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(71) Applicant *(for all designated States except US)*: **CURAGEN CORPORATION** [US/US]; 555 Long Wharf Drive, 11th Floor, New Haven, CT 06511 (US).

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(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"

(57) Abstract: The present invention provides open reading frames encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.

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INTERNATIONAL SEARCH REPORT

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A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/12 C07K14/47 C07K16/18 G01N33/566 C12Q1/68
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According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

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Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
BIOSIS, EMBASE, MEDLINE, CAB Data, PAJ, EPO-Internal, WPI Data, STRAND

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	COLE S.T.: "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence." NATURE, vol. 393, 11 June 1998 (1998-06-11), XP002144873 sequence ---	
A	LAMERDIN J.E.: "Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a serine protease gene cluster." EMEST DATABASE ENTRY, 8 February 1999 (1999-02-08), XP002144874 sequence --- -/--	

[X] Further documents are listed in the continuation of box C.

[ ] Patent family members are listed in annex.

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Date of the actual completion of the international search	Date of mailing of the international search report
21 August 2000	23.11.00

Name and mailing address of the ISA	Authorized officer
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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	M.D. ADAMS ET AL.: "The genome sequence of Drosophila melanogaster." SCIENCE, vol. 287, 24 March 2000 (2000-03-24), pages 2185-2195, XP002144875 the whole document	6

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

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INTERNATIONAL SEARCH REPORT

Inte onal application No.
PCT/US 00/08621

Box I Observations where certain claims were found uns archable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 27 to 32 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

claims 1 to 32 partially

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

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FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claim : 1 to 32 partially

Isolated nucleic acid molecule encoding a polypeptide comprising an amino acid sequence that is at least 85% identical to a polypeptide including an amino acid sequence selected from a group consisting of SEQ ID NO 2n wherein n is 1, oligonucleotides less than 100 nucleotides in length and comprising at least 6 contiguous nucleotides from the above sequence, polypeptides encoded by said nucleotides, antibodies that bind to said polypeptide, pharmaceutical composition comprising said polypeptide and methods of detection, screening, therapeutic uses involving said polypeptide.

2. Claim : .

Inventions 2 to 3161

claims 1 to 32 partially :

Isolated nucleic acid molecule encoding a polypeptide comprising an amino acid sequence that is at least 85% identical to a polypeptide including an amino acid sequence selected from a group consisting of SEQ ID NO 2n wherein n is 2 to 3161, oligonucleotides less than 100 nucleotides in length and comprising at least 6 contiguous nucleotides from the above sequence, polypeptides encoded by said nucleotides, antibodies that bind to said polypeptide, pharmaceutical composition comprising said polypeptide and methods of detection, screening, therapeutic uses involving said polypeptide.

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(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"

(57) Abstract

The present invention provides open reading frames ORFX, encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.

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NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

BACKGROUND OF THE INVENTION

The invention relates generally to nucleic acids and polypeptides encoded thereby, and methods of using these nucleic acids and polypeptides.

SUMMARY OF THE INVENTION

The invention is based in part on the discovery of nucleic acids that include open reading frames encoding novel polypeptides, and on the polypeptides encoded thereby. The nucleic acids and polypeptides are collectively referred to herein as "ORFX".

Accordingly, in one aspect, the invention provides an isolated nucleic acid molecule (SEQ ID NO:2*n*-1, wherein *n* is an integer between 1-3161), that encodes novel polypeptide, or a fragment, homolog, analog or derivative thereof. The nucleic acid can include, *e.g.*, a nucleic acid sequence encoding a polypeptide at least 85% identical to a polypeptide comprising the amino acid sequences of SEQ ID NO:2*n*, wherein *n* is an integer between 1-3161. The nucleic acid can be, *e.g.*, a genomic DNA fragment, or a cDNA molecule.

Also included in the invention is a vector containing one or more of the nucleic acids described herein, and a cell containing the vectors or nucleic acids described herein.

The invention is also directed to host cells transformed with a recombinant expression vector comprising any of the nucleic acid molecules described above.

In another aspect, the invention includes a pharmaceutical composition that includes an ORFX nucleic acid and a pharmaceutically acceptable carrier or diluent.

In a further aspect, the invention includes a substantially purified ORF polypeptide, *e.g.*, any of the ORFX polypeptides encoded by an ORFX nucleic acid, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition that includes a ORFX polypeptide and a pharmaceutically acceptable carrier or diluent.

In a still a further aspect, the invention provides an antibody that binds specifically to an ORFX polypeptide. The antibody can be, *e.g.*, a monoclonal or polyclonal antibody, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition including ORFX antibody and a pharmaceutically acceptable carrier or diluent. The invention is also directed to isolated antibodies that bind to an epitope on a polypeptide encoded by any of the nucleic acid molecules described above.

The invention also includes kits comprising any of the pharmaceutical compositions described above.

The invention further provides a method for producing an ORFX polypeptide by providing a cell containing a ORFX nucleic acid, *e.g.*, a vector that includes a ORFX nucleic acid, and culturing the cell under conditions sufficient to express the ORFX polypeptide encoded by the nucleic acid. The expressed ORFX polypeptide is then recovered from the cell. Preferably, the cell produces little or no endogenous ORFX polypeptide. The cell can be, *e.g.*, a prokaryotic cell or eukaryotic cell.

The invention is also directed to methods of identifying an ORFX polypeptide or nucleic acids in a sample by contacting the sample with a compound that specifically binds to the polypeptide or nucleic acid, and detecting complex formation, if present.

The invention further provides methods of identifying a compound that modulates the activity of a ORFX polypeptide by contacting ORFX polypeptide with a compound and determining whether the ORFX polypeptide activity is modified.

The invention is also directed to compounds that modulate ORFX polypeptide activity identified by contacting a ORFX polypeptide with the compound and determining whether the compound modifies activity of the ORFX polypeptide, binds to the ORFX polypeptide, or binds to a nucleic acid molecule encoding a ORFX polypeptide.

In a another aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a sample from the subject and measuring the amount of ORFX polypeptide in the subject sample.

The amount of ORFX polypeptide in the subject sample is then compared to the amount of ORFX polypeptide in a control sample. An alteration in the amount of ORFX polypeptide in the subject protein sample relative to the amount of ORFX polypeptide in the control protein sample indicates the subject has a tissue proliferation-associated condition. A control sample is preferably taken from a matched individual, *i.e.*, an individual of similar age, sex, or other general condition but who is not suspected of having a tissue proliferation-associated condition. Alternatively, the control sample may be taken from the subject at a time when the subject is not suspected of having a tissue proliferation-associated disorder. In some embodiments, the ORFX is detected using a ORFX antibody.

In a further aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a nucleic acid sample, *e.g.*, RNA or DNA, or both, from the subject and measuring the amount of the ORFX nucleic acid in the subject nucleic acid sample. The amount of ORFX nucleic acid sample in the subject nucleic acid is then compared to the amount of an ORFX nucleic acid in a control sample. An alteration in the amount of ORFX nucleic acid in the sample relative to the amount of ORFX in the control sample indicates the subject has a tissue proliferation-associated disorder.

In a still further aspect, the invention provides method of treating or preventing or delaying a ORFX-associated disorder. The method includes administering to a subject in which such treatment or prevention or delay is desired a ORFX nucleic acid, a ORFX polypeptide, or an ORFX antibody in an amount sufficient to treat, prevent, or delay a tissue proliferation-associated disorder in the subject.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides novel polypeptides and nucleotides encoded thereby. The polynucleotides and their encoded polypeptides can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc.

Included in the invention are 3161 novel nucleic acid sequences and their encoded polypeptides. The sequences are collectively referred to as "ORFX nucleic acids" or ORFX polynucleotides" and the corresponding encoded polypeptide is referred to as a "ORFX polypeptide" or ORFX protein". For example, an ORFX nucleic acid according to the invention is a nucleic acid including an ORF1 nucleic acid, and an ORF polypeptide according to the invention is a polypeptide that includes the amino acid sequence of an ORF1 polypeptide. Unless indicated otherwise, "ORFX" is meant to refer to any of the ORF1-3161 sequences disclosed herein.

Table 1 provides a summary of the ORFX nucleic acids and their encoded polypeptides are summarized in Table 1. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention is provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 1 of Table 1, entitled "ORF #", denotes an ORF number assigned to a nucleic acid containing an open reading frame according to the invention.

Column 2 of Table 1, entitled "Internal Identification number (Nucleic Acid Sequence Identification Number, Polypeptide Sequence Identification Number), provides an internal identification number for the indicated ORF, along with sequence identification numbers (SEQ ID NOs.) corresponding to the indicated ORF. In general, for an ORF*n* according to the invention (wherein *n* is any integer from 1 to 3161), a nucleic acid corresponding to the ORF is SEQ ID NO:2*n*-1, and an amino acid sequence encoded by the ORF is SEQ ID NO:2*n*. For example, a nucleic acid sequence corresponding to an ORF1 nucleic acid is SEQ ID NO:1, and a polypeptide sequence corresponding to an ORF1 polypeptide is SEQ ID NO:2. Similarly, a

nucleic acid sequence corresponding to an ORF4 nucleic acid is SEQ ID NO:7, and a polypeptide sequence corresponding to an ORF4 polypeptide is SEQ ID NO:8; a nucleic acid sequence corresponding to an ORF198 nucleic acid sequence is SEQ ID NO:395, and a polypeptide sequence corresponding to an ORF198 polypeptide is SEQ ID NO:396. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention are provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 2 of Table 1, entitled "Protein Similarity", lists previously described proteins that are related to polypeptides encoded by the ORFs. Genbank identifiers for the previously described proteins are provided. These can be retrieved from http://www.ncbi.nlm.nih.gov/.

To determine similarity to previously described proteins, polypeptides encoded by ORFX DNA sequences were tested using the Framesearch Algorithm against a nonredundant version of the GenPept Database from NCBI/Genbank. DNA sequences that had a score of '90' or above (Framesearch algorithm score, Edelman et. al. GCG Genetics) to a known protein were selected. Open reading frames were extended beyond the region of the protein matched using standard DNA translation and codon tables. Novel proteins that lacked a protein match were translated against the standard genetic codons and proteins with an ORF at least 80 amino acids and containing a Methionine start are included in the Table.

Column 3 of Table 3, entitled "Protein Domains", lists previously described protein domains, designated by pfam entries, that are present in polypeptides encoded by the ORFs, Also included in column 3 are proteins in which these domains are present. The pfam entries can be retrieved from http://pfam.wustl.edu/. DNA sequences were translated in all six frames and tested using the Hmmer Algorithm against the Pfam Database (References to the algorithm and Pfam database can be found at http://pfam.wustl.edu). Translated DNA sequences that matched a protein domain entry in the Pfam database AND had a score of'7.5' were selected.

Column 4 of Table 3, entitled "Protein Classification", lists the type of classification assigned for the protein, based on its homology. Examples of proteins in the classification include the following proteins:

Amylases

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

Amyloid

The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. Amyloid deposition is also associated with type II diabetes mellitus.

Angiopoeitin

Members of the angiopoeitin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

Apoptosis-related proteins

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell

death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of anti-aging drugs.

Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

Colony-stimulating factor-related proteins

Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

Complement-related proteins

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I diabetes mellitus, meningitis neurological disorders such as nemaline myopathy, neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

Cytochrome

The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

Kinesins

Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

Cytokines, Interferon, Interleukin

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

G-protein coupled receptors

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and dwarfism.

Thioesterases

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The key to the molecule type is as follows:

Abbrev:	Title:
amylase	amylase protein
amylaseinhib	amylase inhibitor
amyloid	amyloid protein
apoptosis	apoptosis associated protein
apoptosisinhib	apoptosis inhibitors
apoptosisrecep	apoptosis receptors
ATPase_associated	ATPase associated protein
biotindep	biotin dependent enzyme/protein
cadherin	cadherin protein
calcium_channel	calcium channel protein
carboxylase	carboxylase protein
cathepsin	cathepsin/carboxypeptidases
cathepsininhib	cathepsin/carboxypeptidase inhibitor
chloride_channel	chloride channel protein
collagen	collagen
complement	complement protein
complementrecept	complement receptor protein
complementinhib	complement inhibitor
csf	colony stimulating factor
csfrecept	colony stimulating factor receptor
cyclin	cyclin protein
cyto450	cytochrome p450 protein
cytochrome	cytochrome related protein
deaminase	deaminase
dehydrogenase	dehydrogenase
desaturase	desaturase
dna_rna_bind	DNA/RNA binding protein/factor
dna_rna_inhib	DNA/RNA binding protein/factor inhibitor
dynein	dynein

elastase	elastase
elastaseinhib	elastase inhibitor
eph	EPH family of tyrosine kinases
esterase	esterase
esteraseinhib	esterase inhibitor
fgf	fibroblast growth factor
fgfreceptor	fibroblast growth factor receptor
gaba	GABA receptor
glucoamylase	glucoamylase
glucoronidase	glucoronidase
glycoprotein	glycoprotein
Guanylyl	guanylylate cyclase
helicase	helicase
histone	histone
HOM	homologous
homeobox	homeobox protein
hydrolase	hydrolase
hydroxysteroid	hydroxysteroid associated protein
hypoxanthine	hypoxanthine associated protein
immunoglob	immunoglobulin
immunoglobrecept	immunoglobulin receptor
interferon	interferon
interleukin	interleukin
interleukinrecept	interleukin receptor
isomerase	isomerase
isomeraseinhibitor	isomerase inhibitor
isomerasereceptor	isomerase receptor
kinase	kinase
kinaseinhibitor	kinase inhibitor
kinasereceptor	kinase receptor
kinesin	kinesin
laminin	laminin associated protein
lipase	lipase
metallothionein	metallothionein
MHC	major histocompatability complex
misc_channel	miscellaneous channel
ngf	nerve growth factor
nuci_recpt	nuclear receptor
nuclease	nuclease
oncogene	oncogene associated protein
oxidase	oxidase
oxygenase	oxygenase
peptidase	peptidase
peroxidase	peroxidase
phosphatase	phosphatase
phosphataseinhib	phosphatase inhibitor

phosphorylase	phosphorylase
PIR	PIR DATABASE (release 56, 29-OCT-1998)
polymerase	polymerase
potassium_channel	potassium channel protein
prostaglandin	prostaglandin
protease	protease
proteaseinhib	protease inhibitor
reductase	reductase
ribosomalprot	ribosomal associated protein
RTR	EMBLDATABASE translated entries not to be incorporated into SWISS-PROT (20-JUL-1998)
SIM	similar
SPTR	EMBL DATABASE translated entries to be incorporated into SWISS-PROT (20-JUL-1998)
struct	structural associated protein
sulfotransferase	sulfotransferase
SWP	SWISS-PROT DATABASE (release 18-OCT-1998)
SWPN	SWISS-PROT Update (release 11-NOV-98)
synthase	synthase
tgf	transforming growth factor
tgfreceptor	transforming growth factor receptor
thioesterase	thioesterase
thiolase	thiolase
tm7	seven transmembrane domain G-protein coupled receptor
tnf	necrosis factor receptor
traffic	tumor necrosis factor
tnfreceptor	tumor trafficking associated protein
TRN	EMBL DATABASE translated entries update (20-JUL-1998)
transcriptfactor	transcription factor
transferase	transferase
transport	transport protein
tubulin	tubulin
ubiquitin	ubiquitin
unclassified	Protein not categorized into one of the aforementioned protein families
water channel	water channel protein

Column 5 of Table 1, entitled, "Cells or Tissues in Which Gene is Expressed", denotes tissues, represented by five digit numbers, in which RNA homologous to the ORF nucleic acid sequences is present. Tissues or cells corresponding to the numbers are provided in Table 2.

ORFX nucleic acids, and their encoded polypeptides, according to the invention are useful in a variety of applications and contexts. For example, various ORFX nucleic acids and polypeptides according to the invention are useful, *inter alia*, as novel members of the protein families indicated in Table 1, and/or according to the presence of domains and sequence relatedness to previously described proteins as summarized in Table 1.

ORFX nucleic acids and polypeptides according to the invention can also be used to identify cell types listed in Table 1 for an indicated ORFX according to the invention. Additional utilities for ORFX nucleic acids and polypeptides according to the invention are disclosed herein.

ORFX Nucleic Acids

The novel nucleic acids of the invention include those that encode an ORFX or ORFX-like protein, or biologically active portions thereof. The nucleic acids include nucleic acids encoding polypeptides that include the amino acid sequence of one or more of SEQ ID NO:2*n*, wherein *n* = 1 to 3161. The encoded polypeptides can thus include, *e.g.*, the amino acid sequences of SEQ ID NO: 2, 4, 6, 8, 10, . . ., 6310, 6312, 6314, 6316, 6318, 6320, and/or 6322.

In some embodiments, a nucleic acid encoding a polypeptide having the amino acid sequence of one or more of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) includes the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof. Additionally, the invention includes mutant or variant nucleic acids of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof, any of whose bases may be changed from the disclosed sequence while still encoding a protein that maintains its ORFX -like activities and physiological functions. The invention further includes the complement of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), including fragments, derivatives,

analogs and homolog thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

Also included are nucleic acid fragments sufficient for use as hybridization probes to identify ORFX-encoding nucleic acids (*e.g.*, ORFX mRNA) and fragments for use as polymerase chain reaction (PCR) primers for the amplification or mutation of ORFX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic acid molecules include, but are not limited to, recombinant DNA molecules contained in a vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated ORFX nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement of any of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n*=1 to 3161) as a hybridization probe, ORFX nucleic acid sequences can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, eds., MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ORFX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at lease 6 contiguous nucleotides of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement thereof. Oligonucleotides may be chemically synthesized and may be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion of this nucleotide sequence. A nucleic acid molecule that is complementary to the nucleotide sequence shown in

is one that is sufficiently complementary to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161),, thereby forming a stable duplex.

As used herein, the term "complementary" refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term "binding" means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Von der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), *e.g.*, a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of ORFX. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the

invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, WI) using the default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2: 482-489, which is incorporated herein by reference in its entirety).

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ORFX polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for a ORFX polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ORFX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) as well as a polypeptide having ORFX activity. Biological activities of the ORFX proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ORFX polypeptide.

The nucleotide sequence determined from the cloning of the human ORFX gene allows for the generation of probes and primers designed for use in identifying the cell types disclosed and/or cloning ORFX homologues in other cell types, *e.g.*, from other tissues, as well as ORFX homologues from other mammals. The probe/primer typically comprises a substantially purified

oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 or more consecutive sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or an anti-sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or of a naturally occurring mutant of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

Probes based on the human ORFX nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a ORFX protein, such as by measuring a level of a ORFX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ORFX mRNA levels or determining whether a genomic ORFX gene has been mutated or deleted.

"A polypeptide having a biologically active portion of ORFX" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ORFX" can be prepared by isolating a portion of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), that encodes a polypeptide having a ORFX biological activity (biological activities of the ORFX proteins are summarized in Table 1), expressing the encoded portion of ORFX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ORFX. For example, a nucleic acid fragment encoding a biologically active portion of ORFX can optionally include a domain as shown in Table 1, column 4.

ORFX variants

The invention further encompasses nucleic acid molecules that differ from the disclosed ORFX nucleotide sequences due to degeneracy of the genetic code. These nucleic acids thus encode the same ORFX protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In addition to the human ORFX nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of ORFX may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ORFX gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a ORFX protein, preferably a mammalian ORFX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ORFX gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ORFX that are the result of natural allelic variation and that do not alter the functional activity of ORFX are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ORFX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ORFX cDNAs of the invention can be isolated based on their homology to the human ORFX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein n = 1 to 3161). In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ORFX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at Tm, 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C. This hybridization is followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of any of SEQ ID NO:$2n$-1 (wherein n = 1 to 3161) corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:$2n$-1 (wherein n = 1 to 3161), or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are

hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well known in the art. See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161), or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA 78*: 6789-6792.

Conservative mutations

In addition to naturally-occurring allelic variants of the ORFX sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161), thereby leading to changes in the amino acid sequence of the encoded ORFX protein, without altering the functional ability of the ORFX protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of any of SEQ ID NO:2n-1 (wherein $n = 1$ to 3161). A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ORFX without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ORFX proteins of the present invention, are predicted to be particularly unamenable to alteration.

Amino acid residues that are conserved among members of an ORFX family members are predicted to be less amenable to alteration. For example, an ORFX protein according to the present invention can contain at least one domain (*e.g.*, as shown in Table 1) that is a typically conserved region in an ORFX family member. As such, these conserved domains are not likely to be amenable to mutation. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved among members of the ORFX family) may not be as essential for activity and thus are more likely to be amenable to alteration.

Another aspect of the invention pertains to nucleic acid molecules encoding ORFX proteins that contain changes in amino acid residues that are not essential for activity. Such ORFX proteins differ in amino acid sequence from any of any of SEQ ID NO:2*n* (wherein n = 1 to 3161), yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein n = 1 to 3161). Preferably, the protein encoded by the nucleic acid is at least about 80% homologous to any of SEQ ID NO:2*n* (wherein n = 1 to 3161), more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NO:2.

An isolated nucleic acid molecule encoding a ORFX protein homologous to the protein of any of SEQ ID NO:2*n* (wherein n = 1 to 3161) can be created by introducing one or more nucleotide substitutions, additions or deletions into the corresponding nucleotide sequence, *i.e.* SEQ ID NO:2*n*-1 for the corresponding *n*, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO:2*n*-1 (wherein n = 1 to 3161) by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline,

phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ORFX is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a ORFX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ORFX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ORFX protein can be assayed for (1) the ability to form protein:protein interactions with other ORFX proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ORFX protein and a ORFX receptor; (3) the ability of a mutant ORFX protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.*, avidin proteins); (4) the ability to bind BRA protein; or (5) the ability to specifically bind an anti-ORFX protein antibody.

Antisense

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein n = 1 to 3161), or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ORFX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a ORFX protein of any of SEQ ID NO:2*n* (wherein n = 1 to 3161) or antisense nucleic acids complementary to a ORFX nucleic acid sequence of SEQ ID NO:2n-1 (wherein n = 1 to 3161) are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid

residues (*e.g.*, the protein coding region of a human ORFX that corresponds to any of SEQ ID NO:2*n* (wherein n = 1 to 3161)). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ORFX disclosed herein (*e.g.*, SEQ ID NO:2n-1 (wherein n = 1 to 3161)), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ORFX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ORFX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ORFX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil,

3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a ORFX protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

Ribozymes and PNA m ieties

Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are

carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave ORFX mRNA transcripts to thereby inhibit translation of ORFX mRNA. A ribozyme having specificity for a ORFX-encoding nucleic acid can be designed based upon the nucleotide sequence of a ORFX DNA disclosed herein (*i.e.*, SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161)). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a ORFX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, ORFX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, ORFX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ORFX (*e.g.*, the ORFX promoter and/or enhancers) to form triple helical structures that prevent transcription of the ORFX gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of ORFX can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide

synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ORFX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ORFX can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ORFX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ORFX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, Proc. *Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or

the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

ORFX polypeptides

The novel protein of the invention includes the ORFX-like protein whose sequence is provided in any of SEQ ID NO:2*n* (wherein n = 1 to 3161). The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in FIG. 1 while still encoding a protein that maintains its ORFX-like activities and physiological functions, or a functional fragment thereof. For example, the invention includes the polypeptides encoded by the variant ORFX nucleic acids described above. In the mutant or variant protein, up to 20% or more of the residues may be so changed.

In general, an ORFX -like variant that preserves ORFX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above. Furthermore, without limiting the scope of the invention, positions of any of SEQ ID NO:2*n* (wherein n = 1 to 3161) may be substitute such that a mutant or variant protein may include one or more substitutions

The invention also includes isolated ORFX proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ORFX antibodies. In one embodiment, native ORFX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ORFX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a ORFX

protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ORFX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ORFX protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ORFX protein having less than about 30% (by dry weight) of non-ORFX protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-ORFX protein, still more preferably less than about 10% of non-ORFX protein, and most preferably less than about 5% non-ORFX protein. When the ORFX protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein having less than about 30% (by dry weight) of chemical precursors or non-ORFX chemicals, more preferably less than about 20% chemical precursors or non-ORFX chemicals, still more preferably less than about 10% chemical precursors or non-ORFX chemicals, and most preferably less than about 5% chemical precursors or non-ORFX chemicals.

Biologically active portions of a ORFX protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ORFX protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2 that include fewer amino acids than the full length ORFX proteins, and exhibit at least one activity of a ORFX protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the ORFX protein. A biologically active portion of a ORFX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

A biologically active portion of a ORFX protein of the present invention may contain at least one of the above-identified domains conserved between the FGF family of proteins. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ORFX protein.

In an embodiment, the ORFX protein has an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein n = 1 to 3161). In other embodiments, the ORFX protein is substantially homologous to any of SEQ ID NO:2*n* (wherein n = 1 to 3161) and retains the functional activity of the protein of any of SEQ ID NO:2*n* (wherein n = 1 to 3161), yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below. Accordingly, in another embodiment, the ORFX protein is a protein that comprises an amino acid sequence at least about 45% homologous, and more preferably about 55, 65, 70, 75, 80, 85, 90, 95, 98 or even 99% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein n = 1 to 3161) and retains the functional activity of the ORFX proteins of the corresponding polypeptide having the sequence of SEQ ID NO:2*n* (wherein n = 1 to 3161).

Determining homology between two or more sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, *Needleman and Wunsch* 1970 *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a

degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NO:2*n*-1 (wherein n = 1 to 3161).

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of positive residues.

Chimeric and fusion proteins

The invention also provides ORFX chimeric or fusion proteins. As used herein, a ORFX "chimeric protein" or "fusion protein" includes a ORFX polypeptide operatively linked to a non-ORFX polypeptide. A "ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to ORFX, whereas a "non-ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ORFX protein, *e.g.*, a protein that is different from the ORFX protein and that is derived from the same or a different organism. Within a ORFX fusion protein the ORFX polypeptide can correspond to all or a portion of a ORFX protein. In one embodiment, a ORFX fusion protein comprises at least one biologically active portion of a ORFX protein. In another embodiment, a ORFX fusion protein comprises at least two biologically active portions of a

ORFX protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ORFX polypeptide and the non-ORFX polypeptide are fused in-frame to each other. The non-ORFX polypeptide can be fused to the N-terminus or C-terminus of the ORFX polypeptide.

For example, in one embodiment a ORFX fusion protein comprises a ORFX polypeptide operably linked to the extracellular domain of a second protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate ORFX activity (such assays are described in detail below).

In another embodiment, the fusion protein is a GST-ORFX fusion protein in which the ORFX sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ORFX.

In yet another embodiment, the fusion protein is a ORFX protein containing a heterologous signal sequence at its N-terminus. For example, the native ORFX signal sequence can be removed and replaced with a signal sequence from another protein. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of ORFX can be increased through use of a heterologous signal sequence.

In another embodiment, the fusion protein is a ORFX-immunoglobulin fusion protein in which the ORFX sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The ORFX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ORFX ligand and a ORFX protein on the surface of a cell, to thereby suppress ORFX-mediated signal transduction *in vivo*. In one nonlimiting example, a contemplated ORFX ligand of the invention is an ORFX receptor. The ORFX-immunoglobulin fusion proteins can be used to modulate the bioavailability of a ORFX cognate ligand. Inhibition of the ORFX ligand/ORFX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the ORFX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ORFX antibodies in a subject, to purify ORFX ligands, and in screening assays to identify molecules that inhibit the interaction of ORFX with a ORFX ligand.

A ORFX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A ORFX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ORFX protein.

ORFX agonists and antagonists

The present invention also pertains to variants of the ORFX proteins that function as either ORFX agonists (mimetics) or as ORFX antagonists. Variants of the ORFX protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ORFX protein. An agonist of the ORFX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ORFX protein. An antagonist of the ORFX protein can inhibit one or more of the activities of the naturally occurring form of the ORFX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ORFX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ORFX proteins.

Variants of the ORFX protein that function as either ORFX agonists (mimetics) or as ORFX antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ORFX protein for ORFX protein agonist or antagonist activity. In one

embodiment, a variegated library of ORFX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ORFX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ORFX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of ORFX sequences therein. There are a variety of methods which can be used to produce libraries of potential ORFX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ORFX sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477.

Polypeptide libraries

In addition, libraries of fragments of the ORFX protein coding sequence can be used to generate a variegated population of ORFX fragments for screening and subsequent selection of variants of a ORFX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a ORFX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ORFX protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ORFX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,

transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recrusive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify ORFX variants (Arkin and Yourvan (1992) PNAS 89:7811-7815; Delgrave *et al.* (1993) Protein Engineering 6:327-331).

Anti-ORFX Antibodies

The invention further encompasses antibodies and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any of the proteins of the invention.

An isolated ORFX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind ORFX using standard techniques for polyclonal and monoclonal antibody preparation. Full-length ORFX protein can be used. Alternatively, the invention provides antigenic peptide fragments of ORFX for use as immunogens. The antigenic peptide of ORFX comprises at least 4 amino acid residues of the amino acid sequence shown in any of SEQ ID NO:2*n* (wherein n = 1 to 3161). The antigenic peptide encompasses an epitope of ORFX such that an antibody raised against the peptide forms a specific immune complex with ORFX. The antigenic peptide may comprise at least 6 aa residues, at least 8 aa residues, at least 10 aa residues, at least 15 aa residues, at least 20 aa residues, or at least 30 aa residues. In one embodiment of the invention, the antigenic peptide comprises a polypeptide comprising at least 6 contiguous amino acids of any of SEQ ID NO:2*n* (wherein n = 1 to 3161).

In an embodiment of the invention, epitopes encompassed by the antigenic peptide are regions of ORFX that are located on the surface of the protein, *e.g.*, hydrophilic regions. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each incorporated herein by reference in their entirety.

As disclosed herein, an ORFX protein sequence of any of SEQ ID NO:2*n* (wherein n = 1 to 3161) , or derivatives, fragments, analogs or homologs thereof, may be utilized as immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and

immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as ORFX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human ORFX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to a ORFX protein sequence of any of SEQ ID NO:2*n* (wherein n = 1 to 3161) or derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed ORFX protein or a chemically synthesized ORFX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against ORFX can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of ORFX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular ORFX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular ORFX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND

CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations are incorporated herein by reference in their entirety

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a ORFX protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*, 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a ORFX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Each of the above citations are incorporated herein by reference. Antibody fragments that contain the idiotypes to a ORFX protein may be produced by techniques known in the art including, but not limited to: (*i*) an $F_{(ab')2}$ fragment produced by pepsin digestion of an antibody molecule; (*ii*) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (*iii*) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (*iv*) F_v fragments.

Additionally, recombinant anti-ORFX antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.*(1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988), *J. Natl Cancer Inst* 80:1553-1559); Morrison(1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525;

Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060. Each of the above citations are incorporated herein by reference.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of a ORFX protein is facilitated by generation of hybridomas that bind to the fragment of a ORFX protein possessing such a domain. Antibodies that are specific for one or more domains within a ORFX protein, *e.g.*, the domain spanning the first fifty amino-terminal residues specific to ORFX when compared to FGF-9, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-ORFX antibodies may be used in methods known within the art relating to the localization and/or quantitation of a ORFX protein (*e.g.*, for use in measuring levels of the ORFX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for ORFX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds [hereinafter "Therapeutics"].

An anti-ORFX antibody (*e.g.*, monoclonal antibody) can be used to isolate ORFX by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-ORFX antibody can facilitate the purification of natural ORFX from cells and of recombinantly produced ORFX expressed in host cells. Moreover, an anti-ORFX antibody can be used to detect ORFX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the ORFX protein. Anti-ORFX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or

phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

ORFX Recombinant Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding ORFX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to includes promoters, enhancers and other expression control elements

(*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, ORFX proteins, mutant forms of ORFX, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ORFX in prokaryotic or eukaryotic cells. For example, ORFX can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (1) to increase expression of recombinant protein; (2) to increase the solubility of the recombinant protein; and (3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the ORFX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerivisae* include pYepSec1 (Baldari, *et al.*, (1987) *EMBO J* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (InVitrogen Corp, San Diego, Calif.).

Alternatively, ORFX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, SF9 cells) include the pAc series (Smith *et al.* (1983) *Mol Cell Biol* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J* 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells. See, *e.g.*, Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv Immunol* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α-fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ORFX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, "Antisense RNA as a molecular tool for genetic analysis," Reviews--Trends in Genetics, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant

host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ORFX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ORFX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ORFX protein. Accordingly, the invention further provides methods for producing ORFX protein using the host cells of the invention. In one embodiment,

the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ORFX has been introduced) in a suitable medium such that ORFX protein is produced. In another embodiment, the method further comprises isolating ORFX from the medium or the host cell.

Transgenic animals

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ORFX-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ORFX sequences have been introduced into their genome or homologous recombinant animals in which endogenous ORFX sequences have been altered. Such animals are useful for studying the function and/or activity of ORFX and for identifying and/or evaluating modulators of ORFX activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ORFX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ORFX-encoding nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human ORFX DNA sequence of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human ORFX gene, such as a mouse ORFX gene, can be isolated based on hybridization to the human ORFX cDNA (described further above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of

expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the ORFX transgene to direct expression of ORFX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan 1986, In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ORFX transgene in its genome and/or expression of ORFX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding ORFX can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a ORFX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ORFX gene. The ORFX gene can be a human gene (*e.g.*, SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161)), but more preferably, is a non-human homologue of a human ORFX gene. For example, a mouse homologue of human ORFX gene of SEQ ID NO:2n-1 (wherein $n = 1$ to 3161) can be used to construct a homologous recombination vector suitable for altering an endogenous ORFX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous ORFX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ORFX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous ORFX protein). In the homologous recombination vector, the altered portion of the ORFX gene is flanked at its 5' and 3' ends by additional nucleic acid of the ORFX gene to allow for homologous recombination to occur between the exogenous ORFX gene carried by the vector and an endogenous ORFX gene in an embryonic stem cell. The additional flanking ORFX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See *e.g.*, Thomas *et al.* (1987) *Cell* 51:503 for a description of

homologous recombination vectors. The vector is introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced ORFX gene has homologously recombined with the endogenous ORFX gene are selected (see *e.g.*, Li *et al.* (1992) *Cell* 69:915).

The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras. See *e.g.*, Bradley 1987, In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Curr Opin Biotechnol* 2:823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, see, *e.g.*, Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, *e.g.*, by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813. In brief, a cell, *e.g.*, a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G_0 phase. The quiescent cell can then be fused, *e.g.*, through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of

this female foster animal will be a clone of the animal from which the cell, *e.g.*, the somatic cell, is isolated.

Pharmaceutical Compositions

The ORFX nucleic acid molecules, ORFX proteins, and anti-ORFX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a ORFX protein or anti-ORFX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use

as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by any of a number of routes, *e.g.*, as described in U.S. Patent Nos. 5,703,055. Delivery can thus also include, *e.g.*, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or stereotactic injection (see *e.g.*, Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Additional Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: (a) screening assays; (b) detection assays (*e.g.*, chromosomal mapping, cell and tissue typing, forensic biology), (c) predictive medicine (*e.g.*, diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics); and (d) methods of treatment (*e.g.*, therapeutic and prophylactic).

The isolated nucleic acid molecules of the invention can be used to express ORFX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ORFX mRNA (*e.g.*, in a biological sample) or a genetic lesion in a ORFX gene, and to modulate ORFX activity, as described further below. In addition, the ORFX proteins can be used to screen drugs or compounds that modulate the ORFX activity or expression as well as to treat disorders characterized by insufficient or excessive production of ORFX protein, for

example proliferative or differentiative disorders, or production of ORFX protein forms that have decreased or aberrant activity compared to ORFX wild type protein. In addition, the anti-ORFX antibodies of the invention can be used to detect and isolate ORFX proteins and modulate ORFX activity.

This invention further pertains to novel agents identified by the above described screening assays and uses thereof for treatments as described herein.

Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, small molecules or other drugs) that bind to ORFX proteins or have a stimulatory or inhibitory effect on, for example, ORFX expression or ORFX activity.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a ORFX protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc Natl Acad Sci U.S.A.* 90:6909; Erb *et al.* (1994) *Proc Natl Acad Sci U.S.A.* 91:11422; Zuckermann *et al.* (1994) *J Med Chem* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2059; Carell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2061; and Gallop *et al.* (1994) *J Med Chem* 37:1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), on chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner USP '409), plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and

Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirla *et al.* (1990) *Proc Natl Acad Sci U.S.A.* 87:6378-6382; Felici (1991) *J Mol Biol* 222:301-310; Ladner above.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a ORFX protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ORFX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ORFX protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I, ^{35}S, ^{14}C, or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX or a biologically active portion thereof can be accomplished, for example, by determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule. As used herein, a "target molecule" is a molecule with which a ORFX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a ORFX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule

associated with the internal surface of a cell membrane or a cytoplasmic molecule. A ORFX target molecule can be a non-ORFX molecule or a ORFX protein or polypeptide of the present invention. In one embodiment, a ORFX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.*, a signal generated by binding of a compound to a membrane-bound ORFX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ORFX.

Determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+}, diacylglycerol, IP_3, etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising a ORFX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to bind to the ORFX protein or biologically active portion thereof. Binding of the test compound to the ORFX protein can be determined either directly or indirectly as described above. In one embodiment, the assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or

biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX can be accomplished, for example, by determining the ability of the ORFX protein to bind to a ORFX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ORFX can be accomplished by determining the ability of the ORFX protein further modulate a ORFX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the ORFX protein to preferentially bind to or modulate the activity of a ORFX target molecule.

The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of ORFX. In the case of cell-free assays comprising the membrane-bound form of ORFX, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ORFX is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton® X-100, Triton® X-114, Thesit®, Isotridecypoly(ethylene glycol ether)$_n$, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either ORFX or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to ORFX, or interaction of ORFX with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For

example, GST-ORFX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ORFX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of ORFX binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either ORFX or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ORFX or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ORFX or target molecules, but which do not interfere with binding of the ORFX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ORFX trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ORFX or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ORFX or target molecule.

In another embodiment, modulators of ORFX expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ORFX mRNA or protein in the cell is determined. The level of expression of ORFX mRNA or protein in the presence of the candidate compound is compared to the level of expression of ORFX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ORFX expression based on this comparison. For example, when expression of ORFX mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ORFX mRNA or protein expression. Alternatively, when expression of ORFX mRNA or protein is less (statistically significantly less) in the presence of the candidate

compound than in its absence, the candidate compound is identified as an inhibitor of ORFX mRNA or protein expression. The level of ORFX mRNA or protein expression in the cells can be determined by methods described herein for detecting ORFX mRNA or protein.

In yet another aspect of the invention, the ORFX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.* (1993) Cell 72:223-232; Madura *et al.* (1993) J Biol Chem 268:12046-12054; Bartel *et al.* (1993) Biotechniques 14:920-924; Iwabuchi *et al.* (1993) Oncogene 8:1693-1696; and Brent WO94/10300), to identify other proteins that bind to or interact with ORFX ("ORFX-binding proteins" or "ORFX-bp") and modulate ORFX activity. Such ORFX-binding proteins are also likely to be involved in the propagation of signals by the ORFX proteins as, for example, upstream or downstream elements of the ORFX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ORFX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a ORFX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ORFX.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a

minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample.

The ORFX sequences of the present invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Pat. No. 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the ORFX sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The ORFX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:2n-1 (wherein n = 1 to 3161), as described above, can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

Use of Partial ORFX Sequences in Forensic Biology

DNA-based identification techniques can also be used in forensic biology. Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, *e.g.*, hair or skin, or body fluids, *e.g.*, blood, saliva, or semen

found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents, *e.g.*, PCR primers, targeted to specific loci in the human genome, that can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (*i.e.* another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NOs:__ are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the ORFX sequences or portions thereof, *e.g.*, fragments derived from the noncoding regions of one or more of SEQ ID NO:2*n*-1 (where $n = 1$ to 3161), having a length of at least 20 bases, preferably at least 30 bases.

The ORFX sequences described herein can further be used to provide polynucleotide reagents, *e.g.*, labeled or label-able probes that can be used, for example, in an *in situ* hybridization technique, to identify a specific tissue, *e.g.*, brain tissue, etc. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such ORFX probes can be used to identify tissue by species and/or by organ type.

In a similar fashion, these reagents, *e.g.*, ORFX primers or probes can be used to screen tissue culture for contamination (*i.e.* screen for the presence of a mixture of different types of cells in a culture).

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic

acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

Other conditions in which proliferation of cells plays a role include tumors, restenosis, psoriasis, Dupuytren's contracture, diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.

An ORFX polypeptide may be used to identify an interacting polypeptide a sample or tissue. The method comprises contacting the sample or tissue with ORFX, allowing formation of a complex between the ORFX polypeptide and the interacting polypeptide, and detecting the complex, if present.

The proteins of the invention may be used to stimulate production of antibodies specifically binding the proteins. Such antibodies may be used in immunodiagnostic procedures to detect the occurrence of the protein in a sample. The proteins of the invention may be used to stimulate cell growth and cell proliferation in conditions in which such growth would be favorable. An example would be to counteract toxic side effects of chemotherapeutic agents on, for example, hematopoiesis and platelet formation, linings of the gastrointestinal tract, and hair follicles. They may also be used to stimulate new cell growth in neurological disorders including, for example, Alzheimer's disease. Alternatively, antagonistic treatments may be administered in which an antibody specifically binding the ORFX -like proteins of the invention

would abrogate the specific growth-inducing effects of the proteins. Such antibodies may be useful, for example, in the treatment of proliferative disorders including various tumors and benign hyperplasias.

Polynucleotides or oligonucleotides corresponding to any one portion of the ORFX nucleic acids of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) may be used to detect DNA containing a corresponding ORF gene, or detect the expression of a corresponding ORFX gene, or ORFX-like gene. For example, an ORFX nucleic acid expressed in a particular cell or tissue, as noted in Table 2, can be used to identify the presence of that particular cell type.

An exemplary method for detecting the presence or absence of ORFX in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes ORFX protein such that the presence of ORFX is detected in the biological sample. An agent for detecting ORFX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to ORFX mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length ORFX nucleic acid, such as the nucleic acid of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to ORFX mRNA or genomic DNA, as described above. Other suitable probes for use in the diagnostic assays of the invention are described herein.

An agent for detecting ORFX protein is an antibody capable of binding to ORFX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or $F(ab')_2$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect ORFX mRNA, protein, or genomic DNA in a biological sample *in vitro* as

well as *in vivo*. For example, *in vitro* techniques for detection of ORFX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ORFX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of ORFX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of ORFX protein include introducing into a subject a labeled anti-ORFX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting ORFX protein, mRNA, or genomic DNA, such that the presence of ORFX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ORFX protein, mRNA or genomic DNA in the control sample with the presence of ORFX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ORFX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ORFX protein or mRNA in a biological sample; means for determining the amount of ORFX in the sample; and means for comparing the amount of ORFX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ORFX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity in, *e.g.*, proliferative or differentiative disorders such as hyperplasias, tumors, restenosis, psoriasis, Dupuytren's

contracture, diabetic complications, or rheumatoid arthritis, etc.; and glia-associated disorders such as cerebral lesions, diabetic neuropathies, cerebral edema, senile dementia, Alzheimer's disease, etc. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the present invention provides a method for identifying a disease or disorder associated with aberrant ORFX expression or activity in which a test sample is obtained from a subject and ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant ORFX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder, such as a proliferative disorder, differentiative disorder, glia-associated disorders, etc. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ORFX expression or activity in which a test sample is obtained and ORFX protein or nucleic acid is detected (*e.g.*, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ORFX expression or activity.)

The methods of the invention can also be used to detect genetic lesions in a ORFX gene, thereby determining if a subject with the lesioned gene is at risk for, or suffers from, a proliferative disorder, differentiative disorder, glia-associated disorder, etc. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding a ORFX-protein, or the mis-expression of the ORFX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of (1) a deletion of one or more nucleotides from a ORFX gene; (2) an addition of one or more nucleotides to a ORFX gene; (3) a substitution of one or more nucleotides of a ORFX gene, (4) a chromosomal

rearrangement of a ORFX gene; (5) an alteration in the level of a messenger RNA transcript of a ORFX gene, (6) aberrant modification of a ORFX gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a ORFX gene, (8) a non-wild type level of a ORFX-protein, (9) allelic loss of a ORFX gene, and (10) inappropriate post-translational modification of a ORFX-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in a ORFX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, *e.g.*, U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, *e.g.*, Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the ORFX-gene (see Abravaya *et al.* (1995) *Nucl Acids Res* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to a ORFX gene under conditions such that hybridization and amplification of the ORFX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990, *Proc Natl Acad Sci USA* 87:1874-1878), transcriptional amplification system (Kwoh, *et al.*, 1989, *Proc Natl Acad Sci USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al*, 1988, *BioTechnology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in a ORFX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Pat. No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in ORFX can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7: 244-255; Kozal *et al.* (1996) *Nature Medicine* 2: 753-759). For example, genetic mutations in ORFX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.* above. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ORFX gene and detect mutations by comparing the sequence of the sample ORFX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert (1977) *PNAS* 74:560 or Sanger (1977) *PNAS* 74:5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeve *et al.*, (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, *e.g.*, PCT International Publ. No. WO 94/16101; Cohen *et al.* (1996) *Adv Chromatogr* 36:127-162; and Griffin *et al.* (1993) *Appl Biochem Biotechnol* 38:147-159).

Other methods for detecting mutations in the ORFX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA

heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ORFX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton *et al* (1988) *Proc Natl Acad Sci USA* 85:4397; Saleeba *et al* (1992) *Methods Enzymol* 217:286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ORFX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a ORFX sequence, *e.g.*, a wild-type ORFX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ORFX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl Acad Sci USA*: 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments of sample and control ORFX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting

alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA, rather than DNA, in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, *e.g.*, Keen *et al.* (1991) *Trends Genet* 7:5.

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, *e.g.*, Myers *et al* (1985) *Nature* 313:495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. See, *e.g.*, Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. See, *e.g.*, Saiki *et al.* (1986) *Nature* 324:163); Saiki *et al.* (1989) *Proc Natl Acad. Sci USA* 86:6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs *et al.* (1989) *Nucleic Acids Res* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. See, *e.g.*, Gasparini *et al* (1992) *Mol Cell Probes* 6:1. It is anticipated that in certain embodiments amplification may also be performed using Taq ligase

for amplification. See, *e.g.*, Barany (1991) *Proc Natl Acad Sci USA* 88:189. In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a ORFX gene.

Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ORFX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

Agents, or modulators that have a stimulatory or inhibitory effect on ORFX activity (*e.g.*, ORFX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, neurological, cancer-related or gestational disorders) associated with aberrant ORFX activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996, *Clin Exp Pharmacol Physiol*, 23:983-985 and Linder, 1997, *Clin Chem*, 43:254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic

conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a ORFX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring Clinical Efficacy

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied in basic drug screening and in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase ORFX gene expression, protein levels, or upregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting decreased ORFX gene expression, protein levels, or downregulated ORFX activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease ORFX gene expression, protein levels, or downregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting increased ORFX gene expression, protein levels, or upregulated ORFX activity. In such clinical trials, the expression or activity of ORFX and, preferably, other genes that have been implicated in, for example, a proliferative or neurological disorder, can be used as a "read out" or marker of the responsiveness of a particular cell.

For example, genes, including ORFX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates ORFX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ORFX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ORFX or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, nucleic acid, peptidomimetic, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (*i*) obtaining a pre-administration sample from a subject prior to administration of the agent; (*ii*) detecting the level of expression of a ORFX protein, mRNA, or genomic DNA in the preadministration sample; (*iii*) obtaining one or more

post-administration samples from the subject; (*iv*) detecting the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the post-administration samples; (*v*) comparing the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the pre-administration sample with the ORFX protein, mRNA, or genomic DNA in the post administration sample or samples; and (*vi*) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ORFX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ORFX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ORFX expression or activity.

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, (*i*) a ORFX polypeptide, or analogs, derivatives, fragments or homologs thereof; (*ii*) antibodies to a ORFX peptide; (*iii*) nucleic acids encoding a ORFX peptide; (*iv*) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to a ORFX peptide) that are utilized to "knockout" endogenous function of a ORFX peptide by homologous recombination (see, *e.g.*, Capecchi, 1989, *Science* 244: 1288-1292); or (*v*) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between a ORFX peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized

include, but are not limited to, a ORFX peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of a ORFX peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, etc.).

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ORFX expression or activity, by administering to the subject an agent that modulates ORFX expression or at least one ORFX activity. Subjects at risk for a disease that is caused or contributed to by aberrant ORFX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ORFX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of ORFX aberrancy, for example, a ORFX agonist or ORFX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

Another aspect of the invention pertains to methods of modulating ORFX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ORFX protein activity associated with the cell. An agent that modulates ORFX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a ORFX protein, a peptide, a ORFX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ORFX protein activity. Examples of such stimulatory agents include active ORFX protein and a nucleic acid molecule encoding ORFX that has been introduced into the cell. In another embodiment, the agent inhibits one or more ORFX protein activity. Examples of such inhibitory agents include antisense ORFX nucleic acid molecules and anti-ORFX antibodies. These modulatory methods can be performed *in vitro*

(*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a ORFX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, upregulates or downregulates) ORFX expression or activity. In another embodiment, the method involves administering a ORFX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ORFX expression or activity.

Determination of the Biological Effect of a Therapeutic

In various embodiments of the present invention, suitable *in vitro* or *in vivo* assays are utilized to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Malignancies

Some ORFX polypeptides are expressed in cancerous cells (*see, e.g.*, Tables 1 and 2). Accordingly, the corresponding ORF protein is involved in the regulation of cell proliferation. Accordingly, Therapeutics of the present invention may be useful in the therapeutic or prophylactic treatment of diseases or disorders that are associated with cell hyperproliferation and/or loss of control of cell proliferation (*e.g.*, cancers, malignancies and tumors). For a review of such hyperproliferation disorders, see *e.g.*, Fishman, *et al.*, 1985. MEDICINE, 2nd ed., J.B. Lippincott Co., Philadelphia, PA.

Therapeutics of the present invention may be assayed by any method known within the art for efficacy in treating or preventing malignancies and related disorders. Such assays include,

but are not limited to, *in vitro* assays utilizing transformed cells or cells derived from the patient's tumor, as well as *in vivo* assays using animal models of cancer or malignancies. Potentially effective Therapeutics are those that, for example, inhibit the proliferation of tumor-derived or transformed cells in culture or cause a regression of tumors in animal models, in comparison to the controls.

In the practice of the present invention, once a malignancy or cancer has been shown to be amenable to treatment by modulating (*i.e.*, inhibiting, antagonizing or agonizing) activity, that cancer or malignancy may subsequently be treated or prevented by the administration of a Therapeutic that serves to modulate protein function.

Premalignant conditions

The Therapeutics of the present invention that are effective in the therapeutic or prophylactic treatment of cancer or malignancies may also be administered for the treatment of pre-malignant conditions and/or to prevent the progression of a pre-malignancy to a neoplastic or malignant state. Such prophylactic or therapeutic use is indicated in conditions known or suspected of preceding progression to neoplasia or cancer, in particular, where non-neoplastic cell growth consisting of hyperplasia, metaplasia or, most particularly, dysplasia has occurred. For a review of such abnormal cell growth see *e.g.*, Robbins & Angell, 1976. BASIC PATHOLOGY, 2nd ed., W.B. Saunders Co., Philadelphia, PA.

Hyperplasia is a form of controlled cell proliferation involving an increase in cell number in a tissue or organ, without significant alteration in its structure or function. For example, it has been demonstrated that endometrial hyperplasia often precedes endometrial cancer. Metaplasia is a form of controlled cell growth in which one type of mature or fully differentiated cell substitutes for another type of mature cell. Metaplasia may occur in epithelial or connective tissue cells. Dysplasia is generally considered a precursor of cancer, and is found mainly in the epithelia. Dysplasia is the most disorderly form of non-neoplastic cell growth, and involves a loss in individual cell uniformity and in the architectural orientation of cells. Dysplasia characteristically occurs where there exists chronic irritation or inflammation, and is often found in the cervix, respiratory passages, oral cavity, and gall bladder.

Alternatively, or in addition to the presence of abnormal cell growth characterized as hyperplasia, metaplasia, or dysplasia, the presence of one or more characteristics of a transformed or malignant phenotype displayed either *in vivo* or *in vitro* within a cell sample derived from a patient, is indicative of the desirability of prophylactic/therapeutic administration of a Therapeutic that possesses the ability to modulate activity of An aforementioned protein. Characteristics of a transformed phenotype include, but are not limited to: (*i*) morphological changes; (*ii*) looser substratum attachment; (*iii*) loss of cell-to-cell contact inhibition; (*iv*) loss of anchorage dependence; (*v*) protease release; (*vi*) increased sugar transport; (*vii*) decreased serum requirement; (*viii*) expression of fetal antigens, (*ix*) disappearance of the 250 kDal cell-surface protein, and the like. See *e.g.*, Richards, *et al.*, 1986. MOLECULAR PATHOLOGY, W.B. Saunders Co., Philadelphia, PA.

In a specific embodiment of the present invention, a patient that exhibits one or more of the following predisposing factors for malignancy is treated by administration of an effective amount of a Therapeutic: (*i*) a chromosomal translocation associated with a malignancy (*e.g.*, the Philadelphia chromosome (*bcr/abl*) for chronic myelogenous leukemia and t(14;18) for follicular lymphoma, etc.); (*ii*) familial polyposis or Gardner's syndrome (possible forerunners of colon cancer); (*iii*) monoclonal gammopathy of undetermined significance (a possible precursor of multiple myeloma) and (*iv*) a first degree kinship with persons having a cancer or pre-cancerous disease showing a Mendelian (genetic) inheritance pattern (*e.g.*, familial polyposis of the colon, Gardner's syndrome, hereditary exostosis, polyendocrine adenomatosis, Peutz-Jeghers syndrome, neurofibromatosis of Von Recklinghausen, medullary thyroid carcinoma with amyloid production and pheochromocytoma, retinoblastoma, carotid body tumor, cutaneous melanocarcinoma, intraocular melanocarcinoma, xeroderma pigmentosum, ataxia telangiectasia, Chediak-Higashi syndrome, albinism, Fanconi's aplastic anemia and Bloom's syndrome).

In another embodiment, a Therapeutic of the present invention is administered to a human patient to prevent the progression to breast, colon, lung, pancreatic, or uterine cancer, or melanoma or sarcoma.

Hyperproliferative and dysproliferative disorders

In one embodiment of the present invention, a Therapeutic is administered in the therapeutic or prophylactic treatment of hyperproliferative or benign dysproliferative disorders. The efficacy in treating or preventing hyperproliferative diseases or disorders of a Therapeutic of the present invention may be assayed by any method known within the art. Such assays include *in vitro* cell proliferation assays, *in vitro* or *in vivo* assays using animal models of hyperproliferative diseases or disorders, or the like. Potentially effective Therapeutics may, for example, promote cell proliferation in culture or cause growth or cell proliferation in animal models in comparison to controls.

Specific embodiments of the present invention are directed to the treatment or prevention of cirrhosis of the liver (a condition in which scarring has overtaken normal liver regeneration processes); treatment of keloid (hypertrophic scar) formation causing disfiguring of the skin in which the scarring process interferes with normal renewal; psoriasis (a common skin condition characterized by excessive proliferation of the skin and delay in proper cell fate determination); benign tumors; fibrocystic conditions and tissue hypertrophy (*e.g.*, benign prostatic hypertrophy).

Neurodegenerative disorders

Some ORFX proteins are found in cell types have been implicated in the deregulation of cellular maturation and apoptosis, which are both characteristic of neurodegenerative disease. Accordingly, Therapeutics of the invention, particularly but not limited to those that modulate (or supply) activity of an aforementioned protein, may be effective in treating or preventing neurodegenerative disease. Therapeutics of the present invention that modulate the activity of an aforementioned protein involved in neurodegenerative disorders can be assayed by any method known in the art for efficacy in treating or preventing such neurodegenerative diseases and disorders. Such assays include *in vitro* assays for regulated cell maturation or inhibition of apoptosis or *in vivo* assays using animal models of neurodegenerative diseases or disorders, or any of the assays described below. Potentially effective Therapeutics, for example but not by way of limitation, promote regulated cell maturation and prevent cell apoptosis in culture, or reduce neurodegeneration in animal models in comparison to controls.

Once a neurodegenerative disease or disorder has been shown to be amenable to treatment by modulation activity, that neurodegenerative disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity. Such diseases include all degenerative disorders involved with aging, especially osteoarthritis and neurodegenerative disorders.

Disorders related to organ transplantation

Some ORFX can be associated with disorders related to organ transplantation, in particular but not limited to organ rejection. Therapeutics of the invention, particularly those that modulate (or supply) activity, may be effective in treating or preventing diseases or disorders related to organ transplantation. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity of an aforementioned protein) can be assayed by any method known in the art for efficacy in treating or preventing such diseases and disorders related to organ transplantation. Such assays include *in vitro* assays for using cell culture models as described below, or *in vivo* assays using animal models of diseases and disorders related to organ transplantation, see *e.g.*, below. Potentially effective Therapeutics, for example but not by way of limitation, reduce immune rejection responses in animal models in comparison to controls.

Accordingly, once diseases and disorders related to organ transplantation are shown to be amenable to treatment by modulation of activity, such diseases or disorders can be treated or prevented by administration of a Therapeutic that modulates activity.

Cardiovascular Disease

GENX has been implicated in cardiovascular disorders, including in atherosclerotic plaque formation. Diseases such as cardiovascular disease, including cerebral thrombosis or hemorrhage, ischemic heart or renal disease, peripheral vascular disease, or thrombosis of other major vessel, and other diseases, including diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage disease, systemic lupus erythematosus, homocysteinemia, and familial protein or lipid processing diseases, and the like, are either directly or indirectly associated with atherosclerosis. Accordingly, Therapeutics of the invention, particularly those that modulate (or supply) activity or formation may be effective in treating or preventing

atherosclerosis-associated diseases or disorders. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity) can be assayed by any method known in the art, including those described below, for efficacy in treating or preventing such diseases and disorders.

A vast array of animal and cell culture models exist for processes involved in atherosclerosis. A limited and non-exclusive list of animal models includes knockout mice for premature atherosclerosis (Kurabayashi and Yazaki, 1996, Int. Angiol. 15: 187-194), transgenic mouse models of atherosclerosis (Kappel *et al.*, 1994, FASEB J. 8: 583-592), antisense oligonucleotide treatment of animal models (Callow, 1995, Curr. Opin. Cardiol. 10: 569-576), transgenic rabbit models for atherosclerosis (Taylor, 1997, Ann. N.Y. Acad. Sci 811: 146-152), hypercholesterolemic animal models (Rosenfeld, 1996, Diabetes Res. Clin. Pract. 30 Suppl.: 1-11), hyperlipidemic mice (Paigen *et al.*, 1994, Curr. Opin. Lipidol. 5: 258-264), and inhibition of lipoxygenase in animals (Sigal *et al.*, 1994, Ann. N.Y. Acad. Sci. 714: 211-224). In addition, *in vitro* cell models include but are not limited to monocytes exposed to low density lipoprotein (Frostegard *et al.*, 1996, Atherosclerosis 121: 93-103), cloned vascular smooth muscle cells (Suttles *et al.*, 1995, Exp. Cell Res. 218: 331-338), endothelial cell-derived chemoattractant exposed T cells (Katz *et al.*, 1994, J. Leukoc. Biol. 55: 567-573), cultured human aortic endothelial cells (Farber *et al.*, 1992, Am. J. Physiol. 262: H1088-1085), and foam cell cultures (Libby *et al.*, 1996, Curr Opin Lipidol 7: 330-335). Potentially effective Therapeutics, for example but not by way of limitation, reduce foam cell formation in cell culture models, or reduce atherosclerotic plaque formation in hypercholesterolemic mouse models of atherosclerosis in comparison to controls.

Accordingly, once an atherosclerosis-associated disease or disorder has been shown to be amenable to treatment by modulation of activity or formation, that disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity.

Cytokine and Cell Proliferation/Differentiation Activity

A GENX protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered

to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan *et al.*, Greene Publishing Associates and Wiley-Interscience (Chapter 3 and Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bertagnoili *et al.*, *J Immunol* 145:1706-1712, 1990; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Bertagnolli, *et al.*, *J Immunol* 149:3778-3783, 1992; Bowman *et al.*, *J Immunol* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described by Kruisbeek and Shevach, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1, pp. 3.12.1-14, John Wiley and Sons, Toronto 1994; and by Schreiber, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan eds. Vol 1 pp. 6.8.1-8, John Wiley and Sons, Toronto 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described by Bottomly *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto 1991; deVries *et al.*, *J Exp Med* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 336:690-692, 1988; Greenberger *et al.*, *Proc Natl Acad Sci U.S.A.* 80:2931-2938, 1983; Nordan, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.6.1-5, John Wiley and Sons, Toronto 1991; Smith *et al.*, *Proc Natl Acad Sci U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, *et* al. In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto 1991; Ciarletta, *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and

cytokine production) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds., Greene Publishing Associates and Wiley-Interscience (Chapter 3Chapter 6, Chapter 7); Weinberger *et al.*, *Proc Natl Acad Sci USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur J Immun* 11:405-411, 1981; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A GENX protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by vital (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by vital, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania species., malaria species. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response.

The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or energy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon re-exposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to energize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the

immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc Natl Acad Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and auto-antibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of auto-antibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic vital diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the

patient. Another method of enhancing anti-vital immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II a chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor

specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bowman *et al.*, *J Virology* 61:1992-1998; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Brown *et al.*, *J Immunol* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J Immunol* 144:3028-3033, 1990; and Mond and Brunswick In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, (eds.) Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *J Immunol* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery *et al.*, *J Immunol* 134:536-544, 1995; Inaba *et al.*, *J Exp Med* 173:549-559, 1991; Macatonia *et al.*, *J Immunol* 154:5071-5079, 1995; Porgador *et al.*, *J Exp Med* 182:255-260, 1995; Nair *et al.*, *J Virol* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J Exp Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *J Clin Investig* 94:797-807, 1994; and Inaba *et al.*, *J Exp Med* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J Immunol* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Internat J Oncol* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell Immunol* 155: 111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc Nat Acad Sci USA* 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A GENX protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson *et al. Cellular Biology* 15:141-151, 1995; Keller *et al.*, *Mol. Cell. Biol.* 13:473-486, 1993; McClanahan *et al.*, *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y 1994; Hirayama *et al.*, *Proc Natl Acad Sci USA* 89:5907-5911, 1992; McNiece and Briddeli, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben *et al.*, *Exp Hematol* 22:353-359, 1994; Ploemacher, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Spooncerat *al.*, In: CULTURE OF HEMATOPOIETIC CELLS. Freshhey, *et al.*, (eds.) Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Sutherland, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

Tissue Growth Activity

A GENX protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation

induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a career as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein

may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, EPIDERMAL WOUND HEALING, pp. 71-112 (Maibach and Rovee, eds.), Year Book Medical

Publishers, Inc., Chicago, as modified by Eaglstein and Menz, *J. Invest. Dermatol* 71:382-84 (1978).

Activin/Inhibin Activity

A GENX protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin a family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-b group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale *et al.*, *Endocrinology* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*, *Proc Natl Acad Sci USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (*e.g.*, act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example,

attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Coligan *et al.*, eds. (Chapter 6.12, MEASUREMENT OF ALPHA AND BETA CHEMOKINES 6.12.1-6.12.28); Taub *et al. J Clin Invest* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al., Eur J Immunol* 25: 1744-1748; Gruber*et al. J Immunol* 152:5860-5867, 1994; Johnston *et al., J Immunol* 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.*

45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell—cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan, *et al.*, Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai *et al.*, *Proc Natl Acad Sci USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp. Med.* 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160 1989; Stoltenborg *et al.*, *J Immunol Methods* 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell—cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute

conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting

deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Neural disorders in general include Parkinson's disease, Alzheimer's disease, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral neuropathy, tumors of the nervous system, exposure to neurotoxins, acute brain injury, peripheral nerve trauma or injury, and other neuropathies, epilepsy, and/or tremors.

EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that particular novel compositions and methods involving nucleic acids, polypeptides, antibodies, detection and treatment have been described. Although these particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made as a matter of routine for a person of ordinary skill in the art to the invention without departing from the spirit and scope of the invention as defined by the claims. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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Table 1

ORF#	Internal Identification Number	Protein similarity	Protein domain	Protein Classification	Cells or Tissues in which Gene is Expressed
1	13076366 (1, 2)	Novel Protein sim. GBank gi|4691395|emb|CAB41562.1| - (AL049727) putative large secreted protein [Streptomyces coelicolor]		UNCLASSIFIED	264636
2	80248091 (3, 4)	Novel Protein sim. GBank gi|2829506|sp|P71559|SUCC_MYCTU - SUCCINYL-COA SYNTHETASE BETA CHAIN (SCS-BETA)	Contains protein domain (PF00549) - CoA-ligases	UNCLASSIFIED	264907, 264600, 264602, 264762, 264769, 264689, 264638, 264567
3	80415924 (5, 6)			UNCLASSIFIED	264910, 264604, 264634, 264905, 264636, 264691, 264907, 264692, 264629
4	82018837 (7, 8)			UNCLASSIFIED	264908, 264909, 264760, 264628, 264635
5	79970035 (9, 10)			UNCLASSIFIED	22279002, 264563
6	79842462 (11, 12)		Contains protein domain (PF00127) - Copper binding proteins, plastocyanin/azurin family	UNCLASSIFIED	264908
7	85515576 (13, 14)	Novel Protein sim. GBank gi|4415926|gb|AAD20157| - (AC006282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	20281099, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 265009, 264910, 264595, 264596, 264758, 264603, 264604, 264760, 264762, 264683, 264766, 264767, 264689, 35695917, 264690, 264692, 264693, 33657109, 264628, 264629, 35696423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566, 264486
8	56924278 (15, 16)	Novel Protein sim. GBank gi|585562|sp|Q06458|NIRB_KLEPN - NITRITE REDUCTASE (NAD(P)H) LARGE SUBUNIT		reductase	264907
9	79394457 (17, 18)			UNCLASSIFIED	265007, 265019, 263972
10	79556459 (19, 20)			UNCLASSIFIED	264906
11	20414027 (21, 22)				264605
12	94141210 (23, 24)	Novel Protein sim. GBank gi|3878145|emb|CAA99871| - (Z75543) similar to potassium channel protein [Caenorhabditis elegans]		misc_channel	264259, 265007, 83373044
13	20750551 (25, 26)			UNCLASSIFIED	264556, 264557, 264564
14	95105114 (27, 28)	Novel Protein sim. GBank gi|2832781|emb|CAA12645| - (AJ225805) inward potassium channel alpha subunit [Egeria densa]	Contains protein domain (PF00023) - Ank repeat	potassium_channel	35696286, 35696052, 264510, 35695917, 264691, 264628, 35696423, 264555, 264558, 264559, 83373044
15	20458307 (29, 30)	Novel Protein sim. GBank gi|1710791|sp|Q10234|RT05_SCHPO - PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S5	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	264604
16	20760356 (31, 32)				264555

17	20292744 (33, 34)	Novel Protein sim. GBank gi|1174884|sp|P44391|URE1_HAEIN - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease		264600
18	80246804 (35, 36)	Novel Protein sim. GBank gi|2281102 (AC002333) - SF16 isolog [Arabidopsis thaliana]			29331827, 264555, 264557, 264638, 264558
19	80076624 (37, 38)			UNCLASSIFIED	22278996, 264907, 264910, 264600, 264693
20	20724558 (39, 40)	Novel Protein sim. GBank gi|2506112|sp|P43672|UUP_ECOLI - ABC TRANSPORTER ATP-BINDING PROTEIN UUP		transport	264602
21	80417554 (41, 42)	Novel Protein sim. GBank gi|1730203|sp|P50442|GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L-ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)		UNCLASSIFIED	22278995, 264906, 265008, 265010, 265011, 264602, 264605, 264766, 264688, 21906764, 264691, 18108376, 264636, 18108387, 264486
22	11705858 (43, 44)				264685
23	80419176 (45, 46)	Novel Protein sim. GBank gi|1877329|emb|CAB07077| - (Z92771) fadE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	264488, 264907, 264909, 264600, 264602, 264603, 264605, 264682, 264766, 32833986, 264636, 264486
24	20291697 (47, 48)				264600
25	80253774 (49, 50)				264593
26	80255394 (51, 52)			UNCLASSIFIED	22278996, 56182435, 265018, 264566
27	80235795 (53, 54)	Novel Protein sim. GBank gi|4808369|emb|CAB42783.1| - (AL049841) putative 30S ribosomal protein S14 [Streptomyces coelicolor]	Contains protein domain (PF00253) - Ribosomal protein S14p/S29e	ribosomalprot	18108370, 35696423, 264635, 264555
28	79483561 (55, 56)			UNCLASSIFIED	264638
29	82448765 (57, 58)	Novel Protein sim. GBank gi|3122290|sp|O08333|K6PF_STRCO - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)	Contains protein domain (PF00365) - Phosphofructokinase	kinase	264601, 264782, 264766, 264769, 264636
30	79199333 (59, 60)			UNCLASSIFIED	264908, 265019, 264687, 21906764, 21906766
31	19848158 (61, 62)			UNCLASSIFIED	264534
32	82449495 (63, 64)	Novel Protein sim. GBank gi|3560504 (AF027770) - unknown [Mycobacterium smegmatis]		UNCLASSIFIED	264905, 264605, 264762, 264766, 264687, 264689
33	79582628 (65, 66)	Novel Protein sim. GBank gi|2129003|pir||G64507 - hypothetical protein MJ1665 - Methanococcus jannaschii		UNCLASSIFIED	264687
34	87467657 (67, 68)			UNCLASSIFIED	60432289, 264600, 264602, 264760, 18108357, 264769, 265020, 264691
35	95005170 (69, 70)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264600, 264687, 264558, 264639
36	19642042 (71, 72)	Novel Protein sim. GBank gi|3287739|sp|P73538|BIOB_SYNY3 - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)		synthase	264566
37	20369215 (73, 74)	Novel Protein sim. GBank gi|2313134|gb|AAD07126.1| - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26695]		dehydrogenase	264603

38	20466334 (75, 76)	Novel Protein sim. GBank gi|3805970|emb|CAA06231| - (AJ004933) periplasmic nitrate reductase, large subunit [Rhodopseudomonas sp.]		reductase	264605
39	94300715 (77, 78)	Novel Protein sim. GBank gi|1929449 (L63543) - endodermin [Xenopus laevis]	Contains protein domain (PF00207) - Alpha-2-macroglobulin family	complement	264905, 264906, 264907, 66712502, 264908, 264909, 264511, 265009, 264910, 55812038, 264758, 265011, 264762, 264682, 264763, 264764, 264766, 265022, 264693, 264628, 264631, 264634, 264635, 264555, 264638, 18108381, 264558, 18108385, 264482
40	20635625 (79, 80)			UNCLASSIFIED	264592
41	80023287 (81, 82)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]			264591, 35695917
42	20724566 (83, 84)			UNCLASSIFIED	264602
43	20467069 (85, 86)	Novel Protein sim. GBank gi|3820584 (AF086791) - carbamoylphosphate synthetase large subunit [Zymomonas mobilis]		synthase	264605
44	13085297 (87, 88)	Novel Protein sim. GBank gi|2494764|sp|Q50729|GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)	Contains protein domain (PF00958) - GMP synthase C terminal domain	synthase	264769, 264636
45	39384711 (89, 90)	Novel Protein sim. GBank gi|1881738 (U89688) - myosin-I binding protein Acan125 [Acanthamoeba castellanii]		UNCLASSIFIED	264769, 264510, 264508
46	95003398 (91, 92)			ngf	264566
47	11698624 (93, 94)			UNCLASSIFIED	264689
48	79407218 (95, 96)				18108385, 264635, 264828
49	21659844 (97, 98)			UNCLASSIFIED	264603
50	80503996 (99, 100)				264508, 264603, 264769, 264689, 264636, 264558, 264486
51	80255569 (101, 102)	Novel Protein sim. GBank gi|3411177 (AF076240) - MocC [Rhizobium leguminosarum bv. viciae]		UNCLASSIFIED	264593, 18108387
52	79208528 (103, 104)	Novel Protein sim. GBank gi|3914992|sp|Q26264|SM41_HEMPU - 41 KD SPICULE MATRIX PROTEIN PRECURSOR (HSM41) (HPSMC)		struct	264634
53	36996970 (105, 106)	Novel Protein sim. GBank gi|3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]		UNCLASSIFIED	264762
54	79570897 (107, 108)			UNCLASSIFIED	264630, 264909, 264766
55	80202703 (109, 110)	Novel Protein sim. GBank gi|1633572 (U52064) - Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]			29331824, 264102, 265018, 18108376
56	8758408 (111, 112)	Novel Protein sim. GBank gi|4321580|gb|AAD15785| - (AF050114) alginate lyase [Pseudomonas sp. W7]			264604
57	11223386 (113, 114)		Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264557

58	91227508 (115, 116)	Novel Protein sim. GBank gi|5616074|gb|AAD45616.1|AF06194 - (AF061943) protate-derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	56182575, 264259, 60432049, 35696052, 66712502, 264909, 265008, 265010, 265011, 264681, 29148784, 35695917, 60170615, 264691, 264692, 264693, 18108374, 35696423, 56182323, 60432113
59	80077371 (117, 118)	Novel Protein sim. GBank gi|1172920|sp|P45830|RFE_MYCLE - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE	Contains protein domain (PF00953) - Glycosyl transferase	transferase	264600, 264689, 264638
60	12958341 (119, 120)				264689
61	80426806 (121, 122)	Novel Protein sim. GBank gi|1710216 (U79260) - unknown [Homo sapiens]		glycoprotein	264766
62	13504966 (123, 124)				264630
63	16474553 (125, 126)			UNCLASSIFIED	265019
64	20724576 (127, 128)	Novel Protein sim. GBank gi|420945|pir||A47041 - transposase homolog (insertion element ISAE1) - Alcaligenes eutrophus		UNCLASSIFIED	264602
65	79326308 (129, 130)	Novel Protein sim. GBank gi|3122312|sp|O06134|KPYK_MYCTU - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	kinase	264563
66	46854384 (131, 132)	Novel Protein sim. GBank gi|3928723|emb|CAA22219| - (AL034355) putative ABC transporter [Streptomyces coelicolor]		transport	22278996, 264558
67	78952543 (133, 134)	Novel Protein sim. GBank gi|231985|sp|P30234|DHA_MYCTU - ALANINE DEHYDROGENASE (40 KD ANTIGEN)		dehydrogenase	265021
68	79817382 (135, 136)				264909
69	79841764 (137, 138)			UNCLASSIFIED	264908
70	79871329 (139, 140)				264906, 264908
71	65897456 (141, 142)			UNCLASSIFIED	264602, 265021
72	87734977 (143, 144)	Novel Protein sim. GBank gi|4415926|gb|AAD20157| - (AC006282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264511, 265008, 264910, 264758, 87168474, 264682, 264768, 264686, 264689, 35695917, 265021, 60170615, 264691, 33657023, 264692, 264693, 264629, 264631, 264639, 22279000
73	80025241 (145, 146)			UNCLASSIFIED	60424179, 264508, 264908, 265007, 264603, 264687, 264689, 264692, 18108387
74	20377410 (147, 148)			UNCLASSIFIED	264605
75	11819032 (149, 150)	Novel Protein sim. GBank gi|2853098|emb|CAA16914| - (AL021767) vacuolar protein sorting [Schizosaccharomyces pombe]		UNCLASSIFIED	264689
76	95105303 (151, 152)	Novel Protein sim. GBank gi|4468811|emb|CAB38212| - (AL035601) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	83373044, 264906, 264557
77	10144718 (153, 154)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264563
78	6758258 (155, 156)			UNCLASSIFIED	264604

79	94140190 (157, 158)	Novel Protein sim. GBank gi|5689453|dbj|BAA83010.1| - (AB028981) KIAA1058 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain		35696286, 22278998, 29331822, 29331824, 29331825, 29331827, 264905, 264906, 264907, 66712502, 264908, 264909, 265008, 265009, 264910, 60170831, 55812038, 33109954, 265017, 265018, 264288, 264768, 56181562, 21906765, 21906769, 29148784, 265020, 264690, 264691, 264692, 264693, 60431528, 35696423, 264631, 264632, 264634, 264636, 264639, 83373044, 264564, 264566, 264567
80	82314840 (159, 160)			UNCLASSIFIED	264769, 264601, 265006, 264910, 264604, 264605, 264634, 264635, 264905, 264762, 264637, 264592, 264628, 264907, 264691, 264908, 264567, 264909, 264766
81	20467247 (161, 162)	Novel Protein sim. GBank gi|1723442|sp|Q10258|YD2A_SCHPO - HYPOTHETICAL 69.0 KD PROTEIN C56F8.10 IN CHROMOSOME I		reductase	264605
82	16331388 (163, 164)	Novel Protein sim. GBank gi|2895866 (AF045770) - methylmalonate semi-aldehyde dehydrogenase [Oryza sativa]		dehydrogenase	264567
83	94741180 (165, 166)	Novel Protein sim. GBank gi|3402673 (AC004697) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264508, 264509, 264905, 264908, 264909, 264511, 264591, 264593, 264594, 264595, 264596, 264758, 264603, 264760, 264681, 18108351, 264762, 264682, 264764, 264684, 264766, 264686, 264632, 264637, 264557, 264638, 264639, 18108385, 264566
84	80355375 (167, 168)	Novel Protein sim. GBank gi|1173364|sp|P45380|SAT1_RAT - SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE TRANSPORTER) (SULFATE/CARBONATE ANTIPORTER)		transport	264508, 264906, 264907, 264908, 264909, 264910, 264760, 264763, 264764, 264766, 264768, 264769, 35695855, 264636, 264637
85	80499600 (169, 170)	Novel Protein sim. GBank gi|2120998|pir||S70682 - glycosyltransferase homolog - Bordetella pertussis		transferase	264605, 264762, 264687, 264769, 18108374, 264636, 264486
86	39559043 (171, 172)	Novel Protein sim. GBank gi|3256023|emb|CAA17228.1| - (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]			264910
87	13856808 (173, 174)			UNCLASSIFIED	264093

88	95344718 (175, 176)	Novel Protein sim. GBank gi|559703|dbj|BAA07552| - (D38549) ha1025 is new [Homo sapiens]			52644507, 52646365, 18108398, 65274572, 56182575, 56994075, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 264094, 264095, 264259, 29331822, 29331824, 56182181, 66714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 264105, 264508, 264905, 264906, 264907, 264908, 29331830, 66712502, 52644045, 56182435, 265007, 265009, 264910, 60170831, 264592, 60431735, 60433356, 33657402, 264757, 60433438, 55812038, 264758, 21906754, 52646317, 33109954, 52644296, 87168474, 265011, 87168559, 264601, 265017, 265018, 264604, 265019, 264448, 264369, 264288, 264766, 52644229, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 60170615, 52644150, 33657023, 65274620, 33657109, 27486261, 27486264, 33657349, 35695763, 264628, 263972, 18108374, 55810764, 35696423, 55811576, 65274791, 35695855, 60431850, 264636, 52644332, 56182323, 60170394, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22279000, 22279002, 264482, 264564, 264486
89	80077389 (177, 178)	Novel Protein sim. GBank gi|1710383|sp|P46352|RIPX_BACSU - PROBABLE INTEGRASE/RECOMBINASE RIPX			264600
90	82115999 (179, 180)			UNCLASSIFIED	264760
91	78906950 (181, 182)	Novel Protein sim. GBank gi|2499891|sp|P76403|YEGQ_ECOLI - PUTATIVE PROTEASE IN BAER-OGRK INTERGENIC REGION		protease	265006
92	79554871 (183, 184)	Novel Protein sim. GBank gi|3367754|emb|CAA20079| - (AL031155) hypothetical protein SC3A7.16c [Streptomyces coelicolor]		UNCLASSIFIED	264691
93	80496778 (185, 186)	Novel Protein sim. GBank gi|2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]		ATPase_associated	264907, 264908, 264910, 265009, 264605, 264769
94	79646649 (187, 188)	Novel Protein sim. GBank gi|1171919|sp|P46920|OPUA_BACSU - GLYCINE BETAINE TRANSPORT ATP-BINDING PROTEIN OPUAA	Contains protein domain (PF00571) - CBS domain	transport	264906
95	11090238 (189, 190)				264594

96	94322125 (191, 192)	Novel Protein sim. GBank gi|4589560|db||BAA76802.1| - (AB023175) KIAA0958 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 264259, 29331822, 29331826, 35696052, 29146499, 264509, 264906, 264907, 264908, 264909, 265007, 265008, 264910, 265009, 264593, 265010, 265017, 264604, 265019, 18108351, 264288, 264766, 264768, 264769, 21906765, 21906767, 21906769, 265020, 264692, 33657182, 35695763, 264628, 264629, 18108379, 264631, 264636, 18108381, 264559, 18108382, 83373044, 22279002
97	79605200 (193, 194)	Novel Protein sim. GBank gi|4583559|emb|CAB40388.1| - (AJ005255) OxyR [Erwinia chrysantheml]		UNCLASSIFIED	264508
98	79427000 (195, 196)	Novel Protein sim. GBank gi|1001693|db||BAA10430| - (D64002) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	264909
99	20466524 (197, 198)	Novel Protein sim. GBank gi|1169479|sp|P43925|EFG_HAEIN - ELONGATION FACTOR G (EF-G)		UNCLASSIFIED	264605
100	79640113 (199, 200)			UNCLASSIFIED	264693
101	80203298 (201, 202)	Novel Protein sim. GBank gi|480897|pir||S37485 - gene msg1 protein - mouse		UNCLASSIFIED	265020, 264102, 263972
102	20467259 (203, 204)	Novel Protein sim. GBank gi|2894166|emb|CAA11773.1| - (AJ223998) PCZA361.18 [Amycolatopsis orientalis]		synthase	264605
103	20466368 (205, 206)	Novel Protein sim. GBank gi|1731040|sp|P54509|YQHH_BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	264605
104	80247572 (207, 208)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264591, 264595, 264602
105	79605206 (209, 210)	Novel Protein sim. GBank gi|1685117 (U70770) - furrowed [Drosophila melanogaster]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complement	264508
106	28382058 (211, 212)	Novel Protein sim. GBank gi|1705505|sp|P54729|BS4_MOUSE - BS4 PROTEIN	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264511, 265009
107	80057791 (213, 214)	Novel Protein sim. GBank gi|4887229|gb|AAD32244.1|AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]		ATPase_associated	29331824, 264591, 21906754, 265019
108	80237936 (215, 216)	Novel Protein sim. GBank gi|2635771|emb|CAB15264| - (Z99120) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis]	Contains protein domain (PF00005) - ABC transporter	transport	18108374, 35695917, 22278996, 264113, 264600, 264602, 264603, 265017, 264910, 264906, 264636, 264766
109	95194148 (217, 218)	Novel Protein sim. GBank gi|2330791|emb|CAB11265| - (Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	264758, 264603, 264630, 264636, 264637
110	79582823 (219, 220)				264687
111	39585458 (221, 222)				264564
112	79856038 (223, 224)			UNCLASSIFIED	264908
113	17959439 (225, 226)			UNCLASSIFIED	265007
114	80502101 (227, 228)			UNCLASSIFIED	264769

115	80251003 (229, 230)	Novel Protein sim. GBank gi|2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	52645156, 52645080, 33656970, 264592, 21906754, 27486264, 18108379, 35696423, 264635, 52644332, 18108382
116	81298689 (231, 232)				264905, 264906, 264907, 264908, 264909, 264910, 264758, 265010, 264763, 264682, 264764, 264766, 264685, 264686, 264768, 264769, 33657023, 264693, 33657109, 264628, 18108374, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 56526486, 264565, 264566
117	79636695 (233, 234)				264639, 264693
118	80222170 (235, 236)		Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263974
119	91013071 (237, 238)	Novel Protein sim. GBank gi|732526 (U22327) - alpha2(IV) collagen [Caenorhabditis elegans]		UNCLASSIFIED	22278996, 29331824, 60432289, 265007, 60433438, 264603, 264605, 18108351, 264769, 264689, 265020, 264534, 27486261, 264558, 83373044, 18108385, 264564
120	8756491 (239, 240)	Novel Protein sim. GBank gi|2131219|pir||S50157 - cyclin-dependent kinase chain SRB10 - yeast (Saccharomyces cerevisiae)		kinase	264603
121	80026153 (241, 242)				264595
122	20457620 (243, 244)	Novel Protein sim. GBank gi|2052147|emb|CAB08137| - (Z94752) ksgA [Mycobacterium tuberculosis]	Contains protein domain (PF00398) - Ribosomal RNA adenine dimethylases	transferase	264605
123	8758278 (245, 246)				264604
124	79104017 (247, 248)	Novel Protein sim. GBank gi|2833385|sp|Q43134|UGST_SORBI - GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR		synthase	18108394, 18108397, 265006, 265007, 265008, 265010, 265011, 18108355, 18108379, 18108380, 18108384
125	87797986 (249, 250)	Novel Protein sim. GBank gi|475542 (U08255) - glutamate receptor delta-1 subunit [Rattus norvegicus]	Contains protein domain (PF00060) - Ligand-gated ion channel	misc_channel	264508, 264906, 265009, 264596, 22279002
126	56701283 (251, 252)	Novel Protein sim. GBank gi|5102785|emb|CAB45200.1| - (AL079308) putative transcriptional regulator [Streptomyces coelicolor]			264511
127	20467267 (253, 254)			UNCLASSIFIED	264605
128	80248473 (255, 256)	Novel Protein sim. GBank gi|130120|sp|P23620|PHOB_PSEAE - PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	264907, 264909, 264910, 264600, 264601, 264603, 264605, 18108351, 264693, 264557
129	95290543 (257, 258)	Novel Protein sim. GBank gi|2506493|sp|P38036|YGCB_ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	35696423, 35695855, 264600, 264602, 264603, 264604, 264605, 264508, 264906, 264564, 264628, 264682, 264565, 264683
130	80085583 (259, 260)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]			264634
131	94995022 (261, 262)	Novel Protein sim. GBank gi|1076038|pir||S54860 - ABC transporter PstC-2 chain - Mycobacterium tuberculosis	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	18108376, 264769, 29331826, 264689, 22278996, 265021, 264600, 264511, 264601, 264602, 264605, 264905, 264636

132	10887692 (263, 264)				264636
133	94630883 (265, 266)	Novel Protein sim. GBank gi|1877340|emb|CAB07068| - (Z92771) accA3 [Mycobacterium tuberculosis]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	264905, 264689
134	79834660 (267, 268)	Novel Protein sim. GBank gi|4585838|emb|CAB40932.1| - (AL049630) putative NADH dehydrogenase [Streptomyces coelicolor]		dehydrogenase	264905, 264605, 265021
135	19885057 (269, 270)	Novel Protein sim. GBank gi|1460074|emb|CAB01049| - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]			264634
136	79846083 (271, 272)	Novel Protein sim. GBank gi|2125896|emb|CAA73511| - (Y13070) folylpolyglutamate synthase [Streptomyces coelicolor]		synthase	264508
137	79619770 (273, 274)				264683, 264685, 264686, 264691, 264692, 264693
138	79635971 (275, 276)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108374, 18108385, 33657109, 33657182, 265010, 22278998, 265006, 265007, 265008, 265009, 264693
139	86688076 (277, 278)	Novel Protein sim. GBank gi|5689912|emb|CAB52075.1| - (AL109732) putative mutase [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01817) - Chorismate mutase	dehydrogenase	22278996, 265007, 264910, 60433356, 265010, 264602, 264605, 264766, 264688, 264769, 264693, 32833986, 18108374, 18108387
140	79825759 (279, 280)			UNCLASSIFIED	264908
141	20700094 (281, 282)				264600
142	80028104 (283, 284)	Novel Protein sim. GBank gi|3581916|emb|CAA20855| - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]		nuclease	264602, 265017
143	11072274 (285, 286)			UNCLASSIFIED	264600
144	95009102 (287, 288)	Novel Protein sim. GBank gi|3334127|sp|P97303|BAC2_MOUSE - TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)			263978, 264600, 264910, 264632, 264508, 264563, 264564, 264591, 264556, 264908, 264629, 264639
145	80027058 (289, 290)	Novel Protein sim. GBank gi|3757569|emb|CAA21315| - (AL031863) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=66.31; 1-evidence_end [Drosophila melanogaster]		UNCLASSIFIED	22278996, 264602
146	13085662 (291, 292)	Novel Protein sim. GBank gi|140807|sp|P24536|YI21_BURCE - INSERTION ELEMENT IS402 HYPOTHETICAL 24 KD PROTEIN	Contains protein domain (PF01675) - Transposase		264687
147	94320366 (293, 294)	Novel Protein sim. GBank gi|2827608|emb|CAA16663| - (AL021646) uvrD2 [Mycobacterium tuberculosis]		helicase	264905, 264906, 264909, 264510, 265009, 60433356, 264600, 264601, 264604, 264605, 264687, 264769, 18108365, 65274791, 18108387
148	80248804 (295, 296)	Novel Protein sim. GBank gi|2916947|emb|CAA17585| - (AL021999) hypothetical protein Rv0986 [Mycobacterium tuberculosis]		transport	265009, 265010, 264600, 264602, 264603, 264604, 264605, 264693, 33657109, 264636

149	80249373 (297, 298)	Novel Protein sim. GBank gi|1723073|sp|Q11040|Y081_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.01	Contains protein domain (PF00005) - ABC transporter	transport	265010, 264600, 264601, 264603, 264604, 27486265, 264636
150	20294748 (299, 300)	Novel Protein sim. GBank gi|3724125|emb|CAA11905| - (AJ224340) maltosephosphorylase [Lactobacillus sanfrancisco]			264600
151	20726398 (301, 302)	Novel Protein sim. GBank gi|729312|sp|P07651|DEOB_ECOLI - PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE)	Contains protein domain (PF01676) - Metalloenzyme superfamily	UNCLASSIFIED	264602
152	95002877 (303, 304)	Novel Protein sim. GBank gi|2497952|sp|P55667|Y4TM_RHISN - HYPOTHETICAL HYDROLASE/PEPTIDASE Y4TM		peptidase	264602
153	80256665 (305, 306)	Novel Protein sim. GBank gi|3123021|sp|Q90508|VIT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2))		UNCLASSIFIED	264593
154	82305966 (307, 308)				264910, 264762, 264691, 264634
155	20429859 (309, 310)	Novel Protein sim. GBank gi|419697|pir||JN0443 - transcription initiation factor sigma homolog hrdB - Streptomyces aureofaciens	Contains protein domain (PF00140) - Sigma-70 factor	mapolymerase	264605
156	39564742 (311, 312)	Novel Protein sim. GBank gi|628710|pir||S41739 - hypothetical protein - Escherichia coli		UNCLASSIFIED	264565
157	10358887 (313, 314)	Novel Protein sim. GBank gi|3695013 (AF052586) - CtrA [Pseudomonas aeruginosa]	Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, NifH/frxC family	hydrolase	264691
158	79761936 (315, 316)	Novel Protein sim. GBank gi|1073072|pir||C55543 - cmaU protein - Pseudomonas syringae pv. syringae		UNCLASSIFIED	264905
159	78890376 (317, 318)			UNCLASSIFIED	265008
160	11075119 (319, 320)		Contains protein domain (PF00400) - WD domain, G-beta repeat		264605
161	80055007 (321, 322)	Novel Protein sim. GBank gi|1173023|sp|P46789|RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00327) - Ribosomal protein L30p/L7e	ribosomalprot	22278996, 264600, 264603, 35695917, 32833986, 35696423, 264636
162	80016371 (323, 324)	Novel Protein sim. GBank gi|5304869|emb|CAB46028.1| - (AL031685) dJ963K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukin	264112, 264532, 22279002
163	11692306 (325, 326)			UNCLASSIFIED	264639
164	80077902 (327, 328)			UNCLASSIFIED	264905, 264907, 264600
165	108560o7 (329, 330)				264691
166	88095003 (331, 332)	Novel Protein sim. GBank gi|2661691|emb|CAA15795| - (AL009204) putative protease [Streptomyces coelicolor]		UNCLASSIFIED	264605, 264486
167	16395460 (333, 334)	Novel Protein sim. GBank gi|4416478|gb|AAD20378| - (AF125999) transposase [Mycobacterium avium]		UNCLASSIFIED	265010
168	80079362 (335, 336)	Novel Protein sim. GBank gi|76177|pir||QQECFT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli			264600
169	80239581 (337, 338)				264556, 264557, 264558, 264559

170	79612364 (339, 340)				264906
171	95293073 (341, 342)	Novel Protein sim. GBank gi|140888|sp|P27847|YIGK_ECOLI - HYPOTHETICAL 15.4 KD PROTEIN IN RECQ-PLDB INTERGENIC REGION (F138)	Contains protein domain (PF01810) - LysE type translocator		264595, 264604
172	37797007 (343, 344)	Novel Protein sim. GBank gi|4210905|gb|AAD12048.1| - (AF045609) AglG [Sinorhizobium meliloti]	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	264769
173	57529660 (345, 346)	Novel Protein sim. GBank gi|132854|sp|P02387|RL2_ECOLI - 50S RIBOSOMAL PROTEIN L2	Contains protein domain (PF00181) - Ribosomal Proteins L2	ribosomalprot	264769
174	95293078 (347, 348)	Novel Protein sim. GBank gi|1881350|dbj|BAA19377| - (AB001488) PROBABLE TRANSPORT PROTEIN, SIMILAR TO ANTIBIOTIC TRANSPORT-ASSOCIATED PROTEIN ACTII IN STREPTOMYCES COELICOLOR. [Bacillus subtilis]		transport	264510, 264593, 264602, 264603, 264605, 264762, 264693
175	79756270 (349, 350)	Novel Protein sim. GBank gi|2072722|emb|CAB08326| - (Z95121) manA [Mycobacterium tuberculosis]		isomerase	264565
176	80066896 (351, 352)	Novel Protein sim. GBank gi|1055198 (U40187) - similar to PIR:A41724 chicken LD (limb deformity) gene product and to formin; also P-rich region similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	264907, 264910, 264681, 264558
177	86684852 (353, 354)	Novel Protein sim. GBank gi|2326738|emb|CAB10952| - (Z98268) hypothetical protein Rv1695 [Mycobacterium tuberculosis]	Contains protein domain (PF01513) - Domain of unknown function	UNCLASSIFIED	264768, 60424179, 264687, 264688, 264769, 29331826, 60432289, 18108376, 264689, 18108387, 32833986, 22278996, 265020, 264600, 264601, 264602, 264603, 264604, 264605, 264635, 264762, 264636, 264906, 264564, 264637, 264638, 264486, 60433356, 264766
178	79559526 (355, 356)	Novel Protein sim. GBank gi|1906596 (U81788) - kinesin-73 [Drosophila melanogaster]		struct	264693, 33657109, 264635
179	20263112 (357, 358)			UNCLASSIFIED	264563
180	80488958 (359, 360)	Novel Protein sim. GBank gi|1169367|sp|P45256|DNAB_HAEIN - REPLICATIVE DNA HELICASE		helicase	264769
181	79585369 (361, 362)	Novel Protein sim. GBank gi|3170615 (AF059485) - DOC4 [Mus musculus]		UNCLASSIFIED	21908767, 264635, 264639, 18108384
182	80577899 (363, 364)			UNCLASSIFIED	264259, 35696052, 56182435, 264511, 265018, 33657109, 264555, 264566
183	11614017 (365, 366)	Novel Protein sim. GBank gi|1076627|pir||S54172 - inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco		UNCLASSIFIED	264690
184	10174167 (367, 368)	Novel Protein sim. GBank gi|4371280|gb|AAD18138| - (AC006260) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264510

185	21660822 (369, 370)	Novel Protein sim. GBank gi|3006178|emb|CAA18398.1| - (AL022304) putative mma transport regulator [Schizosaccharomyces pombe]		UNCLASSIFIED	264604
186	80070329 (371, 372)	Novel Protein sim. GBank gi|2829802|sp|P94408|YCLF_BACSU - HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION		transport	264595
187	80186611 (373, 374)			UNCLASSIFIED	264369
188	20464942 (375, 376)	Novel Protein sim. GBank gi|3150260|emb|CAA19179| - (AL023634) cyclin [Schizosaccharomyces pombe]		kinase	264605
189	82338215 (377, 378)	Novel Protein sim. GBank gi|2145853|pir||S72938 - hflX protein - Mycobacterium leprae		UNCLASSIFIED	35696052, 264602, 264605, 264762, 264689, 35695917, 18108370, 18108372, 264638, 264565
190	80086821 (379, 380)	Novel Protein sim. GBank gi|1881244|dbj|BAA19271| - (AB001488) SIMILAR TO PYRUVATE OXIDASE AND ACETOLACTATE SYNTHASE. [Bacillus subtilis]	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	synthase	264563
191	88095012 (381, 382)	Novel Protein sim. GBank gi|120226|sp|P28725|FKBP_STRCH - FK506-BINDING PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE)	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	264508, 264604, 264605, 264769, 264555
192	16333379 (383, 384)				264567
193	79910127 (385, 386)				264908, 264693
194	20464949 (387, 388)				264605
195	13518389 (389, 390)	Novel Protein sim. GBank gi|4980892|gb|AAD35474.1|AE00171 - (AE001718) ABC transporter, ATP-binding protein [Thermotoga maritima]		transport	264636
196	95005569 (391, 392)	Novel Protein sim. GBank gi|1705461|sp|P53656|BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate	gaba	264600, 264689, 264638
197	80248665 (393, 394)	Novel Protein sim. GBank gi|3122305|sp|Q27778|K6PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)	Contains protein domain (PF00365) - Phosphofructokinase	kinase	264602, 264682, 264692, 18108374
198	79163635 (395, 396)				264636
199	78890715 (397, 398)	Novel Protein sim. GBank gi|1781203|emb|CAB06110| - (Z83859) gnd [Mycobacterium tuberculosis]	Contains protein domain (PF00393) - 6-phosphogluconate dehydrogenases		265008
200	79413849 (399, 400)	Novel Protein sim. GBank gi|2642222 (AF030885) - telomere-associated recQ-like helicase [Ustilago maydis]		UNCLASSIFIED	264595, 264596
201	86945924 (401, 402)	Novel Protein sim. GBank gi|2894379|emb|CAA74911.1| - (Y14573) ring finger protein [Hordeum vulgare]		UNCLASSIFIED	29331826, 265007, 264512, 33657402, 264596, 265017, 18108351, 264682, 264683, 264767, 264629, 55810764, 264634, 264635, 58182323, 60432113, 22279000

202	79588046 (403, 404)	Novel Protein sim. GBank gi|231772|sp|P30598|CHS1_USTMA - CHITIN SYNTHASE 1 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 1)	Contains protein domain (PF01644) - Chitin synthase	synthase	264600
203	79843927 (405, 406)	Novel Protein sim. GBank gi|1504042|dbj|BAA13220| - (D86984) similar to yeast adenylate cyclase (S56776) [Homo sapiens]			22278995, 29331822, 29331825, 29331827, 264906, 21906754, 264683, 21906766, 21906769, 35696423, 264556
204	79855186 (407, 408)			UNCLASSIFIED	264909
205	10090583 (409, 410)	Novel Protein sim. GBank gi|2633808|emb|CAB13310| - (Z99111) similar to hypothetical proteins [Bacillus subtilis]		transport	264909
206	8758473 (411, 412)			UNCLASSIFIED	264604
207	20754522 (413, 414)	Novel Protein sim. GBank gi|2134381|pir||S60678 - polybromo 1 protein - chicken		UNCLASSIFIED	264556
208	20289261 (415, 416)				264605
209	80071069 (417, 418)	Novel Protein sim. GBank gi|2501040|sp|O05814|SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE--TRNA LIGASE) (PRORS)			264605, 264689
210	80168800 (419, 420)				264905, 264907, 264909, 264766, 264687, 264691, 264629, 18108374, 264638
211	80034539 (421, 422)				263978
212	82442474 (423, 424)	Novel Protein sim. GBank gi|5031809|ref|NP_005536.1|pISLR - immunoglobulin superfamily containing leucine-rich repeat		UNCLASSIFIED	264508, 264905, 264906, 264907, 264908, 264600, 264762, 264534, 264632, 264634, 264635, 264639, 264486
213	80249562 (425, 426)	Novel Protein sim. GBank gi|3122359|sp|O33123|LEU2_MYCLE - 3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	isomerase	22278996, 264508, 264600, 264602, 264603, 264605, 33657023, 264565, 264486
214	80079381 (427, 428)	Novel Protein sim. GBank gi|116236|sp|P19421|CH60_COXBU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (HEAT SHOCK PROTEIN B)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	eph	264600, 264693
215	14973283 (429, 430)			UNCLASSIFIED	264629
216	80177716 (431, 432)	Novel Protein sim. GBank gi|3417297 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	264448
217	79603634 (433, 434)	Novel Protein sim. GBank gi|2506924|sp|P49754|VP41_HUMAN - VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG (S53)			264508
218	80258475 (435, 436)	Novel Protein sim. GBank gi|1173288|sp|P38106|RSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN		rnapolymerase	264594
219	20438797 (437, 438)	Novel Protein sim. GBank gi|1781097|emb|CAB06231| - (Z83864) gltB [Mycobacterium tuberculosis]		synthase	264604
220	13499572 (439, 440)	Novel Protein sim. GBank gi|2984703 (AF052427) - unknown [Trypanosoma cruzi]		nucleaseinhib	264689
221	11287498 (441, 442)	Novel Protein sim. GBank gi|4587313|dbj|BAA76709.1| - (AB025248) alpha-1,2-mannosidase [Bacillus sp. M-90]		UNCLASSIFIED	264555

222	79862802 (443, 444)	Novel Protein sim. GBank gi|1877268|emb|CAB07049| - (Z92770) hypothetical protein Rv0143c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 264769, 35696423
223	83053869 (445, 446)			UNCLASSIFIED	264906, 264907, 264603
224	79557920 (447, 448)				264684, 264693
225	79559541 (449, 450)	Novel Protein sim. GBank gi|2274851|dbj|BAA21515| - (D64159) 3-7 gene product [Homo sapiens]		UNCLASSIFIED	264692
226	79172397 (451, 452)	Novel Protein sim. GBank gi|868245 (U29488) - C56C10.7 gene product [Caenorhabditis elegans]		UNCLASSIFIED	22278998, 264112, 33657023, 263981
227	81777196 (453, 454)			UNCLASSIFIED	35695917, 264636, 264907
228	79872285 (455, 456)				264768, 264907, 264908, 264692, 264593, 264639
229	79838266 (457, 458)				264906, 264910
230	11013209 (459, 460)			UNCLASSIFIED	264631
231	20622207 (461, 462)	Novel Protein sim. GBank gi|1835114|emb|CAA71733| - (Y10744) homoserine O-acetyltransferase [Leptospira meyeri]			264906, 264600, 264603, 264692
232	80055035 (463, 464)			UNCLASSIFIED	264600, 264603, 264605, 264687, 264769
233	80063054 (465, 466)	Novel Protein sim. GBank gi|2642340 (AF032970) - imidazolone proplonate hydrolase [Pseudomonas putida]	Contains protein domain (PF00449) - Urease	hydrolase	264604
234	7523998 (467, 468)	Novel Protein sim. GBank gi|3510505 (AF030881) - pol polyprotein [Fugu rubripes]		UNCLASSIFIED	264369
235	80203671 (469, 470)			UNCLASSIFIED	264106
236	78940001 (471, 472)	Novel Protein sim. GBank gi|2104609|emb|CAB08805| - (Z95398) PckA [Mycobacterium leprae]		carboxylase	264905
237	11755273 (473, 474)				264681
238	79461401 (475, 476)			UNCLASSIFIED	264639
239	82435190 (477, 478)	Novel Protein sim. GBank gi|2495617|sp|Q57252|YDIJ_HAEIN - HYPOTHETICAL PROTEIN HI1163	Contains protein domain (PF00037) - 4Fe-4S ferredoxins and related iron-sulfur cluster binding domains.		264906, 265010, 264603, 264762, 264682, 264636, 264638, 264486
240	21635575 (479, 480)	Novel Protein sim. GBank gi|3183458|sp|P75796|YLIA_ECOLI - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YLIA		transport	264259, 264769
241	80377307 (481, 482)	Novel Protein sim. GBank gi|3875920|emb|CAB04111| - (Z81503) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65450 comes from this gene; cDNA EST EMBL:D68888 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264908, 264909, 264764, 264639
242	82148454 (483, 484)			UNCLASSIFIED	264489, 264907, 264908, 264511, 264760, 264764, 264692, 264635, 264637
243	79633207 (485, 486)			UNCLASSIFIED	264906
244	80248682 (487, 488)	Novel Protein sim. GBank gi|2624302|emb|CAA15575| - (AL008967) ald [Mycobacterium tuberculosis]		dehydrogenase	264600, 264602, 264605, 264769, 264689
245	79863543 (489, 490)	Novel Protein sim. GBank gi|2920625 (AF044499) - vgrE protein [Escherichia coli]		UNCLASSIFIED	264907, 264758
246	79162929 (491, 492)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01106) - NifU-like domain		264637, 18108381, 18108387, 264565

247	79873185 (493, 494)	Novel Protein sim. GBank gi|1839006|emb|CAB06648| - (Z85982) argB [Mycobacterium tuberculosis]		kinase	264909, 264691, 35696423, 18108387
248	80488983 (495, 496)	Novel Protein sim. GBank gi|1168574|sp|P42464|ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	35696286, 264907, 264511, 264602, 264768, 264688, 265021, 35695855, 18108385
249	79764645 (497, 498)			UNCLASSIFIED	264907, 264910, 265011, 264762, 264636
250	79619980 (499, 500)				21906768, 264692
251	84359489 (501, 502)			UNCLASSIFIED	52645158, 29331822, 29331824, 52644045, 265018, 21906765, 21906768, 265020, 27486261, 27486265, 35695763, 18108376, 264556, 264559, 264565
252	79737756 (503, 504)	Novel Protein sim. GBank gi|3327166|dbj|BAA31651| - (AB014576) KIAA0676 protein [Homo sapiens]			264685, 264687, 264632
253	20443124 (505, 506)	Novel Protein sim. GBank gi|3036880|emb|CAA18513| - (AL022374) putative ATP-dependent DNA helicase [Streptomyces coelicolor]		helicase	264604
254	80027421 (507, 508)	Novel Protein sim. GBank gi|3915488|sp|O34961|YJMB_BACSU - HYPOTHETICAL SYMPORTER IN COTT-RAPA INTERGENIC REGION		UNCLASSIFIED	264508, 264906, 264602, 264687, 265021, 264486
255	11398315 (509, 510)	Novel Protein sim. GBank gi|1665720|dbj|BAA04134| - (D17312) diarrheal toxin [Bacillus cereus]		UNCLASSIFIED	264593
256	80028158 (511, 512)	Novel Protein sim. GBank gi|465787|sp|P34422|YL31_CAEEL - HYPOTHETICAL 86.0 KD PROTEIN F44B9.1 IN CHROMOSOME III	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	264602, 264692
257	20289282 (513, 514)	Novel Protein sim. GBank gi|1172039|sp|P42315|SCOA_BACSU - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE SUBUNIT A (SUCCINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT A)	Contains protein domain (PF01144) - Coenzyme A transferase	transferase	264605
258	20459464 (515, 516)	Novel Protein sim. GBank gi|3127836|emb|CAA18902| - (AL023496) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264604
259	79910152 (517, 518)			collagen	264681, 264686, 264692
260	20379437 (519, 520)			UNCLASSIFIED	264692, 264556
261	20285883 (521, 522)	Novel Protein sim. GBank gi|123761|sp|P24221|HUTH_STRGR - HISTIDINE AMMONIA-LYASE (HISTIDASE)	Contains protein domain (PF00221) - Phenylalanine and histidine ammonia lyases	UNCLASSIFIED	264600
262	80189317 (523, 524)			UNCLASSIFIED	265017, 264369
263	88095045 (525, 526)	Novel Protein sim. GBank gi|3924708|emb|CAA84646| - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...		UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264909, 264512, 264910, 264758, 264596, 264604, 265019, 264605, 264760, 18108351, 264763, 264764, 264288, 264766, 264768, 264769, 264691, 264692, 264693, 264628, 264634, 264635, 264555, 264636, 264638, 264639
264	87370826 (527, 528)	Novel Protein sim. GBank gi|3043734|dbj|BAA25531| - (AB011177) KIAA0605 protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	protease	264259, 264908, 21906754, 265018, 265019, 265020

265	95355646 (529, 530)	Novel Protein sim. GBank gi|4589624|dbj|BAA76834.1| - (AB023207) KIAA0990 protein [Homo sapiens]		kinase	264488, 35696286, 29331824, 56182181, 35696052, 264508, 264905, 264906, 264907, 66712502, 264908, 264909, 264511, 264512, 264910, 264592, 264595, 264758, 264596, 55811386, 264600, 265017, 264603, 264604, 264605, 264760, 18108351, 264762, 264681, 264764, 264288, 264766, 264768, 264769, 21906765, 21906767, 21906769, 265020, 264691, 33657023, 33657109, 33657182, 264628, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 83373044, 56526486, 87168518, 264564, 264566, 264486
266	79588075 (531, 532)				264600
267	11362222 (533, 534)			UNCLASSIFIED	264828
268	79909566 (535, 536)			UNCLASSIFIED	264687, 264769, 264689
269	80025810 (537, 538)			UNCLASSIFIED	264602
270	84361144 (539, 540)	Novel Protein sim. GBank gi|4507367|ref|NP_003182.1|pTARS - threonyl-tRNA synthetase		UNCLASSIFIED	264693
271	79552301 (541, 542)			UNCLASSIFIED	264909, 264693
272	9874778 (543, 544)	Novel Protein sim. GBank gi|4980738|gb|AAD35331.1|AE00170 - (AE001707) glucose-1-phosphate adenylyltransferase [Thermotoga maritima]		synthase	264908
273	12840694 (545, 546)	Novel Protein sim. GBank gi|1168224|sp|P44569|5NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR		UNCLASSIFIED	264688
274	39524246 (547, 548)				264564
275	82787041 (549, 550)	Novel Protein sim. GBank gi|3253159 (AF005355) - translation initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	264907, 264908, 264909, 264766, 264768, 264691, 264632, 264636
276	86671073 (551, 552)	Novel Protein sim. GBank gi|134920|sp|P21997|SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			265008, 60432229
277	80079735 (553, 554)	Novel Protein sim. GBank gi|129021|sp|P20964|OBG_BACSU - SPO0B-ASSOCIATED GTP-BINDING PROTEIN		ribosomalprot	264600, 18108387
278	12966947 (555, 556)			UNCLASSIFIED	264689
279	95292719 (557, 558)	Novel Protein sim. GBank gi|79839|pir||S03812 - uvrB protein - Micrococcus luteus		nuclease	264508, 264604, 21906764, 264638, 264557, 264404
280	5603617 (559, 560)				264259
281	80249599 (561, 562)	Novel Protein sim. GBank gi|3123160|sp|Q18964|YLN2_CAEEL - HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II			18108392, 264634, 264555, 264556, 264557, 264558
282	18598682 (563, 564)			UNCLASSIFIED	265019
283	20614211 (565, 566)			UNCLASSIFIED	264555

284	91212160 (567, 568)	Novel Protein sim. GBank gi|2429094 (U58632) - acetyl xylan esterase; AxeA [Thermotoga neapolitana]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	UNCLASSIFIED	35696052, 29331828, 264508, 264905, 264600, 264602, 264605, 264682, 264764, 56181562, 21906764, 18108376, 264636, 264559, 18108387
285	8757940 (569, 570)			UNCLASSIFIED	264603
286	80503235 (571, 572)	Novel Protein sim. GBank gi|2072674|emb|CAB08305| - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	ATPase_associated	35696052, 264769, 264638
287	12745521 (573, 574)			UNCLASSIFIED	264689
288	20756502 (575, 576)	Novel Protein sim. GBank gi|765323|bbs|157676 - (S74439) silk fibroin heavy chain (C-terminal) [Bombyx mori=silkworms, Peptide Partial, 633 aa] [Bombyx mori]		collagen	264557
289	80043804 (577, 578)	Novel Protein sim. GBank gi|1870009|emb|CAB06860| - (Z92539) hypothetical protein Rv1019 [Mycobacterium tuberculosis]	Contains protein domain (PF00440) - Bacterial regulatory proteins, tetR family	ribosomalprot	264593, 264600
290	80430175 (579, 580)			UNCLASSIFIED	264768
291	20747431 (581, 582)	Novel Protein sim. GBank gi|2506664|sp|P40120|YDCG_ECOLI - 59.4 PROTEIN IN TRG-RIML INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264601
292	80052555 (583, 584)	Novel Protein sim. GBank gi|625182 (L39015) - mitochondrial glutamyl-tRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	264605
293	80062519 (585, 586)	Novel Protein sim. GBank gi|1718065|sp|P53528|UVRD_MYCLE - PUTATIVE DNA HELICASE II HOMOLOG		helicase	264909, 264605, 264687, 264689, 264692
294	79830303 (587, 588)	Novel Protein sim. GBank gi|117422|sp|P10040|CRB_DROME - CRUMBS PROTEIN PRECURSOR (95F)	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696052, 264906, 265011, 264628, 55811576
295	79444180 (589, 590)	Novel Protein sim. GBank gi|1181619|dbj|BAA11565| - (D82364) a variant of TSC-22 [Gallus gallus]			52644507, 29331822, 264592, 265020, 264639
296	79607076 (591, 592)	Novel Protein sim. GBank gi|3649789|dbj|BAA33403| - (AB012226) SecA [Vibrio alginolyticus]		synthase	264508
297	79631297 (593, 594)	Novel Protein sim. GBank gi|5689967|emb|CAB52004.1| - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264905, 264687, 264638
298	80418898 (595, 596)			UNCLASSIFIED	264905, 264691, 264639, 264766

299	95293298 (597, 598)	Novel Protein sim. GBank gi|220637|dbj|BAA01477| - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type		264488, 263994, 56994075, 22278997, 22278998, 22278999, 20281099, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264906, 264907, 264908, 52644045, 264909, 264511, 265008, 264910, 264595, 264596, 264758, 33657084, 87168559, 265018, 265019, 264764, 264288, 264768, 264687, 56181562, 264769, 21906765, 21906768, 21906769, 33657023, 264692, 33657109, 27486261, 18108370, 264628, 264629, 55811576, 35695855, 264631, 264634, 264635, 264638, 264639, 83373044, 18108387, 87168518, 22279000, 22279002, 264565, 264566, 264567
300	20711340 (599, 600)			UNCLASSIFIED	264602
301	13511332 (601, 602)	Novel Protein sim. GBank gi|145922 (M20981) - iron dicitrate transport protein precursor [Escherichia coli]		transport	264687
302	9875260 (603, 604)	Novel Protein sim. GBank gi|1174661|sp|P44594|TGT_HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)			264908
303	79574895 (605, 606)				264689
304	20711344 (607, 608)	Novel Protein sim. GBank gi|67985|pir||HJNVAV - helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus		helicase	264602
305	80412520 (609, 610)	Novel Protein sim. GBank gi|728867|sp|P40602|APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR			264763
306	8515876 (611, 612)	Novel Protein sim. GBank gi|1657554|gb|AAB18082.1| - (U73857) hypothetical protein [Escherichia coli]		UNCLASSIFIED	263978
307	80222901 (613, 614)			UNCLASSIFIED	265010, 21906768, 265020, 18108374, 263977
308	80064305 (615, 616)	Novel Protein sim. GBank gi|1710612|sp|Q10793|RNH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNASE HII)	Contains protein domain (PF01351) - Ribonuclease HII	nuclease	264910, 264600, 264605, 264687, 264689, 264638, 18108387
309	80504136 (617, 618)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]			264769
310	80053616 (619, 620)				264603
311	11090659 (621, 622)	Novel Protein sim. GBank gi|1144522 (U34957) - phosphoribosylaminoimidazolesuccinocarboxamide synthase [Mycobacterium tuberculosis]		synthase	264602
312	80054347 (623, 624)			UNCLASSIFIED	264566
313	80046168 (625, 626)				264603, 264567

314	87645112 (627, 628)	Novel Protein sim. GBank gi|3661583 (AF092175) - ikaros [Danio rerio]	Contains protein domain (PF00320) - GATA zinc finger	dna_rna_bind	264259, 60432289, 29331828, 264905, 264906, 264908, 264909, 265008, 264910, 60432229, 33657402, 60433438, 33109954, 265011, 265017, 264603, 265018, 264288, 264766, 264692, 35695763, 264628, 264629, 264639, 60170394, 22279002, 264566
315	82356091 (629, 630)	Novel Protein sim. GBank gi|1652620|dbj|BAA17540| - (D90907) pyridine nucleotide transhydrogenase beta subunit [Synechocystis sp.]			264508, 264600, 264762, 264687, 264768, 52644229, 264769, 264689, 264635, 264636, 264638, 264486
316	79911071 (631, 632)			UNCLASSIFIED	264693
317	20466944 (633, 634)	Novel Protein sim. GBank gi|118244|sp|P24176|DAPE_ECOLI - SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (SDAP)		UNCLASSIFIED	264605
318	94141836 (635, 636)	Novel Protein sim. GBank gi|4680229|gb|AAD27583.1|AF11827 - (AF118274) DNb-5 [Homo sapiens]	Contains protein domain (PF00526) - Dictyostelium (slime mold) repeats	transport	264908, 264909, 264910, 264593, 264594, 264760, 264288, 264768, 264769, 21906769, 264691, 264693, 264628, 65274791, 264635, 264636, 264638, 83373044, 22279002, 264566
319	17289360 (637, 638)	Novel Protein sim. GBank gi|1149693|emb|CAA60220| - (X86499) rbsC [Clostridium perfringens]		transport	265018
320	13527675 (639, 640)	Novel Protein sim. GBank gi|2811033|sp|O05314|GLGC_MYCTU - GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE)		synthase	264687
321	94134387 (641, 642)	Novel Protein sim. GBank gi|1680716 (U68234) - all-trans-retinoic acid 4-hydroxylase [Danio rerio]		cyto450	264509, 264906, 264907, 264908, 265009, 264596, 264764, 264628, 264634, 264635, 264638, 264639, 83373044, 264567
322	66489053 (643, 644)	Novel Protein sim. GBank gi|1160355 (U33058) - UNC-89 [Caenorhabditis elegans]		UNCLASSIFIED	55811150, 264691, 60431528, 55810764
323	94653725 (645, 646)			UNCLASSIFIED	264488, 265009, 264593, 264628, 264635
324	79174383 (647, 648)				264687
325	79862691 (649, 650)			UNCLASSIFIED	264693
326	28774974 (651, 652)			UNCLASSIFIED	264288, 18108385
327	79776267 (653, 654)	Novel Protein sim. GBank gi|451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]			264488, 264905, 264509, 264910
328	80253202 (655, 656)			UNCLASSIFIED	264592
329	10173821 (657, 658)			UNCLASSIFIED	264510
330	86597767 (659, 660)	Novel Protein sim. GBank gi|4191358 (AF087825) - claudin-7 [Mus musculus]		UNCLASSIFIED	264259, 264908
331	79754888 (661, 662)	Novel Protein sim. GBank gi|80741|pir||S20912 - regulatory protein whiB - Streptomyces coelicolor		transcriptfactor	264910, 264687, 264689, 264636, 264567
332	80071440 (663, 664)	Novel Protein sim. GBank gi|114049|sp|P19480|AHPF_SALTY - ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F (ALKYL HYDROPEROXIDE REDUCTASE F52A PROTEIN)		reductase	35696423, 264636, 264638, 264565
333	13009555 (665, 666)				264687

334	80230771 (667, 668)	Novel Protein sim. GBank gi|322228|pir||S32227 - glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - Corynebacterium glutamicum	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Valine dehydrogenase	dehydrogenase	264905, 264600, 264604, 264486
335	80057026 (669, 670)	Novel Protein sim. GBank gi|2193938|emb|CAB09602| - (Z96800) glpQ2 [Mycobacterium tuberculosis]		esterase	264907, 264603, 264693, 18108374, 264636, 18108387
336	80414319 (671, 672)			UNCLASSIFIED	265009, 264766, 264686
337	11090829 (673, 674)				264602
338	95413134 (675, 676)	Novel Protein sim. GBank gi|5454074|ref|NP_006303.1|pSMRT - silencing mediator for retinoid and thyroid hormone receptors	Contains protein domain (PF00249) - Myb-like DNA-binding domain	nucl_recpt	264569, 18108397, 22278998, 29331822, 20281099, 29331824, 56182181, 66714117, 29331825, 35696052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 265008, 264910, 265009, 264758, 55812038, 65274444, 265011, 87168559, 265017, 265018, 265019, 264760, 55811150, 264681, 264762, 18108351, 264682, 264764, 264766, 264685, 264686, 264768, 52844229, 264689, 55811957, 35695917, 264692, 264693, 264628, 18108370, 18108374, 55811576, 35696423, 35695855, 264635, 264555, 264636, 264556, 264637, 264557, 18108380, 264638, 264558, 264639, 18108381, 83373044, 18108385, 87168518, 60432113
339	11398513 (677, 678)	Novel Protein sim. GBank gi|4001713|dbj|BAA35087.1| - (AB015879) DnaK [Porphyromonas gingivalis]		eph	264593
340	80504149 (679, 680)	Novel Protein sim. GBank gi|2842699|sp|Q92353|UBPC_SCHPO - PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C6G9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)		ubiquitin	264905, 265019, 264769, 18108374
341	11075198 (681, 682)	Novel Protein sim. GBank gi|2688580 (AE001166) - conserved hypothetical protein [Borrelia burgdorferi]	Contains protein domain (PF00290) - Tryptophan synthase alpha chain	isomerase	264605
342	80054196 (683, 684)	Novel Protein sim. GBank gi|1684738|emb|CAA70601| - (Y09452) Yed j hypothetical protein [Pseudomonas syringae]			264603, 264604
343	20466792 (685, 686)				264605
344	80428870 (687, 688)	Novel Protein sim. GBank gi|2117275|emb|CAB09104| - (Z95618) hypothetical protein Rv0807 [Mycobacterium tuberculosis]		UNCLASSIFIED	264600, 264605, 264768, 18108370, 18108374, 35695855
345	80258853 (689, 690)	Novel Protein sim. GBank gi|3023317|sp|Q48935|APHA_MYCRA - ACETYLPOLYAMINE AMINOHYDROLASE		histone	264593
346	79831058 (691, 692)	Novel Protein sim. GBank gi|4239787|emb|CAA75437| - (Y15166) NADP-glutamate dehydrogenase [Pseudomonas aeruginosa]	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Valine dehydrogenase	dehydrogenase	264905

347	79158195 (693, 694)	Novel Protein sim. GBank gi|731675|sp|P38795|YHN4_YEAST - HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION		UNCLASSIFIED	265006, 265008, 265010, 265018, 263967, 263981
348	80020208 (695, 696)	Novel Protein sim. GBank gi|1073610|pir||S47672 - ugpB protein - Escherichia coli		transport	264602, 18108351, 18108387
349	17282112 (697, 698)				265007
350	80502370 (699, 700)	Novel Protein sim. GBank gi|3261599|emb|CAB00917| - (Z77137) hypothetical protein Rv1277 [Mycobacterium tuberculosis]		nuclease	265009, 264769, 264689, 18108370
351	80501805 (701, 702)	Novel Protein sim. GBank gi|2959367|emb|CAA17921| - (AL022117) hypothetical protein [Schizosaccharomyces pombe]		glycoprotein	264769, 264905, 264908
352	11611585 (703, 704)	Novel Protein sim. GBank gi|4416302|gb|AAD20307| - (AF105716) copia-type pol polyprotein [Zea mays]		protease	264595
353	80061653 (705, 706)	Novel Protein sim. GBank gi|1174887|sp|P42873|URE1_STAXY - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	264604
354	56626130 (707, 708)			UNCLASSIFIED	264628
355	80046344 (709, 710)			UNCLASSIFIED	264909, 264595, 264683, 22279002
356	80043835 (711, 712)	Novel Protein sim. GBank gi|115157|sp|P16574|BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA	Contains protein domain (PF00072) - Response regulator receiver domain	transcriptfactor	264909, 264591, 264592
357	80070566 (713, 714)	Novel Protein sim. GBank gi|497637 (J03939) - cytochrome oxidase d subunit I [Escherichia coli]		oxidase	264605
358	37032756 (715, 716)	Novel Protein sim. GBank gi|2290990 (AF006000) - Brg1 [Bordetella pertussis]		UNCLASSIFIED	264768
359	80501488 (717, 718)			UNCLASSIFIED	264604, 264769
360	80026748 (719, 720)			UNCLASSIFIED	264594
361	80584075 (721, 722)	Novel Protein sim. GBank gi|3510639 (AF049344) - UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 [Rattus norvegicus]		transferase	22278996, 264259, 29331822, 29331824, 264605, 55811957, 265022
362	13089485 (723, 724)	Novel Protein sim. GBank gi|113764|sp|P25718|AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		amylase	264688
363	79750145 (725, 726)				264568
364	82443593 (727, 728)	Novel Protein sim. GBank gi|2029816|sp|P95171|NUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)	Contains protein domain (PF00420) - NADH-ubiquinone/plastoquinone oxidoreductase chain 4L	dehydrogenase	264769, 264602, 264604, 264508, 264762, 264638, 264486

365	88040288 (729, 730)	Novel Protein sim. GBank gi|4929268|gb|AAD33924.1| - (AF144237) LOMP protein [Homo sapiens]	Contains protein domain (PF00412) - LIM domain containing proteins		264488, 21906766, 21906767, 55811576, 21906769, 29148629, 22278995, 22278996, 265020, 265022, 264634, 264691, 264593, 33657023, 33657402, 264693, 264639, 264594, 29331824, 264758, 18108385, 29331827, 87168559, 265018, 22279000, 265019, 264482, 264761, 264681, 18108351
366	81821838 (731, 732)				265017, 264757
367	95357471 (733, 734)	Novel Protein sim. GBank gi|4503843|ref|NP_003908.1|pG2AD - UNKNOWN	Contains protein domain (PF01602) - Adaptin N terminal region	glycoprotein	60424179, 65274572, 56182575, 22278994, 56994075, 22278998, 264259, 29331822, 29331824, 56182181, 60424269, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264905, 264828, 56182435, 265006, 264512, 265008, 264591, 55812038, 55811386, 265010, 87168559, 265017, 265018, 264604, 265019, 55811150, 264448, 264369, 264288, 264686, 264768, 56181562, 21906768, 21906769, 55811957, 35695917, 265022, 60170815, 33657023, 65274620, 18108365, 263967, 33657109, 33657349, 35695763, 264628, 18108376, 55811576, 65274791, 35695855, 56182323, 83373044, 60432113, 264563, 264564, 264567
368	79607265 (735, 736)				264509
369	95292917 (737, 738)	Novel Protein sim. GBank gi|3913029|sp|P94967|ALR_MYCSM - ALANINE RACEMASE		UNCLASSIFIED	264508, 264604, 264605, 264636
370	88090966 (739, 740)	Novel Protein sim. GBank gi|3249559 (AF018261) - EH domain binding protein Epsin [Rattus norvegicus]			264905, 264592, 264605, 264766, 264691
371	95292599 (741, 742)	Novel Protein sim. GBank gi|2995299|emb|CAA18328| - (AL022268) putative tRNA delta(2)-isopentenylpyrophosphate transferase [Streptomyces coelicolor]	Contains protein domain (PF01715) - IPP transferase	transferase	264905, 264908, 264510, 264600, 264601, 264602, 264603, 265018, 264604, 264605, 265021, 264692, 264636, 264564
372	80021107 (743, 744)	Novel Protein sim. GBank gi|2506393|sp|P31576|FIXX_ECOLI - FERREDOXIN LIKE PROTEIN			264564
373	79863766 (745, 746)			UNCLASSIFIED	264909
374	79847568 (747, 748)	Novel Protein sim. GBank gi|3341640|emb|CAA13164| - (AJ231122) z61f [Vibrio cholerae]		UNCLASSIFIED	264905, 264906
375	91230181 (749, 750)	Novel Protein sim. GBank gi|5456934|gb|AAD43716.1| - (AF152322) protocadherin gamma A2 [Homo sapiens]		cadherin	65274572, 264259, 29331826, 56182435, 60433356, 60433438, 264757, 55812038, 264758, 55811957, 264690, 33657023
376	80505214 (751, 752)	Novel Protein sim. GBank gi|1805408|dbj|BAA08970| - (D50453) homologues to nitrile hydratase region 3'-hypothetical protein P47K of P. chlororaphis [Bacillus subtilis]		UNCLASSIFIED	264769
377	10339083 (753, 754)				264906

378	80056153 (755, 756)			UNCLASSIFIED	265008, 264555
379	80503437 (757, 758)	Novel Protein sim. GBank gi|1076013|pir||A49930 - carB protein homolog - Mycobacterium bovis (strain BCG) (fragment)	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	synthase	264769
380	80060937 (759, 760)	Novel Protein sim. GBank gi|216556|dbj|BAA02174| - (D12651) glucose dehydrogenase [Escherichia coli]	Contains protein domain (PF01011) - PQQ enzyme repeat	dehydrogenase	264604
381	11769027 (761, 762)			UNCLASSIFIED	264684
382	80054377 (763, 764)				264592
383	83259025 (765, 766)	Novel Protein sim. GBank gi|3327136|dbj|BAA31636| - (AB014561) KIAA0661 protein [Homo sapiens]			264595, 265017, 265021, 264638, 87168518, 22279002
384	95314255 (767, 768)			UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264288, 264766, 263967, 65274791, 35695855, 263981, 83373044, 264567
385	10237679 (769, 770)				264692
386	79633434 (771, 772)	Novel Protein sim. GBank gi|1073456|pir||S47810 - probable alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	dehydrogenase	264906
387	17960637 (773, 774)	Novel Protein sim. GBank gi|1460074|emb|CAB01049| - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]	Contains protein domain (PF01841) - Transglutaminase-like superfamily	UNCLASSIFIED	264760
388	87741376 (775, 776)	Novel Protein sim. GBank gi|4240169|dbj|BAA74863.1| - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	homeobox	35696286, 264905, 66712502, 60432229, 264593, 60433356, 264686, 264688, 21906765, 264691, 22279000, 264482
389	79316971 (777, 778)			UNCLASSIFIED	18108394, 22278996, 264630, 264556, 22279002
390	80079949 (779, 780)			UNCLASSIFIED	264600
391	7657302 (781, 782)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]			264482
392	79796056 (783, 784)			UNCLASSIFIED	264908
393	33206031 (785, 786)	Novel Protein sim. GBank gi|3378523|emb|CAA08867| - (AJ009832) cyclomaltodextrinase glucanotransferase [Thermotoga neapolitana]		synthase	264602, 21906764
394	10104463 (787, 788)				264693
395	80229010 (789, 790)			UNCLASSIFIED	264508, 264563
396	20436224 (791, 792)	Novel Protein sim. GBank gi|2677780 (U70327) - unknown [Paretroplus polyactis]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	264556
397	80417014 (793, 794)	Novel Protein sim. GBank gi|4507909|ref|NP_000368.1|pWAS| - Wiskott-Aldrich syndrome (eczema-thrombocytopenia)			265007, 265009, 264508, 264556, 264629, 264766
398	91230517 (795, 796)	Novel Protein sim. GBank gi|1518458 (U45998) - mitochondrial solute carrier [Onchocerca volvulus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	18108398, 22278995, 22278996, 56994075, 22278999, 264259, 29331824, 29331826, 264905, 264908, 265007, 265008, 265009, 21906754, 33657084, 265017, 264448, 264288, 264766, 21906765, 21906766, 21906767, 265020, 265021, 33657023, 33657109, 264628, 35696423, 35695855, 264952, 18108380, 264567, 18108391

399	80055278 (797, 798)	Novel Protein sim. GBank gi|3358091|dbj|BAA31995| - (AB015974) glycerol kinase [Pseudomonas tolaasii]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	kinase	264592, 264595
400	94117490 (799, 800)	Novel Protein sim. GBank gi|728835|sp|P39192|ALU5_HUMAN - !!!! ALU SUBFAMILY SC WARNING ENTRY !!!!	Contains protein domain (PF00560) - Leucine Rich Repeat	cadherin	18108394, 56182575, 22278995, 22278997, 22278999, 264259, 29331824, 265006, 265007, 265009, 60432229, 33657402, 21906754, 265010, 265017, 265018, 265019, 18108351, 18108357, 21906765, 265021, 265022, 264691, 264692, 33657023, 18108370, 65274791, 264634, 264636, 60170394, 56182323
401	11397491 (801, 802)	Novel Protein sim. GBank gi|4928292|gb|AAD33527.1|AF13211 - (AF132117) FhuA [Staphylococcus aureus]		transport	264594
402	95420294 (803, 804)	Novel Protein sim. GBank gi|5689487|dbj|BAA83027.1| - (AB028998) KIAA1075 protein [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	phosphatase	65274572, 56182575, 35696286, 22278996, 22278998, 264093, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264906, 264907, 264909, 265006, 264511, 265007, 265008, 264910, 264591, 33657402, 60433356, 60433438, 264596, 21906754, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264681, 18108351, 264682, 264448, 264288, 264684, 264766, 264767, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 264690, 264693, 65274620, 35695763, 264628, 18108370, 264629, 18108379, 35696423, 55811576, 264635, 264636, 264557, 264639, 18108385, 22279002, 264563, 264564, 264565, 264566
403	80439913 (805, 806)			UNCLASSIFIED	264768, 264632, 264639, 264563
404	11809865 (807, 808)				264682
405	79471280 (809, 810)	Novel Protein sim. GBank gi|2661649|emb|CAA15755| - (AL009198) dnaE2 [Mycobacterium tuberculosis]		polymerase	265009, 264682
406	79634172 (811, 812)		Contains protein domain (PF00159) - Pancreatic hormone peptides	UNCLASSIFIED	18108357, 264693
407	80478229 (813, 814)			UNCLASSIFIED	264769
408	80079956 (815, 816)			UNCLASSIFIED	264600
409	5640527 (817, 818)	Novel Protein sim. GBank gi|3047117 (AF058919) - similar to ATP-dependent RNA helicases [Arabidopsis thaliana]		helicase	264259

410	95357496 (819, 820)	Novel Protein sim. GBank gi|475016|dbj|BAA06184| - (D29801) Unknown [Mus musculus]		UNCLASSIFIED	264489, 52646365, 52646842, 56181686, 35696286, 52645080, 29331822, 29331824, 56182181, 29331825, 60424269, 35696052, 33656970, 264508, 264509, 264905, 264906, 264907, 264908, 52644045, 264909, 264510, 265007, 264512, 265008, 264910, 33657402, 264758, 52646317, 55811386, 265010, 265011, 265017, 264604, 265018, 55811150, 264762, 264764, 264766, 264687, 264768, 264769, 52644229, 21906766, 265020, 265021, 264534, 52644150, 264692, 33657023, 65274620, 33657109, 33657182, 27486261, 35695763, 264628, 264629, 60431528, 18108376, 263978, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 56182323, 264559, 60432113, 22279002, 264563, 264565, 264486
411	80501670 (821, 822)			UNCLASSIFIED	264769
412	80241662 (823, 824)				264907, 264910, 263973, 22279002
413	11076446 (825, 826)	Novel Protein sim. GBank gi|3261784|emb|CAB08997| - (Z95558) htpX [Mycobacterium tuberculosis]		eph	264605
414	82050554 (827, 828)	Novel Protein sim. GBank gi|129036|sp|P20707|ODO1_AZOVI - 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE)		dehydrogenase	18108374, 264760, 264769, 264602, 264638, 264603, 264909, 264605
415	84453144 (829, 830)	Novel Protein sim. GBank gi|4868350|gb|AAD31273.1|AF13202 - (AF132025) rhophilin [Drosophila melanogaster]		UNCLASSIFIED	264908, 87168518
416	80402775 (831, 832)	Novel Protein sim. GBank gi|2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium etli]		kinase	264488, 264600, 264602, 264764, 264636
417	20153797 (833, 834)	Novel Protein sim. GBank gi|1709171|sp|P52311|MTX2_XANOR - MODIFICATION METHYLASE XORII (CYTOSINE-SPECIFIC METHYLTRANSFERASE XORII) (M.XORII)	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase		264605
418	94125841 (835, 836)			UNCLASSIFIED	264689, 264693
419	95314273 (837, 838)			collagen	264908, 264910, 264764, 264639
420	37036349 (839, 840)	Novel Protein sim. GBank gi|3261659|emb|CAB03751| - (Z81368) hypothetical protein Rv2419c [Mycobacterium tuberculosis]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	phosphatase	264769
421	95292942 (841, 842)	Novel Protein sim. GBank gi|2916942|emb|CAA17580| - (AL021999) hypothetical protein Rv0981 [Mycobacterium tuberculosis]	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	264906, 264600, 264601, 264603, 264604, 264760, 264769
422	79471293 (843, 844)	Novel Protein sim. GBank gi|231752|sp|Q00767|CH61_STRAL - 60 KD CHAPERONIN 1 (PROTEIN CPN60 1) (GROEL PROTEIN 1) (HSP58)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	eph	22278996, 264682, 18108376, 18108387
423	79604948 (845, 846)			UNCLASSIFIED	264509

424	78966557 (847, 848)	Novel Protein sim. GBank gi|4826814|ref|NP_004977.1|pKTN1 - kinectin 1 (kinesin receptor)		struct	265019
425	80431450 (849, 850)	Novel Protein sim. GBank gi|1703701|bbs|178462 - KRP5=kinesin-related protein [rats, testes, Peptide Partial, 167 aa]	Contains protein domain (PF00225) - Kinesin motor domain	struct	264909, 265007, 55811386, 264768, 55810764
426	80064522 (851, 852)				264605, 264559
427	80057232 (853, 854)	Novel Protein sim. GBank gi|231829|sp|P29929|COBN_PSEDE - COBN PROTEIN		UNCLASSIFIED	264603, 264636
428	79487798 (855, 856)			UNCLASSIFIED	264683
429	80091252 (857, 858)	Novel Protein sim. GBank gi|81286|pir||S22697 - extensin - Volvox carteri (fragment)		UNCLASSIFIED	35696423, 35695763, 35695855, 265017, 264564, 264762
430	80504192 (859, 860)	Novel Protein sim. GBank gi|1806154|emb|CAB06451| - (Z84395) hypothetical protein Rv0688 [Mycobacterium tuberculosis]		reductase	264508, 264905, 264509, 264908, 264909, 265008, 264600, 264687, 264769, 264689, 264636, 264638, 18108385, 264486
431	20624249 (861, 862)				264566
432	16525372 (863, 864)				265020
433	81494303 (865, 866)	Novel Protein sim. GBank gi|3123552|emb|CAA18609| - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]		UNCLASSIFIED	264907, 264908, 264909, 264910, 264592, 264595, 264758, 264604, 264760, 264762, 264763, 264636, 264637, 22279002
434	94326323 (867, 868)	Novel Protein sim. GBank gi|2495272|sp|Q99626|CDX2_HUMAN - HOMEOBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEOBOX PROTEIN 2) (CDX-3)	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	55812038, 56182181, 56181562, 29331828, 35696052, 55810764, 55811576, 65274791, 35695855, 60432113, 55811150, 264636, 264766
435	80502738 (869, 870)	Novel Protein sim. GBank gi|114105|sp|P08532|ARAH_ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH		transport	264595, 264769
436	41085953 (871, 872)			UNCLASSIFIED	265020, 22279002
437	11399291 (873, 874)			UNCLASSIFIED	264593
438	11773835 (875, 876)			UNCLASSIFIED	264686
439	80019495 (877, 878)	Novel Protein sim. GBank gi|3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana]			264905, 264600, 264602, 264604
440	79841062 (879, 880)	Novel Protein sim. GBank gi|2291232|gb|AAB65351.1| - (AF016427) Contains similarity to Pfam domain: PF00004 (AAA), Score=268.1, E-value=3.7e-77, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00004) - ATPases associated with various cellular activities (AAA)	ATPase_associated	35696052, 264905, 264908, 264909, 265011, 35698423
441	20396935 (881, 882)	Novel Protein sim. GBank gi|5639946|gb|AAD45904.1|AF16132 - (AF161328) histidine kinase CstS [Corynebacterium diphtheriae]			264605
442	85281058 (883, 884)	Novel Protein sim. GBank gi|1184790 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264909
443	82456427 (885, 886)	Novel Protein sim. GBank gi|5689893|emb|CAB52056.1| - (AL109732) putative ATP-binding RNA helicase [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	35696052, 264508, 264906, 264512, 264604, 264762, 264769, 264689, 264636
444	11395897 (887, 888)	Novel Protein sim. GBank gi|1783249|dbj|BAA11726| - (D83026) homologous to citrate-sodium symport (citrate transporters); hypothetical [Bacillus subtilis]		UNCLASSIFIED	264591

445	79552709 (889, 890)			UNCLASSIFIED	264693
446	79810937 (891, 892)	Novel Protein sim. GBank gi|5531272|emb|CAB50897.1| - (AJ243800) WSC4 homologue [Kluyveromyces lactis]			264509
447	80438888 (893, 894)	Novel Protein sim. GBank gi|538413 (L36315) - zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264768, 55811576
448	80238110 (895, 896)	Novel Protein sim. GBank gi|1542914|emb|CAB02185| - (Z80108) fmt [Mycobacterium tuberculosis]	Contains protein domain (PF00551) - Formyl transferase	dehydrogenase	264508, 264600, 264603, 264605, 264682, 264769, 18108362, 264634, 18108387
449	20460634 (897, 898)	Novel Protein sim. GBank gi|118794|sp|P10443|DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	264605, 264559
450	94631210 (899, 900)	Novel Protein sim. GBank gi|4589506|dbj|BAA76775.1| - (AB023148) KIAA0931 protein [Homo sapiens]	Contains protein domain (PF00481) - Protein phosphatase 2C	phosphatase	65274572, 22278998, 29331824, 29331826, 264906, 264910, 264592, 52646317, 265017, 21906767, 55811957, 56526486, 22279002
451	21433609 (901, 902)			UNCLASSIFIED	264486
452	10267276 (903, 904)				264692
453	52560096 (905, 906)	Novel Protein sim. GBank gi|2650614 (AE001104) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	264907, 264600
454	39523922 (907, 908)	Novel Protein sim. GBank gi|2493000|sp|Q09450|SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)		transferase	264603
455	13089692 (909, 910)			UNCLASSIFIED	264687
456	79563081 (911, 912)			UNCLASSIFIED	264691
457	79831273 (913, 914)	Novel Protein sim. GBank gi|4468699|emb|CAB38153.1| - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]			264905
458	79581227 (915, 916)	Novel Protein sim. GBank gi|3411053 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	55812038, 265010, 265018, 264681
459	80567359 (917, 918)	Novel Protein sim. GBank gi|4506075|ref|NP_002733.1|pPRKC - protein kinase C, mu	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	22278997, 264259, 29331826, 265018, 264448, 264369, 21906765, 35696423
460	79245890 (919, 920)	Novel Protein sim. GBank gi|113158|sp|P25516|ACO1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO-LYASE 1) (ACONITASE 1)		UNCLASSIFIED	264906
461	95287618 (921, 922)	Novel Protein sim. GBank gi|1168574|sp|P42464|ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	264602, 264605, 264768, 264769, 265021, 33657023, 264559

462	79606589 (923, 924)	Novel Protein sim. GBank gi|1346891|sp|P45597|PTF1_XANCP - MULTIPHOSPHORYL TRANSFER PROTEIN (MTP) (CONTAINS: PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I); PHOSPHOCARRIER PROTEIN HPR (PROTEIN H); PTS SYSTEM, FRUCTOSE-SPECIFIC IIA COMPONENT ...	Contains protein domain (PF00391) - PEP-utilizing enzymes	UNCLASSIFIED	264907
463	79796417 (925, 926)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264905, 264906, 264908, 264909, 264910, 264591, 264595, 265011, 264632, 264635, 264636, 264637, 264638, 264639
464	82340151 (927, 928)			UNCLASSIFIED	264634
465	83005730 (929, 930)	Novel Protein sim. GBank gi|5689776|emb|CAB52137.1| - (AJ242832) calpain [Homo sapiens]	Contains protein domain (PF00648) - Calpain family cysteine protease	cathepsin	265017, 21906764, 265020
466	20460645 (931, 932)	Novel Protein sim. GBank gi|1806175|emb|CAB06470| - (Z84395) rpsC [Mycobacterium tuberculosis]	Contains protein domain (PF00417) - Ribosomal protein S3, N-terminal domain.	ribosomalprot	264605, 264559
467	80409035 (933, 934)	Novel Protein sim. GBank gi|543705|sp|P36949|RBSB_BACSU - D-RIBOSE-BINDING PROTEIN PRECURSOR		UNCLASSIFIED	264764
468	52562208 (935, 936)			UNCLASSIFIED	264692
469	19520527 (937, 938)	Novel Protein sim. GBank gi|2114024|emb|CAB08957| - (Z95558) grcC1 [Mycobacterium tuberculosis]		UNCLASSIFIED	264488
470	80502756 (939, 940)	Novel Protein sim. GBank gi|2909459|emb|CAA17347| - (AL021929) cobQ [Mycobacterium tuberculosis]		synthase	264602, 264769
471	17937351 (941, 942)	Novel Protein sim. GBank gi|114921|sp|P17447|BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN		transport	265019
472	80047458 (943, 944)				264596, 264685, 264557
473	20558793 (945, 946)	Novel Protein sim. GBank gi|862343 (L10908) - Gcap1 gene product [Mus musculus]		UNCLASSIFIED	264369
474	80593365 (947, 948)			UNCLASSIFIED	22278997, 264692, 264288
475	82454665 (949, 950)			UNCLASSIFIED	264907, 264908, 264511, 265009, 264762, 264448, 264636, 264638
476	94143857 (951, 952)	Novel Protein sim. GBank gi|5453656|ref|NP_006329.1|pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	65274572, 60432049, 264259, 264508, 52644045, 55812038, 264758, 265011, 264288, 264686, 52644229, 65274791, 264638, 264566
477	79175833 (953, 954)			UNCLASSIFIED	264636
478	79633483 (955, 956)			UNCLASSIFIED	264690, 264693
479	80189746 (957, 958)			collagen	264686, 35695855, 265008, 264631, 264910, 264632, 264638, 265018, 264369, 264909
480	79390729 (959, 960)	Novel Protein sim. GBank gi|1127551 (U18939) - orf2 [Battrachocottus baikalensis]		mapolymerase	264369
481	79624578 (961, 962)			UNCLASSIFIED	264693
482	83050611 (963, 964)	Novel Protein sim. GBank gi|4063042 (AF068065) - GP900; mucin-like glycoprotein [Cryptosporidium parvum]		UNCLASSIFIED	264909, 264686, 264768, 264693, 55811576, 56182323, 18108385

483	20293306 (965, 966)	Novel Protein sim. GBank gi|2104303|emb|CAB08632| - (Z95387) hypothetical protein Rv2610c [Mycobacterium tuberculosis]	Contains protein domain (PF00534) - Glycosyl transferases group 1		264600
484	11618046 (967, 968)	Novel Protein sim. GBank gi|3450883 (AF083334) - fibroin [Antheraea pernyi]		UNCLASSIFIED	264594
485	80191234 (969, 970)			UNCLASSIFIED	264369, 21906765, 22279000, 22279002
486	80059042 (971, 972)	Novel Protein sim. GBank gi|5042272|emb|CAB44526.1| - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]		dehydrogenase	264604
487	11813339 (973, 974)				264638
488	91222383 (975, 976)	Novel Protein sim. GBank gi|5724778|gb|AAC53522.2| - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]	Contains protein domain (PF00620) - RhoGAP domain		264686, 66714117, 264768, 18108385, 55811576, 265008, 265008, 265009, 265019, 22279002, 264259, 18108370, 264907, 264764, 56182323, 264288, 264693
489	10867710 (977, 978)	Novel Protein sim. GBank gi|3882223|dbj|BAA34471.1| - (AB018294) KIAA0751 protein [Homo sapiens]		kinase	264639
490	95361124 (979, 980)	Novel Protein sim. GBank gi|82091|pir||A25494 - hydroxyproline-rich glycoprotein - tomato (fragment)		collagen	22278996, 29331822, 29331828, 264107, 264909, 264110, 265009, 264592, 264593, 60433356, 264288, 264693, 263974, 263976, 20281071, 60432113
491	80496412 (981, 982)	Novel Protein sim. GBank gi|2894206|emb|CAA17072| - (AL021840) hypothetical protein Rv3258c [Mycobacterium tuberculosis]		UNCLASSIFIED	264769
492	87421264 (983, 984)				264600
493	11692942 (985, 986)			UNCLASSIFIED	264638
494	87726604 (987, 988)	Novel Protein sim. GBank gi|5262605|emb|CAB45743.1| - (AL080150) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264489, 35696286, 60432289, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 33657402, 264762, 264764, 264768, 264769, 264688, 21906765, 21906769, 35695917, 265020, 264693, 33657109, 264629, 35696423, 35695855, 264634, 264638
495	80028599 (989, 990)	Novel Protein sim. GBank gi|2791517|emb|CAA16054| - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]	Contains protein domain (PF00005) - ABC transporter	transport	264602, 264682, 264638
496	78985624 (991, 992)	Novel Protein sim. GBank gi|230281|pdb|1R69| - 434 Repressor (Amino-Terminal Domain) (R1-69)	Contains protein domain (PF01381) - Helix-turn-helix		264601, 265021
497	78949661 (993, 994)	Novel Protein sim. GBank gi|129736|sp|P28225|PDXH_ECOLI - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDASE)		oxidase	265006

498	88095488 (995, 996)	Novel Protein sim. GBank gi|1145789 (U41662) - neuroligin 2 [Rattus norvegicus]	Contains protein domain (PF00135) - Carboxylesterases	esterase	264259, 29331826, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264591, 33657402, 264758, 265010, 265011, 264600, 264601, 264605, 264683, 264764, 264766, 264767, 264768, 264687, 264769, 21906767, 33657023, 264693, 264628, 264629, 35696423, 264630, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 18108385, 264563, 264564, 264565, 264566, 264567
499	20438222 (997, 998)	Novel Protein sim. GBank gi|97480|pir||S19739 - integral membrane protein - Rhodobacter capsulatus		UNCLASSIFIED	264605
500	11076810 (999, 1000)				264605
501	13418034 (1001, 1002)	Novel Protein sim. GBank gi|5708250|emb|CAB52363.1| - (AL109747) putative integral membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264688
502	80021176 (1003, 1004)	Novel Protein sim. GBank gi|4468678|emb|CAB38132.1| - (AL035591) glucose-6-phosphate isomerase [Streptomyces coelicolor]	Contains protein domain (PF00342) - Phosphoglucose isomerase	isomerase	22278996, 265011, 264602, 264605, 264635
503	20264483 (1005, 1006)			UNCLASSIFIED	264564
504	10887321 (1007, 1008)			UNCLASSIFIED	264687
505	95003068 (1009, 1010)			UNCLASSIFIED	264369
506	16454292 (1011, 1012)	Novel Protein sim. GBank gi|4033509|sp|P02598|CALM_TETPY - CALMODULIN	Contains protein domain (PF00036) - EF hand	struct	265010
507	20451598 (1013, 1014)	Novel Protein sim. GBank gi|2501069|sp|Q46127|SYW_CLOLO - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN--TRNA LIGASE) (TRPRS)		UNCLASSIFIED	264604
508	79841424 (1015, 1016)	Novel Protein sim. GBank gi|466068|sp|P34618|YO82_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN ZK1236.2 IN CHROMOSOME III		UNCLASSIFIED	264908
509	11776386 (1017, 1018)				264638
510	83373465 (1019, 1020)			UNCLASSIFIED	264687, 264639
511	16525578 (1021, 1022)				265007
512	20399484 (1023, 1024)	Novel Protein sim. GBank gi|2497419|sp|P55635|Y4RB_RHISN - PUTATIVE INTEGRASE/RECOMBINASE Y4RB		UNCLASSIFIED	264565
513	79457404 (1025, 1026)	Novel Protein sim. GBank gi|1276897 (U41809) - cyclin J [Drosophila melanogaster]	Contains protein domain (PF00134) - Cyclin	cyclin	264683, 264689, 35696423, 264639
514	79813805 (1027, 1028)	Novel Protein sim. GBank gi|1184790 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264909
515	79462591 (1029, 1030)				22278999, 264690
516	9862020 (1031, 1032)	Novel Protein sim. GBank gi|2127400|pir||S65770 - maltooligosyltrehalose trehalohydrolase - Arthrobacter sp. (strain Q36)		amylase	264910

517	95292994 (1033, 1034)	Novel Protein sim. GBank gi|2983605 (AE000725) - ribose 5 phosphate isomerase B [Aquifex aeolicus]		isomerase	265018, 264605, 264764, 264766, 264687, 264691, 264565
518	8491831 (1035, 1036)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264487
519	91677886 (1037, 1038)	Novel Protein sim. GBank gi|5689365|dbj|BAA83073.1| - (AB024075) B120 [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	dna_rna_bind	52644507, 22278997, 22278998, 60432049, 264259, 52645080, 29331824, 66714117, 60424269, 29331826, 35696052, 264905, 29331830, 66712502, 264511, 265007, 264591, 60432229, 33657402, 60433438, 21906754, 33109954, 52644296, 87168474, 87168559, 265017, 265018, 264604, 265019, 264681, 264448, 264369, 264288, 264685, 21906765, 21906766, 21906767, 21906769, 265021, 60170615, 33657023, 264692, 52645129, 33657109, 27486262, 27486264, 35695763, 18108370, 264629, 52644332, 56182323, 264639, 83373044, 18108385, 56526486, 60432113
520	79869188 (1039, 1040)				264769
521	11076821 (1041, 1042)	Novel Protein sim. GBank gi|1169126|sp|P46839|CTPA_MYCLE - CATION-TRANSPORTING P-TYPE ATPASE A		transport	264605
522	80435060 (1043, 1044)	Novel Protein sim. GBank gi|1172869|sp|P44331|RBSK_HAEIN - RIBOKINASE	Contains protein domain (PF00294) - pfkB family carbohydrate kinase	kinase	264905, 264768
523	18356013 (1045, 1046)	Novel Protein sim. GBank gi|2132243|pir||S61028 - hypothetical protein YPL236c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	264629
524	80261805 (1047, 1048)	Novel Protein sim. GBank gi|4033608|dbj|BAA35136| - (AB012308) B2HC [Anthocidaris crassispina]		ATPase_associated	264092, 264596, 265011
525	79610046 (1049, 1050)				264907
526	36827630 (1051, 1052)	Novel Protein sim. GBank gi|4106610|emb|CAA21365| - (AL031866) ORF42, len=386 aa , similarity to an aminotransferase, in P95957 Sulfolobus solfataricus, (401 aa), 33.1% identity in 393 aa overlap, Fasta scores: opt:468, E(): 8.5e-24, in Q64602 R. norvegicus,(425 aa), 28.6% ident...		UNCLASSIFIED	264758
527	80504729 (1053, 1054)			UNCLASSIFIED	264769
528	65484134 (1055, 1056)			UNCLASSIFIED	56182575, 265017, 265018
529	17936810 (1057, 1058)	Novel Protein sim. GBank gi|731088|sp|P24215|UXUA_ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)		hydrolase	265019
530	10887336 (1059, 1060)	Novel Protein sim. GBank gi|42144|emb|CAA25200| - (X00513) NusA protein (nusA) [Escherichia coli]		UNCLASSIFIED	264687
531	80226576 (1061, 1062)			UNCLASSIFIED	264555, 264556, 264557, 264558, 18108385
532	90933444 (1063, 1064)	Novel Protein sim. GBank gi|5262640|emb|CAB45758.1| - (AL080170) hypothetical protein [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264488, 264490, 264259, 264592, 264760, 265021, 264690, 263976, 264558

533	87761531 (1065, 1066)	Novel Protein sim. GBank gi|4883636|gb|AAD31593.1|AF11229 - (AF112299) integral inner nuclear membrane protein MAN1 [Homo sapiens]			264907, 264909, 264768, 35695917, 264630, 264555
534	82368264 (1067, 1068)	Novel Protein sim. GBank gi|2995352|emb|CAA04606.1| - (AJ001206) pep1 [Streptomyces coelicolor]		UNCLASSIFIED	264905, 265011, 264601, 264602, 264605, 264762, 264768, 265020, 264693, 264836
535	79641850 (1069, 1070)	Novel Protein sim. GBank gi|3878636|emb|CAA88953| - (Z49128) similar to cAMP-dependant protein kinase; cDNA EST EMBL:T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk492f4.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	ATPase_associated	264906
536	79907207 (1071, 1072)	Novel Protein sim. GBank gi|2495628|sp|P55757|YOHL_SERMA - HYPOTHETICAL 10.1 KD PROTEIN IN BIOA 5'REGION		reductase	18108376, 264905, 264906, 264907, 264909
537	94147448 (1073, 1074)				265008, 264605, 65274791
538	87821963 (1075, 1076)	Novel Protein sim. GBank gi|134920|sp|P21997|SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	collagen	29331822, 29331824, 29331825, 29331826, 29331827, 264908, 52644045, 33657402, 265017, 264762, 264883, 264288, 264685, 21906765, 35695763, 264558, 60170394, 264559, 22279002
539	28396269 (1077, 1078)	Novel Protein sim. GBank gi|2498433|sp|Q12341|HAT1_YEAST - HISTONE ACETYLTRANSFERASE		histone	264602, 265019
540	79637077 (1079, 1080)				264693
541	87762268 (1081, 1082)	Novel Protein sim. GBank gi|3882241|dbj|BAA34480.1| - (AB018303) KIAA0760 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	18108394, 22278997, 22278998, 264259, 264112, 265009, 33657402, 55812038, 52646317, 265017, 21906765, 264693, 55811576, 264635, 56526486, 264566
542	95295836 (1083, 1084)	Novel Protein sim. GBank gi|5042272|emb|CAB44526.1| - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]		dehydrogenase	264910, 265018, 264689, 264638, 264486
543	79796290 (1085, 1086)			UNCLASSIFIED	264602, 264908
544	20437191 (1087, 1088)	Novel Protein sim. GBank gi|2791398|emb|CAA15994| - (AL021184) hypothetical protein Rv1464 [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
545	80434504 (1089, 1090)				264768, 264634, 264907, 264592, 264909
546	80249016 (1091, 1092)	Novel Protein sim. GBank gi|4887211|gb|AAD32237.1|AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]			264600, 264602, 21906765
547	11077563 (1093, 1094)	Novel Protein sim. GBank gi|1350855|sp|P19176|RPOC_PSEPU - DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT)		rnapolymerase	264604
548	82114936 (1095, 1096)	Novel Protein sim. GBank gi|2330021 (AF019250) - kinesin-related protein; KRP; Costal2 [Drosophila melanogaster]		UNCLASSIFIED	264488, 264905, 264910, 264760, 264693, 264639, 264563, 264564

549	95421904 (1097, 1098)	Novel Protein sim. GBank gi|4337460|gb|AAD18133| - (AF056195) neuroblastoma-amplified protein [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 18108398, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 29331826, 35696052, 265007, 265008, 264910, 264592, 33657402, 33109954, 265017, 265018, 265019, 18108351, 264448, 264764, 264369, 264288, 264766, 264686, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264691, 33657023, 264692, 264693, 65274620, 52645129, 33657109, 27486261, 27486262, 27486264, 33657349, 55811576, 18108387, 60432113, 22279002
550	10886616 (1099, 1100)				264688
551	80439990 (1101, 1102)	Novel Protein sim. GBank gi|3122893|sp|P94985|SYFB_MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)		UNCLASSIFIED	264908, 264909, 264768
552	94672870 (1103, 1104)			UNCLASSIFIED	264689, 264639, 264563
553	80106002 (1105, 1106)	Novel Protein sim. GBank gi|552087 (M33753) - crumbs protein [Drosophila melanogaster]	Contains protein domain (PF00008) - EGF-like domain	glycoprotein	55811957, 264628
554	79618379 (1107, 1108)	Novel Protein sim. GBank gi|5019771|gb|AAD37857.1|AF13326 - (AF133263) histidine protein kinase-response regulator hybrid protein CvgSY [Pseudomonas syringae pv. syringae]		kinase	264906
555	78996347 (1109, 1110)	Novel Protein sim. GBank gi|131515|sp|P02908|PTGA_SALTY - PTS SYSTEM, GLUCOSE-SPECIFIC IIA COMPONENT (EIIA-GLC) (GLUCOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIII-GLC)	Contains protein domain (PF00358) - phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1	transport	264762
556	20457127 (1111, 1112)	Novel Protein sim. GBank gi|3914014|sp|P96380|MFD_MYCTU - TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)		transcriptfactor	264508, 264605, 264559
557	19523405 (1113, 1114)	Novel Protein sim. GBank gi|5042273|emb|CAB44527.1| - (AL078618) nuoE, NADH dehydrogenase subunit [Streptomyces coelicolor]		dehydrogenase	264488
558	20724429 (1115, 1116)	Novel Protein sim. GBank gi|1170933|sp|P45331|METE_HAEIN - 5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)		UNCLASSIFIED	264602
559	80084353 (1117, 1118)	Novel Protein sim. GBank gi|4980567|gb|AAD35173.1|AE00169 - (AE001694) iron(III) ABC transporter, permease protein [Thermotoga maritima]		UNCLASSIFIED	264634

560	80066533 (1119, 1120)	Novel Protein sim. GBank gi|2492595|sp|Q53193|Y4TR_RHISN - PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TR	Contains protein domain (PF00005) - ABC transporter	transport	18108396, 264906, 264602, 264604, 18108374
561	20293187 (1121, 1122)			UNCLASSIFIED	264600
562	11698161 (1123, 1124)			UNCLASSIFIED	264689
563	79761420 (1125, 1126)	Novel Protein sim. GBank gi|4104925 (AF042276) - poly(hydroxyalcanoate) granule associated protein GA2 [Pseudomonas putida]		UNCLASSIFIED	264910, 264691
564	56716390 (1127, 1128)	Novel Protein sim. GBank gi|2792310 (AF040570) - unknown [Amycolatopsis mediterranei]		dehydrogenase	264592
565	56465618 (1129, 1130)	Novel Protein sim. GBank gi|3449294|dbj|BAA32462| - (AB011532) MEGF6 [Rattus norvegicus]	Contains protein domain (PF00008) - EGF-like domain	synthase	265010
566	94323888 (1131, 1132)	Novel Protein sim. GBank gi|4539568|emb|CAB38487.1| - (AL035636) putative helicase [Streptomyces coelicolor]		helicase	264909, 264510, 265008, 264910, 264758, 264600, 264602, 264604, 264605, 264768, 264687, 264689, 35695917, 264693, 65274620, 264486
567	79560955 (1133, 1134)			UNCLASSIFIED	264681, 264691, 264593
568	94681793 (1135, 1136)	Novel Protein sim. GBank gi|100506|pir||S17455 - Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flaveria trinervia (fragment)	Contains protein domain (PF00390) - Malic enzyme	dehydrogenase	264689
569	39506897 (1137, 1138)	Novel Protein sim. GBank gi|3915843|sp|O31212|RS2_STRCO - 30S RIBOSOMAL PROTEIN S2	Contains protein domain (PF00318) - Ribosomal protein S2	ribosomalprot	264565
570	78375927 (1139, 1140)			UNCLASSIFIED	18108376, 18108387, 264565
571	79793961 (1141, 1142)	Novel Protein sim. GBank gi|115122|sp|P21627|BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD		transport	264907, 264909
572	36996838 (1143, 1144)			UNCLASSIFIED	264762
573	20715521 (1145, 1146)	Novel Protein sim. GBank gi|4539223|emb|CAB39881.1| - (AL049497) putative integral membrane protein [Streptomyces coelicolor]		UNCLASSIFIED	265007, 264601
574	13521592 (1147, 1148)				264636
575	13076416 (1149, 1150)	Novel Protein sim. GBank gi|118794|sp|P10443|DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	264687
576	20482246 (1151, 1152)	Novel Protein sim. GBank gi|5457625|emb|CAB49116.1| - (AJ248283) PAB2227 [Pyrococcus abyssi]			264605
577	66727 ,02 (1153, 1154)	Novel Protein sim. GBank gi|5042274|emb|CAB44528.1| - (AL078618) nuoD, NADH dehydrogenase subunit [Streptomyces coelicolor]	Contains protein domain (PF00346) - Respiratory-chain NADH dehydrogenase, 49 Kd subunit	dehydrogenase	35696052, 264636
578	11804477 (1155, 1156)				264638
579	11794723 (1157, 1158)	Novel Protein sim. GBank gi|1723081|sp|Q11046|Y089_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.09		transport	264682, 264556

580	80059417 (1159, 1160)				22278999, 35696052, 264555, 264556, 264558
581	79230833 (1161, 1162)			UNCLASSIFIED	265008, 264564
582	80049617 (1163, 1164)	Novel Protein sim. GBank gi|3243131 (AF045777) - titin [Drosophila melanogaster]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	265021, 264555, 264557
583	79321392 (1165, 1166)	Novel Protein sim. GBank gi|2501162|sp|P77726|YAJR_ECOLI - HYPOTHETICAL 49.0 KD PROTEIN IN ABPA-CYOE INTERGENIC REGION		transport	264594
584	79845024 (1167, 1168)			UNCLASSIFIED	264488, 264906, 264766, 264687, 35696423
585	79581454 (1169, 1170)	Novel Protein sim. GBank gi|3882221|dbj|BAA34470.1| - (AB018293) KIAA0750 protein [Homo sapiens]		UNCLASSIFIED	265018, 264684, 21906769
586	38277486 (1171, 1172)			UNCLASSIFIED	264908, 265007
587	80497359 (1173, 1174)	Novel Protein sim. GBank gi|4467250|emb|CAB37575| - (AL035569) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]		hydrolase	264600, 264602, 264605, 264769, 264690, 264557
588	79557239 (1175, 1176)	Novel Protein sim. GBank gi|5689519|dbj|BAA83043.1| - (AB029014) KIAA1091 protein [Homo sapiens]		UNCLASSIFIED	265020, 264692
589	79805828 (1177, 1178)			UNCLASSIFIED	22278996, 264907, 264909, 264510, 265009, 265010, 264687, 264769, 35695917, 18108376, 264634, 264636, 264638
590	79815629 (1179, 1180)			UNCLASSIFIED	264906, 264909
591	10313540 (1181, 1182)	Novel Protein sim. GBank gi|2143293|emb|CAB09390| - (Z95972) rpoB [Mycobacterium tuberculosis]		mapolymerase	264691
592	13889767 (1183, 1184)			MHC	263972
593	82348699 (1185, 1186)	Novel Protein sim. GBank gi|4511983|gb|AAD21543.1| - (AF088896) electrotransfer ubiquinone oxidoreductase [Zymomonas mobilis]		dehydrogenase	264511, 264762, 264769, 264486
594	20212392 (1187, 1188)	Novel Protein sim. GBank gi|1272368 (U51896) - LfgE [Vibrio parahaemolyticus]		UNCLASSIFIED	264605
595	10064064 (1189, 1190)	Novel Protein sim. GBank gi|131490|sp|P20966|PTFB_ECOLI - PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU) (FRUCTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-FRU)			264769
596	13085170 (1191, 1192)			UNCLASSIFIED	264636
597	80259003 (1193, 1194)			UNCLASSIFIED	264592
598	94140216 (1195, 1196)			UNCLASSIFIED	264758, 55810764, 264555, 264556, 264637, 83373044
599	20385137 (1197, 1198)	Novel Protein sim. GBank gi|125329|sp|P04951|KDSB_ECOLI - 3-DEOXY-MANNO-OCTULOSONATE CYTIDYLYLTRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS)		UNCLASSIFIED	264603
600	10357663 (1199, 1200)				264906
601	79610404 (1201, 1202)	Novel Protein sim. GBank gi|2127414|pir||S60064 - hypothetical protein 2 - Corynebacterium glutamicum		UNCLASSIFIED	264510

602	79250602 (1203, 1204)	Novel Protein sim. GBank gi|3522961|gb|AAC34243.1| - (AC004411) putative pto kinase [Arabidopsis thaliana]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	265007
603	11466067 (1205, 1206)			UNCLASSIFIED	264595
604	81675420 (1207, 1208)				264758
605	20436657 (1209, 1210)	Novel Protein sim. GBank gi|1175322|sp|P44917|Y883_HAEIN - HYPOTHETICAL PROTEIN HI0883		UNCLASSIFIED	264605
606	80334582 (1211, 1212)	Novel Protein sim. GBank gi|5020264|gb|AAD38043.1|AF15136 - (AF151363) Cdc42 GTPase-activating protein [Mus musculus]		UNCLASSIFIED	264764
607	95361506 (1213, 1214)	Novel Protein sim. GBank gi|188864 (M74027) - mucin [Homo sapiens]		UNCLASSIFIED	264508, 264906, 85658542, 264682, 264687, 264689, 264534, 18108376, 35696423, 264636, 264555, 264638
608	11810888 (1215, 1216)			UNCLASSIFIED	264682
609	80064775 (1217, 1218)	Novel Protein sim. GBank gi|2496701|sp|P55562|Y4LL_RHISN - HYPOTHETICAL 91.8 KD PROTEIN Y4LL	Contains protein domain (PF00989) - PAS domain	UNCLASSIFIED	264605
610	79629413 (1219, 1220)				264692
611	87586205 (1221, 1222)				264508, 264905, 264907, 264908, 264909, 264511, 264910, 264758, 264604, 264684, 264766, 264689, 264692, 264628, 264635, 264636, 264637, 264558
612	95287851 (1223, 1224)	Novel Protein sim. GBank gi|1877366|emb|CAB07118| - (Z92772) recD [Mycobacterium tuberculosis]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	nuclease	264600, 264601, 264604, 264769, 264558, 264565
613	7523475 (1225, 1226)			UNCLASSIFIED	264369
614	79969348 (1227, 1228)	Novel Protein sim. GBank gi|5114231|gb|AAD40238.1|AF13670 - (AF136709) histidine kinase YycG [Staphylococcus aureus]		kinase	18108372, 264563
615	39586998 (1229, 1230)	Novel Protein sim. GBank gi|1339950|dbj|BAA12741| - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]		synthase	264600, 264602, 264629
616	20465331 (1231, 1232)	Novel Protein sim. GBank gi|544367|sp|P35673|GALE_ERWAM - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	264605
617	91227222 (1233, 1234)	Novel Protein sim. GBank gi|2498097|sp|Q60769|TNP3_MOUSE - TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20)	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	tnf	52645156, 21906765, 35696423, 21906768, 21906769, 22278994, 35696286, 22278998, 265020, 265021, 265007, 265008, 264636, 52644150, 33657023, 264692, 264693, 29331822, 29331824, 55812038, 83373044, 56182181, 60424269, 66714117, 29331825, 33657109, 29331826, 33657182, 29331827, 35696052, 29331828, 27486262, 33657349, 56526486, 265018, 265019, 22279002, 264482, 264448, 29331830, 66712502, 264909

618	20632843 (1235, 1236)	Novel Protein sim. GBank gi|5459386|emb|CAB50746.1| - (AL096839) putative aminotransferase [Streptomyces coelicolor]		isomerase	264603
619	91227224 (1237, 1238)				56994075, 29331826, 33656970, 265008, 33657402, 33109954, 87168559, 264448, 18108374, 83373044
620	81183143 (1239, 1240)	Novel Protein sim. GBank gi|464335|sp|Q05922|DUS2_MOUSE - DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 (DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1)		phosphatase	29148498, 264758, 264369, 29148627
621	80239251 (1241, 1242)			UNCLASSIFIED	264556, 264558, 264639
622	20456427 (1243, 1244)	Novel Protein sim. GBank gi|2633557|emb|CAB13060| - (Z99110) yjdF [Bacillus subtilis]		UNCLASSIFIED	264605
623	10131798 (1245, 1246)	Novel Protein sim. GBank gi|1857710|gb|AAB48482| - (U87224) contactin associated protein [Rattus norvegicus]	Contains protein domain (PF00054) - Laminin G domain	laminin	264906
624	19534127 (1247, 1248)	Novel Protein sim. GBank gi|1705703|sp|P52225|CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK		cytochrome	264596
625	13084619 (1249, 1250)	Novel Protein sim. GBank gi|2894252|emb|CAA17114.1| - (AL021841) hypothetical protein Rv3342 [Mycobacterium tuberculosis]		UNCLASSIFIED	264688
626	88062603 (1251, 1252)	Novel Protein sim. GBank gi|416592|sp|P32323|AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	29331822, 264905, 264908, 33657023, 33657109, 264558
627	80255457 (1253, 1254)	Novel Protein sim. GBank gi|3098418 (AF040944) - P140 [Mus musculus]		UNCLASSIFIED	18108394, 264112, 264593, 265022, 264635
628	80077096 (1255, 1256)	Novel Protein sim. GBank gi|1711543|sp|P50526|SSP1_SCHPO - SERINE/THREONINE-PROTEIN KINASE SSP1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264600
629	79851602 (1257, 1258)	Novel Protein sim. GBank gi|1143204 (U34305) - ORF2; Method: conceptual translation supplied by author. [Shigella sonnei]		isomerase	264906, 264907
630	39565156 (1259, 1260)	Novel Protein sim. GBank gi|3236368 (AF064748) - S3-12 [Mus musculus]		UNCLASSIFIED	264490
631	20598718 (1261, 1262)	Novel Protein sim. GBank gi|140687|sp|P11666|YGGB_ECOLI - HYPOTHETICAL 30.9 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 4) (F286)			263978
632	27843890 (1263, 1264)			UNCLASSIFIED	264906, 264600, 264605, 264769, 264689, 264486
633	80477772 (1265, 1266)			UNCLASSIFIED	264769
634	17938808 (1267, 1268)				265019
635	79574506 (1269, 1270)			UNCLASSIFIED	264689
636	79910981 (1271, 1272)			UNCLASSIFIED	264596, 264762, 264693

637	82455798 (1273, 1274)	Novel Protein sim. GBank gi|2326739|emb|CAB10953| - (Z98268) recN [Mycobacterium tuberculosis]		nuclease	264906, 264907, 264510, 264511, 264601, 264602, 264603, 264604, 264605, 18108351, 264782, 264766, 264687, 264769, 264689, 35695917, 264693, 264634, 264638, 264639, 264559, 18108385
638	14997457 (1275, 1276)	Novel Protein sim. GBank gi|4678662|emb|CAB41074.1| - (AL049645) putative large ATP-binding protein [Streptomyces coelicolor]			264636
639	80204210 (1277, 1278)	Novel Protein sim. GBank gi|4589628|dbj|BAA76836.1| - (AB023209) KIAA0992 protein [Homo sapiens]		struct	264112, 263974
640	17929579 (1279, 1280)	Novel Protein sim. GBank gi|1432083 (U60981) - homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana]	Contains protein domain (PF01466) - Skp1 family	rnapolymerase	265009, 265010
641	79636398 (1281, 1282)			UNCLASSIFIED	264693
642	19898737 (1283, 1284)			UNCLASSIFIED	264565
643	81516220 (1285, 1286)			UNCLASSIFIED	264906, 264908, 264758, 264288, 264632, 264635, 264639, 264564
644	11751367 (1287, 1288)			UNCLASSIFIED	264684
645	95010907 (1289, 1290)			UNCLASSIFIED	264906, 264762, 264693, 264639, 264559
646	80069083 (1291, 1292)				264595, 264566
647	80257085 (1293, 1294)	Novel Protein sim. GBank gi|4507613|ref|NP_003738.1|pTNKS - TANKYRASE	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	264909, 264591
648	80077428 (1295, 1296)	Novel Protein sim. GBank gi|1044963|bbs|169646 - protamine [Monodonta turbinata, gonads, Peptide, 106 aa]		UNCLASSIFIED	264600
649	80247447 (1297, 1298)			UNCLASSIFIED	263978
650	11798316 (1299, 1300)			UNCLASSIFIED	264686
651	11776932 (1301, 1302)	Novel Protein sim. GBank gi|1346916|sp|P12283|PURA_ECOLI - ADENYLOSUCCINATE SYNTHETASE (IMP--ASPARTATE LIGASE)			264602, 264638
652	85516704 (1303, 1304)			UNCLASSIFIED	264905, 264907, 264909, 263978, 264637
653	82124947 (1305, 1306)	Novel Protein sim. GBank gi|1722977|sp|Q10638|Y03C_MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C		UNCLASSIFIED	22278998, 264510, 264511, 264512, 264593, 21906754, 264603, 264760, 18108376, 264556
654	95010589 (1307, 1308)			UNCLASSIFIED	264906, 264595, 264632
655	79320692 (1309, 1310)	Novel Protein sim. GBank gi|130327|sp|P26647|PLSC_ECOLI - 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT)	Contains protein domain (PF01553) - Acyltransferase	transferase	264592
656	80416739 (1311, 1312)			UNCLASSIFIED	264602, 264605, 264766, 264691
657	20811010 (1313, 1314)			UNCLASSIFIED	264557, 264558

658	87761915 (1315, 1316)	Novel Protein sim. GBank gi|5689493|dbj|BAA83030.1| - (AB029001) KIAA1078 protein [Homo sapiens]		UNCLASSIFIED	22278996, 60432049, 29331822, 29331824, 29331828, 265007, 265009, 33657402, 33657084, 265017, 264448, 21906765, 21906766, 263967, 20281149, 18108370, 18108374, 264482
659	87718663 (1317, 1318)	Novel Protein sim. GBank gi|2137872|pir||I48724 - zinc finger protein PZF - mouse	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	22278999, 60432049, 66714117, 29331827, 265007, 264766, 56181562, 18108359, 18108365, 18108370, 18108381
660	81897922 (1319, 1320)			UNCLASSIFIED	264757
661	80026023 (1321, 1322)	Novel Protein sim. GBank gi|134180|sp|P15401|SACY_BACSU - LEVANSUCRASE AND SUCRASE SYNTHESIS OPERON ANTITERMINATOR	Contains protein domain (PF00874) - Transcriptional antiterminator bglG family	UNCLASSIFIED	264510, 265009, 264600, 264602, 264603, 264604, 264605, 32833986, 18108376, 264636, 18108387, 22279000
662	20463731 (1323, 1324)	Novel Protein sim. GBank gi|4545229|gb|AAD22450.1|AF11618 - (AF116183) SecA homolog [Actinobacillus actinomycetemcomitans]		UNCLASSIFIED	264605
663	20628080 (1325, 1326)	Novel Protein sim. GBank gi|5689250|dbj|BAA82881.1| - (AB024335) similar to orf5 [Comamonas testosteroni]		dehydrogenase	264605
664	80508512 (1327, 1328)	Novel Protein sim. GBank gi|1652848|dbj|BAA17766| - (D90909) DNA photolyase [Synechocystis sp.]		UNCLASSIFIED	264769
665	80079053 (1329, 1330)	Novel Protein sim. GBank gi|116841|sp|P21640|COBJ_PSEDE - PRECORRIN-3B C17 METHYLTRANSFERASE (PRECORRIN-3 METHYLTRANSFERASE) (PRECORRIN-3 METHYLASE)		isomerase	264600
666	79603142 (1331, 1332)	Novel Protein sim. GBank gi|3261829|emb|CAB10927| - (Z98260) hypothetical protein Rv1230c [Mycobacterium tuberculosis]		glycoprotein	264907, 265007
667	94631802 (1333, 1334)	Novel Protein sim. GBank gi|5688851|dbj|BAA82702.1| - (AB017438) Orf5 [Streptomyces coelicolor]		UNCLASSIFIED	264689, 264602, 264593
668	82051891 (1335, 1336)	Novel Protein sim. GBank gi|3581853|emb|CAA20809| - (AL031541) 50S ribosomal protein L20 [Streptomyces coelicolor]	Contains protein domain (PF00453) - Ribosomal protein L20	ribosomalprot	264905, 264906, 264908, 264600, 264601, 264603, 264605, 264760, 264689, 264636, 264638, 264639
669	12967154 (1337, 1338)			UNCLASSIFIED	264637
670	80238549 (1339, 1340)	Novel Protein sim. GBank gi|2582531 (AF026444) - 2-isopropylmalate synthase [Streptomyces coelicolor]		synthase	264905, 264906, 264908, 264601, 264762, 264766, 264689, 264638, 18108385, 264486
671	79601368 (1341, 1342)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264690, 264692, 264693, 264636, 18108387
672	79834371 (1343, 1344)	Novel Protein sim. GBank gi|2114430 (U92703) - Olf-1/EBF-like-3 transcription factor [Mus musculus]		transcriptfactor	264910, 265017
673	82285798 (1345, 1346)	Novel Protein sim. GBank gi|4589285|gb|AAD26430.1|AF13515 - (AF135154) ferric alcaligin siderophore receptor [Bordetella pertussis]			264759
674	79199259 (1347, 1348)			UNCLASSIFIED	264629

675	87895870 (1349, 1350)	Novel Protein sim. GBank gi|4980755|gb|AAD35347.1|AE00170 - (AE001708) D-alanine--D-alanine ligase [Thermotoga maritima]	Contains protein domain (PF01820) - D-ala D-ala ligase	UNCLASSIFIED	264488, 22278999, 66714117, 264508, 264511, 265008, 60433438, 264600, 264601, 264602, 264603, 264604, 264605, 264762, 264687, 264769, 60431602, 18108374, 264636, 264638
676	78899607 (1351, 1352)	Novel Protein sim. GBank gi|1723566|sp|Q10479|YDF7_SCHPO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07			265010
677	21644312 (1353, 1354)	Novel Protein sim. GBank gi|887208 (U03976) - dynein heavy chain isotype 5C [Tripneustes gratilla]		ATPase_associated	264591, 264632
678	84225200 (1355, 1356)	Novel Protein sim. GBank gi|1586274|prf||2203365A - laminin alpha5 [Mus musculus]	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	264758, 264682, 264557
679	79868855 (1357, 1358)	Novel Protein sim. GBank gi|3928723|emb|CAA22219| - (AL034355) putative ABC transporter [Streptomyces coelicolor]		UNCLASSIFIED	22278998, 264693
680	20726424 (1359, 1360)				264600, 264602
681	94322017 (1361, 1362)	Novel Protein sim. GBank gi|5174493|ref|NP_006050.1|pLAMC - laminin, gamma 3	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	264102, 264907, 264908, 265006, 264693, 263972, 83373044, 264566
682	11392476 (1363, 1364)			UNCLASSIFIED	264595
683	80083680 (1365, 1366)	Novel Protein sim. GBank gi|4758208|ref|NP_004081.1|pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	264634
684	20465367 (1367, 1368)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]			264605
685	80246735 (1369, 1370)				264909, 263967, 263981
686	79208608 (1371, 1372)				264631
687	80085629 (1373, 1374)				264693, 264635
688	79853412 (1375, 1376)	Novel Protein sim. GBank gi|2688962 (AF027768) - LspA [Serratia marcescens]		peptidase	264907, 264638
689	88064256 (1377, 1378)	Novel Protein sim. GBank gi|3046931 (AF049330) - PPAR gamma coactivator [Mus musculus]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264906, 264907, 265007, 265009, 60433438, 21906754, 264760, 18108358, 21906766, 21906769, 265021, 18108361, 263974, 18108379, 264557, 18108385, 22279002
690	80389750 (1379, 1380)	Novel Protein sim. GBank gi|2498941|sp|Q15428|SP62_HUMAN - SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)		UNCLASSIFIED	264510, 264511, 264764, 264769
691	81854392 (1381, 1382)			UNCLASSIFIED	264757
692	83608936 (1383, 1384)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	55812038, 55811957, 265018, 55811150, 18108351, 264908, 60431528, 264594
693	79586116 (1385, 1386)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264635
694	82455983 (1387, 1388)	Novel Protein sim. GBank gi|267327|sp|Q01033|VG48_HSVSA - HYPOTHETICAL GENE 48 PROTEIN			22278996, 264510, 264602, 264603, 264762, 264687, 264769, 264693

695	94147849 (1389, 1390)	Novel Protein sim. GBank gi|4468339|emb|CAB38059.1| - (AJ010901) MUC4 [Homo sapiens]	Contains protein domain (PF00094) - von Willebrand factor type D domain	UNCLASSIFIED	56182575, 264509, 264905, 264907, 29331830, 264908, 264909, 264511, 265007, 264910, 264758, 264764, 264288, 65274791
696	79830982 (1391, 1392)	Novel Protein sim. GBank gi|2649950 (AE001058) - glutamine ABC transporter, ATP-binding protein (glnQ) [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	264905, 264595
697	11767889 (1393, 1394)	Novel Protein sim. GBank gi|1731343|sp|Q10694|YY25_MYCTU - HYPOTHETICAL 24.4 KD PROTEIN CY49.25	Contains protein domain (PF01836) - Transposase	UNCLASSIFIED	264682
698	66695862 (1395, 1396)			UNCLASSIFIED	264688, 35695917
699	79582558 (1397, 1398)			UNCLASSIFIED	264682
700	79639098 (1399, 1400)				264693
701	80230242 (1401, 1402)	Novel Protein sim. GBank gi|1001236|dbj|BAA10477| - (D84003) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	264488, 264510, 264511, 264602, 264605, 264689
702	79814789 (1403, 1404)			UNCLASSIFIED	264909
703	20446820 (1405, 1406)	Novel Protein sim. GBank gi|2498935|sp|Q46338|SOXG_CORSP - SARCOSINE OXIDASE GAMMA SUBUNIT		oxidase	264604
704	94312224 (1407, 1408)	Novel Protein sim. GBank gi|3150513 (AF067219) - contains similarity to the kelch/MIPP family [Caenorhabditis elegans]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	264288, 56181562, 33657109, 264629, 55811576
705	17932141 (1409, 1410)	Novel Protein sim. GBank gi|421091|pir||S30730 - hypothetical protein o206 - Escherichia coli		UNCLASSIFIED	265006
706	20288062 (1411, 1412)	Novel Protein sim. GBank gi|3024872|sp|Q55790|Y074_SYNY3 - HYPOTHETICAL 52.8 KD PROTEIN SLR0074			264600
707	20638065 (1413, 1414)	Novel Protein sim. GBank gi|3420608|gb|AAC31907.1| - (AF075709) ABC transporter ATP-binding subunit [Pseudomonas putida]		transport	264603
708	20708292 (1415, 1416)				264601, 264692
709	88001439 (1417, 1418)	Novel Protein sim. GBank gi|3649741|emb|CAA03985| - (AJ000281) mucin [Homo sapiens]		struct	18108398, 264637, 264908, 264909
710	11356683 (1419, 1420)	Novel Protein sim. GBank gi|3080425|emb|CAA18744.1| - (AL022604) putative protein [Arabidopsis thaliana]			264369
711	17931418 (1421, 1422)				265019
712	80258164 (1423, 1424)	Novel Protein sim. GBank gi|4758686|ref|NP_002323.1|pLRP1 - low density lipoprotein related protein 1 (alpha-2-macroglobulin receptor)	Contains protein domain (PF00058) - Low-density lipoprotein receptor repeat class B	apolipoprotein	264591
713	79263126 (1425, 1426)	Novel Protein sim. GBank gi|1703266|sp|Q11056|AMI2_MYCTU - PUTATIVE AMIDASE CY50.19C		hydrolase	264906, 264907
714	27847651 (1427, 1428)	Novel Protein sim. GBank gi|4502351|ref|NP_001692.1|pBAAT - bile acid Coenzyme A: amino acid N-acyltransferase; glycine N-choloyltransferase			264508, 264555

715	79639423 (1429, 1430)	Novel Protein sim. GBank gi|1789035 (AE000352) - orf, hypothetical protein [Escherichia coli]		UNCLASSIFIED	264907
716	79559072 (1431, 1432)				264692
717	79491842 (1433, 1434)	Novel Protein sim. GBank gi|2494074|sp|P55653|GABD_RHISN - PROBABLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)		dehydrogenase	264636
718	94319658 (1435, 1436)	Novel Protein sim. GBank gi|3873679|emb|CAA94886| - (Z71178) similar to pro-collagen domains; cDNA EST EMBL:D27978 comes from this gene; cDNA EST EMBL:D27977 comes from this gene; cDNA EST EMBL:D34199 comes from this gene; cDNA EST EMBL:D64392 comes from this gene; cDNA EST EMBL...	Contains protein domain (PF00093) - von Willebrand factor type C domain	kinase	18108392, 22278994, 22278998, 265008, 265018, 264681, 18108354, 264684, 264685, 264686, 264687, 264689, 21906769, 18108361, 264691, 264692, 55810764, 264635, 18108381, 18108382, 83373044, 18108388
719	17679564 (1437, 1438)	Novel Protein sim. GBank gi|2104302|emb|CAB08631| - (Z95387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]		UNCLASSIFIED	265011
720	79841684 (1439, 1440)				264908
721	15020180 (1441, 1442)	Novel Protein sim. GBank gi|123530|sp|P04929|HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	264629
722	9862603 (1443, 144[illegible])	Novel Protein sim. GBank gi|498253 (U02372) - integrase [Vibrio cholerae]			264910
723	19755599 (1445, 1446)	Novel Protein sim. GBank gi|2253054|emb|CAB10705| - (Z97559) hypothetical protein Rv2114 [Mycobacterium tuberculosis]		UNCLASSIFIED	264691
724	10126494 (1447, 1448)	Novel Protein sim. GBank gi|4063015 (AF083061) - protease PrtA [Pseudomonas fluorescens]	Contains protein domain (PF00353) - Hemolysin-type calcium-binding proteins	protease	264909
725	79878679 (1449, 1450)			UNCLASSIFIED	264905, 264907
726	13086282 (1451, 1452)			UNCLASSIFIED	264636
727	13522872 (1453, 1454)				264634
728	20268471 (1455, 1456)	Novel Protein sim. GBank gi|2633910|emb|CAB13411| - (Z99112) similar to hypothetical proteins [Bacillus subtilis]			264567
729	11293753 (1457, 1458)			UNCLASSIFIED	264490
730	19900373 (1459, 1460)	Novel Protein sim. GBank gi|2494660|sp|Q45291|GALE_BRELA - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	264564
731	80058750 (1461, 1462)	Novel Protein sim. GBank gi|1146192 (L47838) - putative [Bacillus subtilis]		UNCLASSIFIED	264605
732	80258175 (1463, 1464)	Novel Protein sim. GBank gi|1168396|sp|P46681|AIP2_YEAST - ACTIN INTERACTING PROTEIN 2		struct	264591, 264594, 264595
733	20446839 (1465, 1466)			UNCLASSIFIED	264604
734	20435987 (1467, 1468)	Novel Protein sim. GBank gi|3184080|emb|CAA19336| - (AL023781) hypothetical protein [Schizosaccharomyces pombe]		ubiquitin	264604

735	11607959 (1469, 1470)	Novel Protein sim. GBank gi|401582|sp|P27432|YICE_ECOLI - HYPOTHETICAL 48.9 KD PROTEIN IN GLTS-SELC INTERGENIC REGION			264594
736	10879734 (1471, 1472)	Novel Protein sim. GBank gi|400831|sp|P31135|POTH_ECOLI - PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTH	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	264636
737	78945340 (1473, 1474)		Contains protein domain (PF00615) - Regulator of G protein signaling domain	UNCLASSIFIED	265020
738	17895353 (1475, 1476)				265008
739	79833670 (1477, 1478)	Novel Protein sim. GBank gi|2506867|sp|P33225|TORA_ECOLI - TRIMETHYLAMINE-N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)		oxidase	264910
740	19881557 (1479, 1480)				264907, 264764, 264634, 264637
741	79827273 (1481, 1482)	Novel Protein sim. GBank gi|3261828|emb|CAB10925| - (Z98260) mrp [Mycobacterium tuberculosis]	Contains protein domain (PF01883) - Domain of unknown function	UNCLASSIFIED	264689, 35696286, 264510, 264908, 18108362
742	82393795 (1483, 1484)	Novel Protein sim. GBank gi|3877494|emb|CAA88472.1| - (Z48583) ATP binding protein with similarity to the CDC48/PAS1/SEC18 family; cDNA EST EMBL:D65037 comes from this gene; cDNA EST EMBL:D68340 comes from this gene; cDNA EST EMBL:D65048 comes from this gene; cDNA EST EMBL:D6845...		UNCLASSIFIED	29331822, 264910, 264762
743	82300051 (1485, 1486)	Novel Protein sim. GBank gi|127420|sp|P19888|MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase	UNCLASSIFIED	264488, 264259, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264596, 264759, 265010, 265011, 18108351, 264763, 264288, 264766, 264768, 264693, 18108370, 264629, 18108372, 264630, 264631, 264634, 264558, 18108385, 264482, 264564, 264567
744	80230421 (1487, 1488)				18108397, 264511, 264690, 264628, 264638, 264692, 264639, 264766
745	9841963 (1489, 1490)	Novel Protein sim. GBank gi|78921|pir||S04846 - UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli		glycoprotein	264906
746	11073229 (1491, 1492)	Novel Protein sim. GBank gi|3386354 (AF074705) - pyochelin synthetase [Pseudomonas aeruginosa]		synthase	264600
747	94322044 (1493, 1494)	Novel Protein sim. GBank gi|2887411|dbj|BAA24848| - (AB007878) KIAA0418 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	oxidase	66714117, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264681, 264288, 264766, 264687, 264768, 264769, 21906768, 35695917, 264691, 264693, 264628, 264634, 264635, 264639, 56182323, 83373044
748	11617923 (1495, 1496)				264690

749	20469119 (1497, 1498)			UNCLASSIFIED	264604
750	20296427 (1499, 1500)	Novel Protein sim. GBank gi|1169727|sp|P44948|FPG_HAEIN - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY-DNA GLYCOSYLASE)			264600
751	21636169 (1501, 1502)	Novel Protein sim. GBank gi|5360068|gb|AAD42851.1|AF15968 - (AF159689) serine/threonine kinase PKN3 [Myxococcus xanthus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264605, 264559
752	82450366 (1503, 1504)	Novel Protein sim. GBank gi|1168662|sp|P44426|BIOA_HAEIN - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate	UNCLASSIFIED	264508, 264907, 264510, 265011, 264762, 264889, 35695855, 264638, 18108387
753	80508718 (1505, 1506)	Novel Protein sim. GBank gi|2851530|sp|P32399|YHGE_BACSU - HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION (ORFB)		UNCLASSIFIED	264909, 264600, 264602, 264604, 264760, 264769, 264634
754	95083741 (1507, 1508)			UNCLASSIFIED	264508, 264906, 264907, 264908, 264909, 264759, 264602, 264764, 264769, 264628, 264629, 264630, 264632, 264634, 264635, 264637, 264638, 83373044, 18108385
755	80185449 (1509, 1510)			UNCLASSIFIED	264448, 264690
756	94631686 (1511, 1512)	Novel Protein sim. GBank gi|3449276|emb|CAA20420| - (AL031317) putative dehydrogenase [Streptomyces coelicolor]			264769, 264689, 264638, 264639
757	79468533 (1513, 1514)			UNCLASSIFIED	264682, 264685
758	78963176 (1515, 1516)	Novel Protein sim. GBank gi|4580331|emb|CAB40107.1| - (AJ001206) putative glycogen debranching enzyme [Streptomyces coelicolor]		amylase	265007, 18108387, 265007, 18108387
759	79475667 (1517, 1518)	Novel Protein sim. GBank gi|2911858 (AF047659) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264684, 264686
760	87628888 (1519, 1520)	Novel Protein sim. GBank gi|3451312|emb|CAA20449| - (AL031324) membrane atpase [Schizosaccharomyces pombe]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	29331822, 264908, 52644045, 56182435, 60170831, 21906754, 265017, 265019, 264681, 264687, 264688, 21906766, 21906768, 265020, 265021, 265022, 264635, 22279000
761	79877966 (1521, 1522)			UNCLASSIFIED	264766
762	80023563 (1523, 1524)	Novel Protein sim. GBank gi|3327158|dbj|BAA31647| - (AB014572) KIAA0872 protein [Homo sapiens]		UNCLASSIFIED	264907, 264593, 265020
763	20294813 (1525, 1526)	Novel Protein sim. GBank gi|4981266|gb|AAD35822.1|AE00174 - (AE001744) lipopolysaccharide core biosynthesis protein KdtB [Thermotoga maritima]			264600
764	39515024 (1527, 1528)				264603

765	80025347 (1529, 1530)	Novel Protein sim. GBank gi|3845093 (AE001371) - erythrocyte membrane protein PfEMP3 [Plasmodium falciparum]		struct	264905, 264906, 264594, 264686, 33657023
766	82417404 (1531, 1532)				264605, 264762, 18108374
767	10296742 (1533, 1534)	Novel Protein sim. GBank gi|541121|pir||S40827 - hypothetical protein o300 - Escherichia coli		UNCLASSIFIED	264907
768	79416080 (1535, 1536)			UNCLASSIFIED	264592, 264595
769	80086554 (1537, 1538)	Novel Protein sim. GBank gi|2982501|emb|CAA06164| - (AJ004832) neuropathy target esterase [Homo sapiens]		esterase	55810764, 264559
770	80417847 (1539, 1540)	Novel Protein sim. GBank gi|283437|pir||S27850 - hypothetical protein - Trypanosoma cruzi (fragment)		UNCLASSIFIED	264905, 264907, 264828, 264909, 265010, 264766, 264628, 264629, 264634, 264636, 264555
771	95329509 (1541, 1542)	Novel Protein sim. GBank gi|4769004|gb|AAD29715.1|AF14059 - (AF140598) ring-box protein 1 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	56182575, 35696286, 264259, 66714117, 264107, 66712502, 56182435, 264112, 55812038, 87168559, 264288, 21906766, 33657023, 65274620, 65274791, 18108381
772	78971362 (1543, 1544)			UNCLASSIFIED	264910
773	78945363 (1545, 1546)			UNCLASSIFIED	265020
774	79856129 (1547, 1548)	Novel Protein sim. GBank gi|5531324|emb|CAB51045.1| - (AJ009579) putative alkane 1-monooxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	264909
775	20620141 (1549, 1550)			UNCLASSIFIED	264555
776	78942693 (1551, 1552)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a		265019
777	79960378 (1553, 1554)	Novel Protein sim. GBank gi|4505461|ref|NP_003624.1|pNRPB - nuclear restricted protein, BTB domain-like (brain)	Contains protein domain (PF01344) - Kelch motif	protease	21906754, 265020, 60170615, 264691
778	20691310 (1555, 1556)			UNCLASSIFIED	264511
779	80054024 (1557, 1558)				264603
780	95288987 (1559, 1560)	Novel Protein sim. GBank gi|1144520 (U34956) - phosphoribosylformylglycinamidine synthase [Mycobacterium tuberculosis]		synthase	264907, 264600, 264601, 264602, 264603, 264604, 264605, 264486
781	80250049 (1561, 1562)				264905, 264907, 265010, 264600, 264601, 18108362, 18108374, 264556
782	8758529 (1563, 1564)	Novel Protein sim. GBank gi|4155447 (AE001517) - proline/betaine transporter [Helicobacter pylori J99]		UNCLASSIFIED	264605
783	16410791 (1565, 1566)				265020
784	80051197 (1567, 1568)			UNCLASSIFIED	264635, 33657023, 29331828, 265017, 264565, 264566
785	56073541 (1569, 1570)	Novel Protein sim. GBank gi|3451335 (AC005525) - F22162_1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	35696052, 264604
786	20438842 (1571, 1572)	Novel Protein sim. GBank gi|136748|sp|P10905|UGPA_ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA		transport	264603
787	80258364 (1573, 1574)			UNCLASSIFIED	264593

788	80507844 (1575, 1576)	Novel Protein sim. GBank gi|2746079 (AF015310) - BTH1 [Brassica napus]		synthase	264909, 264602, 264603, 264769, 264638
789	17294715 (1577, 1578)	Novel Protein sim. GBank gi|2351849 (U93357) - 40 kDa heat shock chaperone protein [Halobacterium cutirubrum]		UNCLASSIFIED	265007
790	86284406 (1579, 1580)	Novel Protein sim. GBank gi|5706378|dbj|BAA83099.1| - (AB026118) MALT1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	22278999, 29331824, 264828, 87168559, 265018, 21906765, 21908767, 21906768, 21906769, 265020, 264692, 22279000, 264583
791	94651627 (1581, 1582)	Novel Protein sim. GBank gi|5689948|emb|CAB51985.1| - (AL109663) putative isoleucyl-tRNA synthetase [Streptomyces coelicolor A3(2)]			264601, 264605, 264636
792	80058786 (1583, 1584)	Novel Protein sim. GBank gi|393194 (L02375) - S-antigen [Plasmodium falciparum]		struct	265021, 264631, 264635, 264556
793	79638730 (1585, 1586)	Novel Protein sim. GBank gi|1345408|dbj|BAA05046| - (D26046) AT motif-binding factor [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264693
794	81839294 (1587, 1588)	Novel Protein sim. GBank gi|105884|pir||S24023 - dopamine receptor D4 - human (fragment)		UNCLASSIFIED	264603, 264604, 264910, 264762, 264906, 264639, 264909, 264757
795	80074988 (1589, 1590)	Novel Protein sim. GBank gi|1877334|emb|CAB07082| - (Z92771) birA [Mycobacterium tuberculosis]		carboxylase	264488, 35696052, 264905, 264907, 265010, 35696423, 264636
796	86669451 (1591, 1592)				60432229, 55811150, 264630, 264637, 264565
797	87771781 (1593, 1594)	Novel Protein sim. GBank gi|2995447|emb|CAA71519| - (Y10495) CDV-1R protein [Mus musculus]		struct	22278998, 264093, 264094, 68714117, 21906767, 21906769, 265020, 265022
798	79865209 (1595, 1596)			transcriptfactor	264687, 264768, 264693
799	79557816 (1597, 1598)	Novel Protein sim. GBank gi|4467250|emb|CAB37575| - (AL035569) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]		hydrolase	264909, 264910, 264636, 264638
800	79970189 (1599, 1600)			UNCLASSIFIED	264488
801	80499399 (1601, 1602)	Novel Protein sim. GBank gi|2791517|emb|CAA16054| - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]		transport	264508, 264511, 265006, 265009, 264769, 264567, 264486
802	79834598 (1603, 1604)	Novel Protein sim. GBank gi|4887211|gb|AAD32237.1|AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]			264905, 264693
803	20467520 (1605, 1606)			struct	264605
804	10174239 (1607, 1608)	Novel Protein sim. GBank gi|1176152|sp|P44507|YHAD_HAEIN - HYPOTHETICAL PROTEIN HI0091		kinase	264510
805	79599993 (1609, 1610)				264508
806	80484113 (1611, 1612)	Novel Protein sim. GBank gi|2764612|emb|CAA04683| - (AJ001330) ornithine transcarbamoylase [Lactobacillus sakei]	Contains protein domain (PF00185) - Aspartate/ornithine carbamoyltransferase	transferase	264769
807	80381812 (1613, 1614)	Novel Protein sim. GBank gi|2833311|sp|Q21828|YNFD_CAEEL - HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III			264764

808	35106817 (1615, 1616)	Novel Protein sim. GBank gi|3913092|sp|Q46170|ARCD_CLOPE - ARGININE/ORNITHINE ANTIPORTER		transport	264909, 264602, 21906764, 18108374
809	81454254 (1617, 1618)	Novel Protein sim. GBank gi|3913016|sp|P74309|ALF1_SYNY3 - FRUCTOSE-BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)	Contains protein domain (PF00274) - Fructose-bisphosphate aldolase class-I	UNCLASSIFIED	264508, 264906, 264909, 265007, 264910, 264758, 264600, 264602, 264603, 264605, 264687, 264769, 264689, 264636, 264486
810	80192761 (1619, 1620)	Novel Protein sim. GBank gi|401472|sp|P30863|YAFB_ECOLI - HYPOTHETICAL OXIDOREDUCTASE IN ASPU-MLTD INTERGENIC REGION	Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	264369
811	80079280 (1621, 1622)			UNCLASSIFIED	264558
812	10297654 (1623, 1624)			UNCLASSIFIED	264692
813	79612280 (1625, 1626)			UNCLASSIFIED	264906
814	80473427 (1627, 1628)	Novel Protein sim. GBank gi|146168 (J01617) - glutaminyl-tRNA synthetase [Escherichia coli]		synthase	264905, 264602, 264605, 264682, 264687, 264769, 264636
815	95419513 (1629, 1630)	Novel Protein sim. GBank gi|4589652|dbj|BAA76848.1| - (AB023221) KIAA1004 protein [Homo sapiens]		UNCLASSIFIED	264488, 22278998, 22278999, 29331822, 29331824, 29331825, 29331827, 29331828, 29146499, 264905, 264908, 265007, 33657402, 60433356, 60433438, 264758, 265011, 265017, 265018, 265019, 264369, 264288, 264685, 21906765, 21906767, 265020, 265021, 264692, 65274620, 33657109, 264629, 18108378, 264635, 264638, 60170394, 56182323, 264564
816	19881910 (1631, 1632)				264600
817	95293316 (1633, 1634)	Novel Protein sim. GBank gi|1781144|emb|CAB06254| - (Z83866) hypothetical protein Rv3069 [Mycobacterium tuberculosis]		UNCLASSIFIED	264595
818	80938190 (1635, 1636)	Novel Protein sim. GBank gi|1477468 (U35244) - vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]			65274572, 22278999, 60424269, 35696052, 55812038, 21906768, 55811957, 35695917, 33657023, 18108370, 18108374, 55810764, 35696423, 55811576, 264636
819	80254977 (1637, 1638)	Novel Protein sim. GBank gi|1001352|dbj|BAA10839| - (D64006) ABC transporter [Synechocystis sp.]		transport	264565
820	80059688 (1639, 1640)	Novel Protein sim. GBank gi|586814|sp|P37484|YYBT_BACSU - HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION		UNCLASSIFIED	264600, 264602, 264604
821	79762590 (1641, 1642)			UNCLASSIFIED	264910
822	80215310 (1643, 1644)			UNCLASSIFIED	264510, 264594, 264637
823	94992299 (1645, 1646)	Novel Protein sim. GBank gi|3878400|emb|CAA95828| - (Z71264) predicted using Genefinder; Weak similarity to Mouse T-complex-associated-testes-expressed-1 protein (PIR Acc. No. A45841); cDNA EST EMBL:D32742 comes from this gene; cDNA EST EMBL:D33617 comes from this gene; cDNA EST...		struct	264509, 264687, 264691
824	80411171 (1647, 1648)	Novel Protein sim. GBank gi|1370076|emb|CAA66887| - (X98235) type I [Drosophila melanogaster]	Contains protein domain (PF01429) - Methyl-CpG binding domain		264910, 264763, 264769, 264693

825	20638600 (1649, 1650)	Novel Protein sim. GBank gi|3025132|sp|P77391|YEAG_ECOLI - HYPOTHETICAL 74.5 KD PROTEIN IN GAPA-RND INTERGENIC REGION		UNCLASSIFIED	264592
826	11075047 (1651, 1652)	Novel Protein sim. GBank gi|3242281|emb|CAA16669| - (AL021646) hypothetical protein Rv3202c [Mycobacterium tuberculosis]			264605
827	80054207 (1653, 1654)	Novel Protein sim. GBank gi|3417424|emb|CAA20312| - (AL031261) putative transport protein [Schizosaccharomyces pombe]			264603
828	95106322 (1655, 1656)	Novel Protein sim. GBank gi|4336692|gb|AAD17897| - (AF101361) Abnormal X segregation [Drosophila melanogaster]		UNCLASSIFIED	52645080, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264512, 264910, 264591, 264758, 264600, 264768, 264768, 21906768, 35695917, 264691, 264628, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 264639, 83373044, 18108385, 264563, 264566, 264486
829	81742215 (1657, 1658)			UNCLASSIFIED	264758, 264634
830	20396091 (1659, 1660)	Novel Protein sim. GBank gi|3820539 (AF080002) - UDP-N-acetylmuramyl tripeptide synthetase MurC [Heliobacillus mobilis]		UNCLASSIFIED	264603
831	87112435 (1661, 1662)			UNCLASSIFIED	66714117, 264910, 264639
832	19536322 (1663, 1664)	Novel Protein sim. GBank gi|1870004|emb|CAB06855| - (Z92539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	264906
833	20726654 (1665, 1666)	Novel Protein sim. GBank gi|2500056|sp|Q46267|PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	264602
834	21428782 (1667, 1668)	Novel Protein sim. GBank gi|2497531|sp|Q46078|KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	kinase	264600, 264602, 264769, 264689, 264636
835	94140482 (1669, 1670)				264768, 263994, 21906767, 264910, 264632, 264635, 264259, 264639, 264693, 83373044, 264758, 35696052, 22279002, 264508, 264905, 264906, 264448, 263972, 264908, 264909
836	66126552 (1671, 1672)	Novel Protein sim. GBank gi|699315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]		transport	35695917, 264557
837	79450450 (1673, 1674)			UNCLASSIFIED	264595
838	79184203 (1675, 1676)	Novel Protein sim. GBank gi|728867|sp|P40602|APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		UNCLASSIFIED	264687
839	79641125 (1677, 1678)	Novel Protein sim. GBank gi|2498533|sp|Q50598|Y0D8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08		UNCLASSIFIED	264906
840	80059851 (1679, 1680)	Novel Protein sim. GBank gi|4557753|ref|NP_000372.1|pMID1 - midline 1 protein	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264762, 264556

841	80376318 (1681, 1682)	Novel Protein sim. GBank gi|139805|sp|P08045|XFIN_XENLA - XFIN PROTEIN	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264764
842	80078724 (1683, 1684)	Novel Protein sim. GBank gi|2114321|dbj|BAA20037| - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	264905, 264908, 265008, 265009, 18108374, 56182323, 264558
843	87002847 (1685, 1686)	Novel Protein sim. GBank gi|3882325|dbj|BAA34522.1| - (AB018345) KIAA0802 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	struct	264091, 29331825, 264906, 264768, 264563
844	17941439 (1687, 1688)	Novel Protein sim. GBank gi|2224721|dbj|BAA20844| - (AB002388) KIAA0390 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	265011
845	18346844 (1689, 1690)				264629
846	79863441 (1691, 1692)	Novel Protein sim. GBank gi|625679|pir||A36929 - virulence regulatory protein VsrB - Pseudomonas solanacearum		kinase	264907
847	78695348 (1693, 1694)				264909
848	78489365 (1695, 1696)			UNCLASSIFIED	265020
849	79756367 (1697, 1698)			UNCLASSIFIED	264566
850	79817849 (1699, 1700)	Novel Protein sim. GBank gi|3183245|sp|P78061|YCJK_ECOLI - PUTATIVE GLUTAMINE SYNTHETASE (GLUTAMATE–AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	264909
851	95320333 (1701, 1702)	Novel Protein sim. GBank gi|5454130|ref|NP_006280.1|pTLN| - talin	Contains protein domain (PF01608) - I/LWEQ domain		264488, 52644507, 264489, 18108398, 65274572, 56182575, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 20281171, 264490, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264107, 264905, 264906, 264907, 264908, 52644045, 56182435, 265006, 265007, 265008, 265009, 264910, 60432229, 60431735, 60433356, 33657402, 60433438, 264595, 264758, 264759, 21906754, 33109954, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 264762, 264681, 18108351, 264763, 264448, 264682, 264764, 264683, 18108354, 264288, 264369, 264685, 264766, 264687, 264768, 264769, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 29148629, 55811957, 35695917, 265020, 265021, 265022, 60170815, 52644150, 264691, 264692, 33657023, 264693, 263966, 33657109, 27486261, 27486262, 27486264, 27486265, 35695763, 60431602, 18108370, 20281069, 264629, 18108374, 18108376, 55811576, 35696423, 35695855, 264634, 264635, 264636, 264555, 60431850, 264556,
852	10147366 (1703, 1704)				264691

853	13032587 (1705, 1706)				264636
854	80052438 (1707, 1708)	Novel Protein sim. GBank gi|3402836|emb|CAA76082| - (Y16136) 2-enoate reductase [Moorella thermoacetica]		reductase	264566
855	79641130 (1709, 1710)				264692
856	11594236 (1711, 1712)			UNCLASSIFIED	264591
857	79210165 (1713, 1714)			UNCLASSIFIED	264630, 264634
858	80248910 (1715, 1716)				265008, 265009, 264601, 264602, 264603, 18108351
859	20296634 (1717, 1718)				264559
860	80041749 (1719, 1720)			UNCLASSIFIED	264489
861	65857045 (1721, 1722)			UNCLASSIFIED	33657023, 264630
862	80079467 (1723, 1724)				264600
863	80579931 (1725, 1726)	Novel Protein sim. GBank gi|2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	264488, 18108398, 35696286, 264259, 18108351, 264288, 265021
864	94939904 (1727, 1728)			UNCLASSIFIED	264259, 264112, 263974
865	80045310 (1729, 1730)	Novel Protein sim. GBank gi|5689884|emb|CAB52047.1| - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01479) - S4 domain		264635, 264600, 264636, 264591, 264602, 264693
866	80162031 (1731, 1732)	Novel Protein sim. GBank gi|4557876|ref|NP_000341.1|pABCR - ATP binding cassette transporter		transport	264288, 264557, 264558
867	80062402 (1733, 1734)				264605
868	10075364 (1735, 1736)			UNCLASSIFIED	264909
869	80062406 (1737, 1738)				264605, 264687, 18108374
870	80249651 (1739, 1740)	Novel Protein sim. GBank gi|628660|pir||S37755 - Adenylyl-transferase - Escherichia coli		transferase	264601, 264636
871	20378295 (1741, 1742)	Novel Protein sim. GBank gi|1708180|sp|Q10602|HEMK_MYCTU - HEMK PROTEIN HOMOLOG		UNCLASSIFIED	264603
872	95197114 (1743, 1744)	Novel Protein sim. GBank gi|1545959|emb|CAA67763| - (X99384) paladin [Mus musculus]		UNCLASSIFIED	35696286, 22278998, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 264910, 264591, 60433356, 264596, 52646317, 87168474, 265010, 264602, 264603, 265017, 265018, 264605, 18108351, 264764, 264766, 264768, 52644229, 264769, 21906765, 265021, 264534, 264691, 52645129, 264628, 264629, 35696423, 65274791, 264631, 264632, 264635, 264636, 264556, 264637, 264638, 264639, 60432113, 22279000, 22279002, 264564
873	20189728 (1745, 1746)	Novel Protein sim. GBank gi|4156104 (AE001569) - putative Outer membrane protein [Helicobacter pylori J99]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264595

874	80077692 (1747, 1748)	Novel Protein sim. GBank gi|134319|sp|P07819|SCRB_BACSU - SUCROSE-6-PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)		UNCLASSIFIED	264600
875	86608446 (1749, 1750)	Novel Protein sim. GBank gi|481000|pir||S37594 - mucin - human (fragment)			264259, 264448, 264288, 264557, 87168518
876	86465157 (1751, 1752)	Novel Protein sim. GBank gi|3128283 (AF010496) - iron(iii) dicitrate transport ATP-binding protein [Rhodobacter capsulatus]	Contains protein domain (PF00005) - ABC transporter	transport	264907, 264601, 264602, 264605, 265020, 60431602
877	87802548 (1753, 1754)	Novel Protein sim. GBank gi|731074|sp|P40349|URB1_USTMA - SIDEROPHORE BIOSYNTHESIS REGULATORY PROTEIN URBS1	Contains protein domain (PF00320) - GATA zinc finger	transcriptfactor	22278998, 264909, 264369
878	80187289 (1755, 1756)	Novel Protein sim. GBank gi|1351614|sp|Q09853|YAED_SCHPO - HYPOTHETICAL 181.5 KD PROTEIN C23D3.13C IN CHROMOSOME I		ATPase_associated	264369, 264555
879	94328962 (1757, 1758)	Novel Protein sim. GBank gi|3875304|emb|CAA98434| - (Z74030) predicted using Genefinder; cDNA EST EMBL:C07609 comes from this gene; cDNA EST EMBL:C09023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com...			56182575, 29331824, 264508, 264906, 265018, 18108351, 264448, 264683, 21906766, 21906768, 60170615, 33657023, 65274620, 33657109, 18108374, 35695855, 264583
880	8491135 (1759, 1760)	Novel Protein sim. GBank gi|137120|sp|P11214|UROT_MOUSE - TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (TPA) (T-PLASMINOGEN ACTIVATOR)	Contains protein domain (PF00051) - Kringle domain	cathepsin	264508
881	11290122 (1761, 1762)			UNCLASSIFIED	264508
882	11077011 (1763, 1764)	Novel Protein sim. GBank gi|2632098|emb|CAA75667| - (Y15513) Prodos protein [Drosophila melanogaster]		UNCLASSIFIED	264558
883	79582969 (1765, 1766)			UNCLASSIFIED	264688
884	13517921 (1767, 1768)	Novel Protein sim. GBank gi|1155068|emb|CAA64425| - (X94976) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	264636
885	80052457 (1769, 1770)	Novel Protein sim. GBank gi|2078027|emb|CAB08467| - (Z95208) hypothetical protein Rv2372c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 18108362
886	11685136 (1771, 1772)				264690
887	94315307 (1773, 1774)	Novel Protein sim. GBank gi|2695834|emb|CAA15904| - (AL021006) sucA [Mycobacterium tuberculosis]		dehydrogenase	35696052, 264906, 264600, 264603, 35695917, 35695855, 264636
888	10083399 (1775, 1776)	Novel Protein sim. GBank gi|5689395|dbj|BAA82981.1| - (AB028952) KIAA1029 protein [Homo sapiens]		UNCLASSIFIED	264908
889	20385917 (1777, 1778)	Novel Protein sim. GBank gi|1881338|dbj|BAA19365| - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE. [Bacillus subtilis]			264603
890	19904337 (1779, 1780)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]			264629

891	13516879 (1781, 1782)	Novel Protein sim. GBank gi|4959396|gb|AAD34331.1|AF11248 - (AF112481) RAD54B protein [Homo sapiens]		UNCLASSIFIED	264636
892	87634157 (1783, 1784)	Novel Protein sim. GBank gi|545526|bbs|143833 - LBP-1b=transcription factor binding to initiation site of HIV-1 (alternatively spliced) [human, Namalwa cells, Peptide, 541 aa]		transcriptfactor	22278996, 22278999, 29331828, 35696052, 264908, 264909, 265009, 265011, 264602, 265019, 264766, 21906765, 21906766, 21906769, 265020, 265021, 56526486
893	79168037 (1785, 1786)	Novel Protein sim. GBank gi|2829688|sp|P80608|CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)		synthase	264689, 263967
894	11102240 (1787, 1788)				263978
895	80239868 (1789, 1790)			UNCLASSIFIED	264508, 264600, 264555, 264559
896	79747803 (1791, 1792)				264632
897	94991923 (1793, 1794)		Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	264686, 29331828, 264511
898	87895109 (1795, 1796)				56182575, 60432289, 56182435, 60432229, 55811957, 22279000, 264486
899	11100463 (1797, 1798)				264601
900	80499768 (1799, 1800)	Novel Protein sim. GBank gi|1750127 (U66480) - YncC [Bacillus subtilis]		transport	264769, 264691, 264563
901	80502410 (1801, 1802)	Novel Protein sim. GBank gi|3122879|sp|O07438|SYA_MYCTU - ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS)	Contains protein domain (PF01411) - tRNA synthetases class II (A)	synthase	264907, 264602, 264605, 264769, 35695917, 18108376, 264563
902	80503301 (1803, 1804)	Novel Protein sim. GBank gi|3355701|emb|CAA20001| - (AL031124) 3-isopropylmalate dehydratase large subunit [Streptomyces coelicolor]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	isomerase	264909, 265008, 264602, 264604, 264769, 264689, 264693
903	82060206 (1805, 1806)	Novel Protein sim. GBank gi|2960120|emb|CAA18018.1| - (AL022121) glpK [Mycobacterium tuberculosis]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	kinase	35696052, 264905, 264510, 264511, 264512, 264605, 264760, 18108351, 264762, 264687, 264768, 264769, 264688, 21906764, 35695917, 27486262, 35695855, 264634, 264636, 264486
904	20451078 (1807, 1808)	Novel Protein sim. GBank gi|728687|sp|P40906|ARGI_COCIM - ARGINASE	Contains protein domain (PF00491) - Arginase family	hydrolase	264604
905	9398483 (1809, 1810)	Novel Protein sim. GBank gi|4567200|gb|AAD23616.1|AC00716 - (AC007168) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264909
906	80052628 (1811, 1812)	Novel Protein sim. GBank gi|3738200|emb|CAA21292| - (AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]			264595, 264605
907	87913201 (1813, 1814)			UNCLASSIFIED	60432289, 264601, 264690
908	11754482 (1815, 1816)			UNCLASSIFIED	264638
909	20727907 (1817, 1818)	Novel Protein sim. GBank gi|3868940|dbj|BAA34296| - (AB015054) Alg2 [Rhizomucor pusillus]		UNCLASSIFIED	264602
910	16776206 (1819, 1820)	Novel Protein sim. GBank gi|4589726|dbj|BAA76883.1| - (AB003137) DnaJ homolog protein [Salix gilgiana]	Contains protein domain (PF00684) - DnaJ central domain (4 repeats)	eph	265009

911	87454340 (1821, 1822)	Novel Protein sim. GBank gi|548774|sp|P35685|RL7A_ORYSA - 60S RIBOSOMAL PROTEIN L7A		ribosomalprot	265010, 264604, 60432113
912	20448863 (1823, 1824)	Novel Protein sim. GBank gi|2314008|gb|AAD07921.1| - (AE000597) CDP-diglyceride hydrolase (cdh) [Helicobacter pylori 26695]		hydrolase	264559
913	20469357 (1825, 1826)			UNCLASSIFIED	264604
914	79183351 (1827, 1828)	Novel Protein sim. GBank gi|417657|sp|Q03604|RIR1_CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)	Contains protein domain (PF00317) - Ribonucleotide reductase	reductase	264636
915	87606703 (1829, 1830)	Novel Protein sim. GBank gi|5689571|db||BAA83069.1| - (AB029040) KIAA1117 protein [Homo sapiens]			18108398, 22278996, 66714117, 264906, 264591, 21906768, 265020, 55811576, 264638
916	79444091 (1831, 1832)	Novel Protein sim. GBank gi|4186110|emb|CAA71790| - (Y10831) putative integrase [Ralstonia eutropha]		UNCLASSIFIED	264595
917	20195985 (1833, 1834)			UNCLASSIFIED	264605
918	91226795 (1835, 1836)	Novel Protein sim. GBank gi|1655699|emb|CAA69032| - (Y07752) pherophorin-S [Volvox carteri]		synthase	264259, 29331826, 264908, 265019, 264448, 265020, 264635, 83373044
919	80436785 (1837, 1838)	Novel Protein sim. GBank gi|5689968|emb|CAB52005.1| - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]			265006, 264512, 264600, 264602, 264604, 264768, 18108370, 264563
920	79606095 (1839, 1840)	Novel Protein sim. GBank gi|1168448|sp|Q05813|AMP1_STRLI - XAA-PRO AMINOPEPTIDASE I (X-PRO AMINOPEPTIDASE I) (AMINOPEPTIDASE P I) (APP) (PEPP I) (AMINOACYLPROLINE AMINOPEPTIDASE I)		peptidase	264508
921	19858634 (1841, 1842)	Novel Protein sim. GBank gi|3850084|emb|CAA21911.1| - (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]		UNCLASSIFIED	264600
922	76982605 (1843, 1844)				265019, 22279002
923	86695830 (1845, 1846)	Novel Protein sim. GBank gi|267079|sp|P29514|TBB6_ARATH - TUBULIN BETA-6 CHAIN		tubulin	264907, 265008, 265009, 265010, 18108351, 264689, 265021, 18108370, 18108374, 18108385
924	21431341 (1847, 1848)				264510
925	20630332 (1849, 1850)	Novel Protein sim. GBank gi|2497688|sp|Q60963|PAFA_MOUSE - PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHO...		esterase	264603
926	79397657 (1851, 1852)	Novel Protein sim. GBank gi|3882325|dbj|BAA34522.1| - (AB018345) KIAA0802 protein [Homo sapiens]			55811957, 263972, 264639
927	37036201 (1853, 1854)			UNCLASSIFIED	264769

928	80070610 (1855, 1856)	Novel Protein sim. GBank gi|156146 (M30316) - xanthine dehydrogenase (AA at 2538) [Calliphora vicina]		dehydrogenase	264605
929	20630336 (1857, 1858)			UNCLASSIFIED	264603
930	5496348 (1859, 1860)	Novel Protein sim. GBank gi|4115936|gb|AAD03446.1| - (AF118223) No definition line found [Arabidopsis thaliana]			264259
931	10245731 (1861, 1862)	Novel Protein sim. GBank gi|4490609|emb|CAB38642.1| - (AJ133495) ribonucelotide reductase major subunit [Staphylococcus aureus]	Contains protein domain (PF00317) - Ribonucleotide reductase	reductase	264486
932	80420613 (1863, 1864)	Novel Protein sim. GBank gi|5459396|emb|CAB50754.1| - (AL096839) putative integral membrane transport protein [Streptomyces coelicolor]		transport	264508, 264905, 264906, 264909, 264600, 264602, 264603, 264605, 264766, 264558, 18108387, 264486
933	94326010 (1865, 1866)	Novel Protein sim. GBank gi|5689523|dbj|BAA83045.1| - (AB029016) KIAA1093 protein [Homo sapiens]	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264508, 264686, 264693, 27486261, 18108370, 65274791, 264636, 264559, 22279002
934	80039105 (1867, 1868)	Novel Protein sim. GBank gi|119111|sp|P12978|EBN2_EBV - EBNA-2 NUCLEAR PROTEIN			264369, 22279002
935	80063162 (1869, 1870)			UNCLASSIFIED	264604, 264605, 264693, 18108370, 18108374
936	80026632 (1871, 1872)	Novel Protein sim. GBank gi|845686 (M32103) - ORF-27 [Staphylococcus aureus]		UNCLASSIFIED	22278995, 22278996, 264602, 264687, 32833986, 18108387
937	80250273 (1873, 1874)	Novel Protein sim. GBank gi|1360669|pir||CGHU1V - collagen alpha 1(V) chain precursor - human		synthase	263978
938	80026633 (1875, 1876)	Novel Protein sim. GBank gi|2226243|emb|CAA74531.1| - (Y14083) hypothetical protein [Bacillus subtilis]		UNCLASSIFIED	264602
939	11071694 (1877, 1878)				264600
940	94144252 (1879, 1880)	Novel Protein sim. GBank gi|3560166|emb|CAA20678| - (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264905, 264906, 264907, 264908, 264909, 264511, 264910, 264592, 33657402, 264596, 264758, 264760, 264683, 264766, 264768, 264769, 33657023, 33657109, 264628, 264629, 264630, 264635, 264636, 264555, 264637, 264556, 264638, 264639, 83373044, 18108385, 264565, 18108391
941	11398414 (1881, 1882)				264593
942	19484122 (1883, 1884)			UNCLASSIFIED	264760
943	80080258 (1885, 1886)	Novel Protein sim. GBank gi|4033729 (AF038595) - apolipoprotein N-acyltransferase [Pseudomonas aeruginosa]		UNCLASSIFIED	264600, 264687, 264689, 264563
944	80216096 (1887, 1888)	Novel Protein sim. GBank gi|2494764|sp|Q50729|GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)		synthase	264511, 264603
945	80052477 (1889, 1890)	Novel Protein sim. GBank gi|732353|sp|P39606|YWCH_BACSU - HYPOTHETICAL 36.6 KD PROTEIN IN QOXD-VPR INTERGENIC REGION	Contains protein domain (PF00818) - Ice nucleation protein repeat	UNCLASSIFIED	264906, 264604, 264605, 265020, 18108387
946	79248402 (1891, 1892)				265017

947	81802699 (1893, 1894)	Novel Protein sim. GBank gi|2896770|emb|CAA17247| - (AL021899) hypothetical protein Rv2033c [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	18108394, 22278996, 264907, 264909, 265008, 265009, 264910, 264758, 264600, 264602, 265018, 264605, 264769, 264689, 264693
948	88165538 (1895, 1896)	Novel Protein sim. GBank gi|2827284 (AF041037) - novel antagonist of FGF signaling [Homo sapiens]		fgf	18108398, 56182575, 22278997, 22278999, 60432049, 29331822, 29331826, 264907, 56182435, 55811386, 265011, 264600, 265017, 265018, 265019, 18108351, 265020, 265021, 265022, 27486265, 263972, 55811576, 264638, 60170394, 264566
949	88081786 (1897, 1898)	Novel Protein sim. GBank gi|4507985|ref|NP_003427.1|pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	29331825, 21906764, 27486261, 21906766, 52644296, 33657349, 87168518, 56994075, 265020, 265021, 87168559, 52644150, 264637
950	79485872 (1899, 1900)	Novel Protein sim. GBank gi|1079461|pir||S43865 - cytokeratin 8, type II - potoroo (fragment)	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264683, 18108361
951	20451411 (1901, 1902)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264604
952	79566954 (1903, 1904)	Novel Protein sim. GBank gi|5305702|gb|AAD41779.1|AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	264910, 264691
953	10196003 (1905, 1906)	Novel Protein sim. GBank gi|2495642|sp|Q47142|YFHS_ECOLI - HYPOTHETICAL 41.6 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION		transport	264510
954	9893326 (1907, 1908)	Novel Protein sim. GBank gi|2360965 (AF016253) - D-amino acid dehydrogenase [Klebsiella aerogenes]		dehydrogenase	264508
955	95313410 (1909, 1910)	Novel Protein sim. GBank gi|5454064|ref|NP_006319.1|pSIP| - SYT interacting protein	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	56994075, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264910, 264758, 264759, 265010, 264601, 264760, 18108351, 264762, 264763, 264764, 264766, 264686, 264767, 264687, 264768, 264769, 264689, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 56182323, 264639, 18108388, 264563, 264564
956	80064224 (1911, 1912)	Novel Protein sim. GBank gi|2052129|emb|CAB08155| - (Z94752) rimJ [Mycobacterium tuberculosis]			264605
957	80056206 (1913, 1914)			UNCLASSIFIED	264603, 18108362
958	80036446 (1915, 1916)	Novel Protein sim. GBank gi|1709787|sp|Q00451|PRF1_LYCES - 36.4 KD PROLINE-RICH PROTEIN		UNCLASSIFIED	264908, 264910, 264762, 263978, 264637
959	80026647 (1917, 1918)	Novel Protein sim. GBank gi|2131050|emb|CAB09260| - (Z95844) opcA [Mycobacterium tuberculosis]		UNCLASSIFIED	264602, 264692
960	37815406 (1919, 1920)	Novel Protein sim. GBank gi|2129478|pir||S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264259
961	20567383 (1921, 1922)				263978
962	11399318 (1923, 1924)				264593

963	80590374 (1925, 1926)			UNCLASSIFIED	264510, 264288, 264555, 264556, 264559, 264486
964	79832019 (1927, 1928)	Novel Protein sim. GBank gi|4589622|db|BAA76833.1| - (AB023206) KIAA0989 protein [Homo sapiens]		UNCLASSIFIED	264112, 264910, 264689
965	91229485 (1929, 1930)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 265017, 264448, 264634, 264558, 83373044
966	95292815 (1931, 1932)			UNCLASSIFIED	264906, 264592, 264596, 264604, 264768, 21906764, 264692, 264693, 264629, 264636, 264638
967	79255708 (1933, 1934)	Novel Protein sim. GBank gi|1731207|sp|Q11156|RGX3_MYCTU - SENSORY TRANSDUCTION PROTEIN REGX3	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	264760
968	79560269 (1935, 1936)	Novel Protein sim. GBank gi|2661836|emb|CAA75187| - (Y14964) putative transport protein [Methylophilus methylotrophus]		transport	264693
969	79919470 (1937, 1938)	Novel Protein sim. GBank gi|5419878|emb|CAB46422.1| - (AL096747) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	35696286, 264685, 264686, 35695917, 264692, 18108374, 264635
970	95085947 (1939, 1940)			UNCLASSIFIED	18108392, 18108394, 18108398, 22278995, 22278996, 22278998, 22278999, 29147620, 264828, 265006, 265007, 265008, 265009, 18108348, 33109954, 265010, 265011, 18108351, 264288, 21906767, 21906768, 18108370, 18108374, 18108377, 264630, 264635, 18108380, 83373044, 18108387, 18108388
971	78919770 (1941, 1942)			UNCLASSIFIED	265007, 265020, 22279002
972	20710704 (1943, 1944)				264557
973	20370183 (1945, 1946)	Novel Protein sim. GBank gi|1723119|sp|P53990|Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174			264604
974	80057103 (1947, 1948)			UNCLASSIFIED	264565
975	10196018 (1949, 1950)			UNCLASSIFIED	264510
976	80205742 (1951, 1952)	Novel Protein sim. GBank gi|3881459|emb|CAA92988.1| - (Z68753) predicted using Genefinder; Similarity to Yeast hypothetical protein YIK9 (SW:YIK9_YEAST); cDNA EST EMBL:D27680 comes from this gene; cDNA EST EMBL:D27679 comes from this gene; cDNA EST EMBL:D64477 comes from this ge...		UNCLASSIFIED	264508, 264906, 264758, 264632, 264639, 264563
977	10355349 (1953, 1954)	Novel Protein sim. GBank gi|549456|sp|Q05335|XYS3_PSEPU - XYLDLEGF OPERON TRANSCRIPTIONAL ACTIVATOR 3		UNCLASSIFIED	264906
978	80025927 (1955, 1956)			UNCLASSIFIED	264600, 264602, 264603, 264604
979	80447820 (1957, 1958)	Novel Protein sim. GBank gi|3171904|emb|CAA75869| - (Y15908) DIA-12C protein [Homo sapiens]		UNCLASSIFIED	264767, 264768, 265006, 265007, 264906
980	80025928 (1959, 1960)			UNCLASSIFIED	264600, 264602, 264605
981	80098550 (1961, 1962)	Novel Protein sim. GBank gi|3599940 (AF017368) - faciogenital dysplasia protein 2 [Mus musculus]		UNCLASSIFIED	264692, 264555, 264556, 264557, 264559

982	80195670 (1963, 1964)	Novel Protein sim. GBank gi|2950220|emb|CAA71575| - (Y10545) fused-ccdB [Escherichia coli]		UNCLASSIFIED	264404
983	90995041 (1965, 1966)	Novel Protein sim. GBank gi|476389|pir||B43402 - myosin heavy chain-B, neuronal - chicken		struct	65274572, 56182575, 264908, 264909, 265007, 265008, 264758, 265010, 55811150, 33657023, 264634, 264557, 264558
984	20466876 (1967, 1968)			UNCLASSIFIED	264605
985	65461368 (1969, 1970)	Novel Protein sim. GBank gi|3451504|emb|CAA07660.1| - (AJ007747) hypothetical protein BbLPS1.21 [Bordetella bronchiseptica]	Contains protein domain (PF00534) - Glycosyl transferases group 1	transferase	56182435, 264600
986	87102868 (1971, 1972)			UNCLASSIFIED	264106, 264110, 265020, 60170615
987	79867231 (1973, 1974)				264909
988	19858661 (1975, 1976)			UNCLASSIFIED	264600
989	88095329 (1977, 1978)			UNCLASSIFIED	264508, 265017, 264534, 264564
990	88057746 (1979, 1980)	Novel Protein sim. GBank gi|5725506|gb|AAD48080.1|AF06015 - (AF060152) METH1 protein [Homo sapiens]	Contains protein domain (PF01421) - Reprolysin (M12B) family zinc metalloprotease	oxidase	264259, 264908, 265009, 264910, 264596, 264369, 264288, 264766, 264628, 264635, 264566
991	10106140 (1981, 1982)			UNCLASSIFIED	264909
992	79845694 (1983, 1984)	Novel Protein sim. GBank gi|2105049|emb|CAB08835| - (Z95436) hypothetical protein Rv3645 [Mycobacterium tuberculosis]	Contains protein domain (PF00211) - Adenylate and Guanylate cyclase catalytic domain	UNCLASSIFIED	264508, 264593
993	10814053 (1985, 1986)				264907
994	11090590 (1987, 1988)	Novel Protein sim. GBank gi|3329297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]		reductase	264602
995	94321911 (1989, 1990)	Novel Protein sim. GBank gi|5106572|gb|AAD39760.1|AF14394 - (AF143946) transcriptional activator SRCAP [Homo sapiens]	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	18108398, 65274572, 22278996, 264490, 60432049, 29331827, 29146498, 264508, 264905, 264907, 264908, 56182435, 265008, 264591, 264592, 60432229, 60431735, 33657402, 264595, 264758, 21906754, 265010, 265017, 265018, 264605, 264760, 264448, 264763, 264768, 21906765, 21906768, 21906769, 55811957, 264692, 264693, 264629, 35696423, 55811576, 35695855, 264636, 264555, 264556, 264558, 83373044, 22279002, 264563
996	91013745 (1991, 1992)	Novel Protein sim. GBank gi|2911719 (AC004227) - KIA001LB [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	phosphatase	83373044, 29331824, 263978, 55811957, 56526486, 87168518, 264910, 264906, 264565, 264566, 264693, 264766
997	80503347 (1993, 1994)	Novel Protein sim. GBank gi|2649101 (AE001001) - ABC transporter, ATP-binding protein [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	35696286, 22278997, 22278999, 264508, 264905, 264908, 265010, 264600, 264602, 264605, 264688, 264769, 265021, 264565, 18108391
998	11397390 (1995, 1996)	Novel Protein sim. GBank gi|123530|sp|P04929|HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR			264595

999	11768047 (1997, 1998)	Novel Protein sim. GBank gi|2506897|sp|P46490|YFCA_HAEIN - HYPOTHETICAL PROTEIN HI0198		UNCLASSIFIED	264682
1000	20727944 (1999, 2000)			UNCLASSIFIED	264602
1001	86673131 (2001, 2002)	Novel Protein sim. GBank gi|2224699|dbj|BAA20833| - (AB002377) KIAA0379 [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	60432049, 264907, 264909, 264511, 264603, 264683, 264684, 264687, 264689, 29148627, 21906769, 264692, 18108385, 22279000
1002	80189603 (2003, 2004)	Novel Protein sim. GBank gi|586121|sp|P37709|TRHY_RABIT - TRICHOHYALIN		struct	265009, 264369, 265020
1003	17933491 (2005, 2006)				265019
1004	16314987 (2007, 2008)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]			264635
1005	79617144 (2009, 2010)	Novel Protein sim. GBank gi|114073|sp|P07672|APT_ECOLI - ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)		UNCLASSIFIED	264508
1006	37815429 (2011, 2012)			UNCLASSIFIED	264259
1007	79620871 (2013, 2014)	Novel Protein sim. GBank gi|4062979|dbj|BAA36210.1| - (AB017138) epsilon subunit of malonate decarboxylase [Pseudomonas putida]		synthase	264905
1008	88094444 (2015, 2016)	Novel Protein sim. GBank gi|2808807|emb|CAA04607.1| - (AJ001206) putative trehalose synthase [Streptomyces coelicolor]		synthase	265007, 264602, 264605, 264760, 264636
1009	57451289 (2017, 2018)	Novel Protein sim. GBank gi|3639077 (AF090113) - AMPA receptor binding protein [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	264102, 264288
1010	94672537 (2019, 2020)	Novel Protein sim. GBank gi|3746332 (AF016307) - possible NADH-dependent oxidase, may function as a demethylase [Sinorhizobium meliloti]		dehydrogenase	264592
1011	85546916 (2021, 2022)	Novel Protein sim. GBank gi|2342647|gb|AAB86591.1| - (U90653) DHHC-domain-containing cysteine-rich protein [Homo sapiens]		UNCLASSIFIED	35696052, 264905, 264764, 264768, 35695917, 264629
1012	95294456 (2023, 2024)	Novel Protein sim. GBank gi|3413411|emb|CAA20272| - (AL031231) guanosine pentaphosphate synthetase/ polyribonucleotide nucleotidyltransferase [Streptomyces coelicolor]	Contains protein domain (PF00013) - KH domain	phosphorylase	35696052, 264905, 264600, 264601, 264602, 264605, 264762, 264766, 264768, 264689
1013	86095772 (2025, 2026)			UNCLASSIFIED	264591, 21906768
1014	86608828 (2027, 2028)				29331824, 265019, 265020

1015	95418879 (2029, 2030)	Novel Protein sim. GBank gi|4159995 (AF063095) - SELIL [Mus musculus]	Contains protein domain (PF00040) - Fibronectin type II domain	struct	22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331825, 29331828, 264907, 56182435, 264510, 264591, 264593, 60433356, 264594, 55812038, 264758, 21906754, 33657084, 265010, 264600, 265017, 265018, 265019, 18108351, 21906765, 21906766, 21906767, 21906768, 55811957, 265022, 33657023, 65274620, 33657182, 32833986, 18108370, 18108377, 55811576, 35696423, 264630, 22279000, 264565
1016	79559694 (2031, 2032)	Novel Protein sim. GBank gi|2506969|sp|P41407|ACPD_ECOLI - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)		esterase	264686, 264693
1017	11069213 (2033, 2034)	Novel Protein sim. GBank gi|5103943|dbj|BAA79259.1| - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA [Aeropyrum pernix]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	transport	264600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gi|4493973|emb|CAB39032.1| - (AL034559) predicted using hexExon; MAL3P7.14 (PFC0925w), Hypothetical protein, len: 489 aa [Plasmodium falciparum]			22278996, 29148627, 264563
1019	11703607 (2037, 2038)			UNCLASSIFIED	264686
1020	80234432 (2039, 2040)				264508, 264509, 264512, 264600, 264762, 264769, 264689, 18108370, 264636, 264638, 264486
1021	37036243 (2041, 2042)	Novel Protein sim. GBank gi|4633807|gb|AAD26859.1|AF12779 - (AF127795) trehalose biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]		synthase	264769
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gi|1781230|emb|CAB06277| - (Z83867) hypothetical protein Rv3137 [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	35696052, 264508, 265008, 265009, 264769, 18108387, 264563
1023	11399341 (2045, 2046)	Novel Protein sim. GBank gi|3777495 (U92083) - calcium transporting ATPase [Pichia angusta]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated	264593
1024	80057128 (2047, 2048)			UNCLASSIFIED	52646842, 33657402, 33657023, 18108379, 55811578, 264631, 264556, 264557, 264559, 18108388, 264566
1025	79644200 (2049, 2050)	Novel Protein sim. GBank gi|3483045|emb|CAA20556| - (AL031371) putative transport system permease protein [Streptomyces coelicolor]		transport	264693
1026	80025948 (2051, 2052)	Novel Protein sim. GBank gi|1174922|sp|Q02322|UVRD_HAEIN - DNA HELICASE II		helicase	264602
1027	17659234 (2053, 2054)	Novel Protein sim. GBank gi|4757728|ref|NP_004886.1|pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	265017

1028	20297928 (2055, 2056)	Novel Protein sim. GBank gi|2791409|emb|CAA16003| - (AL021184) acn [Mycobacterium tuberculosis]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	264600
1029	94665090 (2057, 2058)			UNCLASSIFIED	264595
1030	88095343 (2059, 2060)			UNCLASSIFIED	264907, 264908, 264510, 264512, 265009, 265010, 265011, 264600, 264602, 264603, 264605, 264769, 18108372, 18108374
1031	95289117 (2061, 2062)			UNCLASSIFIED	264905, 264906, 264909, 264595, 264692, 264630, 264634, 264638
1032	94673275 (2063, 2064)	Novel Protein sim. GBank gi|4503895|ref|NP_000145.1|pGALK - galactokinase 1		UNCLASSIFIED	264689
1033	86464818 (2065, 2066)	Novel Protein sim. GBank gi|2982990 (AE000682) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	35896052, 264906, 264510, 18108354, 264687, 264769, 264689, 60431602, 18108385, 264486
1034	79245937 (2067, 2068)	Novel Protein sim. GBank gi|405895 (U00007) - methionyl-tRNA synthetase [Escherichia coli]		UNCLASSIFIED	264906
1035	79956355 (2069, 2070)			UNCLASSIFIED	264692
1036	85804998 (2071, 2072)				264905, 66712502, 264908, 264766
1037	87896058 (2073, 2074)			UNCLASSIFIED	29331824, 264909, 60433438, 265019
1038	20481015 (2075, 2076)	Novel Protein sim. GBank gi|790819 (L39891) - polycystic kidney disease-associated protein [Homo sapiens]	Contains protein domain (PF01477) - PLAT/LH2 domain		264604, 264634
1039	87260021 (2077, 2078)	Novel Protein sim. GBank gi|2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	264092, 264093, 264094, 264683, 264689, 263967
1040	80026840 (2079, 2080)	Novel Protein sim. GBank gi|2352095 (U97022) - DNA topoisomerase I [Fervidobacterium islandicum]	Contains protein domain (PF01131) - Prokaryotic DNA topoisomerase	isomerase	264595
1041	10156682 (2081, 2082)	Novel Protein sim. GBank gi|3256535|dbj|BAA29218.1| - (AP000001) 301aa long hypothetical 2-phosphoglycerate kinase [Pyrococcus horikoshii]		kinase	264907
1042	11084375 (2083, 2084)	Novel Protein sim. GBank gi|2058299|emb|CAA66953| - (X98309) ARI protein [Drosophila melanogaster]			264605
1043	80057136 (2085, 2086)	Novel Protein sim. GBank gi|1870167|emb|CAA70125| - (Y08921) mslK [Streptomyces reticuli]	Contains protein domain (PF00005) - ABC transporter	transport	264565, 264567
1044	80025952 (2087, 2088)			UNCLASSIFIED	265006, 264602, 265017
1045	52415482 (2089, 2090)	Novel Protein sim. GBank gi|5689890|emb|CAB52053.1| - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]			29331825, 264637
1046	11754862 (2091, 2092)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]		helicase	264686
1047	37036258 (2093, 2094)	Novel Protein sim. GBank gi|4210471|dbj|BAA74535.1| - (AB019033) orfSA [Pseudomonas sp.]		UNCLASSIFIED	264769
1048	79186400 (2095, 2098)	Novel Protein sim. GBank gi|3413419|emb|CAA20279| - (AL031232) hypothetical protein SC10H5.07 [Streptomyces coelicolor]	Contains protein domain (PF00220) - Neurohypophysial hormones, N-terminal Domain	UNCLASSIFIED	264687
1049	81755108 (2097, 2098)	Novel Protein sim. GBank gi|5051636|gb|AAD38326.1|AF07372 - (AF073727) EH domain-binding mitotic phosphoprotein [Homo sapiens]		UNCLASSIFIED	264905, 264634
1050	79471521 (2099, 2100)			UNCLASSIFIED	264686

1051	80475471 (2101, 2102)			UNCLASSIFIED	18108374, 264769, 265010, 265011, 264601, 265009, 264604, 264605, 264636, 18108351, 264692
1052	82442962 (2103, 2104)	Novel Protein sim. GBank gi|3123275|sp|P35136|SERA_BACSU - D-3-PHOSPHOGLYCERATE DEHYDROGENASE (PGDH)	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases	dehydrogenase	264508, 264762, 264687, 264486
1053	94851640 (2105, 2106)	Novel Protein sim. GBank gi|5441319|emb|CAB46717.1| - (AL034396) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]			264686, 18108374, 29331824, 83373044, 21906754, 52645156, 56182435, 264689, 29331827, 27486261, 35696052, 21906765, 35696423, 21906768, 56182575, 21906769, 55811957, 87168518, 35696286, 22278997, 265020, 265011, 265021, 265022, 265007, 265018, 22279000, 22279002, 264482, 264906, 52644150, 264909, 264288, 29331822, 52645080, 264766
1054	79580225 (2107, 2108)			UNCLASSIFIED	264686
1055	80594138 (2109, 2110)	Novel Protein sim. GBank gi|5052508|gb|AAD38584.1|AF14560 - (AF145609) BcDNA.GH02833 [Drosophila melanogaster]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	264907, 264602, 264681, 264288, 21906768, 33657109, 55810764, 35695855, 264631
1056	17882319 (2111, 2112)	Novel Protein sim. GBank gi|3021676|dbj|BAA25358| - (D86033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens]		rnapolymerase	264906
1057	85667216 (2113, 2114)	Novel Protein sim. GBank gi|1226281 (U50308) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264682
1058	80376576 (2115, 2116)				264764
1059	94662754 (2117, 2118)	Novel Protein sim. GBank gi|1170016|sp|P46808|GREA_MYCLE - TRANSCRIPTION ELONGATION FACTOR GREA (TRANSCRIPT CLEAVAGE FACTOR GREA)		transcriptfactor	35696052, 35695855, 265009, 264636
1060	79481169 (2119, 2120)	Novel Protein sim. GBank gi|2499087|sp|Q09332|UGGG_DROME - UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	29146499, 264681, 264683, 264687
1061	11034025 (2121, 2122)	Novel Protein sim. GBank gi|90254|pir||A28334 - protein-tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse		phosphatase	264634
1062	39567937 (2123, 2124)	Novel Protein sim. GBank gi|3334200|sp|O49954|GCSP_SOLTU - GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)		dehydrogenase	264593
1063	8490481 (2125, 2126)	Novel Protein sim. GBank gi|2499966|sp|Q41228|PSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A)			264508
1064	78891783 (2127, 2128)	Novel Protein sim. GBank gi|82654|pir||JA0086 - 10K zein precursor - maize			265007, 265008, 18108351, 18108385

1065	80021208 (2129, 2130)	Novel Protein sim. GBank gi|2120998|pir||S70682 - glycosyltransferase homolog - Bordetella pertussis		transferase	264600, 264602, 264689
1066	17896879 (2131, 2132)	Novel Protein sim. GBank gi|2506362|sp|P15042|DNLJ_ECOLI - DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+))		synthase	265009
1067	10132178 (2133, 2134)				264909
1068	82062057 (2135, 2136)	Novel Protein sim. GBank gi|4007669|emb|CAA22355| - (AL034443) putative oxidoreductase [Streptomyces coelicolor]	Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	264688, 18108362, 264558, 264600, 264760
1069	83002954 (2137, 2138)	Novel Protein sim. GBank gi|4589484|dbj|BAA76770.1| - (AB023143) KIAA0926 protein [Homo sapiens]		UNCLASSIFIED	264604
1070	82101992 (2139, 2140)	Novel Protein sim. GBank gi|120304|sp|P15932|FLGK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)		UNCLASSIFIED	264604, 264760
1071	20710589 (2141, 2142)	Novel Protein sim. GBank gi|1750397 (U81261) - glutamate synthase large subunit [Pseudomonas aeruginosa]		synthase	264602
1072	82356540 (2143, 2144)			UNCLASSIFIED	264687, 264688, 21906784, 35696052, 35695917, 35695855, 264600, 264601, 264602, 265009, 264605, 264508, 264905, 264690, 264906, 264762, 264628, 264766
1073	79814400 (2145, 2146)				264909
1074	80105992 (2147, 2148)	Novel Protein sim. GBank gi|477532|pir||A49175 - Motch B protein - mouse (fragment)	Contains protein domain (PF00008) - EGF-like domain	synthase	264906
1075	81850293 (2149, 2150)	Novel Protein sim. GBank gi|3893109|emb|CAA76940| - (Y17920) CALO protein [Drosophila melanogaster]		UNCLASSIFIED	56994075, 22278998, 264594, 264757, 264596, 265018, 265019, 264681, 264369, 264688, 265020, 18108364, 18108374
1076	80477264 (2151, 2152)	Novel Protein sim. GBank gi|1176203|sp|P46442|YHCM_ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375)		ATPase_associated	264769
1077	79831334 (2153, 2154)	Novel Protein sim. GBank gi|4033487|sp|Q44472|TUD4_AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE		kinase	264905
1078	20288874 (2155, 2156)			UNCLASSIFIED	264600
1079	80494518 (2157, 2158)	Novel Protein sim. GBank gi|3413828|emb|CAA20296| - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	18108394, 264769, 264634, 264636
1080	11767188 (2159, 2160)			UNCLASSIFIED	264684
1081	94747080 (2161, 2162)				83373044, 265019, 22279002, 264482, 18108351, 264682, 264908, 264693, 264487
1082	81490656 (2163, 2164)			UNCLASSIFIED	264758, 264768, 264769, 21906767, 264511, 264910, 264634, 264635, 264905, 264636, 264906, 264637, 264907, 264908, 264764, 264638, 20281099, 264766, 264595

1083	87446717 (2165, 2166)	Novel Protein sim. GBank gi|1722945|sp|Q10523|Y01N_MYCTU - HYPOTHETICAL 44.6 KD PROTEIN CY427.23		UNCLASSIFIED	60424179, 264905, 264906, 264510, 60432229, 264759, 87168474, 264605, 264769, 264689, 18108364, 18108376, 35695855, 264636
1084	37799306 (2167, 2168)	Novel Protein sim. GBank gi|418384|sp|P32057|WCAI_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI		UNCLASSIFIED	264769
1085	86475368 (2169, 2170)	Novel Protein sim. GBank gi|1899190 (U90204) - heat shock protein 60 [Tsukamurella tyrosinosolvens]	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	eph	60432229, 264687
1086	79608269 (2171, 2172)	Novel Protein sim. GBank gi|1172956|sp|P46176|RL14_ACYKS - 50S RIBOSOMAL PROTEIN L14	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomalprot	264486
1087	79603979 (2173, 2174)	Novel Protein sim. GBank gi|4160198|emb|CAA15431| - (AL008583) dJ327J16.3 (novel CHROMObox family protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHRromatin Organization MOdifier) domain	helicase	29331827, 264693
1088	79854963 (2175, 2176)	Novel Protein sim. GBank gi|2983155 (AE000693) - phosphoglucomutase/phosphomannomutase [Aquifex aeolicus]		UNCLASSIFIED	264905, 264601, 18108387
1089	80216800 (2177, 2178)	Novel Protein sim. GBank gi|4981768|gb|AAD36290.1|AE00177 - (AE001778) NADH dehydrogenase, 30 kDa subunit, putative [Thermotoga maritima]	Contains protein domain (PF00329) - Respiratory-chain NADH dehydrogenase, 30 Kd subunit	UNCLASSIFIED	264488, 264511, 265011, 264682, 264768, 264689, 21906764, 35695917, 265020, 32833986, 18108370, 35695855
1090	11083825 (2179, 2180)	Novel Protein sim. GBank gi|4007680|emb|CAA22366| - (AL034443) putative oxidoreductase [Streptomyces coelicolor]			264604
1091	12917471 (2181, 2182)	Novel Protein sim. GBank gi|2495562|sp|P77239|YLCD_ECOLI - HYPOTHETICAL 44.3 KD PROTEIN IN NFRB-PHEP INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264637
1092	80252286 (2183, 2184)				264566
1093	80496304 (2185, 2186)	Novel Protein sim. GBank gi|2960098|emb|CAA17996.1| - (AL022121) nth [Mycobacterium tuberculosis]	Contains protein domain (PF00730) - Endonuclease III	nuclease	264769, 35695917, 35695855, 264600, 264602, 264603, 264605, 18108351
1094	10880972 (2187, 2188)	Novel Protein sim. GBank gi|1001642|dbj|BAA10373| - (D64002) dGTP triphosphohydrolase [Synechocystis sp.]		UNCLASSIFIED	264686
1095	87457250 (2189, 2190)	Novel Protein sim. GBank gi|4585587|emb|CAB40855.1| - (AL049628) putative adenine glycosylase [Streptomyces coelicolor]	Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family	nuclease	264906, 265007, 264595, 264600, 264602, 264603, 264604, 264605, 264762, 264766, 264769, 264636, 264558, 18108387, 60432113, 264482, 264486
1096	80025977 (2191, 2192)	Novel Protein sim. GBank gi|115001|sp|P19206|BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)		synthase	264600, 264602, 264603, 264604, 264605, 35695917, 264692, 264631
1097	79239560 (2193, 2194)			UNCLASSIFIED	265019
1098	79186424 (2195, 2196)	Novel Protein sim. GBank gi|114135|sp|P08205|ARGA_ECOLI - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)		synthase	264687

1099	39523838 (2197, 2198)	Novel Protein sim. GBank gi|3915144|sp|O33017|TRMD_MYCLE - TRNA (GUANINE-N1)-METHYLTRANSFERASE (M1G-METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)		UNCLASSIFIED	264603
1100	85736571 (2199, 2200)	Novel Protein sim. GBank gi|3023255|sp|Q64420|ACOD_MESAU - ACYL-COA DESATURASE (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE)		desaturase	264259, 264636
1101	80491857 (2201, 2202)	Novel Protein sim. GBank gi|1174735|sp|P43012|TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)	Contains protein domain (PF01396) - Topoisomerase DNA binding C4 zinc finger	isomerase	264769
1102	79777614 (2203, 2204)			UNCLASSIFIED	264910, 264909
1103	81897259 (2205, 2206)	Novel Protein sim. GBank gi|1906596 (U81788) - kinesin-73 [Drosophila melanogaster]		struct	264757
1104	95003115 (2207, 2208)	Novel Protein sim. GBank gi|2935448 (AF048976) - synaptic ras GTPase-activating protein p135 SynGAP [Rattus norvegicus]		UNCLASSIFIED	29331822, 21906754, 264555, 264556, 264558, 22279002
1105	80255121 (2209, 2210)				264566
1106	79314110 (2211, 2212)			UNCLASSIFIED	264555, 264369
1107	80470019 (2213, 2214)				264906, 264769
1108	80440618 (2215, 2216)	Novel Protein sim. GBank gi|1173421|sp|P43416|SECY_STRSC - PREPROTEIN TRANSLOCASE SECY SUBUNIT		transport	264907, 264510, 264511, 264600, 264602, 264605, 264768, 264769
1109	80064615 (2217, 2218)	Novel Protein sim. GBank gi|2995310|emb|CAA18338| - (AL022268) putative ATP-dependent helicase [Streptomyces coelicolor]		helicase	264602, 264605, 264636
1110	80503554 (2219, 2220)				264908, 264593, 265010, 264601, 264603, 264604, 264605, 264682, 264769, 264693, 264636
1111	80071744 (2221, 2222)	Novel Protein sim. GBank gi|2622039 (AE000868) - type I restriction modification system, subunit S [Methanobacterium thermoautotrophicum]			18108370, 264557
1112	95010088 (2223, 2224)				264908
1113	82456352 (2225, 2226)	Novel Protein sim. GBank gi|3218376|emb|CAA19628| - (AL023862) putative oxidoreductase [Streptomyces coelicolor]		UNCLASSIFIED	264600, 264602, 264604, 264605, 264762, 264769, 264565
1114	14998014 (2227, 2228)	Novel Protein sim. GBank gi|1083428|pir||S54876 - NAD(F)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse		dehydrogenase	264636
1115	11765583 (2229, 2230)			UNCLASSIFIED	264686
1116	79841152 (2231, 2232)				264908

1117	95305465 (2233, 2234)	Novel Protein sim. GBank gi|3255965|emb|CAA94089| - (Z70200) U5 snRNP-specific 200kD protein [Homo sapiens]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108392, 264488, 263994, 264489, 18108398, 56182575, 22278995, 22278996, 35696286, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 29146498, 264508, 264905, 264509, 264906, 264907, 264908, 66712502, 264909, 52644045, 56182435, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 60170831, 264591, 264592, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264596, 264758, 264759, 21906754, 33109954, 33657084, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 264604, 265018, 264605, 265019, 264760, 55811150, 264681, 264762, 18108351, 264448, 264682, 264764, 264683, 264288, 264369, 264684, 264685, 264766, 264767, 264686, 264687, 264768, 264769, 264688, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148784, 35695917, 265020, 265021, 265022, 60170615, 264690, 264691, 33657023, 264692, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763,
1118	79563326 (2235, 2236)			UNCLASSIFIED	264691
1119	79642463 (2237, 2238)			UNCLASSIFIED	264907
1120	79480463 (2239, 2240)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		collagen	29331827, 265018, 265019, 264681, 265021, 60170615, 18108387
1121	79471716 (2241, 2242)	Novel Protein sim. GBank gi|1644450 (U67864) - MEX-3 [Caenorhabditis elegans]	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	264683, 264632, 18108388
1122	79456246 (2243, 2244)			UNCLASSIFIED	264639, 264563
1123	79637119 (2245, 2246)	Novel Protein sim. GBank gi|98800|pir||S17768 - 3-dehydroquinate synthase (EC 4.6.1.3) - Mycobacterium tuberculosis		synthase	264693, 27486265
1124	79811596 (2247, 2248)			UNCLASSIFIED	264909
1125	79757861 (2249, 2250)			UNCLASSIFIED	264910
1126	79758914 (2251, 2252)	Novel Protein sim. GBank gi|138154|sp|P03643|VGG_BPPHX - MAJOR SPIKE PROTEIN (G PROTEIN) (GPG)		eph	264905, 264909, 264910
1127	11800930 (2253, 2254)			UNCLASSIFIED	264682
1128	8364885 (2255, 2256)	Novel Protein sim. GBank gi|5002704|emb|CAB44358.1| - (AJ242630) DNA polymerase I [Methylobacterium sp. DM4]	Contains protein domain (PF00476) - DNA polymerase family A	polymerase	264511

1129	80422480 (2257, 2258)	Novel Protein sim. GBank gi|5689485|dbj|BAA83026.1| - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	265011, 264766
1130	79420151 (2259, 2260)			UNCLASSIFIED	264595
1131	80055391 (2261, 2262)	Novel Protein sim. GBank gi|4981328|gb|AAD35881.1|AE00174 - (AE001747) bioY protein [Thermotoga maritima]		UNCLASSIFIED	35696286, 22278998, 28331828, 264603, 264605, 264559
1132	82062248 (2263, 2264)	Novel Protein sim. GBank gi|1841552 (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	22278996, 264906, 265009, 264600, 264602, 264604, 264605, 264760, 32833986, 18108374
1133	17290437 (2265, 2266)			UNCLASSIFIED	265018
1134	80235376 (2267, 2268)			UNCLASSIFIED	264512, 264534
1135	80029393 (2269, 2270)	Novel Protein sim. GBank gi|4539171|emb|CAB39700.1| - (AL049485) conserved hypothetical protein [Streptomyces coelicolor]			264508, 264600, 264602, 264603, 18108376
1136	79842052 (2271, 2272)	Novel Protein sim. GBank gi|4982454|gb|AAD36931.1|AE00182 - (AE001823) ATP-dependent protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	264906, 264908
1137	90931557 (2273, 2274)	Novel Protein sim. GBank gi|4972746|gb|AAD34768.1| - (AF132180) unknown [Drosophila melanogaster]	Contains protein domain (PF00515) - TPR Domain	collagen	22278998, 22278999, 35696052, 264907, 265009, 60433356, 264596, 265010, 264448, 264682, 264767, 264689, 265020, 264692, 55811576, 35695855, 264631, 264632, 22279002
1138	79841163 (2275, 2276)	Novel Protein sim. GBank gi|731607|sp|P38739|YHC8_YEAST - HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR		struct	264908
1139	79633561 (2277, 2278)	Novel Protein sim. GBank gi|3650031 (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]		UNCLASSIFIED	264693
1140	39480358 (2279, 2280)			UNCLASSIFIED	264593
1141	79638019 (2281, 2282)			UNCLASSIFIED	265019, 264693
1142	19635848 (2283, 2284)			UNCLASSIFIED	264631
1143	87762158 (2285, 2286)	Novel Protein sim. GBank gi|3928000|emb|CAA05880| - (AJ003125) procollagen I N-proteinase [Homo sapiens]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	oxidase	56182575, 264908, 264600, 264632, 87168518
1144	80088988 (2287, 2288)			UNCLASSIFIED	264635, 264636, 264907, 264593, 264908, 264566, 264909
1145	14810262 (2289, 2290)			UNCLASSIFIED	264112
1146	82062092 (2291, 2292)			UNCLASSIFIED	264769, 264689, 35696286, 264760, 264905, 264486, 264559
1147	80071761 (2293, 2294)				264557
1148	80048431 (2295, 2296)	Novel Protein sim. GBank gi|2499003|sp|P76422|THID_ECOLI - PHOSPHOMETHYLPYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)		kinase	264591
1149	11607438 (2297, 2298)	Novel Protein sim. GBank gi|2896734|emb|CAA17213.1| - (AL021897) hypothetical protein Rv1097c [Mycobacterium tuberculosis]			264591

1150	81325074 (2299, 2300)	Novel Protein sim. GBank gi|2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]		ATPase_associated	264488, 35696286, 264907, 264908, 264909, 264910, 264593, 264596, 264758, 264764, 264766, 264768, 264693, 264628, 60431850, 264564, 264566, 264567
1151	80070874 (2301, 2302)	Novel Protein sim. GBank gi|4324655|gb|AAD16978| - (AF108191) DNA polymerase III alpha subunit [Streptomyces coelicolor]		polymerase	264595
1152	80235547 (2303, 2304)	Novel Protein sim. GBank gi|3874275|emb|CAB07311.1| - (Z92825) predicted using Genefinder; Similarity to Yeast low afinity glucose transporter HXT4 (PS:32467); cDNA EST EMBL:C12555 comes from this gene; cDNA EST yk404c10.3 comes from this gene; cDNA EST yk404c10.5 comes from thi...		glycoprotein	264488, 22278998, 264905, 264629, 264486
1153	80027783 (2305, 2306)				264910, 264555, 264557
1154	83002995 (2307, 2308)	Novel Protein sim. GBank gi|4240315|dbj|BAA74936.1| - (AB020720) KIAA0913 protein [Homo sapiens]		UNCLASSIFIED	265008
1155	79411098 (2309, 2310)			UNCLASSIFIED	264690, 264636
1156	57147843 (2311, 2312)	Novel Protein sim. GBank gi|586655|sp|P37617|ATZN_ECOLI - ZINC-TRANSPORTING ATPASE (ZN(II)-TRANSLOCATING P-TYPE ATPASE)	Contains protein domain (PF00122) - E1-E2 ATPase	transport	264603
1157	95287711 (2313, 2314)	Novel Protein sim. GBank gi|418480|sp|P32139|YIHR_ECOLI - HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION		UNCLASSIFIED	264906, 264907, 264758, 264766, 264769, 264689, 264638, 264566
1158	82454917 (2315, 2316)	Novel Protein sim. GBank gi|2496481|sp|Q50724|Y09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C			264906, 264762, 264687, 264769, 264689, 18108374, 35695855
1159	79186451 (2317, 2318)				264687
1160	91229893 (2319, 2320)	Novel Protein sim. GBank gi|1136406|dbj|BAA11490| - (D79995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]			29331822, 29331824, 66714117, 29331826, 60433356, 265018, 265019, 83373044, 18108385, 22279000, 22279002, 264563
1161	7417143 (2321, 2322)				264369
1162	79635357 (2323, 2324)	Novel Protein sim. GBank gi|2443342|dbj|BAA22380| - (D88764) alpha 2 type I collagen [Rana catesbeiana]		UNCLASSIFIED	264693
1163	79563186 (2325, 2326)	Novel Protein sim. GBank gi|4503375|ref|NP_001376.1|pDPYS - dihydropyrimidinase		UNCLASSIFIED	29331827, 264906
1164	79650829 (2327, 2328)	Novel Protein sim. GBank gi|5052554|gb|AAD38607.1|AF14563 - (AF145632) BcDNA.GH06032 [Drosophila melanogaster]		transport	18108398, 29331827, 29331828, 29146498, 29146499, 18108354, 21906768, 29148627, 21906769, 264693, 18108382, 18108385
1165	80491888 (2329, 2330)			UNCLASSIFIED	264602, 264605, 264769, 18108370, 18108374, 264565
1166	88096456 (2331, 2332)	Novel Protein sim. GBank gi|4589476|dbj|BAA76766.1| - (AB023139) KIAA0922 protein [Homo sapiens]			264488, 35696286, 22278999, 264259, 66714117, 60432289, 35696052, 264905, 56182435, 265006, 60433438, 264759, 21906754, 33109954, 265017, 265019, 264448, 264288, 264766, 264685, 35696423, 35695855, 264558, 18108385, 60432113

1167	79963862 (2333, 2334)	Novel Protein sim. GBank gi|2580433|dbj|BAA23138| - (D76414) ppGpp hydrolase [Staphylococcus aureus]		kinase	264488
1168	88094678 (2335, 2336)			UNCLASSIFIED	264259, 29331827, 56182435, 60433438, 265019, 33657023, 35695855, 264566
1169	11805403 (2337, 2338)			UNCLASSIFIED	264681
1170	21632244 (2339, 2340)			UNCLASSIFIED	264602
1171	20434582 (2341, 2342)	Novel Protein sim. GBank gi|2772914 (AF029249) - precollagen D [Mytilus edulis]		UNCLASSIFIED	264556
1172	79610113 (2343, 2344)	Novel Protein sim. GBank gi|4757846|ref|NP_004317.1|pBCL9 - B-cell CLL/lymphoma 9		UNCLASSIFIED	55810764, 35696052, 264634, 264486
1173	80235713 (2345, 2346)	Novel Protein sim. GBank gi|2564053|dbj|BAA22946| - (AB007832) Bm trachealess [Bombyx mori]			264508, 264906, 264907, 264909, 264591, 264632, 264638, 264639
1174	20293077 (2347, 2348)	Novel Protein sim. GBank gi|2911027|emb|CAA17520| - (AL021958) mmsA [Mycobacterium tuberculosis]		dehydrogenase	264600
1175	20711847 (2349, 2350)	Novel Protein sim. GBank gi|118333|sp|P23234|DCIP_ENTCL - INDOLE-3-PYRUVATE DECARBOXYLASE (INDOLEPYRUVATE DECARBOXYLASE)	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	carboxylase	264601
1176	80252645 (2351, 2352)	Novel Protein sim. GBank gi|1144520 (U34956) - phosphoribosylformylglycinamidine synthase [Mycobacterium tuberculosis]	Contains protein domain (PF00586) - AIR synthase related protein	synthase	264509, 264905, 264593, 264602, 264605
1177	80064647 (2353, 2354)	Novel Protein sim. GBank gi|119791|sp|P28643|FABG_CUPLA - 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	264605
1178	94128641 (2355, 2356)	Novel Protein sim. GBank gi|5031697|ref|NP_005594.1|pFIC1 - familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent)	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated	65274572, 18108398, 22278998, 22278999, 29331826, 264508, 264908, 264828, 33657402, 33109954, 264769, 21906765, 21906766, 21906768, 55811957, 33657023, 264629, 55811576, 35696423, 264636, 264556, 56182323, 60432113, 22279000, 22279002
1179	80055575 (2357, 2358)	Novel Protein sim. GBank gi|2960090|emb|CAA17988.1| - (AL022121) dppA [Mycobacterium tuberculosis]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	transport	264603
1180	11794446 (2359, 2360)	Novel Protein sim. GBank gi|2558614|emb|CAA04787| - (AJ001493) dehydroquinate dehydratase [Streptomyces coelicolor]	Contains protein domain (PF01220) - Dehydroquinase class II	synthase	264638
1181	17946362 (2361, 2362)				
1182	81494264 (2363, 2364)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	265017
1183	79574044 (2365, 2366)				265007, 265009, 264564, 264909, 264693
1184	52559933 (2367, 2368)	Novel Protein sim. GBank gi|4091877 (AF061331) - alpha galactosidase precursor [Saccharopolyspora erythraea]			264689, 35696423, 264638, 18108385
1185	79491185 (2369, 2370)	Novel Protein sim. GBank gi|2129478|pir||S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264602
				glycoprotein	263967

1186	20224012 (2371, 2372)			UNCLASSIFIED	264559
1187	79246834 (2373, 2374)			UNCLASSIFIED	29331825, 265017, 18108351
1188	79831387 (2375, 2376)	Novel Protein sim. GBank gi|2996039 (AF054525) - hypothetical protein [Synechococcus PCC7002]		UNCLASSIFIED	264905, 264906
1189	79609367 (2377, 2378)				264692
1190	78930589 (2379, 2380)			UNCLASSIFIED	265018
1191	80310105 (2381, 2382)			UNCLASSIFIED	264600, 264605, 264764, 35695855, 264638, 264486
1192	13521641 (2383, 2384)		Contains protein domain (PF01581) - FMRFamide related peptide family		264636
1193	11103584 (2385, 2386)			UNCLASSIFIED	263978
1194	78893947 (2387, 2388)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	265007, 265008
1195	20445442 (2389, 2390)	Novel Protein sim. GBank gi|1790277 (AE000459) - putative oxidoreductase [Escherichia coli]		UNCLASSIFIED	264605
1196	13000688 (2391, 2392)				264689
1197	11392317 (2393, 2394)	Novel Protein sim. GBank gi|2497360|sp|Q50715|IMDH_MYCTU - INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD)	Contains protein domain (PF00571) - CBS domain	dehydrogenase	264594
1198	95290101 (2395, 2396)				264603
1199	81882011 (2397, 2398)	Novel Protein sim. GBank gi|1709525|sp|P54673|P3K1_DICDI - PHOSPHATIDYLINOSITOL 3-KINASE 1 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)			264259, 264757, 33109954, 21906768
1200	9848880 (2399, 2400)			UNCLASSIFIED	264910
1201	80503751 (2401, 2402)	Novel Protein sim. GBank gi|2499877|sp|P70645|BLMH_RAT - BLEOMYCIN HYDROLASE (BLM HYDROLASE) (BMH)		cathepsin	264766, 264769
1202	80082633 (2403, 2404)	Novel Protein sim. GBank gi|606342 (U18997) - ORF_o622; reading frame open far upstream of start; possible frameshift, linking to previous ORF [Escherichia coli]		ribosomalprot	264600, 264558
1203	82125373 (2405, 2406)			UNCLASSIFIED	264768, 264769, 35695917, 264910, 264760, 264906, 264907, 264829, 264908, 264909, 264766
1204	80503916 (2407, 2408)	Novel Protein sim. GBank gi|2500728|sp|Q59912|SECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT			264905, 264769, 264636
1205	80053961 (2409, 2410)			UNCLASSIFIED	264566
1206	80241965 (2411, 2412)			UNCLASSIFIED	264556, 264557, 264558
1207	79841192 (2413, 2414)				29331824, 264909, 265021, 18108370
1208	87755217 (2415, 2416)	Novel Protein sim. GBank gi|2645560 (AF027954) - Bcl-2-related ovarian killer protein [Rattus norvegicus]	Contains protein domain (PF00452) - Apoptosis regulator proteins, Bcl-2 family	apoptosis	29331824, 29331825, 29331827, 265007, 264764, 264683, 264769, 264688, 264689

1209	79185742 (2417, 2418)	Novel Protein sim. GBank gi|1175033|sp|P44398|XYLA_HAEIN - XYLOSE ISOMERASE	Contains protein domain (PF00259) - Xylose isomerase	isomerase	264687, 264688
1210	56426884 (2419, 2420)			UNCLASSIFIED	264907, 264693
1211	94665655 (2421, 2422)	Novel Protein sim. GBank gi|421095|pir||S30688 - hypothetical protein o246 - Escherichia coli		transferase	264591, 264592, 264595
1212	79167929 (2423, 2424)	Novel Protein sim. GBank gi|3880625|emb|CAB07858| - (Z93785) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL:D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf		264689, 263967
1213	79859633 (2425, 2426)	Novel Protein sim. GBank gi|226292|prf||1505375A - vir gene [Bordetella pertussis]		kinase	264909
1214	10144306 (2427, 2428)	Novel Protein sim. GBank gi|5726285|gb|AAD48396.1|AF12616 - (AF126162) HERV-H LTR associating protein 2 [Homo sapiens]		UNCLASSIFIED	264908
1215	80050106 (2429, 2430)	Novel Protein sim. GBank gi|2326739|emb|CAB10953| - (Z98268) recN [Mycobacterium tuberculosis]		UNCLASSIFIED	265009, 264601, 264602, 264603, 33657109
1216	20438324 (2431, 2432)	Novel Protein sim. GBank gi|417329|sp|P33038|MURA_ENTCL - UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (ENOYLPYRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOLPYRUVYL TRANSFERASE) (EPT)		transferase	264604
1217	95011344 (2433, 2434)			UNCLASSIFIED	264905, 264907, 264908, 264591, 264766, 264691, 264693, 264629, 264630, 264636, 264564
1218	11093680 (2435, 2436)	Novel Protein sim. GBank gi|1805460|dbj|BAA09022| - (D50453) homologue of succinate semialdehyde dehydrogenase GabD of E. coli [Bacillus subtilis]		dehydrogenase	264601
1219	91216252 (2437, 2438)				56181686, 29331822, 60432289, 264601, 264692, 264629
1220	91241524 (2439, 2440)	Novel Protein sim. GBank gi|4240315|dbj|BAA74936.1| - (AB020720) KIAA0913 protein [Homo sapiens]		oncogene	52644507, 264905, 264909, 265008, 265019, 265020, 52644150, 33657023, 264693, 33657182, 35695763, 264634, 22279000, 22279002, 264482
1221	83045055 (2441, 2442)	Novel Protein sim. GBank gi|2143886|pir||I52523 - nucleoporin p62 homolog - rat (fragment)		UNCLASSIFIED	264768, 265020, 264906
1222	20711865 (2443, 2444)	Novel Protein sim. GBank gi|730805|sp|P39663|SPHR_SYNP7 - ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN SPHR	Contains protein domain (PF00486) - Transcriptional regulatory protein, C terminal	phosphatase	264601
1223	11615647 (2445, 2446)				264593
1224	80432645 (2447, 2448)	Novel Protein sim. GBank gi|1172627|sp|P46546|PROB_CORGL - GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK)	Contains protein domain (PF01472) - PUA domain	kinase	264593, 264600, 264601, 264603, 264605, 264768, 18108376, 264635, 18108387

1225	80434427 (2449, 2450)				264768
1226	80237518 (2451, 2452)	Novel Protein sim. GBank gi|2105050|emb|CAB08836| - (Z95436) hypothetical protein Rv3644c [Mycobacterium tuberculosis]		polymerase	264905, 264512, 264689
1227	79422138 (2453, 2454)	Novel Protein sim. GBank gi|1706768|sp|P98133|FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP340)		UNCLASSIFIED	264908, 264637, 264639
1228	79209027 (2455, 2456)	Novel Protein sim. GBank gi|1653901|dbj|BAA18811| - (D90917) acriflavine resistance protein [Synechocystis sp.]	Contains protein domain (PF00873) - AcrB/AcrD/AcrF family		264605, 264634
1229	94329135 (2457, 2458)			UNCLASSIFIED	87168474, 265011, 87168559, 264681, 264689, 264693, 65274620, 18108374
1230	80049357 (2459, 2460)	Novel Protein sim. GBank gi|116230|sp|P28598|CH60_BACSU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	eph	264909, 264605, 18108388
1231	79843141 (2461, 2462)			UNCLASSIFIED	264908
1232	79853104 (2463, 2464)	Novel Protein sim. GBank gi|1215733 (U48718) - OphC [Agrobacterium tumefaciens]		transport	264909
1233	80255179 (2465, 2466)	Novel Protein sim. GBank gi|116298|sp|P20730|CHHC_BOMMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)		UNCLASSIFIED	265017, 264564
1234	79242158 (2467, 2468)	Novel Protein sim. GBank gi|729671|sp|P40280|H2A_MAIZE - HISTONE H2A	Contains protein domain (PF00125) - Core histone H2A/H2B/H3/H4	histone	265008, 265010, 18108381
1235	79914423 (2469, 2470)				264634, 264762
1236	81927147 (2471, 2472)			UNCLASSIFIED	265018, 55811150, 264565, 264757
1237	83371782 (2473, 2474)	Novel Protein sim. GBank gi|3875133|emb|CAA94750| - (Z70750) similar to actin binding domain; cDNA EST EMBL:T00093 comes from this gene; cDNA EST EMBL:D34443 comes from this gene; cDNA EST EMBL:D37508 comes from this gene; cDNA EST EMBL:D64247 comes from this gene; cDNA EST EMBL...			264758, 264601, 264766, 264687, 18108372, 264555, 264559
1238	87411577 (2475, 2476)	Novel Protein sim. GBank gi|3885470 (AF061443) - G protein-coupled receptor LGR4 [Rattus norvegicus]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264259, 29331822, 29331824, 35696052, 264508, 264906, 52644045, 52646317, 264288, 264769, 264693, 264632, 264634, 264558, 87168518, 264563
1239	82197449 (2477, 2478)	Novel Protein sim. GBank gi|4007990|gb|AAC95339| - (AF084363) DOK protein [Mus musculus]		oncogene	264509, 264511, 264759, 264760, 264764, 264557
1240	80497259 (2479, 2480)	Novel Protein sim. GBank gi|1176192|sp|P45420|YHCD_ECOLI - HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN GLTF-NANT INTERGENIC REGION PRECURSOR			264769
1241	80020711 (2481, 2482)	Novel Protein sim. GBank gi|121383|sp|P19904|GLNA_VIBAL - GLUTAMINE SYNTHETASE (GLUTAMATE–AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	264601, 264604, 264638
1242	79775890 (2483, 2484)				264908, 264907, 264908, 264634

1243	79779458 (2485, 2486)	Novel Protein sim. GBank gi|3355671|emb|CAA19971| - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	18108374, 35695917, 35695855, 265009, 264508, 264909
1244	10284821 (2487, 2488)	Novel Protein sim. GBank gi|2970646 (AF051945) - Xin [Mus musculus]		UNCLASSIFIED	264691
1245	80437103 (2489, 2490)	Novel Protein sim. GBank gi|4586338|dbj|BAA76357.1| - (AB016787) cytochrome o ubiquinol oxidase B [Pseudomonas putida]	Contains protein domain (PF00115) - Cytochrome C and Quinol oxidase polypeptide I	oxidase	264768
1246	80059321 (2491, 2492)	Novel Protein sim. GBank gi|3581849|emb|CAA20805| - (AL031541) putative phenylalanyl-tRNA synthetase beta chain [Streptomyces coelicolor]		UNCLASSIFIED	264604, 264636, 264557, 264564
1247	80064831 (2493, 2494)	Novel Protein sim. GBank gi|2621684 (AE000842) - adhesion protein [Methanobacterium thermoautotrophicum]			264758, 264605, 264639
1248	88070353 (2495, 2496)	Novel Protein sim. GBank gi|1352403|sp|P09467|F16P_HUMAN - FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1-6-bisphosphatase	UNCLASSIFIED	18108392, 264259, 29331826, 264106, 264508, 264907, 264828, 265009, 60433356, 264757, 264758, 21906754, 265010, 265011, 265018, 265019, 264760, 18108351, 18108354, 265021, 18108376, 18108377, 264630, 18108385
1249	80056657 (2497, 2498)	Novel Protein sim. GBank gi|2791407|emb|CAA16001| - (AL021184) hypothetical protein Rv1473 [Mycobacterium tuberculosis]		transport	264908, 265010, 264600, 264603, 264691, 18108376
1250	12694385 (2499, 2500)	Novel Protein sim. GBank gi|112785|sp|P05100|3MG1_ECOLI - DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	264689
1251	79850448 (2501, 2502)				264909
1252	79458087 (2503, 2504)			UNCLASSIFIED	264683, 263976
1253	80050121 (2505, 2506)	Novel Protein sim. GBank gi|5670176|gb|AAD46616.1|AF16131 - (AF161317) NRAMP manganese transport protein MntA [Salmonella typhimurium]		glycoprotein	264600, 264603, 18108376
1254	87716767 (2507, 2508)	Novel Protein sim. GBank gi|103160|pir||S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	35696286, 264910, 264764, 264688, 21906767, 55811957, 264692, 264556, 264639
1255	79169728 (2509, 2510)				264636
1256	87889508 (2511, 2512)	Novel Protein sim. GBank gi|2995353|emb|CAA04608.1| - (AJ001206) pep2 [Streptomyces coelicolor]		UNCLASSIFIED	60432289, 264600, 264605, 264764, 264687, 264769, 264689, 27486265, 18108374, 18108376
1257	80201435 (2513, 2514)	Novel Protein sim. GBank gi|3193306 (AF069300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB:AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	264094, 265019
1258	20708150 (2515, 2516)			UNCLASSIFIED	264602, 263978
1259	80186012 (2517, 2518)			UNCLASSIFIED	264906, 264448, 264908
1260	80084606 (2519, 2520)			UNCLASSIFIED	264634, 264639

1261	87412802 (2521, 2522)	Novel Protein sim. GBank gi|5689511|dbj|BAA83039.1| - (AB029010) KIAA1087 protein [Homo sapiens]	Contains protein domain (PF01699) - Sodium/calcium exchanger protein	cadherin	29331824, 264906, 264909, 264768, 264769, 264689, 264693, 264639, 18108384, 264563
1262	13504589 (2523, 2524)	Novel Protein sim. GBank gi|95100|pir||S21334 - hypothetical protein 4 - Agrobacterium tumefaciens		UNCLASSIFIED	264634
1263	20710997 (2525, 2526)				264602
1264	80083396 (2527, 2528)	Novel Protein sim. GBank gi|3550958 (AF004840) - CDO [Rattus norvegicus]		struct	264634
1265	80253579 (2529, 2530)			UNCLASSIFIED	264563
1266	79914604 (2531, 2532)			UNCLASSIFIED	264766, 264636, 264638, 264567
1267	80558918 (2533, 2534)	Novel Protein sim. GBank gi|1085002|pir||S55056 - mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264259, 21906754, 264369
1268	88178473 (2535, 2536)	Novel Protein sim. GBank gi|4886445|emb|CAB43370.1| - (AL050269) hypothetical protein [Homo sapiens]	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	18108398, 22278995, 56994075, 60424269, 29331827, 264109, 264512, 265007, 265008, 265009, 264595, 33109954, 33657084, 87168559, 264600, 265018, 265019, 264369, 264688, 21906767, 265020, 52644150, 264691, 33657023, 33657349, 18108374, 264556, 18108385, 60432113, 22279002, 264486
1269	79821946 (2537, 2538)	Novel Protein sim. GBank gi|3334791|emb|CAA19939| - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264905, 264906, 264687, 264693
1270	80031420 (2539, 2540)	Novel Protein sim. GBank gi|2851634|sp|Q50591|Y0D1_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01	Contains protein domain (PF01574) - IMP dehydrogenase / GMP reductase N terminus	dehydrogenase	265010, 264601
1271	79840499 (2541, 2542)			ATPase_associated	35696052, 264908
1272	79462878 (2543, 2544)				264686, 264689
1273	80220315 (2545, 2546)	Novel Protein sim. GBank gi|1655665|emb|CAB03731| - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	264509, 264639
1274	95010802 (2547, 2548)			UNCLASSIFIED	264905, 264908, 264909, 264769
1275	20730763 (2549, 2550)	Novel Protein sim. GBank gi|123726|sp|P10413|HTPG_ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C62.5)	Contains protein domain (PF00183) - Hsp90 protein	eph	264602
1276	21148644 (2551, 2552)	Novel Protein sim. GBank gi|2129478|pir||S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264369
1277	20438195 (2553, 2554)			UNCLASSIFIED	264556
1278	11088365 (2555, 2556)	Novel Protein sim. GBank gi|1175473|sp|P44555|YAAJ_HAEIN - HYPOTHETICAL PROTEIN HI0183		UNCLASSIFIED	264603
1279	21658756 (2557, 2558)	Novel Protein sim. GBank gi|1929513 (U64318) - ATP synthase subunit beta [Moorella thermoacetica]		synthase	264605
1280	79310959 (2559, 2560)	Novel Protein sim. GBank gi|4938504|emb|CAB43862.1| - (AL078465) putative protein [Arabidopsis thaliana]		struct	263976

1281	94323988 (2561, 2562)	Novel Protein sim. GBank gi|1136501 (U39546) - surface protein MCA-32 [Rattus norvegicus]	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	29331825, 29331828, 264766, 83373044
1282	87537695 (2563, 2564)	Novel Protein sim. GBank gi|3328190 (AF074266) - proto-oncogene AF4 [Mus musculus]		UNCLASSIFIED	265008
1283	20466305 (2565, 2566)	Novel Protein sim. GBank gi|3261721|emb|CAB07057| - (Z92770) hypothetical protein Rv0153c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
1284	20636325 (2567, 2568)	Novel Protein sim. GBank gi|3929022 (AF057696) - LspB [Haemophilus ducreyi]			264604
1285	80427330 (2569, 2570)	Novel Protein sim. GBank gi|417154|sp|P33126|HS82_ORYSA - HEAT SHOCK PROTEIN 82	Contains protein domain (PF00183) - Hsp90 protein	eph	264766, 264689, 263967
1286	20465254 (2571, 2572)	Novel Protein sim. GBank gi|2078004|emb|CAB08451| - (Z95207) gorA [Mycobacterium tuberculosis]		reductase	264605, 264639
1287	80417530 (2573, 2574)			UNCLASSIFIED	265011, 264602, 264766, 264687, 264769, 264689, 18108370, 264636, 18108385, 264563
1288	95338101 (2575, 2576)	Novel Protein sim. GBank gi|5353510|gb|AAD42161.1|AF08891 - (AF088916) emilin precursor [Homo sapiens]	Contains protein domain (PF00386) - C1q domain	collagen	35696052, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 33657402, 264595, 264758, 265011, 265019, 264760, 18108351, 264681, 264764, 264288, 264685, 264766, 264687, 264768, 264769, 265020, 265021, 264534, 264692, 18108370, 264628, 18108374, 35696423, 264555, 264556, 264557, 264558, 18108385, 264564, 264566, 264567, 264486, 18108391
1289	11813647 (2577, 2578)			UNCLASSIFIED	264637
1290	19526027 (2579, 2580)	Novel Protein sim. GBank gi|1169995|sp|P46023|GPCR_LYMST - G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	264563
1291	80470266 (2581, 2582)	Novel Protein sim. GBank gi|2072674|emb|CAB08305| - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	265007, 265008, 264769
1292	94723316 (2583, 2584)	Novel Protein sim. GBank gi|1835755 (U86338) - zinc finger protein Png-1 [Mus musculus]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcriptfactor	264092, 264259, 29331822, 29331824, 264508, 264906, 264909, 264512, 265008, 265009, 264591, 265019, 264369, 264288, 264686, 264768, 264693, 18108374, 264632, 56182323, 264639, 83373044, 22279002, 264482, 264563
1293	80067536 (2585, 2586)			UNCLASSIFIED	265006, 55812038, 264369, 264556
1294	82125908 (2587, 2588)	Novel Protein sim. GBank gi|2129173|pir||F64453 - oxaloacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii		biotindep	264602, 264605, 264760, 18108351, 264689, 33657023, 264559
1295	11686851 (2589, 2590)	Novel Protein sim. GBank gi|5441779|emb|CAB46803.1| - (AL096811) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]		dehydrogenase	264689

1296	11687904 (2591, 2592)			UNCLASSIFIED	264591, 264639
1297	79639300 (2593, 2594)	Novel Protein sim. GBank gi|4982191|gb|AAD36686.1|AE00180 - (AE001805) DNA-directed DNA polymerase I [Thermotoga maritima]	Contains protein domain (PF01367) - 5'-3' exonuclease	polymerase	264693
1298	94239506 (2595, 2596)	Novel Protein sim. GBank gi|1943770 (U97191) - F53F10.1 gene product [Caenorhabditis elegans]		struct	18108348, 265017
1299	80255378 (2597, 2598)				264488, 264906, 264909, 22279002, 264566
1300	80064867 (2599, 2600)	Novel Protein sim. GBank gi|3445181 (AC005498) - R31665_2 [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264605
1301	17939614 (2601, 2602)	Novel Protein sim. GBank gi|4062973|dbj|BAA36204.1| - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]		UNCLASSIFIED	264906
1302	95416198 (2603, 2604)				85658542, 265020
1303	9684121 (2605, 2606)				264908
1304	79377196 (2607, 2608)			UNCLASSIFIED	264508
1305	19905899 (2609, 2610)				264566
1306	13069230 (2611, 2612)	Novel Protein sim. GBank gi|3242273|emb|CAB07017| - (Z92669) hypothetical protein Rv0236c [Mycobacterium tuberculosis]		UNCLASSIFIED	264636
1307	82201029 (2613, 2614)			UNCLASSIFIED	264907, 264592, 264764
1308	21426814 (2615, 2616)	Novel Protein sim. GBank gi|1502421 (U59433) - 3-ketoacyl acyl carrier protein reductase [Bacillus subtilis]	Contains protein domain (PF00516) - Envelope glycoprotein GP120	reductase	264555
1309	79263011 (2617, 2618)	Novel Protein sim. GBank gi|95819|pir||S16298 - ferric enterobactin transport protein fepC - Escherichia coli		transport	264906, 18108354
1310	20466319 (2619, 2620)	Novel Protein sim. GBank gi|5459220|emb|CAB48893.1| - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264605
1311	87613142 (2621, 2622)				35696286, 29331827, 264908, 265008, 264764, 264766, 264686, 21906767, 21906769, 35695917, 264691, 264693
1312	88061720 (2623, 2624)	Novel Protein sim. GBank gi|4455118|gb|AAD21084| - (AF125158) zinc finger DNA binding protein 99 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	22278995, 22278998, 22278999, 264905, 264908, 265011, 265017, 265019, 264687, 21906768, 265020, 265021, 33657023, 22279002, 264564
1313	91225458 (2625, 2626)	Novel Protein sim. GBank gi|4929733|gb|AAD34127.1|AF15189 - (AF151890) CGI-132 protein [Homo sapiens]	Contains protein domain (PF00886) - Ribosomal protein S16	ribosomalprot	22278996, 22278999, 264259, 20281099, 29146498, 264508, 264908, 66712502, 60433356, 60433438, 265011, 265017, 264683, 264288, 21906765, 21906767, 29148627, 21906768, 35695917, 265021, 33657023, 33657109, 18108370, 18108377, 35695855, 60432113, 22279000, 264563, 18108390
1314	56926053 (2627, 2628)				264693
1315	84357192 (2629, 2630)	Novel Protein sim. GBank gi|2589223 (AF026565) - ring finger protein [Mus musculus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264691

1316	95361609 (2631, 2632)	Novel Protein sim. GBank gi|5689407|db|BAA82987.1| - (AB028958) KIAA1035 protein [Homo sapiens]		kinase	56182575, 56181686, 20281171, 29331822, 29331824, 60424269, 29331825, 35696052, 52644045, 264591, 60432229, 265018, 265019, 55811150, 56181562, 21906765, 21906767, 21906768, 35695917, 60170615, 33657023, 65274620, 33657109, 35695763, 35695855, 18108387, 87168518, 60432113, 22279002, 264564
1317	88055167 (2633, 2634)	Novel Protein sim. GBank gi|4836757|gb|AAD30541.1|AF13491 - (AF134918) semaphorin subclass 4 member G [Mus musculus]		UNCLASSIFIED	264093, 264906, 264909, 264369, 264684
1318	95322893 (2635, 2636)	Novel Protein sim. GBank gi|4680204|gb|AAD27567.1|AF11417 - (AF114171) hypothetical protein [Sorghum bicolor]		UNCLASSIFIED	18108392, 18108348, 265011, 265017, 18108359, 18108362, 56182323, 18108385, 22279000
1319	94238546 (2637, 2638)				264908, 264909, 265006, 265008, 264592, 265019, 264766, 56181562, 18108368, 264628, 264629, 18108377, 264636
1320	86603567 (2639, 2640)	Novel Protein sim. GBank gi|4240183|db|BAA74870.1| - (AB020654) KIAA0847 protein [Homo sapiens]		UNCLASSIFIED	35696286, 55812038, 265018, 21906768, 265020, 263978, 22279002
1321	86676351 (2641, 2642)	Novel Protein sim. GBank gi|4886505|emb|CAB43377.1| - (AL050276) hypothetical protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	transcriptfactor	60432049, 29331828, 264907, 264908, 264909, 264910, 55812038, 264601, 264762, 264764, 264766, 264768, 264769, 264628, 18108374, 264634, 264635, 18108385
1322	87755272 (2643, 2644)	Novel Protein sim. GBank gi|5262591|emb|CAB45736.1| - (AL080143) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	29331828, 264908, 265020, 33657023, 264693, 264404
1323	94845931 (2645, 2646)	Novel Protein sim. GBank gi|5459516|db|BAA82407.1| - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 56994075, 264259, 29331822, 29331827, 264104, 56182435, 87168474, 18108351, 264288, 21906766, 21906767, 35695917, 265020, 264693, 65274791, 56182323, 18108387
1324	87737614 (2647, 2648)	Novel Protein sim. GBank gi|5031717|ref|NP_005704.1|pGPBP - goodpasture antigen-binding protein	Contains protein domain (PF01852) - START domain		22278998, 22278998, 29331828, 264905, 264907, 29331830, 264908, 264510, 265008, 264595, 264759, 21906754, 265018, 264288, 264768, 264769, 21906768, 265022, 18108376, 264631, 264632, 264634, 264636, 264638, 264563, 264564, 264565, 264566
1325	94847471 (2649, 2650)	Novel Protein sim. GBank gi|3294501 (U64857) - similar to the DPTI/Kunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor [Caenorhabditis elegans]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	protease	35696286, 264905, 264906, 264907, 264908, 264909, 264910, 264593, 33657402, 264758, 85658542, 264760, 264768, 264769, 264691, 35696423
1326	87316289 (2651, 2652)	Novel Protein sim. GBank gi|1397275 (U61947) - C06G3.8 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264259, 66712502, 264682, 264683, 264635

1327	95322897 (2653, 2654)	Novel Protein sim. GBank gi|728832|sp|P39189|ALU2_HUMAN - !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!	Contains protein domain (PF00279) - Plant lipid transfer protein family	UNCLASSIFIED	18108398, 22278996, 22278997, 22278999, 264091, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264105, 264905, 56182435, 264112, 265008, 265009, 21906754, 265010, 265011, 265017, 265019, 264681, 264448, 264764, 264684, 264288, 264685, 264768, 264688, 21906767, 21906769, 29148629, 265020, 264690, 264691, 264692, 264693, 263967, 33657109, 33657182, 27486262, 33657349, 18108370, 18108374, 55810764, 35695855, 264634, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264567
1328	87753493 (2655, 2656)			UNCLASSIFIED	264488, 22278997, 29331826, 264595, 18108351, 264766, 22279002, 264482, 264567
1329	87755276 (2657, 2658)	Novel Protein sim. GBank gi|4678224|gb|AAD26969.1|AC00713 - (AC007135) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	22278996, 29331827, 264684, 264692, 33657109
1330	87727737 (2659, 2660)	Novel Protein sim. GBank gi|437310 (L23504) - nodulin [Medicago truncatula]		UNCLASSIFIED	264259, 29331825, 264512, 265019, 265021, 264555, 264558, 56526486
1331	87376764 (2661, 2662)	Novel Protein sim. GBank gi|4589586|dbj|BAA76815.1| - (AB023188) KIAA0971 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331826, 29331827, 35696052, 29331828, 60170831, 264448, 264686, 21906765, 55811957, 265020, 33657023, 33657109, 263973, 55811576, 35696423, 35695855, 56182323
1332	94845937 (2663, 2664)	Novel Protein sim. GBank gi|5459516|dbj|BAA82407.1| - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331826, 60432289, 29331827, 35696052, 52644045, 56182435, 264510, 21906754, 87168559, 265018, 265019, 264448, 264288, 264369, 264686, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 52644150, 33657023, 56182323, 18108387, 60432113, 22279002
1333	88098476 (2665, 2666)	Novel Protein sim. GBank gi|5689527|dbj|BAA83047.1| - (AB029018) KIAA1095 protein [Homo sapiens]		UNCLASSIFIED	60432289, 66712502, 264591, 60433356, 60433438, 55812038, 265010, 264639, 56526486
1334	87592388 (2667, 2668)	Novel Protein sim. GBank gi|2662536 (AF036685) - Similar to protein-tyrosine phosphatase [Caenorhabditis elegans]		phosphatase	264905
1335	87644798 (2669, 2670)	Novel Protein sim. GBank gi|4240285|dbj|BAA74921.1| - (AB020705) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED	22278998, 22278999, 29331827, 264509, 264511, 265007, 265008, 265009, 60433438, 21906754, 87168559, 265017, 264288, 21906765, 21906767, 21906768, 21906769, 265020, 33657109, 27486264, 18108374, 264556, 264638, 264557, 60170394, 264559, 18108385, 264563

1336	87787890 (2671, 2672)	Novel Protein sim. GBank gi|465445|sp|P33485|VNUA_PRVKA - PROBABLE NUCLEAR ANTIGEN			264509, 264905, 264512, 264764, 264893, 264635, 264637
1337	94312042 (2673, 2674)	Novel Protein sim. GBank gi|5689471|dbj|BAA83019.1| - (AB028990) KIAA1067 protein [Homo sapiens]		UNCLASSIFIED	56182575, 56994075, 22278998, 22278999, 264092, 264259, 60432289, 29331826, 264906, 264908, 264909, 264112, 265008, 265009, 60433356, 55812038, 33657084, 265011, 265017, 265018, 265019, 264682, 264448, 264683, 264369, 264688, 264689, 21906766, 21906769, 265020, 264691, 27486261, 20281069, 18108379, 55811576, 35695855, 56182323, 60432113, 22279002, 264567
1338	80366114 (2675, 2676)			UNCLASSIFIED	29331822, 265010, 264288, 264689, 18108370, 35695855
1339	80249231 (2677, 2678)	Novel Protein sim. GBank gi|1176422 (U43194) - rhophilin [Mus musculus]		UNCLASSIFIED	35696052, 264909, 264688, 264556, 264558
1340	88316311 (2679, 2680)				264905, 264907, 87168559, 264764
1341	86101485 (2681, 2682)				264681, 264685, 264686, 264692
1342	80089017 (2683, 2684)	Novel Protein sim. GBank gi|5019564|emb|CAB44507.1| - (AL035542) dJ994E9.5 (hs6M1-17 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	264629
1343	80082862 (2685, 2686)	Novel Protein sim. GBank gi|4557543|ref|NP_001384.1|pECM2 - extracellular matrix protein 2	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	264910, 264686, 264534
1344	20562559 (2687, 2688)				263978
1345	91225546 (2689, 2690)	Novel Protein sim. GBank gi|2144101|pir||I55210 - tricarboxylate carrier - rat (fragment)		glycoprotein	264909, 60170394
1346	80255717 (2691, 2692)	Novel Protein sim. GBank gi|3881052|emb|CAA19523| - (AL023843) predicted using Genefinder; similar to serine/threonine kinase; cDNA EST yk246a12.3 comes from this gene; cDNA EST yk358c10.5 comes from this gene; cDNA EST EMBL:M89047 comes from this gene; cDNA EST yk246a12.5 comes...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278998, 264907, 264681, 264685, 264689, 265020, 264693, 22279000, 22279002, 264566
1347	80417393 (2693, 2694)	Novel Protein sim. GBank gi|4504379|ref|NP_003658.1|pHG38 - orphan G protein-coupled receptor HG38	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264906, 264908, 264909, 265006, 264910, 265011, 265017, 264764, 264766, 264767, 264769, 264631, 264634, 264638, 264567, 264486
1348	87352335 (2695, 2696)	Novel Protein sim. GBank gi|3399720|dbj|BAA32100| - (AB010999) peptidylarginine deiminase type IV [Rattus norvegicus]		UNCLASSIFIED	264488, 264489, 264508, 264509, 264510, 264511, 264512, 264591, 264592, 264601, 264684, 264685, 264769, 264532, 264534, 264555, 264556, 264557, 264558, 22279002, 264486

1349	91225548 (2697, 2698)	Novel Protein sim. GBank gi|2144101|pir||I55210 - tricarboxylate carrier - rat (fragment)		UNCLASSIFIED	52646842, 35696286, 22278996, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 264910, 60170831, 264591, 60433438, 264757, 21906754, 265017, 265018, 264605, 264760, 264762, 264288, 264766, 264689, 21906765, 21906766, 21906767, 21906768, 55811957, 35695917, 265020, 264534, 264691, 264692, 33657023, 264693, 33657349, 18108374, 18108376, 35696423, 60170394, 22279000, 22279002, 264563, 264564
1350	87093136 (2699, 2700)			UNCLASSIFIED	52646842, 264259, 29331825, 264908, 264511, 264604, 264288, 21906769, 265020, 33657182, 33657349, 18108374, 35695855, 264555, 264558, 18108385, 22279002, 264486
1351	87361327 (2701, 2702)	Novel Protein sim. GBank gi|4887239|gb|AAD32246.1| - (AF064564) BAW protein [Fugu rubripes]		UNCLASSIFIED	264906, 264907, 264638
1352	80076386 (2703, 2704)			UNCLASSIFIED	264693, 263981
1353	95345417 (2705, 2706)	Novel Protein sim. GBank gi|2144101|pir||I55210 - tricarboxylate carrier - rat (fragment)			35696286, 60424269, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264758, 264596, 55811386, 265011, 264605, 55811150, 264762, 264764, 264766, 52644229, 56181562, 35695917, 265022, 33657023, 264693, 35695763, 60431528, 264629, 263978, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566
1354	95350845 (2707, 2708)	Novel Protein sim. GBank gi|4689108|gb|AAD27763.1|AF07703 - (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 29331826, 264906, 265008, 33657402, 21906754, 265011, 87168559, 264684, 264369, 264769, 264689, 21906765, 21906768, 52644150, 33657023, 264692, 264693, 18108374, 83373044, 87168518, 22279000
1355	88260186 (2709, 2710)	Novel Protein sim. GBank gi|1469199|dbj|BAA09487| - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	22278996, 22278997, 264259, 66714117, 264511, 21906754, 265010, 264769, 264689, 21906765, 21906768, 21906769, 264532, 27486262, 264629, 264638, 264556, 264638, 264639, 264482, 264484

1356	95313991 (2711, 2712)	Novel Protein sim. GBank gi|1113865 (U40342) - ninein [Mus musculus]		struct	18108397, 22278995, 22278998, 22278998, 264094, 29331828, 264905, 265006, 265007, 265008, 265010, 265017, 265018, 265019, 264764, 18108354, 264689, 21906765, 265022, 18108384, 35696423, 83373044, 18108387
1357	88260268 (2713, 2714)	Novel Protein sim. GBank gi|897693|emb|CAA90330| - (Z50026) phosphatidylcholine transfer protein [Bos taurus]	Contains protein domain (PF01852) - START domain		264259, 29331822, 29331825, 264510, 87168559, 265018, 264448, 264288, 21906765, 21906766, 21906768, 265021, 264693, 18108376
1358	38719455 (2715, 2716)	Novel Protein sim. GBank gi|556219 (L36831) - transcription regulator [Mus musculus]			264757
1359	87771643 (2717, 2718)			UNCLASSIFIED	264907, 264909, 264510, 264511, 264512, 18108351, 264764, 264534, 33657023, 18108374, 264634, 264635, 264638, 264639, 18108385, 264486, 264567
1360	87738272 (2719, 2720)	Novel Protein sim. GBank gi|2598282|emb|CAA75612| - (Y15417) acetate--CoA ligase [Coprinus cinereus]		synthase	60432289, 264605
1361	87593527 (2721, 2722)	Novel Protein sim. GBank gi|5689443|dbj|BAA83005.1| - (AB028976) KIAA1053 protein [Homo sapiens]	Contains protein domain (PF00536) - SAM domain (Sterile alpha motif)	UNCLASSIFIED	35696286, 22278997, 22278999, 264259, 29331826, 264508, 264509, 264905, 264907, 264908, 265007, 265009, 33109954, 21906754, 87168474, 265011, 264761, 264683, 264288, 264766, 264769, 264689, 21906768, 265020, 265021, 33657023, 55811576, 35696423, 264634, 60432113, 22279002, 264482, 264486
1362	85287961 (2723, 2724)	Novel Protein sim. GBank gi|5689411|dbj|BAA82989.1| - (AB028960) KIAA1037 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	eph	56182575, 56181686, 60432049, 264259, 29331822, 56182181, 29331827, 35696052, 29331828, 264905, 264906, 264908, 264595, 55812038, 85658542, 55811150, 264681, 264288, 264369, 56181562, 60431528, 55810764, 35696423, 60431850, 264558
1363	85758476 (2725, 2726)	Novel Protein sim. GBank gi|1130494 (U35776) - ADP-ribosylation factor 1-directed GTPase activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	264488, 29331826, 264907, 264687, 264689, 264693
1364	88179488 (2727, 2728)				60432289, 60433356, 60433438, 87168559, 264603, 18108351, 21906766, 35696423, 60432113
1365	83003108 (2729, 2730)	Novel Protein sim. GBank gi|4589562|dbj|BAA76803.1| - (AB023176) KIAA0959 protein [Homo sapiens]		oncogene	264766
1366	87003262 (2731, 2732)	Novel Protein sim. GBank gi|1084944|pir||S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	265007

1367	87721210 (2733, 2734)	Novel Protein sim. GBank gi|4884088|emb|CAB43240.1| - (AL050019) hypothetical protein [Homo sapiens]	Contains protein domain (PF01342) - SAND domain	UNCLASSIFIED	264488, 52646842, 52646365, 22278995, 56994075, 35696286, 22278998, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35696052, 264905, 264907, 264908, 264909, 264510, 265006, 265007, 264512, 264910, 265009, 60170831, 33657402, 55812038, 21906754, 265011, 87168559, 265017, 265019, 18108351, 264448, 264682, 264683, 264288, 264369, 264686, 264767, 264689, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265021, 265022, 264534, 60170615, 264690, 264691, 18108362, 33657023, 33657109, 33657349, 264628, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264635, 264555, 264637, 264556, 52644332, 60170394, 264558, 18108381, 18108385, 56526486, 22279000, 264563, 264567
1368	94320078 (2735, 2736)	Novel Protein sim. GBank gi|464561|sp|P35289|RB15_RAT RAS-RELATED PROTEIN RAB-15	Contains protein domain (PF00071) - Ras family	oncogene	264259, 29331822, 29331826, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264908, 264909, 264510, 265007, 264910, 60433438, 264758, 85658542, 87168559, 264600, 264601, 264760, 264764, 264765, 264768, 52644229, 264689, 35695917, 265020, 265021, 264631, 264632, 264634, 264637, 52644332, 264558, 264639, 83373044, 264563, 264566, 264486, 264567
1369	86634033 (2737, 2738)	Novel Protein sim. GBank gi|2062702 (U90550) - butyrophilin [Homo sapiens]		UNCLASSIFIED	265008, 60432229, 60433356, 33657084, 21906764, 21906769, 264555, 264638, 264559, 264567
1370	95316910 (2739, 2740)	Novel Protein sim. GBank gi|5031823|ref|NP_005823.1|pKCNM - potassium large conductance calcium-activated channel, subfamily M, beta member 2		potassium_channel	22278996, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264758, 265011, 265019, 264764, 264766, 264768, 21906767, 35695917, 18108362, 35696423, 264632, 264635, 264636, 264555, 264638, 264558, 264639, 18108385, 65274727, 264404, 264563, 264566, 264486
1371	95336512 (2741, 2742)	Novel Protein sim. GBank gi|5032203|ref|NP_005714.1|pTSPA - tetraspan 5	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	glycoprotein	22278996, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264905, 264509, 29331830, 66712502, 265008, 265009, 264758, 33657084, 85658542, 265010, 265018, 265019, 264762, 264448, 35695917, 33657109, 33657182, 33657349, 35695855, 264558, 22279002, 264563

1372	80248517 (2743, 2744)	Novel Protein sim. GBank gi|840708|dbj|BAA09334| - (D50685) trans-sialidase [Trypanosoma cruzi]		collagen	UNCLASSIFIED	263978
1373	80499421 (2745, 2746)					264769, 21906765, 21906767, 22278999, 264691, 264910, 55812038, 265010, 264681, 264684
1374	85087036 (2747, 2748)	Novel Protein sim. GBank gi|111876|pir||JC1241 - beta-interferon-induced protein - rat		interferon		264907, 264510, 265007, 264512, 265008, 60432229, 264689, 65274791, 264555, 264556, 264557, 83373044, 60432113
1375	84236942 (2748, 2750)	Novel Protein sim. GBank gi|5649176|gb|AAD03500.2| - (AF051155) G beta-like protein GBL [Rattus norvegicus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase		52844507, 52845156, 52846842, 52846365, 56182575, 56181686, 22278998, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 52845080, 29331824, 29331825, 60432289, 29331828, 29331827, 29331828, 35696052, 33656970, 284905, 264509, 264908, 264907, 264908, 29331830, 264909, 265006, 264511, 265007, 265008, 265009, 33657402, 60433356, 52646317, 33109954, 33657084, 52644296, 87168474, 87168559, 264600, 265017, 265018, 265019, 55811150, 18108351, 264448, 264764, 264288, 264369, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 65274620, 52845129, 33657109, 27486261, 33657349, 27486265, 35695763, 18108376, 55810764, 35696423, 35695855, 264630, 264631, 264634, 264636, 264555, 264638, 18108385, 87168518, 60432113, 22279000, 22279002, 264563, 264564, 264566, 264567
1376	87398050 (2751, 2752)	Novel Protein sim. GBank gi|138350|sp|P28968|VGLX_HSVEB - GLYCOPROTEIN X PRECURSOR		UNCLASSIFIED		264768, 264769, 35695917, 22278997, 264691, 264259, 29331822, 264693, 35696052, 264508, 264509, 264905, 264906, 264628, 264908, 264629, 18108372, 264809, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 56526488, 265010, 265011, 264600, 264583, 264762, 264564, 264565, 264764, 264488, 264768
1377	86964242 (2753, 2754)	Novel Protein sim. GBank gi|1663648 (U75321) - chromaffin granule ATPase II homolog [Mus musculus]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated		29331824, 264591, 265019, 264686, 264768, 55811957, 264693, 22279002

1378	87595071 (2755, 2756)	Novel Protein sim. GBank gi|4107015|dbj|BAA36293| - (AB001772) PEM-5 [Clona savignyi]			22278994, 22278998, 264093, 264094, 264259, 29331824, 29331827, 265009, 265018, 265019, 18108351, 264369, 264288, 29148627, 55811957, 264691, 18108368, 33657109, 18108368, 264635, 263981, 18108385
1379	85679344 (2757, 2758)	Novel Protein sim. GBank gi|3252872 (AF035620) - BRCA1-associated protein 2 [Homo sapiens]			265020
1380	87627962 (2759, 2760)	Novel Protein sim. GBank gi|4837737|gb|AAD30662.1| - (AF096834) germ cell specific Y-box binding protein [Homo sapiens]		nucl_recpt	264510, 264512, 265009, 264288, 264564
1381	88179656 (2761, 2762)	Novel Protein sim. GBank gi|4731580|gb|AAD28508.1|AF12538 - (AF125384) L82A [Drosophila melanogaster]		UNCLASSIFIED	87168559, 265017, 264628, 22279002
1382	94847576 (2763, 2764)		Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	22278994, 22278997, 22278999, 29331822, 29331824, 29331826, 265007, 60432229, 60433356, 85658542, 265017, 265018, 264685, 264768, 21906766, 35695917, 33657023, 27486261, 27486262, 35695763, 35695855, 87168518, 22279002
1383	87860598 (2765, 2766)			UNCLASSIFIED	18108396, 264692
1384	86915895 (2767, 2768)			UNCLASSIFIED	264488, 264508, 264509, 264905, 264906, 264908, 264909, 264511, 264512, 264910, 264760, 18108351, 264766, 264769, 35695855, 264630, 264636, 264555, 264638, 264483, 264564, 264486
1385	86378788 (2769, 2770)	Novel Protein sim. GBank gi|2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]		UNCLASSIFIED	35696052, 55811386, 264688, 21906765, 265020, 33657023, 18108385
1386	91013049 (2771, 2772)	Novel Protein sim. GBank gi|2384910 (AF022982) - contains similarity to the A-type potassium current class of channel proteins [Caenorhabditis elegans]		tnf	60432289, 29331828, 264906, 264907, 56182435, 265011, 264681, 60170615, 33657023, 83373044, 264566
1387	87797958 (2773, 2774)	Novel Protein sim. GBank gi|4160304|emb|CAA10600| - (AJ132192) HS1 binding protein 3 [Mus musculus]		UNCLASSIFIED	264591
1388	95101652 (2775, 2776)	Novel Protein sim. GBank gi|4895164|gb|AAD32753.1|AC00723 - (AC007231) putative disease resistance protein [Arabidopsis thaliana]		glycoprotein	65274572, 22278999, 264259, 29331826, 29331827, 35696052, 264509, 264907, 264908, 264909, 265006, 265008, 60170831, 33657402, 60433438, 264596, 21906754, 87168559, 264600, 265017, 264683, 18108354, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 264692, 33657023, 33657109, 35695855, 264558, 60170394, 83373044, 22279000

1389	91256016 (2777, 2778)	Novel Protein sim. GBank gi|5689387|dbj|BAA82977.1| - (AB028948) KIAA1025 protein [Homo sapiens]	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	UNCLASSIFIED	65274572, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29146499, 264906, 66712502, 55812038, 265017, 265018, 265019, 18108351, 264369, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 264692, 33657023, 33657349, 18108370, 18108374, 55811576, 264555, 264556, 264557, 60170394, 83373044, 22279000, 264563, 264564
1390	94111916 (2779, 2780)	Novel Protein sim. GBank gi|3702295 (AC005783) - R33083_1 [Homo sapiens]		peptidase	52645156, 52646365, 264259, 52645080, 29331825, 29331826, 264906, 52644045, 265009, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264760, 264682, 264288, 264686, 264687, 56181562, 52644229, 21906765, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 27486261, 27486264, 65274791, 264631, 264555, 52644332, 87168518, 22279000, 264567
1391	91227345 (2781, 2782)	Novel Protein sim. GBank gi|1346910|sp|P28650|PUA1_MOUSE - ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (IMP--ASPARTATE LIGASE)	Contains protein domain (PF00709) - Adenylosuccinate synthetase		29331826, 29331828, 29331830, 264448, 264288, 33657023, 18108365, 264555, 264556, 83373044
1392	94311097 (2783, 2784)	Novel Protein sim. GBank gi|726286 (U22394) - mSin3A [Mus musculus]			52646842, 65274572, 22278994, 22278995, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656970, 264907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52646317, 55811386, 52644296, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 264369, 264766, 21906764, 21906767, 35695917, 265020, 265021, 33657109, 52645129, 27486261, 27486262, 27486265, 33657349, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264636, 52644332, 18108382, 18108365, 87168518, 60432113, 22279000, 264484, 264566, 18108391
1393	80409472 (2785, 2786)		Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264763, 264631
1394	15028819 (2787, 2788)			UNCLASSIFIED	264629
1395	95361471 (2789, 2790)	Novel Protein sim. GBank gi|2274845|dbj|BAA21534| - (D88461) N-WASP [Rattus rattus]		UNCLASSIFIED	265009, 18108381

1396	95363253 (2791, 2792)	Novel Protein sim. GBank gi|2135904|pir||I54810 - pHL E1F1 - human			22278997, 22278999, 264259, 29331825, 60432289, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 265006, 265007, 265008, 265009, 60433358, 265010, 264602, 265017, 265018, 265019, 18108354, 52644229, 18108358, 21906767, 29148627, 21906768, 21906769, 29148629, 29148784, 265021, 265022, 18108368, 18108374, 56182323, 18108385, 264563, 264567
1397	87631317 (2793, 2794)			UNCLASSIFIED	35696286, 264907, 66712502, 264510, 35695917, 264892, 264693, 35696423
1398	91233667 (2795, 2796)	Novel Protein sim. GBank gi|5420389|emb|CAB46680.1| - (AJ243460) proteophosphoglycan [Leishmania major]			264259, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 87168474, 265018, 265019, 264682, 264768, 21906767, 265020, 33657023, 27486261, 55811576, 264632, 264639, 83373044, 87168518, 22279002
1399	87631076 (2797, 2798)	Novel Protein sim. GBank gi|2496887|sp|Q09232|YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	264768, 18108370, 264555, 264557
1400	95419064 (2799, 2800)	Novel Protein sim. GBank gi|283920|pir||S27939 - tensin - chicken	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	56182575, 22278994, 22278997, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264908, 56182435, 264112, 265009, 265011, 265017, 265018, 265019, 264760, 264762, 264765, 264288, 264685, 264687, 56181562, 264769, 21906766, 21906767, 55811957, 264691, 264692, 264628, 264629, 55811576, 264634, 264555, 264637, 264557, 264638, 18108381, 264558, 18108384, 60432113, 22279000
1401	91226379 (2801, 2802)	Novel Protein sim. GBank gi|3256185|emb|CAA15485| - (AL008635) dJ510H16.1 [Homo sapiens]	Contains protein domain (PF00790) - VHS domain	UNCLASSIFIED	65274572, 60432289, 264909, 264758, 264768, 21906769, 22279002
1402	95361475 (2803, 2804)	Novel Protein sim. GBank gi|1515427 (U57523) - nel homolog [Homo sapiens]	Contains protein domain (PF00008) - EGF-like domain	tgf	264905, 264907, 264908, 264909, 264112, 264693, 33657109, 264634
1403	94147933 (2805, 2806)	Novel Protein sim. GBank gi|5262615|emb|CAB45747.1| - (AL080156) hypothetical protein [Homo sapiens]			65274572, 66712502, 265017, 264448, 264288, 21906765, 21906769, 264693, 55811576, 65274791, 60432113
1404	90935393 (2807, 2808)			UNCLASSIFIED	65274572, 22278998, 29331822, 29331828, 66712502, 265008, 60433438, 265017, 264693, 18108385

1405	95095068 (2809, 2810)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]			264488, 56994075, 35696286, 29331822, 29331824, 29331826, 29331828, 35696052, 264508, 264906, 264907, 264908, 264510, 264511, 264910, 33657402, 264594, 264758, 264600, 264604, 264762, 18108351, 264764, 33657023, 33657109, 264628, 264634, 83373044, 22279002, 264563, 264482, 264486, 264567
1406	87612369 (2811, 2812)	Novel Protein sim. GBank gi|624076|gb|AAC96425.1| - (U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (9X); similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13993 [Paramecium bursaria Chlorella virus 1]		collagen	264907, 264605
1407	94129872 (2813, 2814)	Novel Protein sim. GBank gi|2827886 (AF015037) - endooligopeptidase A related protein; EOPA related protein [Oryctolagus cuniculus]		UNCLASSIFIED	35696286, 22278999, 264094, 264259, 66714117, 29331826, 29331827, 29331828, 29146498, 264107, 264908, 265006, 265008, 264910, 60433438, 265011, 265017, 18108351, 264448, 264288, 264686, 21906765, 21906769, 264692, 33657109, 18108370, 264628, 263972, 18108374, 35696423, 55811576, 264631, 264557, 264558, 83373044, 18108385, 87168518, 60432113, 22279002
1408	95361477 (2815, 2816)	Novel Protein sim. GBank gi|2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	oncogene	264488, 264489, 35696286, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 265008, 265009, 264910, 33657402, 264757, 264758, 265011, 264601, 265017, 264760, 264762, 264683, 264685, 264766, 264687, 264689, 21906767, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 56182323, 264639, 264563, 264564, 264565, 264566, 264567
1409	66644385 (2817, 2818)	Novel Protein sim. GBank gi|2662165|dbj|BAA23714| - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			264693
1410	86612587 (2819, 2820)	Novel Protein sim. GBank gi|2493790|sp|Q60994|ACR3_MOUSE - 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ)	Contains protein domain (PF00386) - C1q domain	complement	29331826, 264112, 264512, 265009, 265010, 264601, 264686, 264769, 21906767, 263974, 264631, 264566

1411	87818641 (2821, 2822)	Novel Protein sim. GBank gi|3123155|sp|P91343|YM3M_CAEEL - HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	22278995, 22278997, 22278999, 29331822, 60432289, 29331828, 264907, 265017, 265019, 264682, 21906767, 21906768, 21906769, 265020, 264690, 264691, 33657023, 33657109, 27486264, 264628, 263972, 264634, 264558, 18108385
1412	84390919 (2823, 2824)			UNCLASSIFIED	264757
1413	95416559 (2825, 2826)	Novel Protein sim. GBank gi|3879121|emb|CAA94370| - (Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	homeobox	56994075, 29331822, 35696052, 29331828, 29331830, 264909, 52644045, 264510, 52644296, 85658542, 87168474, 265017, 265018, 264681, 264687, 21906768, 35695917, 265020, 52644150, 264692, 263967, 27486264, 35695763, 264639, 18108387, 264566
1414	94675860 (2827, 2828)	Novel Protein sim. GBank gi|3252981 (AF068921) - Ras-binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264682, 264683, 265022, 264636
1415	94326948 (2829, 2830)	Novel Protein sim. GBank gi|1871187 (U90439) - unknown protein [Arabidopsis thaliana]			52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 66712502, 29331830, 52644045, 264113, 264511, 33657402, 264757, 21906754, 55811386, 265017, 265018, 265019, 264761, 264683, 264369, 264288, 264686, 264689, 21906766, 21906767, 29148627, 21906769, 55811957, 265020, 265021, 264690, 33657023, 65274620, 52645129, 27486262, 27486264, 60431528, 264629, 35695855, 56182323, 264559, 60432113, 264404, 22279002, 264482

1416	94325977 (2831, 2832)	Novel Protein sim. GBank gi|5106557|gb|AAD39749.1|AF12305 - (AF123052) MLL septin-like fusion protein [Homo sapiens]	Contains protein domain (PF00735) - Cell division protein	struct	18108392, 18108394, 18108397, 18108398, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 29331822, 35696052, 29331828, 29146498, 264905, 264907, 264908, 264828, 264909, 264113, 265006, 265007, 265008, 265009, 60170831, 264595, 18108348, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264762, 18108351, 264681, 264763, 264682, 264683, 264766, 52644229, 264688, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 55811957, 29148629, 265020, 52644150, 18108361, 33657023, 18108362, 18108368, 264628, 18108370, 264629, 18108374, 18108379, 55811576, 65274791, 264634, 264636, 56182323, 18108381, 60170394, 18108385, 56526486, 87168518, 22279000
1417	87826663 (2833, 2834)	Novel Protein sim. GBank gi|4958935|dbj|BAA78095.1| - (AB027570) suppressor of potassium transport defect 3 [Rattus norvegicus]		ATPase_associated	264107, 264448
1418	87594276 (2835, 2836)			UNCLASSIFIED	264259, 264908, 265010, 52644229, 21906764, 21906768, 264690, 264639, 18108388
1419	87757168 (2837, 2838)	Novel Protein sim. GBank gi|2072294 (U95097) - mitotic phosphoprotein 43 [Xenopus laevis]		struct	264259, 60432289, 265006, 87168474, 264288
1420	87298628 (2839, 2840)	Novel Protein sim. GBank gi|5174421|ref|NP_006023.1|pCPNE - copine VI (neuronal)		ATPase_associated	29331824, 265007, 264563
1421	94746986 (2841, 2842)	Novel Protein sim. GBank gi|3876090|emb|CAA93459.1| - (Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this gen...		kinase	18108358, 18108396, 18108397, 21906766, 18108398, 21906767, 56182575, 21906768, 21906769, 56181686, 55811957, 35695917, 35696286, 22278996, 22278997, 22278998, 22278999, 265021, 265022, 60170615, 264259, 33657023, 29331822, 56182181, 29331824, 66714117, 29331825, 33657109, 29331826, 27486261, 29331828, 35696052, 33657349, 264905, 264509, 20281149, 18108370, 264907, 60431528, 66712502, 263972, 55811576, 35696423, 35695855, 264512, 265007, 60431850, 60432229, 60431735, 56182323, 264558, 60170394, 83373044, 55812038, 264758, 18108385, 21906754, 55811386, 87168518, 87168559, 60432113, 265017, 265018, 265019, 22279002, 55811150, 264563, 264682, 264763, 264448, 264566, 264486, 18108391

1422	88178777 (2843, 2844)	Novel Protein sim. GBank gi|4505939|ref|NP_000928.1|pPOLR - polymerase (RNA) II (DNA directed) polypeptide A (220kD)		rnapolymerase	56994075, 35696286, 87168559, 55811957, 55811576, 264555, 264557, 87168518
1423	86997762 (2845, 2846)			UNCLASSIFIED	264686, 264489, 264692, 264594, 264603, 265018, 264908
1424	95201610 (2847, 2848)	Novel Protein sim. GBank gi|437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]	Contains protein domain (PF00620) - RhoGAP domain	struct	29331822, 29331825, 29331827, 29146498, 264905, 264906, 264908, 264909, 265007, 264910, 265009, 33109954, 265010, 87168559, 265019, 264766, 264687, 21906765, 21906766, 21906767, 21906768, 29148627, 55811957, 29148629, 265021, 264691, 264692, 56526486, 22279002, 264563
1425	21662314 (2849, 2850)	Novel Protein sim. GBank gi|100798|pir||S14959 - proline-rich protein - wheat		UNCLASSIFIED	265007, 264558
1426	94322115 (2851, 2852)	Novel Protein sim. GBank gi|2078441 (U56964) - weak similarity to S. cerevisiae intracellular protein transport protein US)1 (SP:P25386) [Caenorhabditis elegans]		UNCLASSIFIED	264488, 60424179, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331827, 56182435, 264910, 60433356, 60433438, 21906754, 265018, 264288, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 33657109, 18108370, 18108376, 264558, 83373044, 18108385, 56526486, 22279002, 264482
1427	91227510 (2853, 2854)	Novel Protein sim. GBank gi|5816074|gb|AAD45616.1|AF06194 - (AF061943) protate-derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278994, 56994075, 22278997, 29331828, 29331830, 264828, 265006, 265007, 265008, 265009, 264683, 264288, 18108354, 21906765, 21906768, 29148629, 33657023, 18108374, 35695855, 83373044, 22279002, 264564
1428	94323008 (2855, 2856)	Novel Protein sim. GBank gi|138350|sp|P28968|VGLX_HSVEB - GLYCOPROTEIN X PRECURSOR		glycoprotein	56181686, 264259, 264907, 265007, 265009, 264595, 265010, 264686, 65274620, 264629, 65274791, 22279002, 264566
1429	87888689 (2857, 2858)			UNCLASSIFIED	264112, 264595, 265017, 265019, 21906765, 263977, 264555
1430	94735021 (2859, 2860)	Novel Protein sim. GBank gi|1181619|dbj|BAA11565| - (D82364) a variant of TSC-22 [Gallus gallus]			264094, 29331824, 264591, 264593, 265018, 264681, 21906765, 21906767, 65274620, 55811576, 264639, 87168518, 22279002
1431	80429081 (2861, 2862)	Novel Protein sim. GBank gi|5420389|emb|CAB46680.1| - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264768, 265020, 264691, 264693, 264638
1432	87463004 (2863, 2864)	Novel Protein sim. GBank gi|414797 (L18966) - pyruvate dehydrogenase phosphatase [Bos taurus]		phosphatase	18108394, 29146498, 265007, 60433438, 264763, 29148629, 263969
1433	87605403 (2865, 2866)	Novel Protein sim. GBank gi|2460316 (AF022147) - uterus-ovary specific putative transmembrane protein [Rattus norvegicus]	Contains protein domain (PF00100) - Zona pellucida-like domain	UNCLASSIFIED	264259, 264510, 264591, 264603, 264565
1434	85713730 (2867, 2868)			UNCLASSIFIED	264682, 264691

1435	94708213 (2869, 2870)	Novel Protein sim. GBank gi|3970850|dbj|BAA34789.1| - (AB015330) HRIHFB2007 [Homo sapiens]			transcriptfactor	22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 33656970, 264508, 264905, 66712502, 29331830, 264909, 265007, 265008, 264910, 265009, 60433356, 60433438, 264596, 21906754, 265010, 265017, 265018, 265019, 18108351, 264762, 264448, 264288, 264769, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264690, 264691, 33657109, 264628, 18108374, 18108376, 55811576, 264636, 60170394, 56182323, 264559, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264482, 264565
1436	86635024 (2871, 2872)	Novel Protein sim. GBank gi|3183977|emb|CAA39515| - (X56044) protein Htf9C [Mus musculus]		UNCLASSIFIED		263978, 264557, 264559
1437	87631082 (2873, 2874)	Novel Protein sim. GBank gi|2496887|sp|Q09232|YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED		22278997, 66714117, 29331826, 264907, 56182435, 265009, 18108351, 264692, 264693
1438	85544280 (2875, 2876)	Novel Protein sim. GBank gi|1905906 (AD000092) - hypothetical human serine-threonine protein kinase R31240_1 [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase		264488, 264508, 264906, 264909, 264757, 264600, 264601, 264605, 264768, 264769, 264690, 35696423, 264558, 264563, 264566
1439	91231894 (2877, 2878)	Novel Protein sim. GBank gi|3876299|emb|CAA94892| - (Z71180) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabdi...	Contains protein domain (PF00450) - Serine carboxypeptidase	cathepsin		264489, 18108394, 65274572, 56182575, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 264107, 264508, 264509, 264907, 66712502, 29331830, 56182435, 264511, 265006, 265007, 265009, 60432229, 60433438, 264595, 55812038, 55811386, 265011, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 18108355, 264767, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 264638, 56182323, 83373044, 18108387, 87168518, 60432113, 22279000, 264486
1440	87423643 (2879, 2880)	Novel Protein sim. GBank gi|2662165|dbj|BAA23714| - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]		UNCLASSIFIED		264887, 264259, 264906, 264907, 264908, 264909, 265008, 265010, 265017, 265018, 265019, 18108351, 264369, 265020, 33657023, 33657109, 60431528, 55811576, 264635

1441	95317662 (2881, 2882)	Novel Protein sim. GBank gi|4493956|emb|CAB11123.2| - (Z98551) predicted using hexExon; MAL3P6.28 (PFC0845c), Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR:...	Contains protein domain (PF00646) - F-box domain.	helicase	18108392, 264488, 263994, 264489, 56182575, 22278994, 22278995, 56994075, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 56182181, 66714117, 29331826, 29331827, 29331828, 35696052, 29146498, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264910, 264592, 264593, 33657402, 60433438, 264595, 264758, 21906754, 85658542, 87168474, 265010, 87168559, 264600, 264602, 265017, 264604, 265018, 264605, 265019, 264760, 264761, 264762, 264681, 264448, 264764, 264683, 264288, 264766, 264768, 264769, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 264691, 264692, 33657023, 65274620, 33657109, 35695763, 264628, 18108370, 264629, 18108374, 55811576, 35696423, 65274791, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 56182323, 264558, 60170394, 264639, 264559, 83373044, 18108385, 18108388, 56526486, 22279000, 22279002, 264563, 264483, 264564, 264566, 264567, 264486
1442	83367491 (2883, 2884)	Novel Protein sim. GBank gi|5103027|dbj|BAA78765.1| - (AB023419) mSox7 [Mus musculus]		transcriptfactor	264906, 265007, 264693, 264558
1443	87109935 (2885, 2886)	Novel Protein sim. GBank gi|4887229|gb|AAD32244.1|AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	struct	52645080, 264691, 264628, 264555
1444	87620478 (2887, 2888)	Novel Protein sim. GBank gi|3874447|emb|CAB02772| - (Z81039) predicted using Genefinder; cDNA EST EMBL:T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...		UNCLASSIFIED	264259, 29331822, 29331824, 66714117, 29331828, 264288, 35695917, 33657023, 264635, 60170394
1445	94990470 (2889, 2890)	Novel Protein sim. GBank gi|2959886|emb|CAA11022| - (AJ222968) L-periaxin [Mus musculus]		UNCLASSIFIED	264369
1446	85079268 (2891, 2892)				264369
1447	86945392 (2893, 2894)	Novel Protein sim. GBank gi|5081610|gb|AAD39464.1|AF13544 - (AF135440) huntington yeast partner C [Mus musculus]	Contains protein domain (PF01846) - FF domain		18108396, 35696286, 22278997, 66714117, 29331828, 265009, 264758, 265018, 264288, 21906766, 21906767, 264692, 264634, 264566
1448	94990477 (2895, 2896)	Novel Protein sim. GBank gi|3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]	Contains protein domain (PF00439) - Bromodomain		29331827, 264509, 264909, 265008, 264595, 18108357, 18108385, 264566, 264486

1449	87860859 (2897, 2898)			UNCLASSIFIED	66714117, 264906, 264908, 264591, 264601, 264764, 264632
1450	87458696 (2899, 2900)	Novel Protein sim. GBank gi|1707074 (U80450) - M01E11.2 [Caenorhabditis elegans]		UNCLASSIFIED	35696286, 35696052, 265008, 265009, 60170831, 33109954, 264683, 264689, 35696423, 35695855, 56526486
1451	87797970 (2901, 2902)	Novel Protein sim. GBank gi|4160304|emb|CAA10600| - (AJ132192) HS1 binding protein 3 [Mus musculus]		UNCLASSIFIED	29331826, 264683, 264693, 263978, 264630
1452	85692899 (2903, 2904)	Novel Protein sim. GBank gi|2832906|dbj|BAA24608.1| - (D89340) dipeptidyl peptidase III [Rattus norvegicus]		peptidase	264681, 33657023, 264629
1453	86130434 (2905, 2906)	Novel Protein sim. GBank gi|728831|sp|P39188|ALU1_HUMAN - !!!! ALU SUBFAMILY J WARNING ENTRY !!!!		kinase	264510, 264768
1454	11204696 (2907, 2908)				264556
1455	87797896 (2909, 2910)			UNCLASSIFIED	29331822, 66714117, 29331825, 264905, 29331830, 265006, 265008, 265009, 265011, 265019, 18108351, 21906768, 33657109, 18108376, 264632, 56182323, 87168518
1456	86320218 (2911, 2912)	Novel Protein sim. GBank gi|729230|sp|P41004|CUT3_SCHPO - CHROMOSOME SEGREGATION PROTEIN CUT3		transport	22278995, 22278996, 22278997, 22278998, 22278999, 29331827, 264107, 265017, 21906765, 21906766, 21906767, 21906769, 29148629, 18108370, 22279000
1457	80076900 (2913, 2914)			UNCLASSIFIED	264107, 264566
1458	87800460 (2915, 2916)	Novel Protein sim. GBank gi|2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		transport	56182575, 22278999, 60432049, 264259, 29331826, 29331827, 29331828, 264102, 264107, 264110, 265009, 60432229, 265019, 265020, 263972, 263976, 264635, 22279002, 264566
1459	95360920 (2917, 2918)	Novel Protein sim. GBank gi|5524667|gb|AAD44333.1|AF15935 - (AF159356) Munc13-4 protein [Rattus norvegicus]	Contains protein domain (PF00168) - C2 domain	kinase	22278997, 264259, 29331824, 29331826, 29331827, 29331828, 265017, 265018, 264760, 264682, 264448, 264288, 264766, 265021, 264692, 33657023, 33657109, 35695855, 264566
1460	95354602 (2919, 2920)			UNCLASSIFIED	29331822, 264591, 55811957, 264691, 264693, 65274620
1461	94741513 (2921, 2922)	Novel Protein sim. GBank gi|1707274 (U80931) - strong similarity to class-III of pyridoxal-phoshate-dependent aminotransferases [Caenorhabditis elegans]	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate	gaba	22278997, 29331822, 35696052, 265009, 264758, 265017, 265018, 265019, 264760, 264369, 264687, 21906765, 21906768, 265022, 33657109, 27486261, 264555, 83373044
1462	87732018 (2923, 2924)			UNCLASSIFIED	264555, 264556
1463	88090605 (2925, 2926)	Novel Protein sim. GBank gi|1770466|emb|CAA66912| - (X98259) M-phase phosphoprotein 8 [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHRromatin Organization MOdifier) domain	struct	60432049, 264259, 29146499, 264906, 264907, 264512, 265017, 264763, 264766, 18108370, 18108374, 264636, 18108385, 18108388

1464	87620482 (2927, 2928)	Novel Protein sim. GBank gi|3874447|emb|CAB02772| - (Z81039) predicted using Genefinder; cDNA EST EMBL:T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...		UNCLASSIFIED	264569, 22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331825, 35696052, 20281100, 264905, 29331830, 264909, 265007, 33657402, 21906754, 265017, 265018, 264682, 264684, 264369, 264288, 264766, 21906765, 21906766, 21906767, 21906769, 35695917, 264691, 33657023, 264692, 35696423, 35695855, 264630, 264631, 264639, 264565
1465	87425192 (2929, 2930)	Novel Protein sim. GBank gi|4589598|dbj|BAA76821.1| - (AB023194) KIAA0977 protein [Homo sapiens]		glucoamylase	264488, 22278994, 56994075, 60432049, 264259, 56182181, 60432289, 29331827, 52644045, 264511, 265007, 265008, 264596, 55812038, 55811386, 264600, 264602, 265017, 265018, 264604, 265019, 18108351, 18108354, 56181562, 21906769, 265021, 33657023, 33657182, 55811576, 264557, 18108382, 60432113
1466	87606227 (2931, 2932)			UNCLASSIFIED	264512, 265017, 264689, 264558
1467	87614328 (2933, 2934)	Novel Protein sim. GBank gi|2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	264683, 264636
1468	95342862 (2935, 2936)	Novel Protein sim. GBank gi|4507241|ref|NP_003137.1|pSSRP - structure specific recognition protein 1			22278998, 264758, 265018, 265019, 21906769, 265020, 33657109, 22279002
1469	79236174 (2937, 2938)	Novel Protein sim. GBank gi|1906596 (U81788) - kinesin-73 [Drosophila melanogaster]		struct	18108394, 18108397, 18108398, 35696052, 29146499, 265007, 265008, 265009, 265010, 265011, 18108354, 18108365, 18108368, 18108374, 18108381, 18108382, 18108384, 18108388
1470	94990482 (2939, 2940)	Novel Protein sim. GBank gi|5649170|gb|AAD43131.2|AF15909 - (AF159092) syld709613 protein [Homo sapiens]		UNCLASSIFIED	18108394, 18108398, 56182575, 264259, 29331822, 29331824, 29331825, 60432289, 264907, 264909, 265007, 264910, 265009, 264591, 60432229, 60433356, 264595, 60433438, 264758, 33109954, 265010, 265011, 265018, 264760, 264448, 264764, 264288, 264369, 18108357, 264769, 18108358, 21906767, 21906769, 55811957, 265021, 18108361, 264691, 18108362, 18108365, 18108368, 264628, 18108379, 264637, 264557, 18108381, 56182323, 18108382, 83373044, 18108384, 18108388, 87168518, 60432113, 264404, 22279002, 264482, 264567, 264487
1471	87826842 (2941, 2942)	Novel Protein sim. GBank gi|3876146|emb|CAB01750| - (Z78542) similar to Mitochondrial carrier proteins; cDNA EST EMBL:T01651 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	29331822, 29331824, 29331825, 264828, 264603, 264689, 264693, 18108374, 55811576

1472	87756616 (2943, 2944)	Novel Protein sim. GBank gi|4680707|gb|AAD27743.1|AF13296 - (AF132968) CGI-34 protein [Homo sapiens]		UNCLASSIFIED	264905, 18108351, 21906765, 264486
1473	87791609 (2945, 2946)	Novel Protein sim. GBank gi|3688780 (AF042180) - testis-specific Y-encoded-like protein [Mus musculus]	Contains protein domain (PF00956) - Nucleosome assembly protein (NAP)	MHC	18108394, 22278995, 56994075, 22278999, 29331822, 29331824, 68714117, 29331825, 29331826, 35696052, 264906, 264907, 56182435, 265007, 264758, 265018, 265019, 264760, 264764, 264288, 264685, 264686, 264768, 21906769, 55811957, 265021, 264691, 264693, 264629, 55811576, 264634, 264638, 56182323, 22279002, 264566, 264486
1474	85800989 (2947, 2948)	Novel Protein sim. GBank gi|2494890|sp|Q92176|CORO_BOVIN - CORONIN-LIKE PROTEIN P57	Contains protein domain (PF00400) - WD domain, G-beta repeat	struct	264488, 35695917, 35696286, 264692, 33657023, 264693, 33657109, 35696052, 264508, 264905, 264906, 264907, 264629, 264908, 264909, 35696423, 35695855, 264511, 264910, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264639, 264758, 60432113, 264604, 264605, 264565, 264566, 264764, 264486, 264685, 264766
1475	86871935 (2949, 2950)		Contains protein domain (PF00041) - Fibronectin type III domain	UNCLASSIFIED	264681, 264682, 264288, 264566
1476	87548855 (2951, 2952)	Novel Protein sim. GBank gi|4757752|ref|NP_004664.1|pANGP - angiopoietin 3	Contains protein domain (PF00147) - Fibrinogen beta and gamma chains, C-terminal globular domain	glycoprotein	60424179, 56181686, 29331824, 60424269, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264512, 265007, 265008, 265009, 264910, 33657402, 264595, 264596, 55812038, 265011, 264601, 264762, 18108351, 264288, 264369, 264685, 264766, 264689, 55811957, 264691, 264692, 264693, 18108370, 60431528, 18108374, 35696423, 264634, 264635, 264636, 60431850, 264555, 264638, 264557, 264639, 18108382, 18108388, 60432113, 22279002
1477	87774279 (2953, 2954)	Novel Protein sim. GBank gi|2498308|sp|Q60870|DP1_MOUSE - POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)		UNCLASSIFIED	264259, 264107, 264905, 265008, 265010, 265011, 264682, 264288, 265020, 265021, 263974
1478	11754412 (2955, 2956)				264686

1479	91640140 (2957, 2958)	Novel Protein sim. GBank gi|5499741|gb|AAD43978.1|AF15296 - (AF152961) chromatin-specific transcription elongation factor FACT 140 kDa subunit [Homo sapiens]		peptidase	56182575, 22278995, 22278996, 22278998, 22278999, 29331822, 29331824, 66714117, 264906, 264907, 56182435, 265006, 60170831, 33657402, 264758, 33109954, 21906754, 265017, 265019, 264448, 264288, 264767, 264687, 52644229, 21906764, 264689, 21906765, 21906768, 21906769, 265020, 265021, 60170615, 264691, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 18108370, 60431528, 263976, 55811576, 264556, 264557, 60170394, 87168518, 264404, 22279000, 22279002, 264563, 264482
1480	94312412 (2959, 2960)	Novel Protein sim. GBank gi|3550456|emb|CAA06329.1| - (AJ005073) Alix [Mus musculus]		UNCLASSIFIED	18108394, 65274572, 56182575, 22278995, 35696286, 56994075, 22278996, 22278997, 22278998, 22278999, 264091, 264259, 35696052, 29146499, 264103, 264105, 264108, 264907, 52644045, 264112, 265007, 265008, 265009, 60433356, 60433438, 264598, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264448, 264682, 264683, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657109, 33657182, 263972, 35695855, 264557, 263981, 83373044, 18108385, 87168518, 264566, 264089, 264486
1481	87021442 (2961, 2962)	Novel Protein sim. GBank gi|4836807|gb|AAD30566.1|AF14679 - (AF146793) PFT27 [Mus musculus]		MHC	265006, 265007, 265010, 18108374
1482	85320442 (2963, 2964)	Novel Protein sim. GBank gi|4585372|gb|AAD25403.1|AF12292 - (AF122923) Wnt inhibitory factor-1 [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264908, 264910, 264758
1483	94115503 (2965, 2966)	Novel Protein sim. GBank gi|535428 (U13736) - calmodulin-like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	264259, 29331822, 52645080, 29331825, 29331826, 33656970, 29331830, 265007, 55812038, 33109954, 265017, 264288, 21906768, 21906769, 264636, 18108380, 87168518, 22279000
1484	94131544 (2967, 2968)	Novel Protein sim. GBank gi|1911774|bbs|180090 - (S83364) putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]		UNCLASSIFIED	264489, 35696286, 264259, 264107, 264909, 265008, 60433356, 33657402, 60433438, 264288, 21906765, 21906766, 29148627, 33657023, 27486262, 18108374, 35696423, 83373044, 60432113
1485	80194441 (2969, 2970)	Novel Protein sim. GBank gi|5360129|gb|AAD42883.1|AF15511 - (AF155117) NY-REN 62 antigen [Homo sapiens]	Contains protein domain (PF00225) - Kinesin motor domain	struct	264369, 265020, 18108374

1486	94125068 (2971, 2972)	Novel Protein sim. GBank gi|4589516|dbj|BAA76780.1| - (AB023153) KIAA0936 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	56182575, 22278999, 264906, 264907, 21906754, 87168474, 265017, 265019, 18108351, 264288, 265020, 264566
1487	86452711 (2973, 2974)	Novel Protein sim. GBank gi|5019275|emb|CAB44431.1| - (AJ132751) xenobiotic/medium-chain fatty acid:CoA ligase form XL-III [Bos taurus]		synthase	21906754, 264486
1488	87732026 (2975, 2976)	Novel Protein sim. GBank gi|5712131|gb|AAD47379.1|AF120499 - (AF120499) DEM1 protein [Homo sapiens]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	fgf	264686, 264769, 264689, 264692, 264693, 264509, 264906, 264907, 18108370, 264908, 264629, 264909, 264510, 265006, 264512, 265007, 265008, 265009, 264555, 264556, 264557, 264558, 264762, 264564, 264682
1489	95104277 (2977, 2978)	Novel Protein sim. GBank gi|2497303|sp|Q62786|FPRP_RAT - PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN)	Contains protein domain (PF00047) - Immunoglobulin domain	prostaglandin	21906767, 22278999, 265022, 264259, 264693, 29331824, 29331825, 29331826, 29331827, 29331828, 264103, 263972, 66712502, 35696423, 35695855, 265007, 265008, 265009, 83373044, 21906754, 56526486, 265017, 264563, 18108351, 264564, 264566, 264369, 264288
1490	87390127 (2979, 2980)			UNCLASSIFIED	56182575, 264259, 29331822, 29331824, 66714117, 29331827, 29331828, 264508, 264905, 66712502, 265007, 265008, 264594, 33657402, 55812038, 87168474, 265018, 18108351, 264369, 264288, 264769, 264689, 21906767, 21906768, 55811957, 60170615, 33657109, 35695855, 264635, 60170394, 56526488, 22279002, 264563
1491	83594305 (2981, 2982)	Novel Protein sim. GBank gi|295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]		UNCLASSIFIED	265007, 264448, 18108372, 264558, 56182323
1492	85805363 (2983, 2984)	Novel Protein sim. GBank gi|1656005 (U71205) - rit [Mus musculus]	Contains protein domain (PF00071) - Ras family	oncogene	22278997, 22278998, 29331822, 264907, 66712502

1493	91677215 (2985, 2986)	Novel Protein sim. GBank gi|5689515|dbj|BAA83041.1| - (AB029012) KIAA1089 protein [Homo sapiens]		UNCLASSIFIED	264488, 52646365, 65274572, 56182575, 22278994, 35696286, 56994075, 22278999, 60432049, 29331824, 29331828, 35696052, 264508, 264905, 264906, 52644045, 264909, 56182435, 265006, 265008, 265009, 60170831, 33657402, 55812038, 265010, 265011, 265017, 265018, 265019, 55811150, 264448, 264682, 264685, 264686, 52644229, 21906765, 21906766, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657023, 18108364, 18108365, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 264629, 18108374, 52644332, 56182323, 87168518, 22279002, 264564, 264566, 264567
1494	87605265 (2987, 2988)	Novel Protein sim. GBank gi|728832|sp|P39189|ALU2_HUMAN - !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!	Contains protein domain (PF01352) - KRAB box	kinase	264907, 265009, 264769, 18108370, 55811576, 264639, 264565, 264486
1495	87605267 (2989, 2990)	Novel Protein sim. GBank gi|4589588|dbj|BAA76816.1| - (AB023189) KIAA0972 protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	22278997, 264259, 264906, 264907, 265009, 264594, 33657084, 265017, 264760, 264448, 33657109, 264630, 264634, 56526486, 264563, 264565, 264566, 264486, 264567
1496	87784322 (2991, 2992)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	35696286, 264906, 265019, 264693
1497	81695428 (2993, 2994)	Novel Protein sim. GBank gi|3874925|emb|CAA92591| - (Z68296) Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE); cDNA EST EMBL:D27610 comes from this gene; cDNA EST EMBL:T01018 comes from this gene; cDNA EST EMBL:D33256 comes from this gene;...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264910, 264758, 265011, 264764, 264288, 264690, 264634, 264635, 56526486
1498	90934938 (2995, 2996)	Novel Protein sim. GBank gi|728836|sp|P39193|ALU6_HUMAN - !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!		oncogene	264488, 65274572, 29331822, 265017, 265018, 21906765, 29148627, 29148629, 18108374, 264637, 264638, 264567
1499	86451589 (2997, 2998)	Novel Protein sim. GBank gi|2570198 (U54556) - microfilarial sheath protein SHP3 [Litomosoides sigmodontis]		glucoamylase	263978, 264566
1500	80499386 (2999, 3000)			UNCLASSIFIED	22278999, 264769, 18108379
1501	85795297 (3001, 3002)	Novel Protein sim. GBank gi|2078483 (U43200) - antifreeze glycopeptide AFGP polyprotein precursor [Boreogadus saida]		UNCLASSIFIED	264559
1502	80206141 (3003, 3004)				264508, 264112, 264604, 264684, 52644150, 55811576, 264632, 264556, 264638, 56182323, 264563, 264486
1503	87012701 (3005, 3006)	Novel Protein sim. GBank gi|3900855 (AC004874) - similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID:g1171989) [Homo sapiens]	Contains protein domain (PF00535) - Glycosyl transferases	transferase	29331822, 265007, 264369

1504	79640051 (3007, 3008)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264693
1505	86102672 (3009, 3010)	Novel Protein sim. GBank gi|4753775|emb|CAB41970.1| - (AJ132545) protein kinase [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	29331826, 35696052, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 55812038, 264759, 264763, 264764, 264689, 35695917, 265022, 33657109, 18108374, 264631, 264635, 264638, 264566
1506	94143219 (3011, 3012)	Novel Protein sim. GBank gi|1304201|dbj|BAA06170| - (D29766) alternatively spliced product [Rattus norvegicus]	Contains protein domain (PF00018) - SH3 domain	glycoprotein	65274572, 56182575, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 60432049, 264259, 52645080, 29331822, 29331827, 264106, 29331830, 264908, 56182435, 264110, 264511, 264512, 55812038, 21906754, 87168559, 264600, 265017, 265018, 264681, 18108354, 264369, 264637, 264689, 21906765, 29148627, 21906768, 21906769, 29148629, 52644150, 33657023, 18108376, 65274791, 56182323, 264558, 264559, 18108385, 87168518, 60432113, 22279000, 264565
1507	83738250 (3013, 3014)	Novel Protein sim. GBank gi|5689513|dbj|BAA83040.1| - (AB029011) KIAA1088 protein [Homo sapiens]		helicase	264639
1508	11618758 (3015, 3016)				264593
1509	87318451 (3017, 3018)	Novel Protein sim. GBank gi|5031975|ref|NP_005875.1|pPAK4 - protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331828, 264591, 33109954, 264563
1510	95362643 (3019, 3020)	Novel Protein sim. GBank gi|113161|sp|P28614|ACOR_ALCEU - ACETOIN CATABOLISM REGULATORY PROTEIN		UNCLASSIFIED	264259, 29331822, 265007, 18108374, 264556
1511	88318073 (3021, 3022)	Novel Protein sim. GBank gi|726831|sp|P39188|ALU1_HUMAN - !!!! ALU SUBFAMILY J WARNING ENTRY !!!!		UNCLASSIFIED	264259, 29331822, 29331824, 29331827, 264509, 264907, 264510, 264511, 265007, 264512, 265008, 87168559, 264288, 265022, 33657023, 35695855, 264637, 264638, 264563
1512	95345390 (3023, 3024)	Novel Protein sim. GBank gi|4559353|gb|AAD23014.1|AC00658 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family		52645156, 18108396, 56994075, 60432289, 265006, 60433356, 60433438, 21906754, 87168474, 87168559, 265018, 264762, 264763, 264687, 21906765, 21906769, 27486262, 35695763, 18108374, 35696423, 264555, 18108385, 18108387, 18108388, 87168518, 264482
1513	87436228 (3025, 3026)	Novel Protein sim. GBank gi|1330394 (U58761) - C01F1.6 gene product [Caenorhabditis elegans]			35696052, 264905, 264906, 264907, 264908, 264909, 264910, 264591, 264766, 264689, 264692, 264629, 264636

1514	95345392 (3027, 3028)	Novel Protein sim. GBank gi|4559353|gb|AAD23014.1|AC00658 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family	UNCLASSIFIED	52644507, 52645156, 52646365, 52646842, 65274572, 22278994, 35696286, 56994075, 264259, 52645080, 29331822, 29331825, 35696052, 29331830, 52644045, 56182435, 265006, 60433356, 60433438, 55812038, 21906754, 52646317, 52644296, 87168474, 87168559, 264448, 52644229, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 27486265, 35695763, 18108376, 35696423, 35695855, 52644332, 18108385, 18108387, 87168518, 60432113
1515	79163536 (3029, 3030)	Novel Protein sim. GBank gi|3879501|emb|CAA87795| - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...		ubiquitin	265020, 264639
1516	88073539 (3031, 3032)	Novel Protein sim. GBank gi|498015 (L27479) - X123 [Homo sapiens]		UNCLASSIFIED	265008, 56182323, 22279002
1517	87793325 (3033, 3034)	Novel Protein sim. GBank gi|3415134 (AF082024) - Phyb1 [Pimpinella brachycarpa]			264091, 18108370, 264404
1518	87350697 (3035, 3036)	Novel Protein sim. GBank gi|728838|sp|P39195|ALU8_HUMAN - !!!! ALU SUBFAMILY SX WARNING ENTRY !!!!		tm7	66714117, 264508, 264509, 264905, 264510, 264910, 264591, 264595, 264288, 264766, 264769, 18108374, 264636, 264638, 264486
1519	94328689 (3037, 3038)	Novel Protein sim. GBank gi|5262681|emb|CAB45771.1| - (AL080198) hypothetical protein [Homo sapiens]			264569, 264489, 60432049, 265009, 33657402, 264596, 21906754, 265019, 264369, 21906765, 21906768, 21906769, 264691, 65274620, 33657182, 27486261, 18108374, 264557, 264639, 87168518, 22279002
1520	87592855 (3039, 3040)	Novel Protein sim. GBank gi|2662161|dbj|BAA23712| - (AB007900) HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	18108392, 60432049, 264259, 29331824, 265007, 60433356, 265010, 21906768, 264636
1521	86970696 (3041, 3042)	Novel Protein sim. GBank gi|5052351|gb|AAD38516.1|AF13542 - (AF135421) GDP-mannose pyrophosphorylase B [Homo sapiens]	Contains protein domain (PF00483) - Nucleotidyl transferase	synthase	18108394, 264259, 66714117, 265011, 264603, 265019, 18108364, 35696423, 264557, 264558, 18108388
1522	78960687 (3043, 3044)			UNCLASSIFIED	29331824, 265018, 265020, 265021
1523	91005151 (3045, 3046)	Novel Protein sim. GBank gi|3776567 (AC005388) - Strong similarity to F21B7.33 gi|2809264 from A. thaliana BAC gb|AC002560. EST gb|N65119 comes from this gene. [Arabidopsis thaliana]		UNCLASSIFIED	65274572, 21906768, 264693
1524	80203723 (3047, 3048)			UNCLASSIFIED	264112, 21906754, 263974
1525	87799867 (3049, 3050)	Novel Protein sim. GBank gi|4759040|ref|NP_004283.1|pRIN1 - ras inhibitor		UNCLASSIFIED	264683, 264687, 264689, 264690, 264692, 264693

1526	95105344 (3051, 3052)	Novel Protein sim. GBank gi|728850|sp|P08640|AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		glycoprotein	35696286, 56182181, 60431735, 264595, 55812038, 264605, 264683, 21906765, 55811957, 265020, 65274791, 264555, 264556, 264557, 264558, 264559, 83373044
1527	88262512 (3053, 3054)	Novel Protein sim. GBank gi|2792496 (AF041107) - tulip 2 [Rattus norvegicus]			56182575, 264259, 60432049, 29331822, 60432289, 264908, 66712502, 60433438, 87168559, 265017, 264288, 21906766, 21906769, 263977, 55811576, 56182323, 18108381
1528	94130918 (3055, 3056)			UNCLASSIFIED	22278995, 22278997, 264259, 66712502, 264596, 265017, 265019, 264682, 264448, 264683, 264764, 264685, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 264693, 83373044, 18108385
1529	94120793 (3057, 3058)	Novel Protein sim. GBank gi|4406663|gb|AAD20053| - (AF131826) Unknown [Homo sapiens]		UNCLASSIFIED	264488, 263994, 56182575, 22278995, 35696286, 22278997, 264259, 29331822, 60432289, 29331827, 35696052, 264509, 264906, 264907, 264908, 264909, 52644045, 56182435, 264511, 265009, 264910, 60433356, 60433438, 265017, 265018, 264760, 264448, 264764, 264369, 264288, 264766, 18108357, 264768, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 52644150, 33657109, 264629, 35695855, 60432113, 22279002, 264563, 264564, 264486, 264567
1530	95012765 (3059, 3060)	Novel Protein sim. GBank gi|2828710 (AF043642) - matrin cyclophilin [Rattus norvegicus]			264488, 264489, 35696286, 29331825, 35696052, 264508, 264905, 264906, 264907, 264909, 264510, 264511, 264512, 264910, 264592, 264595, 18108351, 264764, 264683, 264684, 264766, 264768, 18108357, 264769, 35695917, 264628, 264629, 18108374, 35695855, 264630, 264631, 264634, 264555, 264636, 264637, 264404, 264563, 264566, 264486
1531	95419351 (3061, 3062)	Novel Protein sim. GBank gi|1905874 (U90878) - carboxyl terminal LIM domain protein [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	56182575, 35696286, 264097, 264259, 29331822, 29331825, 29331826, 29331827, 35696052, 264509, 56182435, 264510, 264511, 265007, 60433356, 55811386, 264681, 264369, 264288, 264766, 264687, 55811957, 35695917, 33657023, 35695763, 55810764, 35696423, 55811576, 263981, 60170394, 56182323, 83373044, 60432113, 264566

1532	85718224 (3063, 3064)	Novel Protein sim. GBank gi|3874716|emb|CAA91265| - (Z66494) cDNA EST EMBL:D65271 comes from this gene; cDNA EST EMBL:D64845 comes from this gene; cDNA EST EMBL:D64449 comes from this gene; cDNA EST EMBL:D67438 comes from this gene; cDNA EST EMBL:D68087 comes from this gene; cDN...		UNCLASSIFIED	264689
1533	94239830 (3065, 3066)	Novel Protein sim. GBank gi|1490324|emb|CAB01543| - (Z78141) unknown [Mus musculus]		struct	29331824, 29146499, 264907, 264112, 265008, 265011, 265017, 265018, 264762, 18108351, 263967, 20281149, 18108374, 263981, 264566
1534	95343941 (3067, 3068)	Novel Protein sim. GBank gi|81286|pir||S22697 - extensin - Volvox carteri (fragment)		UNCLASSIFIED	264905, 264907, 264766, 264637
1535	90936732 (3069, 3070)				65274572, 22278997, 264259, 60432049, 29331822, 60432289, 29331827, 29146499, 265006, 265008, 60170831, 60433438, 33109954, 87168559, 265018, 18108357, 21906768, 29148629, 265021, 265022, 18108377, 56182323, 60432113, 22279000, 22279002
1536	87602856 (3071, 3072)	Novel Protein sim. GBank gi|106024|pir||B32891 - finger protein 2, placental - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264686, 18108357, 18108394, 21906767, 21906768, 29148629, 35696286, 265020, 265021, 52644150, 264693, 66714117, 29331825, 29331826, 264508, 264905, 20281149, 264909, 18108374, 35696423, 35695855, 265009, 264634, 264636, 264638, 18108385, 56526486, 265017, 265018, 264563, 264762, 18108351, 264448, 264369, 264766
1537	95354556 (3073, 3074)	Novel Protein sim. GBank gi|3876332|emb|CAB02096| - (Z79754) cDNA EST EMBL:T01054 comes from this gene; cDNA EST EMBL:D73600 comes from this gene; cDNA EST yk426f12.5 comes from this gene; cDNA EST yk342f10.5 comes from this gene; cDNA EST yk475c5.5 comes from this gene; cDNA ES...			65274572, 56182575, 60432049, 264259, 29331826, 265006, 265007, 60433356, 60433438, 264601, 18108351, 264448, 264369, 264288, 33657023, 65274620, 33657109, 60432113
1538	85724628 (3075, 3076)	Novel Protein sim. GBank gi|403440 (M81787) - [Gallus domesticus skeletal muscle mRNA, partial cds.], gene product [Gallus gallus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	18108394, 18108397, 264909, 265008, 265009, 265010, 18108351, 264638, 18108382, 18108385, 18108388

1539	95337628 (3077, 3078)	Novel Protein sim. GBank gi|3218411|emb|CAA19575.1| - (AL023859) SPBC19C7.07c, putative tRNA splicing endonuclease ga mma subunit, ten:284aa, similar eg. to YAR008W, YAH8_YEAST, P39707, YAR008W, tRNA splicing endonuclease gamma subunit, (275aa), fasta scores, opt:269, E():6.4e-2...		nuclease	22278994, 22278996, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60424269, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 56182435, 265009, 33657402, 60433356, 60433438, 55812038, 21906754, 87168559, 265017, 265018, 265019, 18108351, 264288, 52644229, 18108359, 21906764, 21906767, 21906768, 35695917, 265020, 265021, 52644150, 33657023, 33657109, 27486261, 18108370, 18108376, 35696423, 55811576, 65274791, 264558, 56182323, 60170394, 83373044, 87168518, 60432113, 22279000, 22279002, 264566
1540	95352858 (3079, 3080)	Novel Protein sim. GBank gi|5052634|gb|AAD38647.1|AF14567 - (AF145672) BcDNA.GH12174 [Drosophila melanogaster]		UNCLASSIFIED	264369, 264691, 263978
1541	95317948 (3081, 3082)	Novel Protein sim. GBank gi|5052349|gb|AAD38515.1|AF13501 - (AF135016) protein phosphatase 2A 48 kDa regulatory subunit [Homo sapiens]		phosphatase	264488, 264489, 22278999, 264259, 29331822, 35696052, 264508, 264509, 264905, 264907, 264908, 264511, 264512, 264910, 264592, 264761, 264762, 264448, 264764, 264288, 264687, 21906769, 55811957, 35695917, 265020, 264691, 33657023, 264692, 33657109, 264628, 18108374, 264632, 264634, 264635, 264639, 18108385, 264563, 264564, 264565, 264566, 264486
1542	90937549 (3083, 3084)	Novel Protein sim. GBank gi|5305702|gb|AAD41779.1|AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	18108392, 18108394, 65274572, 29331822, 264508, 265007, 265008, 265009, 265011, 264682, 18108354, 18108355, 52644150, 18108368, 264636, 18108381, 18108382
1543	84348768 (3085, 3086)	Novel Protein sim. GBank gi|728832|sp|P39189|ALU2_HUMAN - !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!		nuclease	264106, 33109954, 265019, 264683, 35695917, 264690, 264692, 33657109
1544	87757295 (3087, 3088)	Novel Protein sim. GBank gi|3493162 (AF084259) - bromodomain-containing protein BP75 [Mus musculus]	Contains protein domain (PF00439) - Bromodomain	nucl_recpt	35696286, 56994075, 22278999, 35696052, 60433356, 60433438, 265011, 264683, 33657109, 35696423, 264631, 87168518, 22279000
1545	85757973 (3089, 3090)	Novel Protein sim. GBank gi|1086591 (U41007) - similar to S. cervisiae nuclear protein SNF2 (SP:P22082) in a a region of gly-arg repeats [Caenorhabditis elegans]		UNCLASSIFIED	264112, 264692, 264693, 55811576
1546	79476589 (3091, 3092)			UNCLASSIFIED	264905, 264686
1547	86999594 (3093, 3094)	Novel Protein sim. GBank gi|2661132 (AF035683) - p21 [Mus musculus]		UNCLASSIFIED	264259, 29331822, 66714117, 265007, 55811386, 265010, 264600, 265017, 265019, 264288, 264768, 265020, 265022, 55811576, 18108380, 264563

1548	94233065 (3095, 3096)	Novel Protein sim. GBank gi|3043692|dbj|BAA25510| - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	29331824, 60431528, 264639, 56182323
1549	95330048 (3097, 3098)	Novel Protein sim. GBank gi|5689519|dbj|BAA83043.1| - (AB029014) KIAA1091 protein [Homo sapiens]		eph	60424179, 22278995, 35696286, 22278998, 22278999, 264092, 264094, 29331822, 56182181, 29331824, 35696052, 264905, 264906, 264908, 264909, 265006, 264511, 265008, 60431735, 60433356, 21906754, 55811386, 87168559, 265017, 265018, 265019, 55811150, 264682, 264288, 264369, 56181562, 264769, 21906765, 21906768, 21906769, 55811957, 265020, 264691, 33657109, 60431528, 35696423, 35695855, 56526486, 60432113, 22279002, 264563, 264566
1550	95201907 (3099, 3100)	Novel Protein sim. GBank gi|544483|sp|P35350|GUSB_BOVIN - POSSIBLE GUSTATORY RECEPTOR TYPE B (PPR1 PROTEIN)	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	65274572, 60432289, 265008, 264910, 265011, 265017, 265019, 264768, 56182323
1551	88077111 (3101, 3102)	Novel Protein sim. GBank gi|4758566|ref|NP_004798.1|pHS6S - heparan-sulfate 6-sulfotransferase		UNCLASSIFIED	22278999, 29331822, 264508, 264509, 264906, 264907, 264909, 265007, 264512, 264910, 21906754, 265018, 265019, 264681, 264764, 264766, 264688, 264769, 21906769, 264692, 35695763, 264635, 264555, 264556, 264557, 264638, 264558, 264563
1552	87617114 (3103, 3104)			UNCLASSIFIED	264259, 29331828, 66712502, 264764, 264288, 264686, 33657109, 264556
1553	94725512 (3105, 3106)	Novel Protein sim. GBank gi|4589570|dbj|BAA76807.1| - (AB023180) KIAA0963 protein [Homo sapiens]	Contains protein domain (PF00304) - Gamma-thionins family	dehydrogenase	56182575, 35696286, 29146499, 264509, 264907, 264908, 264909, 56182435, 265006, 265008, 265009, 264910, 264757, 264758, 265017, 55811150, 18108351, 264764, 56181562, 35695917, 264693, 33657109, 18108374, 35696423, 65274791, 35695855, 264635, 264555, 56182323, 18108382, 83373044, 22279000
1554	94233069 (3107, 3108)	Novel Protein sim. GBank gi|3043692|dbj|BAA25510| - (AB011156) KIAA0584 protein [Homo sapiens]	Contains protein domain (PF00446) - Gonadotropin-releasing hormones	transferase	35696286, 22278997, 264259, 29331822, 29331824, 29331825, 29331828, 265007, 265009, 60432229, 33657402, 55812038, 265011, 265019, 264681, 264369, 264686, 264767, 264768, 21906765, 21906769, 35695917, 264693, 18108370, 60431528, 55811576, 264631, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002

1555	87332970 (3109, 3110)	Novel Protein sim. GBank gi|2257495|dbj|BAA21392| - (AB004534) pi015 [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264259, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 264910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21906765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526486
1556	91229268 (3111, 3112)			UNCLASSIFIED	83373044, 264758, 265022, 264600, 35696052, 264630, 35696423, 265018, 264632, 264682, 29331822, 265020, 265011
1557	87640609 (3113, 3114)	Novel Protein sim. GBank gi|3329611 (AF078783) - contains similarity to C3HC4-type zinc fingers (Pfam; zf-C3HC4.hmm, score; 34.08); most similar to drosophila goliath protein (SW: Q06003) [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	60432289, 264509, 264906, 264907, 264908, 264909, 264910, 264758, 55811386, 264761, 264762, 264766, 264769, 264690, 263978, 264634, 264635, 264639, 264564, 264486
1558	94840376 (3115, 3116)	Novel Protein sim. GBank gi|5360105|gb|AAD42871.1|AF15510 - (AF155105) putative zinc finger protein NY-REN-34 antigen [Homo sapiens]			22278994, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 264448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811576, 83373044, 87168518, 22279000, 22279002
1559	88224865 (3117, 3118)	Novel Protein sim. GBank gi|112908|sp|P02750|A2GL_HUMAN - LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264259, 29331822, 60432289, 35696052, 264107, 264110, 21906754, 33109954, 87168559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35695855
1560	84580675 (3119, 3120)	Novel Protein sim. GBank gi|3880146|emb|CAA92704| - (Z68319) Similarity to Human hnRNP F protein (PIR Acc. No. S43484); cDNA EST EMBL:D34218 comes from this gene; cDNA EST EMBL:D37248 comes from this gene; cDNA EST EMBL:D71817 comes from this gene; cDNA EST EMBL:D74531 comes fro...		UNCLASSIFIED	264908, 264603, 264638
1561	86609159 (3121, 3122)				264510, 264594
1562	83359682 (3123, 3124)			UNCLASSIFIED	263967
1563	85508694 (3125, 3126)			UNCLASSIFIED	264910, 264764, 264766
1564	87766371 (3127, 3128)	Novel Protein sim. GBank gi|1168287|sp|P45953|ACDV_RAT - ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD)	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	18108394, 35696286, 264259, 29331822, 60432289, 35696052, 29331828, 264508, 66712502, 264908, 56182435, 265007, 264910, 60170831, 21906754, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 21906765, 21906768, 265021, 60170615, 264692, 35696423, 35695855, 264557, 56182323, 60432113, 22279002, 264482

1565	87783381 (3129, 3130)	Novel Protein sim. GBank gi|129726|sp|P05307|PDI_BOVIN - PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55)		isomerase	264488, 264689, 18108398, 55811957, 264534, 264259, 264508, 264905, 264509, 264908, 18108372, 264510, 264511, 264512, 265008, 264630, 265009, 264910, 264635, 264636, 264591, 264555, 264592, 264637, 264593, 264594, 264595, 264596, 265011, 264603, 22279002, 18108351, 264762, 264565, 264567
1566	87424749 (3131, 3132)	Novel Protein sim. GBank gi|3880445|emb|CAA20329| - (AL031266) VM106R.1 [Caenorhabditis elegans]		tnf	22278996, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 66712502, 264908, 265008, 18108351, 52644229, 21906765, 21906767, 21906768, 21906769, 33657109, 264555, 264639, 264482
1567	84999006 (3133, 3134)	Novel Protein sim. GBank gi|4929699|gb|AAD34110.1|AF15187 - (AF151873) CGI-115 protein [Homo sapiens]		UNCLASSIFIED	58182575, 21906769, 264692
1568	87648761 (3135, 3136)	Novel Protein sim. GBank gi|4827063|ref|NP_005072.1|pZNF1 - zinc finger protein 142 (clone pHZ-49)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	29331827, 29331830, 264511, 265009, 264758, 21906767, 21906768, 264691, 264693, 22279000, 22279002
1569	90936668 (3137, 3138)	Novel Protein sim. GBank gi|5689451|dbj|BAA83009.1| - (AB028980) KIAA1057 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	65274572, 29331822, 29331824, 29331828, 264905, 56182435, 265007, 265019, 264764, 21906765, 21906769, 55811957, 60170615, 52644150, 264692, 33657023, 33657109, 18108377, 264563, 264567
1570	86943981 (3139, 3140)	Novel Protein sim. GBank gi|1255430 (U53155) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264595, 264682, 265021
1571	91210340 (3141, 3142)	Novel Protein sim. GBank gi|4507731|ref|NP_001061.1|pTUBG - tubulin, gamma polypeptide	Contains protein domain (PF00091) - Tubulin/FtsZ family	tubulin	22278996, 35696286, 22278997, 264091, 264259, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 56182435, 264510, 265007, 264758, 265011, 18108351, 264448, 264288, 264369, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 264693, 18108370, 18108377, 35696423, 35695855, 264634, 264555, 264558, 18108384
1572	81201664 (3143, 3144)			UNCLASSIFIED	35696052, 264905, 264906, 264908, 264910, 264758, 264766, 35695917, 264637
1573	80207066 (3145, 3146)			UNCLASSIFIED	263972

1574	94216142 (3147, 3148)	Novel Protein sim. GBank gi|4758334|ref|NP_004256.1|pFADS - delta-6 fatty acid desaturase	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	cytochrome	18108394, 264887, 18108397, 18108398, 22278998, 22278997, 22278999, 264259, 29331825, 29331827, 29146498, 29146499, 264107, 264907, 264909, 52644045, 264511, 265008, 264910, 265009, 264591, 21906754, 265011, 265019, 18108351, 264682, 264763, 264764, 18108354, 264369, 264288, 264685, 264766, 264686, 264768, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 264690, 264691, 264693, 20281069, 18108370, 18108374, 18108379, 35695855, 264634, 18108384, 18108385, 22279002, 264563, 264566
1575	95340019 (3149, 3150)	Novel Protein sim. GBank gi|3881810|emb|CAA94856| - (Z70783) similar to EF-hand calcium binding protein; cDNA EST EMBL:C08700 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00036) - EF hand	phosphatase	56994075, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 264909, 265006, 265008, 265009, 265010, 87168559, 55811150, 264448, 18108354, 264369, 264288, 18108357, 55811957, 265020, 265021, 60170615, 264691, 33657023, 33657109, 60431528, 65274791, 35695855, 18108385, 60432113, 22279002, 264482
1576	95314019 (3151, 3152)	Novel Protein sim. GBank gi|2773195 (AF039711) - contains similarity to Physcomitrella patens glyceraldehyde 3-phosphate dehydrogenase (GB:X72381) [Caenorhabditis elegans]		UNCLASSIFIED	264569, 264092, 264094, 264095, 264259, 264508, 264905, 264509, 264907, 264909, 264510, 264511, 265006, 264910, 21906754, 265010, 265011, 87168559, 264761, 264762, 264288, 264766, 264769, 264691, 264693, 35695855, 264632, 264634, 264635, 264638, 83373044, 264486
1577	87613800 (3153, 3154)	Novel Protein sim. GBank gi|2499130|sp|P70315|WASP_MOUSE - WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)		UNCLASSIFIED	264511, 265011, 264681, 264369, 264686, 264689, 264629, 264555, 264558, 264559
1578	87123138 (3155, 3156)				264259, 29331826, 265017, 264689, 264693, 60432113
1579	88085141 (3157, 3158)	Novel Protein sim. GBank gi|2978255|dbj|BAA25190| - (AB007407) myeloid zinc finger protein-2 [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	35696286, 264908, 264909, 60433438, 55811386, 264369, 264685, 33657023, 264555, 264556, 264557, 87168518
1580	87255702 (3159, 3160)	Novel Protein sim. GBank gi|4324682|gb|AAD16986| - (AF109674) late gestation lung protein 1 [Rattus norvegicus]	Contains protein domain (PF00188) - SCP-like extracellular protein	glycoprotein	22278999, 35696052, 29331830, 52644045, 55812038, 87168474, 265018, 264448, 265022, 264638, 56526486, 22279000
1581	95087431 (3161, 3162)	Novel Protein sim. GBank gi|2088838 (AF003386) - F59E12.4 gene product [Caenorhabditis elegans]			22278995, 29331822, 29331824, 29331826, 56182435, 264595, 55812038, 87168559, 265017, 264288, 21906764, 55811957, 35695917, 264692, 55811576, 264637, 56182323, 264559, 83373044, 60432113

1582	95358052 (3163, 3164)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		phosphatase	264259, 60432289, 29331827, 264509, 264905, 264906, 264907, 264909, 264910, 264762, 264288, 264768, 264769, 264632, 264555, 264639, 56526486, 22279000
1583	87622715 (3165, 3166)	Novel Protein sim. GBank gi|5578958|emb|CAB51351.1| - (AL050306) dJ475B7.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	60170831, 33657402, 264682, 21906766, 35695855, 264563
1584	95337722 (3167, 3168)	Novel Protein sim. GBank gi|5531815|gb|AAD44482.1| - (AF078850) steroid dehydrogenase homolog [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	60424179, 52646842, 65274572, 56182575, 22278995, 35696286, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 60424269, 60432289, 29331827, 29331828, 35696052, 29146498, 66712502, 29331830, 52644045, 56182435, 264510, 264512, 265008, 60433356, 33657402, 60433438, 55812038, 21906754, 55811386, 52644296, 87168474, 87168559, 265018, 265019, 264448, 264369, 264288, 18108358, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108374, 55810764, 55811576, 35696423, 65274791, 35695855, 56182323, 83373044, 18108387, 87168518, 60432113, 22279002
1585	87626117 (3169, 3170)	Novel Protein sim. GBank gi|4240132|dbj|BAA74846.1| - (AB020630) KIAA0823 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	phosphatase	35696286, 22278998, 264259, 29331822, 29331824, 29331825, 264905, 265006, 265007, 265008, 60433356, 33109954, 87168474, 265011, 265017, 264604, 264369, 264288, 264685, 264769, 18108359, 21906765, 18108364, 18108370, 264629, 263972, 18108383, 18108388, 264482, 264564
1586	88067081 (3171, 3172)	Novel Protein sim. GBank gi|3786494 (AF098993) - No definition line found [Caenorhabditis elegans]			265017, 265018, 264689, 33657023, 263978, 264636, 264563
1587	87617126 (3173, 3174)	Novel Protein sim. GBank gi|3253159 (AF005355) - translation initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	264907, 264908, 264511, 264910, 264591, 264594, 264629, 264631, 264563, 264483, 264567
1588	87802536 (3175, 3176)	Novel Protein sim. GBank gi|1077573|pir||S52680 - probable ribosomal protein L34, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00468) - Ribosomal protein L34	UNCLASSIFIED	264259, 29331828, 264905, 265006, 264758, 21906754, 264761, 264762, 21906765, 21906769, 60170615, 52644150, 33657109, 35695855, 56182323, 18108385
1589	90980653 (3177, 3178)	Novel Protein sim. GBank gi|2137756|pir||I48746 - semaphorin C - mouse (fragment)		UNCLASSIFIED	65274572, 264490, 29331822, 66714117, 29331827, 29331828, 56182435, 265008, 60170831, 264595, 264758, 264598, 265011, 264686, 21906766, 21906768, 55811957, 27486265, 264639, 18108385, 56526486, 60432113

1590	95319825 (3179, 3180)			UNCLASSIFIED	264489, 22278996, 264259, 29331824, 29331825, 29331826, 29331827, 265006, 60433356, 21906754, 265017, 265018, 265019, 264448, 264765, 264288, 52644229, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 27486265, 35695763, 56526486, 60432113, 22279000, 22279002
1591	86877160 (3181, 3182)				264564
1592	87882533 (3183, 3184)	Novel Protein sim. GBank gi|4557749|ref|NP_000237.1|pMHC2 - MHC class II transactivator		MHC	264259, 264905, 29331830, 264595, 265017, 264448, 264288, 264690, 264629, 87168518
1593	94991661 (3185, 3186)			UNCLASSIFIED	65274572, 60432049, 264509, 60433356, 21906754, 21906767, 21906768, 18108370, 35696423, 22279000, 264565, 264567
1594	87773752 (3187, 3188)	Novel Protein sim. GBank gi|3877072|emb|CAA87060| - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]		UNCLASSIFIED	264488, 29331827, 264905, 264906, 264907, 264908, 264909, 264910, 264592, 264593, 264757, 264602, 264604, 264760, 264681, 264288, 264766, 264768, 29148629, 35695917, 264692, 264628, 264629, 264630, 264632, 264634, 264635, 264636, 264639, 264563, 264564, 264566
1595	79919425 (3189, 3190)	Novel Protein sim. GBank gi|3152703 (AF065389) - tetraspan NET-4 [Homo sapiens]	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	UNCLASSIFIED	29331826, 264908, 55811957
1596	79933928 (3191, 3192)			UNCLASSIFIED	29146498, 264758, 263967
1597	86971857 (3193, 3194)	Novel Protein sim. GBank gi|5257114|gb|AAD41244.1|AF09448 - (AF094480) cholesterol 24-hydroxylase [Homo sapiens]	Contains protein domain (PF00067) - Cytochrome P450	cyto450	264092, 29331824, 264508, 264682, 264369, 264686, 264630, 264563
1598	87862939 (3195, 3196)				264259, 264634
1599	87649829 (3197, 3198)	Novel Protein sim. GBank gi|4506797|ref|NP_000324.1|pSCA7 - spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	Contains protein domain (PF01581) - FMRFamide related peptide family	UNCLASSIFIED	52645080, 29331824, 29331826, 264511, 265009, 265011, 264605, 264448, 264764, 265020, 264692, 264693, 18108370, 264635, 18108385
1600	80056002 (3199, 3200)				29331826, 264603, 264691, 264563
1601	15023246 (3201, 3202)			UNCLASSIFIED	264635
1602	86926987 (3203, 3204)	Novel Protein sim. GBank gi|5305704|gb|AAD41780.1|AF12853 - (AF128535) cytoplasmic phosphoprotein PACSIN2 [Mus musculus]	Contains protein domain (PF00018) - SH3 domain	struct	29146499, 264112, 264762, 18108351, 29148627, 263974
1603	80502072 (3205, 3206)	Novel Protein sim. GBank gi|283920|pir||S27939 - tensin - chicken		collagen	264490, 29331824, 264907, 264909, 264511, 265008, 264592, 265010, 265011, 264762, 264764, 264369, 264288, 264687, 264769, 264693, 264628, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 18108385
1604	80221813 (3207, 3208)	Novel Protein sim. GBank gi|4768831|gb|AAD29633.1|AF11682 - (AF116827) unknown [Homo sapiens]		ATPase_associated	263977

1605	91221129 (3209, 3210)			struct	264905, 264509, 264906, 264907, 264908, 264909, 264604, 264766, 264768, 264692, 264693, 33657109, 264629, 35695855, 264635, 264636, 264637
1606	94312703 (3211, 3212)	Novel Protein sim. GBank gi|4505313|ref|NP_003794.1|pMYOM - UNKNOWN	Contains protein domain (PF00047) - Immunoglobulin domain	struct	22278996, 22278999, 264259, 33657402, 265017, 18108351, 264448, 21906767, 21906769, 52644150, 264691, 87168518
1607	10871805 (3213, 3214)	Novel Protein sim. GBank gi|5174473|ref|NP_005888.1|pIPP| - Intracisternal A particle-promoted polypeptide		transcriptfactor	264689
1608	80428900 (3215, 3216)	Novel Protein sim. GBank gi|2224629|dbj|BAA20802| - (AB002342) KIAA0344 [Homo sapiens]		UNCLASSIFIED	264094, 264906, 264907, 264909, 264910, 264591, 264603, 264768, 264693, 264634, 264635, 264637, 264639
1609	94311572 (3217, 3218)	Novel Protein sim. GBank gi|4884073|emb|CAB43213.1| - (AL049934) hypothetical protein [Homo sapiens]			52644507, 52645156, 52646365, 52646842, 56182575, 22278994, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29147620, 29331826, 35696052, 33656970, 264508, 264509, 264907, 52644045, 56182435, 264510, 264511, 264512, 33657402, 21906754, 52646317, 33109954, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264769, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 52645129, 27486261, 27486262, 35695763, 264628, 18108370, 18108376, 35696423, 264638, 52644332, 18108387, 87168518, 22279000, 264563, 264486
1610	85468200 (3219, 3220)	Novel Protein sim. GBank gi|283920|pir||S27939 - tensin - chicken		UNCLASSIFIED	264593, 264757, 55812038, 265018, 265020, 264691, 264692, 264693, 264631, 264634, 264635, 264555, 22279000, 264564
1611	94122843 (3221, 3222)	Novel Protein sim. GBank gi|107284|pir||A35415 - peroxidase (EC 1.11.1.7), thyroid (Grave's disease) - human (fragment)	Contains protein domain (PF00008) - EGF-like domain	peroxidase	35696286, 21906765, 264691, 35696423
1612	85746031 (3223, 3224)	Novel Protein sim. GBank gi|3874846|emb|CAA94337| - (Z70307) Similarity to B.subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST EMBL:C09951 comes from this gene; cDNA EST EMBL:C08265 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264509, 18108370, 18108387, 264486
1613	82247354 (3225, 3226)			UNCLASSIFIED	264759

1614	91228634 (3227, 3228)	Novel Protein sim. GBank gi|4680673|gb|AAD27726.1|AF13295 - (AF132951) CGI-17 protein [Homo sapiens]	Contains protein domain (PF01605) - eRF1-like proteins	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 264908, 264512, 265009, 265011, 265017, 265018, 265019, 18108351, 264683, 264288, 264766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 35696423, 35695855, 60170394, 56182323, 83373044, 264566
1615	86121909 (3229, 3230)	Novel Protein sim. GBank gi|5689485|dbj|BAA83026.1| - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264691, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002
1616	94311819 (3231, 3232)	Novel Protein sim. GBank gi|3876260|emb|CAB01696| - (Z78418) cDNA EST EMBL:D71020 comes from this gene; cDNA EST EMBL:D73593 comes from this gene; cDNA EST EMBL:C07649 comes from this gene; cDNA EST EMBL:C09081 comes from this gene; cDNA EST yk399f2.3 comes from this gene; cDNA ...		UNCLASSIFIED	264488, 52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35696286, 22278996, 22278997, 22278999, 52645080, 29331822, 29331824, 29331825, 29331827, 29331828, 35696052, 33656970, 264905, 264909, 264594, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264448, 264684, 52644229, 21906764, 264689, 21906765, 21906766, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 18108376, 35696423, 35695855, 264557, 52644332, 264558, 18108385, 87168518
1617	88090742 (3233, 3234)	Novel Protein sim. GBank gi|466053|sp|P34679|YO41_CAEEL - HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) - DHHC zinc finger domain	peptidase	35696052, 264905, 264509, 264907, 264908, 264510, 264511, 264764, 264766, 264768, 264689, 264693, 18108374, 264635, 264636, 264638
1618	86272860 (3235, 3236)	Novel Protein sim. GBank gi|4240231|dbj|BAA74894.1| - (AB020678) KIAA0871 protein [Homo sapiens]		struct	35696286, 22278999, 264092, 29331824, 29331825, 35696052, 33657084, 21906765, 27486264
1619	95354580 (3237, 3238)	Novel Protein sim. GBank gi|5031763|ref|NP_005515.1|pHRY| - hairy (Drosophila)-homolog	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	52646842, 65274572, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 56182435, 265007, 265008, 264910, 60170831, 60432229, 60433356, 60433438, 265019, 264448, 264288, 264686, 21906768, 265021, 60170615, 33657023, 65274620, 33657109, 18108374, 18108376, 35696423, 35695855, 56182323, 56526486
1620	87344655 (3239, 3240)	Novel Protein sim. GBank gi|1351047|sp|P45843|SCRT_DROME - SCARLET PROTEIN		UNCLASSIFIED	264684

1621	87076708 (3241, 3242)			UNCLASSIFIED	264910
1622	94741739 (3243, 3244)	Novel Protein sim. GBank gi|3822553 (AF098788) - nuclear calmodulin-binding protein [Gallus gallus]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	18108392, 65274572, 18108398, 22278996, 22278997, 22278999, 29146498, 29146499, 264905, 264908, 264909, 264828, 52644045, 264592, 60433358, 21906754, 264602, 265017, 264369, 21906768, 55811957, 265021, 60170615, 264635, 264557, 60170394, 83373044, 18108385, 22279000, 22279002, 264568
1623	87779106 (3245, 3246)	Novel Protein sim. GBank gi|731086|sp|P40389|UV22_SCHPO - UV-INDUCED PROTEIN UVI22		ribosomalprot	18108398, 264259, 264909, 56182435, 87168474, 264448, 21906768, 35695917, 264691, 87168518, 264563
1624	87338178 (3247, 3248)	Novel Protein sim. GBank gi|3875666|emb|CAB05478| - (Z83104) cDNA EST EMBL:T00015 comes from this gene; cDNA EST EMBL:D33665 comes from this gene; cDNA EST EMBL:D36540 comes from this gene; cDNA EST yk240f8.3 comes from this gene; cDNA EST yk387c8.3 comes from this gene; cDNA ES...		UNCLASSIFIED	66714117, 29331825, 264909, 265008, 264758
1625	95354748 (3249, 3250)	Novel Protein sim. GBank gi|4589622|dbj|BAA76833.1| - (AB023206) KIAA0989 protein [Homo sapiens]		kinase	264489, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331824, 29331825, 29331827, 29331828, 264102, 264106, 264508, 33657084, 265017, 265018, 18108351, 264683, 264369, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 264691, 65274620, 18108368, 263972, 18108376, 35696423, 264631, 264634, 22279000, 22279002
1626	94734369 (3251, 3252)	Novel Protein sim. GBank gi|5679070|gb|AAD46844.1|AF16090 - (AF160904) BcDNA.HL05936 [Drosophila melanogaster]			52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 60432289, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 265009, 60432229, 60433356, 60433438, 21906754, 52646317, 52644296, 265011, 87168559, 264604, 265018, 264448, 264369, 264288, 264766, 52644229, 264689, 21906765, 21906768, 35695917, 265021, 265022, 52644150, 33657023, 65274620, 27486261, 27486262, 27486265, 35695763, 263972, 52644332, 60170394, 87168518, 60432113, 264567
1627	83368773 (3253, 3254)			UNCLASSIFIED	264288
1628	85708459 (3255, 3256)	Novel Protein sim. GBank gi|3668087 (AC004667) - hypothetical protein [Arabidopsis thaliana]		eph	264288, 264686, 264767, 22279002

1629	84993841 (3257, 3258)	Novel Protein sim. GBank gi|4240175|dbj|BAA74866.1| - (AB020650) KIAA0843 protein [Homo sapiens]		struct	264555
1630	87779027 (3259, 3260)			UNCLASSIFIED	29331822, 29331827, 265010, 264693, 264634, 22279002
1631	87758454 (3261, 3262)	Novel Protein sim. GBank gi|1915892|emb|CAA69995| - (Y08740) tom-1A protein [Gallus gallus]		UNCLASSIFIED	55811957, 264259, 33657023, 264693, 29331822, 29331824, 29331827, 29331828, 264906, 264908, 55811576, 264910, 264634, 264636, 264637, 56182323, 264559, 264758, 18108385, 264563, 264764, 264766
1632	87871692 (3263, 3264)	Novel Protein sim. GBank gi|2558501|dbj|BAA22896| - (D63850) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	264687, 264769, 264691, 264692, 29146499, 264509, 264905, 264907, 264511, 264512, 264482, 264681, 264763, 264682, 264683
1633	87773683 (3265, 3266)				264488, 264259, 264907, 264908, 264909, 264628, 264629, 264631
1634	85992817 (3267, 3268)	Novel Protein sim. GBank gi|4887229|gb|AAD32244.1|AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	struct	265007, 264637, 22279002
1635	94232600 (3269, 3270)			UNCLASSIFIED	65274572, 22278998, 35696052, 52644045, 264511, 265008, 265009, 265010, 265011, 265018, 265019, 264448, 264369, 21906765, 21906768, 265021, 264690, 264482
1636	80413227 (3271, 3272)				
1637	80070435 (3273, 3274)	Novel Protein sim. GBank gi|4557511|ref|NP_001339.1|pDAPK - death-associated protein kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	UNCLASSIFIED kinase	22278995, 264594, 264763, 265020 264558
1638	87101854 (3275, 3276)	Novel Protein sim. GBank gi|3420051 (AC004680) - unknown protein [Arabidopsis thaliana]			21906765, 21906767, 22278996, 35696286, 22278999, 264259, 264692, 264693, 29331824, 33657109, 264508, 264906, 18108370, 264629, 265007, 33657402, 21906754, 264602, 264604, 264764, 264683, 264566, 264288
1639	94322194 (3277, 3278)	Novel Protein sim. GBank gi|5420389|emb|CAB46680.1| - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 18108394, 65274572, 56182575, 35696286, 29331824, 29331826, 29331827, 35696052, 264908, 56182435, 264112, 265006, 265008, 264757, 264758, 55811386, 264603, 264760, 18108351, 264764, 264288, 264766, 264768, 21906767, 55811957, 264691, 33657023, 65274620, 18108370, 55810764, 55811576, 264558, 264639, 83373044, 18108385, 87168518

1640	94143185 (3279, 3280)	Novel Protein sim. GBank gi|2842469|emb|CAA16847.1| - (AL021747) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 56994075, 35696286, 60432049, 60432289, 29331827, 35696052, 52644045, 56182435, 264510, 265006, 265007, 265008, 264910, 265009, 33657402, 55812038, 265010, 265011, 265017, 265018, 264288, 52644229, 21906765, 21906766, 21906768, 35695917, 265021, 60170615, 52644150, 33657023, 33657109, 33657349, 18108374, 35696423, 65274791, 35695855, 264632, 264555, 56182323, 22279000
1641	87625160 (3281, 3282)			UNCLASSIFIED	29146499, 265006, 265007, 265008, 265009, 55812038, 265010, 265011, 264555, 264556, 264558, 18108383
1642	94312557 (3283, 3284)	Novel Protein sim. GBank gi|1575333 (U60416) - myr 6 myosin heavy chain [Rattus norvegicus]	Contains protein domain (PF01843) - DIL domain	struct	22278999, 29147620, 29331826, 29331828, 33656970, 55812038, 265010, 265018, 265019, 18108351, 264689, 265020, 265022, 264690, 33657023, 65274620, 35695763, 52644332, 18108381, 60170394, 56182323, 18108388, 87168518, 22279002, 264564
1643	94131766 (3285, 3286)				29331825, 29331827, 29331828, 21906754, 265019, 264288, 264693, 33657349, 18108370, 18108376, 264555, 83373044, 22279002, 264482
1644	88095125 (3287, 3288)			UNCLASSIFIED	264905, 264907, 264908, 264910, 265009, 264757, 264758, 264761, 264762, 264763, 264766, 264768, 264769, 264628, 264629, 264630, 264631, 264632, 264563, 264564, 264565, 264566, 264567
1645	95013858 (3289, 3290)			UNCLASSIFIED	264685, 264693
1646	95382691 (3291, 3292)	Novel Protein sim. GBank gi|1076802|pir||S49915 - extensin like protein - maize		UNCLASSIFIED	22278994, 56994075, 35696286, 264259, 29331824, 29331825, 29331826, 60432289, 264508, 60433356, 60433438, 87168559, 265018, 264687, 35695917, 264692, 33657023, 33657182, 27486261, 27486265, 33657349, 60432113, 264563, 264564
1647	94278428 (3293, 3294)	Novel Protein sim. GBank gi|5002573|emb|CAB44338.1| - (Y17466) alpha-N-acetylgalactosamine alpha-2,6-sialyltransferase [Fugu rubripes]		UNCLASSIFIED	29331822, 264906, 264908, 264369, 21906768, 60170615, 264639, 22279000
1648	87642098 (3295, 3296)		Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	265009, 264686, 55811957, 35695917, 55810764, 264556, 56182323, 264558, 18108385

1649	95347628 (3297, 3298)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]		cadherin	264488, 22278995, 35696286, 22278996, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 66712502, 264908, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264591, 264593, 60433438, 264598, 55812038, 21906754, 265011, 264601, 264602, 265017, 265018, 265019, 264682, 264448, 264764, 264683, 264288, 264766, 264685, 264687, 264768, 264688, 264769, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 55811957, 35695917, 265021, 265022, 52644150, 264692, 33657023, 33657109, 20281149, 18108370, 264628, 18108374, 18108376, 35696423, 35695855, 264632, 264634, 264635, 264636, 18108380, 264639, 264558, 18108382, 18108384, 18108385, 18108387, 264080, 264404, 60432113, 22279000, 22279002, 264482, 264565, 264566, 264487
1650	87418539 (3299, 3300)	Novel Protein sim. GBank gi|3647335|emb|CAA21059| - (AL031644) possible zinc-finger protein [Schizosaccharomyces pombe]			265011, 264602, 21906767, 18108374, 18108377, 18108385
1651	91639773 (3301, 3302)	Novel Protein sim. GBank gi|4884278|emb|CAB43247.1| - (AL050037) hypothetical protein [Homo sapiens]		synthase	264488, 52645156, 18108397, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264508, 264908, 29331830, 264910, 60432229, 21906754, 265010, 265011, 265017, 265019, 264448, 18108354, 264288, 264688, 21906765, 21906766, 21906768, 21906769, 265022, 264692, 264693, 264629, 35695855, 264556, 264637, 264557, 264559, 83373044, 56526486, 22279000, 22279002, 264564
1652	86598622 (3303, 3304)	Novel Protein sim. GBank gi|1657837 (U73200) - p116Rip [Mus musculus]	Contains protein domain (PF00169) - PH domain	struct	22278997, 29146498, 56182435, 21906754, 264369, 21906765, 21906768, 21906769, 265020, 52644150, 33657109, 22279000, 22279002
1653	94255993 (3305, 3306)	Novel Protein sim. GBank gi|3776054|emb|CAA06273| - (AJ004999) Tapasin [Gallus gallus]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	18108398, 22278995, 22278998, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331830, 264909, 265006, 265009, 60432229, 60433356, 60433438, 21906754, 265017, 265019, 264448, 264683, 264288, 265021, 265022, 264692, 18108364, 65274791, 18108384, 60432113, 264567
1654	79756471 (3307, 3308)			UNCLASSIFIED	33657109, 264565

1655	86689346 (3309, 3310)	Novel Protein sim. GBank gi|3355717|emb|CAA73496| - (Y13053) seryl-tRNA synthetase [Zea mays]		synthase	52644507, 35696286, 22278998, 22278999, 29331824, 29331825, 29331828, 33656970, 264908, 52644045, 264511, 264910, 52646317, 264288, 52644229, 33657023, 33657109, 52644332, 264557, 56182323, 56526486, 60432113
1656	79962297 (3311, 3312)	Novel Protein sim. GBank gi|1890141|dbj|BAA18947| - (D83206) P24 protein [Mus musculus]		UNCLASSIFIED	29331822, 29331824, 29331825, 264563
1657	87771994 (3313, 3314)	Novel Protein sim. GBank gi|4557645|ref|NP_001524.1|pHNRP - heterogeneous nuclear ribonucleoprotein L	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	29331827, 265009, 21906766, 21906767, 265020, 265022, 33657109, 264638, 56526486, 264482
1658	87773778 (3315, 3316)	Novel Protein sim. GBank gi|3877072|emb|CAA87060| - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]	Contains protein domain (PF00829) - Ribosomal prokaryotic L21 protein	UNCLASSIFIED	52646365, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 264905, 264908, 52644045, 265006, 60433356, 264757, 60433438, 21906754, 265011, 18108351, 264448, 264369, 264288, 264766, 264768, 21906765, 21906767, 21906768, 21906769, 29148629, 265021, 265022, 18108362, 263969, 263971, 18108374, 35696423, 18108383, 22279000, 264482
1659	88230101 (3317, 3318)	Novel Protein sim. GBank gi|539218|pir||S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	52646317, 21906766, 21906767, 21906768, 87168518, 22278996, 265020, 22278999, 87168559, 264603, 265017, 264631, 265018, 265019, 22279002, 264482, 264635, 264565
1660	94315313 (3319, 3320)	Novel Protein sim. GBank gi|2497012|sp|Q10010|YSV4_CAEEL - HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III		UNCLASSIFIED	264488, 35696286, 264259, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265009, 264910, 264592, 264598, 265010, 264600, 264602, 265017, 265018, 264605, 264760, 264764, 264288, 264766, 264686, 264768, 264769, 264689, 21906766, 35695917, 264690, 33657023, 264693, 33657109, 264629, 35696423, 35695855, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264639, 264559, 18108385, 18108388, 264563, 264483, 264564, 264565, 264566, 264486, 264567

1661	94234071 (3321, 3322)	Novel Protein sim. GBank gi|4759100|ref|NP_004759.1|pSFRS - splicing factor, arginine/serine-rich 11	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264488, 22278998, 264259, 29331824, 29331826, 29331827, 29331828, 264509, 66712502, 29331830, 264908, 52644045, 265007, 264512, 60433356, 60433438, 55812038, 21906754, 265019, 264448, 264766, 264768, 264769, 21906768, 21906769, 265020, 33657023, 33657109, 65274791, 87168518, 264482, 264563, 264564, 264565, 264567
1662	94135172 (3323, 3324)	Novel Protein sim. GBank gi|1730502|sp|P52875|PF27_MOUSE - TRANSMEMBRANE PROTEIN PFT27			18108392, 29331822, 29331828, 20281100, 264106, 265006, 265007, 265008, 18108348, 21906766, 18108365, 18108366, 18108374, 83373044, 18108385
1663	94217146 (3325, 3326)	Novel Protein sim. GBank gi|4884136|emb|CAB43275.1| - (AL050107) hypothetical protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	kinase	52645156, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331826, 29331827, 29331828, 33656970, 29331830, 264908, 56182435, 264511, 60433356, 33657402, 33109954, 87168474, 87168559, 265017, 265018, 264605, 18108351, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 264691, 33657023, 264693, 263967, 33657109, 264630, 52644332, 83373044, 87168518, 60432113, 22279000
1664	94234076 (3327, 3328)	Novel Protein sim. GBank gi|3043692|dbj|BAA25510| - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	264488, 263994, 35696286, 29331824, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 60170831, 264591, 264592, 264595, 87168474, 265011, 264600, 264601, 264604, 264605, 264760, 264762, 18108351, 264681, 264682, 264763, 264683, 264764, 264288, 264684, 264766, 264687, 264768, 264769, 21906764, 21906765, 21906767, 35695917, 265021, 264534, 60170615, 264690, 264691, 264692, 33657109, 33657182, 264628, 18108370, 264629, 35696423, 35695855, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264566, 264486

1665	91226952 (3329, 3330)	Novel Protein sim. GBank gi|1083506|pir||S50065 - sialoadhesin - mouse	Contains protein domain (PF00047) - Immunoglobulin domain	immunoglob	264488, 29331826, 29331828, 264509, 264906, 264907, 264909, 264510, 264511, 264910, 264592, 264593, 264595, 264758, 264596, 264600, 264760, 264762, 264764, 264766, 264768, 264629, 264630, 264634, 264636, 83373044, 264564, 264566, 264567, 264486
1666	95358160 (3331, 3332)	Novel Protein sim. GBank gi|3913431|sp|O42643|DDX8_SCHPO - PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C	Contains protein domain (PF00575) - S1 RNA binding domain	helicase	56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29146498, 265009, 33109954, 87168559, 265019, 264288, 264688, 21906767, 21906769, 264691, 33657182, 18108370, 18108374, 18108385, 22279002
1667	91228655 (3333, 3334)	Novel Protein sim. GBank gi|5689535|dbj|BAA83051.1| - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	transport	264259, 29331822, 29331826, 264905, 264906, 264908, 264510, 265009, 264595, 264758, 265011, 87168559, 265017, 265018, 265019, 264448, 264766, 264686, 21906765, 21906767, 21906769, 265020, 265021, 60170615, 264690, 264692, 264693, 18108368, 18108370, 263972, 55810764, 264555, 83373044, 60432113, 22279000, 22279002
1668	88095135 (3335, 3336)	Novel Protein sim. GBank gi|2076894|gb|AAB53983.1| - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind), Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]		kinase	66714117, 264508, 264509, 264906, 264907, 264908, 264511, 264910, 264764, 264687, 264689, 33657109, 35696423, 35695855, 264632
1669	91227846 (3337, 3338)	Novel Protein sim. GBank gi|3875371|emb|CAA85414.1| - (Z36948) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes fr...		UNCLASSIFIED	29331825, 33109954, 264369, 264767, 264689, 33657109, 83373044
1670	87628009 (3339, 3340)			UNCLASSIFIED	264259, 29331824, 29331827, 60433438, 265022, 264636
1671	87346372 (3341, 3342)	Novel Protein sim. GBank gi|462451|sp|P34244|KKK1_YEAST - PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35696286, 22278997, 29331825, 264909, 21906754, 265017, 265018, 265019, 264682, 264683, 264768, 264688, 21906766, 21906767, 21906768, 21906769, 264691, 264555, 264556, 22279000, 264566
1672	86291834 (3343, 3344)	Novel Protein sim. GBank gi|1814270 (U74586) - double-stranded RNA specific adenosine deaminase [Rattus norvegicus]		deaminase	264906, 264909, 264632, 18108381

1673	88095137 (3345, 3346)	Novel Protein sim. GBank gi|2076894|gb|AAB53983.1| - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind), Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	264488, 264569, 18108394, 56994075, 22278996, 264259, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60170831, 264592, 264594, 264595, 264758, 264601, 264760, 264762, 264683, 264764, 264288, 264766, 264686, 264768, 264687, 264769, 264689, 264690, 33657023, 264692, 264693, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264631, 264632, 264634, 264635, 264637, 264556, 264638, 264639, 264563, 264482, 264564, 264565, 264566, 264567, 264486
1674	88258028 (3347, 3348)	Novel Protein sim. GBank gi|5262467|emb|CAB45693.1| - (AL080062) hypothetical protein [Homo sapiens]		kinase	29331822, 29331824, 264906, 52644045, 60433356, 87168559, 264448, 264288, 264686, 264691
1675	87606466 (3349, 3350)	Novel Protein sim. GBank gi|3128366 (AF010496) - 50S ribosomal protein l9 [Rhodobacter capsulatus]		UNCLASSIFIED	56181686, 35696286, 22278997, 22278998, 264259, 29331824, 29331827, 35696052, 66712502, 264764, 264288, 264686, 264687, 35695917, 265020, 264690, 264693, 35695763, 18108370, 35696423, 35695855, 264637, 264639, 18108385, 264564
1676	95358086 (3351, 3352)	Novel Protein sim. GBank gi|4164065|gb|AAD05327| - (AF111091) latrophilin 3 splice variant bbaf [Bos taurus]		UNCLASSIFIED	264259, 29331827, 29331828, 264106, 264907, 265009, 264600, 265019, 264288, 21906765, 265020, 265022, 35695855, 83373044, 18108385
1677	87408587 (3353, 3354)	Novel Protein sim. GBank gi|3327046|dbj|BAA31591| - (AB014516) KIAA0616 protein [Homo sapiens]		UNCLASSIFIED	264908
1678	86866829 (3355, 3356)			UNCLASSIFIED	29331824, 264102
1679	91214108 (3357, 3358)	Novel Protein sim. GBank gi|550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	264488, 18108392, 18108394, 52646842, 18108397, 18108398, 35696286, 29331824, 265006, 265007, 265008, 265009, 18108348, 265011, 18108351, 264683, 18108354, 18108358, 18108359, 21906765, 29148627, 29148629, 264690, 18108361, 18108362, 18108364, 18108365, 18108368, 264628, 18108379, 35696423, 35695855, 264635, 18108381, 18108382, 18108383, 18108384, 18108385, 18108388
1680	91005372 (3359, 3360)	Novel Protein sim. GBank gi|2394478 (AF024500) - No definition line found [Caenorhabditis elegans]		transport	65274572, 22278994, 22278999, 66714117, 29331827, 56182435, 21906754, 265018, 264288, 21906769
1681	94324150 (3361, 3362)	Novel Protein sim. GBank gi|5689537|dbj|BAA83052.1| - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	22278996, 29331822, 264908, 264593, 264604, 265019, 264683, 55811957, 264690, 33657023, 35696423, 83373044, 264563
1682	86042710 (3363, 3364)			UNCLASSIFIED	264909, 265017, 264605

1683	94316213 (3365, 3366)	Novel Protein sim. GBank gi|5031717|ref|NP_005704.1|pGPBP - goodpasture antigen-binding protein	Contains protein domain (PF01852) - START domain	UNCLASSIFIED	263994, 35696286, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 265007, 265009, 264910, 264593, 264758, 265010, 265011, 264760, 264761, 264762, 264763, 264764, 264369, 264766, 264768, 35695917, 264692, 33657109, 35696423, 35695855, 264634, 264635, 264636, 264638, 264639, 83373044, 264486
1684	80063409 (3367, 3368)			UNCLASSIFIED	264563, 264566
1685	94323182 (3369, 3370)	Novel Protein sim. GBank gi|1255371 (U53147) - coded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase. [Caenorhabditis elegans]	Contains protein domain (PF00625) - Guanylate kinase	kinase	60424179, 52646842, 22278994, 35696286, 22278998, 264259, 52645080, 29331824, 29331826, 265007, 33657084, 265018, 264681, 264448, 264683, 264369, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 65274620, 33657109, 27486262, 264635, 52644332, 56182323, 22279000
1686	87820710 (3371, 3372)	Novel Protein sim. GBank gi|2244707|dbj|BAA21115.1| - (AB005287) thrombospondin 1 [Bos taurus]		UNCLASSIFIED	56182575, 264259, 264508, 264905, 264509, 264907, 264908, 264510, 264511, 265006, 264512, 265009, 264910, 264758, 265010, 265011, 264605, 18108351, 264764, 264766, 18108357, 264768, 18108362, 264628, 264630, 264631, 264634, 264635, 264637, 264638, 264639, 264565, 264486, 264567
1687	94719400 (3373, 3374)	Novel Protein sim. GBank gi|4680679|gb|AAD27729.1|AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264906, 264907, 264908, 264510, 265006, 265007, 264910, 264556, 18108381, 18108383, 265011
1688	82158442 (3375, 3376)			UNCLASSIFIED	264905, 264910, 264760, 264629, 264555
1689	94325049 (3377, 3378)	Novel Protein sim. GBank gi|4240193|dbj|BAA74875.1| - (AB020659) KIAA0852 protein [Homo sapiens]		UNCLASSIFIED	264569, 35696286, 22278999, 264508, 264908, 264909, 56182435, 33657402, 60433438, 55812038, 265017, 265018, 264448, 264764, 264288, 264686, 29148629, 35695917, 265020, 265021, 263972, 18108374, 65274791, 83373044, 264089
1690	83255346 (3379, 3380)	Novel Protein sim. GBank gi|3800736 (AF031572) - seven-pass transmembrane receptor precursor [Mus musculus]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264369, 21906766, 264692, 264639, 87168518
1691	88095223 (3381, 3382)	Novel Protein sim. GBank gi|2773208 (AF039713) - No definition line found [Caenorhabditis elegans]			264768, 33657109, 29331827, 29148629, 264510, 264106, 264910, 264109, 264508, 60170831, 264563, 264905, 264564, 264691, 264637, 264628, 264907, 264908, 33657023, 264567, 264766, 263974
1692	86106709 (3383, 3384)				264106
1693	87012775 (3385, 3386)	Novel Protein sim. GBank gi|121271|sp|P02207|GLB_LAMFL - GLOBIN	Contains protein domain (PF00042) - Globin	UNCLASSIFIED	29331826, 264508, 264905, 264907, 264595, 265010, 265011, 21906768, 33657023, 264629, 263978, 264558

1694	94208168 (3387, 3388)	Novel Protein sim. GBank gi|5453932|ref|NP_006225.1|pPOLR - polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Contains protein domain (PF01193) - RNA polymerases L / 13 to 16 kDa subunit	rnapolymerase	35696286, 22278996, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331828, 35696052, 29146499, 264905, 264908, 52644045, 264511, 265006, 265007, 265009, 264592, 60433356, 21906754, 265010, 265011, 18108351, 264763, 264682, 264448, 264683, 264288, 264768, 264689, 21906768, 60170615, 264691, 264692, 264693, 18108370, 18108374, 263978, 35696423, 35695855, 264556, 18108381, 18108385, 87168518, 264482, 264486
1695	94719325 (3389, 3390)	Novel Protein sim. GBank gi|4680679|gb|AAD27729.1|AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	264634
1696	87824038 (3391, 3392)	Novel Protein sim. GBank gi|4220517|emb|CAA22990| - (AL035356) hypothetical protein [Arabidopsis thaliana]			22278997, 264259, 265010, 18108351, 264764, 21906766, 18108370
1697	85740963 (3393, 3394)	Novel Protein sim. GBank gi|505652 (U10362) - GP36b glycoprotein [Homo sapiens]		glycoprotein	264682
1698	87445285 (3395, 3396)	Novel Protein sim. GBank gi|5052031|gb|AAD38411.1|AF15573 - (AF155739) axotrophin [Mus musculus]			56994075, 22278998, 22278999, 264509, 33657402, 264758, 87168474, 87168559, 265017, 265018, 264448, 264687, 29148627, 21906769, 29148629, 265020, 265022, 33657023, 264558, 87168518, 22279002
1699	87424793 (3397, 3398)			UNCLASSIFIED	35696286, 264635
1700	87859161 (3399, 3400)	Novel Protein sim. GBank gi|543344|pir||S41647 - zinc finger 5 protein - mouse	Contains protein domain (PF00096) - Zinc finger, C2H2 type	nucl_recpt	29331824, 52644045, 265008, 265009, 263969, 263971
1701	86570488 (3401, 3402)			UNCLASSIFIED	264092, 264110, 263977
1702	87795092 (3403, 3404)	Novel Protein sim. GBank gi|3877439|emb|CAA96652| - (Z72510) similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST yk274e3.5 c...		MHC	22278995, 22278997, 264092, 29146498, 29146499, 264107, 264508, 264907, 264110, 264112, 265009, 60170831, 21906754, 265011, 265017, 264762, 18108351, 264288, 21906765, 35695917, 265021, 60170615, 263967, 33657109, 18108370, 263972, 263974, 18108374, 263976, 35695855, 264555, 263981, 60170394, 18108385, 56526486, 87168518, 60432113
1703	79568651 (3405, 3406)	Novel Protein sim. GBank gi|451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	264909, 265017, 264628, 264629, 264638
1704	86622979 (3407, 3408)	Novel Protein sim. GBank gi|1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	264369
1705	87795175 (3409, 3410)	Novel Protein sim. GBank gi|4519621|dbj|BAA75670.1| - (AB017614) OASIS protein [Mus musculus]			264569, 35696286, 264907, 265010, 264687, 264768, 264692, 264693, 264636, 264566
1706	87790967 (3411, 3412)	Novel Protein sim. GBank gi|3123034|sp|Q15011|Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025			22278996, 22278998, 264259, 264509, 265018, 264764, 264685, 264686, 21906768, 21906769, 265022, 264691, 264558, 22279000

1707	88041230 (3413, 3414)	Novel Protein sim. GBank gi|4321664|gb|AAD15797| - (AF055470) ZNF258 [Homo sapiens]		UNCLASSIFIED	18108396, 22278997, 264259, 29147620, 29331826, 29146498, 264905, 264906, 265008, 264593, 264595, 264758, 264596, 265018, 264760, 18108351, 264764, 264766, 264689, 264693, 18108370, 35696423, 55811576, 264558, 87168518, 60432113, 264567
1708	91220519 (3415, 3416)	Novel Protein sim. GBank gi|5174591|ref|NP_005947.1|pMTHF - 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase	Contains protein domain (PF01268) - Formate--tetrahydrofolate ligase	synthase	56182575, 22278996, 56994075, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 29146498, 29146499, 29331830, 265009, 60170831, 33657402, 33109954, 87168559, 265019, 18108351, 264448, 21906765, 21906767, 21906768, 29148627, 29148629, 29148784, 60170615, 52644150, 33657023, 33657109, 18108374, 55811576, 264559, 18108385, 22279000, 264563
1709	80222583 (3417, 3418)			UNCLASSIFIED	264107, 55811957, 263974, 263976, 263977, 263981
1710	20754572 (3419, 3420)			UNCLASSIFIED	264556
1711	91013729 (3421, 3422)	Novel Protein sim. GBank gi|5031735|ref|NP_005760.1|pHEC- - N-acetylglucosamine 6-O-sulfotransferase		sulfotransferase	65274572, 29331824, 29331826, 264768, 60431528, 35696423, 60432113, 264563
1712	95330184 (3423, 3424)	Novel Protein sim. GBank gi|5454168|ref|NP_006453.1|pXAP4 - HBV associated factor	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	kinase	56994075, 264093, 264259, 29331822, 264099, 29331824, 29331827, 264107, 264110, 264511, 264592, 265011, 265018, 264683, 264686, 264689, 265020, 33657023, 263967, 33657109, 263974, 35696423, 35695855, 264630, 264636, 264558, 264566
1713	94143453 (3425, 3426)	Novel Protein sim. GBank gi|160409 (M69183) - mature-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED	22278995, 264508, 264758, 18108351, 18108370, 263974, 18108374, 264634, 56182323, 83373044, 60432113
1714	87420048 (3427, 3428)				22278997, 264757, 21906765, 265020, 265021, 264692, 56526486
1715	94260257 (3429, 3430)	Novel Protein sim. GBank gi|5689537|dbj|BAA83052.1| - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	264509, 264905, 264906, 264907, 264908, 264909, 264910, 264591, 265011, 264766, 264768, 264769, 264691, 264692, 264632, 264634, 264635, 264636, 264637, 264556, 264639, 264564
1716	87400449 (3431, 3432)	Novel Protein sim. GBank gi|4589468|dbj|BAA76761.1| - (AB012808) mBOCT [Mus musculus]		transport	56182575, 29331824, 60432289, 264109, 264909, 265007, 264600, 265019, 264686, 265020, 264693, 55811576, 264558, 60432113, 22279002

1717	87563223 (3433, 3434)	Novel Protein sim. GBank gi|2765411|emb|CAA74749| - (Y14391) GTP-binding protein [Homo sapiens]		UNCLASSIFIED	264569, 264259, 29331825, 29331826, 29331828, 35696052, 264509, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264592, 264595, 264758, 264759, 265017, 264681, 264764, 264766, 264686, 18108357, 35695917, 264690, 264692, 264693, 264628, 264629, 35696423, 264630, 264631, 264635, 264636, 18108380, 264638, 264639, 18108388, 18108391
1718	87032628 (3435, 3436)	Novel Protein sim. GBank gi|2833262|sp|Q14999|Y076_HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA0936)		UNCLASSIFIED	265011, 264681, 264682, 264684, 264688, 264689, 21906765, 265021, 264691, 33657023, 264693, 18108370, 35695855, 264632, 264634, 264636, 18108388, 22279002
1719	94315259 (3437, 3438)	Novel Protein sim. GBank gi|4505197|ref|NP_003473.1|pMLL2 - myeloid/lymphoid or mixed-lineage leukemia 2		UNCLASSIFIED	18108396, 65274572, 35696286, 22278997, 60432049, 58182181, 66714117, 60432289, 29331826, 35696052, 29331828, 264906, 29331830, 56182435, 264592, 60431735, 60433438, 55812038, 264759, 265010, 264600, 264601, 265017, 264448, 264764, 264288, 264769, 21906766, 21906769, 55811957, 265020, 265021, 52644150, 33657023, 33657109, 33657182, 27486262, 33657349, 35695763, 18108370, 60431528, 18108374, 35696423, 55811576, 35695855, 264631, 56182323, 264559, 264564, 264486
1720	94853063 (3439, 3440)	Novel Protein sim. GBank gi|2129478|pir||S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	56182575, 22278999, 264259, 29331824, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 264758, 21906754, 265011, 264601, 264760, 264762, 264288, 264766, 264686, 18108357, 264689, 21906765, 55811957, 264693, 20281149, 264629, 18108374, 55811576, 65274791, 264630, 20281071, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 56182323, 87168518
1721	91722288 (3441, 3442)	Novel Protein sim. GBank gi|4886461|emb|CAB43381.1| - (AL050280) hypothetical protein [Homo sapiens]		UNCLASSIFIED	22278994, 22278999, 29331822, 265006, 265007, 265008, 55812038, 21906754, 60174639, 265011, 87168559, 18108351, 18108354, 21906765, 21906766, 21906768, 21906769, 265020, 33657109, 18108370, 18108374, 264556, 60170394, 83373044, 18108385, 264486
1722	94134549 (3443, 3444)	Novel Protein sim. GBank gi|5689375|dbj|BAA82968.1| - (AB030644) tudor repeat associator with PCTAIRE 2 [Rattus norvegicus]	Contains protein domain (PF00567) - Tudor domain	kinase	56994075, 29331824, 29331828, 265009, 18108351, 21906768, 265020, 33657023, 18108374, 83373044

1723	95358181 (3445, 3446)	Novel Protein sim. GBank gi|4426962|gb|AAD20633| - (AF126062) Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264488, 264687, 264769, 21906767, 21906768, 56182575, 55811957, 22278997, 22278998, 265020, 264259, 264692, 33657023, 29331822, 29331824, 29331825, 60432289, 33657182, 33656970, 33657349, 29146499, 264508, 264907, 18108370, 264629, 264908, 264909, 18108374, 55811576, 264510, 265006, 264511, 265007, 264910, 264632, 264591, 60432229, 264592, 60433356, 264594, 60433438, 264595, 83373044, 55812038, 33109954, 33657084, 87168518, 87168474, 265010, 265011, 87168559, 264600, 60432113, 264604, 265019, 264563, 264448, 264682, 264566, 264764, 264288, 264567, 264486, 264369, 264766
1724	87713806 (3447, 3448)	Novel Protein sim. GBank gi|2340162 (AF005083) - dsRBP-ZFa [Xenopus laevis]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264905, 18108359, 264693, 264628, 264631, 264636, 264555, 264556, 264558, 264559
1725	85655191 (3449, 3450)	Novel Protein sim. GBank gi|3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	35696286, 264259, 29331822, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264910, 265009, 264591, 264601, 264760, 18108351, 264681, 264764, 264288, 264766, 264768, 21906769, 35695917, 264628, 35696423, 264630, 264631, 264632, 264635, 264636, 264638, 87168518, 264566
1726	85754255 (3451, 3452)			UNCLASSIFIED	29146498, 264683, 264689
1727	85296382 (3453, 3454)	Novel Protein sim. GBank gi|4689348|gb|AAD27861.1|AF13256 - (AF132562) BcDNA.LD14270 [Drosophila melanogaster]		UNCLASSIFIED	264905, 265011, 264689, 21906768

1728	95349515 (3455, 3456)	Novel Protein sim. GBank gi|4406549|gb|AAD20027| - (AF131738) Unknown [Homo sapiens]			UNCLASSIFIED	60424179, 18108397, 56182575, 22278995, 56994075, 35696286, 22278997, 22278998, 22278999, 264094, 60432049, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331826, 29331827, 35696052, 264905, 264906, 264907, 29331830, 66712502, 264908, 56182435, 264511, 265008, 265009, 60432229, 60433356, 33657402, 60433438, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 55811150, 264681, 264448, 264682, 264763, 264683, 264288, 264684, 264369, 264685, 264766, 264687, 264769, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 264535, 264691, 264692, 33657023, 264693, 33657109, 18108370, 264628, 263972, 264629, 18108374, 18108376, 55810764, 65274791, 35695855, 264631, 264634, 264635, 60431850, 264636, 264638, 60170394, 264639, 83373044, 56526486, 87168518, 60432113, 22279000, 22279002, 264564, 264566
1729	91227948 (3457, 3458)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	264906, 264907, 264908, 264511, 264555, 83373044, 264596, 264566
1730	85483474 (3459, 3460)				UNCLASSIFIED	29331822, 29331825, 29331828, 264907, 264908, 264909, 265011, 264764, 264629
1731	88266068 (3461, 3462)	Novel Protein sim. GBank gi|631600|pir||S47094 - hypothetical protein - rabbit			UNCLASSIFIED	52646842, 264907, 264909, 56182435, 55811388, 87168559, 265018, 265019, 264760, 52644229, 55811576
1732	91218878 (3463, 3464)	Novel Protein sim. GBank gi|4240231|dbj|BAA74894.1| - (AB020678) KIAA0871 protein [Homo sapiens]			struct	56182575, 29331822, 29331824, 29331827, 66712502, 264591, 33657402, 60433356, 265019, 21906768, 21906769, 35695917, 265020, 265021, 264636, 56182323
1733	87617178 (3465, 3466)	Novel Protein sim. GBank gi|1575756 (U70674) - m-Numb [Mus musculus]	Contains protein domain (PF00640) - Phosphotyrosine interaction domain (PTB/PID).	synthase		264907, 264910, 33657402, 265010, 264681, 264683, 264684, 264686, 264769, 264691, 264692, 264693, 264628, 264638, 264558
1734	87795261 (3467, 3468)					264693

1735	88318638 (3469, 3470)	Novel Protein sim. GBank gi|4836807|gb|AAD30566.1|AF14679 - (AF146793) PFT27 [Mus musculus]	Contains protein domain (PF01169) - Uncharacterized protein family UPF0016		264488, 18108394, 18108398, 22278998, 60432049, 264259, 29331822, 264908, 265006, 265007, 265008, 265009, 264591, 33657402, 265010, 265011, 87168559, 265017, 18108351, 264682, 18108354, 264769, 264689, 21906765, 21906768, 21906769, 29148629, 29148764, 265021, 265022, 52644150, 18108364, 18108365, 33657109, 18108370, 18108374, 18108380, 18108385, 87168518, 264563, 18108390
1736	95362884 (3471, 3472)	Novel Protein sim. GBank gi|4885647|ref|NP_005472.1|pTRAP - thyroid hormone receptor-associated protein complex component		UNCLASSIFIED	264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1737	88165549 (3473, 3474)	Novel Protein sim. GBank gi|2143607|pir||S68695 - B/K protein - rat	Contains protein domain (PF00168) - C2 domain	kinase	29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1738	85788811 (3475, 3476)	Novel Protein sim. GBank gi|2225941|emb|CAA69714| - (Y08460) Mdes protein [Mus musculus]		UNCLASSIFIED	264908, 264909, 265008, 264910, 264566
1739	87328576 (3477, 3478)		Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	UNCLASSIFIED	35696052, 264603, 264557
1740	83592939 (3479, 3480)	Novel Protein sim. GBank gi|4809|emb|CAA44309| - (X62452) YCR601 [Saccharomyces cerevisiae]		traffic	264604, 21906764, 18108364, 264629, 35695855, 264636
1741	95010100 (3481, 3482)	Novel Protein sim. GBank gi|4883898|gb|AAD31695.1|AF13042 - (AF130420) serine protease-like protein isoform [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	60432289, 29331827, 264509, 265009, 60432229, 264759, 265017, 264767, 264688, 264689, 21906769, 265020, 33657109
1742	85788814 (3483, 3484)	Novel Protein sim. GBank gi|4505193|ref|NP_003667.1|pMLD| - membrane fatty acid (lipid) desaturase		UNCLASSIFIED	264906, 264910, 264758, 265011, 264631, 264638, 264566
1743	86966475 (3485, 3486)				265017, 265020, 264692
1744	91224003 (3487, 3488)	Novel Protein sim. GBank gi|728832|sp|P39189|ALU2_HUMAN - !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!		UNCLASSIFIED	22278998, 264508, 264907
1745	20290075 (3489, 3490)			UNCLASSIFIED	264558
1746	94326110 (3491, 3492)	Novel Protein sim. GBank gi|731756|sp|P38873|YHY6_YEAST - HYPOTHETICAL 175.8 KD PROTEIN IN GND1-IKI1 INTERGENIC REGION	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	65274791, 264639, 264559
1747	94324333 (3493, 3494)	Novel Protein sim. GBank gi|1658503 (U75467) - Atu [Drosophila melanogaster]		transcriptfactor	52646842, 29331824, 29331825, 52644045, 56182435, 265007, 52646317, 87168474, 265018, 18108351, 264369, 264769, 264689, 35695917, 60170615, 264691, 33657023, 65274791, 35695855, 60170394, 22279000, 264482

1748	88003580 (3495, 3496)	Novel Protein sim. GBank gi|4504511|ref|NP_001530.1|pHSJ2 - heat shock protein, DNAJ-like 2	Contains protein domain (PF00684) - DnaJ central domain (4 repeats)	eph	264489, 56182575, 29331824, 56182435, 264112, 265007, 265019, 264764, 21906768, 265020, 264691, 55811576, 264635, 264555, 264556, 264557, 264559
1749	83363091 (3497, 3498)	Novel Protein sim. GBank gi|5650780|gb|AAD45948.1|AF15196 - (AF151968) RGS protein RGS-17 [Gallus gallus]	Contains protein domain (PF00615) - Regulator of G protein signaling domain	oncogene	264106
1750	94321664 (3499, 3500)	Novel Protein sim. GBank gi|4996894|gb|AAC28444.2| - (AF065164) hyperpolarization-activated, cyclic nucleotide-gated channel 2 [Homo sapiens]			33657402, 264288, 52644150, 263974, 83373044
1751	83373058 (3501, 3502)	Novel Protein sim. GBank gi|2760161|dbj|BAA24184| - (AB010054) outer arm dynein light chain 2 [Anthocidaris crassispina]	Contains protein domain (PF00560) - Leucine Rich Repeat	ATPase_associated	265010, 264369
1752	86456530 (3503, 3504)	Novel Protein sim. GBank gi|3915482|sp|P74346|YG29_SYNY3 - HYPOTHETICAL 36.0 KD PROTEIN SLR1629	Contains protein domain (PF00849) - RNA pseudouridylate synthase	deaminase	264510, 264593, 264682, 21906765, 18108370
1753	94235159 (3505, 3506)	Novel Protein sim. GBank gi|2852636 (AF007155) - unknown [Homo sapiens]	Contains protein domain (PF01553) - Acyltransferase	phosphatase	56994075, 22278996, 264908, 60170831, 264682, 264764, 264369, 264288, 264685, 264687, 21906766, 264692, 264693, 65274620, 65274791, 35695855, 264637, 264564
1754	88095323 (3507, 3508)	Novel Protein sim. GBank gi|731421|sp|P39981|YEH4_YEAST - HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION		transport	264488, 35696286, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 264591, 33657402, 264594, 264757, 264758, 264600, 264604, 264762, 264763, 264685, 264766, 264691, 264628, 35696423, 264632, 264634, 264637, 264638, 263981, 264558, 264639, 264563, 264564, 264565, 264566, 264567
1755	79470282 (3509, 3510)	Novel Protein sim. GBank gi|1176422 (U43194) - rhophilin [Mus musculus]		UNCLASSIFIED	264686
1756	92962614 (3511, 3512)	Novel Protein sim. GBank gi|4432860|gb|AAD20708| - (AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]			52646842, 22278994, 22278995, 56994075, 22278996, 22278997, 264259, 29331822, 60432289, 29331827, 33656970, 265006, 265009, 60432229, 60433356, 60433438, 33109954, 21906754, 265017, 265018, 265019, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 27486262, 27486264, 18108376, 20281152, 264558, 18108388, 67168518, 60432113, 22279000, 22279002, 264482
1757	95357380 (3513, 3514)	Novel Protein sim. GBank gi|5441615|emb|CAB46856.1| - (AJ388557) zinc finger protein [Canis familiaris]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	22278997, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264593, 265019, 264766, 21906768, 65274620, 18108385, 60432113, 264566, 264487

1758	87612971 (3515, 3516)	Novel Protein sim. GBank gi|3881040|emb|CAA16403| - (AL021497) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	22278994, 22278999, 29331822, 29331824, 29331825, 33656970, 264508, 265006, 265007, 265009, 264591, 33657402, 33109954, 87168474, 264600, 265017, 265018, 21906769, 265020, 265021, 33657023, 33657109, 264629, 18108374, 35695855, 264632, 52644332, 22279002, 264563
1759	36994372 (3517, 3518)			UNCLASSIFIED	264759
1760	87329716 (3519, 3520)	Novel Protein sim. GBank gi|5262748|emb|CAB45688.1| - (AJ133120) Proline rich synapse associated protein 2 [Rattus norvegicus]		UNCLASSIFIED	56182575, 60432049, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264910, 60432229, 264592, 264595, 55812038, 264758, 264762, 18108351, 264764, 264766, 264768, 264769, 21906765, 55811957, 35695917, 264690, 264692, 264628, 264629, 55811576, 35696423, 264632, 264634, 264636, 264557, 264639, 60432113, 264565, 264486
1761	87409586 (3521, 3522)	Novel Protein sim. GBank gi|127749|sp|P10569|MYSC_ACACA - MYOSIN IC HEAVY CHAIN	Contains protein domain (PF00618) - Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	UNCLASSIFIED	29331822, 264910, 264685, 264686
1762	95319887 (3523, 3524)	Novel Protein sim. GBank gi|3169158 (AC004770) - BC209730_2 [Homo sapiens]	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	desaturase	22278999, 264259, 264905, 264907, 60170831, 265010, 265011, 265017, 264448, 21906765, 21906766, 21906767, 21906768, 265021, 264690, 33657109, 18108374, 264558, 60170394
1763	91224013 (3525, 3526)	Novel Protein sim. GBank gi|4809026|gb|AAD30062.1| - (AF132856) suppressor of G2 allele of skp1 homolog [Homo sapiens]			56181686, 29331825, 35696052, 264905, 264906, 264909, 264763, 264682, 264769, 35695917, 265022, 33657023, 18108374, 35696423, 264634
1764	87757697 (3527, 3528)	Novel Protein sim. GBank gi|1360669|pir||CGHU1V - collagen alpha 1(V) chain precursor - human	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	22278998, 264259, 35696052, 29331828, 56182435, 265008, 265017, 265018, 264448, 264288, 21906766, 21906767, 29148627, 35695917, 264691, 33657023, 60432113, 22279002
1765	91230091 (3529, 3530)	Novel Protein sim. GBank gi|486806|pir||S35503 - finger protein neuralized - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	264488, 18108394, 22278995, 22278997, 22278999, 264259, 264104, 264508, 264905, 264907, 264511, 265007, 265008, 264910, 265009, 21906754, 265010, 265017, 264603, 265018, 265019, 18108351, 264682, 264448, 264369, 264288, 264766, 18108359, 21906766, 21906767, 29148627, 29148629, 35695917, 265020, 265021, 264692, 264628, 264629, 18108374, 263976, 264636, 83373044, 22279000, 22279002

1766	95081201 (3531, 3532)	Novel Protein sim. GBank gi|2499087|sp|Q09332|UGGG_DROME - UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	52645156, 87168559, 60170615, 33657023, 264693, 33657109, 27486261, 264555, 83373044
1767	87755998 (3533, 3534)	Novel Protein sim. GBank gi|4176443|emb|CAA18263.1| - (AL022238) dJ1042K10.4 (novel protein) [Homo sapiens]		UNCLASSIFIED	265017, 265019, 264686, 264768, 265020, 264692
1768	80253216 (3535, 3536)			UNCLASSIFIED	29331824, 29331825, 264591, 56182323
1769	87388988 (3537, 3538)			UNCLASSIFIED	264563
1770	95413144 (3539, 3540)	Novel Protein sim. GBank gi|115204|sp|P00736|C1R_HUMAN - COMPLEMENT C1R COMPONENT PRECURSOR	Contains protein domain (PF00089) - Trypsin	complement	264488, 264768, 264769, 56182575, 55811957, 264690, 264691, 35696052, 264905, 264509, 264906, 264907, 264628, 264908, 264909, 264910, 264634, 264635, 264636, 264556, 264757, 264758, 55812038, 65274444, 264760, 264563, 264762, 264764, 264684, 264766
1771	94233542 (3541, 3542)	Novel Protein sim. GBank gi|3914191|sp|P56558|OGT1_RAT - UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT)	Contains protein domain (PF00515) - TPR Domain	transferase	264758, 264600, 264369, 55811957, 265020, 83373044, 22279000
1772	87643510 (3543, 3544)	Novel Protein sim. GBank gi|4959442|gb|AAD34351.1|AF12136 - (AF121360) DNZDHHC/NEW1 zinc finger protein 11 [Drosophila melanogaster]	Contains protein domain (PF01529) - DHHC zinc finger domain		22278998, 29331828, 33109954, 265018, 265019, 264764, 21906765, 265020, 265021, 264556
1773	94116824 (3545, 3546)	Novel Protein sim. GBank gi|3978464 (AF085693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	potassium_channel	65274572, 56182575, 22278996, 35696286, 22278999, 264259, 29331824, 60424269, 29331825, 60432289, 35696052, 264106, 264509, 264906, 264907, 29331830, 264908, 52644045, 264511, 265006, 265007, 265008, 60170831, 60433438, 264758, 55811386, 87168559, 265017, 264604, 265019, 55811150, 264288, 56181562, 264689, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265022, 52644150, 264691, 33657023, 264692, 264693, 60431528, 35696423, 35695855, 264636, 56182323, 18108387, 56526486, 22279000, 22279002, 264563, 264564, 264565, 264566, 264567
1774	94232573 (3547, 3548)	Novel Protein sim. GBank gi|2495899|sp|Q15034|Y032_HUMAN - HYPOTHETICAL PROTEIN KIAA0032	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	UNCLASSIFIED	65274572, 56182575, 35696052, 55812038, 33109954, 21906754, 265017, 21906767, 21906768, 21906769, 265020, 264691, 264636, 56182323, 22279002

1775	95359330 (3549, 3550)	Novel Protein sim. GBank gi|1469199|dbj|BAA09487| - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 56994075, 35696286, 22278997, 29331822, 29331826, 60432289, 29331828, 35696052, 29331830, 66712502, 264828, 56182435, 264511, 265007, 265009, 60170831, 60432229, 60433438, 55812038, 21906754, 85658542, 87168559, 264601, 265017, 265018, 265019, 264762, 264448, 264288, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 265022, 264691, 33657023, 264692, 33657109, 27486261, 33657349, 18108370, 18108377, 35696423, 55811576, 35695855, 264632, 264634, 264636, 264639, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000, 22279002, 264482, 264486
1776	94133756 (3551, 3552)	Novel Protein sim. GBank gi|4589676|dbj|BAA76857.1| - (AB023230) KIAA1013 protein [Homo sapiens]			264910
1777	87447171 (3553, 3554)	Novel Protein sim. GBank gi|3219939|sp|P87115|YDK9_SCHPO - HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I		nucl_recpt	56994075, 29331826, 265008, 87168474, 265017, 265018, 264761, 55811150, 264764, 56181562, 264689, 21906765, 21906768, 21906769, 35695917, 264690, 33657023, 35695763, 60431528, 35696423, 55811576, 35695855, 22279000, 22279002, 264564
1778	94851624 (3555, 3556)	Novel Protein sim. GBank gi|3875648|emb|CAA91454.1| - (Z66561) Similarity to Human rab13 protein (PIR Acc. No. A49647). Contains the ATP/GTP-binding site motif (PROSITE PS00017); cDNA EST EMBL:M89412 comes from this gene; cDNA EST yk212g9.3 comes from this gene; cDNA EST yk212g9...		UNCLASSIFIED	29331826, 29331827, 35696052, 264512, 265007, 265009, 265017, 265019, 264762, 18108351, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264691, 264693, 18108370, 264556, 83373044
1779	94133758 (3557, 3558)	Novel Protein sim. GBank gi|4589676|dbj|BAA76857.1| - (AB023230) KIAA1013 protein [Homo sapiens]		UNCLASSIFIED	29148627, 35696286, 29147620, 265006, 265007, 265008, 18108385, 65274727, 264482, 264369, 264766
1780	87023497 (3559, 3560)		Contains protein domain (PF00807) - Apidaecin	UNCLASSIFIED	264107, 33657109, 56526486
1781	84047477 (3561, 3562)			UNCLASSIFIED	264508, 264906, 264639
1782	88094607 (3563, 3564)	Novel Protein sim. GBank gi|729225|sp|P41237|CTXN_RAT - CORTEXIN			264259, 29331822, 264508, 264905, 264906, 264907, 264908, 265007, 265009, 264910, 264591, 264758, 264764, 264288, 264768, 264769, 264635, 264636, 264637, 264639, 264563
1783	85717905 (3565, 3566)	Novel Protein sim. GBank gi|2257543|dbj|BAA21436| - (AB004538) protein arginine N-methyltransferase [Schizosaccharomyces pombe]		interferon	264768

1784	95197093 (3567, 3568)	Novel Protein sim. GBank gi|1755049 (U55042) - myosin X [Bos taurus]	Contains protein domain (PF00169) - PH domain	struct	35696286, 264259, 35696052, 264508, 264905, 264906, 264907, 66712502, 264908, 264909, 265007, 265008, 265009, 264910, 264591, 264594, 264757, 264758, 264759, 265010, 265011, 264601, 264602, 264604, 264605, 18108351, 264762, 264763, 264764, 264369, 264766, 264687, 264768, 264688, 21906768, 35695917, 264690, 264691, 264692, 264693, 264628, 18108374, 35696423, 264631, 264632, 264635, 264637, 264638, 264639, 18108385, 22279000, 22279002, 264565, 264566, 264486
1785	95357475 (3569, 3570)	Novel Protein sim. GBank gi|4589552|dbj|BAA76798.1| - (AB023171) KIAA0954 protein [Homo sapiens]		UNCLASSIFIED	65274572, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 264905, 264906, 264908, 66712502, 56182435, 264511, 265007, 60433356, 55811150, 264683, 264369, 264687, 52644229, 21906767, 52644150, 33657023, 65274620, 33657182, 65274791, 35695855, 264555, 65274727, 22279002
1786	85296465 (3571, 3572)	Novel Protein sim. GBank gi|117788|sp|P26770|CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)		UNCLASSIFIED	264908, 35696423, 264636
1787	87434784 (3573, 3574)	Novel Protein sim. GBank gi|3877175|emb|CAA90338.1| - (Z50028) cDNA EST yk321h8.5 comes from this gene; cDNA EST EMBL:D68896 comes from this gene; cDNA EST yk395f9.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264905, 264908, 264909, 264595, 264764, 264766, 264692, 60431528, 264629, 264636, 264564, 264566
1788	91228779 (3575, 3576)			UNCLASSIFIED	264488, 83373044
1789	88094529 (3577, 3578)	Novel Protein sim. GBank gi|2088669 (AF003130) - F55A12.9 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264488, 29331828, 264909, 18108351, 264288, 265021, 264555, 264636
1790	82489734 (3579, 3580)				35696052, 264905, 264906, 264907, 264908, 264909, 265008, 264910, 264758, 265011, 265019, 264764, 264766, 264769, 264628, 264635

1791	95197259 (3581, 3582)	Novel Protein sim. GBank gi|2114321|dbj|BAA20037| - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	264488, 264686, 264687, 264768, 18108394, 264789, 18108397, 264259, 264691, 264692, 33657023, 264693, 264509, 264905, 264906, 264628, 264907, 264629, 264908, 264909, 264510, 265006, 264511, 265008, 264630, 265009, 264631, 264910, 264632, 264634, 264635, 264555, 264636, 264592, 264637, 264593, 264638, 18108381, 264639, 264758, 265010, 265011, 264602, 22279000, 264604, 264760, 264564, 264681, 264762, 264565, 264763, 264683, 264566, 264764, 264288, 264684, 264567, 18108354, 18108391, 264685, 264766
1792	87792690 (3583, 3584)	Novel Protein sim. GBank gi|4337106|gb|AAD18082| - (AF129756) BAT4 [Homo sapiens]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED	22278997, 264259, 264508, 265007, 33657402, 87168559, 264369, 33657023, 35695855, 20281071, 264559, 18108387, 87168518
1793	95337877 (3585, 3586)	Novel Protein sim. GBank gi|5579331|gb|AAD45504.1|AF14573 - (AF145732) endoplasmic reticulum alpha-mannosidase I [Homo sapiens]	Contains protein domain (PF01532) - Glycosyl hydrolase family 47	ATPase_associated	65274572, 22278995, 22278996, 22278997, 22278999, 264093, 264259, 29331824, 66714117, 60432289, 29331827, 29331828, 264103, 264105, 29331830, 265007, 264910, 265009, 60170831, 60433356, 21906754, 265010, 265017, 265019, 264681, 264682, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 52644150, 33657023, 33657109, 18108370, 18108374, 65274791, 20281071, 60432113, 22279000, 264482, 264564
1794	87759806 (3587, 3588)	Novel Protein sim. GBank gi|4914604|emb|CAB43677.1| - (AL050369) hypothetical protein [Homo sapiens]	Contains protein domain (PF01798) - Putative snoRNA binding domain	UNCLASSIFIED	18108394, 22278995, 22278999, 264259, 29331822, 29331824, 29331825, 29146498, 29146499, 264508, 264905, 52644045, 264112, 265006, 265008, 264910, 60433356, 264757, 55812038, 87168474, 265011, 265017, 18108351, 264763, 264448, 264683, 264369, 21906765, 21906766, 21906767, 21906769, 29146784, 35695917, 60170615, 33657023, 264629, 18108374, 18108376, 35696423, 35695855, 264556, 264557, 264638, 264558, 18108385, 264564
1795	79747856 (3589, 3590)			UNCLASSIFIED	264632, 264635, 264636, 264595, 264596, 264907, 264566, 264909
1796	86599486 (3591, 3592)	Novel Protein sim. GBank gi|585084|sp|Q07803|EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)		glycoprotein	264488, 264907, 264909, 264594, 264595, 264766, 264687, 21906765, 21906767, 264628, 264630, 264559

1797	91223219 (3593, 3594)	Novel Protein sim. GBank gi|1842111 (U87586) - decoy [Arabidopsis thaliana]		ribosomalprot	22278996, 22278997, 22278998, 22278999, 29331822, 264910, 60170831, 21906754, 52644229, 21906765, 21906768, 21906769, 35695917, 265022, 52644150, 264691, 33657023, 263967, 33657109, 22279000
1798	91221276 (3595, 3596)	Novel Protein sim. GBank gi|2832906|dbj|BAA24608.1| - (D89340) dipeptidyl peptidase III [Rattus norvegicus]		peptidase	22278994, 56994075, 22278997, 22278998, 22278999, 264259, 29331826, 60432289, 29331828, 33656970, 265008, 60432229, 264757, 60433438, 21906754, 33657084, 87168559, 265017, 18108351, 264682, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 33657182, 27486261, 27486265, 33657349, 263973, 18108374, 55811576, 35695855, 18108385, 87168518, 22279000, 264486
1799	86321713 (3597, 3598)	Novel Protein sim. GBank gi|5689541|dbj|BAA83054.1| - (AB029025) KIAA1102 protein [Homo sapiens]		eph	264908, 21906754, 21906767, 21906769, 265020, 33657023, 264692, 264693, 264404, 22279000
1800	87080116 (3599, 3600)			UNCLASSIFIED	264691, 264556, 264566
1801	95060723 (3601, 3602)	Novel Protein sim. GBank gi|4680679|gb|AAD27729.1|AF13295 - (AF132954) CGI-20 protein [Homo sapiens]			52644045, 265007, 264632
1802	87771012 (3603, 3604)	Novel Protein sim. GBank gi|134920|sp|P21997|SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			35696286, 66714117, 264508, 264509, 56182435, 264512, 18108351, 264688, 55811957, 264692, 55811576, 35695855, 264486
1803	95060725 (3605, 3606)	Novel Protein sim. GBank gi|4680679|gb|AAD27729.1|AF13295 - (AF132954) CGI-20 protein [Homo sapiens]			264686, 264488, 264687, 264489, 264768, 264769, 264689, 21906769, 35696286, 35695917, 264259, 264691, 264692, 264693, 20281099, 18108364, 35696052, 264508, 264509, 264905, 264906, 18108370, 264628, 264907, 66712502, 264908, 264909, 18108374, 18108376, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264631, 264632, 264634, 264635, 264591, 264636, 264637, 264592, 264638, 264593, 264639, 264594, 83373044, 264758, 264596, 18108385, 18108387, 265011, 264760, 264563, 18108351, 264762, 264564, 264448, 264565, 264763, 264683, 264764, 264566, 264288, 264486, 264567, 264765, 264766

1804	87770203 (3607, 3608)	Novel Protein sim. GBank gi|3879914|emb|CAA98538.1| - (Z74043) predicted using Genefinder; cDNA EST EMBL:C13850 comes from this gene; cDNA EST EMBL:C11575 comes from this gene; cDNA EST yk343f4.5 comes from this gene [Caenorhabditis elegans]			52646365, 22278997, 22278999, 264905, 264908, 264909, 264910, 21906754, 264766, 21906765, 21906768, 35695917, 265020, 265022, 264691, 264637, 264639, 22279000, 264564, 264566
1805	95330375 (3609, 3610)	Novel Protein sim. GBank gi|5453644|ref|NP_006461.1|pEBBP - estrogen-responsive B box protein			29331824, 29331825, 29331826, 29331827, 29331828, 87168559, 264288, 264687, 52644229, 35698423, 264636, 60432113
1806	94133762 (3611, 3612)	Novel Protein sim. GBank gi|4589676|dbj|BAA76857.1| - (AB023230) KIAA1013 protein [Homo sapiens]		struct	264094, 264105, 264908, 35698423, 265006, 265007, 265008, 264555, 264592, 265011, 265018, 264369
1807	86943032 (3613, 3614)				29331824, 264908, 264910, 33657023, 263978
1808	87642711 (3615, 3616)	Novel Protein sim. GBank gi|4884079|emb|CAB43235.1| - (AL050008) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264488, 35696286, 66714117, 35696052, 66712502, 264592, 60433438, 52644296, 265010, 264683, 264369, 264689, 55811957, 35695917, 33657109, 35695763, 55810764, 18108379, 35696423, 35695855, 56182323, 264563, 264564, 264487
1809	95321468 (3617, 3618)	Novel Protein sim. GBank gi|1916927 (U87965) - putative G protein [Mus musculus]		UNCLASSIFIED	264594, 55811150, 264686, 29148629, 29148784, 264690, 264629, 18108374, 264556, 264557, 264558
1810	88096316 (3619, 3620)	Novel Protein sim. GBank gi|1352944|sp|P47179|YJ9P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264488, 35696052, 264905, 264906, 264907, 264908, 264909, 264511, 265009, 264910, 264592, 264593, 264594, 33657402, 264757, 264595, 264758, 264596, 264759, 264600, 264601, 264762, 264683, 264764, 264288, 264684, 264766, 264767, 264686, 264768, 264687, 264769, 264689, 265021, 264690, 264691, 264693, 264628, 264629, 18108374, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264566, 264486, 264567
1811	88086272 (3621, 3622)	Novel Protein sim. GBank gi|2134984|pir||I37275 - death-associated protein kinase (EC 2.7.1.-) - human	Contains protein domain (PF00023) - Ank repeat	kinase	264488, 264259, 264508, 264509, 264905, 264906, 264907, 56182435, 264511, 264512, 264910, 264758, 265011, 264600, 264604, 18108354, 264766, 264686, 264769, 264534, 60170615, 33657023, 264629, 264631, 264639, 264563, 264482, 264483
1812	79245772 (3623, 3624)				29331822, 29331824, 265019, 18108351, 21906769

1813	88090972 (3625, 3626)	Novel Protein sim. GBank gi|5051636|gb|AAD38326.1|AF07372 - (AF073727) EH domain-binding mitotic phosphoprotein [Homo sapiens]	Contains protein domain (PF01417) - ENTH domain	glucoamylase	56182575, 264259, 29331824, 66714117, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 265007, 264910, 264591, 264593, 55812038, 265011, 265018, 264760, 264682, 264764, 264683, 264369, 264766, 264768, 264769, 21906766, 21906768, 264691, 264693, 18108374, 35695855, 264634, 264635, 264637, 264639, 264559, 22279000, 22279002, 264566
1814	88178047 (3627, 3628)	Novel Protein sim. GBank gi|3643608 (AC005395) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 35696286, 22278998, 264092, 264094, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264107, 52644045, 56182435, 265009, 60432229, 60433356, 87168474, 87168559, 264369, 264288, 21906765, 35695917, 265021, 265022, 33657023, 33657109, 18108374, 35696423, 264638, 56526486, 264482
1815	85296473 (3629, 3630)	Novel Protein sim. GBank gi|117788|sp|P26770|CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)		struct	22278999, 264508, 264509, 264907, 264908, 264910, 265011, 264760, 264766, 264634, 264636
1816	83738845 (3631, 3632)	Novel Protein sim. GBank gi|1176623|sp|P41846|YO96_CAEEL - HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III		UNCLASSIFIED	18108394, 18108397, 264509, 264907, 264908, 264909, 265009, 264591, 265011, 265017, 264687, 264689, 265022, 264691, 18108362, 18108368, 18108370, 18108374, 18108379, 264635, 264557, 264564, 264567
1817	88095268 (3633, 3634)	Novel Protein sim. GBank gi|3766377|emb|CAA21429| - (AL031907) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	histone	264488, 22278997, 22278999, 60432049, 29331822, 29331824, 60432289, 52644045, 60170831, 265017, 265018, 265019, 18108351, 264682, 52644229, 21906765, 21906767, 21906768, 52644150, 33657023, 33657109, 27486262, 18108370, 18108374, 60170394, 56182323, 22279002
1818	85806775 (3635, 3636)	Novel Protein sim. GBank gi|3879121|emb|CAA94370| - (Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	35696286, 60433356, 264758, 264369, 264686, 21906769, 264693, 264632
1819	87759572 (3637, 3638)	Novel Protein sim. GBank gi|5031865|ref|NP_005771.1|pLHFP - lipoma HMGIC fusion partner		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331826, 264908, 265007, 265008, 265009, 60432229, 265017, 265018, 265019, 264448, 264288, 21906768, 21906769, 265020, 18108381, 18108384, 22279000, 22279002, 264567

1820	87769455 (3639, 3640)				264905, 264907, 264594
1821	80431510 (3641, 3642)				264907, 264768, 263978
1822	91221523 (3643, 3644)	Novel Protein sim. GBank gi|4884130|emb|CAB43272.1| - (AL050101) hypothetical protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 35696052, 29331828, 264908, 29331830, 60170831, 264591, 264593, 60433356, 264596, 265017, 265019, 18108351, 264763, 264683, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 18108364, 18108370, 35695855, 22279000, 22279002
1823	85522330 (3645, 3646)			UNCLASSIFIED	264488, 264259, 264511, 264288, 264768, 264693, 35696423, 264634, 18108385, 264486
1824	86612025 (3647, 3648)	Novel Protein sim. GBank gi|477072|pir||A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	264907, 264908, 264909, 264511, 264631, 264634, 264635, 264637, 264638, 264639, 264758, 264566
1825	87430125 (3649, 3650)	Novel Protein sim. GBank gi|3036803|emb|CAA18493| - (AL022373) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60432049, 264910, 264487
1826	91723612 (3651, 3652)	Novel Protein sim. GBank gi|4680685|gb|AAD27732.1|AF13295 - (AF132957) CGI-23 protein [Homo sapiens]		ATPase_associated	52644507, 52645156, 52646842, 22278994, 22278996, 56994075, 264259, 60432049, 52645080, 35696052, 66712502, 52644045, 265008, 265009, 60432229, 60433356, 60433438, 52646317, 52644296, 265011, 87168559, 264448, 264288, 264369, 264688, 52644229, 264689, 21906765, 21906768, 265020, 60170615, 52644150, 33657023, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 83373044, 87168518, 264404, 22279002
1827	81647212 (3653, 3654)				264758

1828	95074017 (3655, 3656)	Novel Protein sim. GBank gi|4503571|ref|NP_001419.1|pENO1 - enolase 1, (alpha)	Contains protein domain (PF00113) - Enol-ase	oncogene	264488, 52646842, 56182575, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264508, 264907, 66712502, 52644045, 56182435, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 60432229, 264593, 60433356, 60433438, 264758, 33109954, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265019, 264761, 264762, 264448, 264764, 264683, 264288, 264369, 18108355, 264768, 18108357, 18108358, 264688, 264769, 264689, 21906768, 21906769, 35695917, 265021, 60170615, 33657023, 33657349, 263972, 55811576, 35695855, 264635, 264555, 264556, 264638, 264557, 87168518, 22279000, 22279002, 264563, 264482, 264565, 264484, 264567
1829	80197720 (3657, 3658)				264508, 264634, 264509, 264482, 29331827, 264908, 265009, 264910
1830	94312942 (3659, 3660)	Novel Protein sim. GBank gi|2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		nuclease	52645156, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 29331822, 29331825, 35696052, 52646317, 52644296, 87168559, 265019, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 35695763, 263974, 35696423, 35695855, 52644332
1831	94138063 (3661, 3662)			UNCLASSIFIED	29331824, 35696052, 29331830, 264595, 264758, 265010, 265019, 265022, 264693, 65274791
1832	84521663 (3663, 3664)	Novel Protein sim. GBank gi|1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....			264602

1833	95314184 (3665, 3666)	Novel Protein sim. GBank gi|5174413|ref|NP_006026.1|pCDC4 - CDC42-binding protein kinase beta (DMPK-like)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278994, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 35696052, 29146499, 264508, 264509, 264906, 264907, 66712502, 264908, 52644045, 264909, 264512, 265008, 264591, 264593, 60433356, 21906754, 33657084, 265011, 265017, 264604, 265018, 265019, 264681, 18108351, 264683, 264288, 264685, 264766, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 265020, 265021, 264690, 264692, 33657023, 65274620, 33657182, 27486264, 33657349, 65274791, 264634, 264635, 264556, 264557, 264558, 264559, 18108385, 56526486, 87168518, 60432113, 22279000, 22279002, 264563
1834	80562790 (3667, 3668)				264259, 264907, 264689, 22279000, 22279002
1835	94135718 (3669, 3670)			UNCLASSIFIED	22278998, 29331822, 29331826, 87168474, 264603, 21906768, 263976, 35695855, 83373044
1836	87348450 (3671, 3672)	Novel Protein sim. GBank gi|4759286|ref|NP_004268.1|pUCP4 - uncoupling protein 4	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	29331825, 264908, 265019, 264764, 264686, 21906765, 264635
1837	94234297 (3673, 3674)	Novel Protein sim. GBank gi|3334400|sp|Q24574|UBPE_DROME - UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	22278995, 29146499, 265006, 265008, 265009, 265010, 264683, 21906765, 29148627, 29148629, 265020, 265021, 265022, 65274620, 18108370, 18108374, 264556, 18108385
1838	94324369 (3675, 3676)	Novel Protein sim. GBank gi|1362599|pir||A56154 - Abl substrate ena (enabled) - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00568) - WH1 domain		29331822, 265017, 264760, 265020, 83373044
1839	87456508 (3677, 3678)	Novel Protein sim. GBank gi|2117310|emb|CAB09116.1| - (Z95620) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	60433438, 264601, 21906765, 21906766, 265021, 33657109, 264556
1840	87391708 (3679, 3680)	Novel Protein sim. GBank gi|127560|sp|P23249|MV10_MOUSE - PROTEIN MOV-10		UNCLASSIFIED	264693
1841	85818445 (3681, 3682)	Novel Protein sim. GBank gi|4572464|gb|AAD23834.1|AF12365 - (AF123653) FEZ1 [Homo sapiens]			56182575, 29331824, 29331826, 60433356, 264764, 264288, 33657023, 263967, 18108370, 18108374, 264631, 264555, 264556, 264639

1842	90992645 (3683, 3684)	Novel Protein sim. GBank gi|1326268 (U58728) - C54H2.1 gene product [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 29331822, 29331824, 29331825, 66714117, 29331826, 29331827, 264907, 264909, 52644045, 56182435, 264510, 265006, 265007, 265009, 264910, 60433356, 264757, 60433438, 55812038, 265017, 18108354, 264686, 264769, 33657023, 264693, 18108364, 33657109, 18108368, 264628, 55810764, 56182323, 18108384, 264563, 264564
1843	95292692 (3685, 3686)			UNCLASSIFIED	264488, 56182435, 264769, 29331826, 29331828, 264511, 265006, 265007, 264910, 264631, 264509, 264690, 264636, 264564, 264691, 60432229, 60432049, 264259, 264629, 33657023, 264486, 264909, 264567, 264595, 264766
1844	87444764 (3687, 3688)	Novel Protein sim. GBank gi|2496887|sp|Q09232|YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	264908, 265022, 33657023, 87168518, 22279002
1845	95096673 (3689, 3690)	Novel Protein sim. GBank [illegible]/5494|sp|Q09819|YAC5_SCHPO - HYPOTHETICAL 45.0 KD PROTEIN C16C9.05 IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger	transcriptfactor	264259, 29331824, 264907, 264908, 66712502, 264510, 265007, 265008, 55812038, 265018, 21906765, 52644150, 33657109, 264555, 264556, 264557, 56182323, 18108382, 83373044, 18108385, 264564
1846	84287872 (3691, 3692)	Novel Protein sim. GBank gi|3881080|emb|CAA21739| - (AL032657) similar to EGF-like domain; cDNA EST yk299a12.3 comes from this gene; cDNA EST EMBL:D35398 comes from this gene; cDNA EST yk331h6.5 comes from this gene; cDNA EST yk299a12.5 comes from this gene; cDNA EST yk467g8.5 c...	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264905, 264908
1847	87821497 (3693, 3694)	Novel Protein sim. GBank gi|5059323|gb|AAD38967.1|AF15152 - (AF151522) hairy and enhancer of split related-1 [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	22278997, 264259, 29331824, 264909, 18108351, 263974, 22279002
1848	86789360 (3695, 3696)	Novel Protein sim. GBank gi|5701854|emb|CAB52191.1| - (AJ245417) G5b protein [Homo sapiens]		tm7	29331825, 29331826, 29331827, 265017, 264683, 264288, 264766, 264768, 21906767, 21906768, 264692, 22279002
1849	84287874 (3697, 3698)	Novel Protein sim. GBank gi|4503665|ref|NP_001989.1|pFBLN - fibulin 2 precursor	Contains protein domain (PF00008) - EGF-like domain	ATPase_associated	56182575, 265018
1850	86689650 (3699, 3700)	Novel Protein sim. GBank gi|4589582|dbj|BAA76813.1| - (AB023186) KIAA0969 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	60432049, 264908
1851	95419789 (3701, 3702)	Novel Protein sim. GBank gi|220637|dbj|BAA01477| - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	29331824, 35696052, 264910, 60433438, 264688, 35695917, 265020, 52644150, 65274620, 52644332

1852	95413170 (3703, 3704)	Novel Protein sim. GBank gi|5174629|ref|NP_006090.1|pPIAS - protein inhibitor of activated STAT3		UNCLASSIFIED	56182575, 35696286, 22278996, 22278997, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 35696052, 52644045, 265007, 264910, 60432229, 60433356, 60433438, 55812038, 65274444, 265018, 265019, 18108351, 264448, 264686, 264687, 21906765, 21906767, 21906769, 265021, 265022, 52644150, 264693, 33657109, 18108370, 18108374, 55811576, 35695855, 56182323, 60432113, 22279002, 264563
1853	91222267 (3705, 3706)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264687, 264768, 52644507, 264769, 21906765, 21906767, 21906768, 22278995, 56994075, 22278999, 52644150, 264259, 264692, 29331822, 29331824, 52645129, 29331827, 33656970, 33657349, 35695763, 264508, 264906, 264628, 264907, 264629, 264909, 35696423, 35695855, 264510, 265006, 264511, 264512, 264630, 265009, 264631, 264910, 264634, 264635, 264637, 264593, 264638, 264639, 33657402, 18108385, 52646317, 52644296, 87168518, 87168559, 264602, 265017, 22279000, 265018, 264760, 264762, 264682, 264448, 264764, 264684, 264567, 264288, 264369, 264766
1854	86038152 (3707, 3708)	Novel Protein sim. GBank gi|2072964 (U93569) - putative p150 [Homo sapiens]		nuclease	264592
1855	91221459 (3709, 3710)	Novel Protein sim. GBank gi|4539520|emb|CAB39994.1| - (AL035424) dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins) [Homo sapiens]	Contains protein domain (PF01344) - Kelch motif	nucl_recpt	18108392, 52646365, 65274572, 56182575, 22278994, 56994075, 22278996, 35696286, 22278999, 264259, 60432049, 264908, 264510, 265007, 265008, 265009, 264595, 21906754, 87168474, 265011, 87168559, 264681, 264288, 264768, 18108359, 21906764, 21906768, 29148627, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108372, 18108374, 18108376, 35696423, 264631, 264636, 18108381, 264482
1856	94231871 (3711, 3712)	Novel Protein sim. GBank gi|3954978|emb|CAA06945| - (AJ006278) acetylglucosaminyltransferase-like protein (Mus musculus]		UNCLASSIFIED	56994075, 264259, 29331828, 264511, 264910, 264758, 264693, 264637, 18108381, 83373044
1857	94324455 (3713, 3714)	Novel Protein sim. GBank gi|4322670|gb|AAD16120| - (AF094508) dentin phosphoryn [Homo sapiens]		ATPase_associated	22278999, 264259, 264906, 60170831, 264448, 264686, 265020, 265022, 33657109, 60170394, 83373044

1858	87628311 (3715, 3716)	Novel Protein sim. GBank gi|4981903|gb|AAD36415.1|AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomalprot	264757
1859	84407464 (3717, 3718)	Novel Protein sim. GBank gi|4240317|dbj|BAA74937.1| - (AB020721) KIAA0914 protein [Homo sapiens]			22278996, 29331824, 265007, 33109954, 265019, 264369, 21906768, 29148784, 27486261, 52644332, 22279002
1860	17929308 (3719, 3720)	Novel Protein sim. GBank gi|4009522 (AF099731) - connexin 31.1 [Homo sapiens]			265019
1861	88086370 (3721, 3722)	Novel Protein sim. GBank gi|2143637|pir||I84505 - calcium-dependent actin-binding protein - rat	Contains protein domain (PF00285) - Citrate synthase		264887, 264259, 29331822, 29331824, 29331825, 265007, 265009, 264591, 33109954, 265010, 265019, 264369, 264288, 264686, 264691, 264693, 27486264, 18108370, 18108374, 263977, 55811576, 56182323, 264639, 22279000, 22279002, 264482
1862	87372923 (3723, 3724)	Novel Protein sim. GBank gi|125493|sp|P07313|KMLC_RABIT - MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35696286, 264259, 87168474, 264369, 21906768, 264558, 264563
1863	85775037 (3725, 3726)	Novel Protein sim. GBank gi|3820909|emb|CAA09299| - (AJ010642) Dof protein [Drosophila melanogaster]		UNCLASSIFIED	264601, 264766, 29148627, 29148629, 264692, 264629, 264635
1864	85547832 (3727, 3728)	Novel Protein sim. GBank gi|4322263|gb|AAD15985| - (AF077738) metallocarboxypeptidase CPX-1 [Mus musculus]	Contains protein domain (PF00754) - F5/8 type C domain	synthase	22278999, 264259, 264907, 265018, 18108370, 264634, 264635, 264555, 264556, 264638, 18108387
1865	87740827 (3729, 3730)	Novel Protein sim. GBank gi|2495727|sp|Q93073|Y256_HUMAN - HYPOTHETICAL PROTEIN KIAA0256			22278999, 264490, 29331822, 66714117, 66712502, 265006, 265007, 265008, 265009, 264591, 60433438, 265010, 265019, 264760, 264448, 264768, 29148627, 29148629, 265020, 265022, 18108385, 60432113
1866	87266816 (3731, 3732)	Novel Protein sim. GBank gi|5262617|emb|CAB45748.1| - (AL080157) hypothetical protein [Homo sapiens]		kinase	18108374, 264769, 18108377, 21906765, 21906766, 35696423, 56182575, 21906769, 29148629, 35696286, 35695917, 265021, 264510, 264511, 264512, 264534, 264535, 60170831, 52644150, 264555, 264691, 264259, 264556, 264692, 264557, 33657023, 60433356, 29331822, 264559, 264595, 29331824, 18108385, 21906754, 33657182, 29331827, 35696052, 33656970, 87168518, 265017, 60431602, 22279000, 264508, 264509, 18108351, 264907, 264682, 264567, 18108372, 264765, 264486
1867	84579159 (3733, 3734)	Novel Protein sim. GBank gi|3859930 (AF078096) - forkhead/winged helix-like transcription factor 7 [Homo sapiens]		UNCLASSIFIED	264094

1868	87357459 (3735, 3736)	Novel Protein sim. GBank gi|3881525|emb|CAA93884| - (Z70038) cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D35254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk357f10.5 comes from this gene [Caenorhabditis elegans]		nuclease	264489, 22278997, 22278999, 29331825, 29331826, 265008, 265009, 33657402, 87168474, 18108351, 21906765, 21906768, 21906769, 265020, 265021, 60170615, 27486264, 264628, 18108374, 264631, 18108385, 87168518, 22279000, 22279002, 264566, 264567
1869	86977292 (3737, 3738)	Novel Protein sim. GBank gi|4826772|ref|NP_004961.1|pIGFA - insulin-like growth factor binding protein, acid labile subunit	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264508, 264509, 264906, 264908, 264909, 264910, 264591, 264600, 18108351, 264683, 264766, 264769, 35695855, 264634, 264558, 264639, 18108385, 264563, 264486
1870	95349488 (3739, 3740)	Novel Protein sim. GBank gi|1869859|emb|CAB06722| - (Z86099) very large tegument protein [human herpesvirus 2]		UNCLASSIFIED	29331824, 60424269, 265007, 265008, 21906754, 265017, 265018, 265019, 264288, 264766, 264686, 264688, 21906768, 21906769, 35695917, 60170615, 264692, 18108368, 35695763, 35696423, 65274791, 264638, 264639, 56526486
1871	80234464 (3741, 3742)			UNCLASSIFIED	264509, 264905, 264595, 264768, 264635, 264636, 264563, 264486
1872	80235355 (3743, 3744)	Novel Protein sim. GBank gi|2460316 (AF022147) - uterus-ovary specific putative transmembrane protein [Rattus norvegicus]		protease	264510, 264594, 264565
1873	80213890 (3745, 3746)				264509, 264512, 265009, 265011, 18108351, 264687, 264691, 18108370, 18108374, 264635
1874	95351136 (3747, 3748)		Contains protein domain (PF00293) - Bacterial mutT protein	UNCLASSIFIED	264488, 35695917, 264259, 264905, 264907, 264908, 264909, 263978, 264511, 264635, 264636, 264637, 264638, 33657402, 264558, 18108385, 264600, 264604, 264764, 264567, 264766
1875	87330516 (3749, 3750)	Novel Protein sim. GBank gi|4589520|dbj|BAA76782.1| - (AB023155) KIAA0938 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264828, 264592, 264557, 264558
1876	87112950 (3751, 3752)	Novel Protein sim. GBank gi|263810|bbs|122920 - collagen alpha chain [Riftia pachyptila=tube worms, Peptide, 1027 aa]		UNCLASSIFIED	264259, 29331822, 60432289, 264908, 264909, 264604, 264764, 264288, 264769, 18108376, 264556, 264558, 264559, 18108385
1877	87315208 (3753, 3754)	Novel Protein sim. GBank gi|3983356|gb|AAC83924.1| - (AF102545) riboflavin binding protein precursor [Scaphiopus couchii]		UNCLASSIFIED	264767, 264686, 264768, 263978, 264693, 264639, 265010, 264563, 264905, 264906, 264907

1878	95351056 (3755, 3756)	Novel Protein sim. GBank gi|4510345|gb|AAD21434.1| - (AC006921) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264569, 264488, 35696286, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 29146498, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 33657402, 264594, 264758, 55812038, 265011, 264602, 264760, 18108351, 264762, 264681, 264682, 264764, 264369, 264288, 264766, 264687, 264768, 264769, 21906766, 35695917, 265021, 60170615, 33657023, 264692, 264693, 33657109, 27486265, 264628, 18108370, 264629, 18108374, 35696423, 264634, 264635, 264555, 264638, 264639, 83373044, 18108385, 56526486, 87168518, 264563, 264564, 264566, 264486, 264567
1879	95310883 (3757, 3758)	Novel Protein sim. GBank gi|4929643|gb|AAD34082.1|AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264905, 264907, 264908, 265007, 264565, 264566
1880	91012978 (3759, 3760)	Novel Protein sim. GBank gi|1550785|emb|CAA69283| - (Y08026) immune associated protein 38 [Mus musculus]		UNCLASSIFIED	264766, 264691, 264692, 83373044
1881	80214949 (3761, 3762)	Novel Protein sim. GBank gi|93144|pir||B40505 - hypothetical protein - suid herpesvirus 1 (strain Indiana-Funkhuser or Becker)		UNCLASSIFIED	264509, 264905, 264908, 264909, 264910, 264762, 264687, 33657023, 264632
1882	86582450 (3763, 3764)	Novel Protein sim. GBank gi|2384956 (AF022985) - No definition line found [Caenorhabditis elegans]			264908, 21906766, 18108370, 263974, 87168518
1883	94216817 (3765, 3766)	Novel Protein sim. GBank gi|1351218|sp|P47226|TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	264908, 264910, 87168559, 21906766, 264636

1884	95310885 (3767, 3768)	Novel Protein sim. GBank gi|4929643|gb|AAD34082.1|AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108394, 56181686, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264512, 265009, 264910, 264592, 264593, 33657402, 55812038, 264758, 55811386, 265010, 265011, 87168559, 264600, 265017, 264604, 265019, 264605, 264760, 55811150, 264761, 264682, 264763, 264683, 264764, 264288, 264369, 264766, 264686, 264768, 264769, 29148784, 35695917, 264690, 264691, 33657023, 264692, 264693, 33657109, 18108370, 264628, 60431528, 264629, 263973, 18108374, 55810764, 55811576, 35696423, 35695855, 264631, 264634, 60431850, 264637, 264638, 56182323, 264639, 18108382, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264486, 264567
1885	87644280 (3769, 3770)	Novel Protein sim. GBank gi|2507155|sp|P37370|VRP1_YEAST - VERPROLIN		UNCLASSIFIED	56182575, 264259, 264905, 264909, 265008, 264596, 264766, 265020, 264628, 60431528, 264634, 56526486, 264080, 264563
1886	86674062 (3771, 3772)	Novel Protein sim. GBank gi|2854158|gb|AAC02577.1| - (AF045641) No definition line found [Caenorhabditis elegans]			22278998, 22278999, 60432049, 264910, 265018, 264766, 21906768, 29148629, 264690, 264693, 264628, 264555, 264486
1887	94139139 (3773, 3774)	Novel Protein sim. GBank gi|5174421|ref|NP_006023.1|pCPNE - copine VI (neuronal)	Contains protein domain (PF00168) - C2 domain	ATPase_associated	29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 264681, 264768, 29148627, 264693, 18108364, 35696423, 65274791, 35695855, 264632, 56182323, 264639, 264563
1888	87822804 (3775, 3776)	Novel Protein sim. GBank gi|3319931|emb|CAB10841| - (Z98046) dJ14O9.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens]	Contains protein domain (PF01454) - MAGE family		263978
1889	91255783 (3777, 3778)	Novel Protein sim. GBank gi|1083308|pir||A56559 - enhancer-trap-locus-1 protein - mouse (fragment)	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	264906, 55812038, 264758, 265010, 265018, 265019, 18108351, 264288, 21906765, 21906768, 21906769, 265021, 33657023, 33657109, 56182323, 83373044, 18108385, 22279000, 22279002
1890	87626705 (3779, 3780)	Novel Protein sim. GBank gi|4240195|dbj|BAA74876.1| - (AB020660) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	18108398, 29147620, 264907, 265009, 264600, 265018, 18108351, 264288, 264689, 21906765, 21906768, 21906769, 264691, 264692, 264693, 264628, 18108370, 264636, 264558, 264404

1891	87013895 (3781, 3782)			UNCLASSIFIED	264686, 264768, 264687, 264692, 264693, 29331822, 29331824, 264508, 264905, 264906, 18108370, 264628, 264907, 264908, 264909, 18108379, 265007, 265008, 264910, 264632, 264591, 264639, 264596, 18108384, 265010, 265011, 264601, 264605, 264563, 264369
1892	87642825 (3783, 3784)	Novel Protein sim. GBank gi|5689535|db||BAA83051.1| - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	struct	22278995, 264509, 87168559, 18108351, 264448, 264682, 265020, 264693, 18108374, 22279000
1893	88533826 (3785, 3786)			laminin	264569, 65274572, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331826, 264906, 265006, 265008, 265009, 264592, 265018, 264681, 264448, 264683, 18108354, 264369, 264684, 264685, 264766, 264687, 264689, 21906768, 265020, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 264628, 18108374, 35695855, 264630, 264632, 264634, 264557, 264558, 60170394, 18108381, 18108385, 22279000
1894	86989120 (3787, 3788)				264508, 264905, 264908, 264907, 264594, 264684, 264690, 264692, 264630, 264635, 264636, 264639, 264563
1895	87631891 (3789, 3790)	Novel Protein sim. GBank gi|5262574|emb|CAB45729.1| - (AL080133) hypothetical protein [Homo sapiens]	Contains protein domain (PF00435) - Spectrin repeat		56182575, 264259, 60432289, 29331826, 264107, 264905, 264908, 264910, 60170831, 264758, 265010, 265018, 264448, 264288, 264768, 33657109, 264628, 55810764, 18108379, 264634, 56182323, 56526486
1896	85673555 (3791, 3792)		Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264907, 265008, 264682, 264686, 21906768, 264629, 264631, 264634, 264555
1897	80565569 (3793, 3794)	Novel Protein sim. GBank gi|728836|sp|P39193|ALU6_HUMAN - !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!		cadherin	264259
1898	87617637 (3795, 3796)	Novel Protein sim. GBank gi|127560|sp|P23249|MV10_MOUSE - PROTEIN MOV-10		helicase	22278996, 22278998, 22278999, 29331824, 29331825, 60432289, 29331827, 35696052, 29331828, 265008, 265019, 264681, 264682, 264448, 264369, 52644229, 21906765, 21906766, 21906768, 21906769, 60170615, 55810764, 22279000
1899	86673097 (3797, 3798)	Novel Protein sim. GBank gi|2909819 (AF031548) - erythrocyte membrane glycoprotein Rh50 [Homo sapiens]	Contains protein domain (PF00909) - Ammonium Transporter Family	glycoprotein	264259, 264508, 264909, 60432229, 264769, 21906765, 21906769
1900	87641858 (3799, 3800)	Novel Protein sim. GBank gi|4102881 (AF017250) - vitellogenin precursor [Oreochromis aureus]		UNCLASSIFIED	264683

1901	95196647 (3801, 3802)	Novel Protein sim. GBank gi|585959|sp|P38378|S61A_RAT PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	Contains protein domain (PF00242) - DNA polymerase (viral) N-terminal domain	transport	264488, 52644507, 52645156, 18108396, 52646365, 52646842, 18108397, 56182575, 22278994, 22278995, 56994075, 35696286, 22278997, 22278998, 264490, 60432049, 264259, 29331822, 52645080, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 29146498, 264906, 264907, 29331830, 264908, 52644045, 264909, 264112, 265006, 264512, 265008, 264910, 265009, 60170831, 60432229, 60433356, 33657402, 60433438, 55812038, 264758, 33109954, 21906754, 33657084, 52644296, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 52644229, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 18108362, 33657023, 264693, 263987, 33657109, 33657182, 27486264, 33657349, 35695763, 18108370, 18108376, 55811576, 35696423, 35695855, 60431850, 264636, 263981, 52644332, 60170394, 83373044, 18108385, 87168518, 60432113, 264564
1902	80202013 (3803, 3804)	Novel Protein sim. GBank gi|4426613|gb|AAD20451| - (AF098796) SLM-1 [Mus musculus]		dna_rna_bind	264107, 263976
1903	87778554 (3805, 3806)	Novel Protein sim. GBank gi|3747107 (AF095741) - unknown [Rattus norvegicus]		UNCLASSIFIED	264259, 29331825, 29331827, 264508, 264907, 265008, 60170831, 60433356, 60433438, 264759, 21906754, 264448, 264288, 265021, 265022, 33657023, 264693, 55811576, 264555, 264556, 22279000
1904	80434213 (3807, 3808)	Novel Protein sim. GBank gi|1352911|sp|P47147|YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION		struct	264509, 264905, 264906, 264907, 264908, 265007, 264910, 264686, 264768, 264687, 264769, 264693, 264628, 18108374, 264634, 264636, 264637, 264565
1905	95351140 (3809, 3810)	Novel Protein sim. GBank gi|3043714|dbj|BAA25521| - (AB011167) KIAA0595 protein [Homo sapiens]	Contains protein domain (PF00293) - Bacterial mutT protein		264488, 264768, 264769, 264689, 29148629, 35695917, 35696286, 264259, 264692, 18108362, 33657023, 29331824, 33657109, 29146499, 264508, 264509, 264905, 264906, 264907, 66712502, 264908, 264909, 35696423, 35695855, 264510, 264511, 264512, 264910, 264634, 264635, 264637, 264638, 33657402, 264758, 85658542, 264602, 264760, 264761, 264482, 264563, 264762, 264483, 264764, 264566, 264288, 264766
1906	12763822 (3811, 3812)			UNCLASSIFIED	264637

1907	95351144 (3813, 3814)	Novel Protein sim. GBank gi|4929585|gb|AAD34053.1|AF15181 - (AF151816) CGI-58 protein [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	hydrolase	65274572, 22278996, 35696286, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 60424269, 29331828, 35696052, 264593, 60433356, 21906754, 55811386, 85658542, 87168559, 265018, 264681, 264682, 264684, 264288, 21906765, 21906766, 21906768, 265020, 265022, 264690, 52644150, 264692, 33657023, 264693, 33657109, 35695855, 264636, 264638, 60432113
1908	95313641 (3815, 3816)	Novel Protein sim. GBank gi|3986770 (AF109906) - NG22 [Mus musculus]		UNCLASSIFIED	264488, 65274572, 56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 60432289, 29331826, 29331827, 29331828, 29146499, 264905, 264906, 264907, 264908, 66712502, 264909, 56182435, 264510, 264511, 265008, 264910, 60170831, 264592, 60433356, 33657402, 264594, 60433438, 264596, 55812038, 33109954, 52646317, 265011, 265017, 264604, 265018, 265019, 264605, 55811150, 264681, 264448, 264288, 264686, 264688, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148629, 35695917, 265020, 265022, 264691, 264692, 18108364, 65274820, 33657109, 33657349, 35695763, 18108374, 263978, 55810764, 55811576, 35696423, 65274791, 264631, 264632, 264556, 264557, 60170394, 56182323, 83373044, 18108385, 60432113, 22279000, 22279002, 264566, 264486
1909	85514505 (3817, 3818)	Novel Protein sim. GBank gi|2224653|dbj|BAA20813| - (AB002354) KIAA0356 [Homo sapiens]		UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 264511, 264910, 264593, 264758, 264764, 264766, 18108370, 264634, 264637, 264486
1910	94216821 (3819, 3820)	Novel Protein sim. GBank gi|1351218|sp|P47226|TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	35696286, 22278996, 22278999, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265007, 264512, 264910, 264758, 265011, 264601, 264602, 264604, 264605, 264761, 264764, 264288, 264766, 264768, 264687, 264769, 35695917, 265021, 52644150, 264692, 264628, 18108370, 264629, 18108372, 18108374, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 18108385, 264565, 264566, 264486

1911	91725345 (3821, 3822)	Novel Protein sim. GBank gi|4809339|gb|AAD30184.1|AC00653 - (AC006530) hypothetical protein [Homo sapiens]	Contains protein domain (PF01119) - DNA mismatch repair protein	nuclease	18108394, 56182575, 56182181, 29331826, 29331827, 33656970, 264906, 265007, 264591, 55812038, 87168559, 264448, 264369, 21906765, 21906768, 265022, 264691, 264693, 18108385, 55811576, 264556, 18108385, 18108388
1912	95413519 (3823, 3824)	Novel Protein sim. GBank gi|5689439|dbj|BAA83003.1| - (AB028974) KIAA1051 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	18108397, 56182575, 56181686, 22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 66714117, 35696052, 264905, 264906, 264907, 264908, 52644045, 56182435, 265007, 265008, 264910, 265009, 264591, 264596, 65274444, 55811386, 87168474, 265011, 87168559, 265018, 265019, 264760, 18108351, 264681, 264369, 264684, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264692, 33657023, 264693, 18108376, 55811576, 35696423, 65274791, 264637, 56182323, 83373044, 56526486, 22279002, 264563, 264566
1913	95305546 (3825, 3826)	Novel Protein sim. GBank gi|5032245|ref|NP_005665.1|pZNF2 - zinc finger protein (C2H2) homologous to mouse MOK-2			56182575, 22278994, 22278995, 56994075, 22278996, 22278998, 22278999, 29331826, 29331827, 265006, 55812038, 265010, 265017, 265018, 265019, 264681, 18108351, 264683, 264764, 264369, 264288, 264685, 264686, 264769, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265022, 264691, 55811576, 264634, 264635, 264638, 56182323, 83373044, 18108385
1914	83423982 (3827, 3828)	Novel Protein sim. GBank gi|4589604|dbj|BAA76824.1| - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	56182575, 29331824, 35696052, 264906, 264908, 264828, 264909, 264592, 264758, 87168559, 18108351, 18108354, 264684, 264686, 33657023, 264693, 264628, 264631, 264632, 264634, 264635, 264639
1915	95340459 (3829, 3830)	Novel Protein sim. GBank gi|5689415|dbj|BAA82991.1| - (AB028962) KIAA1039 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331824, 29331826, 29331827, 264508, 264909, 265009, 265017, 265019, 264768, 264769, 264689, 264628, 264635, 264637, 264639, 83373044, 264565
1916	79640761 (3831, 3832)				264693, 264639

1917	87821680 (3833, 3834)	Novel Protein sim. GBank gi|5689391|dbj|BAA82979.1| - (AB028950) KIAA1027 protein [Homo sapiens]		struct	264769, 264689, 21906765, 21906768, 22278996, 264259, 264691, 264693, 29331824, 29331825, 29331826, 29331828, 264905, 264908, 264628, 264907, 264908, 264909, 264510, 264630, 264910, 264634, 264635, 264638, 264637, 264638, 263981, 264639, 264758, 18108385, 21906754, 265011, 264604, 264563, 18108351, 264762, 264763, 264566, 264764, 264766
1918	95302785 (3835, 3836)	Novel Protein sim. GBank gi|5281517|gb|AAD41524.1|AF15483 - (AF154831) PV-1 [Rattus norvegicus]		struct	264488, 18108392, 18108357, 21906765, 21906767, 21906768, 56182575, 21906769, 22278994, 35696286, 35695917, 22278996, 22278997, 265021, 265022, 264534, 264690, 264691, 264692, 33657023, 264693, 29331824, 29331825, 33657109, 29331826, 52645129, 35696052, 29331828, 27486262, 27486284, 35695763, 264508, 264905, 264509, 264906, 264628, 264907, 18108370, 264908, 264629, 264909, 18108372, 18108374, 263978, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264631, 265009, 264910, 264634, 264635, 264555, 264636, 264556, 264637, 264557, 264593, 264638, 264594, 60170394, 264595, 264559, 264596, 83373044, 264758, 52646317, 18108385, 52644296, 56528486, 87168518, 265010, 265011, 87168559, 264600, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 264760, 264761, 264482, 264564, 18108351, 264762, 264682, 264565, 264448, 264764, 264566, 264486, 264567, 264369, 264288, 264766, 264487, 264685
1919	94143847 (3837, 3838)	Novel Protein sim. GBank gi|3878584|emb|CAB01237| - (Z77667) cDNA EST EMBL:C08125 comes from this gene; cDNA EST EMBL:C09753 comes from this gene [Caenorhabditis elegans]		oxidase	22278997, 29331822, 265007, 60170831, 60432229, 60433438, 264448, 264682, 264288, 55811857, 33657023, 33657109, 65274791, 56182323, 22279002
1920	91229953 (3839, 3840)	Novel Protein sim. GBank gi|1809231 (AC000115) - coded for by human cDNAs R76043 (NID:g850725), R65857 (NID:g838485) and H12868 (NID:g877688) [Homo sapiens]		UNCLASSIFIED	264510, 264511, 264512, 264566
1921	79555226 (3841, 3842)	Novel Protein sim. GBank gi|4580997|gb|AAD24571.1|AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	264693

1922	87641863 (3843, 3844)	Novel Protein sim. GBank gi|38595|sp|P02845|VIT2_CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40]		UNCLASSIFIED	264686, 264688, 264490, 18108370, 264909, 18108374, 265008, 264557, 264564, 18108351
1923	94323589 (3845, 3846)	Novel Protein sim. GBank gi|119110|sp|P03211|EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	264488, 264489, 22278995, 264094, 264259, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 264511, 264512, 265007, 264910, 265009, 264591, 264592, 264593, 264594, 264595, 264758, 264596, 264759, 265011, 265017, 265018, 265019, 55811150, 264681, 264762, 264448, 264764, 264288, 264369, 264766, 264767, 264686, 264687, 264768, 264769, 56181562, 264689, 21906766, 264691, 33657023, 264693, 65274620, 33657109, 18108370, 264628, 264629, 35696423, 264630, 264631, 264632, 264634, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264564, 264565, 264566, 264567
1924	87338925 (3847, 3848)	Novel Protein sim. GBank gi|3877655|emb|CAA96657| - (Z72511) possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL:D75164 comes from this gene; cDNA EST EMBL:C1...	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		29331826, 264906, 264908, 264595, 265017, 265018, 265019, 265021, 264691, 264693, 264637, 18108385, 264565
1925	87628338 (3849, 3850)	Novel Protein sim. GBank gi|4981903|gb|AAD36415.1|AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomalprot	22278995, 22278996, 22278997, 264259, 29331824, 66714117, 29146499, 264909, 52644045, 265008, 265009, 264758, 265011, 265017, 264605, 264448, 264288, 264692, 33657109, 18108374, 60170394
1926	88094739 (3851, 3852)	Novel Protein sim. GBank gi|2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	264905, 264906, 264907, 264910, 264593, 265018, 264760, 264764, 264288, 264692, 264693, 263978, 264631, 264634, 264637, 264563
1927	85654857 (3853, 3854)	Novel Protein sim. GBank gi|3043632|dbj|BAA25480| - (AB011126) KIAA0554 protein [Homo sapiens]			264689, 264631
1928	87799054 (3855, 3856)	Novel Protein sim. GBank gi|1665761|dbj|BAA13377| - (D87433) KIAA0246 [Homo sapiens]	Contains protein domain (PF00193) - Extracellular link domain	tnf	264489, 264259, 265017, 265021, 264692
1929	86997236 (3857, 3858)	Novel Protein sim. GBank gi|5001993|gb|AAD37247.1|AF13432 - (AF134321) chimeric AFGP/trypsinogen-like serine protease precursor [Dissostichus mawsoni]		UNCLASSIFIED	264508, 264591, 33657402, 265017, 264768, 264632, 264556, 264639

1930	87889128 (3859, 3860)	Novel Protein sim. GBank gi|1709230|sp|P52963|NBL4_MOUSE - NBL4 PROTEIN		phosphatase	35696286, 29331828, 264905, 264907, 264908, 264909, 264511, 264910, 264758, 264601, 265017, 265019, 264605, 264760, 264764, 264766, 264686, 264769, 265022, 35696423, 264638, 60432113
1931	87797279 (3861, 3862)	Novel Protein sim. GBank gi|404634 (U01840) - serine/threonine kinase [Mus musculus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264906, 264908, 60432229, 264758, 264764, 264288, 265020, 264692, 264634, 264637
1932	15030972 (3863, 3864)				264684, 264691, 264635
1933	11613668 (3865, 3866)			UNCLASSIFIED	264595
1934	84426360 (3867, 3868)	Novel Protein sim. GBank gi|4115748|dbj|BAA36494| - (AB022023) nonmuscle myosin heavy chain B [Bos taurus]		struct	56182575, 56182435, 264510, 264757, 264758, 55812038, 55811386, 265018, 55811150, 21906765, 264691, 264631, 264635, 264637
1935	87752511 (3869, 3870)			UNCLASSIFIED	264686, 265011, 264511, 264905, 18108351, 264564, 264681, 264259, 18108370, 264566, 264764, 264369, 264595
1936	95414338 (3871, 3872)	Novel Protein sim. GBank gi|4827040|ref|NP_005110.1|pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit			60432289, 265007, 265010, 265011, 265019, 33657109, 18108374
1937	94847141 (3873, 3874)	Novel Protein sim. GBank gi|543187|pir||S37771 - ankyrin, erythrocyte - mouse	Contains protein domain (PF00023) - Ank repeat	kinase	85658542, 21906767, 35695917, 60170615, 264693, 33657109
1938	87403277 (3875, 3876)	Novel Protein sim. GBank gi|4544431|gb|AAD22340.1|AC00695 - (AC006955) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00888) - Cullin family	collagen	264488, 29146498, 264905, 264559
1939	91004978 (3877, 3878)	Novel Protein sim. GBank gi|500858|dbj|BAA03210| - (D14168) 50kDa lectin [Bombyx mori]		UNCLASSIFIED	65274572, 22278999, 60432289, 56182435, 60433356, 265017, 21906765, 21906766, 21906768, 55811957, 27486264, 35696423, 60432113, 264564
1940	87348810 (3879, 3880)	Novel Protein sim. GBank gi|1946300|emb|CAA73132| - (Y12529) hypothetical protein [Silene latifolia]	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	264488, 29331822, 264448, 264683, 264288, 265020, 33657023, 264631
1941	94147177 (3881, 3882)	Novel Protein sim. GBank gi|4206386 (AF060570) - rig-1 protein [Mus musculus]		UNCLASSIFIED	56994075, 22278998, 264259, 29331824, 29331827, 264905, 265008, 33657084, 265017, 265018, 264288, 264687, 21906765, 21906766, 21906767, 265020, 52644150, 27486264, 83373044, 18108387, 60432113, 22279002, 264565
1942	87641870 (3883, 3884)	Novel Protein sim. GBank gi|4927204|gb|AAD33049.1|AF13391 - (AF133911) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	264488, 18108398, 29331825, 27486261, 264509, 18108370, 18108374, 264482
1943	94325298 (3885, 3886)	Novel Protein sim. GBank gi|3122952|sp|O15736|TIPD_DICDI - TIPD PROTEIN	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	22278998, 29331822, 29331827, 35696052, 264511, 265009, 264592, 60432229, 265017, 265018, 265019, 264684, 264692, 33657109, 65274791, 264636

1944	94232958 (3887, 3888)	Novel Protein sim. GBank gi|1799570|dbj|BAA13432| - (D87671) TIP120 [Rattus norvegicus]		UNCLASSIFIED	65274572, 22278994, 22278995, 22278996, 22278998, 22278999, 264259, 52645080, 29331824, 29331826, 29331827, 66712502, 56182435, 264512, 264910, 60170831, 60432229, 60433356, 33657402, 60433438, 264596, 33109954, 21906754, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264369, 264686, 264768, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 60170615, 264692, 33657023, 18108370, 18108374, 35696423, 35695855, 264634, 60170394, 264639, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264563
1945	87641872 (3889, 3890)	Novel Protein sim. GBank gi|4927204|gb|AAD33049.1|AF13391 - (AF133911) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	264488, 22278996, 264510, 264511, 18108351, 264683, 264486, 264567
1946	87443990 (3891, 3892)	Novel Protein sim. GBank gi|2498104|sp|Q27969|AD50_BOVIN - ADRENAL MEDULLA 50 KD PROTEIN		UNCLASSIFIED	60432289, 29331827, 35696052, 265007, 265008, 60433356, 60433438, 264369, 56181562, 21906767, 52644150, 264693, 27486264, 264637, 87168518, 264563
1947	86438862 (3893, 3894)	Novel Protein sim. GBank gi|3914801|sp|O54888|RPA2_RAT - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)		rnapolymerase	22278998, 264905, 264906, 264908, 264909, 264512, 264758, 264762, 264682, 264683, 264764, 264288, 264768, 264688, 21906768, 264693, 18108374, 35695855, 264635, 264637, 264638, 18108385, 22279002
1948	95199174 (3895, 3896)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		struct	264909, 60170831, 264591, 264594, 265010, 265011, 264764, 264369, 264689, 264631, 264638
1949	7640129 (3897, 3898)				264369
1950	87788531 (3899, 3900)	Novel Protein sim. GBank gi|3876766|emb|CAA93466.1| - (Z69637) predicted using Genefinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	Contains protein domain (PF00857) - Isochorismatase family	UNCLASSIFIED	264488, 264768, 264688, 264689, 264259, 29331822, 33657109, 29331828, 264103, 264509, 18108370, 35695855, 264510, 265008, 265009, 33657402, 18108385, 265018, 264563, 55811150, 18108351, 264369, 264288, 18108354
1951	86988253 (3901, 3902)	Novel Protein sim. GBank gi|2626753|dbj|BAA23424| - (AB008782) sulfate transporter [Arabidopsis thaliana]	Contains protein domain (PF00916) - Sulfate transporter family	transport	56182575, 22278997, 52645080, 29331824, 29331825, 29331827, 55812038, 52646317, 265018, 265019, 264369, 21906765, 21906767, 55811957, 265020, 265021, 33657023, 264693, 35695763, 56182323, 22279002
1952	87069775 (3903, 3904)	Novel Protein sim. GBank gi|4929633|gb|AAD34077.1|AF15184 - (AF151840) CGI-82 protein [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	264591, 264593, 264594, 264595, 264555, 264556, 264557, 264558, 264565

1953	20470371 (3905, 3906)	Novel Protein sim. GBank gi|1168715|sp|P31721|C1QB_RAT - COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264259, 264558
1954	91226025 (3907, 3908)	Novel Protein sim. GBank gi|4240271|dbj|BAA74914.1| - (AB020698) KIAA0891 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	264488, 263994, 18108394, 35696286, 22278998, 29331822, 66714117, 29331826, 29331827, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265008, 265007, 265008, 264910, 265009, 60170831, 60432229, 265011, 265017, 264603, 264604, 265019, 18108351, 264685, 264768, 264769, 35695917, 265020, 265021, 264691, 33657023, 264692, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 264630, 264635, 264636, 264555, 264556, 264638, 264557, 264639, 264558, 264559, 83373044, 18108385, 264563, 264564, 264566, 264486, 264567
1955	95308310 (3909, 3910)			UNCLASSIFIED	56182575, 56181686, 22278994, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331828, 29331827, 35696052, 264508, 29331830, 265008, 265009, 264591, 55812038, 87168474, 265017, 265018, 265019, 264448, 264766, 21906765, 21906768, 21906767, 55811957, 265020, 265021, 52645129, 33657109, 27486264, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 264635, 60431850, 264639, 83373044
1956	95092121 (3911, 3912)	Novel Protein sim. GBank gi|1665821|dbj|BAA13407| - (D87469) Similar to D.melanogaster cadherin-related tumor suppressor [Homo sapiens]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264488, 56182575, 22278996, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35698052, 29331828, 264508, 264906, 264908, 264909, 264511, 265007, 264910, 264591, 55812038, 265010, 265018, 18108351, 264768, 56181562, 264689, 21906768, 21906769, 265022, 264691, 264628, 18108374, 55810764, 55811576, 35695855, 264631, 264632, 264635, 264637, 264639, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002, 264563, 264564

1957	94326510 (3913, 3914)	Novel Protein sim. GBank gi|4589674|dbj|BAA76856.1| - (AB023229) KIAA1012 protein [Homo sapiens]		UNCLASSIFIED	52646842, 56182575, 22278997, 22278998, 22278999, 29331824, 66714117, 29331827, 29146498, 264593, 33657402, 33109954, 87168474, 265018, 264448, 264369, 264288, 264766, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264692, 65274620, 27486264, 33657349, 27486265, 35695855, 22279002, 264482
1958	95313902 (3915, 3916)	Novel Protein sim. GBank gi|4240227|dbj|BAA74892.1| - (AB020676) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	22278999, 264092, 264094, 264259, 60432049, 29331824, 56182181, 66714117, 264107, 264109, 264909, 264511, 60170831, 60432229, 21906754, 265010, 21906769, 35695917, 265022, 65274620, 263967, 263976, 35696423, 264631, 264632, 264634, 264635, 18108385, 22279000, 22279002
1959	85701470 (3917, 3918)	Novel Protein sim. GBank gi|2281983|emb|CAB10860| - (Z98056) hyypothetical protein [Schizosaccharomyces pombe]		ubiquitin	264593, 265019
1960	80308608 (3919, 3920)	Novel Protein sim. GBank gi|2274851|dbj|BAA21515| - (D64159) 3-7 gene product [Homo sapiens]		struct	264905, 264906, 264907, 264908, 264909, 265006, 265007, 264910, 264595, 265017, 264604, 265018, 18108351, 264764, 264369, 264766, 264768, 21906765, 18108368, 264629, 18108379, 264635, 264636, 264637, 264638, 264486
1961	16292607 (3921, 3922)				264635
1962	91008385 (3923, 3924)			UNCLASSIFIED	65274572, 264592, 264593, 265019, 264691
1963	90936017 (3925, 3926)	Novel Protein sim. GBank gi|3721653|dbj|BAA33581| - (AB012933) acyl-CoA synthetase 5 [Rattus norvegicus]		eph	65274572, 18108398, 35696286, 29331825, 60432289, 29331827, 264828, 265006, 265009, 60433356, 60433438, 21906754, 265020, 265021, 33657023, 33657109, 27486265, 35695855, 264555
1964	94317605 (3927, 3928)	Novel Protein sim. GBank gi|5262638|emb|CAB45757.1| - (AL080169) hypothetical protein [Homo sapiens]		cadherin	264488, 264092, 264259, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 265009, 264910, 264592, 264593, 264594, 264595, 264758, 264600, 264603, 264604, 264605, 264760, 264762, 264448, 264764, 264288, 264685, 264766, 264768, 264769, 21906766, 264691, 264692, 264693, 18108370, 264628, 264629, 18108374, 264630, 264631, 264634, 264636, 264637, 264638, 18108382, 83373044, 18108385, 264483, 264564, 264565, 264566, 264486, 264567
1965	94317445 (3929, 3930)	Novel Protein sim. GBank gi|4107017|dbj|BAA36294| - (AB001773) PEM-6 [Ciona savignyi]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264488, 264510, 264760, 264768, 264486

1966	94192058 (3931, 3932)	Novel Protein sim. GBank gi|4929707|gb|AAD34114.1|AF15187 - (AF151877) CGI-119 protein [Homo sapiens]	Contains protein domain (PF01027) - Uncharacterized protein family	glycoprotein	22278999, 264092, 264259, 29331826, 29331828, 29146498, 264595, 265011, 264448, 18108354, 264288, 264684, 264766, 264685, 264686, 265022, 264691, 264692, 18108370, 18108377, 264555, 18108381, 18108385, 264486, 264567
1967	87396123 (3933, 3934)	Novel Protein sim. GBank gi|2957270 (AF044576) - phospholipase C PLC210 [Caenorhabditis elegans]	Contains protein domain (PF00388) - Phosphatidylinositol-specific phospholipase C, X domain	esterase	29331824, 265010, 265017, 264288, 21906764, 263981, 56526486
1968	88095641 (3935, 3936)	Novel Protein sim. GBank gi|2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696286, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 265008, 264910, 265009, 264594, 264757, 264758, 264604, 264605, 264760, 264762, 264682, 264764, 264685, 264766, 264767, 264689, 264691, 264693, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 18108380, 264564, 264565, 264566, 264567
1969	84328529 (3937, 3938)	Novel Protein sim. GBank gi|2911274 (U20329) - spidroin 1 [Nephila clavipes]		UNCLASSIFIED	22278995, 22278996, 35696052, 264906, 264908, 18108351, 264482
1970	80596049 (3939, 3940)	Novel Protein sim. GBank gi|4050087 (AF109907) - S164 [Homo sapiens]		UNCLASSIFIED	264908, 264288, 264766, 264636
1971	94843914 (3941, 3942)	Novel Protein sim. GBank gi|134206|sp|P09593|SANT_PLAFV - S-ANTIGEN PROTEIN PRECURSOR		collagen	264488, 264489, 22278998, 264259, 60432049, 66714117, 29331826, 60432289, 29331827, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 264591, 264592, 60432229, 60433356, 264595, 264596, 264600, 264604, 264605, 264760, 18108351, 264448, 264764, 264288, 264766, 264768, 264769, 21906765, 33657023, 264692, 18108370, 264629, 35696423, 65274791, 35695855, 264632, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 60432113, 22279000, 264563, 264564, 264565, 264566, 264486
1972	87645444 (3943, 3944)	Novel Protein sim. GBank gi|4519623|dbj|BAA75671.1| - (AB017616) homologous to the yeast YGR163 gene [Mus musculus]	Contains protein domain (PF01462) - Leucine rich repeat N-terminal domain		22278999, 264259, 29331822, 56182181, 60432289, 29331827, 52644045, 264909, 265006, 264511, 265008, 52644296, 265018, 265019, 264761, 264689, 21906768, 21906769, 264691, 264693, 33657109, 33657182, 264556, 52644332, 264558, 60432113
1973	86395533 (3945, 3946)			UNCLASSIFIED	29331826, 264692, 35696423, 264631, 264555, 264556, 264557, 264558, 264559
1974	80396629 (3947, 3948)	Novel Protein sim. GBank gi|3309543 (AF036382) - MLL [Fugu rubripes]		UNCLASSIFIED	264682, 264764, 264563

1975	94316479 (3949, 3950)			UNCLASSIFIED	264488, 66714117, 29331826, 29331828, 56182435, 265006, 264757, 55812038, 265010, 265017, 264369, 55811957, 65274791, 35695855, 56182323, 60432113
1976	95358914 (3951, 3952)			UNCLASSIFIED	264259, 35696052, 265018, 265020, 265021, 33657109, 56526486
1977	94852664 (3953, 3954)	Novel Protein sim. GBank gi|2499528|sp|Q07782|NASU_RAT - SODIUM/SULFATE COTRANSPORTER (NA(+)/SULFATE COTRANSPORTER)		homeobox	264908, 264596, 265021, 264566
1978	87447645 (3955, 3956)	Novel Protein sim. GBank gi|103421|pir||A33471 - transcription factor NTF1 - fruit fly (Drosophila melanogaster) (fragment)		transcriptfactor	60170831, 264566
1979	87627709 (3957, 3958)	Novel Protein sim. GBank gi|2244815|emb|CAB10238.1| - (Z97336) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	29331826, 29146498, 264905, 264907, 265007, 265009, 265010, 265018, 264686, 18108359, 21906768, 35695917, 265020, 60170615, 264693, 18108368, 18108370, 264631, 264635, 264556, 264558, 18108384, 22279000, 264565
1980	86577059 (3959, 3960)	Novel Protein sim. GBank gi|4759290|ref|NP_004642.1|pUSP1 - Ubiquitin carboxyl-terminal hydrolase, X-linked		ubiquitin	264489
1981	87606974 (3961, 3962)	Novel Protein sim. GBank gi|4406693|gb|AAD20060| - (AF131849) Unknown [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331825, 29331828, 29146498, 29146499, 264107, 264906, 264910, 264595, 21906754, 265010, 265017, 265018, 265019, 264448, 264288, 21906767, 33657023, 27486264, 18108370, 18108374, 18108376, 264630, 264631, 264635, 18108385, 87168518, 22279000, 264482, 264564
1982	90995367 (3963, 3964)	Novel Protein sim. GBank gi|5689523|dbj|BAA83045.1| - (AB029016) KIAA1093 protein [Homo sapiens]			65274572, 29331825, 35696052, 33656970, 264909, 265008, 55811386, 264760, 264686, 264691, 27486264
1983	95098668 (3965, 3966)	Novel Protein sim. GBank gi|3417297 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	22278998, 35696286, 264259, 29331822, 20281099, 29331824, 60432289, 29331827, 264509, 264905, 264906, 264907, 66712502, 264908, 52644045, 264909, 264510, 264512, 264910, 265009, 264591, 264592, 60433356, 60433438, 264758, 265010, 264600, 264603, 264604, 264760, 264762, 264763, 264764, 264766, 264687, 264768, 264769, 21906765, 55811957, 35695917, 264690, 264692, 264693, 264628, 264629, 263978, 18108379, 35696423, 35695855, 20281071, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 83373044, 18108385, 22279000, 22279002

1984	85760989 (3967, 3968)	Novel Protein sim. GBank gi|2896695|emb|CAA17174.1| - (AL021897) fadD14 [Mycobacterium tuberculosis]		synthase	264688, 21906766, 55811957, 56994075, 265020, 265021, 22278999, 265022, 264259, 29331822, 33657182, 29146499, 264628, 18108370, 264908, 264629, 55811576, 35695855, 265006, 265007, 264591, 21906754, 33657084, 265010, 265017, 265019, 264288
1985	85636897 (3969, 3970)	Novel Protein sim. GBank gi|5712131|gb|AAD47379.1|AF12049 - (AF120499) DEM1 protein [Homo sapiens]		glycoprotein	264760, 264288, 263978, 55811576, 264637, 56182323, 18108385, 264564
1986	80200507 (3971, 3972)			UNCLASSIFIED	264488, 264629
1987	87011117 (3973, 3974)	Novel Protein sim. GBank gi|4868443|gb|AAD31319.1|AF14457 - (AF144573) Mx-interacting protein kinase PKM [Mesocricetus auratus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		22278999, 29331830, 265007, 265018, 21906768, 33657023, 264692, 264693, 18108377, 264635, 60170394, 22279002
1988	94122108 (3975, 3976)			UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264910, 264591, 264593, 264758, 264764, 264686, 264768, 265021, 264692, 264628, 264629, 35695855, 264630, 264635, 264636, 264637, 264638, 264639, 264483
1989	91225225 (3977, 3978)	Novel Protein sim. GBank gi|2801701 (AF042379) - spindle pole body protein spc97 homolog GCP2 [Homo sapiens]		tubulin	60432049, 60432289, 52644045, 56182435, 264112, 265007, 33657402, 52644229, 21906765, 21906768, 21906769, 55811957, 33657023, 263967, 33657109, 18108370, 22279000, 22279002
1990	85699888 (3979, 3980)	Novel Protein sim. GBank gi|5701727|dbj|BAA83074.1| - (AB024729) alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homologue [Homo sapiens]			264508, 264757, 264764, 18108381
1991	95353114 (3981, 3982)	Novel Protein sim. GBank gi|4240287|dbj|BAA74922.1| - (AB020706) KIAA0899 protein [Homo sapiens]	Contains protein domain (PF01602) - Adaptin N terminal region	glycoprotein	18108394, 56182575, 22278994, 35696286, 56994075, 22278997, 22278999, 29331822, 29331824, 29331825, 60432289, 29331828, 264508, 264906, 264907, 264908, 56182435, 264510, 265007, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264762, 18108351, 264763, 264683, 264369, 264288, 264685, 264766, 264687, 264769, 21906765, 21906768, 21906769, 55811957, 265020, 60431528, 263974, 18108379, 35695855, 264555, 264557, 264639, 83373044, 18108384, 87168518, 60432113, 22279000, 22279002, 264564, 264486
1992	95317232 (3983, 3984)	Novel Protein sim. GBank gi|2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struct	29331827, 264906, 264907, 264909, 265007, 264603, 264766, 264686, 264768, 21906768, 264628, 264635, 264636, 18108385, 56526486, 264566, 264567
1993	80054763 (3985, 3986)	Novel Protein sim. GBank gi|2565091 (U80761) - CTG26 alternate open reading frame [Homo sapiens]		UNCLASSIFIED	264592, 35696423

1994	94329114 (3987, 3988)	Novel Protein sim. GBank gi|5630077|gb|AAD45822.1|AC00601 - (AC006017) similar to ALR; similar to AAC51735 (PID:g2358287) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	mapolymerase	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 264908, 265006, 60432229, 33657402, 60433356, 264757, 60433438, 264758, 33109954, 265011, 265017, 265018, 265019, 264684, 264369, 264685, 264686, 264768, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 18108362, 264693, 65274620, 18108370, 264635, 264555, 264556, 264557, 56182323, 83373044, 56526486, 22279000, 22279002, 264564
1995	95414353 (3989, 3990)	Novel Protein sim. GBank gi|4827040|ref|NP_005110.1|pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit		UNCLASSIFIED	264488, 18108396, 22278994, 56994075, 22278998, 35696286, 22278997, 22278999, 264259, 29147620, 56182181, 29331824, 60432289, 29331826, 29331827, 35696052, 29146499, 264905, 264907, 66712502, 56182435, 265006, 265007, 265008, 265009, 60431735, 60433356, 33657402, 264595, 55812038, 33657084, 55811386, 85658542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 56181562, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 21906769, 29148629, 29148784, 265020, 265021, 264690, 18108361, 264693, 27486262, 27486264, 27486265, 18108370, 60431528, 18108374, 18108377, 35696423, 55811576, 65274791, 35695855, 264631, 264634, 264635, 264555, 264636, 60431850, 264557, 264558, 264559, 83373044, 20798451, 87168518, 264404, 60432113, 264567
1996	80254186 (3991, 3992)	Novel Protein sim. GBank gi|791146|emb|CAA60020| - (X86028) extensin-like protein [Vigna unguiculata]		UNCLASSIFIED	264564
1997	87028423 (3993, 3994)	Novel Protein sim. GBank gi|2642034 (AF034547) - protein phosphatase M130 myosin binding subunit [Ovis aries]	Contains protein domain (PF00023) - Ank repeat	phosphatase	264908, 264909, 264592, 264593
1998	85262704 (3995, 3996)	Novel Protein sim. GBank gi|4589634|dbj|BAA76839.1| - (AB023212) KIAA0995 protein [Homo sapiens]		UNCLASSIFIED	264113, 264685, 264555, 264567

1999	94324903 (3997, 3998)	Novel Protein sim. GBank gi|5225312|gb|AAD40846.1|AF07244 - (AF072441) calcineurin binding protein cabin 1 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	18108394, 18108397, 35696286, 60424269, 29331827, 29331828, 35696052, 265006, 264512, 55811386, 265010, 265018, 265019, 55811150, 18108351, 264763, 264682, 264369, 264685, 264686, 56181562, 265020, 264691, 33657023, 264693, 33657109, 27486264, 18108370, 18108379, 35695855, 264634, 264635, 264636, 264555, 264557, 56182323, 18108382, 264559, 83373044, 60432113, 22279000, 264563, 264564, 264566
2000	95413705 (3999, 4000)	Novel Protein sim. GBank gi|1723232|sp|Q10155|YATA_SCHPO - HYPOTHETICAL 90.6 KD PROTEIN C1D4.10 IN CHROMOSOME I		UNCLASSIFIED	52646365, 52646842, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331826, 29331827, 29331828, 35696052, 264106, 29331830, 52644045, 265007, 265008, 60170831, 264592, 264593, 33657402, 60433438, 21906754, 52644296, 265017, 265018, 265019, 264761, 264369, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 33657023, 65274620, 52645129, 27486261, 27486262, 27486264, 35695763, 35696423, 35695855, 264631, 52644332, 56182323, 60170394, 83373044, 56526486, 22279002, 264566, 264567
2001	95072534 (4001, 4002)	Novel Protein sim. GBank gi|107560|pir||B38637 - Ras inhibitor (clone JC265) - human (fragment)		UNCLASSIFIED	264769, 52644229, 65274572, 21906768, 22278996, 35696286, 35695917, 265020, 22278999, 264534, 264490, 264259, 264692, 60432289, 33657109, 35696052, 264508, 264509, 18108370, 60431528, 18108374, 35696423, 65274791, 35695855, 264510, 264511, 264512, 265009, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 60433438, 83373044, 264759, 18108385, 265011, 264600, 264601, 60432113, 264603, 264604, 264605, 264448, 264288, 264765
2002	80236368 (4003, 4004)	Novel Protein sim. GBank gi|729433|sp|P38657|ER60_BOVIN - PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (ERP60) (58 KD MICROSOMAL PROTEIN) (P58)	Contains protein domain (PF00085) - Thioredoxin	isomerase	264907, 265006, 264910, 264603, 264692, 264629, 18108374, 264556, 264557
2003	80074449 (4005, 4006)	Novel Protein sim. GBank gi|86388|pir||A27040 - neurofilament triplet M protein - chicken (fragment)		UNCLASSIFIED	264905, 264906, 264908, 264910, 264596, 265017, 18108351, 264692, 264629, 264634, 264565

2004	95317318 (4007, 4008)	Novel Protein sim. GBank gi|4884249|emb|CAB43230.1| - (AL049996) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	52645158, 52646842, 52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331824, 29331826, 29331827, 35696052, 29331828, 33656970, 29331830, 264908, 264592, 60433356, 33657402, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264763, 264683, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 18108374, 18108376, 18108377, 35696423, 35695855, 264631, 52644332, 264558, 18108385, 56526486, 87168518, 60432113, 264483
2005	87400864 (4009, 4010)	Novel Protein sim. GBank gi|3879501|emb|CAA87795| - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...		ubiquitin	264488, 264908
2006	95351177 (4011, 4012)	Novel Protein sim. GBank gi|4106673|emb|CAA22613| - (AL035064) queuine trna-ribosyltransferase [Schizosaccharomyces pombe]	Contains protein domain (PF01702) - Queuine tRNA-ribosyltransferase	UNCLASSIFIED	56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424269, 66714117, 35696052, 264906, 66712502, 264909, 264510, 60433356, 85658542, 265010, 265018, 265019, 264682, 264448, 264288, 264768, 29148627, 21906769, 29148784, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 55810764, 55811576, 35695855, 87168518, 60432113, 264563, 264482
2007	94325556 (4013, 4014)	Novel Protein sim. GBank gi|2662161|dbj|BAA23712| - (AB007900) HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	264488, 263994, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265007, 264910, 264592, 264595, 264758, 265011, 264760, 264762, 264764, 264766, 264685, 264767, 264768, 264769, 55811957, 35695917, 265020, 264691, 264693, 264628, 264629, 65274791, 35695855, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 264566
2008	85084428 (4015, 4016)	Novel Protein sim. GBank gi|1550783|emb|CAA69257| - (Y07960) homeodomain protein [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264909, 264768, 35695855

2009	85749240 (4017, 4018)	Novel Protein sim. GBank gi|3882305|dbj|BAA34512.1| - (AB018335) KIAA0792 protein [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 264910, 264591, 265017, 264681, 264683, 21906768, 264691, 33657182, 33657349, 264631, 87168518, 264404, 22279002, 264563
2010	95422458 (4019, 4020)	Novel Protein sim. GBank gi|5262629|emb|CAB45753.1| - (AL080164) hypothetical protein [Homo sapiens]	Contains protein domain (PF00057) - Low-density lipoprotein receptor domain class A	eph	52644507, 52645156, 52646365, 52646842, 18108397, 65274572, 22278994, 56994075, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264511, 265007, 264512, 265008, 265009, 60432229, 60433356, 21906754, 52646317, 33109954, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264685, 264687, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 264691, 264692, 33657023, 263967, 52645129, 35695763, 18108376, 35696423, 65274791, 35695855, 264631, 264634, 60431850, 264637, 264638, 52644332, 60170394, 18108385, 87168518, 22279002, 264564, 264565, 264566, 264567
2011	94328149 (4021, 4022)	Novel Protein sim. GBank gi|3347953 (AF076183) - cytosolic sorting protein PACS-1a [Rattus norvegicus]		UNCLASSIFIED	56182575, 56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29331828, 35696052, 264906, 66712502, 265006, 265007, 265008, 265010, 265011, 265017, 265019, 264681, 264448, 264683, 264369, 264288, 264685, 264766, 264687, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 65274620, 33657109, 264629, 264557, 264559, 83373044, 87168518, 60432113, 22279002
2012	87772137 (4023, 4024)	Novel Protein sim. GBank gi|1086678 (U41020) - coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBP-2 basic-helix-loop-helix-leucine zipper transcription factor [Caenorhabditis elegans]	Contains protein domain (PF00409) - Kinesin light chain repeat	UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29146498, 87168559, 265019, 264682, 264288, 264686, 21906764, 265020, 265022, 33657023, 264693, 33657109, 55811576, 264632, 264558, 56182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264567
2013	94843842 (4025, 4026)	Novel Protein sim. GBank gi|4507985|ref|NP_003427.1|pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	18108398, 264908, 265007, 265010, 265018, 265019, 264689, 21906767, 265020, 264692
2014	87347940 (4027, 4028)	Novel Protein sim. GBank gi|127720|sp|P20938|MYP0_HETFR - MYELIN P0 PROTEIN PRECURSOR		UNCLASSIFIED	264488, 29331826, 264907, 264636, 264555, 264639, 264558

2015	88094922 (4029, 4030)	Novel Protein sim. GBank gi|81286|pir||S22697 - extensin - Volvox carteri (fragment)		UNCLASSIFIED	56182575, 35696286, 264259, 35696052, 264508, 264906, 264907, 264510, 264512, 87168474, 265010, 264681, 264288, 264689, 264628, 35696423, 35695855, 264639, 264563, 264564
2016	85298641 (4031, 4032)	Novel Protein sim. GBank gi|285046|pir||S26413 - t-complex protein Tcp-10 - mouse		struct	264102, 264508, 264110, 265009, 33109954, 21906768, 265021, 33657109, 27486262, 263972, 18108374, 263976, 264555, 264564
2017	79464293 (4033, 4034)			UNCLASSIFIED	264685, 264636
2018	79637067 (4035, 4036)	Novel Protein sim. GBank gi|124735|sp|P18175|INVO_PIG - INVOLUCRIN			264693
2019	87787900 (4037, 4038)	Novel Protein sim. GBank gi|2143910|pir||S68216 - phosphatase-1 glycogen-binding (GL)-chain - rat		phosphatase	264107, 264110, 264112, 265017, 263976
2020	94674476 (4039, 4040)	Novel Protein sim. GBank gi|2078483 (U43200) - antifreeze glycopeptide AFGP polyprotein precursor [Boreogadus saida]		UNCLASSIFIED	264259, 264508, 264591, 265018, 264682, 264288, 264688, 22279002
2021	86718818 (4041, 4042)	Novel Protein sim. GBank gi|585084|sp|Q07803|EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)			56994075, 264593, 33109954, 21906754, 21906768, 33657023, 33657109, 27486261, 87168518
2022	95295665 (4043, 4044)	Novel Protein sim. GBank gi|4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]			264757, 264767, 60170615, 18108385
2023	87722976 (4045, 4046)	Novel Protein sim. GBank gi|5410230|gb|AAD42992.1|AF07334 - (AF073344) ubiquitin specific protease 3 [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	18108394, 22278999, 264259, 264905, 264906, 264908, 264595, 264762, 264769, 264634, 264636, 87168518, 60432113, 22279000, 264482, 264565
2024	87896443 (4047, 4048)				60433438, 265017, 264686, 264692, 264693, 264636
2025	87858863 (4049, 4050)	Novel Protein sim. GBank gi|4755188|gb|AAD29055.1|AC00701 - (AC007018) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF00637) - 7-fold repeat in Clathrin and VPS	UNCLASSIFIED	22278997, 264509, 264906, 264909, 55812038, 265017, 265021, 265022, 60170615, 264556
2026	94122114 (4051, 4052)	Novel Protein sim. GBank gi|1655699|emb|CAA69032| - (Y07752) pherophorin-S [Volvox carteri]		UNCLASSIFIED	56994075, 60432049, 264508, 66712502, 264112, 60170831, 87168559, 264288, 264688, 264689, 21906766, 33657109, 18108370, 264638, 18108385, 60432113, 22279000, 22279002, 264564, 264566, 264567
2027	80249001 (4053, 4054)			UNCLASSIFIED	263978, 264634, 264486

2028	94699884 (4055, 4056)	Novel Protein sim. GBank gi|1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	Contains protein domain (PF00632) - HECT-domain (ubiquitin-transferase).	ubiquitin	52644507, 52645156, 52646842, 56182575, 56994075, 35696286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 35696052, 264906, 264907, 264908, 29331830, 52644045, 56182435, 265006, 265009, 60432229, 33657402, 264595, 264757, 55812038, 21906754, 52646317, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 18108354, 264288, 264369, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 65274620, 33657109, 52645129, 18108368, 27486261, 27486262, 27486264, 27486265, 35695763, 264629, 55811576, 35696423, 35695855, 264635, 264636, 52644332, 264558, 83373044, 56526486, 22279000, 22279002, 264563
2029	95362032 (4057, 4058)	Novel Protein sim. GBank gi|3599940 (AF017368) - faciogenital dysplasia protein 2 [Mus musculus]	Contains protein domain (PF00621) - RhoGEF domain	UNCLASSIFIED	265009, 264595, 85658542, 264555, 264556, 264557, 264558, 264559, 83373044
2030	91213734 (4059, 4060)	Novel Protein sim. GBank gi|5630080|gb|AAD45825.1|AC00489 - (AC004890) similar to HUB1; similar to BAA24380 (PID:g2789430) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	18108394, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 264108, 66712502, 264828, 265009, 265018, 265019, 264681, 264682, 264684, 264685, 56181562, 264689, 21906769, 265022, 264692, 264693, 264628, 18108370, 18108374, 264634, 264636, 264556, 18108385, 87168518, 22279002, 264565
2031	80245281 (4061, 4062)				264591, 55811957, 18108365, 264557, 264558, 18108382, 18108384
2032	91232607 (4063, 4064)	Novel Protein sim. GBank gi|5689491|dbj|BAA83029.1| - (AB029000) KIAA1077 protein [Homo sapiens]	Contains protein domain (PF00884) - Sulfatase	hydrolase	65274572, 35696286, 29331824, 264908, 265009, 264593, 265018, 264288, 264686, 264769, 21906766, 21906767, 29148627, 264628, 35696423, 264634, 264556, 18108381, 60170394, 264559, 83373044, 18108385, 264482, 264484
2033	95000809 (4065, 4066)	Novel Protein sim. GBank gi|2494828|sp|Q64686|CAG7_RAT - ALPHA-N-ACETYLGALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (ST6GALNACIII) (STY)		synthase	56181562, 264628, 264632, 264555, 264556
2034	91232529 (4067, 4068)	Novel Protein sim. GBank gi|4826984|ref|NP_005147.1|pROD1 - UNKNOWN	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	22278996, 22278999, 264907, 29331830, 265008, 265018, 264681, 264682, 264684, 21906767, 21906768, 21906769, 33657109, 83373044, 56526486

2035	83553451 (4069, 4070)				264369, 264686, 265022, 56526486, 264567
2036	87115833 (4071, 4072)				29331827, 29331826, 264682, 264369, 29148627, 60432113
2037	94324833 (4073, 4074)	Novel Protein sim. GBank gi|2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331824, 60432289, 29331826, 29331828, 35696052, 264907, 29331830, 66712502, 56182435, 265008, 265009, 60170831, 264594, 55812038, 33109954, 21906754, 87168559, 265017, 265018, 265019, 264762, 264369, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 35695763, 35695855, 264632, 264634, 264636, 56182323, 83373044, 60432113, 22279000, 22279002, 264563
2038	95422384 (4075, 4076)	Novel Protein sim. GBank gi|3880625|emb|CAB07858| - (Z93785) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA .ST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL:D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	22278995, 22278996, 56994075, 264259, 29331824, 35696052, 264905, 264906, 52644045, 265007, 265009, 87168559, 265017, 18108351, 264448, 264369, 264766, 264767, 264686, 18108358, 21906765, 21906769, 52644150, 33657023, 264692, 18108362, 33657109, 27486262, 18108370, 18108374, 18108379, 35696423, 65274791, 264632, 264636, 18108383, 83373044, 18108385, 87168518, 22279000, 22279002, 264563, 264564, 264566
2039	85514626 (4077, 4078)	Novel Protein sim. GBank gi|2224653|dbj|BAA20813| - (AB002354) KIAA0356 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278997, 264259, 29331822, 264905, 264906, 264907, 264908, 264909, 264510, 265009, 264910, 264593, 264758, 265011, 265018, 264762, 264288, 264766, 264768, 264769, 21906766, 33657023, 264692, 264693, 33657109, 35696423, 264631, 264632, 264634, 264635, 264636, 264637, 264639, 87168518, 264486
2040	95308417 (4079, 4080)			UNCLASSIFIED	264592
2041	95071736 (4081, 4082)	Novel Protein sim. GBank gi|2500625|sp|P70700|RPA2_MOUSE - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135)		rnapolymerase	264488, 22278998, 35696052, 264905, 264907, 264908, 264910, 265018, 264605, 265019, 18108351, 264768, 264769, 21906766, 265021, 265022, 264692, 33657109, 264628, 264629, 35696423, 35695855, 264637, 264638, 264563, 264564, 264565, 264567

2042	95307447 (4083, 4084)	Novel Protein sim. GBank gi|4406590|gb|AAD20040| - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]	Contains protein domain (PF00568) - WH1 domain	UNCLASSIFIED	60424179, 35696286, 264259, 29331826, 35696052, 29331828, 264508, 264509, 264907, 264909, 264510, 264511, 265009, 264910, 264591, 60433356, 264595, 265017, 265019, 264681, 264764, 264369, 264765, 264684, 264288, 264766, 264686, 52644229, 264769, 21906765, 35695917, 264535, 52644150, 264691, 264692, 18108365, 27486261, 27486262, 27486265, 18108374, 35696423, 65274791, 35695855, 264555, 264558, 60170394, 18108385, 264404, 22279000, 22279002, 264482, 264563, 264564, 264566
2043	94328076 (4085, 4086)	Novel Protein sim. GBank gi|5052554|gb|AAD38607.1|AF145632) BcDNA.GH06032 [Drosophila melanogaster]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	264488, 52644507, 52646365, 56994075, 22278997, 22278999, 20281171, 264259, 29331822, 29331824, 66714117, 29331826, 29331828, 33656970, 29146498, 264509, 264908, 52644045, 56182435, 265006, 33657402, 21906754, 52644296, 87168559, 265017, 265018, 265019, 264681, 264288, 264766, 264685, 264686, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 33657349, 35695763, 18108374, 55811576, 35695855, 18108380, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264567
2044	87106927 (4087, 4088)	Novel Protein sim. GBank gi|2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	264093, 29331827, 264905, 66712502, 264592, 264689, 21906765, 21906769, 265020, 264692, 264482, 264566
2045	79635532 (4089, 4090)				264692
2046	87320849 (4091, 4092)	Novel Protein sim. GBank gi|4406698|gb|AAD20062| - (AF131852) Unknown [Homo sapiens]			264259, 264906, 264683, 22279002
2047	84578801 (4093, 4094)	Novel Protein sim. GBank gi|4101720 (AF006466) - lymphocyte specific formin related protein [Mus musculus]			22278999, 29147620, 29331824, 29146498, 264508, 265007, 265008, 265019, 264605, 264681, 29148627, 29148629, 265021, 33657023, 18108365, 33657109, 33657182, 18108377, 264556, 264638, 264559, 18108388
2048	84606378 (4095, 4096)			UNCLASSIFIED	264909
2049	88094690 (4097, 4098)	Novel Protein sim. GBank gi|4589656|dbj|BAA76850.1| - (AB023223) KIAA1006 protein [Homo sapiens]		UNCLASSIFIED	264488, 264259, 29331824, 29331828, 35696052, 264906, 264907, 264908, 264909, 264910, 264603, 264763, 21906767, 21906768, 264829, 264634, 264637, 22279002, 264564, 264585, 264566, 264567

2050	79633835 (4099, 4100)			UNCLASSIFIED	264693
2051	87780168 (4101, 4102)			UNCLASSIFIED	264488, 264259, 264509, 264906, 264907, 264769, 18108374, 35696423, 264563, 264566, 264486
2052	88096393 (4103, 4104)	Novel Protein sim. GBank gi|4529889|gb|AAD21812.1| - (AF134726) G9A [Homo sapiens]	Contains protein domain (PF00856) - SET domain	kinase	264488, 263994, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264369, 264766, 264686, 264768, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264556, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264486, 264567, 264488, 263994, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264369, 264766, 264686, 264768, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264556, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264486, 264567
2053	87763078 (4105, 4106)	Novel Protein sim. GBank gi|2995449|emb|CAA75113| - (Y14848) midline 1 protein [Mus musculus]		UNCLASSIFIED	22278996, 22278997, 264259, 29331822, 264102, 264508, 35695917, 263972, 264482
2054	95358937 (4107, 4108)	Novel Protein sim. GBank gi|3876326|emb|CAB02090| - (Z79754) similar to C2 domain [Caenorhabditis elegans]	Contains protein domain (PF00168) - C2 domain		60424179, 264094, 264259, 29331825, 60424269, 264906, 60432229, 60433356, 87168559, 265019, 264760, 264288, 264686, 21906769, 33657023, 264693, 55810764, 55811576, 264635, 56182323, 60432113
2055	88259449 (4109, 4110)	Novel Protein sim. GBank gi|5353746|gb|AAD42226.1|AF15913 - (AF159133) SIR2-like protein [Oryza sativa subsp. indica]		UNCLASSIFIED	264488, 29331826, 60432289, 29331828, 60433356, 265019, 264683, 264684, 265021, 33657109, 18108374, 264637, 18108385, 87168518, 60432113, 22279000, 264564

2056	88177396 (4111, 4112)	Novel Protein sim. GBank gi|4826960|ref|NP_005042.1|pQARS - glutamine-tRNA synthetase	Contains protein domain (PF00749) - tRNA synthetases class I (E and Q)	synthase	264488, 52645156, 56182575, 22278994, 35696286, 56994075, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 60432289, 29331827, 29331828, 33656970, 264104, 264906, 264908, 265006, 265008, 60170831, 264591, 60432229, 60433438, 18108348, 21906754, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 264760, 18108351, 264681, 264682, 264448, 264683, 264369, 264288, 264685, 264687, 264688, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 265022, 33657023, 18108362, 33657109, 18108368, 33657182, 27486261, 27486264, 27486265, 33657349, 264628, 18108370, 264629, 18108374, 18108377, 18108379, 35696423, 55811576, 20281152, 264636, 264952, 18108385, 18108388, 87168518, 264482, 264565, 264566, 264567
2057	87877905 (4113, 4114)	Novel Protein sim. GBank gi|728850|sp|P08640|AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		UNCLASSIFIED	52646842, 52646365, 56182575, 35696286, 22278996, 22278997, 22278998, 264093, 52645080, 35696052, 29331828, 33656970, 265009, 52646317, 55811386, 52644296, 52644229, 21906769, 35695917, 265021, 60170615, 52644150, 33657109, 33657182, 27486261, 27486262, 35695763, 35696423, 35695855, 52644332
2058	86276896 (4115, 4116)				265007, 265008, 264591
2059	79866684 (4117, 4118)	Novel Protein sim. GBank gi|119714|sp|P13983|EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	29331825, 264682, 264686, 264691, 264693, 22279002
2060	83050800 (4119, 4120)	Novel Protein sim. GBank gi|2811122 (U87318) - NaDC-2 [Xenopus laevis]		UNCLASSIFIED	56182575, 29331824, 29331826, 264910, 55811957, 18108370, 55811576

2061	95362204 (4121, 4122)	Novel Protein sim. GBank gi|2496947|sp|Q09298|YQO9_CAEEL - HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29331828, 264906, 66712502, 29331830, 264908, 264909, 264112, 264511, 265007, 265009, 264910, 264591, 33657402, 21906754, 85658542, 265017, 265019, 264448, 264683, 264288, 264684, 264369, 264686, 264687, 18108358, 264689, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 33657109, 20281149, 18108379, 35695855, 264634, 264556, 264557, 264558, 18108382, 264559, 83373044, 18108384, 56526486, 60432113
2062	87028440 (4123, 4124)	Novel Protein sim. GBank gi|4502091|ref|NP_001139.1|pANK2 - ankyrin 2, neuronal	Contains protein domain (PF00023) - Ank repeat	struct	264905, 264628, 264907, 264629, 264908, 264909, 18108374, 263978, 35695855, 264512, 264635, 60431850, 264636, 264760, 264563, 18108351, 264762, 264565, 264764, 264487, 264766
2063	87601272 (4125, 4126)	Novel Protein sim. GBank gi|4589562|dbj|BAA76803.1| - (AB023178) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	oncogene	22278994, 22278999, 264259, 29331827, 264906, 264909, 52644045, 264686, 21906767, 55811957, 264692, 18108365, 263972, 55811576, 18108384, 22279002, 264482, 264563, 264564, 264484
2064	95317253 (4127, 4128)	Novel Protein sim. GBank gi|1754515|dbj|BAA13413.1| - (D87515) aminopeptidase-B [Rattus norvegicus]		hydrolase	264488, 52646365, 56994075, 35696286, 22278997, 22278998, 264259, 29331826, 60432289, 29331827, 29331828, 35696052, 264509, 265007, 265008, 60432229, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264761, 18108351, 264682, 264369, 264288, 52644229, 21906765, 21906767, 21906768, 35695917, 33657109, 18108368, 18108374, 35696423, 35695855, 52644332, 264559, 60432113, 22279000, 22279002, 264566, 264486
2065	95092238 (4129, 4130)	Novel Protein sim. GBank gi|2507144|sp|Q04205|TENS_CHICK - TENSIN		kinase	264569, 18108394, 56182181, 60432289, 29331826, 264905, 264906, 264908, 60431735, 60433356, 55811386, 85658542, 265018, 55811150, 264681, 264766, 264692, 60431528, 263974, 55810764, 35695855, 264631, 264634, 264635, 60431850, 264557, 83373044, 18108388, 22279000, 22279002
2066	85793402 (4131, 4132)	Novel Protein sim. GBank gi|160171 (M58295) - circumsporozoite protein [Plasmodium yoelii]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	56182575, 264259, 264906, 264764, 264288, 56182323, 264567

2067	95303892 (4133, 4134)				35696286, 22278997, 22278998, 60432049, 264259, 60432289, 60433438, 264682, 264448, 264369, 264288, 18108355, 21906765, 21906768, 265022, 33657109, 35696423, 35695855, 264558, 264404, 264563, 264486
2068	84344754 (4135, 4136)			UNCLASSIFIED	264687
2069	94319177 (4137, 4138)	Novel Protein sim. GBank gi|3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	60424179, 56182575, 22278995, 22278996, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 33656970, 264509, 264905, 56182435, 265009, 60433356, 87168559, 265017, 265018, 264604, 265019, 264448, 264764, 264766, 21906765, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 33657109, 263976, 264555, 264557, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002
2070	85791380 (4139, 4140)	Novel Protein sim. GBank gi|5712131|gb|AAD47379.1|AF12049 - (AF120499) DEM1 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264905, 264628, 264908, 264638
2071	86946116 (4141, 4142)	Novel Protein sim. GBank gi|3551531|dbj|BAA33016| - (AB017437) avena [Gallus gallus]	Contains protein domain (PF00568) - WH1 domain		18108398, 265006, 265007, 265008, 265009, 264594, 265010, 265011, 18108351, 18108354, 18108364, 18108365, 18108368, 264634, 18108381, 18108385, 18108388, 18108391
2072	91718429 (4143, 4144)		Contains protein domain (PF00184) - Neurohypophysial hormones, C-terminal Domain		22278995, 35696286, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 265008, 33657402, 21906754, 265011, 265019, 18108351, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264690, 264692, 35696423, 264555, 264556, 264558, 22279000
2073	27925664 (4145, 4146)	Novel Protein sim. GBank gi|1504026|dbj|BAA13212| - (D86976) similar to C.elegans protein (Z37093) [Homo sapiens]		UNCLASSIFIED	264556
2074	94324767 (4147, 4148)	Novel Protein sim. GBank gi|4240317|dbj|BAA74937.1| - (AB020721) KIAA0914 protein [Homo sapiens]			29331822, 264909, 264511, 265009, 264594, 264595, 265010, 265011, 265017, 265018, 265019, 264448, 264683, 265020, 265021, 18108370, 264632, 83373044, 264567

2075	94314886 (4149, 4150)	Novel Protein sim. GBank gi|5138930|gb|AAD40382.1| - (AF093680) transcription factor IIB [Homo sapiens]			18108394, 22278994, 22278996, 35696286, 22278998, 22278999, 264259, 29331822, 29331825, 29331827, 35696052, 29331828, 264905, 264907, 264908, 264510, 265007, 264910, 265009, 33657084, 264760, 264448, 264288, 264766, 264767, 264689, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 33657023, 27486262, 27486265, 35696423, 35695855, 264631, 264634, 264639, 87168518, 22279002, 264563, 264488, 18108391
2076	87594118 (4151, 4152)				264259, 29331826, 264508, 264908, 264510, 265007, 265011, 264288, 264637, 18108385
2077	11389877 (4153, 4154)			UNCLASSIFIED	264592
2078	87539364 (4155, 4156)	Novel Protein sim. GBank gi|4220590|dbj|BAA74579| - (D87908) nuclear protein np95 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	ubiquitin	29331825, 265017, 265018, 264288, 265020, 265021, 264634, 56526486
2079	88095916 (4157, 4158)	Novel Protein sim. GBank gi|4240255|dbj|BAA74906.1| - (AB020690) KIAA0883 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	264768, 22278997, 265021, 264690, 264259, 264692, 29331822, 264693, 29331824, 29331828, 264508, 264509, 264906, 264907, 264628, 20281069, 264909, 265007, 265009, 264632, 264636, 264591, 264592, 264639, 264758, 264759, 33109954, 264604, 265018, 265019, 22279002, 264563, 264564, 264448, 264684, 264567, 264685
2080	94136689 (4159, 4160)	Novel Protein sim. GBank gi|2408021|emb|CAB16219.1| - (Z99162) putative vacuolar protein [Schizosaccharomyces pombe]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	56182575, 264092, 29331824, 29331826, 29331830, 265017, 265018, 265020, 83373044
2081	94847186 (4161, 4162)	Novel Protein sim. GBank gi|5524734|gb|AAD44360.1|AF16635 - (AF166350) ST7 protein [Homo sapiens]	Contains protein domain (PF00431) - CUB domain	eph	22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 33657402, 85658542, 265011, 265018, 265019, 21906767, 21906768, 264693, 18108385, 22279000, 22279002
2082	87628629 (4163, 4164)	Novel Protein sim. GBank gi|3880558|emb|CAA94234| - (Z70271) predicted using Genefinder; similar to collagen; cDNA EST yk308e7.3 comes from this gene; cDNA EST yk308e7.5 comes from this gene; cDNA EST yk385a8.3 comes from this gene; cDNA EST yk385a8.5 comes from this gene [Caeno...		collagen	264907, 265019
2083	94141000 (4165, 4166)	Novel Protein sim. GBank gi|2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	56182575, 22278996, 22278997, 264259, 29331822, 29331825, 264509, 264112, 265009, 264593, 21906754, 265018, 265019, 264448, 264288, 264685, 21906769, 265020, 265022, 264691, 18108370, 85274791, 264631, 264555, 264563
2084	95199298 (4167, 4168)	Novel Protein sim. GBank gi|728836|sp|P39193|ALU6_HUMAN - !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!		UNCLASSIFIED	265018, 264763, 264683, 264691

2085	94989476 (4169, 4170)	Novel Protein sim. GBank gi|1655699|emb|CAA69032| - (Y07752) pherophorin-S [Volvox carteri]		UNCLASSIFIED	56182575, 60432289, 264908, 56182435, 87168474, 264763, 264369, 264686, 264693, 18108370, 56182323
2086	91234404 (4171, 4172)	Novel Protein sim. GBank gi|3875032|emb|CAA88936| - (Z49125) similarity to Trichostrongylus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D37644 comes from this gene; cDNA EST EMBL:D36149 come...		UNCLASSIFIED	35696286, 264259, 35696052, 264906, 264907, 264908, 264909, 264910, 264759, 264604, 264762, 264768, 264769, 35695917, 263978, 35696423, 35695855, 264632, 264634, 264637, 264638, 264639, 56182323, 18108385, 264482, 264486
2087	21436337 (4173, 4174)			UNCLASSIFIED	264489
2088	94111527 (4175, 4176)	Novel Protein sim. GBank gi|3880930|emb|CAA16334.1| - (AL021481) similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T0080...			264488, 22278994, 35696286, 22278996, 29331827, 35696052, 33657402, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264448, 264683, 264369, 264685, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35696423, 35695855, 83373044, 87168518, 22279000, 264567
2089	95422801 (4177, 4178)	Novel Protein sim. GBank gi|4758118|ref|NP_004623.1|pDAP3 - Death associated protein 3		cadherin	18108392, 264488, 52644507, 18108394, 18108397, 52646842, 18108398, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 264093, 264094, 60432049, 264259, 29331822, 20281099, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29146498, 29146499, 264102, 264106, 264107, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 66712502, 264828, 52644045, 264909, 56182435, 264110, 264112, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264592, 264593, 60433356, 33657402, 60433438, 264595, 55812038, 264758, 21906754, 33657084, 55811386, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 55811150, 264762, 18108351, 264682, 264448, 264763, 264764, 264683, 264369, 18108354, 264288, 264685, 264766, 264686, 264687, 264768, 52644229, 264688, 18108358, 56181562, 264769, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 55811957, 29148629, 29148784, 35695917, 265020, 265021, 265022, 60170615, 264690,

2090	88222470 (4179, 4180)				22278995, 22278998, 22278999, 264259, 29331826, 35696052, 264910, 33657402, 60433438, 33109954, 87168474, 87168559, 265018, 265019, 264681, 264684, 264686, 264687, 264688, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265022, 60170615, 33657023, 35696423, 35695855, 264952, 18108387, 22279000
2091	95309161 (4181, 4182)	Novel Protein sim. GBank gi|4580997|gb|AAD24571.1|AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	263994, 264905, 264908, 264511, 264512, 265008, 264910, 55811386, 264288, 264768, 56181562, 21906765, 21906768, 21906769, 265022, 264628, 264563, 264567
2092	88223605 (4183, 4184)			homeobox	22278997, 22278999, 66712502, 87168559, 264683, 265021, 264486
2093	87406073 (4185, 4186)	Novel Protein sim. GBank gi|2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264905, 264906, 264907, 264908, 264510, 265006, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2094	91230929 (4187, 4188)	Novel Protein sim. GBank gi|4929551|gb|AAD34036.1|AF15179 - (AF151799) CGI-40 protein [Homo sapiens]		MHC	35696286, 265017, 265018, 265019, 18108388
2095	95351526 (4189, 4190)	Novel Protein sim. GBank gi|1363238|pir||A57284 - spermatid perinuclear RNA-binding protein Spnr - mouse	Contains protein domain (PF00035) - Double-stranded RNA binding motif	dna_rna_bind	35696286, 52644045, 265006, 265007, 265008, 87168559, 18108351, 21906769, 29148784, 265020, 33657023, 27486262, 18108374, 18108388
2096	94119760 (4191, 4192)	Novel Protein sim. GBank gi|3834423 (AF070689) - cytoplasmic dynein intermediate chain isoform DIC1a [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase_associated	264488, 264489, 65274572, 56182575, 22278996, 22278997, 22278999, 264259, 60432289, 29331826, 35696052, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 52644045, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264592, 60433356, 60433438, 264758, 264596, 55812038, 21906754, 264601, 264602, 264605, 264762, 264681, 18108351, 264764, 264683, 264288, 264687, 264768, 264769, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 52644150, 264691, 264692, 33657023, 264693, 27486261, 35695763, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264637, 263981, 264638, 264639, 264563, 264483, 264565, 264566, 264486, 264567

2097	95322772 (4193, 4194)	Novel Protein sim. GBank gi|5174501|ref|NP_006051.1|pLYF1 - zinc finger protein, subfamily 1A, 1 (Ikaros)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	65274572, 264511, 265010, 264600, 265017, 264448, 264288, 265021, 60170615, 264692, 33657109, 18108370, 264636, 264483
2098	87780340 (4195, 4196)	Novel Protein sim. GBank gi|4758208|ref|NP_004081.1|pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	56994075, 264259, 264288, 265020, 264563
2099	95412927 (4197, 4198)	Novel Protein sim. GBank gi|2695659 (AF026954) - pyruvate dehydrogenase phosphatase regulatory subunit precursor; PDPr [Bos taurus]		phosphatase	65274572, 264905, 65274444, 264691, 264636, 264555
2100	95332656 (4199, 4200)	Novel Protein sim. GBank gi|3881189|emb|CAB16514| - (Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...	Contains protein domain (PF00025) - ADP-ribosylation factor family	nucl_recpt	56182575, 22278995, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 29146498, 264909, 265008, 265009, 264910, 264591, 60432229, 60433356, 33657402, 264758, 21906754, 85658542, 87168474, 265017, 265018, 265019, 264681, 18108351, 264762, 264448, 264369, 264288, 18108355, 264686, 21906765, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108374, 35696423, 264558, 83373044, 87168518, 60432113, 22279000, 22279002
2101	87762604 (4201, 4202)	Novel Protein sim. GBank gi|4589468|dbj|BAA76761.1| - (AB012808) mBOCT [Mus musculus]		UNCLASSIFIED	264091, 29331824, 264105, 265007, 265010, 18108380
2102	87770461 (4203, 4204)	Novel Protein sim. GBank gi|3874149|emb|CAA97423.1| - (Z73103) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264489, 35696286, 264259, 35696052, 264508, 264905, 264907, 264908, 264909, 264511, 264512, 264591, 264593, 60433356, 264758, 264601, 264605, 264760, 18108351, 264448, 264764, 264288, 264767, 264768, 21906769, 35695917, 18108374, 264634, 264555, 264559, 264563, 264482, 264486
2103	95413576 (4205, 4206)	Novel Protein sim. GBank gi|4240159|dbj|BAA74858.1| - (AB020642) KIAA0835 protein [Homo sapiens]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcriptfactor	65274572, 56994075, 22278999, 264259, 29331824, 29331825, 35696052, 29331828, 66712502, 265009, 60170831, 264595, 33109954, 85658542, 87168559, 265017, 265019, 264448, 21906765, 21906768, 265022, 33657023, 27486262, 33657349, 35695763, 60431528, 18108374, 55811576, 56182323, 18108387, 87168518, 60432113, 264584
2104	85776161 (4207, 4208)			UNCLASSIFIED	264592, 264604, 22279000

2105	94848080 (4209, 4210)	Novel Protein sim. GBank gi|1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8....		UNCLASSIFIED	264488, 56182575, 22278994, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264508, 264905, 264509, 264907, 29331830, 52644045, 264510, 264511, 265007, 264512, 265009, 60170831, 60432229, 33657402, 60433356, 264595, 60433438, 264758, 33657084, 87168474, 265010, 87168559, 265017, 265018, 265019, 264762, 18108351, 264684, 18108354, 264288, 264686, 52644229, 18108359, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 60170615, 52644150, 264692, 33657023, 264693, 33657109, 60431528, 18108374, 65274791, 35695855, 264635, 60170394, 264639, 264558, 18108385, 18108387, 56526486, 87168518, 60432113, 264564, 264566, 264567
2106	83365475 (4211, 4212)				265006, 265019
2107	79822662 (4213, 4214)	Novel Protein sim. GBank gi|3881524|emb|CAA93883| - (Z70038) ZK1067.4 [Caenorhabditis elegans]			264906, 264639
2108	94233976 (4215, 4216)	Novel Protein sim. GBank gi|3176689 (AC003671) - Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb|Z35927 from S. cerevisiae. [Arabidopsis thaliana]		UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264758, 265011, 264600, 264601, 264764, 264766, 264767, 264768, 264769, 264693, 264629, 35695855, 264632, 264634, 264635, 264638, 264639, 83373044, 264486
2109	80478719 (4217, 4218)			UNCLASSIFIED	18108348, 264769, 18108370, 18108374, 264555, 264556, 264557, 264558
2110	87729075 (4219, 4220)	Novel Protein sim. GBank gi|481043|pir||S37671 - bat2 protein - human		UNCLASSIFIED	264564
2111	87818419 (4221, 4222)			UNCLASSIFIED	264766, 35695917, 264630, 264567, 264486
2112	87293783 (4223, 4224)	Novel Protein sim. GBank gi|2143639|pir||I56542 - calmodulin-binding protein - rat	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	struct	264508, 264906, 264591, 264682, 22279002
2113	78941388 (4225, 4226)	Novel Protein sim. GBank gi|4426629|gb|AAD20459| - (AF100960) protocadherin [Rattus norvegicus]	Contains protein domain (PF00028) - Cadherin domain	cadherin	265008
2114	87889342 (4227, 4228)	Novel Protein sim. GBank gi|3327184|dbj|BAA31660| - (AB014585) KIAA0685 protein [Homo sapiens]			66714117, 29331826, 29331827, 60433438, 55812038, 265017, 265019, 264689, 21906769, 55811957, 265020, 265021, 33657109, 60170394, 264558
2115	90993785 (4229, 4230)	Novel Protein sim. GBank gi|4757890|ref|NP_004328.1|pC8OR - chromosome 8 open reading frame 1		UNCLASSIFIED	65274572, 264689, 264691, 264692, 60432113

2116	88259387 (4231, 4232)	Novel Protein sim. GBank gi|2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	35696286, 22278999, 56182181, 29331824, 29331825, 29331827, 35696052, 264907, 56182435, 265008, 264591, 55812038, 55811386, 87168559, 264288, 264369, 21906769, 29148629, 33657023, 35695763, 55811576, 35696423, 18108385
2117	87788904 (4233, 4234)	Novel Protein sim. GBank gi|2330021 (AF019250) - kinesin-related protein; KRP; Costal2 [Drosophila melanogaster]		struct	29331824, 264511, 265009, 33109954, 265017, 265018, 264288, 264689, 265020, 264692, 56526486, 264482
2118	87078894 (4235, 4236)	Novel Protein sim. GBank gi|1079307|pir||B56573 - nuclear pore complex glycoprotein p62 - African clawed frog		glycoprotein	264259, 264905, 264907, 264908, 264510, 264511, 265009, 264910, 265010, 264602, 264288, 264768, 264693, 263967, 263972, 264638, 264559
2119	86999317 (4237, 4238)	Novel Protein sim. GBank gi|4321407|gb|AAD15748| - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]		UNCLASSIFIED	264693, 18108385
2120	87789395 (4239, 4240)	Novel Protein sim. GBank gi|4885527|ref|NP_005480.1|pNSP3 - novel SH2-containing protein 3	Contains protein domain (PF00017) - Src homology domain 2	eph	264091, 264259, 29331826, 29331828, 265017, 264604, 264288, 264685, 265020, 264691, 18108370, 55810764, 264555, 264636, 60432113
2121	80021375 (4241, 4242)	Novel Protein sim. GBank gi|4757728|ref|NP_004886.1|pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	264601, 264766, 263978
2122	91230931 (4243, 4244)	Novel Protein sim. GBank gi|4929551|gb|AAD34036.1|AF15179 - (AF151799) CGI-40 protein [Homo sapiens]			18108394, 56182575, 22278997, 29331822, 29331824, 29331825, 29331826, 29331828, 264907, 56182435, 265007, 264910, 265010, 265018, 264686, 265020, 55811578, 264555, 264637, 18108382, 83373044, 18108383, 18108384, 56526486, 264565, 264567
2123	86787998 (4245, 4246)	Novel Protein sim. GBank gi|2224551|dbj|BAA20764| - (AB002303) KIAA0305 [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	struct	18108396, 264757, 265011, 18108351, 264691, 264634, 18108385
2124	83005951 (4247, 4248)	Novel Protein sim. GBank gi|5689455|dbj|BAA83011.1| - (AB028982) KIAA1059 protein [Homo sapiens]	Contains protein domain (PF00801) - PKD domain	transport	29331822, 264906, 264907, 264591, 264639, 264563
2125	95354041 (4249, 4250)	Novel Protein sim. GBank gi|728831|sp|P39188|ALU1_HUMAN - !!!! ALU SUBFAMILY J WARNING ENTRY !!!!		UNCLASSIFIED	264259, 264509, 264907, 264511, 85658542, 264763, 21906765, 35695917, 264636, 264486
2126	95084231 (4251, 4252)	Novel Protein sim. GBank gi|4539264|emb|CAB39853.1| - (AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	264488, 264489, 29331827, 35696052, 264905, 264509, 264908, 264909, 264510, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264598, 264758, 264601, 264603, 265018, 264604, 264605, 264760, 264681, 264762, 264683, 264764, 264684, 264288, 264685, 264689, 60170615, 33657023, 33657109, 55810764, 264635, 264636, 264637, 264638, 264639, 83373044, 264564, 264566

2127	81118652 (4253, 4254)	Novel Protein sim. GBank gi|4868435|gb|AAD31315.1|AF14323 - (AF143236) apoptosis related protein APR-2 [Homo sapiens]			35696286, 29331826, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265009, 264910, 264758, 265011, 264600, 264601, 264604, 264762, 264763, 264766, 264687, 264768, 264769, 264689, 35695917, 264690, 264691, 264692, 264693, 264629, 18108374, 35695855, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264567
2128	87414262 (4255, 4256)				56182575, 35696286, 56182181, 29331824, 60432289, 35696052, 264905, 264907, 66712502, 264908, 264909, 264510, 264512, 265009, 264910, 264591, 55812038, 265018, 264764, 264288, 264369, 264687, 264768, 55811957, 264692, 18108368, 264628, 264632, 264634, 264635, 264637, 56182323, 264639, 18108384, 18108388, 264563, 264567
2129	95102089 (4257, 4258)			UNCLASSIFIED	66714117, 264828, 264595, 55812038, 55811150, 55811957, 264693, 18108374, 263978, 65274791, 18108381, 83373044, 22279000
2130	95417144 (4259, 4260)	Novel Protein sim. GBank gi|2649255 (AE001012) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	263981
2131	85723065 (4261, 4262)	Novel Protein sim. GBank gi|1086886 (U41276) - Similar to potassium channel protein. [Caenorhabditis elegans]	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	potassium_channel	35696052, 264909, 264768, 35695917
2132	95361096 (4263, 4264)	Novel Protein sim. GBank gi|5689373|dbj|BAA82973.1| - (AB028944) KIAA1021 protein [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated	264488, 22278999, 264259, 29331827, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264910, 264591, 264592, 264595, 264758, 21906754, 33109954, 87168474, 265011, 264600, 264601, 264605, 265019, 264760, 18108351, 264681, 264762, 264764, 264288, 264684, 264766, 264686, 264687, 264768, 264769, 264688, 21906769, 264690, 52644150, 264691, 264693, 18108370, 264628, 264629, 18108372, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264636, 264555, 264637, 18108380, 264639, 264558, 56182323, 56526486, 264564, 264565, 264566, 264567

2133	95351539 (4265, 4266)	Novel Protein sim. GBank gi|4220489 (AC006069) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60424179, 52646365, 52646842, 56994075, 35696286, 22278997, 22278998, 60432049, 56182181, 66714117, 60424269, 29331826, 29331828, 35696052, 264905, 264906, 264907, 66712502, 29331830, 56182435, 265006, 264512, 265008, 60431735, 60433358, 33657402, 55812038, 33109954, 21906754, 55811386, 265010, 264603, 265017, 265018, 265019, 55811150, 18108351, 264682, 264369, 264288, 52644229, 56181562, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 33657023, 33657109, 60431528, 18108374, 35696423, 65274791, 35695855, 264634, 60431850, 18108380, 56182323, 83373044, 18108385, 18108387, 60432113, 22279002, 264563, 264566
2134	95412697 (4267, 4268)	Novel Protein sim. GBank gi|3875351|emb|CAB09415| - (Z96047) DY3.6 [Caenorhabditis elegans]			56181686, 35696286, 21906754, 55811386, 265011, 265017, 18108351, 264765, 264766, 264688, 21906768, 35695917, 265020, 33657023, 264628, 35695855, 264632, 264555, 264556, 264557, 264558, 18108382, 22279002
2135	88079813 (4269, 4270)	Novel Protein sim. GBank gi|5689559|dbj|BAA83063.1| - (AB029034) KIAA1111 protein [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	22278999, 29331828, 35696052, 264906, 264908, 264910, 265009, 264591, 264758, 52646317, 265011, 87168559, 264601, 18108351, 264448, 264683, 264684, 264689, 18108359, 264691, 33657023, 264692, 35695763, 264629, 35695855, 264631, 264635, 264636, 264637, 56182323, 264639, 22279002, 264564
2136	84346479 (4271, 4272)	Novel Protein sim. GBank gi|2662167|dbj|BAA23715| - (AB007903) KIAA0443 [Homo sapiens]		UNCLASSIFIED	264639
2137	87637716 (4273, 4274)	Novel Protein sim. GBank gi|4884110|emb|CAB43262.1| - (AL050090) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264569, 264909, 33109954, 264763, 21906768, 60170394, 18108385, 264563
2138	87395446 (4275, 4276)	Novel Protein sim. GBank gi|5174779|gb|AAD40696.1| - (U87804) 50 kDa protein [Caulobacter crescentus]		ATPase_associated	264259, 29331828, 35696052, 264909, 265006, 265017, 265018, 18108351, 264288, 21906768, 33657023, 33657109, 264628, 18108374, 35695855, 264634, 264555, 264556, 264557, 264558, 264559
2139	94843882 (4277, 4278)	Novel Protein sim. GBank gi|3850821|emb|CAA77135| - (Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]			264905, 264910, 264591, 55812038, 55811386, 85658542, 264760, 18108351, 18108359, 55811957, 265020, 265021, 33657023, 18108384, 55811576, 83373044, 18108385, 56526486, 264482

2140	87645655 (4279, 4280)	Novel Protein sim. GBank gi|4417293|gb|AAD20418| - (AC007019) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264259, 29331824, 264104, 264109, 264509, 265006, 264759, 265018, 264448, 264288, 21906768, 55811957, 265021, 33657023, 27486265, 35696423, 264636, 264556, 264557, 264559, 264566
2141	79623986 (4281, 4282)			UNCLASSIFIED	265020, 264693
2142	80041222 (4283, 4284)			UNCLASSIFIED	263978
2143	94140051 (4285, 4286)	Novel Protein sim. GBank gi|2135766|pir||S53362 - mucin 5AC (clone JER47) - human (fragment)		UNCLASSIFIED	22278997, 29331827, 264907, 265020, 60432113
2144	94320114 (4287, 4288)	Novel Protein sim. GBank gi|2078483 (U43200) - antifreeze glycopeptide AFGP polyprotein precursor [Boreogadus saida]		UNCLASSIFIED	65274572, 264259, 29331824, 29331827, 264906, 264908, 264591, 265011, 87168559, 264600, 265019, 264288, 264768, 21906765, 21906767, 55811576, 35696423, 65274791, 22279002
2145	20564305 (4289, 4290)			UNCLASSIFIED	263978
2146	87010515 (4291, 4292)	Novel Protein sim. GBank gi|1255871 (U53341) - short region of weak similarity to bovine membrane receptor p63 (PIR:S28503) [Caenorhabditis elegans]		UNCLASSIFIED	264909, 60433356, 264686
2147	80432911 (4293, 4294)	Novel Protein sim. GBank gi|3080398|emb|CAA18718.1| - (AL022603) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264907, 264768, 264769, 18108385
2148	80048811 (4295, 4296)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!		UNCLASSIFIED	264593
2149	87362022 (4297, 4298)	Novel Protein sim. GBank gi|119863|sp|P20693|FCE2_MOUSE - LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE RECEPTOR) (FC-EPSILON-RII) (CD23)	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	29331824, 29331826, 35696052, 264758, 87168474, 265018, 52644150, 33657109
2150	94140059 (4299, 4300)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278998, 29331822, 29331824, 29331828, 264764, 264769, 21906766, 264486
2151	95353241 (4301, 4302)	Novel Protein sim. GBank gi|5689407|dbj|BAA82987.1| - (AB028958) KIAA1035 protein [Homo sapiens]			22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 29331828, 264508, 264511, 60433356, 264758, 264596, 33109954, 60174639, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264288, 264689, 21906765, 21906766, 21906768, 265020, 60170615, 33657109, 33657182, 33657349, 18108370, 264635, 264557, 60170394, 18108385, 87168518, 22279000
2152	79321640 (4303, 4304)	Novel Protein sim. GBank gi|3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]		kinase	18108397, 18108398, 265007, 264591, 265011, 18108351, 18108368, 18108374, 18108388

2153	88313371 (4305, 4306)	Novel Protein sim. GBank gi|4758704|ref|NP_004216.1|pMASL - MFH-amplified sequences with leucine-rich tandem repeats 1	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264488, 263994, 52646842, 22278996, 22278998, 22278999, 264259, 29331822, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264758, 87168474, 87168559, 265017, 265019, 264760, 264288, 264369, 264766, 264687, 264769, 52644229, 21906768, 21906768, 35695917, 33657023, 33657109, 35695855, 264631, 264632, 264635, 264636, 264639, 18108385, 264483, 264564, 264486
2154	87408034 (4307, 4308)	Novel Protein sim. GBank gi|225150|prf||1209265U - chorion protein B11 [Bombyx mori]		UNCLASSIFIED	56994075, 264094, 265009, 265019, 264288, 21906767, 35695917
2155	87424072 (4309, 4310)			UNCLASSIFIED	18108392, 18108398, 22278996, 264259, 29331824, 265008, 265010, 265011, 265017, 265019, 264288, 264686, 265020, 264693, 264628, 58182323
2156	84295205 (4311, 4312)	Novel Protein sim. GBank gi|3970966 (AC004974) - spa-1-like; similar to AF026504 (PID:g2555183) [Homo sapiens]			265007, 264684
2157	87316344 (4313, 4314)				264591
2158	86444218 (4315, 4316)	Novel Protein sim. GBank gi|1076211|pir||S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	264596
2159	80083729 (4317, 4318)	Novel Protein sim. GBank gi|4650844|dbj|BAA77027.1| - (AB026190) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_rna_bind	29331822, 264112, 265009, 264691, 33657023, 264634
2160	16283674 (4319, 4320)	Novel Protein sim. GBank gi|2879925|dbj|BAA24826| - (AB007897) KIAA0437 [Homo sapiens]			264634
2161	87739131 (4321, 4322)			UNCLASSIFIED	265008
2162	94319526 (4323, 4324)	Novel Protein sim. GBank gi|1504006|dbj|BAA13202| - (D86966) similarto human ZFY protein. [Homo sapiens]		UNCLASSIFIED	65274572, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 265007, 264910, 264591, 264592, 264593, 55812038, 264596, 264758, 265011, 264600, 264762, 264763, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 264689, 265020, 264691, 264628, 264629, 263978, 264632, 264634, 264557, 264638, 264639, 18108385, 264563, 264566, 264567
2163	95417158 (4325, 4326)	Novel Protein sim. GBank gi|3876537|emb|CAA98270| - (Z73974) cDNA EST yk291f5.3 comes from this gene; cDNA EST yk291f5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	56182575, 22278998, 264093, 264683, 33657023, 65274620, 60432113
2164	80569456 (4327, 4328)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	collagen	264603, 264637, 264565

2165	94329169 (4329, 4330)	Novel Protein sim. GBank gi|1086794 (U41107) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	56994075, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 29331830, 56182435, 265009, 21906754, 33657084, 265011, 265019, 264448, 264288, 264369, 21906765, 21906768, 21906769, 265020, 265021, 264691, 264692, 33657023, 65274620, 35695855, 264556, 60170394, 83373044, 60432113, 22279002, 264567
2166	87618934 (4331, 4332)	Novel Protein sim. GBank gi|2706522|emb|CAA75816| - (Y15895) ubiquitin activating enzyme [Drosophila melanogaster]		ubiquitin	52645156, 22278994, 22278998, 66714117, 29331828, 52644045, 265018, 265019, 264369, 21906765, 21906767, 21906768, 21906769, 265021, 265022, 264693, 27486262, 35695763, 18108376, 56526486, 87168518, 264567
2167	87716864 (4333, 4334)	Novel Protein sim. GBank gi|2224713|dbj|BAA20840| - (AB002384) KIAA0386 [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 29331824, 29331828, 29146498, 56182435, 265008, 265009, 264592, 264593, 33657402, 33109954, 265011, 265017, 265018, 18108351, 264369, 21906764, 21906765, 21906768, 29148627, 21906769, 52644150, 33657109, 35696423, 18108381, 18108384, 18108385, 60432113, 264567
2168	86999334 (4335, 4336)	Novel Protein sim. GBank gi|4321407|gb|AAD15748| - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	Contains protein domain (PF00664) - ABC transporter transmembrane region.	transport	66714117, 29331827, 264907, 264511, 264591, 265018, 264764, 264683, 264766, 264768, 264566
2169	87886937 (4337, 4338)				264629, 264555, 264559
2170	94141033 (4339, 4340)	Novel Protein sim. GBank gi|5106521|gb|AAD39741.1|AF10536 - (AF105365) K-Cl cotransporter KCC4 [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 22278997, 22278998, 264259, 29331825, 264509, 264906, 56182435, 60433438, 55812038, 264596, 55811386, 265019, 264762, 264763, 264448, 264764, 264684, 264288, 264766, 264685, 56181562, 264689, 55811957, 265020, 264535, 264691, 33657109, 60431528, 18108374, 35696423, 55811576, 65274791, 264634, 264639, 264558, 87168518, 60432113, 264564
2171	80194050 (4341, 4342)			UNCLASSIFIED	264369, 265020, 264558
2172	85452460 (4343, 4344)			UNCLASSIFIED	264259, 264558
2173	87036740 (4345, 4346)	Novel Protein sim. GBank gi|4309681|gb|AAD15478| - (AC006930) R33423_1 [Homo sapiens]		UNCLASSIFIED	264369
2174	95003288 (4347, 4348)	Novel Protein sim. GBank gi|2493778|sp|Q09456|YQ35_CAEEL - PUTATIVE CUTICLE COLLAGEN C09G5.5			264906, 35695855, 264555, 264557

2175	94325850 (4349, 4350)	Novel Protein sim. GBank gi|1263287 (U47855) - fibroin-3 [Araneus diadematus]			UNCLASSIFIED	264488, 35696286, 20281099, 29331826, 60432289, 35696052, 264109, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264591, 264594, 264595, 264596, 264758, 55812038, 265011, 264600, 264603, 264760, 264762, 264448, 264764, 264288, 264766, 264686, 264687, 21906766, 55811957, 35695917, 265020, 265022, 264691, 264692, 33857023, 264693, 264628, 264629, 55811578, 35696423, 65274791, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264558, 18108385, 60432113, 264563, 264564, 264565, 264566, 264486, 264567
2176	88223392 (4351, 4352)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	oncogene		52644507, 52646842, 22278994, 35696286, 22278996, 22278999, 29331826, 29331827, 35696052, 29331828, 33856970, 29331830, 264910, 33857402, 264758, 52644296, 87168559, 265018, 264689, 21906765, 21906767, 21906769, 35695917, 52644150, 264690, 33657023, 33657109, 52645129, 33657182, 27486261, 27486262, 33857349, 18108376, 18108377, 35695855, 87168518, 60432113, 264404, 22279000, 264486
2177	94128942 (4353, 4354)	Novel Protein sim. GBank gi|5454072|ref|NP_006416.1|pSLU7 - step II splicing factor SLU7		kinase		18108392, 22278997, 22278999, 264093, 33657402, 265019, 264448, 264766, 264689, 21906767, 21906768, 21906769, 265021, 33657023, 18108370, 18108374, 60432113, 22279002
2178	87601557 (4355, 4356)	Novel Protein sim. GBank gi|473407 (U08215) - NST-1 [Mus musculus]	Contains protein domain (PF00012) - Hsp70 protein	eph		264488, 22278996, 22278999, 29331824, 29331825, 29331826, 29331827, 52644296, 87168474, 18108370, 35695855, 22279002
2179	87316275 (4357, 4358)				UNCLASSIFIED	60424269, 264760, 264628, 264632

2180	95351397 (4359, 4360)	Novel Protein sim. GBank gi|3122317|sp|P90648|KMHB_DICDI - MYOSIN HEAVY CHAIN KINASE B (MHCK B)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52644507, 22278994, 35696286, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 33656970, 264508, 264509, 264906, 264908, 29331830, 264909, 264510, 265006, 265007, 33657402, 55812038, 21906754, 87168474, 87168559, 265017, 265018, 265019, 264763, 264682, 264683, 264684, 264288, 264686, 21906765, 21906766, 21906769, 265020, 265021, 265022, 52644150, 33657023, 33657109, 27486265, 33657349, 18108374, 35696423, 35695855, 263981, 60170394, 18108385, 56526486, 87168518, 60432113, 22279000, 264482, 264566, 264567, 264486
2181	85764930 (4361, 4362)	Novel Protein sim. GBank gi|3024689|sp|Q15542|T2D4_HUMAN - TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT (TAFII-100) (TAFII100)		kinase	29331827, 264369, 18108376, 264564
2182	87637731 (4363, 4364)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278996, 22278997, 22278999, 264259, 29331822, 56182435, 264112, 264764, 264288, 21906767, 21906768, 21906769, 33657109, 18108376, 60170394, 22279000, 22279002
2183	85460649 (4365, 4366)	Novel Protein sim. GBank gi|3873406|gb|AAC77482.1| - (U17129) unknown [Rhodococcus erythropolis]			264760
2184	87760690 (4367, 4368)	Novel Protein sim. GBank gi|3114713 (AF061346) - Edp1 protein [Mus musculus]		Inf	29331822, 29331825, 29331826, 56182435, 265011, 264685, 264686, 21906768, 18108370, 264629, 264631, 264636, 264557
2185	87826463 (4369, 4370)	Novel Protein sim. GBank gi|5106956|gb|AAD39906.1|AF11361 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]			29331824, 264907, 66712502, 264757, 265019, 264288, 264692, 56526486
2186	87739227 (4371, 4372)	Novel Protein sim. GBank gi|2864625|emb|CAA16972| - (AL021811) putative protein [Arabidopsis thaliana]		ATPase_associated	264259, 29331822, 29331824, 29331826, 56182435, 264592, 55812038, 264760, 264766, 55811957, 33657023, 55811576, 56182323, 264563
2187	87388173 (4373, 4374)			UNCLASSIFIED	35696052, 264905, 264906, 264907, 264908, 264510, 264511, 265008, 264910, 264758, 265019, 264762, 264681, 264766, 264769, 35695917, 264692, 35696423, 264631, 264635, 264637, 18108388, 264566, 264486
2188	87771708 (4375, 4376)	Novel Protein sim. GBank gi|5107816|gb|AAD40129.1|AF14941 - (AF149413) contains similarity to histone deacetylases; Pfam PF00850, Score=13.3, E=5e-10, N=1 [Arabidopsis thaliana]		histone	18108398, 56994075, 264259, 29331824, 29331825, 66714117, 29331827, 264906, 29331830, 265018, 265020, 265021, 56182323, 264559, 22279000, 22279002
2189	85693573 (4377, 4378)	Novel Protein sim. GBank gi|3452357 (AF075724) - unknown [Legionella pneumophila]	Contains protein domain (PF01596) - O-methyltransferase		22278996, 264259, 29331826, 21906754, 264369, 264288, 263967

2190	87639197 (4379, 4380)	Novel Protein sim. GBank gi|132575|sp|P29315|RINI_RAT - RIBONUCLEASE INHIBITOR		nucleaseinhib	22278996, 22278999, 29331822, 29331824, 29331826, 265008, 264910, 60170831, 55812038, 52644296, 265010, 265018, 264685, 264688, 56181562, 21906769, 35695917, 265022, 60170394, 22279000
2191	95198928 (4381, 4382)	Novel Protein sim. GBank gi|5327002|emb|CAB46272.1| - (Y18503) XAP-5-like protein [Homo sapiens]			29331825, 29331826, 29331830, 264510, 264511, 264910, 264593, 264594, 264556, 264559
2192	11126316 (4383, 4384)	Novel Protein sim. GBank gi|462600|sp|P34400|MI10_CAEEL - MIG-10 PROTEIN	Contains protein domain (PF00169) - PH domain		264558
2193	94140073 (4385, 4386)	Novel Protein sim. GBank gi|5420389|emb|CAB46680.1| - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	56181686, 29331825, 29331827, 264508, 264909, 265008, 264592, 60432229, 264288, 264684, 264766, 35695917, 33657023, 60431602, 60431528, 55810764, 55811576, 65274791, 35695855, 60431850, 56182323, 60432113
2194	21418714 (4387, 4388)	Novel Protein sim. GBank gi|2773341 (AF040954) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]			264592
2195	88083023 (4389, 4390)	Novel Protein sim. GBank gi|2832763|emb|CAA15685.1| - (AL009191) /prediction=(method:; /prediction=(method:; /match=(desc:; /match=(desc:; /motif=(desc: [Drosophila melanogaster]		UNCLASSIFIED	22278996, 22278999, 35696052, 265006, 21906754, 265017, 35695917, 265021, 265022, 35695855
2196	95091631 (4391, 4392)	Novel Protein sim. GBank gi|5262487|emb|CAB45699.1| - (AL080076) hypothetical protein [Homo sapiens]		collagen	56182575, 35696286, 22278997, 22278999, 264259, 29331822, 66714117, 60432289, 29331827, 35696052, 29331828, 264508, 52644045, 56182435, 264510, 265007, 265008, 265009, 60433438, 55812038, 265010, 265011, 264448, 264288, 264686, 264687, 52644229, 21906765, 21906766, 21906767, 35695917, 265022, 264691, 33657023, 264693, 18108370, 18108376, 35696423, 55811576, 65274791, 35695855, 264636, 56182323, 18108385
2197	95073813 (4393, 4394)	Novel Protein sim. GBank gi|4929567|gb|AAD34044.1|AF15180 - (AF151807) CGI-49 protein [Homo sapiens]			264768, 264769, 21906765, 21906766, 21906767, 29148627, 55811957, 35696286, 265020, 22278998, 265021, 264259, 33657023, 264693, 29331824, 35696052, 29331828, 18108370, 35695855, 264113, 265008, 264910, 60432229, 56182323, 33657402, 264758, 83373044, 21906754, 265018, 265019, 22279002, 264482, 264448, 264565, 264288, 264369
2198	88060914 (4395, 4396)	Novel Protein sim. GBank gi|3548787 (AC005622) - R30953_1 [Homo sapiens]		UNCLASSIFIED	

2199	88054355 (4397, 4398)	Novel Protein sim. GBank gi|2739372 (AC002505) - hypothetical protein [Arabidopsis thaliana]			264105, 264110, 264112, 264688, 55811957, 33657023, 264692, 263967, 20281071, 56526486
2200	87405385 (4399, 4400)	Novel Protein sim. GBank gi|3043634|dbj|BAA25481| - (AB011127) KIAA0555 protein [Homo sapiens]		struct	29331824, 264763, 264768
2201	94316872 (4401, 4402)	Novel Protein sim. GBank gi|3913470|sp|O57314|DHBX_ANAPL - PUTATIVE STEROID DEHYDROGENASE SPM2	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	29331824, 35696052, 264905, 264907, 33657402, 55811386, 265017, 265018, 265019, 264288, 21906768, 35695917, 265020, 265022, 33657023, 33657109, 27486261, 18108370, 35696423, 35695855, 264555, 264556, 83373044, 87168518, 60432113
2202	91672385 (4403, 4404)	Novel Protein sim. GBank gi|5262665|emb|CAB45767.1| - (AL080186) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264489, 264259, 29331824, 60432289, 35696052, 264905, 264909, 264592, 265017, 265018, 265019, 18108351, 264762, 264448, 264369, 264288, 264766, 21906765, 21906766, 264690, 264691, 264692, 33657109, 264634, 264636, 264555, 264639, 264558, 264559, 83373044, 18108385, 264404, 22279002, 264482
2203	87761832 (4405, 4406)	Novel Protein sim. GBank gi|1172845|sp|P46629|RB25_RABIT - RAS-RELATED PROTEIN RAB-25	Contains protein domain (PF00071) - Ras family	glycoprotein	52646365, 56994075, 264259, 29331822, 29331826, 29331827, 29331828, 264910, 265010, 265011, 87168559, 265018, 265019, 264605, 264288, 21906769, 35695917, 33657023, 264692, 33657109, 35695763, 18108376, 264638, 22279000, 264566, 264567
2204	88088671 (4407, 4408)	Novel Protein sim. GBank gi|121036|sp|P29348|GBT3_RAT GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-3 SUBUNIT (GUSTDUCIN ALPHA-3 CHAIN)	Contains protein domain (PF00503) - G-protein alpha subunit	UNCLASSIFIED	
2205	94147589 (4409, 4410)	Novel Protein sim. GBank gi|4589480|dbj|BAA76768.1| - (AB023141) KIAA0924 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	18108394, 18108397, 56182575, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 265008, 265009, 60432229, 265010, 265011, 265018, 264683, 264288, 264369, 264686, 21906766, 21906768, 21906769, 264690, 264691, 264693, 18108368, 55811576, 65274791, 264634, 18108381, 18108384, 60432113, 22279002, 264563, 264566
2206	20620008 (4411, 4412)			UNCLASSIFIED	264591
2207	87787970 (4413, 4414)	Novel Protein sim. GBank gi|4557753|ref|NP_000372.1|pMID1 - midline 1 protein	Contains protein domain (PF00622) - SPRY domain		29331822, 56182181, 29331827, 35696052, 52644045, 265006, 265019, 56181562, 55811957, 265021, 33657023, 35695763, 35695855, 60170394, 60432113, 264566
2208	86100830 (4415, 4416)				264906, 265019, 18108351, 21906769
2209	87800420 (4417, 4418)	Novel Protein sim. GBank gi|3986746 (AF105228) - tuftelin [Bos taurus]		struct	264112, 265009, 264691, 18108365, 18108374, 264634, 20281166

2210	57152407 (4418, 4420)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	264603
2211	87341720 (4421, 4422)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene	264685, 264686, 18108365, 22279002, 264482
2212	91223924 (4423, 4424)	Novel Protein sim. GBank gi|3776027|emb|CAA09214| - (AJ010475) RNA helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278995, 22278997, 22278999, 264092, 264094, 29331822, 66714117, 29331828, 29331828, 264907, 52644045, 265009, 60170831, 21906754, 87168559, 265017, 265019, 18108351, 264683, 18108354, 264369, 264766, 264687, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 33657109, 18108370, 18108374, 264638, 58182323, 18108384, 18108387, 87168518, 264565
2213	91219309 (4425, 4426)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]			58182575, 22278996, 22278997, 35696052, 264905, 66712502, 264908, 264828, 58182435, 264112, 265008, 60431735, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 18108351, 264765, 21906765, 21906768, 21906769, 265020, 265021, 264693, 264629, 263974, 263976, 18108379, 55811576, 264556, 264637, 264558, 83373044, 22279002, 264482, 264483

2214	95361453 (4427, 4428)	Novel Protein sim. GBank gi|4504325|ref|NP_000173.1|pHADH - hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha su	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	dehydrogenase	264488, 52644507, 18108394, 56182575, 22278994, 22278995, 35696286, 56994075, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 52645080, 29331822, 29147620, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 20281100, 264509, 264907, 66712502, 264908, 29331830, 52644045, 56182435, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 264593, 60433356, 60433438, 33109954, 33657084, 52644298, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 18108351, 264448, 264682, 264763, 264288, 264687, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 264532, 60170615, 264690, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 33657182, 27486262, 27486264, 27486265, 35695763, 18108370, 264629, 60431528, 18108374, 18108376, 55810764, 35696423, 35695855, 264634, 264636, 52644332, 264638, 264558, 60170394, 18108381, 56182323, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22279002, 264482, 264564, 264565, 264566,
2215	95419208 (4429, 4430)	Novel Protein sim. GBank gi|1947160 (AF000298) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]			264909, 265006, 264555, 264558, 87168518
2216	87614046 (4431, 4432)	Novel Protein sim. GBank gi|1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]		UNCLASSIFIED	264693
2217	80589404 (4433, 4434)	Novel Protein sim. GBank gi|5031707|ref|NP_005503.1|pGARP - glycoprotein A repetitions predominant	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264288, 33657109, 264556
2218	85518254 (4435, 4436)	Novel Protein sim. GBank gi|3878636|emb|CAA88953| - (Z49128) similar to cAMP-dependant protein kinase; cDNA EST EMBL:T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk492f4.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		35696423, 264563
2219	87614048 (4437, 4438)	Novel Protein sim. GBank gi|1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	Contains protein domain (PF01963) - TraB family		264682, 264683, 264688, 264689, 264693, 18108370, 18108376

2220	95354165 (4439, 4440)	Novel Protein sim. GBank gi|4507261|ref|NP_003145.1|pSTAT - statherin			264488, 18108394, 18108395, 35696286, 264259, 264097, 60432289, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 264593, 264594, 60433356, 264595, 55812038, 264758, 85658542, 265010, 264601, 264603, 265019, 264605, 264760, 264762, 264448, 264764, 264369, 264766, 18108357, 264768, 264687, 18108358, 264769, 55811957, 264690, 264691, 33657023, 264692, 18108362, 18108368, 264628, 264629, 18108374, 263978, 264634, 264635, 264636, 264637, 264638, 18108385, 264483, 264566, 264486, 264567
2221	88060927 (4441, 4442)	Novel Protein sim. GBank gi|3549154 (AC005625) - R27328_1 [Homo sapiens]			
2222	84425892 (4443, 4444)			UNCLASSIFIED	264908, 265020, 35695855
2223	95091649 (4445, 4446)			UNCLASSIFIED	265010, 264685, 264690, 264693, 264628, 263974, 263976, 55811576, 264555, 264638, 83373044, 264483
2224	87388515 (4447, 4448)	Novel Protein sim. GBank gi|3876005|emb|CAA84799| - (Z35719) cDNA EST EMBL:D67419 comes from this gene; cDNA EST EMBL:C13853 comes from this gene; cDNA EST EMBL:C11578 comes from this gene; cDNA EST yk234a7.3 comes from this gene; cDNA EST yk234a7.5 comes from this gene; cDNA ES...	Contains protein domain (PF01958) - Domain of unknown function	UNCLASSIFIED	264259, 264509, 56182435, 265006, 265008, 265009, 264757, 21906754, 18108351, 264693, 18108374, 18108385
2225	85749484 (4449, 4450)	Novel Protein sim. GBank gi|1255847 (U53338) - C05E11.1 gene product [Caenorhabditis elegans]		transport	22278994, 22278995, 22278999, 52644045, 264600, 265019, 21906765, 21906769
2226	86978953 (4451, 4452)	Novel Protein sim. GBank gi|4826524|emb|CAB42852.1| - (AL049848) hypothetical protein [Homo sapiens]			264259, 29331822, 29331824, 29331825, 29331827, 264508, 264906, 265007, 264691, 264634, 264486
2227	87721135 (4453, 4454)			UNCLASSIFIED	22278999, 265006, 265008, 18108354, 29148629, 29148784, 27486261, 18108374, 264637, 18108384
2228	91227337 (4455, 4456)	Novel Protein sim. GBank gi|606976 (U16800) - ribonucleoprotein [Xenopus laevis]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	264091, 264092, 264094, 29331822, 29331825, 66714117, 264693, 263972, 264639, 83373044, 264563
2229	88060931 (4457, 4458)	Novel Protein sim. GBank gi|3549155 (AC005625) - R27328_2 [Homo sapiens]		UNCLASSIFIED	

2230	95342915 (4459, 4460)	Novel Protein sim. GBank gi|226154|prf||1412350A - DNA polymerase [Human adenovirus type 2]		UNCLASSIFIED	264488, 264768, 52644507, 264769, 21906765, 21906766, 21906767, 21906769, 22278995, 35695917, 22278996, 22278997, 22278998, 22278999, 265021, 264259, 52645129, 29331827, 264508, 264509, 264907, 18108370, 18108374, 35696423, 35695855, 265007, 264910, 264555, 33657402, 21906754, 18108387, 265010, 265018, 265019, 264760, 264288, 264567
2231	88060937 (4461, 4462)	Novel Protein sim. GBank gi|3549154 (AC005625) - R27328_1 [Homo sapiens]		UNCLASSIFIED	264563
2232	87762581 (4463, 4464)	Novel Protein sim. GBank gi|5281316|gb|AAD41476.1|AF13312 - (AF133124) transcription factor IIIC63 [Homo sapiens]		transcriptfactor	18108394, 56182575, 22278995, 35696286, 22278997, 22278999, 264259, 29331827, 35696052, 264907, 56182435, 265006, 265007, 265008, 264910, 264758, 55812038, 264603, 265018, 265019, 18108351, 264682, 264764, 264683, 264369, 264288, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 264690, 52644150, 264691, 33657023, 264693, 18108370, 18108374, 55811576, 35695855, 264639, 18108385, 264564
2233	87755292 (4465, 4466)	Novel Protein sim. GBank gi|4249733|gb|AAD13780| - (AF109377) IdiBp [Mus musculus]			264906, 33657402, 265018, 264288, 264686, 265020, 264635, 18108385
2234	87771817 (4467, 4468)	Novel Protein sim. GBank gi|1706559|sp|P54352|EAS_DROME - ETHANOLAMINE KINASE (EASILY SHOCKED PROTEIN)		kinase	56182435, 264369, 264688, 21906765, 265020, 264693, 264556, 56526486
2235	91012316 (4469, 4470)	Novel Protein sim. GBank gi|4972734|gb|AAD34762.1| - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278997, 264563
2236	88003131 (4471, 4472)	Novel Protein sim. GBank gi|1082675|pir||B53814 - p20 protein - human	Contains protein domain (PF00011) - Hsp20/alpha crystallin family	eph	264569, 264687, 264769, 265022, 264259, 60432049, 264691, 29331826, 60432289, 20281149, 264906, 264907, 264511, 265008, 265009, 264634, 264635, 264636, 264555, 264556, 264557, 264558, 60433356, 264595, 264559, 60433438, 60432113, 264761, 264762, 264763, 264764
2237	91012318 (4473, 4474)	Novel Protein sim. GBank gi|4972734|gb|AAD34762.1| - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264488, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 22278995, 22278996, 22278997, 22278998, 265020, 265021, 22278999, 264259, 29331824, 29331826, 29331827, 35695763, 18108376, 35695855, 265007, 60432229, 33657402, 60433356, 60433438, 83373044, 18108385, 21906754, 18108387, 60432113, 22279000, 265019, 22279002, 264482, 18108351, 264288

2238	94998857 (4475, 4476)		Contains protein domain (PF00286) - Viral coat protein			264509, 264907, 264629, 264634, 264564
2239	87798688 (4477, 4478)					29331825, 265009, 264369, 33657109, 18108370, 18108374, 264557, 264559
2240	94121471 (4479, 4480)	Novel Protein sim. GBank gi|2982311 (AF051240) - probable ubiquitin-conjugating enzyme E2 [Picea mariana]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme		ubiquitin	264488, 65274572, 56182575, 35696286, 22278997, 22278999, 264259, 29331827, 35696052, 264508, 52644045, 56182435, 264511, 265007, 265008, 265009, 60433356, 60433438, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 18108351, 264683, 264288, 264768, 264687, 264688, 264769, 21906765, 21906768, 21906789, 35695917, 265021, 265022, 60170615, 52644150, 33657023, 33657182, 33657349, 35695763, 18108370, 35696423, 35695855, 87168518, 22279000
2241	80091951 (4481, 4482)				UNCLASSIFIED	264693, 264629
2242	91228075 (4483, 4484)	Novel Protein sim. GBank gi|2494312|sp|P70541|E2BG_RAT - TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)			synthase	22278995, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 264509, 265007, 265009, 264586, 21906754, 265010, 265011, 265017, 265018, 265019, 264448, 264369, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657109, 27486262, 27486264, 18108374, 35695855, 264634, 264637, 56182323, 83373044, 56526486, 87168518, 264564
2243	78902026 (4485, 4486)				UNCLASSIFIED	265008
2244	85723527 (4487, 4488)	Novel Protein sim. GBank gi|2291143 (AF016417) - Similar to BZIP transcription factor [Caenorhabditis elegans]			UNCLASSIFIED	264604
2245	95318545 (4489, 4490)	Novel Protein sim. GBank gi|470340 (U00043) - similar to beta-mannosyltransferase [Caenorhabditis elegans]	Contains protein domain (PF00534) - Glycosyl transferases group 1		UNCLASSIFIED	52645156, 22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331827, 264907, 264512, 60433438, 264758, 21906754, 265011, 264603, 264764, 264687, 21906767, 21906768, 21906769, 55811957, 265022, 264691, 264629, 35696423, 264638, 18108387, 60432113, 22279000, 22279002, 264566

2246	94848710 (4491, 4492)	Novel Protein sim. GBank gi|4996096|dbj|BAA78326.1| - (AB028069) activator of S phase Kinase [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	65274572, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 35696052, 264106, 264905, 264907, 265006, 265007, 265008, 60433438, 33109954, 87168559, 265018, 265019, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 27486264, 18108370, 18108374, 65274791, 35695855, 60432113
2247	87862542 (4493, 4494)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U86 [Human herpesvirus 6]		UNCLASSIFIED	52645156, 52646365, 52645080, 35696052, 33656970, 52646317, 33657084, 265017, 21906768, 21906769, 35695917, 33657109, 52645129, 33657182, 27486261, 27486262, 33657349, 27486265, 18108387
2248	95412996 (4495, 4496)	Novel Protein sim. GBank gi|4758502|ref|NP_004123.1|pHABP - hyaluronan-binding protein 2	Contains protein domain (PF00089) - Trypsin	cathepsin	264488, 264259, 264907, 29331830, 264909, 265007, 265009, 264595, 21906754, 65274444, 264603, 265019, 264762, 264448, 264288, 264689, 21906766, 55811957, 265021, 264691, 18108374, 264634, 264635, 264636, 264555, 264638, 264557, 264558, 264559, 18108383, 83373044, 18108385, 264486
2249	94685662 (4497, 4498)	Novel Protein sim. GBank gi|4038461 (AF107772) - TcSTI1 [Trypanosoma cruzi]	Contains protein domain (PF00515) - TPR Domain	eph	264766, 264628, 264636, 264637
2250	79827508 (4499, 4500)	Novel Protein sim. GBank gi|3738140|emb|CAA21241| - (AL031852) valyl-trna synthetase, mitochondrial precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	264908, 18108374
2251	87385863 (4501, 4502)	Novel Protein sim. GBank gi|3218467|emb|CAA07090.1| - (AJ006529) putative phosphatase [Gallus gallus]		UNCLASSIFIED	264259, 35696052, 264508, 56182435, 265009, 264592, 264593, 264760, 264448, 264684, 264288, 264690, 264628, 55811576, 264555, 264556, 264557, 264558, 264559, 264566
2252	87735867 (4503, 4504)	Novel Protein sim. GBank gi|4929325|gb|AAD33953.1|AF14531 - (AF145316) vacuolar proton pump delta polypeptide [Homo sapiens]	Contains protein domain (PF01813) - ATP synthase subunit D	synthase	264092, 264094, 264259, 29331822, 66714117, 29331828, 264102, 264103, 264104, 264105, 264109, 264112, 264511, 265007, 60433356, 265010, 18108351, 21906767, 21906768, 264691, 263974, 263977, 264486, 264567
2253	91010703 (4505, 4506)			UNCLASSIFIED	65274572, 265019

2254	95320031 (4507, 4508)	Novel Protein sim. GBank gi|4502847|ref|NP_001271.1|pCIRB - cold inducible RNA-binding protein	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	264569, 18108394, 18108398, 56182575, 58994075, 35696286, 22278999, 264094, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 264106, 264508, 264509, 264908, 264907, 29331830, 66712502, 264908, 264909, 264510, 265006, 264511, 265007, 265008, 265009, 60170831, 60432229, 60433358, 60433438, 264758, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264764, 264288, 264369, 264766, 264686, 264768, 264769, 21906765, 21906767, 55811957, 264691, 33657023, 264692, 18108362, 65274620, 263969, 264628, 18108370, 60431528, 263972, 264629, 18108372, 18108377, 18108379, 55811576, 35696423, 35695855, 264630, 264634, 264635, 264636, 264558, 263981, 264638, 56182323, 60170394, 264558, 18108381, 18108382, 83373044, 18108385, 87168518, 60432113, 22279002, 264482, 264564, 264565, 264488, 264587, 18108391
2255	91010546 (4509, 4510)	Novel Protein sim. GBank gi|5541865|emb|CAB51072.1| - (AL096858) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	struct	65274572, 56182575, 22278997, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264508, 264905, 264906, 264907, 66712502, 264908, 56182435, 264510, 264511, 265008, 264593, 264595, 21906754, 33109954, 87168474, 265011, 265017, 265019, 264682, 264764, 264369, 264288, 264766, 264685, 264686, 264768, 21906765, 21906766, 21906768, 21906769, 265020, 60170615, 52644150, 264690, 264692, 264693, 33657109, 33657349, 264632, 264636, 52644332, 56182323, 22279000, 22279002
2256	87020531 (4511, 4512)	Novel Protein sim. GBank gi|3327174|dbj|BAA31655| - (AB014580) KIAA0680 protein [Homo sapiens]		UNCLASSIFIED	264768, 264688, 18108374
2257	80088235 (4513, 4514)			UNCLASSIFIED	22278996, 22278999, 264681, 21906765, 21906766, 264567
2258	88090516 (4515, 4516)	Novel Protein sim. GBank gi|3025448 (AC004528) - R32184_2 [Homo sapiens]	Contains protein domain (PF00060) - Ligand-gated ion channel	misc_channel	264908, 264592, 264764

2259	95364155 (4517, 4518)	Novel Protein sim. GBank gi|4884140|emb|CAB43278.1| - (AL050110) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108396, 65274572, 56182575, 22278997, 22278998, 264259, 29331822, 29331827, 264905, 66712502, 264908, 264909, 56182435, 265007, 265008, 60432229, 33657084, 87168559, 18108351, 264448, 264683, 264288, 264369, 56181562, 265021, 60170615, 264690, 33657109, 60431528, 18108374, 52644332, 56182323, 18108385, 22279000, 22279002, 264482
2260	88084119 (4519, 4520)	Novel Protein sim. GBank gi|3080663 (AC004614) - similar to f-spondin proteins AB006086 (PID:g2529225) [Homo sapiens]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	oxidase	56182575, 265020, 264905, 264906, 264908, 35696423, 264511, 264635, 55812038, 264758, 265018, 265019, 264605, 264760, 264563
2261	88074157 (4521, 4522)	Novel Protein sim. GBank gi|3334526|emb|CAA16138| - (AL021306) predicted using FGENEH [Homo sapiens]		UNCLASSIFIED	
2262	91639292 (4523, 4524)	Novel Protein sim. GBank gi|4877759|gb|AAD31421.1|AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]			56182575, 22278999, 29331822, 29331825, 60432289, 29331827, 35696052, 264508, 66712502, 52644045, 56182435, 265006, 265008, 265009, 60433356, 55812038, 265010, 265017, 265019, 264288, 264369, 21906765, 21906767, 55811957, 35695917, 52644150, 33657023, 33657109, 55811576, 65274791, 56182323
2263	87602495 (4525, 4526)	Novel Protein sim. GBank gi|3341697 (AC003672) - hypothetical protein [Arabidopsis thaliana]			22278994, 22278997, 264907, 264828, 52644150, 18108381, 264893, 18108374
2264	87756525 (4527, 4528)	Novel Protein sim. GBank gi|1657601 (U66220) - unknown [Nannocystis exedens]		UNCLASSIFIED	264686, 264488, 264768, 264769, 264691, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 35695855, 264510, 264511, 264512, 265007, 265009, 264638, 264639, 264757, 264758, 18108385, 265011, 264760, 264564, 264565, 264764, 264566, 264486, 264766
2265	86918663 (4529, 4530)	Novel Protein sim. GBank gi|477072|pir||A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264689, 264910, 264764
2266	87773458 (4531, 4532)	Novel Protein sim. GBank gi|3150479 (AF067212) - partial CDS [Caenorhabditis elegans]	Contains protein domain (PF01305) - Ribosomal protein L15 amino terminal region	ribosomalprot	22278995, 22278997, 22278999, 264259, 265006, 265007, 265009, 60433438, 21906754, 265010, 265011, 265017, 264448, 264683, 264288, 264689, 21906765, 21906768, 35695917, 265021, 18108374, 264638, 22279000, 22279002, 264566, 264487

2267	87395838 (4533, 4534)	Novel Protein sim. GBank gi|3560229|emb|CAA20697.1| - (AL031530) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 35696052, 29331828, 264905, 264509, 264907, 264908, 264909, 264512, 265009, 264910, 264593, 33657402, 265010, 265018, 264762, 264448, 264288, 264369, 264768, 52644229, 35695917, 264691, 33657023, 18108382, 33657109, 35696423, 264634, 18108381, 87168518, 264566
2268	85693867 (4535, 4536)	Novel Protein sim. GBank gi|728832|sp|P39189|ALU2_HUMAN - !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!		cadherin	264488, 264259, 264509, 264595, 265010, 265017, 264766, 18108385, 264486
2269	88177977 (4537, 4538)	Novel Protein sim. GBank gi|103418|pir||S17885 - TcD37 protein - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	56182575, 60432049, 265007, 265009, 264591, 87168559, 264605, 18108351, 21906764, 265020, 264629, 60431528, 264638, 18108385, 18108387, 60432113
2270	80410327 (4539, 4540)				264763
2271	91010392 (4541, 4542)			cyto450	264909, 56182435, 265008, 55812038, 55811957, 33657023, 264693, 33657109, 55810764, 55811576, 56182323
2272	84208220 (4543, 4544)			UNCLASSIFIED	264905, 264908
2273	95014271 (4545, 4546)	Novel Protein sim. GBank gi|4176370 (AC005058) - similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	Contains protein domain (PF00462) - Glutaredoxin		52645156, 22278996, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264909, 265006, 264593, 60433438, 21906754, 265018, 264689, 21906765, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486264, 18108376, 35696423, 35695855, 264630, 52644332, 264558, 56182323, 22279002
2274	91640217 (4547, 4548)	Novel Protein sim. GBank gi|1480112|emb|CAA67961| - (X99642) HP1-BP74 protein [Mus musculus]	Contains protein domain (PF00538) - linker histone H1 and H5 family	histone	52645156, 22278997, 22278999, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 52644045, 264511, 265008, 265009, 60170831, 264591, 21906754, 33109954, 265011, 265018, 18108351, 264448, 264288, 264684, 264766, 21906765, 21906766, 21906767, 21906768, 52644150, 264693, 18108364, 35695763, 18108374, 35696423, 264634, 264557, 264638, 52644332, 83373044, 18108385, 56526486, 87168518, 22279002
2275	88082501 (4549, 4550)	Novel Protein sim. GBank gi|3165406 (AC004755) - fos37502_2 [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	
2276	11287447 (4551, 4552)			UNCLASSIFIED	264555, 264556

2277	88084123 (4553, 4554)	Novel Protein sim. GBank gi|2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278999, 35696052, 265008, 265019, 264369, 265020, 265022, 55810764, 264404, 22279002
2278	94133079 (4555, 4556)	Novel Protein sim. GBank gi|2618702 (AC002510) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	18108394, 22278997, 29331826, 60433356, 60433438, 21906754, 265018, 33657023, 264639, 83373044, 264565
2279	80419375 (4557, 4558)	Novel Protein sim. GBank gi|119714|sp|P13983|EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	264766, 264565
2280	94239723 (4559, 4560)				265008, 33109954, 265010, 265019, 265020
2281	95293048 (4561, 4562)	Novel Protein sim. GBank gi|4240299|dbj|BAA74928.1| - (AB020712) KIAA0905 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transport	264092, 264259, 29331822, 29331824, 29331826, 35696052, 264107, 264906, 264909, 52644045, 265006, 33657402, 60433356, 264758, 265011, 265019, 264681, 264683, 264684, 264686, 21906765, 21906767, 21906768, 21906769, 60170615, 264690, 52644150, 18108362, 264692, 18108368, 18108374, 263978, 264631, 18108381, 264559, 18108385, 56526486, 22279000, 264566, 264567
2282	87602829 (4563, 4564)	Novel Protein sim. GBank gi|1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]		UNCLASSIFIED	264488, 264259, 29331822, 29331824, 29331827, 29331828, 29331830, 33657402, 60433438, 87168474, 265019, 18108351, 21906767, 21906769, 55811957, 33657023, 52645129, 33657109, 33657182, 27486262, 263972, 55811576, 87168518, 20281169
2283	95362386 (4565, 4566)	Novel Protein sim. GBank gi|2495729|sp|Q92556|Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)		UNCLASSIFIED	60424179, 56182575, 22278994, 35696286, 22278997, 22278999, 29331822, 29331824, 56182181, 29331825, 29331827, 35696052, 29146499, 264905, 66712502, 264908, 265007, 265009, 60432229, 264593, 60431735, 60433356, 33109954, 33657084, 55811386, 87168474, 265010, 265011, 265018, 265019, 55811150, 264683, 264369, 264288, 264688, 21906765, 21906767, 21906768, 29148627, 21906769, 55811957, 265020, 265022, 33657182, 27486261, 18108370, 264628, 18108374, 55810764, 18108379, 55811576, 35696423, 35695855, 264630, 60431850, 263981, 18108382, 83373044, 18108385, 18108387, 60432113, 22279000, 264482, 264567

2284	95414955 (4567, 4568)	Novel Protein sim GBank gi|2498797|sp|Q64311|PNAD_MOUSE - PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA)			60424179, 52644507, 18108394, 52646842, 22278994, 35696286, 22278998, 22278997, 22278999, 264259, 60432049, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331830, 52644045, 56182435, 33657402, 60433438, 33109954, 21906754, 85658542, 87168559, 265018, 265019, 55811150, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 33657023, 33657182, 27486262, 27486264, 27486265, 18108376, 55810764, 35696423, 35695855, 60431850, 87168518, 60432113, 264482, 264564
2285	87781484 (4569, 4570)	Novel Protein sim. GBank gi|3342234 (U93909) - nuclear antigen EBNA-1 [Cercopithecine herpesvirus 15]		collagen	35696052, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264595, 264760, 18108351, 264682, 264763, 264685, 264766, 264686, 264768, 264693, 264629, 35695855, 264631, 264634
2286	87737825 (4571, 4572)	Novel Protein sim. GBank gi|3873414 (U00043) - similar to D. melanogaster trithorax protein [Caenorhabditis elegans]		kinase	35696286, 56182435, 60170831, 264591, 60432229, 264592, 264593, 264594, 264595, 55812038, 264596, 87168474, 35695917, 264692, 55811576, 264555, 264557
2287	82986696 (4573, 4574)	Novel Protein sim. GBank gi|630905|pir||S42731 - collagen alpha 1 chain - sea urchin (Hemicentrotus pulcherrimus) (fragment)	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	UNCLASSIFIED	264682
2288	94133083 (4575, 4576)	Novel Protein sim. GBank gi|728832|sp|P39189|ALU2_HUMAN - !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!		tm7	22278995, 56994075, 22278997, 22278999, 264259, 60432289, 264508, 264512, 265008, 33657402, 265017, 265018, 265019, 18108351, 264448, 21906765, 21906766, 21906767, 21906768, 33657023, 264557, 22279000, 22279002
2289	88084133 (4577, 4578)	Novel Protein sim. GBank gi|2887497 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	
2290	88084137 (4579, 4580)	Novel Protein sim. GBank gi|2887497 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264683
2291	84295281 (4581, 4582)	Novel Protein sim. GBank gi|3253120 (AC005175) - R31449_3 [Homo sapiens]		struct	08394, 264907, 265006, 265009, 33109954, 52646317, 265010, 18108351, 264681, 264686, 264692, 18108370, 18108374, 18108385

2292	94328834 (4583, 4584)	Novel Protein sim. GBank gi|4803672|emb|CAB42643.1| - (AJ133769) nuclear transport receptor [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 56994075, 29331824, 29331825, 35696052, 56182435, 60433438, 55812038, 33109954, 87168474, 87168559, 265018, 18108351, 264763, 264448, 264369, 264288, 56181562, 264769, 21906765, 21906766, 21906767, 21906769, 265021, 265022, 33657023, 264693, 65274620, 33657109, 27486264, 264629, 55810764, 55811576, 35695855, 56182323, 56526486, 87168518, 22279000, 264567
2293	87759213 (4585, 4586)	Novel Protein sim. GBank gi|3252981 (AF068921) - Ras-binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	264488, 18108397, 35696286, 264092, 264259, 29331822, 29331826, 264906, 264908, 264511, 264512, 265009, 264910, 18108351, 264764, 264369, 264288, 264685, 264766, 265020, 265022, 264534, 35696423, 264631, 264637, 18108381, 56182323, 264639, 18108385, 264404, 264563, 264565
2294	86693580 (4587, 4588)	Novel Protein sim. GBank gi|2062680 (U88964) - HEM45 [Homo sapiens]	Contains protein domain (PF00929) - Exonuclease	nuclease	22278997, 22278998, 22278999, 264259, 29331822, 60432289, 29331828, 35696052, 265018, 264684, 264288, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264692, 33657109, 18108376, 35696423, 35695855, 264634, 22279000, 22279002, 264563, 264486
2295	95312200 (4589, 4590)			UNCLASSIFIED	22278996, 60432289, 264682, 264683, 264689, 18108374
2296	80030781 (4591, 4592)				263974, 263978
2297	94321251 (4593, 4594)	Novel Protein sim. GBank gi|5689501|dbj|BAA83034.1| - (AB029005) KIAA1082 protein [Homo sapiens]		transcriptfactor	264488, 65274572, 56182575, 22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 35696052, 264907, 264908, 52644045, 56182435, 264112, 265006, 265007, 264910, 265009, 60433356, 33657402, 264595, 55812038, 21906754, 265011, 265018, 265019, 264448, 264764, 264288, 264766, 21906765, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 55811576, 56182323, 60170394, 83373044, 18108385, 56526486, 264564, 264486

2298	95312207 (4595, 4596)	Novel Protein sim. GBank gi|3875051|emb|CAB02849| - (Z81050) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65564 comes from this gene; cDNA EST EMBL:D69046 comes from this gene; cDNA EST yk366b12.3 comes from this gene; cDNA EST yk366b12.5 comes from this gene ...	collagen	60424178, 56181686, 22278995, 35696286, 22278998, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 60424269, 35696052, 29331828, 68712502, 56182435, 264510, 265006, 60433438, 21906754, 33109954, 55811386, 265010, 265018, 55811150, 264762, 18108351, 264682, 264683, 264288, 264684, 264686, 264688, 56181562, 264689, 55811957, 29148784, 21906767, 29148629, 55811957, 29148784, 35695917, 265020, 18108362, 33657023, 18108364, 33657109, 60431602, 18108370, 60431528, 18108374, 55810764, 35696423, 35695855, 264630, 264634, 60431850, 18108380, 56182323, 264558, 83373044, 18108385, 60432113, 22279000, 264482, 264567, 264486
2299	80193720 (4597, 4598)		UNCLASSIFIED	264369
2300	94124346 (4599, 4600)	Novel Protein sim. GBank gi|2443886 (AC002294) - Unknown protein [Arabidopsis thaliana]		264488, 22278996, 22278999, 264259, 29331824, 66714117, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 265008, 264910, 265009, 264758, 265010, 87168559, 264600, 265018, 264760, 264762, 18108351, 264764, 264766, 264768, 264769, 21906766, 21906767, 35695917, 265021, 264691, 33657023, 35695763, 18108370, 18108374, 35696423, 35695855, 264631, 264636, 264638, 18108385, 22279002, 264563
2301	91235725 (4601, 4602)	Novel Protein sim. GBank gi|2143637|pir||B4505 - calcium-dependent actin-binding protein - rat	sIruct	264908, 264758, 265017, 21906765, 83373044, 264563
2302	88084141 (4603, 4604)	Novel Protein sim. GBank gi|2887497 (AC004144) - R34001_1 [Homo sapiens]	UNCLASSIFIED	52644045, 265019, 264288, 33657023, 18108370, 18108385
2303	94141439 (4605, 4606)	Novel Protein sim. GBank gi|4884194|emb|CAB43220.1| - (AL049948) hypothetical protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain sIruct	264259, 60432049, 264907, 264909, 264910, 60432229, 33657402, 265011, 265018, 264762, 264448, 264769, 264637, 264638, 83373044, 264486
2304	94840434 (4607, 4608)	Novel Protein sim. GBank gi|2494162|sp|Q10005|YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR	UNCLASSIFIED	264259, 29331824, 21906767, 33657182, 33657349
2305	90935911 (4609, 4610)	Novel Protein sim. GBank gi|4972686|gb|AAD34738.1| - (AF132150) unknown [Drosophila melanogaster]		65274572, 22278998, 264808, 265006, 21906769, 264891, 264486

2306	95334940 (4611, 4612)	Novel Protein sim. GBank gi|4929565|gb|AAD34043.1|AF15180 - (AF151806) CGI-48 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	264488, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264907, 29331830, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 33657402, 21906754, 85658542, 265010, 265011, 264601, 265017, 265018, 264604, 265019, 18108351, 264448, 264288, 264766, 264769, 21906765, 21906766, 21906767, 21906768, 29148629, 29148784, 35695917, 265020, 265021, 265022, 33657023, 264692, 18108370, 18108374, 18108376, 35696423, 35695855, 264630, 264634, 264635, 264638, 264637, 264638, 264639, 18108382, 18108385, 18108387, 264563, 264566, 264486
2307	79415283 (4613, 4614)			UNCLASSIFIED	264828
2308	87606409 (4615, 4616)	Novel Protein sim. GBank gi|4758732|ref|NP_004522.1|pMOCS - molybdenum cofactor synthesis 2		synthase	35696286, 264259, 29331822, 29331824, 264112, 264512, 264757, 21906754, 264288, 264690, 27486264, 264631, 264634, 264404
2309	95357218 (4617, 4618)	Novel Protein sim. GBank gi|3878059|emb|CAB17070| - (Z99942) cDNA EST EMBL:D73444 comes from this gene; cDNA EST EMBL:D70905 comes from this gene; cDNA EST EMBL:D72208 comes from this gene; cDNA EST EMBL:D75030 comes from this gene; cDNA EST LMBL:D72944 comes from this gene; cDN...		glycoprotein	18108397, 22278996, 22278997, 22278998, 22278999, 60432049, 29331822, 29331826, 60432289, 66712502, 60432229, 60433356, 60433438, 65274444, 265010, 264600, 264681, 264448, 264683, 264288, 21906766, 21906768, 265020, 264691, 264692, 264693, 65274620, 65274791
2310	79601668 (4619, 4620)			UNCLASSIFIED	264508
2311	87721189 (4621, 4622)	Novel Protein sim. GBank gi|2137337|pir||I46281 - gene mCBP protein - mouse	Contains protein domain (PF00013) - KH domain	transcriptfactor	18108397, 56182575, 22278996, 56994075, 264259, 29331824, 29331827, 264508, 264907, 56182435, 264510, 264511, 265006, 264512, 265007, 265008, 265009, 60433438, 33109954, 265010, 265011, 264603, 265017, 18108351, 264762, 264683, 264288, 264369, 264686, 33657023, 20281149, 20281069, 264628, 263972, 55811576, 35696423, 20281071, 264632, 264636, 18108385, 18108387, 87168518, 22279000, 264563, 264486

2312	87549681 (4623, 4624)	Novel Protein sim. GBank gi|2911264 (AC002550) - Unknown gene product [Homo sapiens]			56182575, 56994075, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 52644045, 60432229, 60433356, 55812038, 33109954, 21906754, 87168474, 265018, 18108351, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 60170615, 33657023, 27486261, 27486264, 35696423, 35695855, 18108385, 22279000, 22279002
2313	80042533 (4625, 4626)	Novel Protein sim. GBank gi|3043626|dbj|BAA25477| - (AB011123) KIAA0551 protein [Homo sapiens]			263981
2314	94313401 (4627, 4628)	Novel Protein sim. GBank gi|5596714|emb|CAB51401.1| - (AL035398) dJ796I17.2 (CGI-51) [Homo sapiens]		UNCLASSIFIED	52644507, 52646365, 52646842, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 52644045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 265017, 265018, 265019, 264288, 264369, 21906765, 21906766, 21906768, 35695917, 52644150, 33657023, 33657109, 52645129, 33657349, 35695763, 18108374, 35696423, 35695855, 52644332, 22279000, 22279002, 264563, 264567
2315	80430119 (4629, 4630)			UNCLASSIFIED	264905, 264906, 264767, 264768, 264693, 55811576, 264635, 56182323, 18108385
2316	94312191 (4631, 4632)	Novel Protein sim. GBank gi|5531827|gb|AAD44488.1| - (AF078856) p47 [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	glycoprotein	52644507, 52645156, 52646365, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264906, 264907, 29331830, 52644045, 56182435, 264511, 265007, 265008, 265009, 60170831, 60433438, 21906754, 52646317, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264681, 264763, 264448, 264683, 264369, 52644229, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 18108362, 52645129, 33657182, 33657349, 35695763, 18108370, 18108376, 35696423, 35695855, 264631, 264556, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113, 22279000, 264566, 264567

2317	87020571 (4633, 4634)			UNCLASSIFIED	22278998, 60432049, 264910, 60432229, 264686, 264687, 264688, 264689, 264558, 18108385
2318	79959879 (4635, 4636)			UNCLASSIFIED	265006, 264910
2319	95101781 (4637, 4638)	Novel Protein sim. GBank gi|5262613|emb|CAB45746.1| - (AL080155) hypothetical protein [Homo sapiens]			264488, 264569, 18108398, 52646365, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 264259, 52645080, 29331825, 29331826, 29331827, 29331828, 29331830, 56182435, 60170831, 60432229, 60431735, 33657402, 21906754, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 264369, 52644229, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 27486264, 33657349, 35695763, 18108370, 18108376, 18108379, 35696423, 264558, 83373044, 18108385, 56526486, 87168518, 264564, 264565, 264566
2320	91622426 (4639, 4640)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!		kinase	22278994, 60432049, 60432289, 29331827, 264511, 265008, 52646317, 265017, 265019, 21906765, 18108372, 18108387, 22279002
2321	94320377 (4641, 4642)	Novel Protein sim. GBank gi|3873837|emb|CAB02700| - (Z81029) Similarity to S.pombe hypothetical protein C1D4.09C (SW:Q10154); cDNA EST EMBL:T00543 comes from this gene; cDNA EST EMBL:T01062 comes from this gene; cDNA EST EMBL:T01321 comes from this gene; cDNA EST EMBL:T02288 com...		UNCLASSIFIED	264488, 264687, 18108394, 264689, 21906765, 18108397, 18108398, 21906767, 21906768, 65274791, 22278995, 35695855, 22278998, 265021, 265022, 264510, 265006, 264511, 264512, 265008, 60170615, 264555, 264636, 264556, 18108361, 264259, 60432229, 33657023, 264557, 264558, 264693, 60433356, 264559, 60433438, 29331824, 18108365, 18108348, 18108384, 29331825, 18108385, 33109954, 29331827, 56526486, 29146499, 265011, 60432113, 265017, 265018, 264508, 264563, 264482, 264509, 18108351, 264448, 264907, 264682, 18108370, 264683, 264908, 264288, 264909, 18108354, 264486, 264567
2322	87803165 (4643, 4644)	Novel Protein sim. GBank gi|5678957|emb|CAB51685.1| - (AL109630) BACR7A4.y [Drosophila melanogaster]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	22278996, 264907, 264511, 264757, 18108351, 264768, 264638

2323	94840445 (4645, 4646)	Novel Protein sim. GBank gi|2494162|sp|Q10005|YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00226) - DnaJ domain	eph	22278994, 22278995, 22278997, 60432049, 264259, 29331822, 33656970, 264509, 56182435, 264511, 265008, 60433356, 60433438, 55812038, 33109954, 21906754, 85658542, 87168474, 265011, 87168559, 265017, 265019, 264760, 264681, 18108351, 264369, 264288, 18108355, 264687, 264688, 21906765, 21906767, 21906768, 55811957, 35695917, 265021, 33657023, 18108362, 27486262, 55811576, 264631, 264555, 83373044, 87168518, 60432113, 22279002
2324	86633607 (4647, 4648)				264592, 264593, 265020
2325	88165074 (4649, 4650)	Novel Protein sim. GBank gi|5419865|emb|CAB46377.1| - (AL096732) hypothetical protein [Homo sapiens]		ATPase_associated	265020
2326	84390962 (4651, 4652)	Novel Protein sim. GBank gi|231885|sp|P29981|CP4C_BLADI - CYTOCHROME P450 4C1 (CYPIVC1)	Contains protein domain (PF00067) - Cytochrome P450	cyto450	265006, 264759, 35695855, 56182323
2327	88081648 (4653, 4654)	Novel Protein sim. GBank gi|4240227|dbj|BAA74892.1| - (AB020676) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	
2328	83388428 (4655, 4656)	Novel Protein sim. GBank gi|1245105 (U46463) - glutamine repeat protein-1 [Mus musculus]		UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 265007, 264512, 264910, 264758, 265010, 264766, 264768, 264769, 33657023, 264693, 264628, 264631, 264634, 264638, 264639, 264488
2329	87604478 (4657, 4658)	Novel Protein sim. GBank gi|1169343|sp|P42209|DIF6_MOUSE - DIFF6 PROTEIN	Contains protein domain (PF00735) - Cell division protein	UNCLASSIFIED	60433438, 264595, 265017, 264766, 264692, 264629, 264635, 264636, 264638, 56182323, 60432113, 264566
2330	87335396 (4659, 4660)			UNCLASSIFIED	265017, 264685, 60432113, 264088
2331	86990463 (4661, 4662)	Novel Protein sim. GBank gi|5679136|gb|AAD46874.1|AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	265009
2332	87784182 (4663, 4664)	Novel Protein sim. GBank gi|2104452|emb|CAB08779| - (Z95397) unknown [Schizosaccharomyces pombe]		ATPase_associated	35696286, 22278998, 29331824, 60424269, 265008, 265008, 265018, 264448, 264764, 21906765, 35695917, 35695855, 264636, 22279000, 264566
2333	88206958 (4665, 4666)	Novel Protein sim. GBank gi|3879985|emb|CAA92691.1| - (Z68318) cDNA EST CEMSD62F comes from this gene; cDNA EST EMBL:C07930 comes from this gene; cDNA EST EMBL:C09493 comes from this gene; cDNA EST yk415e8.3 comes from this gene; cDNA EST yk415e8.5 comes from this gene; cDNA EST...		UNCLASSIFIED	56182575, 56994075, 29331826, 29331828, 264107, 33657402, 87168559, 264683, 35695917, 265021, 33657023, 263976
2334	94319788 (4667, 4668)	Novel Protein sim. GBank gi|4966270|gb|AAB52261.2| - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E-value=1e-13, N=1 [C...	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	56182575, 29331825, 21906768, 264636, 83373044

2335	80046103 (4669, 4670)	Novel Protein sim. GBank gi|3283350 (AF062378) - calmodulin-binding protein SHA1 [Mus musculus]	Contains protein domain (PF00612) - IQ calmodulin-binding motif	struct	18108351, 21906769, 264555
2336	95196121 (4671, 4672)	Novel Protein sim. GBank gi|1929056|emb|CAA72805| - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]		kinase	264907, 35695917, 18108379
2337	95345810 (4673, 4674)	Novel Protein sim. GBank gi|4495063|emb|CAB39181.1| - (Z85986) dJ108K11.3 (similar to yeast suppressor protein SRP40) [Homo sapiens]		UNCLASSIFIED	35696286, 22278999, 56182181, 29331825, 60424269, 56182435, 33657402, 55812038, 55811386, 265017, 265018, 265019, 21906768, 35695917, 264691, 33657023, 33657109, 263972, 35696423, 35695855, 60432113
2338	87634045 (4675, 4676)	Novel Protein sim. GBank gi|2224689|dbj|BAA20829| - (AB002372) KIAA0374 [Homo sapiens]	Contains protein domain (PF00323) - Mammalian defensin	UNCLASSIFIED	18108394, 29331822, 66714117, 60432289, 264906, 56182435, 265009, 60433438, 264596, 265010, 265019, 18108354, 264288, 264369, 55811957, 265021, 33657023, 263976, 55811576, 264632, 56182323, 264639
2339	85663319 (4677, 4678)	Novel Protein sim. GBank gi|3873550|emb|CAA22127| - (AL033534) serine-rich protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35696286, 264592, 264369, 264691, 264558
2340	90937716 (4679, 4680)				65274572, 22278994, 35696286, 22278997, 22278999, 264259, 29331822, 60432289, 29331826, 29331830, 265009, 33657402, 33109954, 265017, 265018, 264766, 264685, 21906769, 35695917, 264691, 264692, 35696423, 87168518, 22279000
2341	87775281 (4681, 4682)				264259, 264908, 264909, 264682, 22279000
2342	95334968 (4683, 4684)	Novel Protein sim. GBank gi|3874563|emb|CAB02797| - (Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264488, 65274572, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 35696052, 264905, 264509, 29331830, 265006, 60170831, 60432229, 60433356, 87168474, 265017, 265018, 265019, 264448, 264369, 264288, 21906765, 21906766, 55811957, 35695917, 265020, 265022, 52644150, 33657023, 65274620, 33657109, 18108370, 18108378, 55810764, 35696423, 55811576, 264556, 264558, 18108385, 60432113, 264563, 264564, 264565, 264566, 264567
2343	87775448 (4685, 4686)	Novel Protein sim. GBank gi|4929741|gb|AAD34131.1|AF15189 - (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	264907, 264512, 265011, 264683
2344	79953198 (4687, 4688)			UNCLASSIFIED	264758
2345	94319799 (4689, 4690)	Novel Protein sim. GBank gi|2506307|sp|P13944|CA1C_CHICK - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)	Contains protein domain (PF00092) - von Willebrand factor type A domain	collagen	264488, 264259, 66712502, 264759, 83373044, 264566

2346	94131820 (4691, 4692)	Novel Protein sim. GBank gi|1255411 (U53153) - one short region of weak similarity to S. cerevisiae protease A inhibitor 3 (SP:P01094) and another short region of weak similarity to S. cerevisiae glucose repression mediator protein (SP:P14922) [Caenorhabditis elegans]	Contains protein domain (PF00515) - TPR Domain	proteaseinhib	35696286, 22278998, 264259, 35696052, 29331828, 33657402, 60433356, 33109954, 87168559, 264603, 265019, 18108351, 264681, 264685, 21906766, 265021, 33657109, 55811576, 35695855, 264637, 52644332, 264557, 83373044, 22279000, 22279002
2347	85330367 (4693, 4694)				22278997, 264511, 264683, 264684, 264768, 264687, 264688, 264691, 264692, 55811576
2348	95196133 (4695, 4696)	Novel Protein sim. GBank gi|1929056|emb|CAA72805| - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]		kinase	18108394, 35696286, 264259, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265011, 264601, 264762, 18108351, 264764, 264288, 264766, 264768, 264689, 35695917, 264693, 264628, 18108370, 264629, 18108374, 35696423, 264631, 264635, 264636, 264637, 264638, 264639, 83373044, 18108385, 264567, 264486
2349	87776502 (4697, 4698)	Novel Protein sim. GBank gi|4884106|emb|CAB43254.1| - (AL050062) hypothetical protein [Homo sapiens]			35696052, 29146499, 264909, 264369
2350	88260594 (4699, 4700)				22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 33109954, 21906754, 265010, 87168559, 265018, 265019, 264761, 264681, 264288, 18108357, 21906766, 21906767, 264691, 264692, 35695855, 87168518, 22279000, 22279002, 264482
2351	86968042 (4701, 4702)	Novel Protein sim. GBank gi|728832|sp|P39189|ALU2_HUMAN - !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!		kinase	56182575, 264909, 265006, 264558
2352	87337196 (4703, 4704)	Novel Protein sim. GBank gi|731637|sp|P38760|YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264259, 264448
2353	91638784 (4705, 4706)	Novel Protein sim. GBank gi|1346955|sp|P48809|RB27_DROME - HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331826, 55812038, 265019, 264692, 264636
2354	87337199 (4707, 4708)	Novel Protein sim. GBank gi|731637|sp|P38760|YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	29331824, 264908, 265006, 265008

2355	91638786 (4709, 4710)	Novel Protein sim. GBank gi|4938503|emb|CAB43861.1| - (AL078465) hnRNP-like protein [Arabidopsis thaliana]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	56994075, 22278996, 35696286, 22278999, 264259, 29331825, 29331826, 29331828, 29146498, 264905, 264908, 265008, 264758, 87168474, 265010, 265017, 264687, 21906765, 21906767, 21906769, 264691, 264692, 263967, 18108370, 87168518, 22279000
2356	95327688 (4711, 4712)	Novel Protein sim. GBank gi|5138920|gb|AAD40377.1| - (AF092135) PTD014 [Homo sapiens]			52644507, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35696052, 29331828, 264908, 66712502, 264512, 265007, 265008, 60170831, 60432229, 60433356, 60433438, 264758, 52646317, 33109954, 21906754, 55811386, 87168474, 265017, 265018, 264605, 265019, 264681, 264682, 264448, 264369, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170615, 33657109, 27486264, 35695763, 55810764, 18108379, 35696423, 55811576, 35695855, 60170394, 56182323, 83373044, 18108385, 56526486, 264404, 60432113, 22279000, 264482, 264563, 264566, 264486, 264567
2357	87775458 (4713, 4714)	Novel Protein sim. GBank gi|4929741|gb|AAD34131.1|AF15189 - (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	264488, 264769, 18108394, 264259, 29331822, 18108370, 18108374, 264510, 265017, 264482, 264563, 264762, 264565, 264566, 264369, 18108354
2358	87777078 (4715, 4716)	Novel Protein sim. GBank gi|4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 22278999, 264509, 264905, 264592, 18108351, 264681, 264682, 264769, 32833986, 18108374, 264556, 18108385, 264482
2359	87755859 (4717, 4718)	Novel Protein sim. GBank gi|1086830 (U41264) - coded for by C. elegans cDNA yk20f8.5; coded for by C. elegans cDNA yk44g1.5; coded for by C. elegans cDNA yk12b7.5; coded for by C. elegans cDNA yk36g6.5; coded for by C. elegans cDNA yk20f8.5; coded for by C. elegans cDNA yk16g12....		UNCLASSIFIED	35696286, 22278998, 264905, 264511, 265007, 265008, 60433438, 264288, 264686, 21906769, 265020, 264692, 35695855, 264558, 56526486, 264563
2360	80046125 (4719, 4720)	Novel Protein sim. GBank gi|3881545|emb|CAA93779| - (Z69904) cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	22278997, 29331826, 263981, 22279000
2361	94232191 (4721, 4722)	Novel Protein sim. GBank gi|746487 (U23514) - No definition line found [Caenorhabditis elegans]			22278995, 22278999, 264512, 265009, 264757, 21906765, 65274620, 18108370, 60431528, 18108374, 264635, 60170394, 264482

2362	91721193 (4723, 4724)	Novel Protein sim. GBank gi|1171093|sp|P19706|MYSB_ACACA - MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)		UNCLASSIFIED	22278999, 264259, 29331822, 29331824, 60432289, 264509, 264512, 60432228, 60433356, 264448, 264682, 264683, 264369, 21906765, 21906768, 21906769, 60432113, 22279000, 22278002
2363	95006635 (4725, 4726)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264907, 264629, 264635
2364	94827104 (4727, 4728)	Novel Protein sim. GBank gi|5639830|gb|AAD45886.1|AF14601 - (AF146018) hydroxypyruvate reductase [Homo sapiens]	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases	reductase	264488, 18108394, 264887, 18108398, 22278998, 56994075, 35696286, 22278997, 22278998, 264259, 66714117, 29331825, 35696052, 264509, 264905, 264906, 264907, 264908, 68712502, 264909, 264511, 265006, 264512, 265007, 265008, 33657402, 264758, 21906754, 87168474, 265010, 87168559, 264603, 265017, 265018, 265019, 264760, 264762, 18108351, 264448, 264764, 264683, 264684, 264288, 18108355, 264766, 18108358, 264689, 18108359, 21906765, 21906766, 21906767, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 18108368, 18108370, 18108374, 35696423, 35695855, 264635, 264556, 264557, 264639, 60170394, 83373044, 18108383, 18108384, 18108385, 18108388, 56526486, 264482, 264564, 264486
2365	94140746 (4729, 4730)	Novel Protein sim. GBank gi|1840045 (U49082) - transporter protein [Homo sapiens]		transport	22278996, 22278998, 22278999, 264907, 264909, 264910, 33657402, 264758, 264600, 264766, 264687, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 83373044, 264566
2366	94312388 (4731, 4732)			UNCLASSIFIED	52644507, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264907, 29331830, 264909, 264511, 265008, 33657402, 264595, 52646317, 265017, 265018, 265019, 264605, 264685, 264766, 264689, 21906766, 21906769, 35695917, 265020, 265021, 265022, 52644150, 35695855, 52644332, 18108385, 18108387, 264564, 264568
2367	94140910 (4733, 4734)	Novel Protein sim. GBank gi|1065457 (U40410) - C54G7.4 gene product [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	35696286, 21906768, 55810764, 65274791, 264567
2368	94322190 (4735, 4736)				26:628

2369	94314334 (4737, 4738)	Novel Protein sim. GBank gi|5360901|dbj|BAA82158.1| - (AB029343) a-helix coiled-coil rod homologue [Homo sapiens]		struct	52644507, 52646842, 35696286, 264092, 264094, 52645080, 35696052, 264107, 29331830, 52644045, 265006, 265007, 265009, 52644296, 52644229, 264689, 21906765, 21906766, 35695917, 265020, 52644150, 263967, 33657109, 27486265, 35695763, 18108370, 263974, 18108374, 18108376, 52644332, 263981, 18108385
2370	79804120 (4739, 4740)			UNCLASSIFIED	264508, 264909, 264596
2371	57280406 (4741, 4742)				264369
2372	87642413 (4743, 4744)			UNCLASSIFIED	263967, 263981
2373	87418611 (4745, 4746)	Novel Protein sim. GBank gi|4589582|dbj|BAA76813.1| - (AB023186) KIAA0969 protein [Homo sapiens]		UNCLASSIFIED	29331826, 265010, 265019, 35695917, 264634, 60432113
2374	94123665 (4747, 4748)	Novel Protein sim. GBank gi|5105131|dbj|BAA80445.1| - (AP000061) 246aa long hypothetical ribonuclease PH [Aeropyrum pernix]	Contains protein domain (PF01138) - 3' exoribonuclease family	UNCLASSIFIED	265006, 265007, 265008, 265009, 265011, 264766, 35695917, 35695855, 263981, 264557, 264565
2375	87731355 (4749, 4750)	Novel Protein sim. GBank gi|1351115|sp|P47758|SRPB_MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)		UNCLASSIFIED	60432049, 29331824, 264907, 52644045, 264512, 60433356, 21906754, 52644296, 87168559, 264448, 21906765, 21906768, 21906769, 33657023, 18108368, 55811576, 52644332
2376	87613744 (4751, 4752)	Novel Protein sim. GBank gi|2645435 (AF007780) - CHD3 [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	ATPase_associated	264259, 29331830, 264909, 264910, 265009, 60433438, 21906754, 265017, 265018, 265019, 264682, 264288, 264685, 21906767, 263972, 35695855, 87168518, 60432113
2377	95319689 (4753, 4754)	Novel Protein sim. GBank gi|5257005|gb|AAD41239.1| - (AF083249) Rb binding protein homolog [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	UNCLASSIFIED	18108394, 65274572, 22278997, 22278999, 264095, 29331822, 29147620, 29331824, 66714117, 29331825, 29331826, 29331828, 33656970, 29146498, 29146499, 264509, 265006, 265007, 265008, 265009, 60170831, 265010, 265011, 265018, 55811150, 18108351, 264764, 264288, 21906767, 21906768, 29148627, 29148629, 265021, 33657023, 33657109, 18108370, 18108374, 18108379, 35696423, 264556, 83373044, 18108385, 18108388, 56526486, 22279000, 22279002, 264563
2378	94137032 (4755, 4756)	Novel Protein sim. GBank gi|1072198 (U40942) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56182575, 35696286, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 56182435, 264510, 265009, 60433356, 87168474, 265011, 265018, 264288, 21906765, 33657023, 264557, 56182323, 83373044, 18108385, 22279002, 264482
2379	65444324 (4757, 4758)	Novel Protein sim. GBank gi|3337357 (AC004481) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	265017, 264288, 21906768

2380	88923062 (4759, 4760)	Novel Protein sim. GBank gi|4502939|ref|NP_001845.1|pCOL1 - collagen, type XI, alpha 1	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	264908, 264910, 265011
2381	87608241 (4761, 4762)	Novel Protein sim. GBank gi|4455609|emb|CAB36555| - (AL031846) dJ742C19.5 (novel Chromobox protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHRromatin Organization MOdifier) domain	helicase	56182575, 264091, 264093, 264259, 29331825, 264105, 264906, 60433356, 21906754, 265017, 265019, 264683, 264288, 264685, 264686, 264687, 264691, 264692, 264693, 55811578, 264636, 264567
2382	91225982 (4763, 4764)	Novel Protein sim. GBank gi|4325130|gb|AAD17276| - (AF119716) dMi-2 protein [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	transport	29331824, 60432289, 264905, 264596, 21906754, 264769, 265022, 264693, 263967, 33657109, 264629, 264631, 264558, 83373044, 60432113, 264482
2383	87442841 (4765, 4766)	Novel Protein sim. GBank gi|1902982|dbj|BAA19005| - (D89049) lectin-like oxidized LDL receptor [Bos taurus]	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	265009, 21906765, 21906766
2384	95354766 (4767, 4768)	Novel Protein sim. GBank gi|2462851 (AF016252) - Spinophilin [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	struct	264488, 52644507, 52645156, 52646365, 35696286, 22278999, 52645080, 29331824, 29331826, 35696052, 29331828, 264906, 264828, 52644045, 265006, 265008, 265009, 33109954, 33657084, 52644296, 265011, 265017, 265018, 264683, 52644229, 21906765, 21906767, 21906768, 265020, 52644150, 33657023, 264693, 65274620, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108374, 35695855, 264634, 264555, 264556, 264557, 52644332, 264558, 264559, 18108385, 22279000, 22279002
2385	95419485 (4769, 4770)			UNCLASSIFIED	264488, 52644507, 52645156, 264887, 52646365, 22278995, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331826, 35696052, 52644045, 265006, 265007, 265008, 265009, 264910, 60432229, 60433356, 52646317, 21906754, 265019, 264448, 264683, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 265021, 265022, 264690, 264691, 264692, 65274620, 33657109, 18108370, 264631, 52644332, 22279000, 22279002, 264563, 264565, 264567
2386	94742649 (4771, 4772)	Novel Protein sim. GBank gi|4929699|gb|AAD34110.1|AF15187 - (AF151873) CGI-115 protein [Homo sapiens]		glycoprotein	264488, 22278995, 22278996, 22278997, 264259, 29146498, 264112, 264511, 60170831, 60432229, 264595, 60433438, 87168474, 87168559, 264682, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 265021, 264690, 33657109, 264628, 18108376, 83373044, 60432113, 22279000, 264564, 264566, 264487

2387	14997990 (4773, 4774)			UNCLASSIFIED	264634
2388	11424604 (4775, 4776)			UNCLASSIFIED	264595
2389	95310650 (4777, 4778)	Novel Protein sim. GBank gi|4758058|ref|NP_004372.1|pCREB - cAMP responsive element binding protein-like 1	Contains protein domain (PF00170) - bZIP transcription factor	dna_rna_bind	264488, 22278998, 22278999, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 264511, 264512, 264910, 264591, 21906754, 264601, 264604, 264761, 18108351, 264764, 264288, 264766, 264768, 264769, 21906765, 21906768, 264692, 264693, 35696423, 264635, 264636, 264555, 83373044, 22279000, 264486
2390	94320912 (4779, 4780)	Novel Protein sim. GBank gi|1644239|dbj|BAA12223| - (D84103) mitochondrial DNA polymerase gamma [Homo sapiens]	Contains protein domain (PF00476) - DNA polymerase family A	polymerase	52644507, 56182575, 22278995, 35696286, 22278996, 22278997, 22278999, 29331822, 29331825, 29331826, 35696052, 264905, 52644045, 265009, 264758, 264759, 33109954, 52644296, 85658542, 265011, 265017, 265018, 264605, 52644229, 21906765, 21906767, 21906768, 21906769, 35695917, 52644150, 33657023, 33657109, 33657349, 35695763, 18108370, 18108374, 18108376, 35696423, 35695855, 264555, 52644332, 56182323, 60170394, 83373044, 56526486
2391	80036194 (4781, 4782)			UNCLASSIFIED	263976
2392	94245016 (4783, 4784)	Novel Protein sim. GBank gi|4240169|dbj|BAA74863.1| - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	35696286, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 265009, 264591, 264758, 264600, 264604, 264762, 264448, 264764, 264369, 264766, 264768, 264769, 264689, 35695917, 264629, 18108374, 263978, 35696423, 35695855, 264631, 264634, 264635, 264638, 264637, 264638, 60170394, 264639, 264565, 264486

2393	95302633 (4785, 4786)	Novel Protein sim. GBank gi|4506667|ref|NP_000993.1|pRPLP - ribosomal protein, large, P0	Contains protein domain (PF00466) - Ribosomal protein L10	ribosomalprot	18108392, 60424179, 264489, 18108394, 18108397, 22278995, 56994075, 35696286, 22278998, 22278997, 22278999, 264093, 60432049, 264259, 29331822, 29147620, 20281099, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35696052, 29146499, 264508, 264509, 264905, 264907, 264908, 66712502, 52644045, 264828, 264909, 56182435, 264112, 264113, 264510, 265006, 264511, 265007, 265008, 265009, 264910, 264591, 264593, 60433356, 264595, 60433438, 52646317, 33109954, 21906754, 55811386, 265010, 265011, 265017, 265018, 265019, 264681, 264762, 18108351, 264763, 264682, 264764, 264683, 264369, 264288, 18108354, 264768, 264686, 264687, 264688, 264689, 18108359, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148629, 29148784, 35695917, 265021, 265022, 33657023, 264692, 264693, 18108384, 33657109, 18108368, 27486261, 27486262, 33657349, 35695763, 18108370, 263972, 264629, 18108374, 263977, 18108376, 263978, 55810764, 35696423, 35695855, 264634, 60431850, 264555, 264637, 264557, 263981, 264558, 18108381, 60170394
2394	94323266 (4787, 4788)	Novel Protein sim. GBank gi|4159888 (AC004908) - zinc finger protein from gene of uncertain exon structure; similar to Q99676 (PID:g3025333) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	35696286, 22278997, 22278998, 56182181, 35696052, 265006, 264592, 55811386, 265010, 265011, 265017, 265019, 264448, 264683, 264288, 21906765, 21906768, 21906769, 55811957, 35695917, 33657023, 65274620, 33657182, 33657349, 35695763, 18108374, 18108376, 55810764, 55811576, 35696423, 60170394, 18108385, 264564, 264566, 264567
2395	95287212 (4789, 4790)	Novel Protein sim. GBank gi|5712756|gb|AAD47636.1|AF160798 - (AF160798) calcium transporter CaT1 [Rattus norvegicus]		dna_rna_bind	264259, 29331824, 264910, 264288, 265021, 83373044, 18108387, 264563, 264566

2396	85096700 (4791, 4792)	Novel Protein sim. GBank gi|106322|pir||B34087 - hypothetical protein (L1H 3' region) - human	Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	52646385, 18108397, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264106, 264907, 29331830, 66712502, 264110, 60170831, 264591, 33657402, 60433438, 55812038, 33109954, 21906754, 33657084, 87168474, 265017, 265018, 265019, 264760, 264448, 264288, 264766, 52644229, 21906766, 21906767, 265020, 265021, 60170615, 264692, 33657023, 65274620, 52645129, 33657182, 27486262, 27486264, 27486265, 264629, 18108374, 35696423, 35695855, 264631, 264556, 52644332, 264558, 83373044, 18108388, 87168518, 22279002, 264482
2397	87280854 (4793, 4794)				52644507, 52645156, 56182575, 264259, 29147620, 264905, 264907, 264908, 264909, 264910, 264758, 52644296, 264603, 264604, 264762, 264681, 264764, 18108357, 264769, 21906768, 264693, 264628, 264635, 264638, 264639, 264564
2398	88047689 (4795, 4796)	Novel Protein sim. GBank gi|3258609 (AC005178) - H53_GS1 [Homo sapiens]		UNCLASSIFIED	
2399	87738965 (4797, 4798)	Novel Protein sim. GBank gi|786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 60432289, 264906, 29331830, 56182435, 264112, 264910, 33109954, 21906754, 87168474, 264600, 265017, 265018, 265019, 264764, 264765, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265022, 60170615, 33657023, 18108370, 18108374, 264556, 60170394, 264558, 87168518, 22279000, 22279002, 264564, 264566, 264487
2400	91214116 (4799, 4800)	Novel Protein sim. GBank gi|2352822|gb|AAB69285.1| - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	21906766, 52646842, 56994075, 33657182, 27486262, 52644296, 265017

2401	91214118 (4801, 4802)	Novel Protein sim. GBank gi|2352822|gb|AAB69285.1| - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]			phosphatase	52644507, 52645156, 52644229, 264688, 21906764, 21906765, 52646385, 52646842, 21906766, 21906767, 21906768, 22278995, 35695917, 56994075, 35696286, 22278998, 22278997, 265020, 22278998, 22278999, 264259, 33657023, 52645080, 264693, 29331824, 33657109, 52645129, 29331826, 33657182, 29331827, 35696052, 27486261, 27486262, 33656970, 33657349, 27486265, 35695763, 264106, 264905, 35696423, 35695855, 265006, 265007, 265008, 265009, 264637, 52644332, 55812038, 52646317, 18108385, 52644296, 87168474, 265010, 87168559, 60432113, 265017, 265018, 265019, 264563, 264288
2402	91221408 (4803, 4804)	Novel Protein sim. GBank gi|4689258|gb|AAD27832.1|AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]				264907, 264908, 264909, 264566
2403	84135432 (4805, 4806)	Novel Protein sim. GBank gi|4929575|gb|AAD34048.1|AF15181 - (AF151811) CGI-53 protein [Homo sapiens]	Contains protein domain (PF00062) - C-type lysozyme/alpha-lactalbumin family			22278999, 35696052, 265018, 264686, 264693, 83373044, 264567
2404	95312605 (4807, 4808)	Novel Protein sim. GBank gi|2315796 (AF016685) - similar to short chain-type dehydrogenases [Caenorhabditis elegans]	Contains protein domain (PF00106) - short chain dehydrogenase		dehydrogenase	35696286, 29331826, 35696052, 265008, 265018, 21906769, 264564
2405	94311851 (4809, 4810)	Novel Protein sim. GBank gi|464178|dbj|BAA03581| - (D14853) polyprotein [Hepatitis C virus]			UNCLASSIFIED	35696286, 29331822, 265007, 21906754, 265017, 265018, 265019, 264763, 264369, 21906765, 35695917, 265020, 265021, 52644150, 264693, 35695855, 264632, 52644332, 22279002
2406	88094501 (4811, 4812)	Novel Protein sim. GBank gi|2773363 (AF041382) - microtubule binding protein D-CLIP-190 [Drosophila melanogaster]	Contains protein domain (PF01302) - CAP-Gly domain		struct	52646842, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264102, 264106, 264906, 52644045, 265007, 265008, 265009, 264910, 264592, 60433356, 60433438, 33109954, 265010, 265011, 265018, 265019, 264369, 264685, 264686, 21906768, 21906769, 52644150, 264693, 52645129, 264628, 35696423, 264632, 56182323, 264639, 22279000, 22279002, 264563
2407	79465005 (4813, 4814)				UNCLASSIFIED	264685, 264686
2408	87391503 (4815, 4816)	Novel Protein sim. GBank gi|423442|pir||S33513 - gene Fif protein - mouse			UNCLASSIFIED	264910, 265010, 264448, 264557

2409	94741770 (4817, 4818)	Novel Protein sim. GBank gi|1176601|sp|P45966|YNZ6_CAEEL - HYPOTHETICAL 20.8 KD PROTEIN T09A5.6 IN CHROMOSOME III		UNCLASSIFIED	22278995, 22278996, 22278997, 264097, 29331822, 29331824, 29331827, 29146498, 52644045, 60433438, 33657084, 87168474, 264760, 21906767, 29148627, 29148629, 52644150, 33657023, 263967, 20281069, 18108374, 20281071, 56182323, 83373044, 18108385, 87168518
2410	87604860 (4819, 4820)	Novel Protein sim. GBank gi|4966262|gb|AAC48052.2| - (U64849) Contains similarity to Pfam domain: PF00646 (F-box), Score=28.7, E-value=4.3e-05, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00080) - Copper/zinc superoxide dismutase (SODC)		22278998, 264259
2411	87534633 (4821, 4822)	Novel Protein sim. GBank gi|3114713 (AF061346) - Edp1 protein [Mus musculus]		tnf	29331824, 29331827, 29331828, 264764, 264369, 33657109, 56182323
2412	87778332 (4823, 4824)	Novel Protein sim. GBank gi|5410336|gb|AAD43038.1| - (AF106685) myelin gene expression factor 2 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	22278998, 29331827, 264907, 265011, 265017, 265018, 265019, 18108351, 21906766, 265020, 33657109, 264559, 18108385
2413	94133820 (4825, 4826)	Novel Protein sim. GBank gi|5262705|emb|CAB45778.1| - (AL080214) hypothetical protein [Homo sapiens]	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264488, 264259, 29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264510, 264511, 264512, 265008, 265009, 264910, 265011, 264682, 264764, 264766, 264686, 264768, 264689, 265021, 33657023, 18108370, 264628, 35695855, 264632, 264634, 264635, 264636, 83373044, 264563, 264564, 264565, 264566, 264567, 264486
2414	94312590 (4827, 4828)	Novel Protein sim. GBank gi|1082340|pir||S52863 - DNA-binding protein R kappa B - human		ubiquitin	52645156, 52646842, 52646365, 18108398, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29331830, 264909, 60433356, 33657402, 264594, 52646317, 21906754, 33657084, 265010, 87168559, 265017, 265018, 265019, 264369, 264684, 264687, 264688, 56181562, 21906764, 264689, 21906765, 21906766, 21906767, 29148627, 21906769, 265020, 265021, 60170615, 33657023, 264693, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 18108370, 60431528, 264629, 18108374, 18108376, 55810764, 264636, 52644332, 264638, 264558, 56182323, 83373044, 18108385, 87168518, 22279002

2415	88089002 (4829, 4830)	Novel Protein sim. GBank gi|423915|pir||A45439 - myosin I heavy chain - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	struct	264259, 264908, 60433356, 33657402, 21906754, 265018, 264687, 264689, 21906769, 55811957, 265021, 264690, 264691, 33657023, 264693, 35696423, 56182323, 56526486
2416	94118356 (4831, 4832)	Novel Protein sim. GBank gi|3025445 (AC004528) - R32184_1 [Homo sapiens]			264638
2417	87733334 (4833, 4834)	Novel Protein sim. GBank gi|1084944|pir||S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins		264094, 29331822, 29331824, 29331827, 264369
2418	94234349 (4835, 4836)	Novel Protein sim. GBank gi|1176572|sp|P45895|YNA4_CAEEL - HYPOTHETICAL 91.0 KD PROTEIN PAR2.4 IN CHROMOSOME III	Contains protein domain (PF00411) - Ribosomal protein S11	UNCLASSIFIED	56994075, 264091, 264259, 29331824, 29331825, 60432289, 29331828, 264905, 264907, 264511, 265009, 60432229, 21906754, 87168559, 265019, 264682, 21906768, 21906769, 265020, 265021, 33657023, 65274620, 18108370, 55811576, 264634, 60170394, 18108385, 22279000, 22279002, 264566
2419	82374249 (4837, 4838)	Novel Protein sim. GBank gi|284006|pir||S18732 - autoantigen, 64K - human		struct	264569, 264762, 264448, 264691, 264631, 264634, 264555, 264556, 264638, 264558
2420	94844244 (4839, 4840)	Novel Protein sim. GBank gi|1076211|pir||S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	29331824, 29331825, 29331828, 60432229, 33109954, 85658542, 87168474, 265018, 264288, 265020, 264564
2421	87805345 (4841, 4842)			UNCLASSIFIED	264909, 264768, 264638
2422	88084714 (4843, 4844)	Novel Protein sim. GBank gi|2224567|dbj|BAA20772| - (AB002311) KIAA0313 [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	transport	18108392, 18108394, 18108398, 264906, 265006, 265010, 18108351, 18108374, 18108385
2423	88058390 (4845, 4846)	Novel Protein sim. GBank gi|4505153|ref|NP_002392.1|pMEKK - MAP/ERK kinase kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 60432049, 29331822, 29331826, 60432289, 29331828, 265008, 265009, 60433356, 21906754, 265017, 265018, 265019, 21906766, 21906768, 21906769, 265020, 265021, 20281149, 263971, 60432113
2424	94854047 (4847, 4848)	Novel Protein sim. GBank gi|2988398 (AC004381) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278997, 60432049, 264259, 29331826, 29331828, 264905, 66712502, 29331830, 60433356, 265011, 265019, 264766, 21906768, 55811957, 264692, 33657023, 33657109, 55811576, 56182323, 83373044, 18108385, 18108388, 60432113, 22279000
2425	87415981 (4849, 4850)	Novel Protein sim. GBank gi|2077932|dbj|BAA19878| - (D86556) Protein Kinase [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264634
2426	87613945 (4851, 4852)	Novel Protein sim. GBank gi|2039368|gb|AAB53003.1| - (U94619) circulating cathodic antigen [Schistosoma mansoni]		UNCLASSIFIED	22278996, 22278998, 264259, 264102, 264512, 265008, 21906767, 18108370, 18108374, 263976

2427	87622693 (4853, 4854)	Novel Protein sim. GBank gi|4680695|gb|AAD27737.1|AF13296 - (AF132962) CGI-28 protein [Homo sapiens]	Contains protein domain (PF00573) - Ribosomal protein L4/L1 family	ribosomalprot	264259, 20281099, 35696052, 265008, 264594, 265011, 264760, 18108351, 264682, 264683, 264369, 264684, 264686, 264687, 264689, 21906766, 264691, 264692, 18108374, 18108377, 264557, 264639, 18108385
2428	85732889 (4855, 4856)	Novel Protein sim. GBank gi|1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]			22278996, 22278999, 35696052, 21906754, 264288, 21906765, 21906768, 21906769, 35695917, 265020, 263972, 22279002
2429	87769276 (4857, 4858)	Novel Protein sim. GBank gi|601931 (M94316) - neurofilament-H [Oryctolagus cuniculus]	Contains protein domain (PF00711) - Beta defensins	UNCLASSIFIED	22278999, 29331824, 264906, 264909, 264511, 265009, 21906754, 265017, 265018, 265019, 264448, 264683, 264288, 21906765, 21906768, 265021, 264693, 18108381
2430	86948827 (4859, 4860)			UNCLASSIFIED	264112, 264691
2431	87649884 (4861, 4862)	Novel Protein sim. GBank gi|3860729|emb|CAA14630| - (AJ235270) CELL DIVISION PROTEIN FTSJ (ftsJ) [Rickettsia prowazekii]	Contains protein domain (PF01728) - FtsJ cell division protein		29331826, 29331827, 35696052, 29146499, 264905, 264906, 264681, 264288, 264689, 21906765, 264692, 35696423
2432	80083033 (4863, 4864)	Novel Protein sim. GBank gi|3876367|emb|CAA93287| - (Z69360) Weak similarity to Elmeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89266 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans]		protease	264634, 264558
2433	80055092 (4865, 4866)	Novel Protein sim. GBank gi|2224593|dbj|BAA20784| - (AB002324) KIAA0326 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264569, 264905, 265018, 264762, 264683, 264691, 264556, 264557, 264639, 264558
2434	19520148 (4867, 4868)				264563
2435	20759044 (4869, 4870)			UNCLASSIFIED	264555
2436	88044008 (4871, 4872)	Novel Protein sim. GBank gi|1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	265008, 264758, 265010, 264689, 27486261, 263972, 18108374, 18108381
2437	83363424 (4873, 4874)	Novel Protein sim. GBank gi|3641352 (AF091234) - putative transcription factor [Mus musculus]		UNCLASSIFIED	29331828, 265007, 265009, 265017, 264760, 264685, 264693, 264565
2438	94143473 (4875, 4876)	Novel Protein sim. GBank gi|3860014 (AF091088) - unknown [Homo sapiens]	Contains protein domain (PF01256) - Uncharacterized protein family UPF0031	UNCLASSIFIED	29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 264910, 265009, 264591, 33657402, 21906754, 265011, 264760, 264764, 264685, 264686, 264768, 35695917, 33657023, 264693, 264631, 264632, 56182323, 264558, 83373044, 264563, 264564, 264565, 264566, 264567

2439	94850650 (4877, 4878)	Novel Protein sim. GBank gi|4263519|gb|AAD15345| - (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]	Contains protein domain (PF01423) - Sm protein	UNCLASSIFIED	60424179, 18108397, 56182575, 56181686, 56994075, 22278996, 35696286, 22278997, 22278999, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 29146498, 264509, 264905, 264906, 52644045, 60431735, 33109954, 21906754, 33657084, 55811386, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 33657109, 33657182, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 60431528, 263977, 55810764, 35696423, 65274791, 35695855, 60431850, 56182323, 60432113, 22279000, 22279002, 264567
2440	87641733 (4879, 4880)			UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264907, 264510, 265018, 265019, 264448, 264369, 265020, 265021, 56182323, 264639, 22279002
2441	87623914 (4881, 4882)	Novel Protein sim. GBank gi|3024889|sp|P56524|Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)		UNCLASSIFIED	264488, 264629, 18108374, 264564
2442	87273590 (4883, 4884)	Novel Protein sim. GBank gi|4506013|ref|NP_002703.1|pPPP1 - protein phosphatase 1, regulatory subunit 7	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	22278996, 22278999, 29331822, 264768, 264693
2443	84305949 (4885, 4886)	Novel Protein sim. GBank gi|1170658|sp|Q02975|KID1_RAT - RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17)	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264906
2444	88086345 (4887, 4888)	Novel Protein sim. GBank gi|4758824|ref|NP_004280.1|pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	264259, 18108382, 18108383, 18108385, 22279000
2445	87338636 (4889, 4890)	Novel Protein sim. GBank gi|2135950|pir||S58222 - PQ-rich protein - human			264259, 35696052, 264369, 18108361
2446	88059293 (4891, 4892)	Novel Protein sim. GBank gi|4753887|emb|CAA05409.2| - (AJ002424) p65 protein [Rattus norvegicus]	Contains protein domain (PF00095) - WAP-type (Whey Acidic Protein) 'four-disulfide core'	proteaseinhib	265011, 264689, 33657023, 263981, 18108385
2447	94845149 (4893, 4894)	Novel Protein sim. GBank gi|4885613|ref|NP_005409.1|pST5| - suppression of tumorigenicity 5		cadherin	56182575, 264259, 29331824, 29331825, 29331827, 60433356, 60433438, 264758, 265018, 264692, 65274620, 60431528, 65274791, 56182323

2448	87749680 (4895, 4896)			UNCLASSIFIED	22278996, 22278997, 22278999, 29331826, 35696052, 264107, 264110, 87168474, 87168559, 18108351, 21906767, 21906769, 27486262, 263976
2449	87869075 (4897, 4898)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!		cadherin	264259, 264828, 265007, 264595, 265021, 56526486
2450	86597784 (4899, 4900)			UNCLASSIFIED	264906
2451	91014563 (4901, 4902)	Novel Protein sim. GBank gi|1710021|sp|P35290|RB24_MOUSE - RAS-RELATED PROTEIN RAB-24 (RAB-16)	Contains protein domain (PF00071) - Ras family	glycoprotein	264093, 29331822, 29331824, 29331825, 66714117, 29331826, 29331828, 35696052, 264907, 66712502, 29331830, 264910, 265009, 264758, 265017, 265018, 264762, 264448, 264288, 21906767, 265021, 33657023, 264693, 33657109, 263969, 83373044, 18108385
2452	91230509 (4903, 4904)	Novel Protein sim. GBank gi|1504034|dbj|BAA13216| - (D86980) KIAA0227 [Homo sapiens]		isomerase	264102, 264112, 264688, 263972, 18108374, 83373044, 264563
2453	84201088 (4905, 4906)	Novel Protein sim. GBank gi|2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	ngfrecep	264509, 264512, 18108385
2454	95310691 (4907, 4908)	Novel Protein sim. GBank gi|1076802|pir||S49915 - extensin like protein - maize	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263994, 66714117, 29331827, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 264591, 264758, 264759, 265010, 265011, 264603, 264604, 264760, 264761, 264762, 18108351, 264764, 264765, 264766, 264686, 264768, 264769, 264534, 264691, 264692, 33657023, 264693, 33657109, 264628, 263978, 35695855, 264634, 264635, 264637, 264638, 264639, 83373044, 18108385, 264563, 264564, 264486
2455	95288301 (4909, 4910)	Novel Protein sim. GBank gi|543817|sp|P35585|AP47_MOUSE - CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)	Contains protein domain (PF00928) - Adaptor complexes medium subunit family	glycoprotein	264488, 22278996, 264259, 35696052, 264905, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264758, 265019, 264760, 264681, 18108351, 264683, 264764, 18108354, 264766, 264768, 264769, 264689, 21906766, 21906767, 21906769, 29148629, 35695917, 265020, 265022, 33657023, 33657109, 18108370, 264628, 264629, 264631, 264632, 264635, 56182323, 60170394, 18108385, 264563, 264564, 264566, 264567
2456	88166700 (4911, 4912)	Novel Protein sim. GBank gi|2588630 (AC003079) - Ankyrin-like; 54% similar to 2022340A (NID:g1092123) in exons spanning 43974 to 11551 of clone. [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	264693

2457	94118375 (4913, 4914)	Novel Protein sim. GBank gi|3025447 (AC004528) - R32184_3 [Homo sapiens]		UNCLASSIFIED	56181686, 264905, 264907, 264511, 264596, 55811386, 264682, 264684, 264685, 264687, 264691, 33657023, 264693, 35695855, 264636, 264555, 56182323, 264558, 56526486, 264563
2458	85875304 (4915, 4916)	Novel Protein sim. GBank gi|2384942 (AF022985) - Similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	264691, 264693, 264834, 264559
2459	87551913 (4917, 4918)	Novel Protein sim. GBank gi|5441942|gb|AAD43187.1|AC00499 - (AC004997) supported by mouse EST AA538043 (NID:g2284036) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport	27486265
2460	94315289 (4919, 4920)	Novel Protein sim. GBank gi|4929701|gb|AAD34111.1|AF15187 - (AF151874) CGI-116 protein [Homo sapiens]		kinase	65274572, 35696286, 22278996, 22278997, 60432049, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 29146499, 264102, 264109, 60433438, 265017, 265018, 265019, 264288, 21906765, 21906766, 21906769, 35695917, 265020, 264691, 33657023, 27486261, 18108374, 35695855, 87168518, 60432113
2461	87645147 (4921, 4922)	Novel Protein sim. GBank gi|4426962|gb|AAD20633| - (AF126062) Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264259, 29331828, 264910, 18108351, 18108370, 18108374
2462	86998002 (4923, 4924)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]			264909, 264758, 264684, 18108374, 264637, 18108385
2463	84388543 (4925, 4926)	Novel Protein sim. GBank gi|5052516|gb|AAD38588.1|AF14561 - (AF145613) BcDNA.GH03108 [Drosophila melanogaster]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264681, 264566
2464	91219957 (4927, 4928)	Novel Protein sim. GBank gi|5410300|gb|AAD43021.1| - (AF100757) COP9 complex subunit 4 [Homo sapiens]	Contains protein domain (PF01399) - PCI domain	protease	264489, 52646842, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 264509, 52644045, 264510, 264511, 264512, 265008, 60170831, 264593, 52646317, 33109954, 33657084, 265017, 265018, 265019, 264762, 264448, 264764, 264288, 264766, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 18108370, 18108381, 60170394, 18108385, 22279002, 264486

2465	95357483 (4929, 4930)	Novel Protein sim. GBank gi|4506401|ref|NP_002871.1|pRAF1 - v-raf-1 murine leukemia viral oncogene homolog 1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	oncogene	18108392, 52644507, 52645156, 52646365, 22278994, 22278995, 35696286, 22278996, 22278998, 264259, 29331822, 29331824, 29331825, 60424269, 60432289, 29331827, 35696052, 29331828, 264907, 29331830, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264910, 33657402, 60433438, 55812038, 21906754, 33109954, 265010, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264369, 264288, 264685, 264767, 21906765, 21906767, 21906768, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 52645129, 33657109, 27486261, 27486264, 35695763, 264628, 263972, 18108374, 35695855, 264636, 264637, 60170394, 56526486, 87168518, 60432113, 264563, 264564, 264566, 264487
2466	85681386 (4931, 4932)	Novel Protein sim. GBank gi|4321619|gb|AAD15788.1| - (AF051098) seven transmembrane domain orphan receptor [Mus musculus]			264369
2467	88059465 (4933, 4934)	Novel Protein sim. GBank gi|3513300 (AC005595) - F16601_1, partial CDS [Homo sapiens]		UNCLASSIFIED	56994075, 264908, 21906768, 33657023
2468	87614696 (4935, 4936)	Novel Protein sim. GBank gi|2143455|pir||I58106 - gene DMR-N9 protein - mouse (fragment)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	29331824, 52644045, 265008, 264910, 265019, 21906765, 21906769, 265021
2469	86294397 (4937, 4938)				264288, 264628
2470	80223831 (4939, 4940)	Novel Protein sim. GBank gi|5420389|emb|CAB46680.1| - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264592, 264692, 264555, 264556, 264557, 264558, 264559, 18108385, 264482
2471	91013681 (4941, 4942)	Novel Protein sim. GBank gi|5419882|emb|CAB46424.1| - (AL096749) DKFZp434G153 [Homo sapiens]		UNCLASSIFIED	65274572, 35696286, 29331827, 265007, 264592, 33109954, 265018, 265019, 264288, 55811957, 265020, 264693, 55811576, 56182323
2472	95060811 (4943, 4944)	Novel Protein sim. GBank gi|4929747|gb|AAD34134.1|AF15189 - (AF151897) CGI-139 protein [Homo sapiens]		UNCLASSIFIED	264092, 60432049, 29331825, 60433356, 265010, 265011, 18108351, 264764, 264288, 264692, 65274620, 18108370, 18108372, 18108374, 264634, 18108385
2473	95421509 (4945, 4946)	Novel Protein sim. GBank gi|4539009|emb|CAB39630.1| - (AL049481) putative protein [Arabidopsis thaliana]			60424179, 65274572, 22278999, 60424269, 29331826, 265008, 60433356, 60433438, 265010, 18108351, 264448, 264288, 264687, 264689, 265021, 264692, 65274620, 60431528, 65274791, 264556, 56182323, 60432113
2474	94315616 (4947, 4948)	Novel Protein sim. GBank gi|3252827 (AC004382) - Unknown gene product [Homo sapiens]			65274572, 56994075, 264259, 29331826, 60170831, 265017, 265018, 265019, 264683, 264369, 265020, 264693, 264563, 264564

2475	94321693 (4949, 4950)	Novel Protein sim. GBank gi|1216486 (U48852) - HT protein [Cricetulus griseus]	Contains protein domain (PF00008) - EGF-like domain	tgf	264259, 29331822, 265006, 265007, 265010, 265011, 264448, 264288, 264369, 264685, 264686, 18108357, 264768, 18108362, 264693, 18108370, 18108374, 18108379, 35696423, 83373044, 18108383, 18108385, 264564, 264565, 264567
2476	94315618 (4951, 4952)	Novel Protein sim. GBank gi|3252827 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 60424269, 66714117, 264905, 265006, 264511, 265008, 265009, 264758, 265010, 265011, 18108351, 264681, 264369, 264288, 264689, 21906767, 265020, 18108374, 264639, 18108382, 83373044, 18108385, 87168518
2477	20718974 (4953, 4954)			UNCLASSIFIED	263978
2478	17659165 (4955, 4956)			UNCLASSIFIED	265017
2479	94314569 (4957, 4958)	Novel Protein sim. GBank gi|1644232|dbj|BAA11082| - (D67066) N-WASP [Bos taurus]		tm7	56994075, 22278999, 21906754, 264682, 21906765
2480	95295605 (4959, 4960)			UNCLASSIFIED	264905, 264907, 264765
2481	94718481 (4961, 4962)	Novel Protein sim. GBank gi|5689469|dbj|BAA83018.1| - (AB028989) KIAA1066 protein [Homo sapiens]		collagen	65274572, 56182575, 22278997, 264094, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 56182435, 265008, 264910, 33657402, 55812038, 264758, 265010, 265011, 265017, 265018, 264760, 264762, 18108351, 264764, 264288, 264766, 264686, 264768, 21906768, 55811957, 265020, 264691, 264692, 264693, 264629, 55811576, 264630, 264634, 264635, 264636, 264637, 264556, 264558, 56182323, 83373044, 60432113, 22279002
2482	87393165 (4963, 4964)	Novel Protein sim. GBank gi|321249|pir||S28407 - guanine nucleotide-exchange activator CDC25 homolog - mouse		UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 264508, 264905, 264509, 264906, 264907, 264908, 264511, 264591, 264768, 264693, 264631, 264632, 264636, 264638, 264639, 264563
2483	87731583 (4965, 4966)			UNCLASSIFIED	264488, 22278995, 264093, 264095, 60432049, 60433356, 60433438, 264448, 264288, 263967, 18108370, 18108385, 18108388, 264482
2484	94187774 (4967, 4968)	Novel Protein sim. GBank gi|728831|sp|P39188|ALU1_HUMAN - !!!! ALU SUBFAMILY J WARNING ENTRY !!!!		kinase	264563
2485	87786556 (4969, 4970)	Novel Protein sim. GBank gi|1185397 (U25281) - SH3 domain binding protein [Rattus norvegicus]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 60432289, 29331827, 265007, 264910, 264593, 264600, 264603, 264604, 265019, 264448, 264288, 264685, 264686, 264769, 264689, 35695917, 265022, 264692, 264693, 56182323

2486	87748978 (4971, 4972)	Novel Protein sim. GBank gi|2662167|dbj|BAA23715| - (AB007903) KIAA0443 [Homo sapiens]			265017, 264555
2487	95343105 (4973, 4974)	Novel Protein sim. GBank gi|464559|sp|P35287|RB14_RAT RAS-RELATED PROTEIN RAB-14	Contains protein domain (PF00071) - Ras family	glycoprotein	22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331822, 35696052, 264106, 264905, 264907, 29331830, 264909, 265006, 264511, 265008, 265009, 60433438, 21906754, 33109954, 87168559, 265018, 264681, 264288, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 264534, 33657023, 264692, 33657109, 263972, 18108377, 35696423, 35695855, 60170394, 18108385, 56526486, 22279000, 22279002, 264563, 264482, 264565, 20281169, 18108391
2488	87652451 (4975, 4976)			UNCLASSIFIED	264910, 264448, 264288, 264684, 264691, 264634
2489	82990585 (4977, 4978)	Novel Protein sim. GBank gi|4886439|emb|CAB43355.1| - (AL050253) hypothetical protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	264686, 264693, 55811576, 22279002
2490	88069609 (4979, 4980)	Novel Protein sim. GBank gi|2588624 (AC003083) - Rap2 interacting protein-like; similar to U73941 (PID:g1916018) [Homo sapiens]		UNCLASSIFIED	264907, 265008, 22279002
2491	91242116 (4981, 4982)	Novel Protein sim. GBank gi|728832|sp|P39189|ALU2_HUMAN - !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!		tm7	264259, 29331826, 265008, 264762, 18108370, 18108376, 18108379
2492	95308202 (4983, 4984)	Novel Protein sim. GBank gi|3355303 (AF001549) - Unknown gene product [Homo sapiens]		transcriptfactor	264488, 22278998, 22278999, 29331828, 264591, 33109954, 265017, 55811150, 21906764, 21906768, 264692, 60431528, 87168518, 60432113, 22279000

2493	95422415 (4985, 4986)	Novel Protein sim. GBank gi|4240307|dbj|BAA74932.1| - (AB020716) KIAA0909 protein [Homo sapiens]	Contains protein domain (PF01424) - R3H domain	struct	18108394, 264887, 65274572, 56182575, 22278995, 56994075, 60432049, 29331822, 29331824, 29331825, 29331826, 29331827, 29146498, 264508, 264905, 264509, 264906, 264907, 29331830, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 264910, 21906754, 265011, 264600, 265017, 265018, 264604, 264605, 265019, 55811150, 264762, 18108351, 264681, 264448, 264683, 264369, 264288, 18108355, 18108357, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264691, 264692, 33657023, 33657349, 18108370, 18108374, 18108376, 55810764, 18108379, 65274791, 264630, 264632, 264634, 264635, 264636, 264555, 264637, 264557, 264558, 264639, 264559, 83373044, 18108385, 87168518, 60432113, 22279000, 22279002, 264482, 264566, 264486
2494	30793118 (4987, 4988)			UNCLASSIFIED	264907, 264601
2495	94234551 (4989, 4990)	Novel Protein sim. GBank gi|5420389|emb|CAB46680.1| - (AJ243460) proteophosphoglycan [Leishmania major]		collagen	263994, 22278997, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264595, 264604, 264448, 264682, 264764, 264288, 264685, 264766, 264769, 264689, 265020, 264692, 65274620, 264629, 55810764, 35696423, 55811576, 264636, 264637, 18108385, 22279000, 264564, 264567, 264486
2496	80018765 (4991, 4992)	Novel Protein sim. GBank gi|4808220|emb|CAB42832.1| - (AL022315) dJ1177I5.1 (PUTATIVE novel protein) [Homo sapiens]		struct	29147620, 264905, 265006, 265007, 18108348, 18108362, 18108370, 18108374, 264555, 264556, 18108381, 18108383, 18108388
2497	91723554 (4993, 4994)			UNCLASSIFIED	52644507, 22278996, 22278999, 29331824, 29331828, 33657402, 21906754, 87168474, 265019, 264369, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 33657023, 18108376, 18108387
2498	87724633 (4995, 4996)	Novel Protein sim. GBank gi|1200503 (U47924) - B [Homo sapiens]		UNCLASSIFIED	29331827, 264512, 264910, 264288, 18108374, 35695855
2499	94685125 (4997, 4998)	Novel Protein sim. GBank gi|3510234 (AC005581) - R31237_1, partial CDS [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264909, 55812038, 264631, 264637, 264558

2500	94648324 (4999, 5000)	Novel Protein sim. GBank gi|3881275|emb|CAA21725| - (AL032655) predicted using Genefinder; similar to Inositol monophosphatase family; cDNA EST yk255e11.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00459) - Inositol monophosphatase family	transport	52644507, 52645156, 22278995, 56994075, 35696286, 22278998, 264259, 52645080, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 35696052, 29331828, 264508, 264509, 264510, 264512, 33657402, 60433438, 21906754, 52644296, 87168474, 87168559, 264603, 264681, 264448, 264683, 264288, 264369, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 33657182, 35695763, 35696423, 35695855, 52644332, 83373044, 18108387, 87168518, 22279002
2501	94303896 (5001, 5002)	Novel Protein sim. GBank gi|4929615|gb|AAD34068.1|AF15183 - (AF151831) CGI-73 protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_rna_bind	65274572, 56182575, 35696286, 22278996, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264910, 264591, 60432229, 33657402, 60433356, 264595, 55812038, 264758, 264596, 87168474, 87168559, 264600, 264601, 264602, 265017, 264604, 265018, 264605, 265019, 18108351, 264448, 264369, 264288, 264766, 18108357, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 264692, 33657023, 264629, 35696423, 55811576, 35695855, 264630, 264634, 264635, 264555, 264636, 264638, 264558, 60170394, 83373044, 18108385, 18108387, 87168518, 60432113, 22279002, 264566
2502	90993716 (5003, 5004)	Novel Protein sim. GBank gi|3041847 (AC004542) - OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:g129308) [Homo sapiens]	Contains protein domain (PF01237) - Oxysterol-binding protein	UNCLASSIFIED	65274572, 264907, 56182435, 265007, 264592, 264760, 18108351, 264448, 264369, 264288, 264684, 264686, 55811957, 265021, 264692, 33657109, 263973, 55811576, 264635, 264555, 264556, 264557, 264558, 56182323, 264559, 87168518, 264563, 264482
2503	87878345 (5005, 5006)	Novel Protein sim. GBank gi|2196874|emb|CAA72638| - (Y11896) BRX protein [Mus musculus]			264905, 264907, 264512, 265008, 265011, 18108351, 264448, 264288, 29148627, 264693, 18108370, 18108374, 18108385

2504	87868706 (5007, 5008)	Novel Protein sim. GBank gi|550420|emb|CAA48220| - (X68101) trg [Rattus norvegicus]			264488, 52644507, 52645156, 52646842, 22278994, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264906, 264908, 52644045, 265009, 60433356, 33657402, 60433438, 264595, 33109954, 87168474, 265017, 265019, 264448, 264288, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 52644150, 264692, 27486261, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 52644332, 56182323, 18108387, 87168518, 60432113, 22279002, 264564
2505	8760559 (5009, 5010)			UNCLASSIFIED	264605
2506	91232326 (5011, 5012)	Novel Protein sim. GBank gi|2137562|pir||I49635 - mouse Dhm1 protein - mouse		nuclease	264488, 52644507, 52645156, 52646365, 65274572, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331826, 29331828, 264509, 56182435, 264112, 264593, 60433356, 55812038, 21906754, 265011, 265017, 265018, 265019, 264605, 264762, 18108351, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170615, 33657023, 27486264, 18108379, 35695855, 264637, 83373044, 18108385, 87168518, 60432113, 22279000, 264563, 264482, 264565
2507	95316233 (5013, 5014)	Novel Protein sim. GBank gi|5174489|ref|NP_006035.1|pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 263994, 264592, 264595, 264369, 264686, 264768, 35695917, 35696423, 264563
2508	95315505 (5015, 5016)	Novel Protein sim. GBank gi|4826433|emb|CAB42889.1| - (AL031447) dJ126A5.2.1 (novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 60432049, 264259, 29331828, 265006, 265007, 60433438, 33657084, 265010, 265017, 265018, 265019, 18108351, 264448, 18108354, 264369, 18108359, 21906765, 21906769, 55811957, 265020, 265022, 27486261, 33657349, 18108377, 35695855, 60432113, 22279002, 264563, 264565
2509	87813741 (5017, 5018)	Novel Protein sim. GBank gi|1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	265007, 265008, 18108357, 264556, 264567

2510	95421379 (5019, 5020)	Novel Protein sim. GBank gi|3293537|gb|AAC25762.1| - (AF071059) zinc finger RNA binding protein [Mus musculus]		dna_rna_bind	65274572, 22278994, 22278996, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 33656970, 264908, 66712502, 265007, 264910, 60170831, 60432229, 60433356, 60433438, 21906754, 87168474, 265017, 265018, 264448, 264288, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486262, 33657349, 18108370, 35695855, 264555, 56182323, 83373044, 60432113, 22279002
2511	87384281 (5021, 5022)	Novel Protein sim. GBank gi|4323152|gb|AAD16228.1| - (AF098863) Ets-protein Spi-C [Mus musculus]			265017, 21906764, 265020, 264692
2512	88084771 (5023, 5024)	Novel Protein sim. GBank gi|4502075|ref|NP_001135.1|pAMFR - autocrine motility factor receptor	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport	22278999, 264259, 29331825, 29331826, 29146499, 264907, 264909, 265006, 265008, 264591, 60432229, 21906754, 264763, 264683, 264766, 18108357, 264689, 21906769, 264693, 18108370, 263972, 18108374, 264558, 22279000
2513	95357843 (5025, 5026)	Novel Protein sim. GBank gi|3004657 (AF017777) - bobby sox [Drosophila melanogaster]		UNCLASSIFIED	60424179, 52645156, 18108394, 22278994, 35696286, 56994075, 22278996, 29331822, 29331824, 60424269, 29331825, 29331827, 33656970, 60431735, 33657084, 87168559, 265017, 264448, 264369, 56181562, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108366, 33657109, 27486261, 27486262, 33657349, 18108374, 55810764, 35696423, 56182323, 264558, 18108385
2514	88094578 (5027, 5028)	Novel Protein sim. GBank gi|2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	264510
2515	87994509 (5029, 5030)	Novel Protein sim. GBank gi|3757727|emb|CAA18783| - (AL022727) dJ80I19.7 (olfactory receptor-like protein (hs6M1-3)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	
2516	87786908 (5031, 5032)			UNCLASSIFIED	264259, 29146498, 264905, 264288, 29148629, 35695917, 27486261, 264634
2517	87784966 (5033, 5034)	Novel Protein sim. GBank gi|4220527|emb|CAA23000| - (AL035356) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264091, 29331824, 29331825, 29331826, 29331828, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 33657402, 264757, 33109954, 265017, 265018, 264605, 264760, 264762, 264763, 264766, 264768, 264769, 33657109, 33657182, 264628, 55811576, 35696423, 264631, 264634, 264637, 264638, 264639, 87168518, 22279002, 264564

2518	94147410 (5035, 5036)	Novel Protein sim. GBank gi|4929591|gb|AAD34056.1|AF15181 - (AF151819) CGI-61 protein [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 264907, 264909, 264511, 265007, 60432229, 60433356, 60433438, 55812038, 265010, 265017, 264448, 264288, 264689, 21906768, 21906769, 265022, 52644150, 264693, 18108370, 263972, 264555, 56182323, 83373044, 18108385, 60432113, 264088
2519	94326180 (5037, 5038)	Novel Protein sim. GBank gi|4263748|gb|AAD15420| - (AC004883) similar to KIAA0766; similar to PID:g3882253 [Homo sapiens]		kinase	264259, 66714117, 29331826, 29331827, 29331828, 264907, 66712502, 265006, 265008, 264594, 265010, 265011, 265018, 264288, 21906769, 265020, 60431528, 55811576, 65274791, 264632, 264555, 264636, 22279002, 264564
2520	87413235 (5039, 5040)	Novel Protein sim. GBank gi|4826722|ref|NP_005085.1|pFATP - fatty acid transport protein 4		transport	264259, 264908, 264910, 264682, 21906769, 265020, 264563
2521	95316244 (5041, 5042)	Novel Protein sim. GBank gi|5174489|ref|NP_006035.1|pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 264489, 263994, 65274572, 22278995, 22278998, 264259, 29331822, 29331826, 264508, 264905, 264509, 264906, 264907, 66712502, 264511, 265006, 265007, 264591, 264592, 264593, 264594, 264595, 264596, 264681, 264448, 264763, 264682, 264764, 264684, 264369, 264288, 264685, 264686, 21906768, 55811957, 264692, 264693, 27486261, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264632, 264558, 18108385, 65274727, 60432113, 264563, 264564, 264565, 264566, 264567
2522	87754052 (5043, 5044)	Novel Protein sim. GBank gi|4580011|gb|AAD24201.1|U81002_ - (U81002) TRAF4 associated factor 1 [Homo sapiens]		transport	264489, 22278997, 20281171, 21906754, 35695917, 263967, 263976, 263981, 20281169
2523	95340467 (5045, 5046)				263969
2524	95340469 (5047, 5048)	Novel Protein sim. GBank gi|1809327 (U76374) - skm-BOP2 [Mus musculus]	Contains protein domain (PF01753) - MYND finger		56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 56182435, 264512, 265008, 60170831, 33657402, 265010, 87168559, 265019, 264288, 21906765, 21906769, 35695917, 265020, 265021, 265022, 52644150, 264691, 33657023, 33657109, 27486261, 35696423, 65274791, 264559, 83373044, 56526486, 87168518, 264567

2525	94126928 (5049, 5050)	Novel Protein sim. GBank gi|2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]		kinase	264488, 22278997, 22278999, 60432049, 60432289, 29331828, 264905, 265008, 55812038, 21906754, 265019, 264369, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 33657109, 60431528, 83373044, 60432113, 22279000, 22279002, 264565
2526	95289404 (5051, 5052)	Novel Protein sim. GBank gi|4589628|dbj|BAA76836.1| - (AB023209) KIAA0992 protein [Homo sapiens]	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomalprot	60424179, 264768, 264687, 264769, 264689, 65274572, 21906767, 56182575, 21906768, 21906769, 55811957, 22278994, 22278995, 35696286, 35695917, 22278996, 22278997, 265020, 22278998, 265021, 22278999, 265022, 264690, 264691, 60432049, 264259, 264097, 33657023, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 27486262, 264508, 264509, 264905, 264907, 18108370, 66712502, 60431528, 264828, 264909, 18108372, 18108374, 56182435, 18108376, 55810764, 55811576, 35696423, 35695855, 265006, 265007, 264512, 265008, 265009, 264634, 264635, 60431850, 264636, 264555, 264592, 60431735, 264638, 33657402, 56182323, 60433356, 60433438, 264595, 55812038, 264596, 264758, 83373044, 52646317, 18108385, 33657084, 18108387, 55811386, 65274727, 56526486, 87168518, 60432113, 265017, 22279000, 265018, 265019, 264564, 18108351, 264448, 264566, 264288, 264486, 264567, 264766
2527	88094580 (5053, 5054)	Novel Protein sim. GBank gi|2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354
2528	88078380 (5055, 5056)	Novel Protein sim. GBank gi|2085786 (AC002086) - similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:g1399185) [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_rna_bind	55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2529	86670926 (5057, 5058)	Novel Protein sim. GBank gi|3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]		synthase	264908, 264769, 265020, 265021, 18108383
2530	80259978 (5059, 5060)				264369, 264556
2531	87768931 (5061, 5062)			UNCLASSIFIED	29331822, 29331824, 60432289, 264508, 264509, 264906, 265011, 264769, 21906768, 33657023, 87168518, 22279000
2532	87419778 (5063, 5064)	Novel Protein sim. GBank gi|2864625|emb|CAA16972| - (AL021811) putative protein [Arabidopsis thaliana]			264593
2533	87000255 (5065, 5066)	Novel Protein sim. GBank gi|437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]		UNCLASSIFIED	264555

2534	87332322 (5067, 5068)	Novel Protein sim. GBank gi|3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]		UNCLASSIFIED	264259, 35696052, 264905, 265017, 21906769, 265020, 265022, 33657109, 22279000
2535	91225056 (5069, 5070)	Novel Protein sim. GBank gi|4468311|emb|CAB37992| - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			65274572, 35696286, 60432289, 29331828, 66712502, 265006, 60432229, 265017, 265018, 265019, 264288, 264369, 264689, 21906768, 265020, 265021, 264636, 60170394, 22279002
2536	94218540 (5071, 5072)	Novel Protein sim. GBank gi|728836|sp|P39193|ALU6_HUMAN - !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!		kinase	18108398, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331826, 29331827, 29331828, 264905, 264511, 265009, 264910, 264596, 52646317, 18108351, 264681, 264683, 18108354, 264288, 264687, 264769, 264689, 21906765, 21906766, 21906767, 265021, 52645129, 33657109, 18108374, 18108380, 56182323, 18108381, 18108388, 87168518, 60432113, 22279000, 22279002, 264567, 18108391
2537	95422283 (5073, 5074)	Novel Protein sim. GBank gi|4557026|ref|NP_003913.1|pHERC - guanine nucleotide exchange factor p532		ubiquitin	65274572, 35696286, 29331822, 29331825, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 265011, 264760, 264288, 264685, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 18108374, 35696423, 35695855, 264636, 264558, 60170394, 56182323, 83373044
2538	36853454 (5075, 5076)			UNCLASSIFIED	
2539	94144916 (5077, 5078)			UNCLASSIFIED	22278998, 22278999, 29331822, 29331825, 29331828, 29146499, 264908, 264112, 60170831, 87168559, 264604, 265019, 264685, 264766, 87168518, 22279000, 264565, 264566
2540	94218545 (5079, 5080)	Novel Protein sim. GBank gi|1362647|pir||S53876 - sex-regulated protein janus A - fruit fly (Drosophila pseudoobscura)		UNCLASSIFIED	22278997, 29331828, 265008, 265009, 264758, 265010, 18108351, 264683, 264288, 21906765, 35695917, 265020, 18108374, 264567
2541	95308238 (5081, 5082)	Novel Protein sim. GBank gi|1711658|sp|P54797|T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264488, 264768, 264689, 264511, 20281171, 264634, 264635, 264691, 264639, 29331824, 264603, 264604, 264905, 264907, 264908, 264766

2542	95298162 (5083, 5084)	Novel Protein sim. GBank gi|5225320|gb|AAD40850.1|AF08310 - (AF083107) sirtuin type 2 [Homo sapiens]	Contains protein domain (PF00220) - Neurohypophysial hormones, N-terminal Domain	UNCLASSIFIED	264488, 18108394, 52646365, 52646842, 65274572, 22278994, 35696286, 22278996, 264259, 52645080, 29331822, 29331824, 29331827, 35696052, 33656970, 264907, 264909, 52644045, 264510, 265006, 264512, 265007, 265008, 265009, 264910, 60431735, 52646317, 52644296, 265010, 265011, 265018, 265019, 18108351, 264683, 264288, 264685, 264687, 52644229, 264769, 21906766, 21906767, 21906769, 52644150, 33657023, 33657109, 52645129, 33657182, 27486261, 27486264, 33657349, 35695763, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264558, 83373044, 18108385, 18108387, 87168518, 264563, 264564
2543	94139088 (5085, 5086)	Novel Protein sim. GBank gi|5419857|emb|CAB46374.1| - (AL096723) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)		65274572, 56182575, 22278999, 264259, 29331826, 264907, 264510, 264511, 264592, 264595, 264764, 264369, 264288, 264684, 264766, 264689, 21906765, 21906767, 21906769, 60170615, 264692, 264693, 55811578, 65274791, 264636, 264556, 18108381, 60170394, 264639, 18108385, 60432113, 22279000
2544	94218549 (5087, 5088)	Novel Protein sim. GBank gi|2498110|sp|Q63191|AEGP_RAT - APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR	Contains protein domain (PF00629) - MAM domain.	glycoprotein	18108397, 52646365, 22278997, 264259, 60432049, 29331822, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 265006, 265007, 265008, 87168559, 265017, 265018, 265019, 18108351, 264448, 264686, 264687, 264689, 21906765, 265020, 265021, 18108370, 18108374, 18108376, 18108381, 18108385, 18108387, 56526486, 22279000, 264482, 264563, 264567
2545	87742645 (5089, 5090)	Novel Protein sim. GBank gi|3327046|dbj|BAA31591| - (AB014516) KIAA0616 protein [Homo sapiens]			29331825, 264906, 265009, 60170831, 265017, 264369, 21906767, 60170615, 264692, 33657109
2546	88093861 (5091, 5092)	Novel Protein sim. GBank gi|2996032 (AF054586) - brain finger protein [Rattus norvegicus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	29331824, 265007, 22279002

2547	94143869 (5093, 5094)	Novel Protein sim. GBank gi|4929607|gb|AAD34064.1|AF15182 - (AF151827) CGI-69 protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264488, 18108394, 52646842, 18108397, 58182575, 22278995, 56994075, 22278996, 22278997, 22278999, 264259, 2331822, 29331824, 29331826, 60432289, 29331827, 35696052, 29331828, 264104, 264508, 264905, 264906, 264908, 66712502, 264909, 58182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 60431735, 264594, 60433438, 21906754, 52646317, 265010, 265011, 264600, 264601, 265018, 265019, 264760, 18108351, 264682, 264448, 264288, 264369, 264684, 264686, 264687, 56181562, 264688, 264689, 21906765, 21906766, 21906767, 21906768, 29148627, 21906789, 55811957, 265020, 265021, 265022, 264690, 264691, 18108362, 264692, 264693, 27486261, 18108370, 18108374, 55810764, 55811576, 35696423, 35695855, 264635, 264636, 264555, 264637, 263981, 264557, 18108380, 264638, 56182323, 264558, 264559, 83373044, 18108385, 87168518, 22279002, 264584, 264566, 264486
2548	88179079 (5095, 5096)			UNCLASSIFIED	264488, 18108394, 52646365, 22278994, 35696286, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 56182435, 264511, 265007, 264512, 60433356, 87168559, 264684, 264369, 52644229, 265021, 33657023, 264692, 18108374, 52644332, 264557, 18108380, 18108381, 18108382, 18108384, 18108385, 60432113, 22279000, 22279002, 264563, 264567
2549	94196893 (5097, 5098)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	Contains protein domain (PF00412) - LIM domain containing proteins	struct	56182575, 22278996, 22278997, 22278998, 22278999, 264259, 264508, 264908, 29331830, 265009, 265010, 265018, 264688, 21906764, 21906765, 21906766, 21906767, 21906769, 265020, 265021, 52644150, 264691, 18108368, 60431602, 18108376, 35696423, 56182323, 18108387, 264567
2550	87778584 (5099, 5100)	Novel Protein sim. GBank gi|2143886|pir||I52523 - nucleoporin p62 homolog - rat (fragment)		UNCLASSIFIED	56182575, 29331822, 264105, 264512, 18108351, 35695917, 264637, 264638

2551	95308400 (5101, 5102)	Novel Protein sim. GBank gi|4337103|gb|AAD18079| - (AF129756) NG26 [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	UNCLASSIFIED	18108396, 65274572, 22278995, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 264905, 56182435, 265007, 60433438, 55812038, 21906754, 65274444, 265017, 265018, 264605, 265019, 264288, 21906766, 21906768, 21906769, 265020, 60170615, 264693, 33657109, 35696423, 264638, 56182323, 83373044, 22279000
2552	95332620 (5103, 5104)			UNCLASSIFIED	56182575, 35696286, 29331824, 29331826, 35696052, 29331828, 264508, 264907, 56182435, 265008, 264591, 33109954, 264760, 55811957, 35695917, 33657023, 33657109, 18108374, 55811576, 35696423, 35695855, 56182323, 264558
2553	95308243 (5105, 5106)	Novel Protein sim. GBank gi|1711658|sp|P54797|T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264686, 264488, 263976, 264768, 29331826, 35696052, 35696423, 264601, 264511, 264602, 264910, 264634, 264760, 264555, 264762, 264906, 264592, 264691, 264566, 264908, 264684, 264567, 264909, 264766
2554	87761520 (5107, 5108)	Novel Protein sim. GBank gi|728835|sp|P39192|ALU5_HUMAN - !!!! ALU SUBFAMILY SC WARNING ENTRY !!!!		cadherin	22278997, 29331822, 264508, 21906769, 33657023, 33657109, 56182323
2555	87627551 (5109, 5110)	Novel Protein sim. GBank gi|4884319|emb|CAB43260.1| - (AL050084) hypothetical protein [Homo sapiens]		nuclease	29331824, 263972
2556	87645533 (5111, 5112)	Novel Protein sim. GBank gi|4106984 (AC003038) - R30923_1 [Homo sapiens]	Contains protein domain (PF00514) - Armadillo/beta-catenin-like repeats	UNCLASSIFIED	22278998, 264509, 33657402, 264683, 264684, 264766, 264689, 33657023, 33657109, 35695855, 264558, 264567
2557	79437803 (5113, 5114)				264595
2558	87617591 (5115, 5116)	Novel Protein sim. GBank gi|119110|sp|P03211|EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	22278997, 29331824, 66714117, 29331825, 264906, 264511, 265018, 264448
2559	88096382 (5117, 5118)	Novel Protein sim. GBank gi|4538998|emb|CAB39619.1| - (AL049481) AIG1-like protein [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 29331822, 29331828, 60433356, 265011, 264288, 264765, 264766, 264769, 21906765, 21906766, 60432113, 264482
2560	87994530 (5119, 5120)	Novel Protein sim. GBank gi|5051399|emb|CAB44995.1| - (AL078630) 573K1.3 (mm17M1-4 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor LIKE) protein)) [Mus musculus]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		
2561	88176575 (5121, 5122)	Novel Protein sim. GBank gi|5326825|gb|AAD42056.1|AF04495 - (AF044953) NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens]		UNCLASSIFIED	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 265007, 60432229, 87168559, 265017, 265018, 265019, 264689, 21906766, 21906769, 35695917, 265020, 33657023, 33657109, 18108374, 264634, 264559, 18108385, 87168518, 22279002

2562	87645539 (5123, 5124)	Novel Protein sim. GBank gi|4106984 (AC003038) - R30923_1 [Homo sapiens]			UNCLASSIFIED	56994075, 22278996, 22278997, 22278999, 264259, 29331822, 60432289, 33657402, 60433356, 21906765, 55811957, 60170615, 33657023, 264693, 35695855, 87168518
2563	88095497 (5125, 5126)	Novel Protein sim. GBank gi|4886447|emb|CAB43371.1| - (AL050270) hypothetical protein [Homo sapiens]			UNCLASSIFIED	264488, 35696286, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264907, 264908, 264909, 52644045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21906767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264583, 264565, 264566, 264486
2564	80502783 (5127, 5128)	Novel Protein sim. GBank gi|1352944|sp|P47179|YJ9P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR			sulfotransferase	29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2565	85530906 (5129, 5130)				UNCLASSIFIED	66714117, 264909, 263978, 264632
2566	80224956 (5131, 5132)	Novel Protein sim. GBank gi|628012|pir|A53933 - myosin I myr 4 - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	struct		18108370, 35695855, 264556, 264558, 18108383
2567	88143590 (5133, 5134)					265020, 60170615
2568	91233099 (5135, 5136)	Novel Protein sim. GBank gi|466009|sp|P34548|YNJ4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III			synthase	60424178, 18108394, 56181686, 56994075, 22278999, 264490, 264259, 29331822, 56182181, 29331824, 60424269, 29331825, 29331826, 29331828, 264509, 29331830, 265007, 265008, 265009, 33657402, 265010, 265011, 265019, 264448, 264683, 264288, 18108354, 264769, 21906766, 21906767, 35695917, 265021, 33657023, 18108362, 33657109, 33657182, 35695763, 60431528, 55810764, 18108379, 83373044, 18108385, 60432113, 264482

2569	95313764 (5137, 5138)	Novel Protein sim. GBank gi|2599560|gb|AAB84166.1| - (AF029674) basic leucine zipper protein LZIP [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	18108394, 56182575, 56181686, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 56182181, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264906, 56182435, 265008, 265009, 264910, 60432229, 264592, 60433356, 60433438, 21906754, 87168559, 265017, 265018, 265019, 264682, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 35695917, 265021, 265022, 52644150, 264690, 264691, 264692, 264693, 65274620, 263967, 35695763, 20281069, 263974, 18108374, 55810764, 35696423, 35695855, 264558, 18108381, 56182323, 18108382, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264566
2570	94136754 (5139, 5140)	Novel Protein sim. GBank gi|4758954|ref|NP_004567.1|pPPP2 - protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	Contains protein domain (PF01240) - Protein phosphatase 2A regulatory subunit PR55	phosphatase	22278998, 29331822, 29331824, 66714117, 29331825, 60432289, 29331827, 35696052, 264907, 264510, 265007, 265009, 264758, 33109954, 265019, 264686, 264689, 265020, 265021, 264691, 264692, 264693, 18108374, 35695855, 264634, 56182323, 264639, 60170394, 83373044, 22279002, 264482
2571	87733750 (5141, 5142)	Novel Protein sim. GBank gi|732218|sp|P34609|YO60_CAEEL - HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III		struct	264508, 264905, 264907, 264828, 18108351, 264555, 264556, 264557, 264558, 264559
2572	87627560 (5143, 5144)	Novel Protein sim. GBank gi|4884319|emb|CAB43260.1| - (AL050084) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35696286, 29331827, 35696052, 264100, 264104, 264110, 264592, 21906754, 29148627, 29148629, 263972, 263974, 18108374, 263976, 35695855, 60170394, 264559, 18108385

2573	95313929 (5145, 5146)	Novel Protein sim. GBank gi|399138|sp|P02745|C1QA_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264488, 60424179, 65274572, 56182575, 56181686, 22278995, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264104, 264107, 264508, 264906, 29331830, 264909, 264510, 265006, 264512, 265008, 265009, 264910, 264591, 264592, 60432229, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264761, 264762, 264763, 264764, 264369, 264288, 264685, 264766, 264686, 264687, 264688, 264769, 56181562, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 21906769, 265020, 265021, 265022, 60170615, 264690, 52644150, 264691, 264692, 33657023, 65274620, 18108365, 18108368, 27486265, 60431602, 264629, 60431528, 263976, 65274791, 35695855, 20281071, 60431850, 264637, 264638, 264558, 264639, 56182323, 60170394, 83373044, 18108384, 87168518, 60432113, 264482, 264564, 264565, 264566, 264567
2574	94746814 (5147, 5148)	Novel Protein sim. GBank gi|3334982 (AC005306) - R27218_1 [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	UNCLASSIFIED	22278995, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 265008, 264910, 264591, 33657402, 265018, 265019, 264448, 264764, 264369, 264288, 18108357, 21906765, 21906766, 21906768, 55811957, 60170615, 264691, 33657023, 264693, 33657109, 33657182, 27486261, 27486264, 33657349, 264636, 264555, 83373044, 18108385, 264482
2575	87754408 (5149, 5150)	Novel Protein sim. GBank gi|4929729|gb|AAD34125.1|AF15188 - (AF151888) CGI-130 protein [Homo sapiens]		UNCLASSIFIED	264910, 264601, 264683, 264689, 264080
2576	95357881 (5151, 5152)	Novel Protein sim. GBank gi|4680681|gb|AAD27730.1|AF13295 - (AF132955) CGI-21 protein [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264259, 35696052, 264906, 60433438, 264681, 18108351, 264288, 52644150, 264628, 35696423
2577	86996621 (5153, 5154)	Novel Protein sim. GBank gi|4337103|gb|AAD18079| - (AF129756) NG26 [Homo sapiens]		UNCLASSIFIED	29331825, 265018, 265019, 264685
2578	87786941 (5155, 5156)			UNCLASSIFIED	264488, 264906, 264908, 264910, 264598, 264603, 264604, 264605, 264766, 21906769, 264628, 264630, 264634, 264639, 264563
2579	87292879 (5157, 5158)			UNCLASSIFIED	29331822, 29331824, 264767

2580	88166788 (5159, 5160)	Novel Protein sim. GBank gi|2588628 (AC003080) - Similar to KIAA0299; 60% similarity to AB002297 (PID:g2224539) [Homo sapiens]			265007, 265018, 264762
2581	87899048 (5161, 5162)	Novel Protein sim. GBank gi|4406642|gb|AAD20049| - (AF131809) Unknown [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	collagen	56994075, 29331824, 29331826, 29331828, 264905, 60433356, 60433438, 264758, 87168559, 21906769, 265022, 35695855, 263981
2582	87786789 (5163, 5164)	Novel Protein sim. GBank gi|2739367 (AC002505) - putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]		eph	264488, 264907, 264908, 264910, 264764, 264684, 264766, 264636, 264555, 264565
2583	91220950 (5165, 5166)	Novel Protein sim. GBank gi|4378112|emb|CAA16521.1| - (AL021578) dJ453C12.2 (similar to transcription factor RBP-L) [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	transcriptfactor	56181686, 264259, 264510, 264512, 264591, 264592, 264593, 264594, 264595, 264596, 264603, 264629, 55810764, 264630, 264637, 264565
2584	80430941 (5167, 5168)			UNCLASSIFIED	264908, 264910, 264768, 264693, 18108374, 55811578, 56182323
2585	80436126 (5169, 5170)	Novel Protein sim. GBank gi|2736151 (AF021935) - mytonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]		kinase	264768
2586	91226136 (5171, 5172)				22278998, 264259, 29331822, 29331824, 29331827, 29331828, 264906, 265007, 265009, 264591, 60433356, 33657402, 265018, 264762, 264288, 21906766, 21906767, 21906769, 265022, 264691, 83373044, 56526486, 22279002
2587	80430943 (5173, 5174)				264908, 265019, 264768, 264693, 55811576, 56182323
2588	80074385 (5175, 5176)			UNCLASSIFIED	264564
2589	85515607 (5177, 5178)	Novel Protein sim. GBank gi|3021598|emb|CAA71415| - (Y10389) nuclear protein [Xenopus laevis]		UNCLASSIFIED	35696052, 264905, 264906, 264907, 264908, 264909, 265009, 265018, 264769, 35698423, 264636
2590	87054526 (5179, 5180)	Novel Protein sim. GBank gi|2104689 (U92793) - alpha glucosidase II, alpha subunit [Mus musculus]	Contains protein domain (PF01055) - Glycosyl hydrolases family 31	glucoamylase	22278995, 29331830, 265008, 265010, 265017, 264639
2591	94192167 (5181, 5182)	Novel Protein sim. GBank gi|5702202|gb|AAD47199.1|AF12916 - (AF129166) long-chain acyl-CoA synthetase 5 [Homo sapiens]		eph	264259, 29331822, 264106, 264906, 56182435, 265007, 265008, 33109954, 264448, 55811957, 265020, 18108370, 55811576, 22279002

2592	95332648 (5183, 5184)	Novel Protein sim. GBank gi|3024998|sp|Q60936|YAB1_MOUSE - HYPOTHETICAL HEART PROTEIN		transport	18108397, 56182575, 35696286, 56994075, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264906, 264909, 265007, 265008, 264910, 60432229, 264594, 60433356, 60433438, 55812038, 18108348, 21906754, 265011, 87168559, 265017, 265019, 264764, 264369, 264288, 264766, 265021, 60170615, 33657023, 33657109, 264629, 35696423, 35695855, 264557, 264638, 60170394, 56182323, 83373044, 56526486, 87168518, 264563, 264482, 264565
2593	87754416 (5185, 5186)	Novel Protein sim. GBank gi|4929729|gb|AAD34125.1|AF15188 - (AF151888) CGI-130 protein [Homo sapiens]		tm7	22278999, 29331825, 264758, 21906754, 52646317, 265010, 18108351, 264288, 264369, 21906768, 264693, 18108370, 264637, 264638, 264482
2594	95305758 (5187, 5188)	Novel Protein sim. GBank gi|4929587|gb|AAD34054.1|AF15181 - (AF151817) CGI-59 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108398, 56182575, 35696286, 22278997, 264093, 264259, 29331822, 29331825, 66714117, 29331826, 264905, 264909, 52644045, 56182435, 264510, 264512, 265007, 264757, 21906754, 87168474, 265017, 264760, 264448, 264764, 264288, 264766, 264689, 21906768, 33657109, 263975, 263977, 264634, 264556, 60170394, 56182323, 56526486, 264482, 264563, 264564, 264566, 264567
2595	79561676 (5189, 5190)			UNCLASSIFIED	264692
2596	87538637 (5191, 5192)	Novel Protein sim. GBank gi|4309681|gb|AAD15478| - (AC006930) R33423_1 [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 265018, 264448, 265021, 60431528
2597	94784089 (5193, 5194)			UNCLASSIFIED	264905, 264509, 264908, 264762, 264766, 35695917, 35695855, 264635, 264636, 83373044, 264486
2598	88094948 (5195, 5196)	Novel Protein sim. GBank gi|1001351|dbj|BAA10838| - (D64006) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	22278998, 264259, 29331824, 87168474, 264683, 21906766, 35695917, 264691, 33657023, 33657109, 18108370, 18108374, 264564, 264565
2599	87642889 (5197, 5198)	Novel Protein sim. GBank gi|3941737 (AF109719) - BAT2 [Mus musculus]		MHC	264766, 264769, 21906768, 33657182, 35695763, 18108370, 18108374, 264635, 264636, 56526486, 22279000, 264566
2600	87787846 (5199, 5200)	Novel Protein sim. GBank gi|4263521|gb|AAD15347| - (AC004044) putative WD-repeat protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	35696286, 264093, 264288, 21906769, 35696423, 35695855

2601	91243070 (5201, 5202)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!		kinase	56182575, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 264906, 265007, 265008, 264591, 60433356, 33657402, 60433438, 21906754, 265011, 265018, 265019, 18108351, 264448, 264369, 21906769, 265020, 60170615, 264693, 33657109, 18108370, 18108376, 56182323, 18108381, 18108385, 22279002, 264563
2602	88180022 (5203, 5204)	Novel Protein sim. GBank gi|4406632|gb|AAD20047| - (AF131801) Unknown [Homo sapiens]			60433438, 21906754, 87168559, 264601, 264369, 264288, 21906767
2603	94325821 (5205, 5206)	Novel Protein sim. GBank gi|3122367|sp|Q61211|LIGA_MOUSE - LIGATIN		UNCLASSIFIED	264488, 65274572, 22278995, 22278996, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 56182435, 264113, 265008, 265009, 60433356, 264757, 60433438, 264759, 33657084, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264683, 18108354, 264288, 264767, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486262, 18108374, 35696423, 65274791, 35695855, 264555, 264636, 264637, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000
2604	94676601 (5207, 5208)	Novel Protein sim. GBank gi|5454030|ref|NP_006468.1|pRRP2 - RAS-related on chromsome 22		oncogene	264259, 35696052, 264508, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 264910, 33657402, 264604, 264605, 264762, 264763, 264682, 264764, 264683, 264768, 264769, 264689, 33657023, 264693, 18108365, 264628, 35696423, 264631, 264632, 264634, 264635, 264637, 18108381, 264639, 83373044, 264565
2605	94316756 (5209, 5210)	Novel Protein sim. GBank gi|3628745|dbj|BAA33366| - (AB013721) mitsugumin 23 [Oryctolagus cuniculus]		UNCLASSIFIED	22278998, 264490, 60432049, 264259, 60432289, 264909, 265008, 60433356, 60433438, 264758, 21906754, 265010, 265011, 265018, 264681, 18108351, 264288, 264766, 264685, 21906765, 21906766, 21906768, 21906769, 264691, 264692, 264693, 65274791, 264634, 264555, 264636
2606	87746406 (5211, 5212)				22278996, 264510, 264512, 265009, 264766, 22279002, 264566

2607	87627742 (5213, 5214)	Novel Protein sim. GBank gi|4826626|gb|AAD30202.1| - (AF135022) mediator [Homo sapiens]			29331822, 29331825, 29331826, 29331827, 29331828, 264906, 264907, 264908, 66712502, 264828, 56182435, 55812038, 265010, 265017, 265018, 265019, 264768, 264689, 21906765, 55811957, 265020, 265022, 264692, 33657023, 264693, 33657109, 18108370, 264639, 56182323
2608	81734786 (5215, 5216)	Novel Protein sim. GBank gi|2226005 (U49973) - ORF2: function unknown [Homo sapiens]			264509, 264907, 264908, 264592, 264758, 264631
2609	94843791 (5217, 5218)	Novel Protein sim. GBank gi|3024889|sp|P56524|Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 65274572, 35696286, 22278997, 22278999, 60432049, 264259, 56182181, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264907, 60433356, 60433438, 55812038, 265011, 87168559, 265017, 265018, 264448, 264765, 264288, 264766, 264689, 21906765, 21906767, 21906769, 265020, 265021, 264691, 264692, 33657109, 27486261, 18108370, 65274791, 264636, 264556, 56182323, 18108385, 56526486
2610	88177654 (5219, 5220)	Novel Protein sim. GBank gi|4336855|gb|AAD17989| - (AF106473) leucine-rich-domain inter-acting protein 1; LeR inter-acting protein 1; LEAP1 [Mus musculus]		transcriptfactor	18108394, 22278994, 56994075, 60432049, 264259, 29331822, 29331825, 60432289, 29331827, 264107, 264109, 264905, 56182435, 264112, 265006, 265007, 265008, 265009, 60433356, 60433438, 265011, 87168559, 265017, 264448, 264682, 264764, 264288, 265021, 33657023, 263967, 33657182, 27486261, 18108374, 263976, 55811576, 264638, 87168518, 60432113
2611	87428890 (5221, 5222)	Novel Protein sim. GBank gi|3876761|emb|CAA92994| - (Z68760) predicted using Genefinder; Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278999, 265017, 264684, 21906768, 22279000
2612	87771198 (5223, 5224)	Novel Protein sim. GBank gi|5679136|gb|AAD46874.1|AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	265009, 264910, 264759, 265017, 21906767, 18108365, 18108388, 60432113
2613	79481496 (5225, 5226)			UNCLASSIFIED	264685
2614	87643948 (5227, 5228)	Novel Protein sim. GBank gi|5533081|gb|AAD45009.1|AF16118 - (AF161181) P55T protein [Mus musculus]	Contains protein domain (PF00625) - Guanylate kinase		22278998, 22278999, 29331825, 264508, 264906, 21906754, 264602, 264766, 264769, 52644229, 21906765, 33657109, 27486264, 18108370, 263972, 264555, 60432113
2615	87381996 (5229, 5230)			UNCLASSIFIED	264768, 18108394, 264692, 264693, 264508, 264509, 264907, 264628, 264908, 264909, 18108377, 264511, 264512, 264910, 264635, 264595, 265010, 264404, 264563, 264764, 264685, 264766

2616	87428895 (5231, 5232)	Novel Protein sim. GBank gi|3876761|emb|CAA92994| - (Z68760) predicted using Genefinder; Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278995, 22278997, 22278998, 60432049, 60432289, 264828, 60433356, 264594, 60433438, 33109954, 87168474, 265011, 265017, 265019, 264288, 264766, 21906765, 21906767, 265020, 265021, 18108376, 18108377, 18108387, 87168518, 264482, 264567
2617	86976888 (5233, 5234)	Novel Protein sim. GBank gi|728831|sp|P39188|ALU1_HUMAN - !!!! ALU SUBFAMILY J WARNING ENTRY !!!!		kinase	265010, 265019, 264369, 264693, 55811576, 22279002
2618	91231662 (5235, 5236)	Novel Protein sim. GBank gi|3319282 (AF049103) - Huntingtin interacting protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	UNCLASSIFIED	264489, 22278996, 264490, 264259, 29331822, 264102, 264509, 264906, 264907, 66712502, 29331830, 265008, 264910, 265009, 60433356, 60433438, 264758, 21906754, 265011, 87168559, 265017, 265018, 264369, 264288, 264766, 264768, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 33657023, 264692, 33657109, 264628, 18108374, 35695855, 18108381, 83373044, 18108385, 18108388, 56526486, 264563
2619	87694000 (5237, 5238)	Novel Protein sim. GBank gi|2431772 (U66411) - putative type III alcohol dehydrogenase [Drosophila melanogaster]	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	dehydrogenase	264259, 60432289, 60433438, 21906754, 264369, 60432113, 264566
2620	95314841 (5239, 5240)	Novel Protein sim. GBank gi|4322567|gb|AAD16097| - (AF090436) dachshund variant 1 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	52644507, 52645156, 52646842, 65274572, 22278995, 56994075, 35696286, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 35696052, 264907, 66712502, 265008, 60433356, 33657402, 52646317, 21906754, 87168474, 265010, 265017, 265018, 264448, 264369, 264288, 264687, 264768, 52644229, 264688, 264689, 21906765, 21906768, 35695917, 52644150, 264692, 33657109, 35695763, 35696423, 264556, 52644332, 18108382, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 22279002
2621	80253495 (5241, 5242)				264594, 264636
2622	81780390 (5243, 5244)	Novel Protein sim. GBank gi|4557341|ref|NP_001174.1|pATP6 - ATPase, H+ transporting, lysosomal subunit 1; vacuolar proton pump; H-ATPase subunit			264488, 264906, 264907, 264908, 264512, 265007, 264758, 35695917, 264634, 264636, 264563, 264482
2623	91639306 (5245, 5246)	Novel Protein sim. GBank gi|3880355|emb|CAB05299| - (Z82285) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	29331824, 35696052, 265007, 265010, 264288, 29148629

2624	91639308 (5247, 5248)	Novel Protein sim. GBank gi|3880355|emb|CAB05299| - (Z82285) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	56181686, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331828, 35696052, 29146499, 66712502, 52644045, 265007, 265008, 60433356, 33109954, 21906754, 265010, 265011, 265019, 264448, 264288, 21906765, 21906766, 21906767, 29148629, 35695917, 265021, 265022, 27486265, 18108370, 60431528, 55811576, 35695855, 56182323, 18108385, 87168518, 22279002, 18108391
2625	86452068 (5249, 5250)	Novel Protein sim. GBank gi|2887429|dbj|BAA24857| - (AB007887) KIAA0427 [Homo sapiens]		UNCLASSIFIED	264091, 264511, 263981
2626	16533797 (5251, 5252)	Novel Protein sim. GBank gi|487416 (L20302) - actin filament protein [Gallus gallus]		struct	265008
2627	87636823 (5253, 5254)	Novel Protein sim. GBank gi|88462|pir||A27307 - proline-rich phosphoprotein (gene PRH1, Db allele) - human		UNCLASSIFIED	22278996, 265007, 265009, 264448, 21906767, 265021, 264558, 87168518
2628	94848254 (5255, 5256)	Novel Protein sim. GBank gi|3123552|emb|CAA18609| - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]		UNCLASSIFIED	22278997, 22278999, 264259, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264907, 264909, 265008, 264591, 60433356, 60433438, 265010, 265017, 265018, 264369, 264288, 18108357, 21906765, 21906768, 265022, 65274791, 264638, 18108387, 87168518, 22279002
2629	87376490 (5257, 5258)	Novel Protein sim. GBank gi|4929595|gb|AAD34058.1|AF15182 - (AF151821) CGI-63 protein [Homo sapiens]		synthase	29331825, 29331826, 264102, 265006, 264766, 35695917, 264691, 33657023, 263972, 18108374, 22279000
2630	79188364 (5259, 5260)			UNCLASSIFIED	264836, 18108385
2631	94845909 (5261, 5262)	Novel Protein sim. GBank gi|321605|pir||JQ1161 - Gag protein - Visna virus (strain EV1)	Contains protein domain (PF00098) - Zinc finger, CCHC class	dna_rna_bind	52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35696286, 56994075, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264905, 264509, 264907, 264908, 264511, 264512, 265007, 265008, 264910, 52646317, 33657084, 52644296, 265010, 87168559, 265017, 265018, 265019, 264760, 264762, 264448, 264288, 264369, 264766, 264768, 52644229, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 35696423, 65274791, 35695855, 264634, 264637, 52644332, 56182323, 60432113, 264566, 264486
2632	36730414 (5263, 5264)				264685

2633	95011617 (5265, 5266)	Novel Protein sim. GBank gi|1139548|db||BAA10889| - (D64009) seizure-related gene product 6 type 2 precursor [Mus musculus]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)		22278995, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331827, 264508, 264906, 265006, 265007, 265008, 265009, 55812038, 33657084, 55811386, 265010, 265011, 87168559, 265018, 265019, 264683, 264288, 264686, 29148629, 33657023, 264693, 33657182, 35695763, 55811576, 264639, 56182323, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264565
2634	87330921 (5267, 5268)	Novel Protein sim. GBank gi|5441611|emb|CAB46854.1| - (AJ388555) hypothetical protein [Canis familiaris]		UNCLASSIFIED	29331826, 263972, 264089
2635	86623144 (5269, 5270)	Novel Protein sim. GBank gi|4680663|gb|AAD27721.1|AF13294 - (AF132946) CGI-12 protein [Homo sapiens]			22278997, 264259, 29331824, 66714117, 29331827, 29331828, 264907, 33657084, 265017, 265018, 264448, 264288, 21906766, 21906767, 21906768, 29148629, 18108376, 55811576, 35695855, 87168518, 22279000
2636	87260534 (5271, 5272)	Novel Protein sim. GBank gi|3879146|emb|CAB07646| - (Z93386) Similarity to Yeast hypothetical 52.9 KD protein (SW:P43616); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D69025 comes ...	Contains protein domain (PF01546) - Peptidase family M20/M25/M40		264569, 29331822, 29331828, 265006, 60170831, 264681, 264765, 264685, 29148627, 21906769, 29148784, 265022, 60170615, 264635, 18108385, 56526486, 22279002, 264567
2637	95011299 (5273, 5274)	Novel Protein sim. GBank gi|4758208|ref|NP_004081.1|pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	264488, 264489, 52644507, 264887, 52646365, 52646842, 22278994, 22278996, 22278999, 20281171, 264259, 29331822, 52645080, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 29146498, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264591, 264592, 60432229, 264593, 264594, 33657402, 60433356, 264757, 60433438, 264596, 264758, 52646317, 21906754, 52644296, 265010, 264600, 264602, 264603, 264605, 264761, 264762, 264681, 264448, 264764, 264765, 264288, 264766, 264686, 264768, 264687, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 60170615, 264691, 33657023, 264692, 264693, 65274620, 27486264, 18108370, 264628, 264629, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 52644332, 264639, 264558, 83373044, 60432113, 264564, 264565, 264566, 264486, 264567

2638	94326733 (5275, 5276)	Novel Protein sim. GBank gi|4929689|gb|AAD34105.1|AF15186 - (AF151868) CGI-110 protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	60424179, 52644507, 52646842, 18108398, 56182575, 22278995, 22278996, 35696286, 22278997, 22278999, 264259, 60432049, 29331822, 60424269, 29331826, 35696052, 29146498, 264905, 52644045, 56182435, 60433356, 33657402, 55812038, 55811386, 265019, 264288, 264769, 52644229, 56181562, 29148627, 29148629, 55811957, 29148784, 35695917, 265021, 52644150, 33657023, 65274620, 33657109, 35695763, 18108374, 55810764, 35696423, 55811576, 35695855, 60431850, 56182323, 60432113, 264404
2639	95361346 (5277, 5278)	Novel Protein sim. GBank gi|2190007|dbj|BAA20355| - (AB004109) phosphatidylserine synthase II [Cricetulus griseus]		synthase	264488, 29331825, 35696052, 264508, 264509, 264909, 264512, 33657402, 60433438, 264758, 85658542, 264600, 265020, 265021, 33657109, 264628, 35696423, 264555, 264639, 264563, 264564, 264565, 264566, 264486
2640	87781330 (5279, 5280)	Novel Protein sim. GBank gi|3158516 (AF067617) - contains similarity to chromo (chromatin organization modifier) domains (Pfam: chromo.hmm. score: 17.76 and 27.94) and to helicases conserved C-terminal domain (Pfam: helicase_C.hmm, score: 67.00) [Caenorhabditis elegans]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	29331822, 29331826, 264906, 33109954, 265017, 265019, 21906768, 35695763, 264636, 264637, 18108387
2641	11669834 (5281, 5282)			UNCLASSIFIED	264828
2642	87412575 (5283, 5284)	Novel Protein sim. GBank gi|2564955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	264259, 29331822, 33657402, 265019, 264369, 264691, 264634, 56526486, 22279002
2643	87643961 (5285, 5286)	Novel Protein sim. GBank gi|4490304|emb|CAB38795.1| - (AL035678) putative protein [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278997, 264259, 29146499, 56182435, 264910, 265010, 18108351, 264682, 264683, 264369, 264684, 264685, 264686, 29148627, 264690, 33657109, 18108370, 263973, 18108374, 264634, 264557, 264558, 18108385, 264482
2644	88177671 (5287, 5288)	Novel Protein sim. GBank gi|3789797|gb|AAC67502.1| - (AF059569) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	nucl_recpt	264107, 264687
2645	17277228 (5289, 5290)			UNCLASSIFIED	265007
2646	94148542 (5291, 5292)	Novel Protein sim. GBank gi|1706722|sp|P49749|EVX2_MOUSE - HOMEOBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2)		UNCLASSIFIED	264909, 264687, 264632, 83373044

2647	91212978 (5293, 5294)			UNCLASSIFIED	56182575, 22278996, 35696286, 22278998, 264259, 29331822, 56182181, 29331825, 60424269, 60432289, 35696052, 66712502, 264908, 265007, 55812038, 33109954, 21906754, 33657084, 265019, 264448, 264288, 56181562, 21906765, 21906766, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 264693, 33657109, 33657349, 60431528, 18108374, 55810764, 35696423, 56182323, 60432113, 22279002, 264564
2648	87600587 (5295, 5296)				29146498, 56182435, 33109954, 265011, 264682, 55811957, 35695917, 264690, 263976, 18108377, 35696423, 60432113
2649	94128783 (5297, 5298)	Novel Protein sim. GBank gi|3041852 (AC004539) - unknown function; similar to Y09105 (PID:g1666171) [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278998, 29331824, 29331826, 60432289, 66712502, 56182435, 60170831, 60432229, 33657402, 33109954, 21906754, 265017, 264686, 264688, 21906765, 21906768, 60170615, 264693, 263967, 18108370, 263976, 60170394, 60432113, 22279002, 264563
2650	87297533 (5299, 5300)	Novel Protein sim. GBank gi|5360271|dbj|BAA81908.1| - (AB029335) HrPET-3 [Halocynthia roretzi]			264685
2651	88088745 (5301, 5302)	Novel Protein sim. GBank gi|4240225|dbj|BAA74891.1| - (AB020675) KIAA0868 protein [Homo sapiens]	Contains protein domain (PF00054) - Laminin G domain	synthase	29331824, 29331826, 29331827, 265007, 55812038, 21906754, 18108366, 18108384, 22279002, 264567
2652	10343125 (5303, 5304)			UNCLASSIFIED	264692
2653	87798735 (5305, 5306)	Novel Protein sim. GBank gi|4493956|emb|CAB11123.2| - (Z98551) predicted using hexExon; MAL3P6.28 (PFC0845c), Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR:...		UNCLASSIFIED	265018, 18108370, 18108387, 264566
2654	95103240 (5307, 5308)				60424179, 65274572, 56182575, 264259, 56182181, 264908, 56182435, 55811957, 35695917, 265021, 263976, 55810764, 65274791, 56182323, 83373044, 65274727
2655	91229018 (5309, 5310)	Novel Protein sim. GBank gi|3875272|emb|CAB02861| - (Z81051) predicted using Genefinder; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk443h5.3 comes from this gene; cDNA EST yk443h5.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transcriptfactor	56182575, 56181686, 264092, 264259, 56182181, 60432289, 264907, 33657402, 55812038, 21906754, 87168559, 265017, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21906768, 33657109, 18108370, 264628, 55811576, 264556, 264639, 83373044, 56526486, 264404, 60432113
2656	84562601 (5311, 5312)	Novel Protein sim. GBank gi|3043718|dbj|BAA25523| - (AB011169) KIAA0597 protein [Homo sapiens]			264693

2657	52561728 (5313, 5314)	Novel Protein sim. GBank gi|5689509|dbj|BAA83038.1| - (AB029009) KIAA1086 protein [Homo sapiens]		dna_rna_bind	264693
2658	88062454 (5315, 5316)	Novel Protein sim. GBank gi|3688089 (AC005757) - R32611_1 [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nucleaseinhib	35696286, 264259, 29331822, 29331824, 29331826, 29331828, 265019, 264683, 21906768, 35695917, 264693, 35695855, 264637, 87168518, 264486, 264567
2659	87600755 (5317, 5318)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01426) - BAH domain	UNCLASSIFIED	264909, 264910, 265018, 264369, 264769, 21906769, 264693, 263972, 18108388
2660	91718472 (5319, 5320)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	Contains protein domain (PF00036) - EF hand	kinase	264488, 65274572, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 35696052, 264908, 56182435, 265008, 265009, 60433356, 264594, 265010, 265018, 55811150, 18108351, 264682, 264684, 264369, 264288, 264687, 21906765, 29148784, 35695917, 60170615, 52644150, 33657023, 33657109, 35696423, 35695855, 264556, 60170394, 18108385, 22279000, 22279002
2661	95342817 (5321, 5322)	Novel Protein sim. GBank gi|4758048|ref|NP_004739.1|pCPR8 - cell cycle progression 8 protein		glycoprotein	60432049, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 264909, 264593, 33109954, 265010, 265017, 265018, 265019, 264760, 264448, 264369, 264288, 21906765, 21906768, 265022, 264691, 33657023, 27486262, 60431528, 18108374, 35695855, 18108388, 264482
2662	80228739 (5323, 5324)				264555, 264556, 264558, 264486
2663	87780623 (5325, 5326)	Novel Protein sim. GBank gi|3874714|emb|CAA91263| - (Z66494) similar to choline dehydrogenase; cDNA EST yk346d5.5 comes from this gene; cDNA EST yk346d5.3 comes from this gene [Caenorhabditis elegans]		dehydrogenase	264906, 264909, 264757, 264758, 264767, 264691, 33657023, 264638
2664	85518329 (5327, 5328)	Novel Protein sim. GBank gi|1389670 (U58977) - Notch homolog Scalloped wings [Lucilia cuprina]	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696286, 264509, 264595, 264288, 264685, 264686
2665	87770662 (5329, 5330)	Novel Protein sim. GBank gi|4884406|emb|CAB43311.1| - (AL050190) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35696286, 22278999, 29331822, 35696052, 264906, 264907, 264909, 264510, 264511, 264512, 264593, 60433438, 265019, 264681, 21906765, 21906766, 21906767, 21906768, 265020, 265022, 35696423, 35695855, 22279002, 264482, 264486
2666	87826472 (5331, 5332)	Novel Protein sim. GBank gi|5106956|gb|AAD39906.1|AF11361 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]		UNCLASSIFIED	29331825, 265007, 264910, 60432229, 265019, 264288, 21906767, 264558, 22279002
2667	87422720 (5333, 5334)	Novel Protein sim. GBank gi|2500570|sp|Q17533|RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0564.1	Contains protein domain (PF01138) - 3' exoribonuclease family	nuclease	264907, 29331830, 264681, 264683, 264288, 35695855, 264332, 264556, 264557, 264558, 264559, 264563, 264565, 264567

2668	91216716 (5335, 5336)	Novel Protein sim. GBank gi|5454186|ref|NP_006327.1|pZYG| - ZYG homolog		UNCLASSIFIED	56181688, 35696286, 22278998, 22278999, 56182181, 29331824, 60424269, 29331825, 35696052, 29331828, 66712502, 56182435, 60433356, 264758, 21906754, 55811386, 265011, 87168559, 265017, 265019, 55811150, 264448, 264369, 264288, 21906765, 21906766, 21906768, 55811957, 35695917, 265020, 265021, 33657023, 264692, 33657109, 35695763, 60431528, 18108374, 35696423, 55811576, 264634, 60431850, 83373044, 18108385, 87168518, 22279000, 264563, 264564
2669	95415721 (5337, 5338)	Novel Protein sim. GBank gi|2147012|pir||JC4899 - proline rich protein - rat			264489, 264689, 21906767, 65274572, 56182575, 21906768, 29148627, 21906769, 29148629, 35696286, 35695917, 22278996, 22278998, 265021, 265022, 60170615, 52644150, 60432049, 264259, 264691, 33657023, 264692, 29331822, 29331824, 29331825, 60432289, 33657109, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264905, 264908, 52644045, 264909, 56182435, 35696423, 65274791, 35695855, 265006, 264910, 264635, 60432229, 264592, 264638, 56182323, 60433356, 60170394, 60433438, 264559, 264595, 55812038, 33109954, 87168559, 60432113, 265019, 264448, 264369, 264684, 264288
2670	87613234 (5339, 5340)	Novel Protein sim. GBank gi|1723523|sp|Q10362|YDBB_SCHPO - HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger		18108370, 263974
2671	91214936 (5341, 5342)	Novel Protein sim. GBank gi|4768277|gb|AAD29444.1|AF06425 - (AF064255) very long-chain acyl-CoA synthetase homolog 2; VLCS-H2 [Homo sapiens]		transport	52646842, 56994075, 264259, 29331822, 29331824, 29331825, 29331827, 33656970, 264509, 265006, 33109954, 21906754, 264682, 264288, 265021, 33657023, 33657109, 33657182, 27486261, 27486262, 27486265, 18108376, 18108385
2672	87399123 (5343, 5344)	Novel Protein sim. GBank gi|4966346|gb|AAD34677.1|AC00634 - (AC006341) Contains two PF|01344 Kelch motif domains. [Arabidopsis thaliana]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	264767

2673	87430749 (5345, 5346)	Novel Protein sim. GBank gi|5457337|emb|CAB41505.2| - (AJ236876) poly(ADP-ribosyl) polymerase-2 [Homo sapiens]	Contains protein domain (PF00644) - Poly(ADP-ribose) polymerase catalytic region.	polymerase	22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331828, 35696052, 60433438, 87168474, 87168559, 265017, 265018, 265019, 264448, 21906768, 21906769, 265020, 265021, 33657109, 27486262, 35695763, 60431850, 60170394, 87168518, 264563
2674	94847721 (5347, 5348)	Novel Protein sim. GBank gi|4758824|ref|NP_004280.1|pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	264488, 22278996, 35696286, 264091, 264259, 29331824, 29331826, 35696052, 264511, 55812038, 85658542, 264768, 21906765, 35695917, 264629, 35696423, 18108383, 87168518
2675	79563835 (5349, 5350)			UNCLASSIFIED	264691
2676	79628393 (5351, 5352)			UNCLASSIFIED	264906, 265008
2677	94329600 (5353, 5354)	Novel Protein sim. GBank gi|1079042|pir||S52154 - acetyl-CoA synthetase - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00501) - AMP-binding enzyme	synthase	18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278996, 35896286, 22278997, 22278999, 264490, 264259, 52645080, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 29146499, 29331830, 264908, 52644045, 265006, 265007, 265008, 265009, 60432229, 60433356, 60433438, 55812038, 265010, 265011, 87168559, 265017, 265018, 18108351, 264682, 264448, 264683, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 60170615, 52644150, 264691, 33657023, 263967, 33657109, 27486264, 27486265, 33657349, 35695763, 18108370, 18108374, 18108377, 55811576, 35696423, 35695855, 83373044, 18108387, 22279000, 22279002, 264564

2678	95001694 (5355, 5356)	Novel Protein sim. GBank gi|86760|pir||A40465 - alanine transaminase (EC 2.6.1.2), cytosolic - human		UNCLASSIFIED	264488, 263994, 264489, 18108394, 52646842, 35696286, 22278999, 264259, 29331825, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 264593, 264594, 264596, 264758, 33109954, 52646317, 21906754, 265010, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 265019, 264605, 264760, 264762, 18108351, 264763, 264682, 264683, 264764, 264288, 264766, 264687, 264768, 264769, 264689, 21906765, 21906767, 35695917, 265020, 265021, 52644150, 264691, 33657023, 264693, 18108364, 18108365, 33657109, 33657349, 264628, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264565, 264566, 264486, 264567
2679	95361544 (5357, 5358)	Novel Protein sim. GBank gi|1709233|sp|P07514|NC5R_BOVIN - NADH-CYTOCHROME B5 REDUCTASE	Contains protein domain (PF00970) - FAD/NAD-binding Cytochrome reductase	reductase	264488, 22278996, 35696286, 264259, 29331826, 29331827, 29331828, 264909, 56182435, 264113, 264511, 265008, 60433438, 264758, 85658542, 87168474, 265011, 265017, 265019, 264288, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 264690, 33657023, 55810764, 35696423, 55811576, 264631, 18108381, 60170394, 83373044, 87168518, 264566
2680	87800356 (5359, 5360)	Novel Protein sim. GBank gi|4589604|dbj|BAA76824.1| - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	264259, 264102, 264905, 264908, 265007, 265008, 33109954, 265011, 18108351, 264768, 33657023, 20281149, 263972, 264630, 264635, 264638
2681	90933844 (5361, 5362)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!		kinase	264489, 22278995, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264512, 264910, 264594, 60433438, 264758, 264603, 264604, 265019, 264605, 264760, 264764, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264486
2682	94138934 (5363, 5364)	Novel Protein sim. GBank gi|423468|pir||JQ1974 - HTF9-C protein - mouse	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	35696286, 264908, 55811386, 265017, 55811150, 55811957, 35695917, 60431528, 55810764, 55811576, 35696423, 65274791, 56526486
2683	87774405 (5365, 5366)	Novel Protein sim. GBank gi|5114351|gb|AAD40286.1| - (AF156271) RING finger protein terf [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	interleukinrecept	264909, 264769, 264635, 264636

2684	85787151 (5367, 5368)	Novel Protein sim. GBank gi|4886469|emb|CAB43385.1| - (AL050284) hypothetical protein [Homo sapiens]			264593
2685	88054299 (5369, 5370)	Novel Protein sim. GBank gi|3342729 (AC005331) - R31341_2 [Homo sapiens]		UNCLASSIFIED	
2686	87628690 (5371, 5372)	Novel Protein sim. GBank gi|4650844|dbj|BAA77027.1| - (AB026190) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF01344) - Kelch motif	struct	264259, 29331822, 60432289, 29331827, 29331830, 264909, 264512, 264596, 264769, 264534, 264555, 264556, 264557, 264558, 60170394, 264559, 264486
2687	87998183 (5373, 5374)	Novel Protein sim. GBank gi|5281314|gb|AAD41475.1|AF13312 - (AF133123) transcription factor IIIC102 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	transcriptfactor	18108394, 18108396, 22278996, 35696286, 22278997, 29331826, 29331828, 66712502, 21906754, 265011, 264760, 264761, 264763, 264689, 21906765, 35696423, 264559, 18108385, 264563
2688	79959584 (5375, 5376)				264908, 264760
2689	94122440 (5377, 5378)	Novel Protein sim. GBank gi|3880023|emb|CAA97339| - (Z73098) Similarity to yeast hypothetical protein (Swiss Prot accession number Q09695); cDNA EST EMBL:D72982 comes from this gene; cDNA EST EMBL:D75947 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00560) - Leucine Rich Repeat		22278997, 22278998, 22278999, 29331824, 35696052, 264906, 264908, 56182435, 264512, 264910, 265009, 60433438, 21906754, 18108351, 264682, 264683, 264767, 21906765, 21906766, 21906768, 33657023, 33657182, 27486262, 27486264, 33657349, 18108370, 18108372, 18108374, 35696423, 35695855, 18108385, 22279002
2690	88003055 (5379, 5380)	Novel Protein sim. GBank gi|2477513 (AC002398) - F25965_3 [Homo sapiens]	Contains protein domain (PF00620) - RhoGAP domain	struct	
2691	91219241 (5381, 5382)	Novel Protein sim. GBank gi|4107276|emb|CAA67130| - (X98506) acetyl-CoA synthetase [Solanum tuberosum]		synthase	65274572, 56182575, 264259, 29331822, 29331824, 29331826, 29331828, 264112, 265009, 55812038, 264596, 33109954, 265017, 264448, 264288, 264369, 264684, 21906769, 60170615, 60431528, 55810764, 264634, 264636, 264556, 264637, 22279002, 264564, 264566
2692	94111914 (5383, 5384)	Novel Protein sim. GBank gi|3513303 (AC005594) - R26984_1 [Homo sapiens]	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	
2693	20438807 (5385, 5386)			UNCLASSIFIED	264592
2694	94111918 (5387, 5388)	Novel Protein sim. GBank gi|3122400|sp|O35682|MUG_MOUSE - MYELOID UPREGULATED PROTEIN			264559
2695	95345513 (5389, 5390)	Novel Protein sim. GBank gi|4972740|gb|AAD34765.1| - (AF132177) unknown [Drosophila melanogaster]		collagen	35696286, 56994075, 22278999, 264259, 35696052, 29331830, 265011, 264288, 56181562, 264690, 264692, 33657023, 27486262, 263976, 18108376, 35696423, 35695855, 60170394, 83373044, 56526486, 22279000, 22279002, 264566
2696	87874040 (5391, 5392)	Novel Protein sim. GBank gi|728831|sp|P39188|ALU1_HUMAN - !!!! ALU SUBFAMILY J WARNING ENTRY !!!!		synthase	264594, 21906768, 18108370, 18108372

2697	91638472 (5393, 5394)	Novel Protein sim. GBank gi|5689473|dbj|BAA83020.1| - (AB028991) KIAA1068 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 265006, 265007, 264512, 265009, 60170831, 60433356, 264595, 264758, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 264761, 18108351, 264448, 264288, 264766, 264688, 264689, 21906765, 21906768, 265020, 265021, 60170615, 33657109, 18108376, 35696423, 35695855, 264555, 264558, 60170394, 264559, 18108387, 56526486, 87168518, 22279002, 264563, 264482
2698	94325891 (5395, 5396)	Novel Protein sim. GBank gi|841318 (U22818) - mutant sterol regulatory element binding protein-2 [Cricetulus griseus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcriptfactor	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 33656970, 264906, 29331830, 264909, 52644045, 264910, 60433356, 33657402, 33109954, 265017, 265018, 265019, 264288, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 265021, 265022, 52644150, 33657023, 33657182, 27486261, 35696423, 65274791, 264638, 60432113, 22279000
2699	87780650 (5397, 5398)			UNCLASSIFIED	264768, 18108357, 264690, 264691
2700	94139836 (5399, 5400)	Novel Protein sim. GBank gi|5174395|ref|NP_006006.1|pB120 - Brain protein 120		UNCLASSIFIED	60424269, 56182435, 60432229, 60433438, 55811386, 265017, 55811150, 264448, 56181562, 55811957, 264693, 33657109, 60431528, 264629, 55810764, 55811576, 65274791, 60431850, 60432113
2701	94148584 (5401, 5402)	Novel Protein sim. GBank gi|1572801 (U70854) - F38A5.1 gene product [Caenorhabditis elegans]			18108394, 52645156, 35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146499, 265006, 60433356, 33657402, 60433438, 264595, 33657084, 18108351, 264288, 264769, 18108359, 21906768, 35695917, 33657023, 27486261, 18108374, 18108379, 35696423, 18108382, 83373044, 18108384, 18108388, 60432113, 22279000
2702	57295366 (5403, 5404)	Novel Protein sim. GBank gi|2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	29331828, 264512, 264555, 264556, 264557, 264558, 264559
2703	87649514 (5405, 5406)	Novel Protein sim. GBank gi|5689399|dbj|BAA82983.1| - (AB028954) KIAA1031 protein [Homo sapiens]	Contains protein domain (PF00642) - Zinc finger C-x8-C-x5-C-x3-H type (and similar).		60432289, 265007, 21906765, 21906768, 265021, 264563

2704	87649515 (5407, 5408)	Novel Protein sim. GBank gi|4335694|gb|AAB63294| - (AF008554) Implantation-associated protein [Rattus norvegicus]			264488, 22278995, 22278998, 29331828, 29146499, 264905, 264906, 264907, 52644045, 264511, 33657402, 264600, 264602, 265017, 264605, 264761, 18108351, 264764, 264687, 264769, 265021, 264691, 264692, 18108382, 264693, 18108370, 18108374, 264634, 264635
2705	87771745 (5409, 5410)				264489, 264509, 264511, 264512, 264910, 264593, 87168474, 264604, 264288, 264687, 264769, 264638, 264566, 264486
2706	94326789 (5411, 5412)	Novel Protein sim. GBank gi|3255952|emb|CAA16821.1| - (AL021728) /prediction=(method:; /match=(desc: [Drosophila melanogaster]		UNCLASSIFIED	264488, 52646842, 65274572, 22278994, 56994075, 22278997, 264259, 29331824, 29331825, 29331826, 29331828, 33656970, 264907, 264908, 264909, 52644045, 56182435, 265006, 265007, 60433438, 55812038, 21906754, 52644296, 265010, 264601, 265017, 265019, 264681, 264448, 264682, 264288, 264686, 264687, 264688, 21906766, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 264690, 264691, 33657023, 264692, 264693, 65274620, 27486264, 263972, 18108374, 18108377, 264635, 264636, 264556, 60170394, 83373044, 65274727, 87168518, 22279000
2707	88089839 (5413, 5414)	Novel Protein sim. GBank gi|3417294 (AC004381) - Unknown gene product [Homo sapiens]			22278996, 22278998, 56182435, 21906754, 87168559, 265017, 264448, 52645129
2708	91011351 (5415, 5416)	Novel Protein sim. GBank gi|545790|bbs|147178 - DARPP-32=dopamine and cAMP-regulated phosphoprotein [human, brain, Peptide, 204 aa]		UNCLASSIFIED	65274572, 264259, 29331822, 29331825, 60432289, 29331826, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109954, 265010, 265011, 264369, 264288, 264765, 264693, 264565
2709	94853988 (5417, 5418)	Novel Protein sim. GBank gi|3169705 (AC004780) - F17127_1 [Homo sapiens]		UNCLASSIFIED	29331822, 18108370, 18108374, 83373044
2710	87627979 (5419, 5420)	Novel Protein sim. GBank gi|4468311|emb|CAB37992| - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			29331824, 264759, 264693, 18108382, 18108388

2711	94111920 (5421, 5422)	Novel Protein sim. GBank gi|3122400|sp|O35682|MUG_MOUSE - MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	264488, 264687, 52645156, 264769, 21906764, 21906765, 21906767, 21906768, 21906769, 55811957, 56994075, 22278997, 22278998, 265020, 265021, 264690, 264259, 264691, 264692, 33657023, 29331822, 29331824, 60424269, 29331826, 33657182, 29331827, 27486262, 33657349, 264508, 264905, 264907, 60431528, 264908, 264909, 55810764, 35696423, 65274791, 35695855, 265007, 264910, 60431850, 60432229, 264557, 264558, 55812038, 33109954, 18108385, 21906754, 33657084, 87168518, 87168474, 87168559, 60432113, 265017, 22279000, 265018, 265019, 22279002, 264760, 55811150, 264681, 18108351, 264565, 264764, 264566, 264288, 264766
2712	94312071 (5423, 5424)	Novel Protein sim. GBank gi|5081315|gb|AAD39343.1|AF07660 - (AF076607) prediabetic NOD sera-reactive autoantigen [Mus musculus]	Contains protein domain (PF00515) - TPR Domain	transferase	264488, 35696286, 22278998, 264259, 29331824, 60432289, 35696052, 264508, 264906, 66712502, 52644045, 265006, 60432229, 33657402, 60433356, 265010, 265019, 18108351, 264681, 264288, 264685, 21906765, 21906766, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 264691, 264692, 33657023, 33657109, 33657182, 33657349, 18108370, 18108374, 35696423, 35695855, 264555, 52644332, 56182323, 87168518, 60432113
2713	88003064 (5425, 5426)	Novel Protein sim. GBank gi|2477513 (AC002398) - F25965_3 [Homo sapiens]		UNCLASSIFIED	66714117, 264906, 264563
2714	13528218 (5427, 5428)			UNCLASSIFIED	264636
2715	94122454 (5429, 5430)	Novel Protein sim. GBank gi|4321968|gb|AAD15897| - (AF067430) Smarce1-related protein [Mus musculus]		UNCLASSIFIED	264508, 264905, 264907, 264908, 264909, 264910, 264758, 265011, 264760, 264764, 264288, 264766, 264768, 264636
2716	88003068 (5431, 5432)	Novel Protein sim. GBank gi|2477513 (AC002398) - F25965_3 [Homo sapiens]		glycoprotein	264091, 264259, 29331822, 66714117, 264908, 264369, 264693, 264556, 264563
2717	80077461 (5433, 5434)	Novel Protein sim. GBank gi|3327046|dbj|BAA31591| - (AB014516) KIAA0616 protein [Homo sapiens]			264593, 264558
2718	79604062 (5435, 5436)				264693
2719	88180423 (5437, 5438)	Novel Protein sim. GBank gi|746495 (U23515) - weakly similar to gastrula zinc finger protein [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 87168559, 265019, 265021, 52644150, 264691

2720	95086242 (5439, 5440)	Novel Protein sim. GBank gi|1335873 (U46690) - ATP-dependent RNA helicase [Mus musculus]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108374, 60424179, 264489, 56182435, 21906765, 21906766, 35696423, 22278997, 265020, 265022, 265005, 265008, 264092, 264636, 60432229, 264691, 264692, 33657023, 264693, 33657402, 83373044, 29331824, 18108366, 60424269, 29331826, 18108385, 52645129, 21906754, 35696052, 29331828, 87168474, 264100, 265010, 265011, 265019, 22279002, 264905, 264482, 264563, 264906, 18108351, 264681, 18108370, 29331830, 264908, 66712502, 52644045, 264909, 264828, 18108354
2721	95345523 (5441, 5442)	Novel Protein sim. GBank gi|4929683|gb|AAD34092.1|AF15185 - (AF151855) CGI-97 protein [Homo sapiens]	Contains protein domain (PF01172) - Uncharacterized protein family UPF0023		22278995, 35696286, 264259, 29331822, 29331824, 66714117, 29331826, 264906, 60433438, 265017, 18108351, 264448, 264288, 264769, 21906766, 265021, 33657109, 263969, 60431528, 264629, 55811576, 65274791, 35695855, 264631, 264637, 60170394, 56182323, 22279000
2722	91638807 (5443, 5444)	Novel Protein sim. GBank gi|3212997|gb|AAC23434.1| - (AC004997) match to ESTs AA667999 (NID:g2626700), AA165465 (NID:g1741481), Z45871 (NID:g575105), and T84026 (NID:g712314); similar to various tre-like proteins including: AF040654 (PID:g2746883), D13644 (PID:g2104571), AL02114...	Contains protein domain (PF00566) - TBC domain	oncogene	35696286, 22278999, 21906754, 265017, 264762, 264288, 21906765, 21906767, 21906768, 35695917, 18108362, 27486262, 35695855, 264558, 264559
2723	87387732 (5445, 5446)			UNCLASSIFIED	264508, 264509, 264906, 264909, 264910, 55812038, 264766, 264687, 264629, 264636, 264486
2724	87639563 (5447, 5448)	Novel Protein sim. GBank gi|4680681|gb|AAD27730.1|AF13295 - (AF132955) CGI-21 protein [Homo sapiens]		ubiquitin	18108396, 22278999, 20281099, 29331824, 29331826, 60432289, 29331828, 60170831, 60432229, 60433438, 18108351, 264682, 21906766, 21906767, 21906769, 35695917, 33657023, 33657109, 18108372, 18108374, 35695855, 22279000, 22279002
2725	94853991 (5449, 5450)	Novel Protein sim. GBank gi|3169705 (AC004780) - F17127_1 [Homo sapiens]		UNCLASSIFIED	264488, 52644507, 264259, 29331827, 21906754, 265011, 18108351, 264448, 264288, 264685, 264689, 35695917, 265020, 33657182, 27486261, 18108370, 18108374, 35696423, 18108385, 22279000
2726	86880599 (5451, 5452)	Novel Protein sim. GBank gi|3342738 (AC005328) - R26660_1, partial CDS [Homo sapiens]		MHC	264488, 264828, 264685

2727	91010470 (5453, 5454)	Novel Protein sim. GBank gi|731267|sp|P39219|RLUA_ECOLI - RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)	Contains protein domain (PF00849) - RNA pseudouridylate synthase	synthase	65274572, 56182575, 22278994, 56994075, 22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 33656970, 264509, 66712502, 264910, 33657402, 60433438, 264758, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 264767, 21906765, 21906767, 21906769, 55811957, 35695917, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 55811576, 35696423, 35695855, 264630, 60431850, 264636, 56182323, 87168518, 60432113, 22279000, 264564, 264565
2728	94126022 (5455, 5456)	Novel Protein sim. GBank gi|3880433|emb|CAA91399| - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	18108394, 56182435, 21906767, 55811957, 35695855, 265021, 264690, 264556, 264259, 264557, 29331822, 264559, 264448, 264288
2729	94126024 (5457, 5458)	Novel Protein sim. GBank gi|2408095|emb|CAB16300| - (Z99168) putative RNA splicing protein [Schizosaccharomyces pombe]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	65274572, 264259, 60432289, 66712502, 56182435, 264448, 264288, 264369, 55811957, 265021, 264557, 60432113
2730	94126026 (5459, 5460)	Novel Protein sim. GBank gi|3880433|emb|CAA91399| - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264887, 29331824, 29331826, 35696052, 264107, 56182435, 265008, 265009, 264592, 60431735, 265011, 264601, 265017, 18108351, 264288, 29148627, 55811957, 265021, 264690, 18108368, 18108374, 264557, 264558, 264559, 18108387, 56526486, 264566, 264486
2731	87723022 (5461, 5462)	Novel Protein sim. GBank gi|1723239|sp|Q10166|YAUB_SCHPO - HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I	Contains protein domain (PF00795) - Carbon-nitrogen hydrolase		264259, 35696052, 265006, 264758, 264762, 264448, 264288, 29148627, 21906769, 87168518, 22279002
2732	94126028 (5463, 5464)	Novel Protein sim. GBank gi|3880433|emb|CAA91399| - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	264687, 264489, 18108358, 56182435, 264689, 35696423, 55811957, 265021, 265006, 265008, 264910, 265009, 264690, 264555, 264259, 264556, 264557, 264558, 264559, 18108383, 33657109, 87168518, 265010, 264601, 60432113, 265017, 264905, 264448, 263972, 264369, 264567
2733	87363060 (5465, 5466)			UNCLASSIFIED	29331825, 264509, 264909
2734	94140286 (5467, 5468)	Novel Protein sim. GBank gi|4519621|dbj|BAA75670.1| - (AB017614) OASIS protein [Mus musculus]	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	60424179, 52644507, 56182575, 264259, 29331828, 264907, 264510, 264910, 60433356, 265019, 55811150, 264681, 264763, 264687, 33657182, 18108370, 60431528, 60431850, 56182323, 83373044

2735	87712336 (5469, 5470)	Novel Protein sim. GBank gi|3850569 (AC005278) - ESTs gb|T21276, gb|T45403, and gb|AA586113 come from this gene. [Arabidopsis thaliana]		glycoprotein	22278996, 60432289, 29331827, 29146498, 264108, 264909, 264112, 33657402, 87168474, 265017, 264762, 264448, 264764, 264684, 21906765, 264693, 33657109, 263976, 264636, 264638, 264557, 22279000, 22279002, 264567
2736	80247655 (5471, 5472)			UNCLASSIFIED	264905, 264628, 264629, 263978, 264632, 264564
2737	87604526 (5473, 5474)				264690
2738	85731808 (5475, 5476)	Novel Protein sim. GBank gi|2558501|dbj|BAA22896| - (D63850) hepatoma-derived growth factor [Mus musculus]			264488, 265009, 264768, 264691
2739	94319834 (5477, 5478)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264684, 83373044, 264566
2740	94148762 (5479, 5480)	Novel Protein sim. GBank gi|3417386|emb|CAA75495| - (Y15197) microtubule-associated protein, MAP-115 [Mus musculus]		UNCLASSIFIED	264488, 56182575, 22278995, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 29146498, 29331830, 265008, 265007, 265009, 60432229, 33657402, 55812038, 87168474, 265010, 265011, 265017, 265018, 265019, 264605, 264681, 264288, 264369, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 264691, 264692, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 60431850, 264639, 56182323, 18108382, 18108385, 65274727, 22279002, 264564
2741	88047518 (5481, 5482)	Novel Protein sim. GBank gi|3242764 (AC005154) - similar to protein U28928 (PID:g861308) [Homo sapiens]		UNCLASSIFIED	22278996, 52644045, 52644229, 21906768, 21906769, 265020, 60170615, 264691
2742	87648644 (5483, 5484)	Novel Protein sim GBank gi|4758412|ref|NP_004472.1|pGALN - UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	264259, 264905, 264758, 55812038, 264369, 29148627
2743	87627991 (5485, 5486)	Novel Protein sim. GBank gi|4468311|emb|CAB37992| - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 264906, 264908, 265006, 60433438, 265017, 18108351, 264448, 264764, 264288, 21906765, 21906767, 264690, 264691, 264693, 263969, 263971, 35695855, 264637, 264558, 18108382, 60432113
2744	94126030 (5487, 5488)	Novel Protein sim. GBank gi|3880433|emb|CAA91399| - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	kinase	18108374, 264488, 56182435, 21906765, 35696423, 35695917, 35695855, 265020, 265021, 264511, 265009, 264490, 264556, 264259, 264557, 56182323, 264558, 264559, 18108383, 29331824, 18108385, 33657109, 29331826, 21906754, 29331827, 29331828, 33657349, 87168518, 265018, 264905, 264482, 264448, 264486, 264369, 264288

2745	87740125 (5489, 5490)	Novel Protein sim. GBank gi|4405795|gb|AAD19826| - (AF038963) RNA helicase [Homo sapiens]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	35696286, 264509, 264905, 264907, 264908, 264909, 264510, 264512, 265008, 264758, 264601, 265017, 264604, 264763, 264288, 264686, 264769, 264693, 35696423, 35695855, 264634, 264636, 264563, 264564, 264565
2746	95418601 (5491, 5492)	Novel Protein sim. GBank gi|4758738|ref|NP_004680.1|pMTA1 - metastasis associated 1	Contains protein domain (PF00320) - GATA zinc finger	UNCLASSIFIED	22278996, 22278998, 22278999, 29331822, 29331826, 29331827, 35696052, 29331828, 264905, 264906, 264907, 264908, 264909, 52644045, 265006, 60170831, 264596, 55812038, 265018, 264683, 264288, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 33657023, 264693, 33657109, 18108368, 18108374, 264558, 18108385, 22279000, 264563
2747	94112677 (5493, 5494)	Novel Protein sim. GBank gi|4557803|ref|NP_000262.1|pNPC1 - Niemann-Pick disease, type C1		glycoprotein	264569, 52644507, 18108394, 22278995, 35696286, 22278997, 22278999, 52645080, 29331824, 56182181, 29331826, 29331827, 35696052, 264907, 264908, 264909, 265009, 33109954, 55811386, 87168474, 265010, 87168559, 264603, 265019, 264760, 264686, 264768, 21906769, 35695917, 60170615, 264692, 33657023, 52645129, 27486264, 60431528, 18108374, 35696423, 35695855, 264556, 56182323, 18108385, 264482
2748	91214983 (5495, 5496)	Novel Protein sim. GBank gi|4191272|emb|CAA09984| - (AJ012295) apaG protein [Rhizobium etli]	Contains protein domain (PF00646) - F-box domain.		65274572, 29331828, 264112, 264511, 265019, 264760, 264767, 264768, 264769, 21906768, 21906769, 265020, 27486262, 56526486, 87168518, 22279000
2749	87346307 (5497, 5498)				264259, 264908, 264510, 265008, 265009, 264760, 264369, 264768, 264563
2750	87336344 (5499, 5500)	Novel Protein sim. GBank gi|1872498 (U74297) - PiUS [Oryctolagus cuniculus]		UNCLASSIFIED	264488, 52644507, 18108396, 56994075, 264259, 29331825, 29331826, 29331827, 29331828, 264508, 265009, 264910, 264591, 264595, 33657084, 265011, 265019, 18108351, 264288, 264686, 264769, 264689, 55811957, 264693, 27486264, 18108370, 18108374, 264558, 18108385, 264482, 264563
2751	87057465 (5501, 5502)			UNCLASSIFIED	29331822, 29331824, 265017, 33657023
2752	88062675 (5503, 5504)	Novel Protein sim. GBank gi|3041859 (AC004534) - OG-2 homeodomain protein-like; similar to U65067 (PID:g1575526) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2753	94138972 (5505, 5506)	Novel Protein sim. GBank gi|3851648 (AF098301) - neural F box protein NFB42 [Rattus norvegicus]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	56182575, 56994075, 22278998, 29331822, 29331824, 29331825, 29331826, 265007, 264593, 55812038, 33109954, 18108351, 264288, 56181562, 21906767, 21906768, 265021, 264693, 18108374, 65274791, 264632, 56182323, 22279002, 264563, 264567
2754	94115513 (5507, 5508)	Novel Protein sim. GBank gi|535428 (U13736) - calmodulin-like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	22278999, 66714117, 29331827, 35696052, 29331828, 264906, 264908, 264909, 265011, 265017, 265018, 265019, 264288, 21906765, 21906767, 265022, 33657023, 264693, 56182323, 18108382, 22279000
2755	88001472 (5509, 5510)	Novel Protein sim. GBank gi|2996653 (AC004510) - R30385_2 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	
2756	11465908 (5511, 5512)			UNCLASSIFIED	264594
2757	95361590 (5513, 5514)	Novel Protein sim. GBank gi|1173539 (U30473) - putative src-like adapter protein; non-catalytic src-like adapter protein containing SH3 and SH2 domains; homolog of mouse SLAP; Method: conceptual translation supplied by author [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	eph	65658542, 264693
2758	79637846 (5515, 5516)	Novel Protein sim. GBank gi|3608372 (AF053768) - brain specific cortactin-binding protein CBP90 [Rattus norvegicus]		struct	264693
2759	91005312 (5517, 5518)	Novel Protein sim. GBank gi|2072200 (U94863) - p40 [Borna disease virus]			65274572, 35696286, 66714117, 29331828, 264508, 56182435, 21906754, 55811957, 264629, 264636, 56182323, 22279002
2760	79824798 (5519, 5520)			UNCLASSIFIED	264908
2761	87639597 (5521, 5522)	Novel Protein sim. GBank gi|4914573|emb|CAB43685.1| - (AL050390) hypothetical protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	nuclease	22278998, 29331822, 29331830, 265010, 265019, 264288, 21906765, 21906768, 21906769, 265020, 56182323, 22279002, 264563
2762	87592699 (5523, 5524)	Novel Protein sim. GBank gi|3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00989) - PAS domain	struct	18108394, 22278998, 264906, 264909, 265006, 265007, 264757, 265010, 265011, 265017, 265019, 18108351, 264448, 264683, 264686, 264768, 265020, 265021, 265022, 264691, 18108362, 264693, 18108365, 33657109, 18108368, 18108370, 18108381, 18108382, 18108384, 18108388, 87168518
2763	87539988 (5525, 5526)	Novel Protein sim. GBank gi|3511122 (AF060503) - zinc finger protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264369, 35696423
2764	94305140 (5527, 5528)	Novel Protein sim. GBank gi|2905643 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases		52646842, 264259, 29331822, 29331825, 29331826, 29331828, 33656970, 264905, 264907, 29331830, 265006, 265009, 21906754, 265019, 264448, 21906769, 27486262, 56182323, 56526486, 87168518, 264487

2765	94315105 (5529, 5530)	Novel Protein sim. GBank gi|4688672|emb|CAA17688.2| - (AL022018) /prediction=(method:; /prediction=(method:; /match=(desc: [Drosophila melanogaster]			264488, 65274572, 22278995, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264512, 264910, 265009, 264592, 264595, 264758, 55812038, 33109954, 265010, 87168559, 264600, 265018, 264760, 264761, 264762, 264763, 264448, 264764, 264288, 264766, 264767, 264768, 56181562, 21906764, 21906765, 21906768, 35695917, 265021, 264691, 264692, 33657023, 33657109, 264628, 18108370, 264629, 18108374, 55811576, 35696423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 264558, 264639, 83373044, 87168518, 22279000, 22279002, 264563, 264482
2768	94315109 (5531, 5532)	Novel Protein sim. GBank gi|5441611|emb|CAB46854.1| - (AJ388555) hypothetical protein [Canis familiaris]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	264488, 65274572, 60432289, 264907, 264909, 264511, 264512, 60433356, 264288, 264685, 264689, 35695917, 265022, 264693, 264628, 65274791, 264635, 264555, 264556, 264557, 264638, 264558, 264559, 83373044, 60432113
2767	80204297 (5533, 5534)	Novel Protein sim. GBank gi|1079451|pir||A55463 - tropomodulin, skeletal muscle - chicken		struct	264112, 263974, 264558
2768	94322238 (5535, 5536)	Novel Protein sim. GBank gi|5441322|emb|CAB46721.1| - (AL031427) dJ167A19.1 (novel protein) [Homo sapiens]		UNCLASSIFIED	264488, 263994, 264489, 35696286, 22278998, 22278999, 264259, 29331822, 60432289, 29331826, 35696052, 264508, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264757, 264596, 265011, 264604, 265019, 264760, 264681, 18108351, 264764, 264288, 264766, 264686, 264768, 18108357, 264769, 264689, 21906766, 21906768, 21906769, 35695917, 265021, 265022, 33657023, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 264639, 83373044, 264563, 264564, 264565, 264566, 264486, 264567

2769	95311088 (5537, 5538)	Novel Protein sim. GBank gi|5419859|emb|CAB46375.1| - (AL098725) hypothetical protein [Homo sapiens]		tubulin		264488, 56182575, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331828, 264908, 29331830, 56182435, 264592, 33657402, 264448, 264369, 264288, 60170615, 264691, 33657023, 264692, 33657109, 18108374, 55811576, 264634, 264636, 56182323, 83373044, 60432113
2770	87730182 (5539, 5540)	Novel Protein sim. GBank gi|5701965|emb|CAB52157.1| - (AL109736) WD repeat protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase		18108398, 22278995, 22278998, 22278999, 264105, 265006, 265019, 18108351, 264687, 21906765, 18108364, 264629, 18108374, 264631, 18108385, 18108388
2771	88084071 (5541, 5542)	Novel Protein sim. GBank gi|3093433 (AC004125) - Unknown gene product [Homo sapiens]		UNCLASSIFIED		264259, 29331822, 29331824, 29331825, 264369
2772	95357309 (5543, 5544)	Novel Protein sim. GBank gi|4885531|ref|NP_005465.1|pNY C - histone deacetylase 5	Contains protein domain (PF00850) - Histone deacetylase family	histone		264259, 29331822, 29331824, 66714117, 60432289, 29331827, 264905, 265009, 264592, 55812038, 65274444, 264766, 21906769, 33657109, 263978, 264555, 264638, 264557, 83373044, 264563, 264564, 264486
2773	94138984 (5545, 5546)	Novel Protein sim. GBank gi|3288888 (AC005253) - R26445_1 [Homo sapiens]		UNCLASSIFIED		18108374, 264686, 264687, 263976, 56182435, 264689, 55810764, 21906766, 35696423, 55811576, 65274791, 58181686, 55811957, 35695855, 264110, 265021, 264112, 265022, 265006, 265008, 264092, 264094, 60431850, 264637, 264691, 264259, 264692, 263981, 264594, 60433356, 56182323, 264693, 264757, 56182181, 55812038, 29331825, 60424269, 18108385, 29331826, 29331827, 27486261, 29331828, 35696052, 55811388, 264107, 60432113, 265017, 55811150, 18108351, 264681, 264906, 18108370, 264484, 264682, 20281069, 264448, 66712502, 264683, 264764, 264288, 264684, 264766, 263974
2774	87819908 (5547, 5548)	Novel Protein sim. GBank gi|465852|sp|P34388|YLS3_CAEEL - HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III	Contains protein domain (PF00380) - Ribosomal protein S9/S16	ribosomalprot		22278995, 35696286, 22278996, 22278999, 264259, 29331826, 60432289, 35696052, 264112, 33657402, 21906754, 87168559, 265017, 265018, 264288, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 33657023, 33657109, 18108370, 263976, 35696423, 35695855, 87168518, 22279000, 264482

2775	95307987 (5549, 5550)	Novel Protein sim. GBank gi|4689132|gb|AAD27775.1|AF07704 - (AF077042) 30S ribosomal protein S7 homolog [Homo sapiens]	Contains protein domain (PF00177) - Ribosomal protein S7p/S5e	ribosomalprot	264488, 22278995, 56994075, 22278996, 35696288, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 265007, 21906754, 265017, 265019, 264448, 264682, 264369, 264288, 18108354, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 60170615, 264691, 18108370, 35696423, 65274791, 35695855, 264634, 60431850, 60170394, 56182323, 264558, 18108388, 22279000, 264563, 264565, 264488, 264567
2776	87791557 (5551, 5552)				56182575, 22278998, 22278999, 264259, 29331822, 29331824, 264908, 29331830, 264510, 33657402, 21906754, 55811386, 265017, 265019, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 55810764, 55811576, 264555, 56526486, 22279000
2777	79818729 (5553, 5554)			UNCLASSIFIED	264907, 264766
2778	82112411 (5555, 5556)			UNCLASSIFIED	264907, 264593, 264760, 264628
2779	87649729 (5557, 5558)	Novel Protein sim. GBank gi|4680711|gb|AAD27745.1|AF13297 - (AF132970) CGI-36 protein [Homo sapiens]		UNCLASSIFIED	22278997, 264259, 29331824, 66714117, 35696052, 265006, 264512, 264448, 264288, 29148627, 18108364, 20281149, 18108370, 264629
2780	94679397 (5559, 5560)	Novel Protein sim. GBank gi|4758524|ref|NP_004825.1|pHGK| - HPK/GCK-like kinase	Contains protein domain (PF00780) - CNH domain	kinase	29146499, 65274791, 264634, 264639
2781	91220057 (5561, 5562)	Novel Protein sim. GBank gi|4469352|gb|AAD21222| - (AF069502) ubiquitin specific protease UBP43 [Mus musculus]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	60424179, 29331824, 60424269, 66714117, 29331826, 56182435, 87168474, 265017, 264764, 56181562, 21906765, 21906766, 21906768, 35695917, 265020, 33657023, 35695855, 56182323, 87168518
2782	94233146 (5563, 5564)	Novel Protein sim. GBank gi|4505013|ref|NP_002310.1|pLRN| - leucine-rich neuronal protein	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	65274572, 22278996, 22278998, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331828, 264905, 264907, 264908, 264909, 52644045, 265009, 265017, 265018, 264604, 265019, 264760, 264683, 264288, 264766, 264685, 264686, 264768, 52644229, 264689, 21906768, 265020, 265021, 264691, 18108362, 264692, 33657023, 264693, 33657109, 33657349, 18108370, 264628, 263978, 35695855, 264557, 56182323, 83373044, 18108385

2783	80016629 (5565, 5566)	Novel Protein sim. GBank gi|728831|sp|P39188|ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		tm7	264909, 264628, 263978, 263981
2784	87614360 (5567, 5568)				264259, 29331822, 29331824, 29331825, 264482
2785	88071930 (5569, 5570)	Novel Protein sim. GBank gi|2134933|pir||S58890 - collapsin response mediator protein - human		UNCLASSIFIED	22278999, 264908, 264758, 265018, 264769, 21906765, 21906768, 21906769, 265020, 264584
2786	87408542 (5571, 5572)	Novel Protein sim. GBank gi|2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264905, 265017
2787	87901266 (5573, 5574)	Novel Protein sim. GBank gi|5174507|ref|NP_006020.1|pMA1| - paraneoplastic neuronal antigen		UNCLASSIFIED	264768, 21906765, 21906768, 55811957, 22278999, 264093, 60170615, 264259, 29331822, 18108365, 29331824, 33657109, 29331827, 35696052, 264100, 264105, 264908, 263977, 55811576, 264635, 264637, 60433438, 60432113, 265017, 265019, 22279002, 55811150, 264369, 264288
2788	88090644 (5575, 5576)	Novel Protein sim. GBank gi|3252826 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	
2789	85491275 (5577, 5578)	Novel Protein sim. GBank gi|2495729|sp|Q92556|Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA8725)		UNCLASSIFIED	264103, 21906769, 264693
2790	87602784 (5578, 5580)	Novel Protein sim. GBank gi|5101772|emb|CAB45135.1| - (AJ242978) p821 [Homo sapiens]		struct	264488, 264769, 264910, 264631, 264636, 264690, 264691, 264259, 264638, 29331824, 264508, 264509, 264905, 264563, 264906, 264628, 18108370, 264907, 264764, 264908, 264288, 264909
2791	88083195 (5581, 5582)	Novel Protein sim. GBank gi|2911266 (AC002550) - Unknown gene product [Homo sapiens]			21906764, 18108368
2792	95083783 (5583, 5584)	Novel Protein sim. GBank gi|2854163|gb|AAC02581.1| - (AF045642) No definition line found [Caenorhabditis elegans]			22278996, 22278997, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 35696052, 264908, 66712502, 29331830, 264909, 60432229, 60433356, 60433438, 33109954, 265010, 265011, 265017, 265018, 265019, 264682, 264448, 264288, 264369, 264768, 52844229, 21906765, 21906768, 265020, 265021, 33657023, 263974, 18108374, 65274791, 35695855, 264636, 264556, 264558, 56182323, 83373044, 18108385, 56526486, 60432113, 22279000, 264567
2793	87425476 (5585, 5586)			UNCLASSIFIED	264259, 60432289, 66712502, 265009, 264636
2794	85794830 (5587, 5588)			UNCLASSIFIED	264689, 265022, 264691, 18108388, 264567

2795	95334888 (5589, 5590)	Novel Protein sim. GBank gi|5454146|ref|NP_006348.1|pUBE2 - ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5)	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	65274572, 56182575, 35696286, 22278998, 22278999, 60432049, 264259, 29331822, 29331825, 66714117, 60432289, 29331826, 29331827, 35696052, 29331828, 264907, 66712502, 56182435, 264511, 265007, 264512, 264910, 60432229, 60433356, 60433438, 33109954, 85658542, 265018, 265019, 264288, 264686, 21906764, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265021, 265022, 52644150, 33657023, 264693, 65274620, 33657109, 35696423, 55811576, 65274791, 56182323, 56526486, 60432113, 22279002, 264482, 264563, 264484, 264567
2796	94848857 (5591, 5592)	Novel Protein sim. GBank gi|4680651|gb|AAD27715.1|AF13294 - (AF132940) CGI-06 protein [Homo sapiens]		UNCLASSIFIED	18108394, 65274572, 56182575, 56994075, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 264509, 264906, 264907, 264908, 66712502, 56182435, 264510, 265006, 264512, 265007, 265008, 264910, 265009, 264591, 264592, 60433356, 264594, 264595, 55812038, 264596, 21906754, 60174639, 87168474, 265010, 265011, 265017, 265018, 265019, 55811150, 264762, 18108351, 264448, 264682, 264369, 264288, 264685, 264766, 264687, 56181562, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 264692, 33657023, 18108362, 264693, 65274620, 33657109, 33657182, 27486265, 33657349, 18108374, 35696423, 65274791, 35695855, 264556, 264557, 56182323, 264558, 60170394, 83373044, 65274727, 87168518, 22279000, 264563, 264564, 264565, 264566, 264567
2797	95110790 (5593, 5594)	Novel Protein sim. GBank gi|4838557|gb|AAD31040.1| - (AF143859) potassium channel modulatory factor DEBT-91 [Mus musculus]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	56182575, 22278995, 22278996, 22278997, 29331827, 29146499, 264509, 264906, 56182435, 264757, 21906754, 265010, 265017, 265019, 264681, 264682, 264683, 264686, 21906765, 21906767, 21906768, 21906769, 29148629, 265020, 52644150, 264690, 33657182, 264629, 18108376, 56182323, 22279002, 264563
2798	86198005 (5595, 5596)	Novel Protein sim. GBank gi|2852645 (AF007160) - unknown [Homo sapiens]		UNCLASSIFIED	264488, 264490, 264259, 264448, 20281149, 20281152, 264556, 264557, 264558, 264559, 264483, 264486, 264567

2799	88090651 (5597, 5598)	Novel Protein sim. GBank gi|3252825 (AC004382) - Unknown gene product [Homo sapiens]			UNCLASSIFIED	22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331828, 35696052, 29331828, 264909, 60433356, 33657402, 33109954, 87168474, 264448, 52644229, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 52644150, 35695855, 264634, 60432113, 22279000
2800	88316481 (5599, 5600)	Novel Protein sim. GBank gi|4240301|dbj|BAA74929.1| - (AB020713) KIAA0906 protein [Homo sapiens]			glycoprotein	264488, 56994075, 264259, 20281099, 29331825, 29331827, 264905, 56182435, 265006, 265011, 87168559, 265017, 265019, 264448, 264288, 264766, 264688, 60170615, 264691, 264692, 27486265, 264628, 264629, 264636, 264557, 264558, 264559, 87168518, 264564, 264566, 264567
2801	86068814 (5601, 5602)		Contains protein domain (PF00627) - UBA domain			265007, 264687
2802	88082477 (5603, 5604)	Novel Protein sim. GBank gi|2337865 (AC002464) - organic cation transporter; 50% similarity to JC4884 (PID:g2143892) [Homo sapiens]	Contains protein domain (PF00083) - Sugar (and other) transporter		transport	264448, 35695855
2803	79577446 (560: 5606)				UNCLASSIFIED	264639
2804	57111131 (5607, 5608)	Novel Protein sim. GBank gi|4559368|gb|AAD23029.1|AC006585 - (AC006585) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF01585) - G-patch domain		peptidase	264566
2805	87398486 (5609, 5610)					264092, 264259, 29331822, 29331824, 29331827, 29331828, 264508, 265007, 265009, 21906754, 264369, 264288, 264632, 60170394, 264563, 264482
2806	87898951 (5611, 5612)	Novel Protein sim. GBank gi|1168973|sp|P44403|CLPB_HAEIN - CLPB PROTEIN			UNCLASSIFIED	22278995, 22278996, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29146498, 265008, 265009, 60433438, 265017, 265018, 265019, 264448, 264288, 21906765, 21906767, 21906769, 29148629, 265022, 52644150, 56182323

2807	91720702 (5613, 5614)	Novel Protein sim. GBank gi|4468310|emb|CAB37991| - (AL031432) dJ465N24.1 (PUTATIVE novel protein similar to predicted yeast and worm proteins) [Homo sapiens]		UNCLASSIFIED	52644507, 52645156, 52646842, 18108398, 56182575, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 35696052, 29331828, 33656970, 264100, 264105, 264907, 52644045, 60433356, 264594, 60433438, 52646317, 21906754, 33109954, 33657084, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264763, 264687, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 27486265, 35695763, 18108370, 18108372, 18108374, 18108376, 263977, 18108377, 35696423, 35695855, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113
2808	95359111 (5615, 5616)	Novel Protein sim. GBank gi|5541863|emb|CAB51071.1| - (AL096857) hypothetical protein [Homo sapiens]		MHC	60432289, 264510, 265010, 265017, 265018, 264681, 264686, 265021, 264690, 22279000, 264566
2809	88083530 (5617, 5618)	Novel Protein sim. GBank gi|2772561 (AC004002) - similar to ciliary dynein beta heavy chain; 78% Similarity to P23098 (PID:g118965) [Homo sapiens]		ATPase_associated	18108351
2810	87259032 (5619, 5620)			UNCLASSIFIED	264569, 22278996, 264091, 264259, 29331828, 29146499, 29148629, 29148784, 264693
2811	91235845 (5621, 5622)			UNCLASSIFIED	22278999, 264259, 66712502, 264693
2812	88093334 (5623, 5624)	Novel Protein sim. GBank gi|3264583 (AC005189) - match to ESTs H97758 (NID:g1118643) and AA085546 (NID:g1628773) [Homo sapiens]		UNCLASSIFIED	264106
2813	91218755 (5625, 5626)	Novel Protein sim. GBank gi|4240273|dbj|BAA74915.1| - (AB020699) KIAA0892 protein [Homo sapiens]		UNCLASSIFIED	56182575, 29331828, 264906, 66712502, 55811386, 265017, 265018, 265019, 264683, 265020, 87168518, 60432113
2814	90980906 (5627, 5628)	Novel Protein sim. GBank gi|3548791 (AC005620) - R33590_1 [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	65274572
2815	79774521 (5629, 5630)			UNCLASSIFIED	264907, 264909
2816	95358229 (5631, 5632)	Novel Protein sim. GBank gi|5420389|emb|CAB46680.1| - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 35696286, 29331825, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264760, 264681, 264766, 264769, 264689, 21906765, 264693, 264628, 18108370, 264629, 264631, 264634, 264563, 264564, 264566, 264486

2817	87749542 (5633, 5634)	Novel Protein sim. GBank gi|1293846 (U56966) - coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3 [Caenorhabditis elegans]			264259, 29331822, 29331827, 264508, 264509, 264905, 264907, 264908, 264909, 56182435, 264510, 265006, 264511, 264512, 264593, 264758, 265010, 264760, 264761, 264764, 264288, 264687, 264769, 55811957, 35695917, 33657109, 263978, 264634, 264636, 264639, 264564, 264565, 264566, 264488, 264567
2818	88073579 (5635, 5636)	Novel Protein sim. GBank gi|549986 (U13149) - possible apospory-associated protein [Pennisetum ciliare]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	66712502
2819	87793527 (5637, 5638)			UNCLASSIFIED	264909, 264511
2820	87765744 (5639, 5640)	Novel Protein sim. GBank gi|4929773|gb|AAD34147.1|AF15209 - (AF152097) CGI-05 protein [Homo sapiens]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	18108394, 52646365, 52644045, 264112, 265009, 21906754, 265017, 18108351, 264683, 264369, 264686, 264769, 21906769, 33657023, 33657109, 18108370, 18108374, 18108377, 18108385
2821	95320511 (5641, 5642)	Novel Protein sim. GBank gi|399144|sp|P02747|C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264636
2822	94260221 (5643, 5644)	Novel Protein sim. GBank gi|2224671|dbj|BAA20820| - (AB002363) KIAA0365 [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 60432289, 264905, 60433356, 33657402, 265011, 264760, 21906765, 60170615, 264638
2823	95320513 (5645, 5646)	Novel Protein sim. GBank gi|399144|sp|P02747|C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264766
2824	95320515 (5647, 5648)	Novel Protein sim. GBank gi|399144|sp|P02747|C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR		UNCLASSIFIED	264907
2825	19742170 (5649, 5650)				264760
2826	94311905 (5651, 5652)	Novel Protein sim. GBank gi|3859683|emb|CAA22020| - (AL033503) conserved hypothetical protein [Candida albicans]			52645156, 22278994, 35696286, 22278997, 22278998, 52645080, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 33656970, 52644045, 52646317, 33657084, 52644296, 265017, 265018, 265019, 264288, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 52644150, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 35696423, 35695855, 52644332, 18108385, 87168518, 264484

2827	95320519 (5653, 5654)	Novel Protein sim. GBank gi|399144|sp|P02747|C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264488, 263994, 264489, 65274572, 29331822, 66714117, 29331827, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 264910, 264591, 60432229, 264592, 264593, 264595, 264596, 21906754, 265011, 264600, 264601, 264602, 265017, 264604, 264605, 264288, 264766, 264767, 264689, 55811957, 264534, 264690, 264691, 264692, 264693, 263972, 264629, 35695855, 264631, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264558, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264567, 264486, 18108391
2828	91229615 (5655, 5656)	Novel Protein sim. GBank gi|3598974 (AF077000) - protein tyrosine phosphatase TD14 [Rattus norvegicus]	Contains protein domain (PF00102) - Protein-tyrosine phosphatase	phosphatase	29331822, 35696052, 264104, 264908, 265007, 264591, 265010, 265011, 265019, 264766, 264686, 55811957, 18108370, 18108374, 55810764, 35696423, 55811576, 56182323, 83373044, 87168518
2829	87651244 (5657, 5658)	Novel Protein sim. GBank gi|4680689|gb|AAD27734.1|AF13295 - (AF132959) CGI-25 protein [Homo sapiens]			22278996, 22278997, 264091, 264093, 60432049, 264259, 29331822, 29331825, 29331827, 29331828, 264905, 264509, 66712502, 264510, 264511, 264593, 60433438, 21906754, 265011, 264603, 18108351, 264288, 21906765, 21906768, 21906769, 29148629, 52644150, 264693, 33657109, 18108374, 264634, 18108385, 60432113, 22279000, 264565, 264486
2830	88087109 (5659, 5660)	Novel Protein sim. GBank gi|2498667|sp|Q61200|NPH1_MOUSE - NEUREXOPHILIN 1			265008, 265019, 264639, 22279002
2831	87614717 (5661, 5662)			UNCLASSIFIED	265017
2832	87631809 (5663, 5664)			UNCLASSIFIED	22278997, 22278999, 52646317, 264288, 264688, 21906767, 60431528, 264638, 22279000
2833	87612938 (5665, 5666)	Novel Protein sim. GBank gi|5262615|emb|CAB45747.1| - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264555, 264556, 264558
2834	86974703 (5667, 5668)	Novel Protein sim. GBank gi|2224567|dbj|BAA20772| - (AB002311) KIAA0313 [Homo sapiens]			263972
2835	87775712 (5669, 5670)	Novel Protein sim. GBank gi|4589532|dbj|BAA76788.1| - (AB023161) KIAA0944 protein [Homo sapiens]		ATPase_associated	60432289, 29331828, 265008, 265010, 265017, 264448, 55811957, 265020, 18108370
2836	85724748 (5671, 5672)	Novel Protein sim. GBank gi|2351568 (U76618) - N-RAP [Mus musculus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcriptfactor	264259, 264112, 265010, 264762, 264764, 263974, 264555, 264558, 264559

2837	87766482 (5673, 5674)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108394, 22278997, 22278998, 29331822, 264907, 264909, 265006, 265007, 265018, 265019, 264682, 264288, 21906766, 21906767, 55811957, 35695917, 18108374, 56182323, 22279000, 22279002
2838	87775392 (5675, 5676)	Novel Protein sim. GBank gi|973378 (U31263) - core protein [Hepatitis C virus]		UNCLASSIFIED	18108394, 18108397, 264259, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2839	85799317 (5677, 5678)			UNCLASSIFIED	264555
2840	87774665 (5679, 5680)	Novel Protein sim. GBank gi|1575515 (U64899) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]			264509, 264511, 265011, 264288, 264769, 265020, 264634, 264636, 264556
2841	86982568 (5681, 5682)	Novel Protein sim. GBank gi|2224605|dbj|BAA20790| - (AB002330) KIAA0332 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	56182575, 35696052, 264907, 264908, 264909, 264910, 264593, 264595, 264766, 265022, 264691, 33657182, 35695763, 18108370, 35695855, 264631, 264559, 264563, 264567
2842	80080086 (5683, 5684)				264600
2843	91012494 (5685, 5686)	Novel Protein sim. GBank gi|5578957|emb|CAB51350.1| - (AL050306) dJ475B7.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]		UNCLASSIFIED	264906, 264907, 264908, 264909, 264910, 264764, 35695855, 83373044, 18108385
2844	56731154 (5687, 5688)	Novel Protein sim. GBank gi|585123|sp|Q08878|FBLC_MOUSE - FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)	Contains protein domain (PF00008) - EGF-like domain		264685
2845	94321719 (5689, 5690)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		homeobox	29146498, 87168474, 264686, 35696423, 83373044, 264564
2846	88318613 (5691, 5692)	Novel Protein sim. GBank gi|5306263|gb|AAD41995.1|AC00623 - (AC006233) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	29331830, 264909, 265008, 265011, 87168559, 264629, 264556
2847	81811757 (5693, 5694)	Novel Protein sim. GBank gi|3399676 (AC005390) - R31180_1 [Homo sapiens]		UNCLASSIFIED	264908, 264766, 264769, 264629, 264637, 264566
2848	87612943 (5695, 5696)	Novel Protein sim. GBank gi|5262615|emb|CAB45747.1| - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264490, 264259, 264508, 264905, 264907, 264510, 265007, 265008, 264591, 264592, 264593, 264594, 264595, 55812038, 265010, 265011, 264604, 264763, 264764, 264765, 264766, 264686, 264628, 264629, 264555, 264636, 264556, 264557, 264638, 264558, 264559, 264563, 264566, 264567
2849	88084283 (5697, 5698)	Novel Protein sim. GBank gi|3342218 (AC004131) - Unknown gene product [Homo sapiens]			29331822, 35696052, 264509, 264906, 265007, 264594, 265018, 264288, 263972, 35696423, 18108384, 56526486, 18108390
2850	87623636 (5699, 5700)			UNCLASSIFIED	35696286, 265008, 265009, 265018, 264288, 35695917, 264693, 18108374, 35695855, 22279000

2851	87820548 (5701, 5702)	Novel Protein sim. GBank gi|4321619|gb|AAD15788.1| - (AF051098) seven transmembrane domain orphan receptor [Mus musculus]		UNCLASSIFIED	264906, 264907, 56182435, 264758, 55811386, 265010, 18108351, 264448, 264369, 21906765, 264691, 264692, 264693, 35695855, 264556, 18108385, 264567
2852	86987023 (5703, 5704)	Novel Protein sim. GBank gi|1825729 (U88308) - similar to drosophila membrane protein PATCHED SP:P18502 (PID:g129645) [Caenorhabditis elegans]		UNCLASSIFIED	264591
2853	87784630 (5705, 5706)	Novel Protein sim. GBank gi|2702347 (AF027503) - putative membrane-associated guanylate kinase 1 [Mus musculus]	Contains protein domain (PF00397) - WW domain	kinase	56182575, 55811150, 264690, 27486262, 27486265, 264632, 56182323, 56526486, 22279002
2854	88083557 (5707, 5708)	Novel Protein sim. GBank gi|2795825 (AC004021) - kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to A45773 (PID:g1079096) [Homo sapiens]	Contains protein domain (PF01344) - Kelch motif	dna_rna_bind	35696286, 29331824, 29331826, 29331828, 264908, 264768, 264693, 22279002, 264482
2855	94723856 (5709, 5710)	Novel Protein sim. GBank gi|1504040|dbj|BAA13219| - (D86983) similar to D.melanogaster peroxidasin(U11052) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278994, 29331822, 29331824, 29331825, 264906, 264908, 265009, 33109954, 265018, 265019, 264448, 21906765, 265020, 264690, 27486265, 83373044, 22279000, 22279002, 264482
2856	88093359 (5711, 5712)	Novel Protein sim. GBank gi|3264583 (AC005189) - match to ESTs H97758 (NID:g1118643) and AA085546 (NID:g1628773) [Homo sapiens]			21906766, 22278997, 265022, 29331822, 29331826, 27486262, 265007, 265009, 265017, 264482, 264563, 18108351
2857	95348286 (5713, 5714)	Novel Protein sim. GBank gi|3041855 (AC004537) - similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	struct	22278995, 35696286, 29331824, 29331825, 35696052, 264103, 264108, 56182435, 21906765, 21906769, 265020, 18108368, 35695763, 22279002, 264563
2858	87434748 (5715, 5716)	Novel Protein sim. GBank gi|462585|sp|P35227|ME18_HUMAN - DNA-BINDING PROTEIN MEL-18 (ZINC FINGER PROTEIN 144)	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	dna_rna_bind	264569, 264887, 22278995, 22278996, 22278997, 22278999, 264259, 29331826, 29331827, 29331828, 264509, 264905, 264906, 29331830, 264908, 52644045, 264909, 264511, 264512, 265007, 265008, 264910, 265009, 264593, 60433356, 264595, 264758, 21906754, 265010, 265011, 264604, 265018, 264760, 18108351, 264763, 264682, 264764, 264765, 264288, 264369, 264685, 264766, 264768, 18108357, 264769, 21906766, 21906767, 265021, 264534, 60170615, 264691, 264692, 18108370, 264629, 18108374, 264631, 264636, 263981, 18108381, 264558, 18108385, 22279002, 264564, 264566, 264486, 264567
2859	90937675 (5717, 5718)	Novel Protein sim. GBank gi|4325320|gb|AAD17331.1| - (AF124427) claudin-15 [Mus musculus]		UNCLASSIFIED	60424179, 65274572, 29331828, 264905, 264511, 264758, 265011, 21906767, 21906769, 55811957, 265021, 56182323

2860	87532599 (5719, 5720)	Novel Protein sim. GBank gi|4469186|emb|CAB38414.1| - (AL031588) dJ1163J1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylate)-Methyltransferases) (isoform 1) [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264510, 264511, 33109954, 18108351, 264683, 264765, 264369, 264686, 21906765, 264691, 264692, 264693, 18108388, 22279002, 264482
2861	86698507 (5721, 5722)	Novel Protein sim. GBank gi|3941730 (AF108083) - BS4 [Homo sapiens]			264369, 264692
2862	87569585 (5723, 5724)	Novel Protein sim. GBank gi|4505013|ref|NP_002310.1|pLRN| - leucine-rich neuronal protein		UNCLASSIFIED	264691, 264638
2863	91220421 (5725, 5726)	Novel Protein sim. GBank gi|3249088 (AC004473) - Contains similarity to goliath protein gb|M97204 from D. melanogster. [Arabidopsis thaliana]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struct	56994075, 35696286, 22278998, 29331822, 29331824, 35696052, 29331828, 264106, 264511, 55812038, 33657084, 55811386, 265018, 265019, 21906765, 21906766, 21906769, 35695917, 265020, 265022, 33657023, 33657109, 33657349, 264629, 18108376, 60431850, 56182323, 18108385, 18108387, 87168518, 22279002
2864	87420030 (5727, 5728)	Novel Protein sim. GBank gi|1079451|pir||A55463 - tropomodulin, skeletal muscle - chicken		struct	264259, 264910
2865	95312191 (5729, 5730)	Novel Protein sim. GBank gi|438840 (L19048) - MSA-2 [Plasmodium falciparum]			22278995, 21906764, 264482
2866	95105480 (5731, 5732)	Novel Protein sim. GBank gi|585703|sp|Q07066|PMP2_RAT - 22 KD PEROXISOMAL MEMBRANE PROTEIN		glycoprotein	65274572, 22278996, 22278998, 22278999, 264259, 29331824, 29331827, 29331828, 60433438, 21906754, 265018, 264448, 264764, 52644150, 83373044
2867	86908001 (5733, 5734)	Novel Protein sim. GBank gi|4580997|gb|AAD24571.1|AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	264488, 264768, 21906768, 22278998, 265022, 264259, 264508, 264905, 264907, 264511, 264910, 264635, 264636, 264637, 265011, 265017, 265018, 265019, 264563, 264088, 264566, 264764, 264369, 264567, 264486, 264288, 264766

2868	95303283 (5735, 5736)	Novel Protein sim. GBank gi|1292868|emb|CAA63923| - (X94232) t-Cell activation protein [Homo sapiens]			18108392, 264488, 22278994, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 264508, 52644045, 264828, 265006, 265007, 265008, 265009, 264591, 60432229, 264593, 60433356, 264595, 21906754, 265017, 265019, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 264691, 33657182, 18108368, 27486261, 27486262, 27486264, 27486265, 18108370, 18108374, 35696423, 35695855, 264632, 56182323, 87168518, 264404, 22279000, 22279002, 264482, 264563, 264564, 264567, 264487
2869	88094412 (5737, 5738)			UNCLASSIFIED	264369
2870	84404574 (5739, 5740)			UNCLASSIFIED	264905, 264908, 264764, 21906769, 264634
2871	88318621 (5741, 5742)	Novel Protein sim. GBank gi|5306263|gb|AAD41995.1|AC00623 - (AC006233) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264907, 265008, 265017, 265018, 264682, 264764, 18108354, 265021, 27486265, 264629, 18108387, 264567
2872	95312197 (5743, 5744)	Novel Protein sim. GBank gi|112205|pir||B39066 - proline-rich protein 15 - rat		kinase	263981
2873	88094252 (5745, 5746)			UNCLASSIFIED	264488, 18108374, 264768, 264687, 264688, 264689, 35696423, 35696286, 35695917, 264510, 264511, 265007, 264512, 265008, 264910, 264534, 264634, 264635, 264555, 264592, 264259, 264558, 60433438, 60432289, 35696052, 265011, 264600, 264601, 60432113, 264508, 264563, 264482, 264509, 264905, 264906, 264564, 18108351, 264763, 18108370, 264907, 264566, 264908, 264764, 264288, 264567, 264909, 264486, 264766, 18108391

2874	94313549 (5747, 5748)	Novel Protein sim. GBank gi|3212854 (AC004005) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	52644507, 52645156, 52646365, 56182575, 22278994, 22278995, 56994075, 35696286, 60432049, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 29331825, 66714117, 29331826, 29331827, 35696052, 29331828, 33656970, 66712502, 52644045, 265007, 265009, 60433356, 264758, 55812038, 18108348, 52646317, 33109954, 33657084, 265017, 264604, 265018, 265019, 264682, 264369, 264288, 264688, 52644229, 21906766, 21906767, 21906768, 55811957, 265020, 265021, 265022, 52644150, 33657023, 52645129, 18108374, 18108376, 35696423, 56182323, 18108387, 87168518, 60432113, 22279000, 22279002, 264563, 264565
2875	88083726 (5749, 5750)	Novel Protein sim. GBank gi|2781386 (AC004010) - similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278996, 22278997, 22278999, 29331826, 29331828, 29146499, 66712502, 265008, 265017, 18108351, 264683, 264689, 21906767, 18108376, 18108377, 55811576, 60170394, 22279000, 264487
2876	88090854 (5751, 5752)	Novel Protein sim. GBank gi|2979530 (AC004449) - R33683_2 [Homo sapiens]	Contains protein domain (PF00167) - Fibroblast growth factor	fgf	
2877	94747029 (5753, 5754)	Novel Protein sim. GBank gi|4704208|emb|CAB41646.1| - (AL035419) dJ1100H13.1 (putative novel protein) [Homo sapiens]			52646365, 65274572, 56182575, 22278997, 22278998, 22278999, 60432049, 52645080, 60424269, 60432289, 29331827, 35696052, 29331828, 66712502, 52644045, 56182435, 60433356, 33657402, 33657084, 265019, 55811150, 264448, 264369, 21906766, 21906768, 21906769, 265020, 33657023, 33657109, 33657182, 27486262, 264629, 60431528, 55811576, 52644332, 56182323, 264558, 83373044, 18108385, 56526486, 60432113, 22279000, 22279002, 264563
2878	88095309 (5755, 5756)	Novel Protein sim. GBank gi|3876775|emb|CAB03067| - (Z81077) predicted using Genefinder; Similarity to Yeast protein 8248 (TR:G587531) [Caenorhabditis elegans]	Contains protein domain (PF01207) - Uncharacterized protein family UPF0034	UNCLASSIFIED	264488, 264259, 29331822, 29331826, 264905, 264509, 264907, 264909, 264510, 265006, 264511, 264512, 33657402, 264758, 21906754, 18108351, 264681, 264682, 264288, 264684, 264685, 264768, 264689, 21906769, 264690, 33657023, 264693, 18108364, 33657109, 264629, 18108374, 264630, 264632, 264556, 264637, 264639, 264558, 18108385, 18108387, 264563, 264564, 264565, 264566, 264486, 264567

2879	87869122 (5757, 5758)	Novel Protein sim. GBank gi|4895145|gb|AAD32752.1| - (AF127374) unknown [Streptomyces lavendulae]	Contains protein domain (PF00315) - Uracil-DNA glycosylase	UNCLASSIFIED	18108359, 264259, 264905, 18108370, 264629, 264908, 264909, 18108374, 18108377, 265006, 264910, 264637, 60170394, 264559, 265017, 264564, 264565, 264567, 264684, 264369
2880	94851439 (5759, 5760)	Novel Protein sim. GBank gi|4680703|gb|AAD27741.1|AF13296 - (AF132966) CGI-32 protein [Homo sapiens]			264488, 52646365, 52646842, 22278994, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 52644045, 264510, 265006, 264511, 265007, 264512, 265009, 264910, 264594, 21906754, 52646317, 52644296, 87168559, 264600, 264604, 264605, 264760, 264764, 264288, 264766, 264768, 264687, 264769, 21906766, 21906769, 35695917, 265021, 264690, 264692, 33657023, 52645129, 33657109, 33657182, 27486262, 33657349, 264629, 18108374, 35695855, 264634, 264635, 264636, 264637, 264638, 264557, 52644332, 264558, 264559, 83373044, 264404, 22279000, 264563, 264483, 264567, 264486
2881	87650539 (5761, 5762)	Novel Protein sim. GBank gi|733571 (U23452) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	22278998, 29331822, 52644045, 21906765, 264639, 60432113
2882	87714367 (5763, 5764)	Novel Protein sim. GBank gi|1118112 (U41559) - No definition line found [Caenorhabditis elegans]			264488, 22278996, 22278999, 29331822, 29331826, 264908, 60170831, 60433356, 55812038, 264681, 264682, 264686, 264687, 264688, 21906768, 21906769, 264693, 263967, 18108374, 55811576, 56182323, 22279002, 264566
2883	95362875 (5765, 5766)	Novel Protein sim. GBank gi|4868008|gb|AAD31087.1|AF10693 - (AF106934) vitamin D receptor-interacting protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264112, 264682
2884	87784643 (5767, 5768)				265018, 264634
2885	83006306 (5769, 5770)	Novel Protein sim. GBank gi|2224697|dbj|BAA20832| - (AB002376) KIAA0378 [Homo sapiens]		UNCLASSIFIED	264686, 264693
2886	91237823 (5771, 5772)	Novel Protein sim. GBank gi|1255889 (U53344) - T07H6.5 gene product [Caenorhabditis elegans]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	60432049, 264259, 29331828, 264908, 264511, 264595, 60433438, 264596, 265017, 264605, 263969, 263972, 264555, 83373044, 87168518, 264566
2887	91227860 (5773, 5774)	Novel Protein sim. GBank gi|3882323|dbj|BAA34521.1| - (AB018344) KIAA0801 protein [Homo sapiens]		UNCLASSIFIED	18108351, 264686, 264629, 264631, 264639, 83373044, 264482
2888	95105816 (5775, 5776)	Novel Protein sim. GBank gi|4508015|ref|NP_003447.1|pZNF2 - zinc finger protein 205	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264488, 264259, 29331828, 264508, 264906, 264593, 264758, 264766, 264769, 18108374, 83373044, 264486

2889	87606562 (5777, 5778)			UNCLASSIFIED	56994075, 29331824, 265009, 264760, 18108354, 264288
2890	78703853 (5779, 5780)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264591, 264766
2891	88094428 (5781, 5782)	Novel Protein sim. GBank gi|3877750|emb|CAB01508| - (Z78064) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65865 comes from this gene; cDNA EST EMBL:D69451 comes from this gene; cDNA EST EMBL:D66026 comes from this gene; cDNA EST EMBL:D69658 comes from this gen...		UNCLASSIFIED	264591, 264595, 264369, 264685, 264693, 264628, 264563, 264566
2892	95419745 (5783, 5784)	Novel Protein sim. GBank gi|4929759|gb|AAD34140.1|AF15190 - (AF151903) CGI-145 protein [Homo sapiens]		UNCLASSIFIED	65274572, 35696286, 29331828, 264110, 265009, 60433438, 265018, 265019, 18108351, 264288, 21906765, 21906766, 21906769, 55811957, 264690, 65274620, 263967, 35695855
2893	87798014 (5785, 5786)			UNCLASSIFIED	264259, 265010, 264682, 18108370, 264555, 264556
2894	87755985 (5787, 5788)	Novel Protein sim. GBank gi|5669015|gb|AAD46135.1| - (AF080171) zinc finger protein ZNF232 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264259, 265006, 60433438, 52644296, 265011, 264369, 35695917, 18108381, 18108382, 18108388
2895	86938778 (5789, 5790)	Novel Protein sim. GBank gi|3924708|emb|CAA84646| - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...	Contains protein domain (PF01437) - Plexin repeat		29331824, 265007, 264762, 264636, 264563
2896	87752122 (5791, 5792)	Novel Protein sim. GBank gi|4885549|ref|NP_005456.1|pPKBG - protein kinase B gamma	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	18108392, 18108394, 18108398, 22278998, 264259, 29331822, 29331824, 29146499, 264906, 264908, 265007, 265009, 265018, 265019, 264369, 264685, 264689, 21906766, 265021, 264693, 33657182, 264639, 18108384, 18108388, 264567
2897	95413057 (5793, 5794)	Novel Protein sim. GBank gi|4502877|ref|NP_001296.1|pCLDN - Clostridium perfringens enterotoxin receptor 1		UNCLASSIFIED	60424179, 56182575, 22278996, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331825, 60424269, 60432289, 29331826, 29331828, 35696052, 264908, 56182435, 265009, 264910, 60170831, 60431735, 60433356, 60433438, 65274444, 55811386, 265018, 18108351, 264448, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 264534, 33657023, 33657109, 35695763, 264628, 264629, 60431528, 18108374, 55810764, 55811576, 35696423, 35695855, 264555, 56182323, 18108385, 264404, 22279000, 22279002, 264566
2898	87750340 (5795, 5796)			UNCLASSIFIED	22278995, 264604, 18108385, 264566

2899	80357670 (5797, 5798)			UNCLASSIFIED	264764, 21906764, 264692
2900	94233538 (5799, 5800)	Novel Protein sim. GBank gi|4581470|emb|CAB40137.1| - (Y18483) SLC7A8 protein [Homo sapiens]		glycoprotein	65274572, 56182575, 35696286, 60432049, 264259, 29331824, 66714117, 29331826, 35696052, 29331828, 66712502, 56182435, 265006, 265007, 265008, 265009, 60433356, 264758, 265018, 264764, 264765, 264288, 264768, 21906764, 21906768, 21906769, 265020, 264692, 264693, 32833986, 264631, 83373044, 60432113
2901	87444731 (5801, 5802)	Novel Protein sim. GBank gi|4759272|ref|NP_004614.1|pTTC4 - tetratricopeptide repeat domain 4		phosphatase	22278995, 22278997, 22278999, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 264910, 265009, 21906754, 33657084, 87168474, 265010, 265018, 21906764, 21906765, 21906766, 21906767, 21906769, 33657023, 264693, 33657109, 33657349, 35696423, 35695855, 263981, 56182323, 22279002
2902	85745271 (5803, 5804)	Novel Protein sim. GBank gi|2414615|emb|CAB16364| - (Z99259) hypothetical protein [Schizosaccharomyces pombe]			264683, 264691
2903	87606733 (5805, 5806)	Novel Protein sim. GBank gi|1079318|pir||S52241 - XLCL2 protein - African clawed frog			264887, 22278994, 264259, 29331826, 29331828, 264905, 52644045, 56182435, 264511, 265017, 265018, 18108351, 264448, 264683, 264769, 264689, 35695917, 52644150, 87168518, 60432113, 22279002
2904	86458072 (5807, 5808)	Novel Protein sim. GBank gi|5639823|gb|AAD45885.1|AF14367 - (AF143676) multispanning nuclear envelope membrane protein nurim [Homo sapiens]		UNCLASSIFIED	52646365, 22278999, 264259, 35696052, 265011, 265017, 264683, 264769, 35695917, 265020, 263967, 18108374, 35695855, 264637, 264952, 18108385, 18108387
2905	84449926 (5809, 5810)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!		oncogene	265009, 264681, 264682
2906	95341051 (5811, 5812)	Novel Protein sim. GBank gi|4889256|gb|AAD27831.1|AF12185 - (AF121858) sorting nexin 8 [Homo sapiens]	Contains protein domain (PF00787) - PX domain	UNCLASSIFIED	22278996, 35696286, 22278998, 264259, 60432289, 29331828, 29331830, 66712502, 265009, 60170831, 33109954, 264448, 264683, 264288, 264689, 21906766, 21906767, 21906768, 55811957, 35695917, 265022, 52644150, 264691, 33657023, 264692, 264693, 35695855, 60432113, 264566

2907	91211383 (5813, 5814)	Novel Protein sim. GBank gi|1707079 (U80451) - contains strong similarity to a DNAJ-like domain (PS:PS00636) [Caenorhabditis elegans]	Contains protein domain (PF00226) - DnaJ domain	eph	52644507, 56182575, 56181686, 22278995, 56994075, 35696286, 60432049, 56182181, 35696052, 60431735, 264595, 55812038, 21906754, 55811386, 265019, 264682, 264369, 56181562, 21906766, 55811957, 35695917, 265020, 265021, 33657023, 33657109, 60431528, 55811576, 35696423, 35695855, 264638, 22279000
2908	80414246 (5815, 5816)	Novel Protein sim. GBank gi|2673917 (AC002561) - putative ATP-dependent RNA helicase [Arabidopsis thaliana]		helicase	265009, 33109954, 18108351, 264766, 265021, 264691, 264692, 18108374, 264556, 264638, 264557, 264558
2909	87420225 (5817, 5818)			eph	264259, 87168474, 265018, 18108365, 264628
2910	86601075 (5819, 5820)	Novel Protein sim. GBank gi|4539335|emb|CAB37483.1| - (AL035539) putative protein [Arabidopsis thaliana]			22278995, 264509, 264512, 265007, 33657402, 265017, 264369, 265022, 18108365, 264628
2911	94216615 (5821, 5822)	Novel Protein sim. GBank gi|4469187|emb|CAB38415.1| - (AL031588) dJ1163J1.3 (novel protein similar to mouse B99) [Homo sapiens]		glucoamylase	52646365, 18108397, 22278995, 22278997, 22278998, 22278999, 29331824, 29331825, 52644045, 265006, 265018, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 18108370, 18108372, 18108374, 22279000
2912	87731803 (5823, 5824)	Novel Protein sim. GBank gi|4929637|gb|AAD34079.1|AF15184 - (AF151842) CGI-84 protein [Homo sapiens]	Contains protein domain (PF00904) - Involucrin repeat		52645156, 264092, 60432049, 264259, 52645080, 29331824, 29331825, 66712502, 33109954, 264760, 264683, 264288, 264686, 265021, 264693, 18108368, 263976, 264404
2913	87713823 (5825, 5826)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	52644507, 52645156, 52646842, 56182575, 35696286, 22278997, 264259, 52645080, 29331827, 35696052, 29331828, 264828, 52644045, 56182435, 55812038, 52646317, 21906754, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264682, 264686, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 27486261, 27486262, 27486265, 35695763, 55811576, 35695855, 52644332, 22279000, 22279002, 264563
2914	87797300 (5827, 5828)				264557

2915	88081972 (5829, 5830)	Novel Protein sim. GBank gi|5174485|ref|NP_006030.1|pKIAA - endocytic receptor (macrophage mannose receptor family)	Contains protein domain (PF00059) - Lectin C-type domain	eph	264569, 264488, 264687, 264768, 21906766, 52646842, 21906767, 21906768, 56182575, 29148629, 35695917, 22278996, 22278997, 22278998, 265021, 22278999, 52644150, 264691, 264259, 60432049, 264692, 52645129, 33657109, 33657182, 29331827, 27486261, 35696052, 29331828, 27486262, 27486264, 27486265, 33657349, 29146498, 29146499, 264906, 264907, 18108370, 264908, 18108372, 52644045, 18108374, 56182435, 35695855, 264112, 264510, 265008, 60432229, 264593, 60433356, 56182323, 18108382, 55812038, 18108385, 33109954, 21906754, 33657084, 87168518, 265010, 265011, 60432113, 265017, 265018, 22279000, 265019, 55811150, 264681, 18108351, 264763, 264448, 264683, 264566, 18108354, 264389, 264288, 264766
2916	95337790 (5831, 5832)	Novel Protein sim. GBank gi|5104851|dbj|BAA80165.1| - (AP000061) 305aa long hypothetical dTDP-4-dehydrorhamnose reductase [Aeropyrum pernix]		dehydrogenase	52645156, 65274572, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 264509, 264906, 29331830, 52644045, 264909, 56182435, 60170831, 264592, 264593, 33657402, 60433356, 52646317, 21906754, 33109954, 33657084, 52644296, 85658542, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486264, 35695763, 18108376, 55811576, 35696423, 65274791, 35695855, 52644332, 264557, 264638, 56182323, 18108387, 87168518, 22279002, 264482
2917	87454546 (5833, 5834)	Novel Protein sim. GBank gi|3169065|emb|CAA19260.1| - (AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe]		UNCLASSIFIED	60433438, 264602, 264682, 87168518, 60432113
2918	85690529 (5835, 5836)	Novel Protein sim. GBank gi|539218|pir||S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)			264638
2919	87641497 (5837, 5838)	Novel Protein sim. GBank gi|2564955 (AF030001) - unknown [Mus musculus]			66714117, 66712502, 263981

2920	87769523 (5839, 5840)				35696286, 22278997, 264259, 52645080, 29331824, 29331826, 29331827, 264828, 264909, 56182435, 264511, 264758, 33109954, 21906754, 52644296, 265010, 265011, 264601, 265017, 265019, 264681, 264687, 21906767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486262, 27486264, 27486265, 35696423, 35695855, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 87168518, 60432113
2921	91639982 (5841, 5842)	Novel Protein sim. GBank gi|4580013|gb|AAD24202.1|U83194_ - (U83194) TRAF4-associated factor 2 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		35696286, 22278997, 264091, 264092, 264094, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29146498, 264104, 264105, 264107, 264509, 264110, 264112, 264512, 60433356, 21906754, 87168474, 265017, 18108351, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 263974, 18108374, 263976, 263977, 18108376, 264555, 263981, 56526486, 87168518, 22279000, 22279002
2922	87749762 (5843, 5844)	Novel Protein sim. GBank gi|4589514|dbj|BAA76779.1| - (AB023152) KIAA0935 protein [Homo sapiens]	Contains protein domain (PF01074) - Glycosyl hydrolases family 38	kinase	264906, 264909, 264511, 265006, 265008, 264593, 33657402, 60174639, 18108351, 264763, 21906765, 29148627, 35695917, 264692, 264629, 263976, 55811576, 35695855, 264555, 264558, 56182323, 60170394, 22279000, 264486
2923	95337799 (5845, 5846)	Novel Protein sim. GBank gi|4835268|emb|CAB42898.2| - (Z83844) dJ37E16.4 (similar to mouse p116Rip protein) [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	264488, 18108397, 22278995, 22278996, 22278997, 22278998, 22278999, 29331825, 29331826, 29331827, 29331830, 264511, 265009, 33657402, 265011, 265017, 265018, 264683, 18108354, 21906765, 21906767, 21906768, 21906769, 52644150, 264691, 264692, 33657109, 263974, 18108376, 264631, 264636, 18108385, 18108387, 22279000, 264563, 264566
2924	87791967 (5847, 5848)	Novel Protein sim. GBank gi|2133095|pir||S72254 - ribosomal protein L36, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00444) - Ribosomal protein L36	ribosomalprot	265017, 264628, 20281152, 264556
2925	95090120 (5849, 5850)	Novel Protein sim. GBank gi|2388986|emb|CAB11718| - (Z98980) actin associated protein [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 35696286, 264259, 60432289, 29331827, 264508, 52644045, 264910, 264591, 60432229, 55812038, 21906754, 264681, 264448, 264683, 264288, 264685, 52644229, 264689, 21906765, 21906766, 21906768, 21906769, 265021, 265022, 60170615, 264692, 33657023, 264693, 33657109, 35696423, 65274781, 56182323

2926	95343003 (5851, 5852)				29331828, 265011, 264768, 264689
2927	80408018 (5853, 5854)	Novel Protein sim. GBank gi|283032|pir||S22456 - hydroxyproline-rich glycoprotein - perennial teosinte			264764, 264288, 264630, 264637
2928	20452179 (5855, 5856)			UNCLASSIFIED	264559
2929	91622920 (5857, 5858)	Novel Protein sim. GBank gi|3413320|emb|CAA06915| - (AJ006215) CMP-N-acetylneuraminic acid synthetase [Mus musculus]		UNCLASSIFIED	264569, 264489, 22278994, 35696286, 22278996, 22278998, 22278999, 264094, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 33656970, 264109, 29331830, 52644045, 265009, 33109954, 52644296, 87168559, 264760, 264762, 264448, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906768, 21906769, 35695917, 264691, 33657023, 264693, 33657109, 18108374, 263976, 35696423, 35695855, 263981, 22279000, 22279002, 264567, 264486
2930	95302755 (5859, 5860)			UNCLASSIFIED	56182575, 56181686, 35696286, 22278996, 22278998, 22278999, 264259, 29331825, 60432289, 29331828, 264905, 52644045, 56182435, 265009, 60170831, 264592, 60432229, 60433356, 87168474, 265010, 265011, 265017, 265018, 265019, 264762, 264448, 264683, 264288, 264766, 21906765, 21906769, 35695917, 60170615, 33657023, 33657109, 264628, 18108370, 18108372, 35696423, 35695855, 264556, 56182323, 60432113, 264567
2931	94312693 (5861, 5862)	Novel Protein sim. GBank gi|3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]	Contains protein domain (PF00471) - Ribosomal protein L33	UNCLASSIFIED	52645156, 22278997, 22278998, 29331822, 52645080, 29331824, 60432289, 33656970, 60433356, 60433438, 33109954, 21906765, 21906766, 21906767, 21906768, 265020, 52644150, 33657023, 33657109, 33657182, 27486265, 35696423, 35695855, 264555, 87168518, 60432113, 264566
2932	79632623 (5863, 5864)				264906, 264907
2933	91720776 (5865, 5866)	Novel Protein sim. GBank gi|3378056 (AF017777) - helicase [Drosophila melanogaster]		helicase	264488, 18108392, 56182575, 22278999, 264091, 264259, 29331825, 60432289, 29331827, 264508, 52644045, 56182435, 265007, 265009, 264592, 60433356, 60433438, 21906754, 265017, 264682, 264288, 52644229, 21906765, 21906766, 21906768, 21906769, 265022, 52644150, 33657023, 33657109, 27486265, 264635, 264636, 60170394, 56182323, 18108385, 60432113, 264565, 264566, 264567

2934	86576025 (5867, 5868)				22278997, 22278999, 29331824, 33657402, 264691, 27486262, 264628, 87168518, 22279000
2935	86410579 (5869, 5870)			UNCLASSIFIED	56182575, 22278995, 60433356, 33657402, 264758, 33109954, 21906754, 265018, 265019, 264448, 264769, 21906764, 21906765, 265021, 264692, 33657023, 33657109, 33657349, 55810764, 22279000
2936	87605863 (5871, 5872)	Novel Protein sim. GBank gi|4153862 (AC005065) - determined by GENSCAN prediction and spliced EST; match to EST R84329 (NID:942735) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	nuclease	22278997, 29331827, 29331828, 265009, 265017, 264605, 265020, 55811576, 18108387, 60432113, 264563
2937	94853096 (5873, 5874)	Novel Protein sim. GBank gi|5174409|ref|NP_006101.1|pCD2B - CD2 antigen (cytoplasmic tail)-binding protein 2		UNCLASSIFIED	56994075, 22278999, 264259, 60432049, 29331822, 56182181, 29331827, 29331828, 264906, 264908, 264909, 56182435, 265006, 264512, 264910, 60170831, 60433356, 265011, 265018, 18108351, 264448, 264288, 264766, 52644229, 21906765, 29148784, 65274791, 264556, 56182323, 60170394, 264558, 60432113, 264565, 264486, 264567
2938	95419773 (5875, 5876)	Novel Protein sim. GBank gi|3319990|emb|CAA76720| - (Y17267) ubiquitin-conjugating enzyme [Mus musculus]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	264488, 56182575, 22278996, 35696286, 22278997, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264107, 264905, 66712502, 52644045, 56182435, 264511, 265008, 265009, 60432229, 33657402, 60433438, 55812038, 21906754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264681, 264288, 264689, 21906765, 21906767, 21906768, 55811957, 35695917, 265020, 60170615, 264690, 264691, 264692, 33657023, 264693, 65274620, 33657109, 18108370, 18108374, 263976, 35696423, 35695855, 264555, 264556, 18108381, 56182323, 60170394, 83373044, 18108385, 56526486, 60432113, 22279002
2939	87786622 (5877, 5878)	Novel Protein sim. GBank gi|3979900|emb|CAA99909| - (Z75547) similar to WD domain, G-beta repeat; cDNA EST yk371b7.5 comes from this gene; cDNA EST yk312h1.5 comes from this gene; cDNA EST yk465d5.5 comes from this gene; cDNA EST yk472c4.5 comes from this gene; cDNA EST yk292f8....	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase_associated	264907, 265018, 264681, 264685, 264686

2940	95011103 (5879, 5880)			UNCLASSIFIED	22278996, 29331822, 29331824, 66714117, 29331826, 29331828, 264905, 264908, 66712502, 29331830, 265011, 265017, 264764, 264369, 21906766, 21906767, 33657023, 33657109, 32833986, 18108374, 18108377, 264634, 83373044, 18108385, 18108387, 264566
2941	21423370 (5881, 5882)	Novel Protein sim. GBank gi|3413872|dbj|BAA32300| - (AB007924) KIAA0455 protein [Homo sapiens]		UNCLASSIFIED	264557
2942	87430203 (5883, 5884)	Novel Protein sim. GBank gi|1172845|sp|P46629|RB25_RABIT - RAS-RELATED PROTEIN RAB-25		glycoprotein	264910, 265010, 264768
2943	95314504 (5885, 5886)	Novel Protein sim. GBank gi|4929653|gb|AAD34087.1|AF15185 - (AF151850) CGI-92 protein [Homo sapiens]		collagen	60432049, 264259, 60432289, 29331827, 29146498, 265008, 264593, 60433356, 60433438, 265010, 265011, 265017, 265018, 264683, 264766, 18108381, 65274727, 60432113, 264567
2944	95081063 (5887, 5888)	Novel Protein sim. GBank gi|4678282|emb|CAB41190.1| - (AL049660) 1-acylcerol-3-phosphate acyltransferase-like protein [Arabidopsis thaliana]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	ATPase_associated	56994075, 22278998, 60432049, 264259, 29331822, 29331824, 60424269, 60432289, 29331826, 29331828, 264905, 264907, 52644045, 264909, 264511, 265006, 265009, 264594, 21906754, 87168559, 264603, 265017, 265018, 18108351, 264682, 264766, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170615, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 33657182, 33657349, 18108370, 18108374, 18108377, 55811576, 35696423, 35695855, 264635, 264555, 264556, 56182323, 60170394, 264558, 264559, 83373044, 56526486, 87168518, 60432113, 22279002, 264482, 264563, 264484, 264567
2945	94233560 (5889, 5890)	Novel Protein sim. GBank gi|728831|sp|P39188|ALU1_HUMAN - !!!! ALU SUBFAMILY J WARNING ENTRY !!!!	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	60424179, 22278995, 22278996, 22278998, 22278999, 264259, 56182181, 29331824, 60424269, 60432289, 35696052, 264908, 265006, 60433356, 55812038, 264759, 55811386, 265018, 264681, 18108351, 264448, 264683, 264369, 264288, 264687, 56181562, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264693, 60431528, 55810764, 35696423, 35695855, 264630, 60170394, 83373044, 22279000, 264566, 264567

2946	84317315 (5891, 5892)	Novel Protein sim. GBank gi|5441952|gb|AAD43195.1|AF07286 - (AF072864) peroxisomal membrane protein PMP 24 [Homo sapiens]		UNCLASSIFIED	264488, 264259, 264508, 264509, 264906, 264907, 264909, 264510, 264511, 265007, 264512, 264910, 264591, 264593, 18108351, 264764, 264288, 264684, 264769, 265021, 264692, 33657109, 264628, 264629, 18108374, 264631, 264634, 264636, 264637, 18108380, 264638, 264639, 83373044, 264565, 264566, 264486, 264567
2947	87362952 (5893, 5894)	Novel Protein sim. GBank gi|3540281|gb|AAC34383.1| - (AF056116) All-1 related protein [Fugu rubripes]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 29146498, 264508, 29331830, 265007, 265008, 265009, 60432229, 21906754, 265010, 265017, 265019, 264766, 264685, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264628, 18108370, 264629, 264630, 18108387, 60432113
2948	87626527 (5895, 5896)	Novel Protein sim. GBank gi|5566614|gb|AAB65654.2| - (AF001533) mitogen-induced [Mus musculus]			52646842, 22278995, 264259, 29331824, 29331825, 29331827, 29331830, 264909, 265007, 265009, 265019, 264763, 264684, 264288, 264685, 264686, 21906767, 264691, 264692, 264693, 18108374, 55811576, 18108385, 22279002, 264563, 264567
2949	88175545 (5897, 5898)	Novel Protein sim. GBank gi|2132923|pir||S67133 - probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	22278996, 22278997, 60432289, 29331826, 29331827, 29331828, 35696052, 29146499, 264104, 264107, 264905, 66712502, 264908, 60433356, 60433438, 87168559, 264764, 52644229, 56181562, 21906767, 21906768, 21906769, 265022, 60170615, 33657023, 35696423, 263981, 264558, 60432113, 22279002
2950	95086870 (5899, 5900)	Novel Protein sim. GBank gi|466102|sp|P34629|YOJ6_CAEEL - PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III	Contains protein domain (PF00883) - Cytosol aminopeptidase family	peptidase	264488, 35696286, 264259, 35696052, 264907, 265007, 264910, 265017, 265018, 264288, 264768, 35695917, 265020, 18108362, 18108370, 18108379, 35696423, 65274791, 35695855, 264556, 56526486, 264486
2951	87392357 (5901, 5902)	Novel Protein sim. GBank gi|4688902|emb|CAB41450.1| - (AJ238248) centaurin beta2 [Homo sapiens]			264693

2952	95329952 (5903, 5904)	Novel Protein sim. GBank gi|5596693|emb|CAB51405.1| - (AL096881) hypothetical protein [Homo sapiens]	Contains protein domain (PF00650) - CRAL/TRIO domain.	transcriptfactor	264687, 52645156, 21906766, 21906769, 22278996, 265020, 264690, 60432049, 264259, 264693, 29331822, 18108365, 29331825, 60432289, 33657109, 18108368, 29331827, 35696052, 27486262, 264508, 264905, 20281149, 264906, 264907, 29331830, 264908, 264909, 35695855, 264511, 265008, 265009, 264910, 264635, 264636, 60432229, 264638, 60433356, 264639, 264758, 87168518, 265017, 22279000, 22279002, 264760, 264563, 264482, 18108351, 264448, 264288
2953	88093575 (5905, 5906)	Novel Protein sim. GBank gi|119522|sp|P10658|SERC_RABIT - PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP)	Contains protein domain (PF00266) - Aminotransferases class-V	UNCLASSIFIED	18108398, 56994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264906, 264907, 264510, 264591, 264594, 33657402, 264595, 264596, 264758, 52646317, 21906754, 33657084, 52644296, 87168559, 264600, 264760, 264681, 18108351, 264764, 264369, 264288, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 18108364, 52645129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565
2954	88086288 (5907, 5908)	Novel Protein sim. GBank gi|4885261|ref|NP_005251.1|pGDF9 - growth differentiation factor 9	Contains protein domain (PF00019) - Transforming growth factor beta like domain	tgf	29331822
2955	87698426 (5909, 5910)	Novel Protein sim. GBank gi|3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331825, 29331826, 35696052, 264908, 52644045, 264512, 60432229, 265018, 265019, 55811150, 264769, 21906767, 21906768, 21906769, 265021, 60170615, 55810764, 264567
2956	85789745 (5911, 5912)	Novel Protein sim. GBank gi|4689254|gb|AAD27830.1|AF12185 - (AF121857) sorting nexin 7 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		22278996, 264259, 29331827, 264908, 21906768
2957	90933301 (5913, 5914)	Novel Protein sim. GBank gi|4503023|ref|NP_000089.1|pCPT2 - carnitine palmitoyltransferase II precursor		cadherin	22278999, 264259, 29331824, 29331827, 265008, 264595, 264758, 265010, 265011, 264448, 264763, 264683, 264288, 264685, 18108357, 29148629, 264690, 18108362, 264693, 18108370, 60431528, 18108374, 264634, 18108381, 56182323, 18108382, 18108385, 18108388, 56526486, 87168518, 264482, 264487
2958	87440014 (5915, 5916)	Novel Protein sim. GBank gi|4240257|dbj|BAA74907.1| - (AB020691) KIAA0884 protein [Homo sapiens]			264595, 264596, 264681, 264369, 264629, 264631, 264567

2959	95109420 (5917, 5918)	Novel Protein sim. GBank gi|988221 (U33005) - Tbc1 [Mus musculus]	Contains protein domain (PF00566) - TBC domain	oncogene		263994, 22278997, 264259, 60432049, 29331828, 29331828, 35696052, 29331830, 68712502, 56182435, 265006, 264512, 265008, 265009, 60433358, 60433438, 264596, 265017, 265018, 264683, 264288, 264766, 264769, 21906766, 21906767, 21906769, 265020, 60170615, 264692, 27486265, 18108374, 65274781, 35695855, 83373044, 56526486, 60432113
2960	87420091 (5919, 5920)			UNCLASSIFIED		35696286, 56182435, 87168474, 265010, 60170615, 35696423, 56182323, 18108383, 87168518, 264483
2961	85413418 (5921, 5922)	Novel Protein sim. GBank gi|5596646|emb|CAB05177.2| - (Z82266) predicted using Genefinder; similar to WD domain, G-beta repeats [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor		22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 264907, 264908, 52644045, 265006, 33657402, 21906754, 87168474, 265011, 87168559, 265017, 21906769, 265020, 60170615, 264692, 33657023, 35695763, 18108370, 18108374, 35696423, 264632, 264636, 18108385, 87168518, 22279002, 264564, 264567
2962	87912700 (5923, 5924)			UNCLASSIFIED		35696286, 22278997, 264092, 264094, 264259, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264509, 264907, 264908, 264909, 264510, 264512, 264593, 264594, 60433438, 264758, 52646317, 264602, 264603, 264605, 264760, 264762, 264764, 264288, 264766, 264686, 264768, 264769, 35695917, 265020, 264691, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264565, 264566, 264567, 264486
2963	95313464 (5925, 5926)	Novel Protein sim. GBank gi|4240223|dbj|BAA74890.1| - (AB020674) KIAA0867 protein [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor		18108392, 56994075, 22278998, 22278999, 29331822, 29331825, 29331826, 29331827, 29331828, 265007, 265008, 264592, 264594, 21906754, 265018, 264760, 264687, 29148627, 29148784, 265020, 33657023, 264693, 65274620, 33657182, 27486261, 264629, 55810764, 35696423, 264555, 264636, 264637, 264557, 264558, 264563
2964	94324617 (5927, 5928)			UNCLASSIFIED		264259, 29331828, 33657402, 265017, 265018, 264692, 18108368, 35696423, 83373044, 18108388

2965	80384762 (5929, 5930)	Novel Protein sim. GBank gi|4885447|ref|NP_005452.1|pKRML - Kreisler (mouse) maf-related leucine zipper homolog		transcriptfactor	264259, 29331826, 264508, 264509, 264905, 264907, 264908, 264909, 264511, 265008, 264910, 264591, 264593, 264594, 33657402, 265011, 264760, 264762, 264764, 264288, 264685, 264766, 264692, 33657109, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264567, 18108391
2966	91725248 (5931, 5932)	Novel Protein sim. GBank gi|5262751|emb|CAB45690.1| - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]			60432289, 264682, 264448
2967	94658303 (5933, 5934)	Novel Protein sim. GBank gi|624225 (U19181) - Rabin3 [Rattus norvegicus]		UNCLASSIFIED	264488, 264508, 264509, 264908, 264909, 264511, 264910, 264594, 264758, 85658542, 264762, 264764, 265021, 264556, 18108381, 264564, 264486
2968	95302776 (5935, 5936)	Novel Protein sim. GBank gi|4929715|gb|AAD34118.1|AF15188 - (AF151881) CGI-123 protein [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		264687, 52645156, 21906765, 52646365, 21906767, 18108398, 35696423, 22278996, 35696286, 22278997, 265020, 22278999, 265021, 265022, 264093, 264636, 264690, 52644150, 264259, 33657023, 52645080, 264693, 29331822, 56182181, 29331824, 66714117, 29331825, 33109954, 52645129, 29331826, 21906754, 33657182, 29331827, 29331828, 35696052, 27486262, 87168518, 87168474, 265010, 87168559, 265018, 22279000, 265019, 22279002, 264563, 18108351, 264906, 264907, 264448, 66712502, 264566, 264369, 264288
2969	95310957 (5937, 5938)	Novel Protein sim. GBank gi|3024743|sp|O24734|THSA_SULS7 - THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT)		eph	52646842, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331828, 264509, 264909, 52644045, 56182435, 265009, 60433438, 55812038, 21906754, 265011, 87168559, 265018, 265019, 264448, 264288, 264369, 52644229, 21906766, 21906768, 21906769, 29148784, 265020, 265021, 52644150, 264691, 33657109, 18108374, 56182323, 60170394, 87168518, 60432113, 22279000
2970	88088071 (5939, 5940)	Novel Protein sim. GBank gi|3165407 (AC004755) - fos37502_1 [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2971	94196930 (5941, 5942)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!		tm7	264488, 56182575, 35696286, 56994075, 29331824, 29331826, 29146499, 264508, 264905, 264907, 264112, 264910, 21906754, 87168559, 265018, 265019, 18108351, 264689, 21906765, 21906767, 21906768, 265020, 265021, 60170615, 18108364, 264628, 264629, 18108374, 264636, 264556, 264558, 83373044, 18108384, 18108385, 87168518, 264564, 264567
2972	86625943 (5943, 5944)	Novel Protein sim. GBank gi|728836|sp|P39193|ALU6_HUMAN - !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!		kinase	265017, 35695917, 265021, 33657109, 22279002, 264563
2973	91215301 (5945, 5946)	Novel Protein sim. GBank gi|2746789 (AF040642) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 264692, 33657349, 55811576, 264563
2974	91673002 (5947, 5948)	Novel Protein sim. GBank gi|786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	18108392, 52644507, 56182575, 56181686, 22278995, 22278998, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331824, 29331825, 66714117, 60424269, 29331826, 29331827, 29331828, 35696052, 66712502, 264908, 52644045, 265007, 264910, 265009, 60433438, 33109954, 21906754, 55811386, 52644296, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264448, 264369, 264288, 52644229, 18108359, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 52644150, 264691, 264692, 33657023, 27486262, 27486264, 35695763, 18108370, 18108376, 55810764, 55811576, 35696423, 35695855, 264630, 264635, 264557, 52644332, 264558, 83373044, 18108387, 87168518, 60432113, 22279000, 264482, 264487
2975	95325213 (5949, 5950)	Novel Protein sim. GBank gi|3880812|emb|CAA19508| - (AL023839) similar to HECT-domain (ubiquitin-transferase).; cDNA EST yk480d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00632) - HECT-domain (ubiquitin-transferase).	ubiquitin	29331824, 29331827, 29331828, 264910, 85658542, 265011, 265018, 264448, 264288, 264769, 21906767, 265020, 264691, 264559, 83373044
2976	87771202 (5951, 5952)	Novel Protein sim. GBank gi|5679136|gb|AAD46874.1|AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	22278996, 264906, 265007, 265010, 265011, 265017, 265019, 18108351, 264685, 264689, 18108370, 264639, 18108385
2977	91725254 (5953, 5954)	Novel Protein sim. GBank gi|5262751|emb|CAB45690.1| - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		UNCLASSIFIED	264509, 264288

2978	87332059 (5955, 5956)	Novel Protein sim. GBank gi|746549 (U23522) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00480) - ROK family	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432289, 29331827, 29146499, 56182435, 265006, 265007, 265009, 60433356, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 264288, 264685, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 35696423, 264639, 60432113, 22279000, 22279002
2979	91725256 (5957, 5958)	Novel Protein sim. GBank gi|5262751|emb|CAB45690.1| - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		complement	264488, 65274572, 56994075, 22278999, 264093, 29331822, 29331824, 264288, 55811957, 33657023, 33657109, 18108370, 55811576, 56182323, 60432113, 264482
2980	86296600 (5959, 5960)				265009, 21906767, 263981, 22279000
2981	87376330 (5961, 5962)			UNCLASSIFIED	264629, 264564
2982	95303675 (5963, 5964)	Novel Protein sim. GBank gi|4929767|gb|AAD34144.1|AF15190 - (AF151907) CGI-149 protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264092, 29331824, 29331827, 29331828, 264905, 264591, 264592, 264594, 264595, 264596, 33657084, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 18108365, 33657182, 33657349, 35696423, 83373044, 22279000, 22279002
2983	91725258 (5965, 5966)	Novel Protein sim. GBank gi|5262751|emb|CAB45690.1| - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]			60424179, 52646842, 18108398, 22278997, 264093, 60432049, 264259, 29331822, 60432289, 33656970, 264905, 52644045, 265006, 60431735, 87168474, 265018, 265019, 18108351, 264448, 21906765, 21906768, 35695917, 33657023, 52645129, 18108370, 35696423, 83373044, 56526486, 60432113, 264404, 22279002
2984	94136467 (5967, 5968)	Novel Protein sim. GBank gi|2393734 (AC002542) - similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619) [Homo sapiens]		ATPase_associated	
2985	87099072 (5969, 5970)	Novel Protein sim. GBank gi|103160|pir||S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	264910, 55812038, 56181562, 55811957, 264628, 55810764, 264632, 264635, 60432113
2986	86284861 (5971, 5972)				55811957, 264566
2987	86455934 (5973, 5974)			UNCLASSIFIED	264369

2988	95357753 (5975, 5976)	Novel Protein sim. GBank gi|4679028|gb|AAD27002.1| - (AF077207) HSPC021 [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 22278995, 22278996, 22278997, 22278999, 264092, 264094, 264259, 60432049, 29331824, 29331826, 60432289, 35696052, 29331828, 264107, 264905, 264907, 264908, 66712502, 264828, 264909, 56182435, 265006, 265007, 265008, 60170831, 60432229, 264593, 60433356, 264757, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264682, 264448, 264369, 264288, 264685, 52644229, 21906765, 21906767, 21906769, 35695917, 265021, 265022, 52644150, 264690, 33657023, 65274620, 263967, 33657109, 27486262, 18108370, 18108372, 18108374, 55810764, 65274791, 35695855, 264635, 264636, 264637, 263981, 264638, 56182323, 83373044, 60432113, 22279000, 264563, 264564, 264565, 264566, 264567
2989	91225118 (5977, 5978)	Novel Protein sim. GBank gi|113671|sp|P23964|ALUF_HUMAN - !!!! ALU CLASS F WARNING ENTRY !!!!		kinase	22278996, 22278997, 264905, 264511, 60170831, 264593, 265019, 21906765, 21906767, 21906768, 18108374
2990	87330444 (5979, 5980)	Novel Protein sim. GBank gi|2829836|sp|P97348|RHOD_MOUSE - RHO-RELATED GTP-BINDING PROTEIN RHOD	Contains protein domain (PF00071) - Ras family	oncogene	265007, 264512, 18108351, 264288, 264689, 265020, 264691, 33657023, 33657109
2991	94325361 (5981, 5982)				
2992	85425164 (5983, 5984)			UNCLASSIFIED	264563
2993	94325363 (5985, 5986)			UNCLASSIFIED	264259, 265019, 264689, 18108385
				UNCLASSIFIED	264488, 29331822, 265017, 264761, 21906769, 65274791, 263981, 264565
2994	94136634 (5987, 5988)	Novel Protein sim. GBank gi|2496549|sp|Q50658|YU02_MYCTU - HYPOTHETICAL 29.7 KD PROTEIN CY339.02		transport	22278994, 22278995, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 265006, 265009, 264910, 33109954, 87168474, 87168559, 265018, 265019, 264448, 264288, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 33657023, 264693, 35695855, 83373044, 18108385, 22279000, 264565, 264566
2995	87591070 (5989, 5990)	Novel Protein sim. GBank gi|2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]			264905, 264907, 265019, 18108351, 264683
2996	91013798 (5991, 5992)	Novel Protein sim. GBank gi|2829912 (AC002291) - Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	65274572, 35696286, 264259, 29331824, 35696052, 29146499, 264508, 264907, 265007, 265008, 60433438, 18108348, 265017, 264681, 264683, 264288, 264766, 264769, 264689, 35695917, 60170615, 33657023, 264692, 264634, 264555, 18108381, 18108382, 18108388, 264484

2997	87627440 (5993, 5994)	Novel Protein sim. GBank gi|4589652|dbj|BAA76848.1| - (AB023221) KIAA1004 protein [Homo sapiens]		homeobox	264488, 56182575, 264259, 66714117, 29331826, 35696052, 264508, 264509, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21906764, 21906766, 21906768, 21906769, 27486261, 18108374, 35696423, 264634, 264635, 264636, 264557, 18108385, 87168518
2998	88095381 (5995, 5996)	Novel Protein sim. GBank gi|3947589|emb|CAA22252| - (AL034364) cDNA EST yk255b9.3 comes from this gene; cDNA EST yk255b9.5 comes from this gene; cDNA EST EMBL:M75923 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	52646365, 22278997, 264508, 264906, 18108351, 21906765, 21906767, 18108370, 18108374, 35696423, 264636, 264639
2999	94847055 (5997, 5998)	Novel Protein sim. GBank gi|115408|sp|P18835|CC19_CAEEL - CUTICLE COLLAGEN 19		UNCLASSIFIED	56182575, 22278996, 29147620, 29331825, 29146498, 29146499, 264905, 66712502, 265006, 265009, 21906754, 85658542, 18108351, 29148627, 29148629, 60170615, 33657109, 27486262, 18108370, 18108374, 264556, 264557, 264558, 60170394, 18108385, 264563
3000	95099370 (5999, 6000)	Novel Protein sim. GBank gi|1163174 (U32575) - similar to yeast Sec6p, Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author [Rattus norvegicus]		UNCLASSIFIED	264887, 22278997, 22278999, 264259, 29331822, 29331824, 35696052, 29146498, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 265008, 265009, 264910, 33657402, 264757, 264595, 264596, 264758, 21906754, 265011, 264600, 265017, 265018, 264605, 265019, 264760, 264761, 264762, 264681, 264682, 264764, 264288, 264685, 264766, 264686, 264768, 264769, 21906765, 21906768, 35695917, 265020, 264691, 264692, 33657023, 264693, 33657109, 33657182, 27486261, 264628, 264629, 18108374, 18108376, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 60170394, 83373044, 20798451, 22279002, 264563, 264486, 264567
3001	88078454 (6001, 6002)	Novel Protein sim. GBank gi|2078470 (AC002073) - Putative gene. Genscan predictions confirmed by EST splicing.; coded for by human cDNAs AA122029 (NID:g1678048), D31562 (NID:g644442), AA158721 (NID:g1733515), R59640 (NID:g830335) and F13082 (NID:g709111) [Homo sapiens]		cathepsin	18108394, 52646842, 56182575, 29331824, 29331825, 29331827, 264910, 33109954, 52644296, 265017, 265019, 264288, 265020, 265021, 52644150, 264692, 35695763, 55810764, 35696423, 56182323, 18108387, 264563, 264564
3002	87718167 (6003, 6004)	Novel Protein sim. GBank gi|3599478 (AF085185) - Myosin-IA [Acanthamoeba castellanii]		UNCLASSIFIED	264488, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 264510, 265009, 21906754, 264682, 264688, 33657023, 264565

3003	86648079 (6005, 6006)	Novel Protein sim. GBank gi|1754969 (U30292) - collagen type XIII alpha-1 chain [Mus musculus]	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	collagen	264512, 264593, 264564, 264567, 264486
3004	88066876 (6007, 6008)	Novel Protein sim. GBank gi|2224629|dbj|BAA20802| - (0002342) KIAA0344 [Homo sapiens]			29331830, 21906769, 264691, 33657109, 263972, 18108385
3005	87794843 (6009, 6010)	Novel Protein sim. GBank gi|4680659|gb|AAD27719.1|AF13294 - (AF132944) CGI-10 protein [Homo sapiens]	Contains protein domain (PF01360) - Monooxygenase	oxygenase	29331822, 29331824, 29331827, 60433438, 265011, 265019, 21906766, 21906767, 21906768, 265020, 33657023, 33657349, 60170394, 22279002, 264567
3006	87422224 (6011, 6012)	Novel Protein sim. GBank gi|3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Ank repeat	MHC	264259, 29331822, 264512, 21906754, 265018, 264687, 21906765, 264691, 264555, 264556, 264558, 18108385
3007	90936005 (6013, 6014)	Novel Protein sim. GBank gi|2565052 (U80738) - CAGH1a [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	52644507, 52645156, 65274572, 264909, 264512, 265018, 264760, 264448, 264765, 264689, 60170615, 18108374, 20281152, 264636, 52644332
3008	80416249 (6015, 6016)				264905, 264593, 264766, 264636
3009	91213387 (6017, 6018)	Novel Protein sim. GBank gi|3127193 (AF062389) - kidney-specific protein [Rattus norvegicus]	Contains protein domain (PF00501) - AMP-binding enzyme	synthase	52646842, 56182575, 22278995, 22278996, 264259, 29331825, 29331826, 29331827, 29331828, 35696052, 264508, 264509, 264907, 56182435, 264511, 265007, 264512, 265008, 264757, 264758, 55812038, 264759, 33109954, 21906754, 265010, 265011, 264600, 265017, 265018, 265019, 264760, 18108351, 264288, 264369, 21906764, 21906765, 21906767, 55811957, 265020, 265021, 264691, 18108368, 27486262, 20281149, 18108370, 55811576, 264637, 264556, 264557, 18108381, 264558, 56182323, 264559, 18108385, 18108388, 22279002, 264486
3010	95317217 (6019, 6020)	Novel Protein sim. GBank gi|4927370|gb|AAD33084.1|AF06797 - (AF067972) DNA cytosine methyltransferase 3 alpha [Homo sapiens]	Contains protein domain (PF01923) - Protein of unknown function	UNCLASSIFIED	264686, 264687, 21906767, 21906769, 55811957, 22278995, 35695917, 22278996, 22278997, 265020, 265021, 60170615, 264692, 33657023, 29331822, 264693, 18108364, 29331824, 33657109, 60432289, 29331827, 27486261, 29331828, 264508, 264909, 55811576, 35695855, 265008, 264556, 60433438, 83373044, 18108387, 65274727, 60432113, 265017, 22279000, 265019, 264564, 264682, 264764
3011	94323597 (6021, 6022)	Novel Protein sim. GBank gi|5052319|gb|AAD38501.1|AF11883 - (AF118838) citrin; adult-onset type II citrullinemia protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	35696052, 56182435, 264758, 21906754, 265018, 264760, 264762, 18108351, 264682, 264448, 21906766, 65274620, 18108374, 264482, 264564
3012	87753087 (6023, 6024)			UNCLASSIFIED	263972

3013	91238799 (6025, 6026)	Novel Protein sim. GBank gi|3702286 (AC005787) - R33374_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	264488, 263994, 35696286, 22278997, 264259, 29331824, 60424269, 66714117, 35696052, 264905, 264906, 264907, 264908, 264909, 56182435, 264511, 264512, 264910, 264591, 264592, 264593, 264594, 33657402, 60433438, 264595, 264596, 55812038, 264758, 33109954, 21906754, 265010, 265018, 264604, 264760, 264682, 264683, 264764, 264369, 264288, 264765, 264766, 264686, 264768, 264687, 21906767, 35695917, 265020, 33657023, 264692, 264693, 33657109, 264628, 264629, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 264563, 264565, 264566, 264567
3014	79877263 (6027, 6028)	Novel Protein sim. GBank gi|3878374|emb|CAA93081| - (Z68879) Similarity to Yeast Chl12p protein (PIR Acc. No. S54453); cDNA EST EMBL:D27950 comes from this gene; cDNA EST EMBL:D27949 comes from this gene; cDNA EST EMBL:D33447 comes from this gene; cDNA EST EMBL:D33316 comes from...		ATPase_associated	264760
3015	86995466 (6029, 6030)				22278995, 22278996, 22278997, 264259, 29331824, 29331828, 264908, 265007, 265008, 264910, 265011, 265017, 265019, 264691, 33657109, 18108370, 35695855, 264556, 264564
3016	87759945 (6031, 6032)	Novel Protein sim. GBank gi|1168819|sp|P41733|CC91_YEAST - CELL DIVISION CONTROL PROTEIN 91		UNCLASSIFIED	52644507, 52646842, 56994075, 52645080, 29331822, 29331824, 35696052, 33656970, 52644045, 264596, 33657084, 265017, 265019, 52644229, 21906767, 35695917, 52644150, 33657023, 33657109, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 35695855, 87168518
3017	95011154 (6033, 6034)	Novel Protein sim. GBank gi|4589658|dbj|BAA76851.1| - (AB023224) KIAA1007 protein [Homo sapiens]			264488, 18108397, 22278996, 35696286, 22278999, 264259, 29331822, 60432289, 264908, 29331830, 264909, 56182435, 265006, 265007, 265008, 265009, 264591, 60433356, 60433438, 52646317, 21906754, 55811386, 265010, 265011, 87168559, 265017, 265018, 265019, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 65274620, 52645129, 33657109, 33657182, 18108370, 263972, 18108374, 264631, 52644332, 83373044, 18108385, 18108388, 56526486, 87168518, 264404, 60432113, 22279000, 264567

3018	11073891 (6035, 6036)				264558
3019	94148231 (6037, 6038)	Novel Protein sim. GBank gi|3219332 (AC004020) - Unknown gene product [Homo sapiens]		oncogene	264569, 52644507, 18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 264908, 56182435, 265007, 265009, 60432229, 264593, 60433356, 55812038, 21906754, 87168474, 265011, 87168559, 265017, 265018, 265019, 264681, 18108351, 264448, 264682, 264683, 18108354, 264685, 264687, 264689, 21906766, 21906768, 21906769, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 52645129, 33657349, 264829, 65274791, 264634, 52644332, 56182323, 18108385, 87168518, 22279000, 22279002, 264563
3020	94318251 (6039, 6040)	Novel Protein sim. GBank gi|3414809 (AF061529) - rjs [Mus musculus]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	ATPase_associated	264488, 263994, 35696286, 264259, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60174639, 264600, 264603, 264760, 264762, 264682, 264763, 264764, 264288, 264369, 264766, 264687, 264688, 264769, 55811957, 35695917, 33657023, 264628, 35696423, 35695855, 264630, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264638, 264639, 83373044, 18108385, 264564, 264567, 264486
3021	80478512 (6041, 6042)	Novel Protein sim. GBank gi|3880889|emb|CAB09005| - (Z95559) cDNA EST yk236d4.5 comes from this gene; cDNA EST EMBL:C13455 comes from this gene; cDNA EST yk329g6.5 comes from this gene; cDNA EST CEMSH45R comes from this gene [Caenorhabditis elegans]			264769, 264629, 264482
3022	87718500 (6043, 6044)			UNCLASSIFIED	264259, 29331826, 29331828, 264288, 264566
3023	95305484 (6045, 6046)	Novel Protein sim. GBank gi|416592|sp|P32323|AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR	Contains protein domain (PF00614) - Phospholipase D. Active site motif	UNCLASSIFIED	264488, 22278995, 35696286, 22278997, 29331826, 35696052, 264907, 29331830, 52644045, 56182435, 60432229, 264592, 60433356, 60433438, 264689, 21906767, 55811957, 35695917, 265021, 18108376, 263978, 264635, 264558, 22279000
3024	86675305 (6047, 6048)			UNCLASSIFIED	60432049, 264760, 21906769, 55811957, 35695917, 264690, 264555, 264559
3025	65706629 (6049, 6050)	Novel Protein sim. GBank gi|295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]			264593, 55811576

3026	87643662 (6051, 6052)	Novel Protein sim. GBank gi|3024052|sp|P97924|KARI_RAT - KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)		UNCLASSIFIED	22278996, 22278997, 264490, 29331825, 264111, 265007, 60170831, 265010, 87168559, 265019, 21906765, 29148627, 263967, 20281149, 20281069, 263975, 263977, 20281071, 56526486, 22279000
3027	94844563 (6053, 6054)	Novel Protein sim. GBank gi|4929647|gb|AAD34084.1|AF15184 - (AF151847) CGI-89 protein [Homo sapiens]	Contains protein domain (PF01529) - DHHC zinc finger domain	UNCLASSIFIED	18108394, 22278995, 22278996, 35696286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264907, 29331830, 264908, 264909, 264510, 265007, 265008, 265009, 264910, 33657402, 264596, 21906754, 265010, 265011, 87168559, 264600, 265018, 18108351, 264682, 264683, 264764, 264288, 264685, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 35695917, 265020, 265021, 265022, 52644150, 264692, 33657023, 264693, 52645129, 33657109, 27486261, 18108374, 55811576, 35696423, 65274791, 264636, 264556, 264557, 264638, 60170394, 264639, 264558, 83373044, 18108385, 56526486, 22279000, 22279002
3028	94231997 (6055, 6056)	Novel Protein sim. GBank gi|3080521|emb|CAA18650| - (AL022599) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 29331824, 29331827, 35696052, 264908, 265007, 265008, 265009, 60170831, 21906754, 265011, 87168559, 265018, 264762, 264683, 264765, 264689, 21906765, 21906768, 21906769, 29148629, 35695917, 265021, 265022, 33657109, 27486265, 264628, 264629, 18108374, 35696423, 35695855, 264638, 60170394, 22279000, 22279002, 264482, 264564
3029	87619284 (6057, 6058)			UNCLASSIFIED	22278997, 22278999, 29331827, 264905, 264509, 264909, 264510, 264511, 264512, 87168474, 265019, 18108351, 21906768, 264534, 264690, 264693, 263969, 18108370, 264558, 22279000, 22279002, 264482
3030	87544928 (6059, 6060)	Novel Protein sim. GBank gi|3757726|emb|CAA18782| - (AL022727) dJ80I19.1 (olfactory receptor-like protein (hs6M1-1)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	
3031	91677953 (6061, 6062)	Novel Protein sim. GBank gi|4530587|gb|AAD22105.1| - (AF132000) TADA1 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 35696052, 264908, 265018, 21906765, 21906766, 21906767, 21906768, 265021, 263974, 18108374, 264558, 56526486, 22279000, 22279002

3032	94130124 (6063, 6064)	Novel Protein sim. GBank gi|1019951 (U37429) - similar to M. musculus MER5 and other AHPC/TSA proteins [Caenorhabditis elegans]	Contains protein domain (PF00534) - Glycosyl transferases group 1	synthase	22278996, 35696286, 264259, 29331824, 29331828, 264907, 29331830, 264758, 33109954, 87168474, 87168559, 265019, 264288, 21906769, 265021, 264693, 35696423, 35695855, 264636, 56182323, 83373044, 87168518
3033	95308321 (6065, 6066)	Novel Protein sim. GBank gi|5031573|ref|NP_005712.1|pACTR - ARP3 (actin-related protein 3, yeast) homolog	Contains protein domain (PF00022) - Actin	struct	35696286, 264259, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265008, 264591, 21906754, 265010, 265019, 264681, 264369, 264768, 21906764, 21906768, 35695917, 33657023, 264628, 35695855, 264632, 264635, 264639, 264482, 264563
3034	80415373 (6067, 6068)			UNCLASSIFIED	264906, 264907, 264510, 264592, 265010, 264762, 264766, 264637, 264638, 264486
3035	91220692 (6069, 6070)	Novel Protein sim. GBank gi|3738207|emb|CAA21262| - (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]		UNCLASSIFIED	264636
3036	91718323 (6071, 6072)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!		kinase	264907, 33657402, 265021
3037	95307434 (6073, 6074)	Novel Protein sim. GBank gi|4406590|gb|AAD20040| - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]			265017
3038	95421807 (6075, 6076)	Novel Protein sim. GBank gi|5360093|gb|AAD42865.1|AF15509 - (AF155099) NY-REN 18 antigen [Homo sapiens]	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	22278996, 22278997, 264259, 264905, 265007, 265009, 60433356, 21906754, 265018, 265019, 18108351, 264687, 21906765, 265020, 265021, 65274620, 27486262, 264636, 56182323, 18108385, 22279000
3039	87332257 (6077, 6078)	Novel Protein sim. GBank gi|4757128|emb|CAB42094.1| - (AJ238717) ZRP protein [Rattus norvegicus]		UNCLASSIFIED	35696286, 29331828, 264109, 264110, 264511, 265007, 21906754, 265011, 264681, 264683, 264687, 21906768, 264691, 18108370, 263972, 264629, 18108374, 263977, 35696423, 264564, 18108391
3040	90933517 (6079, 6080)	Novel Protein sim. GBank gi|4884278|emb|CAB43247.1| - (AL050037) hypothetical protein [Homo sapiens]			264692, 264558, 18108382, 18108385, 264567
3041	88312357 (6081, 6082)	Novel Protein sim. GBank gi|3876073|emb|CAB04122.1| - (Z81505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this ...		UNCLASSIFIED	56994075, 22278997, 22278998, 29331827, 33656970, 33109954, 21906754, 87168559, 264600, 264683, 21906765, 21906768, 22279002
3042	85749402 (6083, 6084)	Novel Protein sim. GBank gi|790236 (U21156) - sarcolemmal associated protein-2 [Oryctolagus cuniculus]		glycoprotein	264636

3043	87773026 (6085, 6086)	Novel Protein sim. GBank gi|854065|emb|CAA58337| - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	35696286, 60424269, 35696052, 264508, 264905, 66712502, 56182435, 55811386, 52644296, 55811150, 35695917, 60170615, 33657109, 18108374, 264634, 60431850
3044	87646182 (6087, 6088)	Novel Protein sim. GBank gi|4104922 (AF042276) - o251 homolog [Pseudomonas putida]	Contains protein domain (PF01209) - ubiE/COQ5 methyltransferase family	glycoprotein	22278996, 22278998, 22278999, 29331824, 56182435, 264511, 265007, 60170831, 60432229, 60433356, 33109954, 18108351, 264288, 35695917, 18108368, 18108370, 60170394
3045	94127598 (6089, 6090)	Novel Protein sim. GBank gi|4589680|dbj|BAA76859.1| - (AB023232) KIAA1015 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	264488, 264259, 35696052, 264508, 264905, 264509, 264906, 264907, 264909, 264511, 265006, 264591, 264593, 33109954, 264604, 264764, 264683, 264288, 264766, 264768, 21906765, 21906768, 55811957, 35695917, 27486262, 18108370, 264628, 18108374, 35695855, 264630, 264632, 264635, 264563, 264564, 264566
3046	88098247 (6091, 6092)			UNCLASSIFIED	22278999, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264906, 52646317, 55811957, 60432113, 22279000, 22279002, 264482, 264564
3047	95089924 (6093, 6094)			UNCLASSIFIED	264488, 22278996, 22278997, 22278999, 29331824, 29331825, 56182435, 264511, 265008, 265009, 265011, 265017, 264766, 21906768, 21906769, 35695917, 52644150, 33657349, 65274791, 35695855, 264555, 60432113, 22279000, 264566
3048	87629419 (6095, 6096)	Novel Protein sim. GBank gi|4588034|gb|AAD25962.1|AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264102, 29146784
3049	88229955 (6097, 6098)	Novel Protein sim. GBank gi|5454158|ref|NP_006286.1|pVARS - valyl-tRNA synthetase 1	Contains protein domain (PF01406) - tRNA synthetases class I (C)	UNCLASSIFIED	22278997, 29331826, 264907, 264758, 87168559, 265018, 264448, 21906766, 265020, 33657109, 35695855, 60432113, 22279000
3050	87643679 (6099, 6100)	Novel Protein sim. GBank gi|4589642|dbj|BAA76843.1| - (AB023216) KIAA0999 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331825, 264909, 265007, 264512, 265019, 264288, 21906766, 265020, 264693, 18108385, 56526486, 87168518, 22279002, 264566
3051	87750599 (6101, 6102)				22278997, 264595, 265019, 264288, 264693, 87168518
3052	57108030 (6103, 6104)	Novel Protein sim. GBank gi|117528|sp|P14755|CRYL_RABIT - LAMBDA-CRYSTALLIN		dehydrogenase	264534

3053	95350373 (6105, 6106)	Novel Protein sim. GBank gi|3947613|emb|CAA19465.1| - (AL023828) cDNA EST EMBL:M89008 comes from this gene; cDNA EST yk282d3.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56181686, 22278995, 35696286, 22278998, 264259, 60432289, 265008, 265009, 60433438, 21906754, 265010, 87168559, 264603, 265018, 265019, 264763, 264764, 264288, 21906765, 21906766, 21906768, 21906769, 35695917, 18108374, 35696423, 264638, 56182323, 22279000, 264563
3054	86943510 (6107, 6108)	Novel Protein sim. GBank gi|1076211|pir||S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	35696286, 35696052, 29331830, 264908, 264909, 264512, 264910, 265017, 264604, 264766, 265020, 33657109, 264628, 35695855, 264636, 264564, 264566, 264486
3055	95350537 (6109, 6110)	Novel Protein sim. GBank gi|4680655|gb|AAD27717.1|AF13294 - (AF132942) CGI-08 protein [Homo sapiens]		transport	60424179, 65274572, 56182575, 35696286, 22278996, 22278999, 60432049, 264259, 60424269, 60432289, 35696052, 56182435, 265006, 265009, 60170831, 60432229, 60431735, 60433356, 264594, 60433438, 21906754, 55811386, 265011, 87168559, 265019, 18108351, 264683, 264288, 264369, 264689, 21906768, 55811957, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 60431528, 18108374, 55810764, 55811576, 35696423, 65274791, 264636, 60431850, 18108381, 56182323, 60170394, 18108385, 60432113, 264564, 264565, 264566
3056	91661636 (6111, 6112)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!		glycoprotein	264488, 264569, 18108394, 52646842, 22278997, 22278998, 22278999, 264259, 66714117, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 264512, 265007, 265008, 265009, 264910, 33657402, 55812038, 264596, 264758, 265010, 265011, 265017, 265019, 264760, 18108351, 264762, 264763, 264764, 264288, 264766, 264687, 18108357, 264768, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264691, 264693, 33657109, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 18108381, 83373044, 18108385, 22279000, 22279002, 264563, 264564, 264565, 264566, 264486, 264567

3057	95412746 (6113, 6114)	Novel Protein sim. GBank gi|3878119|emb|CAA88860| - (Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...		struct	264508, 264905, 264907, 264908, 264909, 264510, 264512, 264910, 264592, 264594, 264767, 18108374, 264635, 264555, 264637, 264639, 264563, 264564, 264565, 264486
3058	79646226 (6115, 6116)			UNCLASSIFIED	264693
3059	87629425 (6117, 6118)	Novel Protein sim. GBank gi|4588034|gb|AAD25962.1|AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264490, 264259, 29331824, 29331825, 29331827, 35696052, 29331828, 265007, 60433438, 265017, 265018, 265019, 264681, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906769, 29148629, 29148784, 265022, 52644150, 18108370, 264636, 18108385, 264563, 264567
3060	79346691 (6119, 6120)			UNCLASSIFIED	264567
3061	87740964 (6121, 6122)			UNCLASSIFIED	264112, 52644296, 21906768, 33657023, 263974, 18108385
3062	87619465 (6123, 6124)	Novel Protein sim. GBank gi|4454690|gb|AAD20963| - (AF070657) glutathione S-transferase subunit 13 homolog [Homo sapiens]		transferase	264908, 265008, 18108351, 264566
3063	80078023 (6125, 6126)	Novel Protein sim. GBank gi|2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	18108359, 264558
3064	91241526 (6127, 6128)	Novel Protein sim. GBank gi|4240315|dbj|BAA74936.1| - (AB020720) KIAA0913 protein [Homo sapiens]	Contains protein domain (PF00403) - Heavy-metal-associated domain	UNCLASSIFIED	52646365, 52646842, 65274572, 56182575, 56181686, 22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 66714117, 264508, 264907, 264908, 56182435, 265009, 60432229, 60433438, 55812038, 52644296, 265018, 264682, 264288, 264686, 264768, 264687, 52644229, 264689, 21906768, 264691, 264692, 264693, 18108370, 18108377, 55811576, 264636, 56182323, 264558, 264639, 18108385, 22279000, 22279002
3065	91639201 (6129, 6130)	Novel Protein sim. GBank gi|5656743|gb|AAD45960.1|AC00506 - (AC005067) Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and genscan [Homo sapiens]		UNCLASSIFIED	22278996, 22278998, 264093, 264094, 264095, 29331824, 60424269, 66714117, 264100, 264907, 265007, 264591, 60432229, 264593, 265011, 265019, 18108351, 264766, 264767, 21906765, 21906768, 264693, 20281069, 22279000, 22279002, 264482, 264566, 264567

3066	91224437 (6131, 6132)	Novel Protein sim. GBank gi|4884268|emb|CAB43245.1| - (AL050028) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108397, 22278995, 56994075, 22278996, 264905, 66712502, 265006, 264512, 264910, 264758, 60174639, 264760, 18108351, 264764, 264683, 18108359, 264692, 18108364, 18108368, 18108370, 18108377, 18108379, 60170394, 264567
3067	95422551 (6133, 6134)	Novel Protein sim. GBank gi|4689258|gb|AAD27832.1|AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]	Contains protein domain (PF00787) - PX domain	struct	264488, 264489, 35696286, 22278996, 56994075, 264259, 29331822, 29331825, 35696052, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264112, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265010, 265011, 87168559, 264601, 264602, 264603, 264604, 264605, 265019, 264760, 264762, 264448, 264763, 264764, 264288, 264369, 264766, 264768, 264687, 264769, 264689, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 264534, 52644150, 264691, 33657023, 264693, 264628, 60431528, 263977, 35695855, 264630, 264631, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 56526486, 87168518, 22279000, 22279002, 264563, 264483, 264564, 264565, 264566, 264567, 264486
3068	85360651 (6135, 6136)				264112
3069	95412753 (6137, 6138)	Novel Protein sim. GBank gi|3878119|emb|CAA88860| - (Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...	Contains protein domain (PF01926) - GTPase of unknown function	struct	22278996, 56994075, 22278998, 22278999, 264259, 264107, 264905, 29331830, 52644045, 264110, 60170831, 264592, 264594, 33657402, 21906754, 33109954, 87168474, 87168559, 265017, 264448, 264764, 264683, 264766, 52644229, 21906765, 21906766, 21906768, 21906769, 60170615, 33657023, 18108370, 18108376, 264634, 264557, 60170394, 56182323, 18108385, 87168518, 22279000, 264482

3070	94319173 (6139, 6140)	Novel Protein sim. GBank gi|3877788|emb|CAB05527| - (Z83110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk468c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM...		synthase	264488, 22278994, 22278995, 22278996, 56994075, 22278997, 22278999, 264259, 29331822, 29147620, 29331824, 66714117, 29331826, 29146498, 29146499, 66712502, 29331830, 52644045, 56182435, 264511, 265007, 264512, 264910, 60170831, 264592, 264758, 33109954, 21906754, 87168474, 265019, 18108351, 264448, 264683, 264288, 52644229, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 264691, 33657023, 27486261, 27486264, 264628, 18108370, 18108377, 55811576, 35695855, 264634, 264635, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 18108387, 56526486, 264404, 264563, 264566
3071	94325573 (6141, 6142)	Novel Protein sim. GBank gi|4502425|ref|NP_001709.1|pBMP6 - bone morphogenetic protein 6 precursor	Contains protein domain (PF00085) - Thioredoxin	tgf	264488, 65274572, 18108398, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35696052, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 52644045, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 264592, 60433356, 33657402, 60433438, 33109954, 52644296, 87168474, 265010, 265017, 264681, 264288, 264685, 264766, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35696423, 55811576, 65274791, 35695855, 264630, 264635, 264636, 264557, 60170394, 83373044, 60432113, 22279000, 22279002, 264563, 264564, 264565, 264566, 264567
3072	95115892 (6143, 6144)	Novel Protein sim. GBank gi|1263289 (U47856) - fibroin-4 [Araneus diadematus]		transcriptfactor	56182575, 29331822, 29331824, 29331825, 29146498, 264908, 52644045, 56182435, 265009, 60433438, 55812038, 18108351, 264683, 264369, 52644229, 52644150, 33657023, 264693, 33657109, 18108374, 55811576, 65274791, 264555, 56182323, 60432113, 264564

3073	88147248 (6145, 6146)	Novel Protein sim. GBank gi|134840|sp|P22528|CORB_HUMAN - CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN)		UNCLASSIFIED	264769
3074	88089351 (6147, 6148)	Novel Protein sim. GBank gi|3419847 (AC004982) - similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens]		UNCLASSIFIED	264488, 265019, 264448, 264288, 21906767, 264693, 18108368, 18108370, 18108374, 264567
3075	88095752 (6149, 6150)	Novel Protein sim. GBank gi|4557349|ref|NP_000456.1|pBARD - BRCA1 associated RING domain 1	Contains protein domain (PF00023) - Ank repeat	homeobox	264509, 264907, 264689, 264693, 56526486
3076	87819219 (6151, 6152)			UNCLASSIFIED	18108398, 29331822, 29331827, 60432229, 265017, 264691, 264693
3077	88734277 (6153, 6154)	Novel Protein sim. GBank gi|3023956|sp|Q00808|HET1_PODAN - VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	65274572, 35696052, 264511, 60170831, 87168474, 264369, 35695917, 33657182, 27486264, 33657349, 35695763, 35695855, 264639
3078	88089355 (6155, 6156)	Novel Protein sim. GBank gi|3900850 (AC004994) - similar to KIAA0600; similar to d1026456 (PID:g3043724) [Homo sapiens]			22279002
3079	87821893 (6157, 6158)	Novel Protein sim. GBank gi|3875410|emb|CAB02876| - (Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]		transport	29331824, 29331826, 264758, 55811386, 265017, 55811150, 52644229, 21906768, 265020, 265021, 264693, 18108376, 264631, 52644332, 22279002
3080	95298274 (6159, 6160)	Novel Protein sim. GBank gi|5257221|gb|AAD41265.1| - (AF117887) protein arginine methyltransferase [Mus musculus]		interferon	264488, 52644507, 22278996, 22278998, 264490, 264259, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 29146499, 264508, 264905, 264828, 52644045, 56182435, 265006, 264591, 264596, 21906754, 60174639, 265010, 264682, 264448, 264763, 264683, 264764, 264288, 264685, 264769, 264688, 264689, 21906765, 21906767, 21906769, 55811957, 35695917, 265020, 60170615, 52644150, 264692, 33657023, 264693, 65274620, 33657109, 27486261, 35695763, 264628, 18108370, 65274791, 264558, 56182323, 60170394, 264482, 264565, 264484
3081	88094864 (6161, 6162)	Novel Protein sim. GBank gi|728831|sp|P39188|ALU1_HUMAN - !!!! ALU SUBFAMILY J WARNING ENTRY !!!!		UNCLASSIFIED	18108398, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264595, 264758, 265011, 265018, 264760, 264761, 264763, 264764, 18108354, 264685, 264766, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264555, 264638, 18108382, 18108385, 264563, 264565, 264566
3082	80310121 (6163, 6164)				264764, 55811957, 264555, 264564

3083	88095756 (6165, 6166)	Novel Protein sim. GBank gi|868241 (U29488) - C56C10.3 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264259, 29331824, 264106, 265008, 264591, 264592, 21906754, 264288, 264767, 21906768, 21906769, 29148784, 264691, 264632, 22279000
3084	87448568 (6167, 6168)	Novel Protein sim. GBank gi|476774|pir||A37475 - probable structural component p38 - borna disease virus			22278995, 60432289, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265007, 264910, 264593, 264595, 264758, 264369, 264288, 264766, 35695917, 265020, 18108374, 35696423, 264631, 264556, 264565, 264566, 264567, 264486
3085	87795781 (6169, 6170)	Novel Protein sim. GBank gi|2565057 (U80741) - CAGH44 [Homo sapiens]		UNCLASSIFIED	265011, 264681
3086	87769942 (6171, 6172)	Novel Protein sim. GBank gi|3894189 (AC005662) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	22278998, 264092, 264259, 29331822, 29331825, 264108, 264112, 18108351, 264687, 263967, 263974, 55810764, 263981, 18108385, 264487
3087	87462988 (6173, 6174)				52646365, 56994075, 22278997, 22278998, 29331824, 29331825, 35696052, 60433438, 33109954, 21906754, 52646317, 265017, 264682, 264369, 264684, 21906767, 21906768, 265020, 264691, 33657023, 33657109, 52645129, 33657182, 27486262, 35695855, 87168518
3088	91224441 (6175, 6176)	Novel Protein sim. GBank gi|3355304 (AF001549) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264591
3089	95361242 (6177, 6178)	Novel Protein sim. GBank gi|4689146|gb|AAD27782.1|AF07704 - (AF077049) lambda-crystallin [Homo sapiens]	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	dehydrogenase	18108397, 65274572, 56182575, 56181686, 56994075, 35696286, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 29331828, 264907, 29331830, 264909, 56182435, 264510, 265007, 60170831, 60432229, 21906754, 55811386, 265017, 265018, 265019, 264760, 55811150, 264288, 264766, 56181562, 21906765, 21906766, 21906767, 21906768, 265021, 60170615, 27486262, 18108370, 60431528, 35696423, 264558, 264559, 60432113, 264486

3090	95342371 (6179, 6180)	Novel Protein sim. GBank gi|1354050 (U47024) - MEM3 [Mus musculus]		UNCLASSIFIED	60424179, 52645156, 65274572, 58182575, 56181686, 22278995, 35696286, 56994075, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264906, 264908, 52644045, 264828, 265006, 265007, 265008, 60170831, 60432229, 60433356, 33657402, 55812038, 264758, 21906754, 33109954, 52646317, 55811386, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 55811150, 18108351, 264681, 264448, 264288, 264369, 18108357, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 60170615, 264690, 52644150, 264691, 33657023, 18108365, 65274620, 33657109, 18108368, 33657182, 27486261, 27486265, 35695763, 18108374, 18108376, 55810764, 35696423, 55811576, 65274791, 35695855, 264557, 56182323, 83373044, 18108387, 18108388, 87168518, 22279000, 22279002, 264563, 264482
3091	95317424 (6181, 6182)	Novel Protein sim. GBank gi|3873932|emb|CAB01859| - (Z79596) Similarity to Bovine aspartyl beta hydroxylase (TR:G162694); cDNA EST EMBL:D27916 comes from this gene; cDNA EST EMBL:D27915 comes from this gene; cDNA EST EMBL:D64881 comes from this gene; cDNA EST EMBL:D68139 comes f...		UNCLASSIFIED	35696286, 29331822, 35696052, 264508, 264509, 264905, 264908, 264908, 264909, 264510, 264758, 265010, 265011, 264683, 264685, 264768, 264768, 264769, 264693, 264628, 35696423, 35695855, 264632, 264635, 264639, 264482, 264563, 264486

3092	95314592 (6183, 6184)	Novel Protein sim. GBank gi|1710756|sp|P15880|RS2_HUMAN - 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	264488, 60424179, 18108396, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264508, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264113, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264591, 264592, 60431735, 264593, 264594, 60433438, 264595, 264758, 21906754, 265010, 265011, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 265019, 264760, 264762, 264681, 18108351, 264763, 264682, 264448, 264764, 264683, 264288, 264369, 264765, 264766, 264686, 264767, 264687, 264768, 264769, 264688, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 29148784, 35695917, 265020, 265021, 264534, 60170615, 264690, 264691, 264692, 65274620, 33657109, 27486262, 264628, 264629, 18108374, 263978, 18108377, 35696423, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264557, 264558, 264639, 60170394, 18108385,
3093	94318457 (6185, 6186)	Novel Protein sim. GBank gi|5002587|emb|CAB44347.1| - (Y17454) LSFR1 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331824, 35696052, 264905, 265006, 60432229, 60431735, 264684, 264369, 264288, 264766, 21906767, 35696423, 83373044, 18108385
3094	94316675 (6187, 6188)	Novel Protein sim. GBank gi|400734|sp|P31044|PBP_RAT - PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (23 KD MORPHINE-BINDING PROTEIN) (P23K)	Contains protein domain (PF01161) - Phosphatidylethanolamine-binding protein	collagen	18108398, 264259, 60432289, 29331827, 264511, 264763, 264288, 264767, 265022, 264691, 264693, 65274791, 56182323, 264564, 264565

3095	94848162 (6189, 6190)	Novel Protein sim. GBank gi|4877759|gb|AAD31421.1|AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]	Contains protein domain (PF01454) - MAGE family	UNCLASSIFIED	18108397, 56182575, 22278995, 35696286, 56994075, 22278997, 22278999, 264259, 60432049, 66714117, 29331825, 60432289, 35696052, 33656970, 29146499, 264508, 264905, 264509, 29331830, 264909, 264510, 264511, 264512, 265007, 265008, 265009, 60170831, 264758, 21906754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264681, 264682, 264683, 264764, 264369, 264288, 264686, 264768, 264769, 264689, 21906765, 21906766, 21906767, 55811957, 35695917, 265020, 265021, 265022, 52644150, 264691, 264692, 33657023, 264693, 263972, 18108376, 55811576, 35696423, 264952, 60170394, 264639, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 264482, 264563, 264564, 264566, 264487, 18108391
3096	87756128 (6191, 6192)	Novel Protein sim. GBank gi|3882221|dbj|BAA34470.1| - (AB018293) KIAA0750 protein [Homo sapiens]	Contains protein domain (PF00307) - Calponin homology (CH) domain	struct	22278995, 22278996, 22278997, 22278999, 29331824, 29331825, 29331826, 29331827, 33656970, 264905, 264908, 265008, 264910, 33657402, 265011, 265017, 265018, 264369, 21906766, 21906767, 21906768, 35695917, 265020, 60170615, 264691, 264692, 264693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264566
3097	88264895 (6193, 6194)	Novel Protein sim. GBank gi|4468288|emb|CAB37981| - (AL022395) dJ273N12.1 (PUTATIVE protein based on EST matches) [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	264488, 29331822, 29331825, 60432289, 29331826, 35696052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87168474, 87168559, 52644229, 21906765, 21906767, 18108376, 35696423, 52644332, 264638, 60432113, 22279002
3098	80258024 (6195, 6196)				264634, 264637, 264565
3099	91243325 (6197, 6198)	Novel Protein sim. GBank gi|303603|dbj|BAA02145.1| - (D12621) cytochrome P-450LTBV [Homo sapiens]		cyto450	264488, 35696286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22279002, 264563
3100	87602421 (6199, 6200)	Novel Protein sim. GBank gi|1083764|pir||B48013 - proline-rich proteoglycan 2 precursor, parotid - rat		UNCLASSIFIED	29331825, 60432289, 35696052, 264910, 60432229, 264592, 264288, 264693, 263967, 264635
3101	79602134 (6201, 6202)			UNCLASSIFIED	264908, 264693, 264628, 264630, 264632

3102	91220892 (6203, 6204)	Novel Protein sim. GBank gi|5305706|gb|AAD41781.1|AF12853 - (AF128536) cytoplasmic phosphoprotein PACSIN2 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	struct	35696286, 22278996, 22278999, 29331827, 35696052, 264909, 264512, 265008, 60170831, 60433356, 33109954, 18108351, 264684, 264689, 21906767, 60170615, 264692, 33657023, 264638, 22279000, 264482, 264564
3103	90938004 (6205, 6206)	Novel Protein sim. GBank gi|464564|sp|P35292|RB17_MOUSE - RAS-RELATED PROTEIN RAB-17		UNCLASSIFIED	35695917, 264565
3104	87340633 (6207, 6208)	Novel Protein sim. GBank gi|5032207|ref|NP_005696.1|pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	264259, 264684, 264532, 33657182, 264558
3105	94148603 (6209, 6210)				22278997, 264259, 29331824, 35696052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264511, 264910, 264591, 264594, 264758, 264760, 264681, 264762, 264764, 264288, 264766, 264768, 264687, 264769, 21906766, 21906768, 35695917, 33657023, 264692, 264693, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 83373044, 264404, 22279002, 264563, 264565, 264566, 264486, 264567
3106	95361416 (6211, 6212)	Novel Protein sim. GBank gi|1938574 (U97190) - B0025.2 gene product [Caenorhabditis elegans]			22278996, 22278997, 22278998, 22278999, 264092, 264093, 264094, 29331822, 264906, 264907, 264908, 52644045, 56182435, 264112, 265008, 265009, 55812038, 265017, 265018, 264683, 264686, 264687, 264768, 52644229, 21906765, 21906768, 21906769, 55811957, 265020, 265022, 264690, 52644150, 264692, 264693, 18108370, 18108377, 55811576, 56182323, 18108385, 18108388, 22279000, 264563
3107	95343272 (6213, 6214)	Novel Protein sim. GBank gi|3341441|emb|CAA76851| - (Y17794) winged-helix transcription factor [Gallus gallus]			22278995, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 264259, 29331822, 29331825, 29331826, 60432289, 29331827, 29331828, 33656970, 264105, 264512, 265009, 60433356, 60433438, 265011, 265017, 265018, 21906765, 21906766, 21906767, 21906769, 265021, 264691, 33657109, 27486261, 27486265, 18108370, 263972, 18108374, 55811576, 18108385, 56526486, 264482, 264487
3108	87340635 (6215, 6216)	Novel Protein sim. GBank gi|5032207|ref|NP_005696.1|pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	56182435, 264288, 264690, 264564

3109	94318461 (6217, 6218)	Novel Protein sim. GBank gi|5002587|emb|CAB44347.1| - (Y17454) LSFR1 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struct	264490, 264908, 265007, 264910, 264593, 264683, 264684, 264687, 21906767, 21906768, 264693, 18108370, 264629, 18108374, 264632, 264638, 22279000
3110	95090716 (6219, 6220)	Novel Protein sim. GBank gi|1076211|pir||S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	264488, 65274572, 22278995, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264906, 264510, 265006, 265007, 265008, 265009, 60432229, 33657402, 60433356, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264288, 264369, 21906766, 21906767, 21906768, 265020, 60170615, 264693, 65274620, 18108370, 264639, 18108384, 22279000, 264563, 18108390
3111	87754512 (6221, 6222)	Novel Protein sim. GBank gi|3282231 (U75454) - C2H2 type zinc finger protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264488, 18108398, 66712502, 265017, 265018, 265019, 264448, 21906767, 265020, 33657023, 18108365, 18108368, 35696423, 52644332, 18108385, 18108388
3112	88043639 (6223, 6224)	Novel Protein sim. GBank gi|3900848 (AC005023) - match to EST AA361117 (NID:g2013436) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	
3113	88207098 (6225, 6226)	Novel Protein sim. GBank gi|2459910 (AF005856) - anon2A5 [Drosophila yakuba]		tm7	18108397, 22278999, 264259, 29331824, 35696052, 264907, 264757, 60433438, 87168559, 264763, 264448, 18108354, 264288, 21906767, 21906769, 35695917, 264690, 264691, 264692, 264693, 18108365, 18108381, 18108384, 18108385, 18108388, 87168518, 22279000, 22279002
3114	79843167 (6227, 6228)	Novel Protein sim. GBank gi|4966270|gb|AAB52261.2| - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E-value=1e-13, N=1 [C...	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	hydrolase	264909, 56182435, 264910, 21906754
3115	94117996 (6229, 6230)	Novel Protein sim. GBank gi|5032225|ref|NP_005676.1|pWBSC - Williams-Beuren syndrome chromosome region 11		transcriptfactor	60424179, 56182575, 264259, 29331824, 60424269, 29331826, 66712502, 264510, 265007, 60431735, 60433356, 55812038, 55811386, 265019, 264288, 264689, 21906769, 264691, 33657023, 264693, 60431528, 263974, 60431850, 56182323, 264559, 22279000, 22279002
3116	79642855 (6231, 6232)			UNCLASSIFIED	264905, 264758, 21906764, 264690
3117	87771288 (6233, 6234)			UNCLASSIFIED	264510, 265011, 18108351, 264288, 264689, 264691, 18108368, 18108372, 263981, 264558, 264564

3118	94665848 (6235, 6236)	Novel Protein sim. GBank gi|3880563|emb|CAB01444.1| - (Z78018) predicted using Genefinder; similar to serine/threonine kinase; cDNA EST yk353d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00008) - EGF-like domain	tgf	52645156, 52646842, 65274572, 56182575, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 264905, 264908, 29331830, 52644045, 56182435, 264510, 264511, 265007, 265008, 265009, 264757, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264605, 265019, 264762, 264448, 264682, 264684, 264288, 264766, 56181562, 21906765, 21906766, 21906768, 21906769, 265020, 265022, 264690, 52644150, 264691, 33657023, 264693, 33657109, 33657349, 264628, 18108370, 60431528, 18108374, 35696423, 65274791, 60170394, 83373044, 87168518, 22279000, 22279002, 264486
3119	85728796 (6237, 6238)		Contains protein domain (PF00328) - Histidine acid phosphatase		265006, 264288
3120	87344040 (6239, 6240)	Novel Protein sim. GBank gi|5019819|gb|AAD37863.1|AF14315 - (AF143152) putative NADH oxidoreductase complex I subunit [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264509, 264510, 264511, 264512, 264288, 264486
3121	94110735 (6241, 6242)	Novel Protein sim. GBank gi|4501877|ref|NP_001088.1|pACR| - acrosin			52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278996, 22278999, 264259, 29331824, 29331827, 35696052, 52644045, 265008, 52646317, 87168474, 87168559, 21906765, 52644150, 33657023, 18108374, 264637
3122	11814528 (6243, 6244)			UNCLASSIFIED	264638
3123	88083003 (6245, 6246)	Novel Protein sim. GBank gi|2439517 (AC002563) - putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860) [Homo sapiens]	Contains protein domain (PF00780) - CNH domain	kinase	18108392, 29331822, 29331824, 29331825, 264905, 265007, 55812038, 265019, 18108351, 264682, 264288, 264766, 21906764, 21906765, 21906768, 21906769, 55811957, 18108365, 18108366, 27486265, 18108374, 18108381, 18108384, 22279000, 22279002, 264482
3124	87786899 (6247, 6248)			UNCLASSIFIED	264905
3125	91216607 (6249, 6250)	Novel Protein sim. GBank gi|4980826|gb|AAD35412.1|AE00171 - (AE001714) oxidoreductase, short chain dehydrogenase/reductase family [Thermotoga maritima]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	56181686, 264259, 66714117, 60432289, 29331826, 29331827, 264907, 264908, 264828, 265009, 60433356, 33657402, 60433438, 264758, 18108351, 264288, 29148627, 29148629, 33657023, 33657109, 18108382, 56526486

3126	95337205 (6251, 6252)			UNCLASSIFIED	22278999, 264490, 264259, 60432049, 29331822, 60432289, 29146498, 52644045, 56182435, 265009, 60433438, 265010, 87168559, 265017, 265018, 55811150, 264763, 264683, 264369, 264685, 29148629, 33657023, 264693, 33657109, 18108374, 55811576, 18108385, 60432113, 22279002
3127	91639233 (6253, 6254)	Novel Protein sim. GBank gi|2828280|emb|CAA16694.1| - (AL021687) putative protein [Arabidopsis thaliana]			35696286, 22278996, 22278999, 29331826, 264908, 60433438, 87168559, 264604, 21906765, 21906769, 33657023, 33657349, 264629, 18108374, 18108377, 22279000, 22279002
3128	87674330 (6255, 6256)	Novel Protein sim. GBank gi|3885828 (AF090133) - lin-7-A [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	misc_channel	22278996, 264259, 52644045, 265008, 21906754, 265017, 265018, 21906768, 18108376, 18108387, 22279000, 22279002
3129	87755412 (6257, 6258)	Novel Protein sim. GBank gi|3135273 (AC003058) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	56182575, 264259, 29331825, 29331828, 52644045, 56182435, 60433356, 264600, 264682, 264763, 264764, 264369, 264288, 264686, 55811957, 264692, 33657023, 33657109, 60432113, 264564, 264566
3130	14993960 (6259, 6260)	Novel Protein sim. GBank gi|3329465 (AF064553) - NSD1 protein [Mus musculus]			264636
3131	95351469 (6261, 6262)	Novel Protein sim. GBank gi|1848277 (U86136) - telomerase-associated protein TP-1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	56182575, 264259, 29331824, 264907, 56182435, 264594, 60433438, 55812038, 33109954, 21906754, 33657084, 87168474, 264448, 264766, 21906769, 55811957, 265020, 265021, 265022, 60170615, 33657023, 33657109, 33657182, 27486261, 33657349, 65274791, 60170394, 56182323, 83373044, 87168518, 264564

3132	95415459 (6263, 6264)	Novel Protein sim. GBank gi|4680647|gb|AAD27713.1|AF13293 - (AF132938) CGI-03 protein [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	ubiquitin	52644507, 52646842, 52646365, 65274572, 56182575, 22278994, 22278995, 35696286, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 52645080, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 52644045, 56182435, 264910, 60170831, 60432229, 60433356, 33657402, 55812038, 52646317, 21906754, 52644296, 85658542, 87168559, 265017, 265018, 265019, 264448, 264288, 264369, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 264692, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 18108374, 18108376, 55811576, 35695855, 18108385, 18108387, 56526486, 87168518, 60432113, 22279002
3133	87379414 (6265, 6266)	Novel Protein sim. GBank gi|4507613|ref|NP_003738.1|pTNKS - TANKYRASE		polymerase	22278994, 22278998, 264905, 265006, 265007, 87168559, 264760, 21906767, 18108374, 22279000, 22279002, 264563
3134	94649816 (6267, 6268)	Novel Protein sim. GBank gi|1729827|sp|P54633|TALA_DICDI - FILOPODIN (TALIN HOMOLOG)			264595, 264369, 264685, 264628, 264566
3135	86389356 (6269, 6270)	Novel Protein sim. GBank gi|3093478 (AF012927) - fibrinogen-binding protein [Streptococcus equi]		struct	22278996, 264095, 29331826, 33657402, 18108348, 263974
3136	94845839 (6271, 6272)	Novel Protein sim. GBank gi|627101|pir||S44092 - probable carrier protein c2 - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	22278998, 264259, 264828, 265006, 265008, 60433438, 265019, 264764, 264288, 264769, 264689, 265020, 27486262, 263972, 65274791, 264557, 264558
3137	88257947 (6273, 6274)	Novel Protein sim. GBank gi|3342730 (AC005331) - R31341_1 [Homo sapiens]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264510, 265008, 21906754, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264682, 264769, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 18108370, 18108374, 22279000, 22279002, 264482, 264486

3138	94130186 (6275, 6276)	Novel Protein sim. GBank gi|4406759|gb|AAD20070| - (AC006836) hypothetical protein [Arabidopsis thaliana]			264569, 264488, 264907, 264511, 264593, 33109954, 87168559, 264681, 264684, 264685, 264686, 264687, 264768, 264688, 264689, 264691, 264692, 264693, 33657109, 264631, 264634, 264635, 264636, 264637, 60170394, 83373044, 18108385, 18108388, 60432113, 22279000, 22279002
3139	87325503 (6277, 6278)	Novel Protein sim. GBank gi|228938|prf||1814452C - Hyp-rich glycoprotein [Zea diploperennis]		UNCLASSIFIED	22278997, 22278998, 22278999, 264905, 265018, 265019, 21906765, 265020, 264636, 264557
3140	91222692 (6279, 6280)	Novel Protein sim. GBank gi|932|emb|CAA37773| - (X53744) 68kDA subunit of signal recognition particle [Canis familiaris]		struct	22278995, 56994075, 35696286, 264908, 264909, 60433356, 21906754, 52644296, 87168474, 87168559, 264683, 264288, 264685, 264686, 265022, 264693, 27486262, 35695855, 264630, 264555, 264566
3141	87323564 (6281, 6282)	Novel Protein sim. GBank gi|3213227 (AF035209) - putative v-SNARE Vti1a [Mus musculus]		UNCLASSIFIED	56182575, 35696286, 29331828, 264909, 265009, 265018, 18108351, 264369, 21906766, 29148627, 265020, 264628, 264629, 264631, 18108385
3142	95419028 (6283, 6284)	Novel Protein sim. GBank gi|2498197|sp|Q95245|C561_PIG - CYTOCHROME B561 (CYTOCHROME B-561)		cytochrome	52645156, 52646365, 22278995, 35696286, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331827, 29146499, 56182435, 265007, 60170831, 60432229, 33657402, 264595, 60433438, 264758, 21906754, 264288, 264766, 264687, 52644229, 21906765, 21906767, 21906768, 60170615, 52644150, 65274620, 33657109, 35695763, 18108370, 18108376, 65274791, 35695855, 264631, 264557, 87168518, 60432113, 22279000
3143	95351475 (6285, 6286)	Novel Protein sim. GBank gi|5420387|emb|CAB46679.1| - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 56182575, 22278996, 22278998, 22278999, 29331822, 29331824, 60432289, 35696052, 29331828, 264508, 264905, 264906, 264907, 264908, 264909, 52644045, 56182435, 264511, 264512, 265008, 264910, 60432229, 33657402, 60433356, 60433438, 55812038, 265011, 265019, 264760, 264763, 264448, 264764, 264684, 264288, 264685, 264686, 264768, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 264690, 33657023, 264693, 263967, 33657109, 264628, 264629, 18108374, 263976, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 87168518, 60432113, 22279000, 22279002, 264563, 264566, 264486

3144	95336329 (6287, 6288)	Novel Protein sim. GBank gi|4884468|emb|CAB43322.1| - (AL050225) hypothetical protein [Homo sapiens]			264488, 18108396, 22278996, 35696286, 22278997, 22278999, 29331826, 29331827, 35696052, 29331828, 264106, 265006, 265007, 265009, 33657402, 85658542, 265011, 18108351, 264448, 264369, 21906765, 21906766, 21906767, 265020, 265021, 52644150, 27486261, 18108370, 18108374, 35696423, 56182323, 83373044, 22279000, 22279002, 264567
3145	86611657 (6289, 6290)	Novel Protein sim. GBank gi|3879709|emb|CAB03330| - (Z81118) Similarity to Human endosomal protein P162 (TR:Q15075); cDNA EST EMBL:Z14487 comes from this gene; cDNA EST EMBL:Z14556 comes from this gene; cDNA EST EMBL:D27011 comes from this gene; cDNA EST EMBL:D27015 comes from t...		UNCLASSIFIED	18108397, 29331824, 29146499, 20281100, 265006, 55812038, 265010, 21906766, 29148627, 21906769, 29148784, 264692, 33657023, 33657109, 35695763, 263981, 56182323, 87168518
3146	87756314 (6291, 6292)	Novel Protein sim. GBank gi|2135746|pir||S69890 - mitogen inducible gene mig-2 - human	Contains protein domain (PF00169) - PH domain	struct	264259, 29331826, 29331828, 29331830, 264510, 264511, 265007, 265009, 264600, 265017, 18108351, 264448, 264369, 21906766, 265021, 264692, 33657109, 18108374, 35696423, 35695855, 60432113, 264564
3147	94848512 (6293, 6294)	Novel Protein sim. GBank gi|3874279|emb|CAB07315.1| - (Z92825) predicted using Genefinder; cDNA EST yk315e12.3 comes from this gene; cDNA EST yk315e12.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	UNCLASSIFIED	56181686, 35696286, 60432049, 264259, 56182181, 29331825, 60432289, 35696052, 56182435, 265008, 264910, 60431735, 60433356, 60433438, 265010, 264448, 264288, 265022, 33657023, 33657109, 60431528, 65274791, 264631, 56182323, 264404, 22279002
3148	95362169 (6295, 6296)	Novel Protein sim. GBank gi|5225322|gb|AAD40851.1|AF08310 - (AF083108) sirtuin type 3 [Homo sapiens]		UNCLASSIFIED	35696286, 35696052, 264511, 85658542, 87168474, 264764, 35696423, 264555, 264556, 264557, 264558, 83373044, 56526486, 60432113
3149	95308548 (6297, 6298)	Novel Protein sim. GBank gi|4200446 (AF102777) - FYVE finger-containing phosphoinositide kinase [Mus musculus]	Contains protein domain (PF01363) - FYVE zinc finger	eph	29331822, 35696052, 264109, 29148629, 18108381
3150	87655472 (6299, 6300)	Novel Protein sim. GBank gi|3378454|emb|CAA76893| - (Y17850) ganglioside-induced differentiation associated protein 1 [Mus musculus]	Contains protein domain (PF00043) - Glutathione S-transferases.	transferase	264259, 29331822, 29331824, 29331825, 29331827, 52646317, 264686, 35695855, 56182323, 264639
3151	87772355 (6301, 6302)	Novel Protein sim. GBank gi|172591 (M63577) - SFP1 [Saccharomyces cerevisiae]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	oncogene	29331822, 265008
3152	85698108 (6303, 6304)			UNCLASSIFIED	21906754, 87168559, 264605, 21906768, 52644150, 27486264, 35696423, 22279000

3153	95317299 (6305, 6306)	Novel Protein sim. GBank gi|4895041|gb|AAD32705.1|AF14395 - (AF143957) coronin-3 [Mus musculus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	struct	264488, 52646365, 35696286, 22278996, 22278997, 22278999, 60432049, 264259, 29331826, 60432289, 33656970, 264508, 264908, 33657402, 264595, 60433438, 87168474, 87168559, 264601, 265019, 264448, 264682, 264764, 264288, 264369, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 29148784, 265021, 265022, 60170615, 52644150, 264690, 264691, 33657023, 65274620, 33657109, 18108370, 35695855, 264638, 60170394, 87168518, 60432113, 22279000, 22279002
3154	87718573 (6307, 6308)	Novel Protein sim. GBank gi|4680661|gb|AAD27720.1|AF13294 - (AF132945) CGI-11 protein [Homo sapiens]		ATPase_associated	22278998, 264259, 29331824, 66712502, 265008, 265010, 265017, 18108354, 264691, 33657023, 264693, 20281149, 18108374
3155	87762394 (6309, 6310)	Novel Protein sim. GBank gi|728837|sp|P39194|ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!		UNCLASSIFIED	29331828, 264509, 264905, 264908, 264510, 264511, 264512, 33657402, 264681, 264683, 33657023, 18108370, 264634, 264639, 18108385, 264563, 264488
3156	87737449 (6311, 6312)	Novel Protein sim. GBank gi|5630076|gb|AAD45821.1|AC00601 - (AC006017) N-acetylgalactosaminyltransferase; similar to Q10473 (PID:g1709559) [Homo sapiens]	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21906754, 33109954, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 264288, 264689, 21906766, 21906768, 21906769, 35695917, 265020, 265022, 264692, 18108370, 35696423, 56182323, 22279002
3157	88259577 (6313, 6314)				18108396, 264259, 29331826, 35696052, 29146498, 87168559, 265017, 264448, 264288, 264691, 18108366, 52645129, 35696423, 52644332
3158	80034118 (6315, 6316)	Novel Protein sim. GBank gi|5306064|gb|AAD41895.1|AF15677 - (AF156778) ASB-3 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	264488, 263974
3159	94124114 (6317, 6318)	Novel Protein sim. GBank gi|5531272|emb|CAB50897.1| - (AJ243800) WSC4 homologue [Kluyveromyces lactis]		UNCLASSIFIED	56182575, 22278999, 29331824, 264106, 60433356, 264758, 265011, 87168559, 264448, 18108354, 264768, 21906768, 265020, 264691, 264692, 33657109, 18108374, 35696423, 264555, 60170394, 22279000
3160	80221068 (6319, 6320)	Novel Protein sim. GBank gi|3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Ank repeat	struct	18108351, 264555, 264556, 264557, 264558, 264559

3161	88074111 (6321, 6322)				264488, 22278995, 22278997, 22278998, 264259, 29331822, 60432289, 29331828, 52644045, 265017, 265018, 264448, 264288, 21906764, 21906767, 265020, 18108374, 264636, 264566

Table 2

Tissue ID	Tissue Name	Tissue Information	Disease Association
20281069	192xN	Protein-protein Interactions	Any
20281071	192xN	Protein-protein Interactions	Any
20281149	192xN	Protein-protein Interactions	Any
20281152	192xN	Protein-protein Interactions	Any
264111	276xN	Protein-protein Interactions	Any
264112	276xN	Protein-protein Interactions	Any
263966	384xN	Protein-protein Interactions	Any
263967	384xN	Protein-protein Interactions	Any
264110	552xN	Protein-protein Interactions	Any
18108379	SPH 52.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108381	SPH 52.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108383	SPH 52.3 (B's Lyphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoeisis, leukemia
18108368	SPH 52.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108384	SPH 52.6 (Brain- Thalmus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108394	SPH 53.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108355	SPH 53.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108359	SPH 53.3 (B's Lyphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoeisis, leukemia
18108361	SPH 53.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108362	SPH 53.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108366	SPH 53.6 (Brain- Thalmus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108354	SPH 54.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108392	SPH 54.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108348	SPH 54.3 (B's Lyphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoeisis, leukemia
18108382	SPH 54.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108395	SPH 54.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108365	SPH 54.6 (Brain- Thalmus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108397	SPH 55.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108398	SPH 55.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108364	SPH 55.3 (B's Lyphoma- Raji)	Lymphoma derived from B cells	
18108388	SPH 55.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108358	SPH 55.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
20281099	SPH 56.2 (MG63)		
20281100	SPH 56.3 (UtSMC)		
264404	SPH.1 (Brain)	Whole Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264510	5PH.10 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264511	5PH.11 (Placenta)	Placenta	Infertility, birth defects
264512	5PH.12 (Thyroid)	Thyroid	Hyperparathyroidism, Hypoparathyroidism
264555	5PH.13 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
264556	5PH.14 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
264557	5PH.15 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
264558	5PH.16 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
264559	5PH.17 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
264569	5PH.19 (One Fetal tissue and two cell lines)	Mixed	
264687	5PH.19.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, immunodeficiencies
264688	5PH.19.2 (hematopoetic stem cells - CRL2043)	Hematopoeitic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264689	5PH.19.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264690	5PH.19.4 (Fetal Liver)	Fetal liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis,Transplantation
264691	5PH.19.5 (Heart)	Heart	Cardiomyopathy, Atherosclerosis,Hypertension, Congenital heart defects, Aortic stenosis ,Atrial septal defect (ASD),Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases,Tuberous sclerosis, Scleroderma, Obesity,Transplantation
264692	5PH.19.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation,Idiopathic thrombocytopenic purpura , Immunodeficiencies,Graft vesus host
264693	5PH.19.7 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264482	5PH.2 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264600	5PH.21 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264601	5PH.22 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
264602	5PH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264603	5PH.24 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264604	5PH.25 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264605	5PH.26 (Placenta)	Placenta	Infertility, birth defects
264634	5PH.28 (Heart)	Heart	Cardiomyopathy, Atherosclerosis,Hypertension, Congenital heart defects, Aortic stenosis ,Atrial septal defect (ASD),Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases,Tuberous sclerosis, Scleroderma, Obesity,Transplantation
264635	5PH.29 (Fetal Kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome
264483	5PH.3 (Bone Marrow)	Bone marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
264636	5PH.30 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264637	5PH.31 (P)ancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264638	5PH.32 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264639	5PH.33 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264484	5PH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
264758	5PH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome
264760	5PH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis,Transplantation

264762	5PH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis,Hypertension, Congenital heart defects, Aortic stenosis ,Atrial septal defect (ASD),Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases,Tuberous sclerosis, Scleroderma, Obesity,Transplantation
264764	5PH.44.4 (Prostate)	Prostate	Prostate Cancer
264766	5PH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation,Idiopathic thrombocytopenic purpura , Immunodeficiencies,Graft vesus host
264768	5PH.44.6 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264769	5PH.44.7 (Uterus)	Uterus	Infertility, birth defects
264905	5PH.48.1 (Burkitt's Lymphoma- Raji)	Burkitt's Lymphoma	Lymphoma, blood cancers
264906	5PH.48.2 (Thalamus- Brain)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264907	5PH.48.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
264908	5PH.48.4 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
264909	5PH.48.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
264910	5PH.48.6 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
265006	5PH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
265007	5PH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
265008	5PH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
265009	5PH.50.4 (fetal lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
265010	5PH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
265011	5PH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
18108385	5PH.51.1 (MCF-7)	Breast Cancer	Breast Cancer
18108370	5PH.51.2 (CCRF-CEM)	Cancer Cell line	Cancer
18108374	5PH.51.3 (K-562)	Cancer Cell line	Cancer
18108351	5PH.51.4 (OVCAR-3)	Ovarian cancer	Ovarian cancer
18108372	5PH.51.5 (HL-60)	Cancer Cell line	Cancer
264486	5PH.6 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmune disease,allergies, immunodeficiencies,transplantation, Graft vesus host,

264508	5PH.8 (Fetal Brain)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264509	5PH.9 (Lymph Node)	Lymph Node	Lymphedema , Allergies
20798451	5RH 56.3(UtSMC)		
264487	5RH.1 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264534	5RH.11 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
264535	5RH.12 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
264563	5RH.19 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264488	5RH.2 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
264564	5RH.20 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264565	5RH.21 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264566	5RH.22 (Placenta)	Placenta	Infertility, birth defects
264567	5RH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264591	5RH.25 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264592	5RH.26 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
264593	5RH.27(thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264594	5RH.28 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264595	5RH.29 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264489	5RH.3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,

264596	5RH.30 (Placenta)	Placenta	Infertility, birth defects
264628	5RH.33 (fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome
264629	5RH.34 (lymph Node)	Lymph Node	Lymphedema , Allergies
264630	5RH.35 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264631	5RH.36 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264632	5RH.37 (Fetal Brain)	Fetal Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264490	5RH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmune disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
264681	5RH.43.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, immunodeficiencies
264682	5RH.43.2 (hematopoetic stem cells - CRL2043)	Hematopoeitic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264683	5RH.43.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264684	5RH.43.4 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis,Transplantation
264685	5RH.43.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation,Idiopathic thrombocytopenic purpura , Immunodeficiencies,Graft vesus host
264686	5RH.43.7 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264757	5RH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome
264759	5RH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis,Transplantation
264761	5RH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis,Hypertension, Congenital heart defects, Aortic stenosis ,Atrial septal defect (ASD),Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases,Tuberous sclerosis, Scleroderma, Obesity,Transplantation
264763	5RH.44.4 (Prostate)	Prostate	Prostate Cancer
264765	5RH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation,Idiopathic thrombocytopenic purpura , Immunodeficiencies,Graft vesus host

264767	5RH.44.6 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264828	5RH.46.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264887	5RH.47.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis,Transplantation
18108377	5RH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
18108380	5RH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
18108396	5RH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108391	5RH.50.4 (fetal lung)	Fetal Lung	Airway diseases, infection
18108357	5RH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
18108390	5RH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
264532	5RH.9 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmume disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
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264080	Mx96		
21906754	NQH 6.1 (HH729)		
22278996	NQH 6.10 (PrEC)	Endothelial cells	heart disease, cancer
22278997	NQH 6.11 (CAEC)	Endothelial cells	heart disease, cancer
22278998	NQH 6.12 (CSC)	Cancer Cell line	Cancer
22278999	NQH 6.13 (NHNPC)	Cancer Cell line	Cancer
22279000	NQH 6.14 (NHMC-RM)	Cancer Cell line	Cancer
22279002	NQH 6.15 (Hypothalmus)	Hypothalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
21906764	NQH 6.2 (In Dated Platelets)	Platelets	Clotting diseases, stroke
21906765	NQH 6.3 (HuVec)	Endothelial cells	heart disease, cancer
87168474	NQH 6.3 (Sized-HUVEC)	Endothelial cells	heart disease, cancer
21906766	NQH 6.4 (UtMVEC- myo)	Cancer Cell line	Cancer
21906767	NQH 6.5 (NHEM-neo)	Cancer Cell line	Cancer
21906768	NQH 6.6 (NHEK)	Cancer Cell line	Cancer
21906769	NQH 6.7 (ByCAEC)	Endothelial cells	heart disease, cancer
22278994	NQH 6.8 (NHA)	Cancer Cell line	Cancer

22278995	NQH 6.9 (PrSC)	Cancer Cell line	Cancer
27486261	NQH 7.1 (Jurkat E6-untreated)	Cancer Cell line	Cancer
27486262	NQH 7.2 (TF1-untreated)	Cancer Cell line	Cancer
27486264	NQH 7.3 (U87-untreated)	Cancer Cell line	Cancer
27486265	NQH 7.4 (THP1-untreated)	Cancer Cell line	Cancer
29331822	NQH 8.1 (Brain- amygdala)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331824	NQH 8.2 (Brain-hippocampus)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331825	NQH 8.3 (Brain- substantia nigra)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331826	NQH 8.4 (small intestine)	Small intestine	digestive diseases, obesity, diabetes
29331827	NQH 8.5 (Spinal cord)	Spinal chord	paralysis, neurodegenerative disorders
29331828	NQH 8.6 (stomach)	Stomach	Stomach cancer
29331830	NQH 8.7 (Trachea)	Trachea	Airway diseases, infection
87168518	NQH 9.1 (Sized-MG-63_treatment pool)		
87168559	NQH 9.2 (Sized-HEPG2 untreated)		
35695763	NQH.10.1 (MCF-7untreated)	Cancer Cell line	Cancer
35695855	NQH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
35695917	NQH.10.3 (JAR)	Cancer Cell line	Cancer
35696052	NQH.10.4 (PA-1)	Cancer Cell line	Cancer
35696286	NQH.10.5 (CADMEC)	Endothelial cells	heart disease, cancer
35696423	NQH.10.6 (CADMEC_LA)	Endothelial cells	heart disease, cancer
52644045	NQH.11.1 (SK-PN-DW)	Cancer Cell line	Cancer
52644150	NQH.11.2 (Chorionic Villus Cells)	Chorionic villus	fertility, birth defects
52644229	NQH.11.3 (A549)	Cancer Cell line	Cancer
52644296	NQH.11.4 (U266B1)	Cancer Cell line	Cancer
52644332	NQH.11.5 (Daoy)	Cancer Cell line	Cancer
52644507	NQH.11.6 (SW1783)	Cancer Cell line	Cancer
52645080	NQH.12.1 (U-118MG)	Cancer Cell line	Cancer
52645129	NQH.12.2 (A204)	Cancer Cell line	Cancer
52645156	NQH.12.3 (T24)	Cancer Cell line	Cancer
52646317	NQH.12.4 (G-401)	Cancer Cell line	Cancer
52646365	NQH.12.5 (CaSki)	Cancer Cell line	Cancer
52646842	NQH.12.6 (SHP-77)	Cancer Cell line	Cancer

60424179	NQH.14.1 (Yale75_breast carcinoma)	Breast carcinoma	Breast Cancer
60424269	NQH.14.2 (Yale78B_ovarytumor)	Ovary tumor	Ovarian cancer
60431528	NQH.14.3 (Yale79_prostateBPH)	Prostate	Prostate Cancer
60431602	NQH.14.4 (Yale80_ProstateAdenocarcinoma)	Prostate	Prostate Cancer
60431735	NQH.14.5 (Yale86_UterineMyoma)	Uterine Myoma	Uterine Cancer
60431850	NQH.14.6 (Yale207_Myometrium)	Myometrium	Fertility
60432049	NQH.15.1 (Yale99_cervix)	Cervix	Osteoporosis, cervical cancer
60432113	NQH.15.2 (Yale45_spleenITP)		Hemophilia, Hypercoagulation,Idiopathic thrombocytopenic purpura , Immunodeficiencies,Graft vesus host
60432229	NQH.15.3 (Yale16_Skin)	Skin	wound healing, melanoma
60432289	NQH.15.4 (Yale137_Parotid)		
60433356	NQH.15.5 (Yale38_SmallIntestine)	Small intestine	digestive diseases, obesity, diabetes
60433438	NQH.15.6 (Yale28_ColonAscending)	Colon	Colon cancer
65274444	NQH.17.1 (Larynx)	Larynx	Cancer
65274572	NQH.17.2 (Duodenum)	Duodenum	
65274620	NQH.17.3 (Kidney, Primary tumors)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome
65274727	NQH.17.4 (Lung Pleura, normal)	Lung	Airway diseases, infection
65274791	NQH.17.5 (Lung, Normal Adult)	Lung	Airway diseases, infection
83373044	NQH.18.230 (Pooled adrenal gland, placenta)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
85658542	NQH.18.560 (Pooled uterus, BeWo pool)	Uterus	Infertility, birth defects
33656970	NQH.9.1 (MG-63_treatment pool)	Cancer Cell line	Cancer
33657023	NQH.9.2 (HEPG2 untreated)		Von Hippel-Lindau (VHL) syndrome, Cirrhosis,Transplantation
33657084	NQH.9.3 (PC3_untreated)	Cancer Cell line	Cancer
33657109	NQH.9.4 (TF-1_TPA)	Cancer Cell line	Cancer
33657182	NQH.9.5 (TF-1_TPO)	Cancer Cell line	Cancer
33657349	NQH.9.6 (TF-1_Hemin)	Cancer Cell line	Cancer
33657402	NQH.9.7 (HFDPC)	Cancer Cell line	Cancer
264259	NQH1(Mixture of eight adult & two fetal tissues)		
264288	NQH2 (Ten tissues plus lymphocyte control)		
264448	NQH3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmune disease,allergies, immunodeficiencies,transplantation, Graft vesus host,
265017	NQH4.1 (lymph node)	Lymph Node	Lymphedema , Allergies

265018	NQH4.2 (fetal kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome
66712502	NQH4.2 (Sized)		
265019	NQH4.3 (pituitary gland)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
66714117	NQH4.3 (Sized)		
265020	NQH4.4 (testis)	testis	Infertility, birth defects
265021	NQH4.5 (fetal liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis,Transplantation
265022	NQH4.6 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
18108376	NQH5.1 (MCF-7)	Breast cancer	Breast Cancer
18108387	NQH5.2 (CCRF-CEM)	Cancer Cell line	Cancer
264952	NRL1: HPLC FRACTIONATION OF RE-LIG		
263971	Old BB3 Baits		
263969	Old BB5 Baits		
263975	ORFSEL		
263972	OTHER Baits		
263978	pGALORF		
264106	PPBAITS		
264088	QC-YA7		
264089	QC-YA8		
264102	Resequenced Interactors		
264369	RRH.1		
60170394	RRH.10.1 (MCF-7untreated)	Breast cancer	Breast Cancer
60170615	RRH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
60170831	RRH.10.3 (JAR)	Cancer Cell line	Cancer
60174639	RRH.11.8 (HeLa)	Cancer Cell line	Cancer
264113	πQEA Baits		
263973	RRQEA_B5 baits		
29146498	SRD 3.1 (SKMC)	Cancer Cell line	Cancer
29146499	SRD 3.2 (SKMC)	Cancer Cell line	Cancer
29147620	SRD 3.3 (RPTEC)	Cancer Cell line	Cancer
29148627	SRD 3.4 (HRCE)	Cancer Cell line	Cancer
29148629	SRD 3.6 (HRE)	Cancer Cell line	Cancer
29148784	SRD 3.7 (HRE)	Cancer Cell line	Cancer
55810764	SRD.7.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
55811150	SRD.7.2 (pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
55811386	SRD.7.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,

55811576	SRD.7.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
55811957	SRD.7.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis,Transplantation
55812038	SRD.7.6 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome
56181562	SRD.8.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
56181686	SRD.8.2 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
56182181	SRD.8.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
56182323	SRD.8.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
56182435	SRD.8.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis,Transplantation
56182575	SRD.8.6 (Fetal Kidney)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome
32833986	SRD4: HL adapter		
56526486	SRD5.1:rr fragments		
33109954	SRD5: long-RXRJ		
56994075	SRD9.1 (CS/SC)	Cancer Cell line	Cancer
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<210> 6
<211> 121
<212> PRT
<213> Homo sapiens

<400> 6
Met Ser Leu Pro Val Pro Leu Ser Leu Ala Ala Arg Gly Gln His Ser
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His Pro Gly Asp Thr Arg Pro Pro Leu Pro Ser Pro Lys Ile Ala Ser
            20   25   30
Pro Met Cys Phe Pro Gln Lys Gly Leu Glu Gly Tyr Tyr Pro Asn Ala
        35   40   45
Pro Ala Thr Pro Ser Leu Gln Lys Val Ile Cys Asp Leu Gln Gly Leu
    50   55   60
Thr Ala Arg Cys Asp Val Ser Cys Cys Gln Ala Glu Arg Gly Leu Gly
65   70   75   80
Glu Pro Cys Arg Asp Val Met Thr Ser Tyr Val Leu Gly Asn Lys Val
                85   90   95
Thr Cys Cys Arg Pro Leu Glu Leu Trp Pro Val Lys Thr Pro Gly Asn
            100   105   110
Pro Met Ala Arg Arg Glu Thr Val Leu
        115   120

<210> 7
<211> 480
<212> DNA
<213> Homo sapiens

<400> 7
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240
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<210> 8
<211> 119
<212> PRT
<213> Homo sapiens

<400> 8
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Gly Ser Ser Leu Gly Val Glu Ser Ala Cys His Arg Pro Trp Pro Glu
20 25 30
Pro Val Arg Glu Trp Cys Val Lys Gly His Leu His Val Gly Lys Arg
35 40 45
Glu Asp Leu Asp Phe Ser Gly Thr Glu Met Gly Pro Pro Ala Cys Gly
50 55 60
Ser His Leu Ala Thr Thr Leu Gly Pro Val Lys Val Gly Ala Arg Arg
65 70 75 80
Val Val Leu Pro Asp Leu Ser Ser Glu Gly Phe Ala Cys Pro Ala Arg
85 90 95
Ala Ala Arg His Arg Gly Pro Ser Gly Thr Pro Met Ala Thr Leu Gly
100 105 110
Lys Thr Gly Leu Leu Thr Arg
115

<210> 9
<211> 428
<212> DNA
<213> Homo sapiens

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428

<210> 10
<211> 138
<212> PRT

<213> Homo sapiens

<400> 10
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Asn Ser Trp Leu Pro Gly Met Leu Asp Asp Leu Phe Gln Ser Met Phe
35 40 45
Leu Cys Ala Leu Leu Leu Phe Trp Leu Cys Val Tyr His Gly Ile Arg
50 55 60
Val Gln Gly Glu Arg Lys Cys Leu Thr Phe Tyr Leu Pro Lys Phe Phe
65 70 75 80
Ile Val Gly Leu Leu Trp Leu Ala Ser Val Thr Leu Gly Ile Trp Gln
85 90 95
Thr Val Asn Glu Leu His Asp Pro Met Tyr Gln Tyr Arg Val Asp Thr
100 105 110
Gly Asn Phe Gln Gly Met Lys Val Phe Phe Met Val Val Ala Ala Val
115 120 125
Tyr Ile Leu Tyr Leu Leu Phe Leu Ile Val
130 135

<210> 11
<211> 453
<212> DNA
<213> Homo sapiens

<400> 11
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360
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453

<210> 12
<211> 130
<212> PRT
<213> Homo sapiens

<400> 12
Met Leu Gln Ala Asn Ser Arg Pro Val Ala Leu Val Lys Val Gln Val
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Ser Ser Ala Asp Leu Pro Gly Ser Thr Ser Thr Leu Leu Gly Ser Ser

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            20                  25                  30
Cys Phe Met Pro Pro Ile Ser Pro Cys Pro Met Ala Ala Trp Ser Ile
        35                  40                  45
Leu Pro Met Pro Val Ala Val Ser Met Pro Leu Ala Cys Ile Leu Ser
    50                  55                  60
Ile Ser Phe Trp Cys Ser Ala Cys Ile Ala Ala Ser Pro Arg Leu Asn
65                  70                  75                  80
Ser Cys Ser Asn Trp Pro Leu Leu Thr Ser Thr Lys Arg Thr Val Ser
                85                  90                  95
Pro Ala Phe Thr Ser Arg Ala Leu Gly Glu Lys Glu Met Ser Cys Arg
            100                 105                 110
Val Thr Ser Thr Val Arg Val Ala Leu Ser Ala Gly Ala Gly Trp Pro
        115                 120                 125
Asn Ala
    130

<210> 13
<211> 2034
<212> DNA
<213> Homo sapiens

<400> 13
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600
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720
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780
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900
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960
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2034

<210> 14
<211> 222
<212> PRT
<213> Homo sapiens

<400> 14
Ile Val Gln Gln Cys Ala Leu Pro Pro Glu Gln Glu Pro Glu Lys Pro
1 5 10 15
Gly Pro Gly Ser Lys Asp Pro Lys Ala Asp Ser Val Arg Ala Ile Ser
20 25 30
Val Arg Thr Leu Tyr Leu Val Ser Thr Thr Val Asp Arg Met Ser His
35 40 45
Val Leu Trp Pro Tyr Leu Leu Gln Phe Leu Thr Pro Val Arg Phe Thr
50 55 60
Gly Ala Leu Thr Pro Leu Cys Arg Ser Leu Val His Leu Ala Gln Lys
65 70 75 80
Arg Gln Glu Ala Gly Ala Asp Ala Phe Leu Ile Gln Tyr Asp Ala His

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                85                  90                  95
Ala Ser Leu Pro Ser Pro Tyr Ala Val Thr Gly Arg Leu Leu Val Val
            100                 105                 110
Ser Ser Ser Pro Tyr Leu Gly Asp Gly Arg Gly Ala Ala Ala Leu Arg
        115                 120                 125
Leu Leu Ser Val Leu His Pro Asn Ile His Pro Leu Leu Gly Gln His
    130                 135                 140
Trp Glu Thr Thr Val Pro Leu Leu Leu Gly Tyr Leu Asp Glu His Thr
145                 150                 155                 160
Glu Glu Thr Leu Pro Gln Glu Glu Trp Glu Glu Lys Leu Leu Met Val
                165                 170                 175
Arg Ala Gly Val Arg Pro Ile Leu Gly Leu Lys Val Leu Ser Gly Leu
            180                 185                 190
Gly Gly Ala Gly Val Ala Glu Ala Gly Pro Pro Ala Ser Thr Ser Pro
        195                 200                 205
Arg Gly Leu Ala Gly Glu Pro Arg Ile Arg Gln His Gln Gly
    210                 215                 220
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<210> 15
<211> 363
<212> DNA
<213> Homo sapiens

<400> 15
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gcgaagaaat acgatctgta caccaagatc accggcggcc agcggatcga cctgttcggc
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gcccagttgc acgaattgcc gcagatctgg ggcgagctgg tggatgccgg attcgagacc
360
ggt
363

<210> 16
<211> 121
<212> PRT
<213> Homo sapiens

<400> 16
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Xaa Ala Leu Leu Ala Arg His Gly Lys Gly His Val Gly Cys Asp Ile
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Cys Lys Pro Ala Val Gly Ser Ile Leu Ala Ser Cys Trp Asn Gln Pro
            20                  25                  30
Ile Met Asp Pro Ala Leu Val Pro Leu Gln Asp Thr Asn Asp Thr Phe
        35                  40                  45
Met Ala Asn Met Gln Lys Asn Gly Thr Tyr Ser Ile Ile Pro Arg Ile
    50                  55                  60
Ala Gly Gly Glu Ile Thr Pro Asp Lys Leu Ile Ala Leu Gly Ala Val
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65                  70                  75                  80
Ala Lys Lys Tyr Asp Leu Tyr Thr Lys Ile Thr Gly Gly Gln Arg Ile
                85                  90                  95
Asp Leu Phe Gly Ala Gln Leu His Glu Leu Pro Gln Ile Trp Gly Glu
            100                 105                 110
Leu Val Asp Ala Gly Phe Glu Thr Gly
        115                 120
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<210> 17
<211> 682
<212> DNA
<213> Homo sapiens

<400> 17
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tcctgagatc cctcattctt tggcaccagg aacagttgca attagtaaac cctggttccc
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tgctgtctca caaatcgcaa ga
682

<210> 18
<211> 110
<212> PRT
<213> Homo sapiens

<400> 18
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Met Asn Phe Leu Lys Leu Ile Ala Val Phe Ile Val Phe Ser His Ala
 1               5                  10                  15
Ser Glu Ser Pro Gln Asp Ser Thr Pro Asn Gln Leu Tyr Ile Trp Gly
            20                  25                  30
Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp
        35                  40                  45
Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val
    50                  55                  60
Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser
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65 70 75 80
Phe Pro Thr Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala
85 90 95
Ile Ser Lys Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg
100 105 110

<210> 19
<211> 515
<212> DNA
<213> Homo sapiens

<400> 19
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cccccatctc aactatgtta gccagtctgg ctgttcactt agtcactaca gtttgcttct
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cgtctgcagt gcagtcttgg gctataagaa acactgggcc actcaatacc tccccccttt
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tggcccttct cctcctctgg tccatgggtg gggttggggg gagcccagtt tcagcaccag
240
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420
gtcctgctgt aggtgtccag tctgaaggaa tgcctgggat acttcctcaa gcagttcctt
480
ctcacagtct cctggctgct ccgcatgtca gatct
515

<210> 20
<211> 130
<212> PRT
<213> Homo sapiens

<400> 20
Met Gly Pro Ala Ser Leu Leu His Pro Ser Leu Gly Lys Asp His Ala
1 5 10 15
Pro Ile Ser Thr Met Leu Ala Ser Leu Ala Val His Leu Val Thr Thr
20 25 30
Val Cys Phe Ser Ser Ala Val Gln Ser Trp Ala Ile Arg Asn Thr Gly
35 40 45
Pro Leu Asn Thr Ser Pro Leu Leu Ala Leu Leu Leu Leu Trp Ser Met
50 55 60
Gly Gly Val Gly Gly Ser Pro Val Ser Ala Pro Ala Ala Gly Ala His
65 70 75 80
Thr Thr Leu Ile Phe Gln Phe Trp Leu Trp Glu Pro Leu Pro Gln Val
85 90 95
Ser Val Pro Gln Ala Pro Gly Leu Ser Phe Phe Tyr Cys Lys Ser Trp
100 105 110
Leu Leu Leu Trp Leu Ala Pro Arg Arg Val Arg Cys Ser Leu Leu Ser
115 120 125
Lys Ser

130

<210> 21
<211> 390
<212> DNA
<213> Homo sapiens

<400> 21
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ttaaccacga caaataccct tctgtccttt taaatgaagc ggcccaggct tcattactgg
240
atacaatgac tgcttgcact gatgggttca caattgagca attggagctt acacgatctc
300
tatgttatga aagagtatta gcacatcgat cctcatggga tcgttcagcc ctggctcaag
360
aattaaagca agttgtccaa ggcatccatn
390

<210> 22
<211> 105
<212> PRT
<213> Homo sapiens

<400> 22
Met Val Ala Glu Asp His Gly Val Lys Arg Val Arg Leu Asp Asp Ala
1 5 10 15
Thr Asn Val Pro Glu Gly Glu Met Ala Arg Ala Ser Ala Asn Glu Gly
20 25 30
Met Thr Pro Val Asn His Asp Lys Tyr Pro Ser Val Leu Leu Asn Glu
35 40 45
Ala Ala Gln Ala Ser Leu Leu Asp Thr Met Thr Ala Cys Thr Asp Gly
50 55 60
Phe Thr Ile Glu Gln Leu Glu Leu Thr Arg Ser Leu Cys Tyr Glu Arg
65 70 75 80
Val Leu Ala His Arg Ser Ser Trp Asp Arg Ser Ala Leu Ala Gln Glu
85 90 95
Leu Lys Gln Val Val Gln Gly Ile His
100 105

<210> 23
<211> 385
<212> DNA
<213> Homo sapiens

<400> 23
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120

ggctgggact acgtggactc gctctacttc tgcttcgtca ccttcagcac catcggcttc
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cgctgctgcc cggctcctgg cgcgc
385

<210> 24
<211> 128
<212> PRT
<213> Homo sapiens

<400> 24
Xaa Ser Glu Ala Asp Ser Leu Ala Gly Trp Lys Pro Ser Val Tyr His
1 5 10 15
Val Leu Leu Ile Leu Gly Leu Phe Ala Val Leu Leu Ser Cys Cys Ala
20 25 30
Ser Ala Met Tyr Thr Ser Val Glu Gly Trp Asp Tyr Val Asp Ser Leu
35 40 45
Tyr Phe Cys Phe Val Thr Phe Ser Thr Ile Gly Phe Gly Asp Leu Val
50 55 60
Ser Ser Gln His Ala Ala Tyr Arg Asn Gln Gly Leu Tyr Arg Leu Gly
65 70 75 80
Asn Phe Leu Phe Ile Leu Leu Gly Val Cys Cys Ile Tyr Ser Leu Phe
85 90 95
Asn Val Ile Ser Ile Leu Ile Lys Gln Val Leu Asn Trp Met Leu Arg
100 105 110
Lys Leu Ser Cys Arg Cys Cys Ala Arg Cys Cys Pro Ala Pro Gly Ala
115 120 125

<210> 25
<211> 337
<212> DNA
<213> Homo sapiens

<400> 25
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gggttgagtg tagggcaaaa gagaaagaag gcaccaagcc tggggtctgg gttttctctc
300
ttacacttgc tgggtggacg gtggtgccac tgaatga
337

<210> 26

<211> 111
<212> PRT
<213> Homo sapiens

<400> 26
Met Gly Glu Thr Val His Phe Leu Leu Gly Leu Arg Gly Lys Ser Leu
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Gln Ser Phe Glu Glu Gly Ser Ser Gln Leu Cys Ile Phe Glu Gly Ser
20 25 30
Val Leu Leu Leu Gly Pro Val Arg Ser Pro Val Gly Ser Arg Leu Glu
35 40 45
Trp Val Glu Pro Gly Gln Val Gly Ala Glu Thr Leu Glu Glu Ser Trp
50 55 60
Ser Asn Ala Leu Cys Ile Trp Arg Gln Asn Gln Gln Arg Val Leu Trp
65 70 75 80
Val Glu Cys Arg Ala Lys Glu Lys Glu Gly Thr Lys Pro Gly Val Trp
85 90 95
Val Phe Ser Leu Thr Leu Ala Gly Trp Thr Val Val Pro Leu Asn
100 105 110

<210> 27
<211> 333
<212> DNA
<213> Homo sapiens

<400> 27
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cacattgcag caaattgtgg atcggtggaa tgcttggttt tgctgttaaa gaaaggagca
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aatcctaact atcaagatat ttcaggctgt aca
333

<210> 28
<211> 111
<212> PRT
<213> Homo sapiens

<400> 28
Pro Thr Ser Asn Ile His Ala Ala Ala Pro Arg Met Glu Arg Ala Met
1 5 10 15
Glu Gln Leu Asn Arg Leu Thr Arg Ser Leu Arg Arg Ala Arg Thr Val
20 25 30
Glu Leu Pro Glu Asp Asn Glu Thr Ala Val Tyr Thr Leu Met Pro Met
35 40 45
Val Met Ala Asp Gln His Arg Ser Val Ser Glu Leu Leu Ser Asn Ser
50 55 60
Lys Phe Asp Val Asn Tyr Ala Phe Gly Arg Val Lys Arg Ser Leu Leu

65 70 75 80
His Ile Ala Ala Asn Cys Gly Ser Val Glu Cys Leu Val Leu Leu Leu
85 90 95
Lys Lys Gly Ala Asn Pro Asn Tyr Gln Asp Ile Ser Gly Cys Thr
100 105 110

<210> 29
<211> 375
<212> DNA
<213> Homo sapiens

<400> 29
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gagagctatt tgagcgccgt gacgccgctg agtcccaaag agattcgtca gctgccccgc
120
tacaatatca cgatcaagcg cgtcgtgaac atgacgggca agggccgcac gccgagctgg
180
tactcgctcg tcgtggctgg caatggtcgg ggcctcgtgg gctatggcga aggcaaagat
240
actaacatca gccgcgcgaa caaaaaggcg ttccacgccg cggtgaaaaa catggacttg
300
gtatcggtcc accggtcgaa gagtggcgcc aacacgctcg agccccccgt cgagggccgc
360
tggggcgcta cgcgt
375

<210> 30
<211> 125
<212> PRT
<213> Homo sapiens

<400> 30
Xaa Pro Ser Val Leu Ala Ile Met Thr Ala Gly Ser Asp Gln Gly Glu
1 5 10 15
Glu Val Asn Ser Glu Ser Tyr Leu Ser Ala Val Thr Pro Leu Ser Pro
20 25 30
Lys Glu Ile Arg Gln Leu Pro Arg Tyr Asn Ile Thr Ile Lys Arg Val
35 40 45
Val Asn Met Thr Gly Lys Gly Arg Thr Pro Ser Trp Tyr Ser Leu Val
50 55 60
Val Ala Gly Asn Gly Arg Gly Leu Val Gly Tyr Gly Glu Gly Lys Asp
65 70 75 80
Thr Asn Ile Ser Arg Ala Asn Lys Lys Ala Phe His Ala Ala Val Lys
85 90 95
Asn Met Asp Leu Val Ser Val His Arg Ser Lys Ser Gly Ala Asn Thr
100 105 110
Leu Glu Pro Pro Val Glu Gly Arg Trp Gly Ala Thr Arg
115 120 125

<210> 31
<211> 375
<212> DNA
<213> Homo sapiens

<400> 31
accggtcttg gcctcagctt tgctctgaaa ttgaagtcgg tgccaaaagt ggggaagagc
60
gggagcaggc acttacgagc ctgcgcgtca gggatgcttc ctgggcccct gagagtgcag
120
agattcctgg atccagagct gcggctgggc ggctgcagct gcgcctggga gtgcagggct
180
cccgccctgc cagctcaaaa ggaaatgggg gctcctgcct gttcctggct cctgttggcc
240
ctgcagagtg cacaaaccta gccgcgcttc ctccactgca gcttacgtct ttgcagcagc
300
cactcccgat gggctgccac tgccatctgt gagaccataa tgtgtgcaat ttgagactca
360
tggcctgcat tgttt
375

<210> 32
<211> 118
<212> PRT
<213> Homo sapiens

<400> 32
Met Gln Ala Met Ser Leu Lys Leu His Thr Leu Trp Ser His Arg Trp
 1   5   10   15
Gln Trp Gln Pro Ile Gly Ser Gly Cys Cys Lys Asp Val Ser Cys Ser
            20   25   30
Gly Gly Ser Ala Ala Arg Phe Val His Ser Ala Gly Pro Thr Gly Ala
        35   40   45
Arg Asn Arg Gln Glu Pro Pro Phe Pro Phe Glu Leu Ala Gly Arg Glu
    50   55   60
Pro Cys Thr Pro Arg Arg Ser Cys Ser Arg Pro Ala Ala Ala Leu Asp
65   70   75   80
Pro Gly Ile Ser Ala Leu Ser Gly Ala Gln Glu Ala Ser Leu Thr Arg
                85   90   95
Arg Leu Val Ser Ala Cys Ser Arg Ser Ser Pro Leu Leu Ala Pro Thr
            100   105   110
Ser Ile Ser Glu Gln Ser
        115

<210> 33
<211> 351
<212> DNA
<213> Homo sapiens

<400> 33
ccatgcagcc caaccgttgg cgataaagtc cgtttaggcg ataccaattt atgggcaacc
60
attgaacaag atttattaac caaaggtgat gagtgtaaat ttggtggcgg taaaagtgtg
120
cgtgatggta tggcgcaaag cggcaccgca actcgcgaca atccaaatgt attggatttt
180
gtgattacca atgtgatgat cattgatgcc aaattaggca ttatcaaagc cgatattggt
240

attcgcgatg gtcgtattgt cggtatcgga caagcaggta accctgacac catggatgac
300
gtcacgccaa acatgattat cggtgctagc acagaagtac ataacggtgc a
351

<210> 34
<211> 117
<212> PRT
<213> Homo sapiens

<400> 34
Pro Cys Ser Pro Thr Val Gly Asp Lys Val Arg Leu Gly Asp Thr Asn
1 5 10 15
Leu Trp Ala Thr Ile Glu Gln Asp Leu Leu Thr Lys Gly Asp Glu Cys
20 25 30
Lys Phe Gly Gly Gly Lys Ser Val Arg Asp Gly Met Ala Gln Ser Gly
35 40 45
Thr Ala Thr Arg Asp Asn Pro Asn Val Leu Asp Phe Val Ile Thr Asn
50 55 60
Val Met Ile Ile Asp Ala Lys Leu Gly Ile Ile Lys Ala Asp Ile Gly
65 70 75 80
Ile Arg Asp Gly Arg Ile Val Gly Ile Gly Gln Ala Gly Asn Pro Asp
85 90 95
Thr Met Asp Asp Val Thr Pro Asn Met Ile Ile Gly Ala Ser Thr Glu
100 105 110
Val His Asn Gly Ala
115

<210> 35
<211> 355
<212> DNA
<213> Homo sapiens

<400> 35
nngctagctg caccaccacc tgttcatgca ggcagagcgg ccacccctca tggaagaaga
60
ggaatccact gtattgggca caggcttcct gctggacctt ggcaagcagg tgcttggctg
120
gtaccaggaa gtccagcgtg tacctcagtg cgtcctcccg ataagtcctc tccaccacct
180
ggaacacctg gcccaacagg gtgggggctg ttgcctcaaa gggtggatac agggcggcga
240
gagtgctctg cacacagtcc tccactggct caggctccat ggctcggcgc cgggccgcgt
300
ccgacgcttg gtcgggcggg cggggccggg cgcgccaccg cctcccttca cgcgt
355

<210> 36
<211> 118
<212> PRT
<213> Homo sapiens

<400> 36
Xaa Leu Ala Ala Pro Pro Pro Val His Ala Gly Arg Ala Ala Thr Pro

```
 1               5                  10                  15
His Gly Arg Arg Gly Ile His Cys Ile Gly His Arg Leu Pro Ala Gly
            20                  25                  30
Pro Trp Gln Ala Gly Ala Trp Leu Val Pro Gly Ser Pro Ala Cys Thr
        35                  40                  45
Ser Val Arg Pro Pro Asp Lys Ser Ser Pro Pro Pro Gly Thr Pro Gly
    50                  55                  60
Pro Thr Gly Trp Gly Leu Leu Pro Gln Arg Val Asp Thr Gly Arg Arg
65                  70                  75                  80
Glu Cys Ser Ala His Ser Pro Pro Leu Ala Gln Ala Pro Trp Leu Gly
                85                  90                  95
Ala Gly Pro Arg Pro Thr Leu Gly Arg Ala Gly Gly Ala Gly Arg Ala
            100                 105                 110
Thr Ala Ser Leu His Ala
        115
```

<210> 37
<211> 492
<212> DNA
<213> Homo sapiens

<400> 37
acgcgtggcc ttcgtctgcc accaggaccg actcagcccc accgggtttc cggacccgcc
60
gcaaccatga caagggcgat gttgtgatct gggtggattc cttctccgac atgctcgagg
120
gatcggatct ctcggcggta gtcacggtgc ttgccgaggc cggctatcgc ccacgggtcc
180
tcgccgacga cgtctgctgc gggttgacgt ggatcactac cggtcagctc gacggtgctc
240
ggcgtcggct gcgcgctggt ctcgacgtgc tggcacccct gtcagacgcc agcgtcccag
300
tcgttgggct agagccgtcc tgcactaccg tctggcgtga tgacgcactc cgcctcctgc
360
cagatgatcc gcgcgtccac cgggtagcca gaaacatgca taccgtcgcc gagatgcttg
420
aggcagcaca gtggacccca ccctcgctag caggccacac cctcgtcgct cagccccatt
480
gtcatcccgc gg
492

<210> 38
<211> 127
<212> PRT
<213> Homo sapiens

<400> 38
```
Met Leu Glu Gly Ser Asp Leu Ser Ala Val Val Thr Val Leu Ala Glu
 1               5                  10                  15
Ala Gly Tyr Arg Pro Arg Val Leu Ala Asp Asp Val Cys Cys Gly Leu
            20                  25                  30
Thr Trp Ile Thr Thr Gly Gln Leu Asp Gly Ala Arg Arg Arg Leu Arg
        35                  40                  45
Ala Gly Leu Asp Val Leu Ala Pro Leu Ser Asp Ala Ser Val Pro Val
```

```
    50                  55                  60
Val Gly Leu Glu Pro Ser Cys Thr Thr Val Trp Arg Asp Asp Ala Leu
65                  70                  75                  80
Arg Leu Leu Pro Asp Asp Pro Arg Val His Arg Val Ala Arg Asn Met
                85                  90                  95
His Thr Val Ala Glu Met Leu Glu Ala Ala Gln Trp Thr Pro Pro Ser
            100                 105                 110
Leu Ala Gly His Thr Leu Val Ala Gln Pro His Cys His Pro Ala
        115                 120                 125
```

<210> 39
<211> 412
<212> DNA
<213> Homo sapiens

<400> 39
aacgaaggtn ccgtacgcgc tctgaaagcc ctgcgtaaag agcgttccga tcgccgggaa
60
gtgatgngca ccgccaaaat gcaggtggtc gaagccgcga gttcaggcaa gattgtcttt
120
gaaatggaag acgtttatta cagcattgcc ggaaaacaac tggtgagcaa cttctctgcg
180
caagtcatgc gtggtgataa aattgcgctg attggcccga acggttgtgg taaaacgacg
240
ttgctgaaac tgatgttaag taagattcag gcagacagcg gccgtgttca ctgcggtact
300
aaactggaag ttgcgtactt cgaccagcac cgtgctgagc tggatcctga gcgtacggtg
360
atggataacc tggccgaagg taagcaggaa gtgatggtaa atggccgtgt an
412

<210> 40
<211> 137
<212> PRT
<213> Homo sapiens

<400> 40
```
Asn Glu Gly Xaa Val Arg Ala Leu Lys Ala Leu Arg Lys Glu Arg Ser
 1               5                  10                  15
Asp Arg Arg Glu Val Met Xaa Thr Ala Lys Met Gln Val Val Glu Ala
            20                  25                  30
Ala Ser Ser Gly Lys Ile Val Phe Glu Met Glu Asp Val Tyr Tyr Ser
        35                  40                  45
Ile Ala Gly Lys Gln Leu Val Ser Asn Phe Ser Ala Gln Val Met Arg
    50                  55                  60
Gly Asp Lys Ile Ala Leu Ile Gly Pro Asn Gly Cys Gly Lys Thr Thr
65                  70                  75                  80
Leu Leu Lys Leu Met Leu Ser Lys Ile Gln Ala Asp Ser Gly Arg Val
                85                  90                  95
His Cys Gly Thr Lys Leu Glu Val Ala Tyr Phe Asp Gln His Arg Ala
            100                 105                 110
Glu Leu Asp Pro Glu Arg Thr Val Met Asp Asn Leu Ala Glu Gly Lys
        115                 120                 125
Gln Glu Val Met Val Asn Gly Arg Val
```

130 135

<210> 41
<211> 1080
<212> DNA
<213> Homo sapiens

<400> 41
gaattcaagt ggacacaggc tccacgcccg cgtctcaccg ataagagcta caagcacaac
60
tactatgacg agcgggtttc gctcgaagag cgtcttgagc gcactgtggc taaggatttc
120
gtcacgacgg aggtcgagcc catgtgggat gcggctgatg tcatgcggat gggtaaggat
180
ctcttcatcc agcacggtct gacgacaaat cggaagtcaa tggagtggtt taagcgttac
240
taccccgatt tccgcgttca cgcggtgaat ttccctgggg atccgtaccc gatccatatc
300
gacgcgacct ttgtgccgct tcgtccgggg ctcatcatca acaacccgaa tcgtccactg
360
ccgcaggagc agaggaagat cttcgaggcc aatgactggc agatcgttga tgctgctcag
420
ccggcgcacg acacgcctcc agaattgtgc tactcgtctg tgtggctatc aatgaactgc
480
ttggtacttg atccgaagac ggtcatctgc gaggcttcgg aagttcatca gatggagcag
540
atggacaagc tgggtatgaa cgtcatcccg gtcgccttcc gtgacgcgta cccattcggt
600
ggaggtctcc actgcgccac agctgatgta tatcgcgaag gtacctgtga ggactacttc
660
ccgaatcagg tcgacgaccc gaccttggtg tgagaaaacc ccgtggtcat gtcatgactg
720
acggatctcg gtggctcggt acggaactta cgttgtccgt taccgggccg ccgggtctga
780
tatggcagta tcacgcctag caaaaaggag catgtcatgg acatggagcc gggcatcatc
840
aacgtcaaac aggaagttcc aggcgtcggt acgatgaacc agaaagtggg attcgtgtcc
900
atgcttcttt ctgcaacggg tatggggttg gtgggtactt tcgggcgtct cagcactcct
960
gtggatccca cgacgggcag taagtacatc atcggtgatt ttttggccac tggtaggatg
1020
atagtcgggg tcctgggatt tctgcttatt atcgtcatac ttggaaaatg gtctgagctc
1080

<210> 42
<211> 230
<212> PRT
<213> Homo sapiens

<400> 42
Glu Phe Lys Trp Thr Gln Ala Pro Arg Pro Arg Leu Thr Asp Lys Ser
1 5 10 15
Tyr Lys His Asn Tyr Tyr Asp Glu Arg Val Ser Leu Glu Glu Arg Leu

```
            20                  25                  30
Glu Arg Thr Val Ala Lys Asp Phe Val Thr Thr Glu Val Glu Pro Met
        35                  40                  45
Trp Asp Ala Ala Asp Val Met Arg Met Gly Lys Asp Leu Phe Ile Gln
    50                  55                  60
His Gly Leu Thr Thr Asn Arg Lys Ser Met Glu Trp Phe Lys Arg Tyr
65                  70                  75                  80
Tyr Pro Asp Phe Arg Val His Ala Val Asn Phe Pro Gly Asp Pro Tyr
                85                  90                  95
Pro Ile His Ile Asp Ala Thr Phe Val Pro Leu Arg Pro Gly Leu Ile
            100                 105                 110
Ile Asn Asn Pro Asn Arg Pro Leu Pro Gln Glu Gln Arg Lys Ile Phe
        115                 120                 125
Glu Ala Asn Asp Trp Gln Ile Val Asp Ala Ala Gln Pro Ala His Asp
    130                 135                 140
Thr Pro Pro Glu Leu Cys Tyr Ser Ser Val Trp Leu Ser Met Asn Cys
145                 150                 155                 160
Leu Val Leu Asp Pro Lys Thr Val Ile Cys Glu Ala Ser Glu Val His
                165                 170                 175
Gln Met Glu Gln Met Asp Lys Leu Gly Met Asn Val Ile Pro Val Ala
            180                 185                 190
Phe Arg Asp Ala Tyr Pro Phe Gly Gly Gly Leu His Cys Ala Thr Ala
        195                 200                 205
Asp Val Tyr Arg Glu Gly Thr Cys Glu Asp Tyr Phe Pro Asn Gln Val
    210                 215                 220
Asp Asp Pro Thr Leu Val
225                 230
```

<210> 43
<211> 358
<212> DNA
<213> Homo sapiens

<400> 43
gggccccca catagtggac acaggtttct gggatgtcag catggagtgc caagaggtgg
60
gtgaccacct ggtggggaat aaggcgcttc tgggacatag aggctgcctt ccagctgcgc
120
ctggcagagc tgttgacaca acagcatggt ctgcagtgcc gggccactgc cacgcacacc
180
gatgtccttt aaggatggat ttgggttttc ggattcgcgt ggcctatcag cgggagtccc
240
agatcctgaa ggaagtgcag agcccagagg ggatgatctc gctgagggac acagctgcct
300
ccctccgcct tgagagagac acaaggcagt tgccactgct caccagtgcc ctgcacgn
358

<210> 44
<211> 105
<212> PRT
<213> Homo sapiens

<400> 44
Met Glu Cys Gln Glu Val Gly Asp His Leu Val Gly Asn Lys Ala Leu

```
 1               5                  10                  15
Leu Gly His Arg Gly Cys Leu Pro Ala Ala Pro Gly Arg Ala Val Asp
            20                  25                  30
Thr Thr Ala Trp Ser Ala Val Pro Gly His Cys His Ala His Arg Cys
        35                  40                  45
Pro Leu Arg Met Asp Leu Gly Phe Arg Ile Arg Val Ala Tyr Gln Arg
    50                  55                  60
Glu Ser Gln Ile Leu Lys Glu Val Gln Ser Pro Glu Gly Met Ile Ser
65                  70                  75                  80
Leu Arg Asp Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp Thr Arg Gln
                85                  90                  95
Leu Pro Leu Leu Thr Ser Ala Leu His
            100                 105
```

<210> 45
<211> 905
<212> DNA
<213> Homo sapiens

<400> 45
gtcgacgata aaggagtatt tgcgcagcag cagtatgatg ctctcgttga ggcgggtttc
60
gcggctcctg gaatcccaga gcagtatggt ggcgacggtg cggatgcgat tgcgtccgca
120
ataatcatgg aagaggtcgc tcgagtctgt gcgtcgtcgt ccaccgtcat atcgtccaat
180
gagcttggta ccgtccctct cctcaaatac ggtagcgagg agcagaggaa acgttatctt
240
tctgaagttg cttcgggtaa ggcacttttc ggatatgcgc tctccgaggc tgatgctgga
300
tcagatccag ctgcacttaa gtgtcgagcc gacgaagatg gggacagttt cgtcctgaat
360
ggcgttaagg cttgggtcac ggaggctggc gaggccaagt acctggtgat atttgcggtt
420
actgacccag acgatccgcg ccacagaatc agcgcgttga tggtccatgc agatgacccg
480
ggcattagct acggggctcc ggagcacaaa atggggatac gcgggtcagt taccagggaa
540
gtggttttca agaatacgcg tatccccaag gaacgagtaa ttggccgtcg agggcacggt
600
ctgagtgttg ctctaggtac gcttgataac tctcgtgtct cgattgctgc tcaagcagtg
660
ggaattgccc aaggagcttt agacattgcc acggattacg tccagaagcg caagcagttt
720
ggccagccac tgtccaattt tgagggaatc cagttcatgc tcgcagacat ggcaatgcgt
780
ttggaggcgg cgcgagcgct gacatactct gcagctgatc gtagtgggcg ccagactgac
840
gatgtgagtt acttcggcgc ggcggccaaa tgtttcgctt ccgacacagc gatggcagtg
900
tgcac
905

<210> 46

<211> 301
<212> PRT
<213> Homo sapiens

<400> 46
Val Asp Asp Lys Gly Val Phe Ala Gln Gln Gln Tyr Asp Ala Leu Val
1 5 10 15
Glu Ala Gly Phe Ala Ala Pro Gly Ile Pro Glu Gln Tyr Gly Gly Asp
20 25 30
Gly Ala Asp Ala Ile Ala Ser Ala Ile Ile Met Glu Glu Val Ala Arg
35 40 45
Val Cys Ala Ser Ser Ser Thr Val Ile Ser Ser Asn Glu Leu Gly Thr
50 55 60
Val Pro Leu Leu Lys Tyr Gly Ser Glu Glu Gln Arg Lys Arg Tyr Leu
65 70 75 80
Ser Glu Val Ala Ser Gly Lys Ala Leu Phe Gly Tyr Ala Leu Ser Glu
85 90 95
Ala Asp Ala Gly Ser Asp Pro Ala Ala Leu Lys Cys Arg Ala Asp Glu
100 105 110
Asp Gly Asp Ser Phe Val Leu Asn Gly Val Lys Ala Trp Val Thr Glu
115 120 125
Ala Gly Glu Ala Lys Tyr Leu Val Ile Phe Ala Val Thr Asp Pro Asp
130 135 140
Asp Pro Arg His Arg Ile Ser Ala Leu Met Val His Ala Asp Asp Pro
145 150 155 160
Gly Ile Ser Tyr Gly Ala Pro Glu His Lys Met Gly Ile Arg Gly Ser
165 170 175
Val Thr Arg Glu Val Val Phe Lys Asn Thr Arg Ile Pro Lys Glu Arg
180 185 190
Val Ile Gly Arg Arg Gly His Gly Leu Ser Val Ala Leu Gly Thr Leu
195 200 205
Asp Asn Ser Arg Val Ser Ile Ala Ala Gln Ala Val Gly Ile Ala Gln
210 215 220
Gly Ala Leu Asp Ile Ala Thr Asp Tyr Val Gln Lys Arg Lys Gln Phe
225 230 235 240
Gly Gln Pro Leu Ser Asn Phe Glu Gly Ile Gln Phe Met Leu Ala Asp
245 250 255
Met Ala Met Arg Leu Glu Ala Ala Arg Ala Leu Thr Tyr Ser Ala Ala
260 265 270
Asp Arg Ser Gly Arg Gln Thr Asp Asp Val Ser Tyr Phe Gly Ala Ala
275 280 285
Ala Lys Cys Phe Ala Ser Asp Thr Ala Met Ala Val Cys
290 295 300

<210> 47
<211> 379
<212> DNA
<213> Homo sapiens

<400> 47
aagcttgtag agctagtccg aagcggactg tcggtacgcc aagctgctaa aagatgtggg
60
atgcatctta ccgctgcgta tgccgtagct acggaagctg ggtgccatat ccggttaagt
120

cagtatgctc ggaaagtccg ccagacgcag ttaagagtgg aatacctgcg ccttcggctg
180
gcgagcctgc ctggtggtga tgctggcgcg gcagtaggaa ttgatcgtcg actgcgttta
240
gatttcgaaa aaggactcac caaatcccag ggtcgacgag aagagttcat acccgtcggc
300
gaagacgcca gcacgtataa cagacttatg aaagcgctgc gccaacgcca tgatgtcatc
360
aaatccggaa agcttgccc
379

<210> 48
<211> 106
<212> PRT
<213> Homo sapiens

<400> 48
Met His Leu Thr Ala Ala Tyr Ala Val Ala Thr Glu Ala Gly Cys His
1 5 10 15
Ile Arg Leu Ser Gln Tyr Ala Arg Lys Val Arg Gln Thr Gln Leu Arg
20 25 30
Val Glu Tyr Leu Arg Leu Arg Leu Ala Ser Leu Pro Gly Gly Asp Ala
35 40 45
Gly Ala Ala Val Gly Ile Asp Arg Arg Leu Arg Leu Asp Phe Glu Lys
50 55 60
Gly Leu Thr Lys Ser Gln Gly Arg Arg Glu Glu Phe Ile Pro Val Gly
65 70 75 80
Glu Asp Ala Ser Thr Tyr Asn Arg Leu Met Lys Ala Leu Arg Gln Arg
85 90 95
His Asp Val Ile Lys Ser Gly Lys Leu Ala
100 105

<210> 49
<211> 309
<212> DNA
<213> Homo sapiens

<400> 49
tgatcatgat gctggcatgg actattctgg tccctgttcc tctctcacct gctgaaggac
60
atccctctaa tttttgtgtc tccttctgta tcatcaaatt ttccctctct actgagtctc
120
ttgcatctcc ttggaagcat gctgtactat gtcccatcct taaagaactc cccttgtctg
180
cacattaccc tctgccagct ggctcatttt tctgctcccc tttacaggga aactcttcaa
240
aaagttatct ccacctcctt ccatctcatg ttctcttgaa cctgcagtac tgggtgctcc
300
ctccttttg
309

<210> 50
<211> 101
<212> PRT

<213> Homo sapiens

<400> 50
Met Met Leu Ala Trp Thr Ile Leu Val Pro Val Pro Leu Ser Pro Ala
1 5 10 15
Glu Gly His Pro Ser Asn Phe Cys Val Ser Phe Cys Ile Ile Lys Phe
20 25 30
Ser Leu Ser Thr Glu Ser Leu Ala Ser Pro Trp Lys His Ala Val Leu
35 40 45
Cys Pro Ile Leu Lys Glu Leu Pro Leu Ser Ala His Tyr Pro Leu Pro
50 55 60
Ala Gly Ser Phe Phe Cys Ser Pro Leu Gln Gly Asn Ser Ser Lys Ser
65 70 75 80
Tyr Leu His Leu Leu Pro Ser His Val Leu Leu Asn Leu Gln Tyr Trp
85 90 95
Val Leu Pro Pro Phe
100

<210> 51
<211> 512
<212> DNA
<213> Homo sapiens

<400> 51
agatctttga agaattgcca cactgtcttc ctccctgctt ataatttcct tattccctag
60
gatgtgatcc ttgttcttgg ggcctcacat ggcagctgga tctctggcga ttgcatctga
120
gttccagaca ccaggatgga aaagaaaaga aggaggggca agaggaaccc ccagatgctc
180
cttaagagct actgcgtggc attcccactt gcatctcatt tgctcgatcg ctgtcactgt
240
gccctaacga gctgcaagga cactggggaa atgagtctgt cttgtacttc atgtgccccc
300
caaaatcttc tgttgctgag ggagaagagg ccagccggta ttgaggaaca actagcactt
360
tctgcttccg cgtcccaggg ggacgtgggt gtgttgaatc cacaccgggg gtgcggacct
420
ctgaggctgg gctggatggg acatcaggtg ggccctctgt ttcatttatg tgacctccca
480
tcaggtcttc tggttggatc ctgctttcta ga
512

<210> 52
<211> 125
<212> PRT
<213> Homo sapiens

<400> 52
Met Glu Lys Lys Arg Arg Arg Gly Lys Arg Asn Pro Gln Met Leu Leu
1 5 10 15
Lys Ser Tyr Cys Val Ala Phe Pro Leu Ala Ser His Leu Leu Asp Arg
20 25 30
Cys His Cys Ala Leu Thr Ser Cys Lys Asp Thr Gly Glu Met Ser Leu

```
        35                  40                  45
Ser Cys Thr Ser Cys Ala Pro Gln Asn Leu Leu Leu Leu Arg Glu Lys
    50                  55                  60
Arg Pro Ala Gly Ile Glu Glu Gln Leu Ala Leu Ser Ala Ser Ala Ser
65                  70                  75                  80
Gln Gly Asp Val Gly Val Leu Asn Pro His Arg Gly Cys Gly Pro Leu
                85                  90                  95
Arg Leu Gly Trp Met Gly His Gln Val Gly Pro Leu Phe His Leu Cys
            100                 105                 110
Asp Leu Pro Ser Gly Leu Leu Val Gly Ser Cys Phe Leu
        115                 120                 125
```

<210> 53
<211> 474
<212> DNA
<213> Homo sapiens

<400> 53
accggtacac ctacgtcacc cgtaaaaacc gacgcaatac ccggatcgcc tcgtcctcaa
60
aaaattcgat cccgtcgtgc gtcgtcacat tgagttcaag gaggcccgct aatggccaaa
120
aagtccaaga ttgtcgccca gaagaaacgt gagaagctcg tagcccaata cgccgaaagg
180
cgcgccgaac tcaaggccat catgaagtgc ccaactgcct cattggacga acgcatggag
240
gcatcgcgta agctgtctcg cctgccgcgc gattcatccc ccgtgcggtt acgtaaccgt
300
gaccaagtcg acgggcgtcc ccgcggctac gttggcaagg ccggtgtgtc ccgtatccgt
360
ttccgtgaga tggcccaccg cggcgaactc cccggaatcg cgaagtcaag ctggtgaagc
420
catggcagta ccgaagcgaa agaagtcccg ttcgaccacg cgtcataggc gggc
474

<210> 54
<211> 101
<212> PRT
<213> Homo sapiens

<400> 54
```
Met Ala Lys Lys Ser Lys Ile Val Ala Gln Lys Lys Arg Glu Lys Leu
 1               5                  10                  15
Val Ala Gln Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Met Lys
            20                  25                  30
Cys Pro Thr Ala Ser Leu Asp Glu Arg Met Glu Ala Ser Arg Lys Leu
        35                  40                  45
Ser Arg Leu Pro Arg Asp Ser Ser Pro Val Arg Leu Arg Asn Arg Asp
    50                  55                  60
Gln Val Asp Gly Arg Pro Arg Gly Tyr Val Gly Lys Ala Gly Val Ser
65                  70                  75                  80
Arg Ile Arg Phe Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Ile
                85                  90                  95
Ala Lys Ser Ser Trp
```

100

<210> 55
<211> 378
<212> DNA
<213> Homo sapiens

<400> 55
ccatggccca ggacagccgg catatcggct acgactacgg tacaccggtg gcgccacagt
60
tcggcgcagc caagcccgca gcgtgctgcc aggcgcaagc gacaaacacc ggcccgtggg
120
tggtgttcga ccatgtgcgt tgcacccacg acacctttct gatcgacgtc tttctcaacc
180
agcccgatgc caccgcgcag caggtcaatg ccgacaaccc gcactacgtc gggcgtttca
240
gccgcatcgg catgggcctg gtggatgaca agggccgttg cattacccag ggcgtatcgc
300
gcgcgttgaa tgcggcgcgc agcaccaagg cgctgaacct gggaccgagt gacgcggcgc
360
agttatcggt gaggcgta
378

<210> 56
<211> 125
<212> PRT
<213> Homo sapiens

<400> 56
Met Ala Gln Asp Ser Arg His Ile Gly Tyr Asp Tyr Gly Thr Pro Val
1 5 10 15
Ala Pro Gln Phe Gly Ala Ala Lys Pro Ala Ala Cys Cys Gln Ala Gln
20 25 30
Ala Thr Asn Thr Gly Pro Trp Val Val Phe Asp His Val Arg Cys Thr
35 40 45
His Asp Thr Phe Leu Ile Asp Val Phe Leu Asn Gln Pro Asp Ala Thr
50 55 60
Ala Gln Gln Val Asn Ala Asp Asn Pro His Tyr Val Gly Arg Phe Ser
65 70 75 80
Arg Ile Gly Met Gly Leu Val Asp Asp Lys Gly Arg Cys Ile Thr Gln
85 90 95
Gly Val Ser Arg Ala Leu Asn Ala Ala Arg Ser Thr Lys Ala Leu Asn
100 105 110
Leu Gly Pro Ser Asp Ala Ala Gln Leu Ser Val Arg Arg
115 120 125

<210> 57
<211> 388
<212> DNA
<213> Homo sapiens

<400> 57
agacccaccc gacacagatc aggagtcgtc atgtccagaa agaagaaggt cggcatcctc
60

accgcaggcg gtgattgccc cgggctcaac gccgctatcc gcggatttgg caaggctgcc
120
atccgccagc acgacatgga gctcatcggt attcaggacg gctttcttgg attggcggga
180
aaccgcacca tctcccttgg cccgcgtgcc ctctcaggca tcttgacggt cggcgggacc
240
atcctgggaa ctagccgtga caaggtcaat cacatgatta tcgacggcga ggaacgggat
300
atggtcccca ccaccgtcga gaattacgag aagctggggc ttgacgcttt ggtgactttg
360
ggtggcggtg gcaccgccaa gaacgcgt
388

<210> 58
<211> 129
<212> PRT
<213> Homo sapiens

<400> 58
Arg Pro Thr Arg His Arg Ser Gly Val Val Met Ser Arg Lys Lys Lys
1 5 10 15
Val Gly Ile Leu Thr Ala Gly Gly Asp Cys Pro Gly Leu Asn Ala Ala
20 25 30
Ile Arg Gly Phe Gly Lys Ala Ala Ile Arg Gln His Asp Met Glu Leu
35 40 45
Ile Gly Ile Gln Asp Gly Phe Leu Gly Leu Ala Gly Asn Arg Thr Ile
50 55 60
Ser Leu Gly Pro Arg Ala Leu Ser Gly Ile Leu Thr Val Gly Gly Thr
65 70 75 80
Ile Leu Gly Thr Ser Arg Asp Lys Val Asn His Met Ile Ile Asp Gly
85 90 95
Glu Glu Arg Asp Met Val Pro Thr Thr Val Glu Asn Tyr Glu Lys Leu
100 105 110
Gly Leu Asp Ala Leu Val Thr Leu Gly Gly Gly Gly Thr Ala Lys Asn
115 120 125
Ala

<210> 59
<211> 417
<212> DNA
<213> Homo sapiens

<400> 59
ggtaccatcg gagctcgaca agaaatggtt gggtgaagtc gtggcttctg ctccacccag
60
tgccctcatg ggtcagccca cctgaatatc ttcatgcctg tgcatttctc ctgatgttca
120
cgtgtgccct gtgtttttac gcatctgtga tcgtgcaccc acgcgtctca gagaggagcc
180
cgtttgggaa tccggagaat gtgcgctggc ggaagagcgt cacacactgg aagcaaacct
240
cagaccgcgt ggacaagacc aaggatgaaa tggaacacga ggccttggtg gaagggaacc
300

tggcaaccga ggcaagccta gtggttctgg acacactgga gatcatcgtg cagacggtga
360
tgctttcaga agcccgggag agcgtcttgg gggcagtgct gaaggttgtg ctgtaca
417

<210> 60
<211> 101
<212> PRT
<213> Homo sapiens

<400> 60
Met Phe Thr Cys Ala Leu Cys Phe Tyr Ala Ser Val Ile Val His Pro
1 5 10 15
Arg Val Ser Glu Arg Ser Pro Phe Gly Asn Pro Glu Asn Val Arg Trp
20 25 30
Arg Lys Ser Val Thr His Trp Lys Gln Thr Ser Asp Arg Val Asp Lys
35 40 45
Thr Lys Asp Glu Met Glu His Glu Ala Leu Val Glu Gly Asn Leu Ala
50 55 60
Thr Glu Ala Ser Leu Val Val Leu Asp Thr Leu Glu Ile Ile Val Gln
65 70 75 80
Thr Val Met Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Ala Val Leu
85 90 95
Lys Val Val Leu Tyr
100

<210> 61
<211> 304
<212> DNA
<213> Homo sapiens

<400> 61
agatcttcac agccttagac ttttttcatg ggtgccttac agttttggag gtccctatcc
60
gcacacatat ttgcaggctt ggagagagtg tgtgggggca tgtactttcg gtgggtcaag
120
tatgaagaag caggccttat aaacacatat tctgacctta acctgtactt cagaagagga
180
ccgctgactc accaaggagg cctgaaggac aaggcagcat ctctgtcttc acatgagtcc
240
tcccctagac cgggcccatg gccaggcctg accacagagc tcccattgcc tttcctgcac
300
gcgt
304

<210> 62
<211> 92
<212> PRT
<213> Homo sapiens

<400> 62
Met Gly Ala Leu Gln Phe Trp Arg Ser Leu Ser Ala His Ile Phe Ala
1 5 10 15

```
Gly Leu Glu Arg Val Cys Gly Gly Met Tyr Phe Arg Trp Val Lys Tyr
20                  25                  30
Glu Glu Ala Gly Leu Ile Asn Thr Tyr Ser Asp Leu Asn Leu Tyr Phe
        35                  40                  45
Arg Arg Gly Pro Leu Thr His Gln Gly Gly Leu Lys Asp Lys Ala Ala
    50                  55                  60
Ser Leu Ser Ser His Glu Ser Ser Pro Arg Pro Gly Pro Trp Pro Gly
65                  70                  75                  80
Leu Thr Thr Glu Leu Pro Leu Pro Phe Leu His Ala
                85                  90
```

<210> 63
<211> 577
<212> DNA
<213> Homo sapiens

<400> 63
cgcgtcaagg gggtctacac cgggacgatt aacgcctcgg tgggagtatt catcaccgcg
60
ctgacggtgc tagctgggtg gctcacccta gccgggcgta tcagtgtcgg ggaactcgtc
120
accgtggtcg ggctggccca aaccctcggc cctccgctgc gagcactggg cgtcgacacc
180
gcgacgatgt tggccaccgc ccacgcctcc ggggaccgat tctgtgagtt gcgtgatagc
240
ccggcagcct ggcagatcca ccccgacgac ggtgcccgca ccacaccggg tgatggcccg
300
gtggagttgc acatcccggt cagggatttc cagcttgacg tcgccggcgg cacccatgtg
360
ggtatcatgg cgcctcaatc ggtctgtgac gccttggccg aggcgataga ccacggctcc
420
gagaccgtct tgaatggggt tcccgccagt cgcctcaacc ctgcccaacg gcgtcgtctg
480
gtgctggtgg ctccccgctc ccccgaactg ttcgacgata ctgcccgtgc gaacatcgtg
540
cttgacagcc agacgactgt cgccaggctg aatgcat
577

<210> 64
<211> 192
<212> PRT
<213> Homo sapiens

<400> 64
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Arg Val Lys Gly Val Tyr Thr Gly Thr Ile Asn Ala Ser Val Gly Val
 1               5                  10                  15
Phe Ile Thr Ala Leu Thr Val Leu Ala Gly Trp Leu Thr Leu Ala Gly
            20                  25                  30
Arg Ile Ser Val Gly Glu Leu Val Thr Val Val Gly Leu Ala Gln Thr
        35                  40                  45
Leu Gly Pro Pro Leu Arg Ala Leu Gly Val Asp Thr Ala Thr Met Leu
    50                  55                  60
Ala Thr Ala His Ala Ser Gly Asp Arg Phe Cys Glu Leu Arg Asp Ser
65                  70                  75                  80
```

```
Pro Ala Ala Trp Gln Ile His Pro Asp Asp Gly Ala Arg Thr Thr Pro
                85                  90                  95
Gly Asp Gly Pro Val Glu Leu His Ile Pro Val Arg Asp Phe Gln Leu
            100                 105                 110
Asp Val Ala Gly Gly Thr His Val Gly Ile Met Ala Pro Gln Ser Val
        115                 120                 125
Cys Asp Ala Leu Ala Glu Ala Ile Asp His Gly Ser Glu Thr Val Leu
    130                 135                 140
Asn Gly Val Pro Ala Ser Arg Leu Asn Pro Ala Gln Arg Arg Arg Leu
145                 150                 155                 160
Val Leu Val Ala Pro Arg Ser Pro Glu Leu Phe Asp Asp Thr Ala Arg
                165                 170                 175
Ala Asn Ile Val Leu Asp Ser Gln Thr Thr Val Ala Arg Leu Asn Ala
            180                 185                 190
```

<210> 65
<211> 339
<212> DNA
<213> Homo sapiens

<400> 65
gtcgaccgcg ccttgggatc gctcgaaggg gccagcctgg accaggtagc ggaagaagtc
60
aagaaggccg ctttcaagat cacccgcgcc gggcaactag tgggcaccat ggcctccgag
120
cgccttggcg taccttcgg catcatcgac ctttcgcttg cccctactgc cgaattggga
180
gattcggggg cccacatcct tgagcatatg ggattggacc aagtaggcac gcacggcaca
240
actgctgctt tggctctgct taacgacgcc gtaaagaaag gcggcatgat ggcctgcccc
300
cgcgtcggcg gtttgtctgg ctccttcatc ccgggctcc
339

<210> 66
<211> 113
<212> PRT
<213> Homo sapiens

<400> 66
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Val Asp Arg Ala Leu Gly Ser Leu Glu Gly Ala Ser Leu Asp Gln Val
 1               5                  10                  15
Ala Glu Glu Val Lys Lys Ala Ala Phe Lys Ile Thr Arg Ala Gly Gln
            20                  25                  30
Leu Val Gly Thr Met Ala Ser Glu Arg Leu Gly Val Pro Phe Gly Ile
        35                  40                  45
Ile Asp Leu Ser Leu Ala Pro Thr Ala Glu Leu Gly Asp Ser Gly Ala
    50                  55                  60
His Ile Leu Glu His Met Gly Leu Asp Gln Val Gly Thr His Gly Thr
65                  70                  75                  80
Thr Ala Ala Leu Ala Leu Leu Asn Asp Ala Val Lys Lys Gly Gly Met
                85                  90                  95
Met Ala Cys Pro Arg Val Gly Gly Leu Ser Gly Ser Phe Ile Pro Gly
            100                 105                 110
```

Ser

<210> 67
<211> 446
<212> DNA
<213> Homo sapiens

<400> 67
tgatcataaa ccacgcgtca ccgaggggat gtggcacacc tacctgcgcg tcgcagatgc
60
cgcacaggca cgggtcaggg gcgttcgcgg cgccagctgg cacaacttcg cgaccggtga
120
caaggggtcc ttcgacgcca acgagcttgc cgtaactcct gatactgaca ccgtcatcca
180
gggagtcggg cccgccctag ccctcctcga ttcagcgtgg ggacgccaga tccacgtgga
240
gacaacaggg tgtcccagtg ccgtggtctg gaatccacgc tcctcgtcga cacatgccga
300
taacccgaca gcccaggcat ggcgcgattt cgtatgcgtc gagaccgggg cctgcaagga
360
caatgcggtc attgttgccc cacacagcga cctcaccatg tccacacgga ttagcgtcga
420
aacgttgtga tcgctgcatg gatatt
446

<210> 68
<211> 133
<212> PRT
<213> Homo sapiens

<400> 68
Met Trp His Thr Tyr Leu Arg Val Ala Asp Ala Ala Gln Ala Arg Val
1 5 10 15
Arg Gly Val Arg Gly Ala Ser Trp His Asn Phe Ala Thr Gly Asp Lys
20 25 30
Gly Ser Phe Asp Ala Asn Glu Leu Ala Val Thr Pro Asp Thr Asp Thr
35 40 45
Val Ile Gln Gly Val Gly Pro Ala Leu Ala Leu Leu Asp Ser Ala Trp
50 55 60
Gly Arg Gln Ile His Val Glu Thr Thr Gly Cys Pro Ser Ala Val Val
65 70 75 80
Trp Asn Pro Arg Ser Ser Ser Thr His Ala Asp Asn Pro Thr Ala Gln
85 90 95
Ala Trp Arg Asp Phe Val Cys Val Glu Thr Gly Ala Cys Lys Asp Asn
100 105 110
Ala Val Ile Val Ala Pro His Ser Asp Leu Thr Met Ser Thr Arg Ile
115 120 125
Ser Val Glu Thr Leu
130

<210> 69
<211> 552
<212> DNA

<213> Homo sapiens

<400> 69
nnaagggtaa ggagaaaagc aaggaccttg caaagagagc ctctgtgccg gagaggctgg
60
ccctcaagga ggagccaaaa gaagacccca gtggagcagc tgtgcccgag atgccaaaaa
120
agtcctccaa gattgccagc ttcatcccca aaggggggaa gctcaacagt gccaagaagg
180
agcnccatgg ccccttccct cagtggaata ccaaaaccag gaatgaaaag catgcccggg
240
aaatccccaa gtgccccagc gccttccaag gaaggggagc ggagccggag tgggaagctg
300
agctcaggac tcccccagca gaagccccag ctggacggca gacactccag ttcctcttcc
360
agcctggcgt cctcagaagg aaaaggccca ggagggacca ccctgaacca cagcatcagc
420
agccagactg tcagtgggtc tgtcgggacc acccagacca caggaagcaa tnnaccgtca
480
gtgttcagct acctcagccc cagcagcaat acaaccatcc caacactgcc acggttgcac
540
ctttcctgta ca
552

<210> 70
<211> 184
<212> PRT
<213> Homo sapiens

<400> 70
Xaa Arg Val Arg Arg Lys Ala Arg Thr Leu Gln Arg Glu Pro Leu Cys
 1   5   10   15
Arg Arg Gly Trp Pro Ser Arg Arg Ser Gln Lys Lys Thr Pro Val Glu
            20   25   30
Gln Leu Cys Pro Arg Cys Gln Lys Ser Pro Pro Arg Leu Pro Ala Ser
        35   40   45
Ser Pro Lys Gly Gly Ser Ser Thr Val Pro Arg Arg Ser Xaa Met Ala
    50   55   60
Pro Ser Leu Ser Gly Ile Pro Lys Pro Gly Met Lys Ser Met Pro Gly
65   70   75   80
Lys Ser Pro Ser Ala Pro Ala Pro Ser Lys Glu Gly Glu Arg Ser Arg
                85   90   95
Ser Gly Lys Leu Ser Ser Gly Leu Pro Gln Gln Lys Pro Gln Leu Asp
            100   105   110
Gly Arg His Ser Ser Ser Ser Ser Ser Leu Ala Ser Ser Glu Gly Lys
        115   120   125
Gly Pro Gly Gly Thr Thr Leu Asn His Ser Ile Ser Ser Gln Thr Val
    130   135   140
Ser Gly Ser Val Gly Thr Thr Gln Thr Thr Gly Ser Asn Xaa Pro Ser
145   150   155   160
Val Phe Ser Tyr Leu Ser Pro Ser Ser Asn Thr Thr Ile Pro Thr Leu
                165   170   175
Pro Arg Leu His Leu Ser Cys Thr
            180

<210> 71
<211> 316
<212> DNA
<213> Homo sapiens

<400> 71
cgcgttgaaa tggcgttcga acttaaacgt ttacatattg actccgtgcc attaaacatt
60
ttgaatcctg ttaaagggac tccatttgaa agcaacgaag ctttacgtcc tttaaatatc
120
ttacgtacct tcgccgtatt ccgtttcatc ttgccaaacg cattgatacg aactgcaggt
180
ggccgcgaag taaatctacg agacttacaa gcttatgctc taaaaggtgg cctaaacggt
240
atcatggttg gtggctactt aactactggc ggtcgttcac ctcaagacga tctccaaatg
300
attcaagact tggagt
316

<210> 72
<211> 105
<212> PRT
<213> Homo sapiens

<400> 72
Arg Val Glu Met Ala Phe Glu Leu Lys Arg Leu His Ile Asp Ser Val
 1   5   10   15
Pro Leu Asn Ile Leu Asn Pro Val Lys Gly Thr Pro Phe Glu Ser Asn
            20   25   30
Glu Ala Leu Arg Pro Leu Asn Ile Leu Arg Thr Phe Ala Val Phe Arg
        35   40   45
Phe Ile Leu Pro Asn Ala Leu Ile Arg Thr Ala Gly Gly Arg Glu Val
    50   55   60
Asn Leu Arg Asp Leu Gln Ala Tyr Ala Leu Lys Gly Gly Leu Asn Gly
65   70   75   80
Ile Met Val Gly Gly Tyr Leu Thr Thr Gly Gly Arg Ser Pro Gln Asp
                85   90   95
Asp Leu Gln Met Ile Gln Asp Leu Glu
            100   105

<210> 73
<211> 384
<212> DNA
<213> Homo sapiens

<400> 73
nntaccggca agatcctggc cgaaggtgac gtcgaggttt ctgaggctat cgactttgct
60
gcttggtatg tcgaccgagc cgaggagctc gagggcgtcg acggtgccca gtttgtgccg
120
ccacgagtga ccgtcgtcac cccgccgtgg aacttcgccc tgtctattac cgccggatcc
180

acccttgccg ctctggccgc cggatcgtca gtactactca agcccgctcc acaggcccgc
240
cactgtgctg ccgtcatctc tgaatgcctg tgggaggctg ggatcccgcg ggacgttctg
300
cagctcgtcg atgttgagga aaatgaggct ggtaaacacc tggtgagcca ccccgaggtc
360
gatcgggtca tcctcacggg aggt
384

<210> 74
<211> 128
<212> PRT
<213> Homo sapiens

<400> 74
Xaa Thr Gly Lys Ile Leu Ala Glu Gly Asp Val Glu Val Ser Glu Ala
 1   5   10   15
Ile Asp Phe Ala Ala Trp Tyr Val Asp Arg Ala Glu Glu Leu Glu Gly
            20   25   30
Val Asp Gly Ala Gln Phe Val Pro Pro Arg Val Thr Val Val Thr Pro
        35   40   45
Pro Trp Asn Phe Ala Leu Ser Ile Thr Ala Gly Ser Thr Leu Ala Ala
    50   55   60
Leu Ala Ala Gly Ser Ser Val Leu Leu Lys Pro Ala Pro Gln Ala Arg
65   70   75   80
His Cys Ala Ala Val Ile Ser Glu Cys Leu Trp Glu Ala Gly Ile Pro
                85   90   95
Arg Asp Val Leu Gln Leu Val Asp Val Glu Glu Asn Glu Ala Gly Lys
            100   105   110
His Leu Val Ser His Pro Glu Val Asp Arg Val Ile Leu Thr Gly Gly
        115   120   125

<210> 75
<211> 405
<212> DNA
<213> Homo sapiens

<400> 75
gaattcgtct cggaatacac gctggaaaat tcggccgaga tgtccggggt gcgctcanac
60
cgcattgagg cgctggccga gctctatgcc gatcccaaga ccagggtggt gagcttctgg
120
accatgggct tcaaccagca cacccgcggc gtctggtgca acaatctcgt ctacaacatc
180
cacctgctga ccggaaaaat ctcgacgccc ggcaacagcc cgttctcgct gaccgggcag
240
ccatcggcct gcggcacggc gcgcgaggtc ggtaccttct cgcatcgcct gcccgccgac
300
atggtggtca ccagcaaggc gcaccgcgac atcgccgaga agatctggca gctgccggaa
360
ggaccagtcc ccgacaagcc cggctaccac gccgtgctgc agagc
405

<210> 76

<211> 135
<212> PRT
<213> Homo sapiens

<400> 76
Glu Phe Val Ser Glu Tyr Thr Leu Glu Asn Ser Ala Glu Met Ser Gly
1 5 10 15
Val Arg Ser Xaa Arg Ile Glu Ala Leu Ala Glu Leu Tyr Ala Asp Pro
20 25 30
Lys Thr Arg Val Val Ser Phe Trp Thr Met Gly Phe Asn Gln His Thr
35 40 45
Arg Gly Val Trp Cys Asn Asn Leu Val Tyr Asn Ile His Leu Leu Thr
50 55 60
Gly Lys Ile Ser Thr Pro Gly Asn Ser Pro Phe Ser Leu Thr Gly Gln
65 70 75 80
Pro Ser Ala Cys Gly Thr Ala Arg Glu Val Gly Thr Phe Ser His Arg
85 90 95
Leu Pro Ala Asp Met Val Val Thr Ser Lys Ala His Arg Asp Ile Ala
100 105 110
Glu Lys Ile Trp Gln Leu Pro Glu Gly Pro Val Pro Asp Lys Pro Gly
115 120 125
Tyr His Ala Val Leu Gln Ser
130 135

<210> 77
<211> 5816
<212> DNA
<213> Homo sapiens

<400> 77
gagcggcgcc ctgctctggc cgttgctccc gctcctgctc ctgctgctgt cggcgcggga
60
cggcgtgcgc gccgcgcagc ctcaggcccc gggttacttg attgcagctc cctctgtttt
120
tcgcgcgggc gtggaggaag tcatcagcgt gaccatcttt aactctccaa gggaagtcac
180
ggtccaggct cagctggtgg cccagggtga gccggtggtg cagagccagg gagccatcct
240
ggataaaggg acaatcaaac tcaaggtgcc cacgggcctc cggggccaag cgcttctgaa
300
agtgtggggc cgcggctggc aggcggagga ggggcccctc tttcacaacc agacctcggt
360
gaccgtggac ggccggggcg cttctgtatt catccagacg gacaagcctg tgtacagacc
420
ccagcaccga gtgctcataa gcatcttcac cgtctctcca aatctgaggc ctgtcaacga
480
gaagctggaa gcctacatcc tggacccccg aggctctcgg atgatagagt ggagacactt
540
aaagccgttc tgctgcggca tcaccaacat gagcttcccc ttgtccgacc agcctgtgtt
600
gggagaatgg ttcatttttg ttgaaatgca aggccacgcg tacaacaagt cttttgaagt
660
tcagaagtat gtgttgccca agtttgagct tctgattgac ccgccccggt atatccaaga
720

cctggacgcc tgtgagacag gcactgtgcg ggccaggtat acctttggga aacctgtggc
780
tggtgcctta atgatcaaca tgactgttaa tggtgtaggg tactacagcc acgaggtggg
840
acgccctgtc ctcagaacaa ccaagatcct cggctcccgg gacttcgaca tctgcgtgag
900
ggacatgatc ccagcggacg tccctgagca cttccggggc agggtcagca tctgggccat
960
ggtgaccagt gtggacggga gccagcaggt cgcgttcgat gactccaccc ccgtgcagag
1020
gcagctggtg gacatccggt actccaagga cacgaggaag cagttcaagc cgggcctggc
1080
ctacgtgggg aaggtggagc tatcctaccc cgatggcagc ccagctgagg gggtgacggt
1140
ccagattaag gcagagctga caccaaagga taacatctac accagtgaag ttgtgtccca
1200
gcgtggacta gtggggtttg aaatcccctc catccccacg tcagcccagc acgtgtggct
1260
ggagaccaag gtgatggcac tgaacgggaa gcccgtgggg gctcagtacc tgcccagcta
1320
cctctccctc ggcagctggt actcccccag ccagtgctac ctgcagctgc agccaccctc
1380
ccacccactg caggttgggg aagaagccta tttttctgtg aagtccacat gtccctgcaa
1440
ctttaccctg tactacgagg tggctgcacg gggcaatatt gtgctatcgg gccagcagcc
1500
tgcccacacc acccagcagc gaagcaagcg ggcggccccc gccctggaga aaccgattcg
1560
tttaacacac ctttctgaga cagagccccc accagcccca gaagctgagg tcgacgtgtg
1620
tgtgacctct cttcatctgg ccgtgacccc cagcatggtc ccccttggtc gcctgctggt
1680
cttctacgtc agggagaatg gagaaggggt cgccgacagc cttcagtttg cagtcgagac
1740
cttcttcgaa aaccaggttt cagtgacgta ttcagcaaat gagacccaac ctggggaggt
1800
tgtcgacctg cggatcaggg ctgcaagggg cagctgtgtg tgcgtcgccg cagttgataa
1860
gagtgtctac ctgctcaggt ctgggttccg gctgactcct gcccaggttt tccaggaact
1920
ggaagattat gatgtttctg attcctttgg cgtgtccagg gaggatggtc ctttttggtg
1980
ggctgggctg acggcacaac gacgccggcg ctcctctgtc ttcccgtggc cttggggcat
2040
caccaaggac tctgggtttg ccttcaccga aacgggactg gtggtgatga ccgaccgagt
2100
gagcctgaac caccggcagg acggtggcct ctacaccgat gaggctgtcc ccgctttcca
2160
gccccacaca gggagcctgg tggcagtggc tccttccagg caccccccca gaacagagaa
2220
gagaaaaagg actttcttcc ccgaaacatg gatttggcat tgtctcaaca tcagtgaccc
2280
atctggtgag gggacactca gtgtgaaggt cccggactcc atcaccagct gggtgggtga
2340

ggccgtggcc ctgtccacct ctcagggctt aggcatcgcc gagccctccc tgctgaagac
2400
cttcaagccc ttcttcgtgg acttcatgct ccccgctctc atcatccgtg gggagcaggt
2460
caagatcccg ctcagtgtct acaactacat gggcacctgc gctgaggtgt acatgaagct
2520
ctcggttccc aagggcatcc agtttgttgg gcatcctggc aaacgccatg tgaccaagaa
2580
gatgtgtgtg gcccccgggg aggctgagcc catctgggtc gttctgtcct tcagcgacct
2640
gggactcaac aacatcacgg ccaaagccct tgcttacgga gacacaaatt gctgccggga
2700
tgggaggtcc agcaaacacc ctgaggagaa tcacgccgac aggagggtcc ccatcggggt
2760
ggatcacgtc aggcgcagtg tgatggttga ggcggaagga gtcccccggg cgtacaccta
2820
cagcgcattc ttctgtccca gtgagagagt ccacatctcc acccccaaca agtatgagtt
2880
ccagtatgtg cagcggccac tgcgcctcac ccgctttgat gtggctgtgc gagctcacaa
2940
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<210> 78
<211> 799
<212> PRT
<213> Homo sapiens

<400> 78
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20 25 30
Thr Ala Ser Ile Ile Gly Asp Val Met Gly Pro Thr Leu Asn His Leu
35 40 45
Asn Asn Leu Leu Arg Leu Pro Phe Gly Cys Gly Glu Gln Asn Met Ile
50 55 60
His Phe Ala Pro Asn Val Phe Val Leu Lys Tyr Leu Gln Lys Thr Gln
65 70 75 80
Gln Leu Ser Pro Glu Val Glu Arg Glu Thr Thr Asp Tyr Leu Val Gln
85 90 95
Gly Tyr Gln Arg Gln Leu Thr Tyr Lys Arg Gln Asp Gly Ser Tyr Ser
100 105 110
Ala Phe Gly Glu Arg Asp Ala Ser Gly Ser Met Trp Leu Thr Ala Phe
115 120 125
Val Leu Lys Ser Phe Ala Gln Ala Arg Ser Phe Ile Phe Val Asp Pro
130 135 140
Arg Glu Leu Ala Ala Ala Lys Ser Trp Ile Ile Gln Gln Gln Gln Ala
145 150 155 160
Asp Gly Ser Phe Leu Ala Val Gly Arg Val Leu Asn Lys Asp Ile Gln
165 170 175
Gly Gly Ile His Gly Ile Val Pro Leu Thr Ala Tyr Val Val Val Ala
180 185 190
Leu Leu Glu Thr Gly Thr Ala Ser Glu Glu Glu Arg Gly Ser Thr Asp
195 200 205
Lys Ala Arg His Phe Leu Glu Ser Ala Ala Pro Leu Ala Met Asp Pro
210 215 220
Tyr Ser Cys Ala Leu Thr Thr Tyr Ala Leu Thr Leu Leu Arg Ser Pro
225 230 235 240
Ala Ala Pro Glu Ala Leu Arg Lys Leu Arg Ser Leu Ala Ile Met Arg
245 250 255
Asp Gly Val Thr His Trp Ser Leu Ser Asn Ser Trp Asp Val Asp Lys
260 265 270
Gly Thr Phe Leu Ser Phe Ser Asp Arg Val Ser Gln Ser Val Val Ser
275 280 285
Ala Glu Val Glu Met Thr Ala Tyr Ala Leu Leu Thr Tyr Thr Leu Leu
290 295 300
Gly Asp Val Ala Ala Ala Leu Pro Val Val Lys Trp Leu Ser Gln Gln

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305                 310                 315                 320
Arg Asn Ala Leu Gly Gly Phe Ser Ser Thr Gln Asp Thr Cys Val Ala
                325                 330                 335
Leu Gln Ala Leu Ala Glu Tyr Ala Ile Leu Ser Tyr Ala Gly Gly Ile
            340                 345                 350
Asn Leu Thr Val Ser Leu Ala Ser Thr Asn Leu Asp Tyr Gln Glu Thr
        355                 360                 365
Phe Glu Leu His Arg Thr Asn Gln Lys Val Leu Gln Thr Ala Ala Ile
    370                 375                 380
Pro Ser Leu Pro Thr Gly Leu Phe Val Ser Ala Lys Gly Asp Gly Cys
385                 390                 395                 400
Cys Leu Met Gln Ile Asp Val Thr Tyr Asn Val Pro Asp Pro Val Ala
                405                 410                 415
Lys Pro Ala Phe Gln Leu Leu Val Ser Leu Gln Glu Pro Glu Ala Gln
            420                 425                 430
Gly Arg Pro Pro Pro Met Pro Ala Ser Ala Ala Glu Gly Ser Arg Gly
        435                 440                 445
Asp Trp Pro Pro Ala Asp Asp Asp Asp Pro Ala Ala Asp Gln His His
    450                 455                 460
Gln Glu Tyr Lys Val Met Leu Glu Val Cys Thr Arg Trp Leu His Ala
465                 470                 475                 480
Gly Ser Ser Asn Met Ala Val Leu Glu Val Pro Leu Leu Ser Gly Phe
                485                 490                 495
Arg Ala Asp Ile Glu Ser Leu Glu Gln Leu Leu Leu Asp Lys His Met
            500                 505                 510
Gly Met Lys Arg Tyr Glu Val Ala Gly Arg Arg Val Leu Phe Tyr Phe
        515                 520                 525
Asp Glu Ile Pro Ser Arg Cys Leu Thr Cys Val Arg Phe Arg Ala Leu
    530                 535                 540
Arg Glu Cys Val Val Gly Arg Thr Ser Ala Leu Pro Val Ser Val Tyr
545                 550                 555                 560
Asp Tyr Tyr Glu Pro Ala Phe Glu Ala Thr Arg Phe Tyr Asn Val Ser
                565                 570                 575
Thr His Ser Pro Leu Ala Arg Glu Leu Cys Ala Gly Pro Ala Cys Asn
            580                 585                 590
Glu Val Glu Arg Ala Pro Ala Arg Gly Pro Gly Trp Phe Pro Gly Glu
        595                 600                 605
Ser Gly Pro Ala Val Ala Pro Glu Glu Gly Ala Ala Ile Ala Arg Cys
    610                 615                 620
Gly Cys Asp His Asp Cys Gly Ala Gln Gly Asn Pro Val Cys Gly Ser
625                 630                 635                 640
Asp Gly Val Val Tyr Ala Ser Ala Cys Arg Leu Arg Glu Ala Ala Cys
                645                 650                 655
Arg Gln Ala Ala Pro Leu Glu Pro Ala Pro Pro Ser Cys Cys Ala Leu
            660                 665                 670
Glu Gln Arg Leu Pro Ala Ser Ser Ser Ser Thr Tyr Gly Asp Asp Leu
        675                 680                 685
Ala Ser Val Ala Pro Gly Pro Leu Gln Gln Asp Val Lys Leu Asn Gly
    690                 695                 700
Ala Gly Leu Glu Val Glu Asp Ser Asp Pro Glu Pro Glu Gly Glu Ala
705                 710                 715                 720
Glu Asp Arg Val Thr Ala Gly Pro Arg Pro Pro Val Ser Ser Gly Asn
                725                 730                 735
Leu Glu Ser Ser Thr Gln Ser Ala Ser Pro Phe His Arg Trp Gly Gln
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            740                 745                 750
Thr Pro Ala Pro Gln Arg His Ser Gly Arg Val Val Gly Ala His Arg
        755                 760                 765
Pro Gly Leu Leu Ser Pro Val Phe Val Tyr Ser Pro Ala Phe Gln Ser
    770                 775                 780
Gly Gly Glu Glu Gly Leu Trp Met Ser Asn Thr Cys Thr Leu Arg
785                 790                 795

<210> 79
<211> 346
<212> DNA
<213> Homo sapiens

<400> 79
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120
ccgatgcaac ggcatcaata ctcaaggcca tgaagtcgtt ggtgcggctc tggaagtact
180
tcaccgcgcc ttccgacaag cccacgtcct tgagcaggaa gtcgcggtag ctggtggccg
240
ccagatactc ggctttttct tcggcggact tgcccggcag gtaatccttg ggcgcgacgt
300
gcatggcgat caatgcccgg ctgtccgctt ccggncnnnc cnncnn
346

<210> 80
<211> 101
<212> PRT
<213> Homo sapiens

<400> 80
Met His Val Ala Pro Lys Asp Tyr Leu Pro Gly Lys Ser Ala Glu Glu
 1               5                  10                  15
Lys Ala Glu Tyr Leu Ala Ala Thr Ser Tyr Arg Asp Phe Leu Leu Lys
            20                  25                  30
Asp Val Gly Leu Ser Glu Gly Ala Val Lys Tyr Phe Gln Ser Arg Thr
        35                  40                  45
Asn Asp Phe Met Ala Leu Ser Ile Asp Ala Val Ala Ser Ala Asp Ala
    50                  55                  60
Tyr Ser Val Gly Phe Pro Gly Phe Gly Gly Met Asn Leu Ala Pro Ile
65                  70                  75                  80
Ser Glu Glu Ala Ala Ala Glu Met Glu Glu Pro Tyr Ile Tyr His Phe
                85                  90                  95
Pro Asp Gly Asn Ala
            100

<210> 81
<211> 429
<212> DNA
<213> Homo sapiens

<400> 81
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120
cctctatgag tggaatccag tctcatggcc ccccccatgg ctcctgttac cctggaggag
180
gctactccat gaggctggct ccggtggcac tgcctcgggg ctgcatgtac atgtgtgtgc
240
atgnntgtgt gcatgtgcgt gtgcacgtgt nngtgtgtgc ccgtgtgcat gtgcccgtgt
300
gcgtgtctgt gctgtgtgtg tgcgtgcatg tgtgcgtgtc tgtgcgtgnc tgtgtgtgtg
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cgtgcatgtg tgtgcacgtg tgtgcatgtg cacgtgtgcg cacccgtgtg catgtccgtg
420
tgcacgcgt
429

<210> 82
<211> 79
<212> PRT
<213> Homo sapiens

<400> 82
Gly Trp Leu Arg Trp His Cys Leu Gly Ala Ala Cys Thr Cys Val Cys
1 5 10 15
Met Xaa Val Cys Met Cys Val Cys Thr Cys Xaa Cys Val Pro Val Cys
20 25 30
Met Cys Pro Cys Ala Cys Leu Cys Cys Val Cys Ala Cys Met Cys Ala
35 40 45
Cys Leu Cys Val Xaa Val Cys Val Arg Ala Cys Val Cys Thr Cys Val
50 55 60
His Val His Val Cys Ala Pro Val Cys Met Ser Val Cys Thr Arg
65 70 75

<210> 83
<211> 411
<212> DNA
<213> Homo sapiens

<400> 83
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cgtgcgctct ttaaaaagcg caaaggcttt tataagttcg atgtgctttt tttcaggccc
120
ggaaagacgc gatccgtaga taaaataggg ccgctttatc gcaaatggct ttatggttac
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240
gatttcgatt ttcgctttgt cgatgccaag ccctatcaaa tcgtttcgca aaaactcgct
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360
gtcgctcttt tctttgagca tgacggaaac gatggaattg acgacggcga c
411

<210> 84
<211> 127
<212> PRT
<213> Homo sapiens

<400> 84
Met Leu Lys Glu Lys Ser Asp Arg Met Met Arg Met Gln Ile Lys Arg
1 5 10 15
Gly Leu Thr Lys Val Gln Lys Ile Val Ala Ala Ser Glu Phe Leu Arg
20 25 30
Asn Asp Leu Ile Gly Leu Gly Ile Asp Lys Ala Lys Ile Glu Ile Ile
35 40 45
His Asn Gly Ile Asp His Arg Pro Phe Phe Pro Gln Leu Gln Ile Asp
50 55 60
Ala Glu Thr Val Thr Ile Lys Pro Phe Ala Ile Lys Arg Pro Tyr Phe
65 70 75 80
Ile Tyr Gly Ser Arg Leu Ser Gly Pro Glu Lys Lys His Ile Glu Leu
85 90 95
Ile Lys Ala Phe Ala Leu Phe Lys Glu Arg Thr Lys Ser Pro His Pro
100 105 110
Leu Val Ile Ala Gly Ala Glu Gly Pro Ser Ser Glu Glu Val His
115 120 125

<210> 85
<211> 333
<212> DNA
<213> Homo sapiens

<400> 85
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120
acccagcgtt tcctggtgga gaacggagta ccggcggaaa agatcaacaa ggtgctggaa
180
ggccgcccgc acattgttga cgcaattacc aacggcgagg tgcaactcgt tttcaatacc
240
accgaggggc cacaggcgct ggctgacagc cgctcgttgc gacgcgctgc cctcttgcat
300
aaagtgccat attacaccac tctttcaggt gca
333

<210> 86
<211> 111
<212> PRT
<213> Homo sapiens

<400> 86
Xaa Arg Val Pro Arg Lys Gly Thr Met Phe Val Ser Val Arg Glu Thr
1 5 10 15
Asp Lys Ala Arg Ile Leu Asp Ala Val Lys Leu Leu Ser Ser Leu Gly
20 25 30
Phe Lys Val Ile Ala Thr Ser Gly Thr Gln Arg Phe Leu Val Glu Asn

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        35                  40                  45
Gly Val Pro Ala Glu Lys Ile Asn Lys Val Leu Glu Gly Arg Pro His
    50                  55                  60
Ile Val Asp Ala Ile Thr Asn Gly Glu Val Gln Leu Val Phe Asn Thr
65                  70                  75                  80
Thr Glu Gly Pro Gln Ala Leu Ala Asp Ser Arg Ser Leu Arg Arg Ala
                85                  90                  95
Ala Leu Leu His Lys Val Pro Tyr Tyr Thr Thr Leu Ser Gly Ala
            100                 105                 110
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<210> 87
<211> 355
<212> DNA
<213> Homo sapiens

<400> 87
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ctcctgagcg atgttcattc ggtaggggta cagggtgacg ggcgtactta tggttctccc
120
attgtgcttc gcccggtgac gagtgaggac gccatgactg cggactgggc acgtatccca
180
tatgacgtac tggaaaagat ctcgactcgc attacgaatg cgtgtccgca aatcaaccgg
240
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300
caccgtgaac atgacatggc ccgcaccttt cttggggcgg gccatgccgt gttag
355

<210> 88
<211> 96
<212> PRT
<213> Homo sapiens

<400> 88
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Thr Arg Glu Glu Met Gly Ala Ala Gly Leu Asp Arg Lys Val Trp Gln
 1               5                  10                  15
Cys Pro Val Val Leu Leu Ser Asp Val His Ser Val Gly Val Gln Gly
            20                  25                  30
Asp Gly Arg Thr Tyr Gly Ser Pro Ile Val Leu Arg Pro Val Thr Ser
        35                  40                  45
Glu Asp Ala Met Thr Ala Asp Trp Ala Arg Ile Pro Tyr Asp Val Leu
    50                  55                  60
Glu Lys Ile Ser Thr Arg Ile Thr Asn Ala Cys Pro Gln Ile Asn Arg
65                  70                  75                  80
Val Val Leu Asp Ile Thr Ser Lys Pro Pro Ala Thr Ile Glu Trp Glu
                85                  90                  95
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<210> 89
<211> 351
<212> DNA
<213> Homo sapiens

<400> 89

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120
ggtgattgga taaggccaga gggttgggcg gggttctgcc cctgctgaag cctggtgggg
180
cccaggtctg tgatctggga ccggaacaac acatctgctc tgggcctgct ggatgtggcg
240
caagccctgg aacagaacca cagcctcaag tccatgccgc tgccactgaa tgacgtaacc
300
caggctcatc gcagccggcc agaactcaca actcgagcgg tccatcagat c
351

<210> 90
<211> 61
<212> PRT
<213> Homo sapiens

<400> 90
Ser Leu Val Gly Pro Arg Ser Val Ile Trp Asp Arg Asn Asn Thr Ser
1 5 10 15
Ala Leu Gly Leu Leu Asp Val Ala Gln Ala Leu Glu Gln Asn His Ser
20 25 30
Leu Lys Ser Met Pro Leu Pro Leu Asn Asp Val Thr Gln Ala His Arg
35 40 45
Ser Arg Pro Glu Leu Thr Thr Arg Ala Val His Gln Ile
50 55 60

<210> 91
<211> 327
<212> DNA
<213> Homo sapiens

<400> 91
nggtgggtcc tctcgcagga caggtaatcc tgagacctac gcagctccct ggagctctgc
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acgtcgaagc ccagcagggc ctcctgcagg tccctggggc agccagcaca cacaaagtcc
120
cggaaggggc tgtagactcc ctgccagcgg ctttcccggg gaaggcaccc acgcccagct
180
gcctcttgca ggtactgctc gggtctggtg ggagggcagc cgtgtccagc acaccctgtg
240
tgtgcagtcc tctccctgcc ccactgccga acgagccctc cacggtgaag ccattgggga
300
acgtgacctt gcccttcccc atgaggt
327

<210> 92
<211> 107
<212> PRT
<213> Homo sapiens

<400> 92
Met Gly Lys Gly Lys Val Thr Phe Pro Asn Gly Phe Thr Val Glu Gly

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 1               5                  10                  15
Ser Phe Gly Ser Gly Ala Gly Arg Gly Leu His Thr Gln Gly Val Leu
            20                  25                  30
Asp Thr Ala Ala Leu Pro Pro Asp Pro Ser Ser Thr Cys Lys Arg Gln
        35                  40                  45
Leu Gly Val Gly Ala Phe Pro Gly Lys Ala Ala Gly Arg Glu Ser Thr
    50                  55                  60
Ala Pro Ser Gly Thr Leu Cys Val Leu Ala Ala Pro Gly Thr Cys Arg
65                  70                  75                  80
Arg Pro Cys Trp Ala Ser Thr Cys Arg Ala Pro Gly Ser Cys Val Gly
                85                  90                  95
Leu Arg Ile Thr Cys Pro Ala Arg Gly Pro Thr
            100                 105
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<210> 93
<211> 394
<212> DNA
<213> Homo sapiens

<400> 93
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atgctcgaat gggacggcgg acatgagcaa taggccgcca aagcacagcg agaggaaggc
120
ggcgcgctct gcggcctcgc ggatgaagga ggggtggtcg cgcaagagac gccccgcgcc
180
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240
gctctatttc gaggctatca ggttgcgtgt caacaaccgt tatcacggcc agtgggtgac
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aatggaagtt gtcgttaccg gcaagcatac caggggactt ctcgatcgtg cagtcactct
360
ggcggaagaa agtgccacag gattcactca cgta
394

<210> 94
<211> 109
<212> PRT
<213> Homo sapiens

<400> 94
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Met Leu Ala Gly Asn Asp Asn Phe His Cys His Pro Leu Ala Val Ile
 1               5                  10                  15
Thr Val Val Asp Thr Gln Pro Asp Ser Leu Glu Ile Glu Arg Phe Arg
            20                  25                  30
Phe Arg Thr Leu Gly His Asp Gln Val Ala Pro Gly Ile Tyr Arg Tyr
        35                  40                  45
Lys Arg Arg Gly Ala Ser Leu Ala Arg Pro Pro Leu Leu His Pro Arg
    50                  55                  60
Gly Arg Arg Ala Arg Arg Leu Pro Leu Ala Val Leu Trp Arg Pro Ile
65                  70                  75                  80
Ala His Val Arg Arg Pro Ile Arg Ala Cys Cys Ser Gly Met Gly Pro
                85                  90                  95
His Arg Asn Ala Pro Arg Gly Thr Ala Cys Arg Thr Arg
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100 105

<210> 95
<211> 531
<212> DNA
<213> Homo sapiens

<400> 95
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120
ccaaattgag gtgacagaag gaagacaaga ggtgtaagct ggagagggaa gggaagaaat
180
cagtggcttt ggccagcctc tgtgccaccc agtacgacag aggagtggga actggccctc
240
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360
gctgagcatg gagctcaccc catgccatag ggtgtgggaa gagggcacag gaggcctcat
420
ccatgggggа aagggttgag gatggacatg ggtggggaga gggcatagac atcccttcct
480
aatctctgtt cccaccacat ttcataggag atgagttagg agatgacagc t
531

<210> 96
<211> 124
<212> PRT
<213> Homo sapiens

<400> 96
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1 5 10 15
Ser Met Leu Ser Leu Ser Glu Leu Leu Ser Phe Pro Val Cys Thr Thr
20 25 30
Gly Thr Pro Met Leu Ser Val Arg Leu Glu Glu Val Met Ser Arg Trp
35 40 45
His Asn Val Gln Cys Leu Trp Pro Ser Arg Ala Pro Glu Gly Gln Phe
50 55 60
Pro Leu Leu Cys Arg Thr Gly Trp His Arg Gly Trp Pro Lys Pro Leu
65 70 75 80
Ile Ser Ser Leu Pro Ser Pro Ala Tyr Thr Ser Cys Leu Pro Ser Val
85 90 95
Thr Ser Ile Trp Gly Gly Tyr Asn Phe Thr Gly Val Thr His Pro Arg
100 105 110
Pro Val His Phe Arg Ile Gln Ala Lys Phe Pro Glu
115 120

<210> 97
<211> 405
<212> DNA
<213> Homo sapiens

<400> 97
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tcgcggtgcc ttgcgcgcgg gctggtaggt ggagaagccg cgcgagtacg cgccgtagag
120
cgacatcgtg tctgagacgt cgaagctcag gcccagcttt ggcgtccagg cgcgctcggt
180
cggtccgccc tcttgcggca attgattcag cgcaatcccg gccatcacat gccagcgctt
240
gtccagggtc atgaaatcct gggcataggc gcgcgaggag cgcagcggcg aattggacag
300
gcgctcgata ttgggcgtga tgtccgaaga cgggaacggg acccgggggg agaagacgtt
360
gcccgggaaa agatcccccg acgccatcgt ggtgtcgacc gagat
405

<210> 98
<211> 122
<212> PRT
<213> Homo sapiens

<400> 98
Met Ala Ser Gly Asp Leu Phe Pro Gly Asn Val Phe Ser Pro Arg Val
 1   5   10   15
Pro Phe Pro Ser Ser Asp Ile Thr Pro Asn Ile Glu Arg Leu Ser Asn
            20   25   30
Ser Pro Leu Arg Ser Ser Arg Ala Tyr Ala Gln Asp Phe Met Thr Leu
        35   40   45
Asp Lys Arg Trp His Val Met Ala Gly Ile Ala Leu Asn Gln Leu Pro
    50   55   60
Gln Glu Gly Gly Pro Thr Glu Arg Ala Trp Thr Pro Lys Leu Gly Leu
65   70   75   80
Ser Phe Asp Val Ser Asp Thr Met Ser Leu Tyr Gly Ala Tyr Ser Arg
                85   90   95
Gly Phe Ser Thr Tyr Gln Pro Ala Arg Lys Ala Pro Arg Ala Tyr Gly
            100   105   110
Pro Ser Ala Ala Arg Pro Ser Lys Arg Glu
        115   120

<210> 99
<211> 545
<212> DNA
<213> Homo sapiens

<400> 99
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tgccccgacg acccagcaaa cgtccccggc tgttcctcat tgaccacgcc gaccggatcg
120
tcgatcccat cactcgggat ttgctggaat ccctggttcg cgaagccggc gacgctgcgg
180
tgatcttggg tgcccagcgt cgcggtcgca tcgattggct ctccccacag atcatccaca
240

acctggccga acaccatttt gagtcgtcct ctggaggtac tcgatgatga ctgaacgttc
300
ccattccacg atcaggttaa ggtggccggc ggtggtggtt ctcgtcctcg ttccgctgct
360
ggtggtcgcc ggattggtcc gggacgacct ggcataccac cgaccggttg ggccgggtga
420
aagcggccgt cgtcaacgag gacaaggccg tcaaggtgcg tggacaactg gttccgatgg
480
gccgccaact caccgccgcc ttgatggact ctggctcgca caccactgat ggccacaccg
540
tcgac
545

<210> 100
<211> 101
<212> PRT
<213> Homo sapiens

<400> 100
Met Gly Thr Phe Ser His His Arg Val Pro Pro Glu Asp Asp Ser Lys
 1   5   10   15
Trp Cys Ser Ala Arg Leu Trp Met Ile Cys Gly Glu Ser Gln Ser Met
            20   25   30
Arg Pro Arg Arg Trp Ala Pro Lys Ile Thr Ala Ala Ser Pro Ala Ser
        35   40   45
Arg Thr Arg Asp Ser Ser Lys Ser Arg Val Met Gly Ser Thr Ile Arg
    50   55   60
Ser Ala Trp Ser Met Arg Asn Ser Arg Gly Arg Leu Leu Gly Arg Arg
65   70   75   80
Gly Arg Trp Val Ser Thr Val Ile Ala Glu Arg Ser Ser Ser Thr Thr
                85   90   95
Ser Gly Ala Asp Ala
            100

<210> 101
<211> 619
<212> DNA
<213> Homo sapiens

<400> 101
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tcatgcacga tccggacttc gatccgatcc ccatggtgaa caaggagctt gacgccttcg
120
aagctgccgg gggtgactat ctcatcctcg ccacggattc cggacgcaag ggatacacga
180
ccgcccgtcc tcacgaggcc ggcggaaaac gctattacca acctggacca gatccgcgaa
240
gtctgcgcca gccgcaacgt caccgcctgt ctacaccccc attggggaac gatggtccag
300
aaccgtgacg aagtgatccg cgtgctcgag aactcctcga tcgggctgtg cctggacact
360
ggtcatctgg cctgtggtgg taccgatgtc gttgagctgg tgcgtaagta cgccaaccgc
420

gtcgacattg tccacgccaa agatgtccat aaggagatgg ccgacaagct tttgcctggc
480
gagatcacct ggtccgaagg cattcgcgcc gggatgttcg cacccatcgg cgacggtgat
540
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600
ctagagcagg acatcatga
619

<210> 102
<211> 173
<212> PRT
<213> Homo sapiens

<400> 102
Thr Arg Ser Leu Thr Pro Ser Lys Leu Pro Gly Val Thr Ile Ser Ser
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Ser Pro Arg Ile Pro Asp Ala Arg Asp Thr Arg Pro Pro Val Leu Thr
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Arg Pro Ala Glu Asn Ala Ile Thr Asn Leu Asp Gln Ile Arg Glu Val
35 40 45
Cys Ala Ser Arg Asn Val Thr Ala Cys Leu His Pro His Trp Gly Thr
50 55 60
Met Val Gln Asn Arg Asp Glu Val Ile Arg Val Leu Glu Asn Ser Ser
65 70 75 80
Ile Gly Leu Cys Leu Asp Thr Gly His Leu Ala Cys Gly Gly Thr Asp
85 90 95
Val Val Glu Leu Val Arg Lys Tyr Ala Asn Arg Val Asp Ile Val His
100 105 110
Ala Lys Asp Val His Lys Glu Met Ala Asp Lys Leu Leu Pro Gly Glu
115 120 125
Ile Thr Trp Ser Glu Gly Ile Arg Ala Gly Met Phe Ala Pro Ile Gly
130 135 140
Asp Gly Asp Ile Asp Phe Ala Ala Ile Val Arg Leu Leu Asp Glu Ala
145 150 155 160
Gly Phe Asp Gly Tyr Tyr Val Leu Glu Gln Asp Ile Met
165 170

<210> 103
<211> 321
<212> DNA
<213> Homo sapiens

<400> 103
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gccattgggg ggagacccct gccgtgggga aagaccctg ccatggggca gacccctgcc
120
actgggggga gacccctgcc gctgggggga gacccgagcc attgggggga gacccctgcc
180
atggggaaag acccctgcca ttgggggaga ntacctgcca ttgggggaga tccctgccgt
240
tgggggggaga tccctgctgt tgggggggaga ntccctcctg taggggaaga cccctgcagg
300

agtggttggg gcgaagaccc c
321

<210> 104
<211> 107
<212> PRT
<213> Homo sapiens

<400> 104
Xaa His Gly Gly Arg Gln Gln Pro Cys Gly Gly Asp Pro Ser His Trp
1 5 10 15
Gly Glu Thr Pro Ala Ile Gly Gly Arg Pro Leu Pro Trp Gly Lys Thr
20 25 30
Pro Ala Met Gly Gln Thr Pro Ala Thr Gly Gly Arg Pro Leu Pro Leu
35 40 45
Gly Gly Asp Pro Ser His Trp Gly Glu Thr Pro Ala Met Gly Lys Asp
50 55 60
Pro Cys His Trp Gly Arg Xaa Pro Ala Ile Gly Gly Asp Pro Cys Arg
65 70 75 80
Trp Gly Glu Ile Pro Ala Val Gly Gly Arg Xaa Pro Pro Val Gly Glu
85 90 95
Asp Pro Cys Arg Ser Gly Trp Gly Glu Asp Pro
100 105

<210> 105
<211> 344
<212> DNA
<213> Homo sapiens

<400> 105
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ccgggtcaac gagggtttgg cgcacggtcc actccgtggc gcccggggtg atgtgcaaca
120
gggcgggccc gcgcgcggcc gggcctgatt ccagcctctc gtgctcgtcc cagtacccat
180
ccagcgcatc gccccagcgg tcggcatccc agccgtggtc gccgtcgagc gcccccaggg
240
cctcaatgtc gtcatcggcg gccagttcca cccggcggaa catctcgttg cggaccatga
300
cccggaaggc gcgggaattc tcggtcagtt tcggcggtgc cggc
344

<210> 106
<211> 62
<212> PRT
<213> Homo sapiens

<400> 106
Cys Ala Thr Gly Arg Ala Arg Ala Arg Pro Gly Leu Ile Pro Ala Ser
1 5 10 15
Arg Ala Arg Pro Ser Thr His Pro Ala His Arg Pro Ser Gly Arg His
20 25 30
Pro Ser Arg Gly Arg Arg Arg Ala Pro Pro Gly Pro Gln Cys Arg His

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        35                  40                  45
Arg Arg Pro Val Pro Pro Gly Gly Thr Ser Arg Cys Gly Pro
    50                  55                  60

<210> 107
<211> 549
<212> DNA
<213> Homo sapiens

<400> 107
acgcgttcct cggacgctgc tagtttgagc gcacaggcat tgggcggggc tcacgggga
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gccgcttaat aaccgaccaa catgaaactc aagggctgcc ccttcctagc ggggaccctg
120
cacagacccg aaaataaggg gttttgctct gccctcctca gttcacgtgg gcaccttgga
180
acactgaaga aggcattttc cgaactcact gtcctacgga cttattctcc gcactgtttt
240
cgcctccttc gccctgttct cgtgactgac aggagcaggg gtcacaagca ggcagcccga
300
gagctctgct cacctggaaa agcatttttg tgtagcttaa atgtgaaggc ctcaggcagt
360
ggcctgttgt cctcctccac atgcgcccat cttcactctt tcatgtgact ggcctgtttt
420
tgaaggcaag gcccctgtca cccttggcta ggccaggtat gttctgcacc gaaaatggcc
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ctgccctctg cattggatgg ctagctctta ggttggttta ttttagcaaa taagcgttac
540
agggtaggc
549

<210> 108
<211> 108
<212> PRT
<213> Homo sapiens

<400> 108
Met Lys Leu Lys Gly Cys Pro Phe Leu Ala Gly Thr Leu His Arg Pro
 1               5                  10                  15
Glu Asn Lys Gly Phe Cys Ser Ala Leu Leu Ser Ser Arg Gly His Leu
            20                  25                  30
Gly Thr Leu Lys Lys Ala Phe Ser Glu Leu Thr Val Leu Arg Thr Tyr
        35                  40                  45
Ser Pro His Cys Phe Arg Leu Leu Arg Pro Val Leu Val Thr Asp Arg
    50                  55                  60
Ser Arg Gly His Lys Gln Ala Ala Arg Glu Leu Cys Ser Pro Gly Lys
65                  70                  75                  80
Ala Phe Leu Cys Ser Leu Asn Val Lys Ala Ser Gly Ser Gly Leu Leu
                85                  90                  95
Ser Ser Ser Thr Cys Ala His Leu His Ser Phe Met
            100                 105

<210> 109
<211> 748
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<212> DNA
<213> Homo sapiens

<400> 109
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aagtcagaag acttatttgt tctggtacct attctgctgt taataaattg ataaatgagt
120
gatattgggg taagttacca atttacttta cagcccttaa gtaaataatc tgctttcctc
180
agcatcatag acttttgaag aggattaatt aagcgcttaa aaaacctgta gactctatta
240
cagtcagtga aaggaataat tctctttaca aagtaaatgc agttgtttta ttttagacaa
300
gagtgttcta aacttcgtga agagttaagg cttcaacatg aagaggataa gaagtcagca
360
atgtctcaac ttttgcagtt gaaagatcga gagaaaaatg cagcaagaga ttcatggcag
420
aagaaagtag aagatctctt aaaccagatt tccttgctga aacagaatct ggagatacag
480
ctttcccagt ctcagacttc tttgcaacaa ctgcaagccc agtttacgca agaacgacag
540
cggcttacgc aagagcttga agaattagag gagcaacatc agcaaagaca caaatcatta
600
aaagaagcac atgtccttgc atttcaaact atggaagagg aaaaggaaaa ggagcaaaga
660
gctcttgaaa atcatttaca acagaagcat tctgcagagc ttcaatcact aaaagatgca
720
cacagagagt caatggaggg cttccgga
748

<210> 110
<211> 157
<212> PRT
<213> Homo sapiens

<400> 110
Met Gln Leu Phe Tyr Phe Arg Gln Glu Cys Ser Lys Leu Arg Glu Glu
 1   5   10   15
Leu Arg Leu Gln His Glu Glu Asp Lys Lys Ser Ala Met Ser Gln Leu
            20   25   30
Leu Gln Leu Lys Asp Arg Glu Lys Asn Ala Ala Arg Asp Ser Trp Gln
        35   40   45
Lys Lys Val Glu Asp Leu Leu Asn Gln Ile Ser Leu Leu Lys Gln Asn
    50   55   60
Leu Glu Ile Gln Leu Ser Gln Ser Gln Thr Ser Leu Gln Gln Leu Gln
65   70   75   80
Ala Gln Phe Thr Gln Glu Arg Gln Arg Leu Thr Gln Glu Leu Glu Glu
                85   90   95
Leu Glu Glu Gln His Gln Gln Arg His Lys Ser Leu Lys Glu Ala His
            100   105   110
Val Leu Ala Phe Gln Thr Met Glu Glu Glu Lys Glu Lys Glu Gln Arg
        115   120   125
Ala Leu Glu Asn His Leu Gln Gln Lys His Ser Ala Glu Leu Gln Ser

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    130                 135                 140
Leu Lys Asp Ala His Arg Glu Ser Met Glu Gly Phe Arg
145                 150                 155

<210> 111
<211> 429
<212> DNA
<213> Homo sapiens

<400> 111
gcgcgcccag agagtgcaca atggtgtcag gatatgggag ccaccggaat cattaaccat
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cgtgaaccgc tcgccccgca ggtcaacgac ttcgggatca ccgggttcga cggcattctc
120
tcggcttatn nacgccacca gcatncgact ttggctgaga tcatcgcacc gttcggacat
180
ctggtcatga tcgacggaac cgactcattc gatctcatgg ccttcaagtc aaagtcgtta
240
acggtgacca gcgagtcgat gttcagccgt ccacagttcg cgacgcccga cgtcgccgaa
300
caaggccggg cactggccag catcgccgac ctcgtcgaga aggggcagat ccgtccgacg
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atgacccgcc atatcgaggg tctgacaacc cagcatgtgc gtgaggccac cgcagccgtc
420
gagtccggc
429

<210> 112
<211> 143
<212> PRT
<213> Homo sapiens

<400> 112
Ala Arg Pro Glu Ser Ala Gln Trp Cys Gln Asp Met Gly Ala Thr Gly
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Ile Ile Asn His Arg Glu Pro Leu Ala Pro Gln Val Asn Asp Phe Gly
            20                  25                  30
Ile Thr Gly Phe Asp Gly Ile Leu Ser Ala Tyr Xaa Arg His Gln His
        35                  40                  45
Xaa Thr Leu Ala Glu Ile Ile Ala Pro Phe Gly His Leu Val Met Ile
    50                  55                  60
Asp Gly Thr Asp Ser Phe Asp Leu Met Ala Phe Lys Ser Lys Ser Leu
65                  70                  75                  80
Thr Val Thr Ser Glu Ser Met Phe Ser Arg Pro Gln Phe Ala Thr Pro
                85                  90                  95
Asp Val Ala Glu Gln Gly Arg Ala Leu Ala Ser Ile Ala Asp Leu Val
            100                 105                 110
Glu Lys Gly Gln Ile Arg Pro Thr Met Thr Arg His Ile Glu Gly Leu
        115                 120                 125
Thr Thr Gln His Val Arg Glu Ala Thr Ala Ala Val Glu Ser Gly
    130                 135                 140

<210> 113
<211> 382
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<212> DNA
<213> Homo sapiens

<400> 113
gtgcactgga cggatgctgg ggaactgagg cctgcccttc tccactcctg ctgcctctgt
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gtggaccgcc tgccacctgg cttcaacgat gtggacgctc tgtgccgggc gctgtcagct
120
gtccacagcc ccaccttctg ccagctggcg tgcggccagg atgggcagct gaagggcttc
180
gcggtgctgg agtatgagac ggctgagatg gcggaggagg cacagcagca ggcggacggc
240
ctgtccctgg ggggcagcca cctgcgagtc tccttctgcg cccctgggac ccccgggcgc
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360
ctccccgagc ccaacatcct gc
382

<210> 114
<211> 125
<212> PRT
<213> Homo sapiens

<400> 114
Met Leu Gly Ser Gly Arg Thr Pro Cys Pro Arg Leu Arg Ala Val Ala
 1   5   10   15
Trp Ala Thr Met Arg Ala Ala Ser Ile Leu Arg Pro Gly Val Pro Gly
            20   25   30
Ala Gln Lys Glu Thr Arg Arg Trp Leu Pro Pro Arg Asp Arg Pro Ser
        35   40   45
Ala Cys Cys Cys Ala Ser Ser Ala Ile Ser Ala Val Ser Tyr Ser Ser
    50   55   60
Thr Ala Lys Pro Phe Ser Cys Pro Ser Trp Pro His Ala Ser Trp Gln
65   70   75   80
Lys Val Gly Leu Trp Thr Ala Asp Ser Ala Arg His Arg Ala Ser Thr
                85   90   95
Ser Leu Lys Pro Gly Gly Arg Arg Ser Thr Gln Arg Gln Gln Glu Trp
            100   105   110
Arg Arg Ala Gly Leu Ser Ser Pro Ala Ser Val Gln Cys
        115   120   125

<210> 115
<211> 4798
<212> DNA
<213> Homo sapiens

<400> 115
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catttcactc cctgtttgga gccatgagtg gccccctgtt gccttcaaga ctgaagccat
120
ccccatcctt cctcccacca acctagaggc tttgcttcgt aaatgctggc cctttccttc
180

atgggctcca ccctctgagt gtgtcatgaa ctcttccact tccttgcctt ggttcgtatt
240
gggtcctctg cccgaggtca gagatttgga cgagcccttc tcctccatct tcacagtctc
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tataagaaaa agctagatct gtccatttta tttctagttt ttggaagaga tgtggataca
420
gagaaatatt actctactat tgaaaaaaat atatatcagt ctgattataa atgtcaactc
480
atactaagtc aatatcaggg aagcagtgtg gagaaggatg tggcaaactg gagattgctg
540
tttccataga aagagggcag ctaatgctta tctccagacc attgttatgc agtaatgtag
600
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660
tattactttt ggcagttaat tttaaaaatc accgtttagg ccaaaacaac atgacatttg
720
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780
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900
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960
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1020
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1140
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gcaaggaagt caaggaattg gggtttgaac ccaagtcgtc tcagttccat tccattgtcc
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2280
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4440
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4798

<210> 116
<211> 1062
<212> PRT
<213> Homo sapiens

<400> 116
Met Met Gly Thr Ser Gln Gly His Val Ala Arg Lys Ser Arg Asn Trp

```
 1               5                  10                  15
Gly Leu Asn Pro Ser Arg Leu Ser Ser Ile Pro Leu Ser Ser Thr Pro
            20                  25                  30
Cys His Leu Ser Pro Ser Ser Leu Ser Pro Phe Ser Val Ala Glu Arg
        35                  40                  45
Lys Pro Pro Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile
    50                  55                  60
Ala Gln Asn Glu Ser Pro Val Leu Gln Ser Gly His Trp Ser Glu Tyr
65                  70                  75                  80
Phe Arg Asn Phe Val Asp Ser Cys Leu Gln Lys Ile Pro Gln Asp Arg
                85                  90                  95
Pro Thr Ser Glu Val Leu Leu Lys His Arg Phe Val Leu Arg Glu Arg
            100                 105                 110
Pro Pro Thr Val Ile Met Asp Leu Ile Gln Arg Thr Lys Asp Ala Val
        115                 120                 125
Arg Glu Leu Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Ile Leu Phe
    130                 135                 140
Gln Glu Ala Pro Asn Gly Pro Gly Ala Glu Ala Pro Glu Glu Glu Glu
145                 150                 155                 160
Glu Ala Glu Pro Tyr Met His Arg Ala Gly Thr Leu Thr Ser Leu Glu
                165                 170                 175
Ser Ser His Ser Val Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser
            180                 185                 190
Ser Ser Val Asn Ser Leu Ala Asp Ala Ser Asp Asn Glu Glu Glu Glu
        195                 200                 205
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Pro Glu Ala Arg
    210                 215                 220
Glu Met Ala Met Met Gln Glu Gly Glu His Thr Val Thr Ser His Ser
225                 230                 235                 240
Ser Ile Ile His Arg Leu Pro Gly Ser Asp Asn Leu Tyr Asp Asp Pro
                245                 250                 255
Tyr Gln Pro Glu Ile Thr Pro Ser Pro Leu Gln Pro Pro Ala Ala Pro
            260                 265                 270
Ala Pro Thr Ser Thr Thr Ser Ser Ala Arg Arg Arg Ala Tyr Cys Arg
        275                 280                 285
Asn Arg Asp His Phe Ala Thr Ile Arg Thr Ala Ser Leu Val Ser Arg
    290                 295                 300
Gln Ile Gln Glu His Glu Gln Asp Ser Ala Leu Arg Glu Gln Leu Ser
305                 310                 315                 320
Gly Tyr Lys Arg Met Arg Arg Gln His Gln Lys Gln Leu Leu Ala Leu
                325                 330                 335
Glu Ser Arg Leu Arg Gly Glu Arg Glu Glu His Ser Ala Arg Leu Gln
            340                 345                 350
Arg Glu Leu Glu Ala Gln Arg Ala Gly Phe Gly Ala Glu Ala Glu Lys
        355                 360                 365
Leu Ala Arg Arg His Gln Ala Ile Gly Glu Lys Glu Ala Arg Ala Ala
    370                 375                 380
Gln Ala Glu Glu Arg Lys Phe Gln Gln His Ile Leu Gly Gln Gln Lys
385                 390                 395                 400
Lys Glu Leu Ala Ala Leu Leu Glu Ala Gln Lys Arg Thr Tyr Lys Leu
                405                 410                 415
Arg Lys Glu Gln Leu Lys Glu Glu Leu Gln Glu Asn Pro Ser Thr Pro
            420                 425                 430
Lys Arg Glu Lys Ala Glu Trp Leu Leu Arg Gln Lys Glu Gln Leu Gln
```

```
        435                 440                 445
Gln Cys Gln Ala Glu Glu Glu Ala Gly Leu Leu Arg Arg Gln Arg Gln
    450                 455                 460
Tyr Phe Glu Leu Gln Cys Arg Gln Tyr Lys Arg Lys Met Leu Leu Ala
465                 470                 475                 480
Arg His Ser Leu Asp Gln Asp Leu Leu Arg Glu Asp Leu Asn Lys Lys
                485                 490                 495
Gln Thr Gln Lys Asp Leu Glu Cys Ala Leu Leu Leu Arg Gln His Glu
            500                 505                 510
Ala Thr Arg Glu Leu Glu Leu Arg Gln Leu Gln Ala Val Gln Arg Thr
        515                 520                 525
Arg Ala Glu Leu Thr Arg Leu Gln His Gln Thr Glu Leu Gly Asn Gln
    530                 535                 540
Leu Glu Tyr Asn Lys Arg Arg Glu Gln Glu Leu Arg Gln Lys His Ala
545                 550                 555                 560
Ala Gln Val Arg Gln Gln Pro Lys Ser Leu Lys Val Arg Ala Gly Gln
                565                 570                 575
Arg Pro Pro Gly Leu Pro Leu Pro Ile Pro Gly Ala Leu Gly Pro Pro
            580                 585                 590
Asn Thr Gly Thr Pro Ile Glu Gln Gln Pro Cys Ser Pro Gly Gln Glu
        595                 600                 605
Ala Val Leu Asp Gln Arg Met Leu Gly Glu Glu Glu Glu Ala Val Gly
    610                 615                 620
Glu Arg Arg Ile Leu Gly Lys Glu Gly Ala Thr Leu Glu Pro Lys Gln
625                 630                 635                 640
Gln Arg Ile Leu Gly Glu Glu Ser Gly Ala Pro Ser Pro Ser Pro Gln
                645                 650                 655
Lys His Gly Ser Leu Val Asp Glu Glu Val Trp Gly Leu Pro Glu Glu
            660                 665                 670
Ile Glu Glu Leu Arg Val Pro Ser Leu Val Pro Gln Glu Arg Ser Ile
        675                 680                 685
Val Gly Gln Glu Glu Ala Gly Thr Trp Ser Leu Trp Gly Lys Glu Asp
    690                 695                 700
Glu Ser Leu Leu Asp Glu Glu Phe Glu Leu Gly Trp Val Gln Gly Pro
705                 710                 715                 720
Ala Leu Thr Pro Val Pro Glu Glu Glu Glu Glu Glu Glu Glu Gly Ala
                725                 730                 735
Pro Ile Gly Thr Pro Arg Asp Pro Gly Asp Gly Cys Pro Ser Pro Asp
            740                 745                 750
Ile Pro Pro Glu Pro Pro Pro Thr His Leu Arg Pro Cys Pro Ala Ser
        755                 760                 765
Gln Leu Pro Gly Leu Leu Ser His Gly Leu Leu Ala Gly Leu Ser Phe
    770                 775                 780
Ala Val Gly Ser Ser Ser Gly Leu Leu Pro Leu Leu Leu Leu Leu Leu
785                 790                 795                 800
Leu Pro Leu Leu Ala Ala Gln Gly Gly Gly Gly Leu Gln Ala Ala Leu
                805                 810                 815
Leu Ala Leu Glu Val Gly Leu Val Gly Leu Gly Ala Ser Tyr Leu Leu
            820                 825                 830
Leu Cys Thr Ala Leu His Leu Pro Ser Ser Leu Phe Leu Leu Leu Ala
        835                 840                 845
Gln Gly Thr Ala Leu Gly Ala Val Leu Gly Leu Ser Trp Arg Arg Gly
    850                 855                 860
Leu Met Gly Val Pro Leu Gly Leu Gly Ala Ala Trp Leu Leu Ala Trp
```

```
865                 870                 875                 880
Pro Gly Leu Ala Leu Pro Leu Val Ala Met Ala Ala Gly Gly Arg Trp
                885                 890                 895
Val Arg Gln Gln Gly Pro Arg Val Arg Arg Gly Ile Ser Arg Leu Trp
            900                 905                 910
Leu Arg Val Leu Leu Arg Leu Ser Pro Met Ala Phe Arg Ala Leu Gln
        915                 920                 925
Gly Cys Gly Ala Val Gly Asp Arg Gly Leu Phe Ala Leu Tyr Pro Lys
    930                 935                 940
Thr Asn Lys Asp Gly Phe Arg Ser Arg Leu Pro Val Pro Gly Pro Arg
945                 950                 955                 960
Arg Arg Asn Pro Arg Thr Thr Gln His Pro Leu Ala Leu Leu Ala Arg
                965                 970                 975
Val Trp Val Leu Cys Lys Gly Trp Asn Trp Arg Leu Ala Arg Ala Ser
            980                 985                 990
Gln Gly Leu Ala Ser His Leu Pro Pro Trp Ala Ile His Thr Leu Ala
        995                 1000                1005
Ser Trp Gly Leu Leu Arg Gly Glu Arg Pro Thr Arg Ile Pro Arg Leu
    1010                1015                1020
Leu Pro Arg Ser Gln Arg Gln Leu Gly Pro Pro Ala Ser Arg Gln Pro
1025                1030                1035                1040
Leu Pro Gly Thr Leu Ala Gly Arg Arg Ser Arg Thr Arg Gln Ser Arg
                1045                1050                1055
Ala Leu Pro Pro Trp Arg
            1060
```

<210> 117
<211> 471
<212> DNA
<213> Homo sapiens

<400> 117
nacgcgttga cgatctgtct ggctggtgta gtgatctgcg ctgtgggtgt cgtcgatgac
60
ctgctcgacc ttcctgcctt ggccaaggca gctggccagg tattagcggc cggcatcgtc
120
gtcacgggcg gagtgcgaat gttttggatc ccgctgccga actccatcat tgctttgggg
180
acgcctactt cgatcttggt gacggtgttc ttcattgtgt tgtgcgccaa tgcggtgaat
240
ttcattgatg gacttgacgg cctggcatcc ggtgtggtgg ccatcgggtc cttggctttc
300
ttctcataca cctacctgct ggctcacgaa caggactttg ttgttgcgac gactaccagt
360
ctcattacgg ctgcgacggc gggcgcctgt ctcggttttt tgccccacaa ctggcatccg
420
gcgaggatgt tcatgggtga ttccggagct ctgctacttg gcttattgct a
471

<210> 118
<211> 157
<212> PRT
<213> Homo sapiens

<400> 118
Xaa Ala Leu Thr Ile Cys Leu Ala Gly Val Val Ile Cys Ala Val Gly
1 5 10 15
Val Val Asp Asp Leu Leu Asp Leu Pro Ala Leu Ala Lys Ala Ala Gly
20 25 30
Gln Val Leu Ala Ala Gly Ile Val Val Thr Gly Gly Val Arg Met Phe
35 40 45
Trp Ile Pro Leu Pro Asn Ser Ile Ile Ala Leu Gly Thr Pro Thr Ser
50 55 60
Ile Leu Val Thr Val Phe Phe Ile Val Leu Cys Ala Asn Ala Val Asn
65 70 75 80
Phe Ile Asp Gly Leu Asp Gly Leu Ala Ser Gly Val Val Ala Ile Gly
85 90 95
Ser Leu Ala Phe Phe Ser Tyr Thr Tyr Leu Leu Ala His Glu Gln Asp
100 105 110
Phe Val Val Ala Thr Thr Thr Ser Leu Ile Thr Ala Ala Thr Ala Gly
115 120 125
Ala Cys Leu Gly Phe Leu Pro His Asn Trp His Pro Ala Arg Met Phe
130 135 140
Met Gly Asp Ser Gly Ala Leu Leu Leu Gly Leu Leu Leu
145 150 155

<210> 119
<211> 302
<212> DNA
<213> Homo sapiens

<400> 119
ntcaaacatg agcagtcgtg gcggccgagg ccgcggtggc tattatcgcg agctttatgg
60
tagccgaggt cgaggcagta aatctaatga aactttcgca aaaaattcgg atgtctactc
120
tcagaaaaag actcgaacag tacgaggcac ctccgaagat ttagcacgat cgctccataa
180
gcttcatatg cgcccgtacc ctgcgtatca tgacattgag ggtatgtggg ctttcccagc
240
ctttactttt tatctggatc atgcacaagc agacccatac gctgccccaa ataaggcacg
300
cn
302

<210> 120
<211> 98
<212> PRT
<213> Homo sapiens

<400> 120
Met Ser Ser Arg Gly Gly Arg Gly Arg Gly Gly Tyr Tyr Arg Glu Leu
1 5 10 15
Tyr Gly Ser Arg Gly Arg Gly Ser Lys Ser Asn Glu Thr Phe Ala Lys
20 25 30
Asn Ser Asp Val Tyr Ser Gln Lys Lys Thr Arg Thr Val Arg Gly Thr
35 40 45
Ser Glu Asp Leu Ala Arg Ser Leu His Lys Leu His Met Arg Pro Tyr

```
    50                  55                  60
Pro Ala Tyr His Asp Ile Glu Gly Met Trp Ala Phe Pro Ala Phe Thr
65                  70                  75                  80
Phe Tyr Leu Asp His Ala Gln Ala Asp Pro Tyr Ala Ala Pro Asn Lys
                85                  90                  95
Ala Arg
```

<210> 121
<211> 318
<212> DNA
<213> Homo sapiens

<400> 121
ngcatggggg gccctgggac cgcacttgtg ccccttttt ttttagggaa aaaattgagc
60
cctaaaggat ttgccgcatt acaggaaagt tttttggtaa gtttggggtt gtttctgtgc
120
tgtgtgagaa ggagtagaag cagctccagt agagtgggcc ttttcatttt tatccagagg
180
aaatttgtag gctgtggcta ttacttcctt ttttttcttt ttttttttg tttagagaca
240
gagtctgnct ctgtcgccag gctggagtga agtggcacga tctcagctca ctgcaacctc
300
tgcctcccag gttcaagc
318

<210> 122
<211> 89
<212> PRT
<213> Homo sapiens

<400> 122

```
Xaa Met Gly Gly Pro Gly Thr Ala Leu Val Pro Leu Phe Phe Leu Gly
 1               5                  10                  15
Lys Lys Leu Ser Pro Lys Gly Phe Ala Ala Leu Gln Glu Ser Phe Leu
            20                  25                  30
Val Ser Leu Gly Leu Phe Leu Cys Cys Val Arg Arg Ser Arg Ser Ser
        35                  40                  45
Ser Ser Arg Val Gly Leu Phe Ile Phe Ile Gln Arg Lys Phe Val Gly
    50                  55                  60
Cys Gly Tyr Tyr Phe Leu Phe Phe Leu Phe Phe Phe Cys Leu Glu Thr
65                  70                  75                  80
Glu Ser Xaa Ser Val Ala Arg Leu Glu
                85
```

<210> 123
<211> 338
<212> DNA
<213> Homo sapiens

<400> 123
acgcgtctag ggtagaaatc aactccagta actgtcattc aacctcagca atgctgggga
60

cgggcagagg cagggcagct gtgtgccaca ttcctgccag ggctggtcag gccccggctc
120
tcaccactcc tcctccctgc tttgaacctg tggaacaaag ggcccctgca ccccaactca
180
ttcctctttg ccacataagg gcctcaagtc atgctgtccc ctctgcctgg gttgcttttt
240
ctccctctgc ttgggtcact gttcacacca ctggccactt tcctcaggga agggccctca
300
ctgcccacac acctaaacat gccccctgct cctccata
338

<210> 124
<211> 96
<212> PRT
<213> Homo sapiens

<400> 124
Met Leu Gly Thr Gly Arg Gly Arg Ala Ala Val Cys His Ile Pro Ala
1 5 10 15
Arg Ala Gly Gln Ala Pro Ala Leu Thr Thr Pro Pro Pro Cys Phe Glu
20 25 30
Pro Val Glu Gln Arg Ala Pro Ala Pro Gln Leu Ile Pro Leu Cys His
35 40 45
Ile Arg Ala Ser Ser His Ala Val Pro Ser Ala Trp Val Ala Phe Ser
50 55 60
Pro Ser Ala Trp Val Thr Val His Thr Thr Gly His Phe Pro Gln Gly
65 70 75 80
Arg Ala Leu Thr Ala His Thr Pro Lys His Ala Pro Cys Ser Ser Ile
85 90 95

<210> 125
<211> 280
<212> DNA
<213> Homo sapiens

<400> 125
ccatggacct ggccagccac catcacctgc ctcctgcctc acccaccctg ggtgcctgcc
60
ggcaaggatt ggagggcaga ctgctggagc gtgagaccag gccaatctgt ctttctggga
120
accttcagcc tccaactgga gctgactgtc aactttcggg tgagaagtca cttttctgca
180
ttcccaccac actatctatc tgtgcaatac ggcagcgtga cagcactcac cttattgagg
240
gcttctgctg tcctggccca ttctggatag gcctgatcta
280

<210> 126
<211> 92
<212> PRT
<213> Homo sapiens

<400> 126
Met Asp Leu Ala Ser His His His Leu Pro Pro Ala Ser Pro Thr Leu

```
 1               5                  10                  15
Gly Ala Cys Arg Gln Gly Leu Glu Gly Arg Leu Leu Glu Arg Glu Thr
            20                  25                  30
Arg Pro Ile Cys Leu Ser Gly Asn Leu Gln Pro Pro Thr Gly Ala Asp
        35                  40                  45
Cys Gln Leu Ser Gly Glu Lys Ser Leu Phe Cys Ile Pro Thr Thr Leu
    50                  55                  60
Ser Ile Cys Ala Ile Arg Gln Arg Asp Ser Thr His Leu Ile Glu Gly
65                  70                  75                  80
Phe Cys Cys Pro Gly Pro Phe Trp Ile Gly Leu Ile
                85                  90
```

<210> 127
<211> 444
<212> DNA
<213> Homo sapiens

<400> 127
cgcgtgatcg ccgtggcgga gggccgcggc gccgactcga tcgcccagct gacaaccgag
60
ctgcaaagcc gtcactgccc tgcggagcag atcacgtccg tcagcatcga catgtcgcca
120
gcgttcatca ggggctgcgc cgagcacctg cccaacgcgc gcgtcacctt cgacaagttc
180
cacgtcatcg ggcacgccaa tgcggccgtg gacaggatgc gccgcatcga gcagcgcagc
240
gacaagtccc tcaaggggat gcgctggtcg ctgctgaaga accgcgccag cctcaagccc
300
gaggctgccg ccgatctgga tgccctgatc gccaggatgg ccactgtgcg caccgcgcgc
360
gcctgggtct acaaggagca gctgcgcgag atcctcgcgc gcaagcagat caacgtggca
420
cgcgacatgc tcaagcactg gtgc
444

<210> 128
<211> 148
<212> PRT
<213> Homo sapiens

<400> 128
```
Arg Val Ile Ala Val Ala Glu Gly Arg Gly Ala Asp Ser Ile Ala Gln
 1               5                  10                  15
Leu Thr Thr Glu Leu Gln Ser Arg His Cys Pro Ala Glu Gln Ile Thr
            20                  25                  30
Ser Val Ser Ile Asp Met Ser Pro Ala Phe Ile Arg Gly Cys Ala Glu
        35                  40                  45
His Leu Pro Asn Ala Arg Val Thr Phe Asp Lys Phe His Val Ile Gly
    50                  55                  60
His Ala Asn Ala Ala Val Asp Arg Met Arg Arg Ile Glu Gln Arg Ser
65                  70                  75                  80
Asp Lys Ser Leu Lys Gly Met Arg Trp Ser Leu Leu Lys Asn Arg Ala
                85                  90                  95
Ser Leu Lys Pro Glu Ala Ala Ala Asp Leu Asp Ala Leu Ile Ala Arg
```

```
            100                 105                 110
Met Ala Thr Val Arg Thr Ala Arg Ala Trp Val Tyr Lys Glu Gln Leu
        115                 120                 125
Arg Glu Ile Leu Ala Arg Lys Gln Ile Asn Val Ala Arg Asp Met Leu
    130                 135                 140
Lys His Trp Cys
145
```

<210> 129
<211> 291
<212> DNA
<213> Homo sapiens

<400> 129
gaggagggac gtaccgtccc cgttatagcc aagctcgaga agccgcaagc tatcgagaac
60
ttggacgaga ttattgacgt ctttgacgcc gtcatggttg cccgtggcga tatggccgtc
120
gagtgcccgc tcgaggaagt tccgctgatc caaaagcaga tcatcgagaa ggctcgttta
180
caggctaagc ccgtcattgt ggccacccag atgcttgagt cgatgatcca cgctccccgt
240
ccgacccgcg ctgaggccgc cgacgtcgcg aacgccatcc ttgacggcgc g
291

<210> 130
<211> 97
<212> PRT
<213> Homo sapiens

<400> 130
```
Glu Glu Gly Arg Thr Val Pro Val Ile Ala Lys Leu Glu Lys Pro Gln
 1               5                  10                  15
Ala Ile Glu Asn Leu Asp Glu Ile Ile Asp Val Phe Asp Ala Val Met
            20                  25                  30
Val Ala Arg Gly Asp Met Ala Val Glu Cys Pro Leu Glu Glu Val Pro
        35                  40                  45
Leu Ile Gln Lys Gln Ile Ile Glu Lys Ala Arg Leu Gln Ala Lys Pro
    50                  55                  60
Val Ile Val Ala Thr Gln Met Leu Glu Ser Met Ile His Ala Pro Arg
65                  70                  75                  80
Pro Thr Arg Ala Glu Ala Ala Asp Val Ala Asn Ala Ile Leu Asp Gly
                85                  90                  95
Ala
```

<210> 131
<211> 416
<212> DNA
<213> Homo sapiens

<400> 131
tccggagcgt ccgtggccct catgggtgtg tcagcgtggt tgctgtctcg ggccgcagag
60

attccaccgg tgctctacct ggaggccgca gccgtcgggg ttcgattctt cggcatctcc
120
cgcggtgtct tccgctacgc cgaacgtctg gtaggccacg acctggctct gcggatgcag
180
ggggcattgc ggatgcgggt ctacgaccgg ctgtcacgta ccnaccctgc tgggnnacgt
240
cgccggggtg acctgctggt acgggttact gccgacgtcg acgcggtgtt ggacatggtc
300
gtgcgggtga tcgttccggc gtgcgcgtca agcctcgtca tcattggcac cacggtcctt
360
ctttgtccga gagaaggttg agttttctta gccggattcc aacacagcct gggggc
416

<210> 132
<211> 126
<212> PRT
<213> Homo sapiens

<400> 132
Ser Gly Ala Ser Val Ala Leu Met Gly Val Ser Ala Trp Leu Leu Ser
 1   5   10   15
Arg Ala Ala Glu Ile Pro Pro Val Leu Tyr Leu Glu Ala Ala Ala Val
            20   25   30
Gly Val Arg Phe Phe Gly Ile Ser Arg Gly Val Phe Arg Tyr Ala Glu
        35   40   45
Arg Leu Val Gly His Asp Leu Ala Leu Arg Met Gln Gly Ala Leu Arg
    50   55   60
Met Arg Val Tyr Asp Arg Leu Ser Arg Thr Xaa Pro Ala Gly Xaa Arg
65   70   75   80
Arg Arg Gly Asp Leu Leu Val Arg Val Thr Ala Asp Val Asp Ala Val
                85   90   95
Leu Asp Met Val Val Arg Val Ile Val Pro Ala Cys Ala Ser Ser Leu
            100   105   110
Val Ile Ile Gly Thr Thr Val Leu Leu Cys Pro Arg Glu Gly
        115   120   125

<210> 133
<211> 327
<212> DNA
<213> Homo sapiens

<400> 133
gccgttgcta tcgctgctgg tatgcgtgca gacgtcactg tttttgatat caatatcgct
60
gcgttgaaga gactcgccga catctaccag ggtcgtgttc acacagtagt atccacccgc
120
gccgaaattg cgaaggcgct agaaaccgct gacgttgtga tcggttctgt ccttattccg
180
ggtagttcta ccccgaagct tgttactacc gatatggttg ctcacatgca gcctgggtct
240
gttcttattg atattgctat agaccaaggc ggctgcttcg aggattcgca ccccaccact
300
tacgatgacc ccactttcac tgtgcac
327

<210> 134
<211> 109
<212> PRT
<213> Homo sapiens

<400> 134
Ala Val Ala Ile Ala Ala Gly Met Arg Ala Asp Val Thr Val Phe Asp
1 5 10 15
Ile Asn Ile Ala Ala Leu Lys Arg Leu Ala Asp Ile Tyr Gln Gly Arg
20 25 30
Val His Thr Val Val Ser Thr Arg Ala Glu Ile Ala Lys Ala Leu Glu
35 40 45
Thr Ala Asp Val Val Ile Gly Ser Val Leu Ile Pro Gly Ser Ser Thr
50 55 60
Pro Lys Leu Val Thr Thr Asp Met Val Ala His Met Gln Pro Gly Ser
65 70 75 80
Val Leu Ile Asp Ile Ala Ile Asp Gln Gly Gly Cys Phe Glu Asp Ser
85 90 95
His Pro Thr Thr Tyr Asp Asp Pro Thr Phe Thr Val His
100 105

<210> 135
<211> 560
<212> DNA
<213> Homo sapiens

<400> 135
taagatgtgg tcctgccctg ttcctgaagg ggctgcagct ctgatggaaa atacagggat
60
ttacactcag ggctacagcc acgggggget gaggcccaag gctgcaatct cgggggaagg
120
ggaagttggc ttttcctggt ggattggaaa catcctcttg gaggcaaaga cttttcctgg
180
atcttacaga cttcccggga tttttagatt agaatattgg gggcaaagga ggctgtcttg
240
ttttaaagca atgctacata gacacagtgg ggaagacctg gttcgacggc agataagcag
300
tgggtgatgg gcttgaggag gagagtcagg gcaaagtcta agactgagca gaaaggaatt
360
cccccatctc ccatggataa gtacgttcta gaacattctc tttgggtcta atactctgaa
420
atgacatctt gtcttcatgc tcgagagaga attacttcac tggctccact tggagtgcca
480
gtgttcagac accaagcctg actgggaggg ttccgttttc ttaacacctt cccaccgccg
540
acttccaagt ccccacgcgt
560

<210> 136
<211> 100
<212> PRT
<213> Homo sapiens

<400> 136
Met Trp Ser Cys Pro Val Pro Glu Gly Ala Ala Ala Leu Met Glu Asn
1 5 10 15
Thr Gly Ile Tyr Thr Gln Gly Tyr Ser His Gly Gly Leu Arg Pro Lys
20 25 30
Ala Ala Ile Ser Gly Glu Gly Glu Val Gly Phe Ser Trp Trp Ile Gly
35 40 45
Asn Ile Leu Leu Glu Ala Lys Thr Phe Pro Gly Ser Tyr Arg Leu Pro
50 55 60
Gly Ile Phe Arg Leu Glu Tyr Trp Gly Gln Arg Arg Leu Ser Cys Phe
65 70 75 80
Lys Ala Met Leu His Arg His Ser Gly Glu Asp Leu Val Arg Arg Gln
85 90 95
Ile Ser Ser Gly
100

<210> 137
<211> 429
<212> DNA
<213> Homo sapiens

<400> 137
accggttgga tggcctgcag gccaaagcgt tcctgcaaac tcagcaggcc ttcagcgcaa
60
gaggcaaaca gctggtcgcg cacctgcttg aggtccaccg attgcgcatc gcccttgagc
120
aaggcgcgcc agttggtttt gtcggccact tggctgcgga acaggtcttc gacaaaaccg
180
gactgctggc gggtcgcaac gcgcatgatc ggcagcgcct ggctggcgcc ctggtcgagc
240
cagcgcgtcg gcagttgggt ggcccgggtg ataccgacct tgatccccga cgaattggcc
300
aggtacacca catggtcggt catgcagaat gtttcgcccc agccgggatc acggcaagtg
360
ccggcgtcgt aatggcaacg ttcggggctc atgatgcaca ggtcacactg ggccagcttg
420
gtcatgccc
429

<210> 138
<211> 141
<212> PRT
<213> Homo sapiens

<400> 138
Met Thr Lys Leu Ala Gln Cys Asp Leu Cys Ile Met Ser Pro Glu Arg
1 5 10 15
Cys His Tyr Asp Ala Gly Thr Cys Arg Asp Pro Gly Trp Gly Glu Thr
20 25 30
Phe Cys Met Thr Asp His Val Val Tyr Leu Ala Asn Ser Ser Gly Ile
35 40 45
Lys Val Gly Ile Thr Arg Ala Thr Gln Leu Pro Thr Arg Trp Leu Asp
50 55 60
Gln Gly Ala Ser Gln Ala Leu Pro Ile Met Arg Val Ala Thr Arg Gln

```
65                  70                  75                  80
Gln Ser Gly Phe Val Glu Asp Leu Phe Arg Ser Gln Val Ala Asp Lys
                85                  90                  95
Thr Asn Trp Arg Ala Leu Leu Lys Gly Asp Ala Gln Ser Val Asp Leu
            100                 105                 110
Lys Gln Val Arg Asp Gln Leu Phe Ala Ser Cys Ala Glu Gly Leu Leu
        115                 120                 125
Ser Leu Gln Glu Arg Phe Gly Leu Gln Ala Ile Gln Pro
    130                 135                 140
```

<210> 139
<211> 341
<212> DNA
<213> Homo sapiens

<400> 139
acgcgtcgtt tgaaggcttg atccgcacgt ccaattcgct ttgcgccaat gcgccgcagc
60
ttgtgaacag cagaatcaag ccgctggtaa atcttcctgg gagcttcata ggcggggatg
120
ctacacgagc tggggagaca ctttgaaccc ggaattgtct gaataattct gtctcaaacc
180
tttgcagcct gtaacgactg agggttcgga tggaaaaaca catgctccag gatgggaccg
240
acggccactt caccgatctc ttcatagccc tggcgtttgt agaaatccag gtagcgcgaa
300
tcgccagcgt cgagcacgac gcctgatgag tgcgggtcat t
341

<210> 140
<211> 113
<212> PRT
<213> Homo sapiens

<400> 140

```
Met Thr Arg Thr His Gln Ala Ser Cys Ser Thr Leu Ala Ile Arg Ala
 1               5                  10                  15
Thr Trp Ile Ser Thr Asn Ala Arg Ala Met Lys Arg Ser Val Lys Trp
            20                  25                  30
Pro Ser Val Pro Ser Trp Ser Met Cys Phe Ser Ile Arg Thr Leu Ser
        35                  40                  45
Arg Tyr Arg Leu Gln Arg Phe Glu Thr Glu Leu Phe Arg Gln Phe Arg
    50                  55                  60
Val Gln Ser Val Ser Pro Ala Arg Val Ala Ser Pro Pro Met Lys Leu
65                  70                  75                  80
Pro Gly Arg Phe Thr Ser Gly Leu Ile Leu Leu Phe Thr Ser Cys Gly
                85                  90                  95
Ala Leu Ala Gln Ser Glu Leu Asp Val Arg Ile Lys Pro Ser Asn Asp
            100                 105                 110
Ala
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<210> 141
<211> 324

<212> DNA
<213> Homo sapiens

<400> 141
gaattcctct tggatagctt cgggtaaatg ggtacagcaa atatcaggag cgcaaccgca
60
acctttactt actggtacat gaacaccatt tacattacag ctatcgtact caccccacgt
120
catgtgaaca gacacataac tgaaaggttt ataaaccaca gtctcacggt acgtatgacc
180
gtcaactgtg aacaccgcta agtaatagcc tgcgggggct tgcatgaact cctttgacca
240
tgcgtaataa atacgtccgt cattagtcac acctgatggg gcgaaacaaa aagaacggca
300
gcagttatca ccgcccatac gcgt
324

<210> 142
<211> 106
<212> PRT
<213> Homo sapiens

<400> 142
Met Gly Gly Asp Asn Cys Cys Arg Ser Phe Cys Phe Ala Pro Ser Gly
 1   5   10   15
Val Thr Asn Asp Gly Arg Ile Tyr Tyr Ala Trp Ser Lys Glu Phe Met
            20   25   30
Gln Ala Pro Ala Gly Tyr Tyr Leu Ala Val Phe Thr Val Asp Gly His
        35   40   45
Thr Tyr Arg Glu Thr Val Val Tyr Lys Pro Phe Ser Tyr Val Ser Val
    50   55   60
His Met Thr Trp Gly Glu Tyr Asp Ser Cys Asn Val Asn Gly Val His
65   70   75   80
Val Pro Val Ser Lys Gly Cys Gly Cys Ala Pro Asp Ile Cys Cys Thr
                85   90   95
His Leu Pro Glu Ala Ile Gln Glu Glu Phe
            100   105

<210> 143
<211> 1325
<212> DNA
<213> Homo sapiens

<400> 143
nacgcgtgga tctgccagct gagcctggag ctgtgcaggc agctgccctg ctacgatgag
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gcaccccagg agaagaactt cctgtacaaa tgcataggca ccaccctggg tgctgcttca
120
agtaaggagg tggtgaggaa gcaccttcaa gagctgctgg agacggccag ataccaggag
180
gaggcagaac gcgagggcct cgcctgctgc ttcgggatct gtgccatctc ccacctcgag
240
gacacgctgg cccagctgga ggacttcgtg aggtcagagg tcttcagaaa atccattggc
300

attctcaaca tttttaagga tcgaagtgag aacgaagtgg agaaggtgaa gagtgctctg
360
atcctgtgct atgggcacgt ggcggcccgg gccccccggg agctggtgct ggccaaggta
420
gagtcagaca tcctccggaa catcntgcca gcacttcagc acnncaagga cccagccctg
480
aagctgtgcc ttgtccagag tgtgtgcatg gtcagccgcg ccatctgcag cagcacccag
540
gctggctcct tccacttcac ccggaaagca gagctggtgg cacagatgat ggagttcatc
600
agggcagagc ccccggactc cttgaggaca cctattcgga agaaagccat gctcacctgc
660
acttacttgg tctccgtgga gccagcgctg gacgagcagg cccgggcgga tgtgatccat
720
ggctgcctgc acagcatcat ggccctgctg cctgagccca aggaggagga cggaggctgc
780
cagaagtccc tgtatctgga gacactgcac gcccttgagg atctgctgac gagcctcctg
840
cagcggaaca tgaccccca aggcctgcag atcatgattg agcacctgag cccatggatc
900
aagtccccaa gaggtcacgt agcggcgcgt gccctaggcc tgagcgccct cctcgtgcgc
960
tacttcctgg agcacctgcg tgtcagtggc gcccaagtag ataccaggtt tccatctgag
1020
cccaggatcc tgtgcaatgg ccctggtgcc cttccacaac ctgggccttc tcatcggcct
1080
cttctcccca cggtgtgcgg acctgtggcc tgccacccgc caggaggccg tggactgtgt
1140
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1200
cgtggcggag cggctcctca gcctcaagga cggcctcgtg caccctgacc ccgccattct
1260
cttccacacc tgccacagtg taggccagat tattgccaag cgcctccccc cagcccttca
1320
cgcgt
1325

<210> 144
<211> 390
<212> PRT
<213> Homo sapiens

<400> 144
Xaa Ala Trp Ile Cys Gln Leu Ser Leu Glu Leu Cys Arg Gln Leu Pro
1 5 10 15
Cys Tyr Asp Glu Ala Pro Gln Glu Lys Asn Phe Leu Tyr Lys Cys Ile
20 25 30
Gly Thr Thr Leu Gly Ala Ala Ser Ser Lys Glu Val Val Arg Lys His
35 40 45
Leu Gln Glu Leu Leu Glu Thr Ala Arg Tyr Gln Glu Glu Ala Glu Arg
50 55 60
Glu Gly Leu Ala Cys Cys Phe Gly Ile Cys Ala Ile Ser His Leu Glu
65 70 75 80
Asp Thr Leu Ala Gln Leu Glu Asp Phe Val Arg Ser Glu Val Phe Arg

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                85                  90                  95
Lys Ser Ile Gly Ile Leu Asn Ile Phe Lys Asp Arg Ser Glu Asn Glu
            100                 105                 110
Val Glu Lys Val Lys Ser Ala Leu Ile Leu Cys Tyr Gly His Val Ala
        115                 120                 125
Ala Arg Ala Pro Arg Glu Leu Val Leu Ala Lys Val Glu Ser Asp Ile
    130                 135                 140
Leu Arg Asn Ile Xaa Pro Ala Leu Gln His Xaa Lys Asp Pro Ala Leu
145                 150                 155                 160
Lys Leu Cys Leu Val Gln Ser Val Cys Met Val Ser Arg Ala Ile Cys
                165                 170                 175
Ser Ser Thr Gln Ala Gly Ser Phe His Phe Thr Arg Lys Ala Glu Leu
            180                 185                 190
Val Ala Gln Met Met Glu Phe Ile Arg Ala Glu Pro Pro Asp Ser Leu
        195                 200                 205
Arg Thr Pro Ile Arg Lys Lys Ala Met Leu Thr Cys Thr Tyr Leu Val
    210                 215                 220
Ser Val Glu Pro Ala Leu Asp Glu Gln Ala Arg Ala Asp Val Ile His
225                 230                 235                 240
Gly Cys Leu His Ser Ile Met Ala Leu Leu Pro Glu Pro Lys Glu Glu
                245                 250                 255
Asp Gly Gly Cys Gln Lys Ser Leu Tyr Leu Glu Thr Leu His Ala Leu
            260                 265                 270
Glu Asp Leu Leu Thr Ser Leu Leu Gln Arg Asn Met Thr Pro Gln Gly
        275                 280                 285
Leu Gln Ile Met Ile Glu His Leu Ser Pro Trp Ile Lys Ser Pro Arg
    290                 295                 300
Gly His Val Ala Ala Arg Ala Leu Gly Leu Ser Ala Leu Leu Val Arg
305                 310                 315                 320
Tyr Phe Leu Glu His Leu Arg Val Ser Gly Ala Gln Val Asp Thr Arg
                325                 330                 335
Phe Pro Ser Glu Pro Arg Ile Leu Cys Asn Gly Pro Gly Ala Leu Pro
            340                 345                 350
Gln Pro Gly Pro Ser His Arg Pro Leu Leu Pro Thr Val Cys Gly Pro
        355                 360                 365
Val Ala Cys His Pro Pro Gly Gly Arg Gly Leu Cys Leu Leu Pro Ala
    370                 375                 380
Val Pro Pro Ala Arg Leu
385                 390
```

<210> 145
<211> 802
<212> DNA
<213> Homo sapiens

<400> 145
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60
cataagcaga cgtagagagt ggtcacatcc atgtcgatgg tgtgcgcgta atgaaggtct
120
acatcaccct ggtgaaggcc tgcaccacta gcgtcggcac catttccccg cgtcggacaa
180
gacatcatgc cccatatctt gacagaatgt ctgacatgag tatgccacgc cgagcagcac
240

cagaggacga caccgatctg gcggacgccg cccgttcatg gcgcagatac ctcatcctcg
300
tcatttgtgg cgttatcgtc gctgtcctcg gactaggcat tttcgggtat cttgcgtggt
360
ggtcattgtg cgatcaagct gccggggtct gtcagcgtgg tgaacccgtt atgtactggt
420
gttcggtggt ctctctggcc attctcggac tcattatcgg ggtcttgacg cagatctggc
480
tggagaagcg ctggtggcac atgcttgcca tcgtcatccc ggctgttttc atcgtcgccg
540
gtatcttttt ctggctcgcc gtctaagaag gggcgtcaca gattccacaa acgacacagg
600
tattgatctc cgttttatcg gctcctagca gccgtggtca acgtatcgct atcaagcgat
660
acaggactcg tcgttcgcat cgttgttgtg ctgctgggaa acaatcccag cgatctactc
720
ggctaccgcc agacagttca ctcacaaccc ctcacgccgg cgcagacatc aaatcccatt
780
ctcgatagac ggcccacacc ac
802

<210> 146
<211> 151
<212> PRT
<213> Homo sapiens

<400> 146
Met Lys Val Tyr Ile Thr Leu Val Lys Ala Cys Thr Thr Ser Val Gly
1 5 10 15
Thr Ile Ser Pro Arg Arg Thr Arg His His Ala Pro Tyr Leu Asp Arg
20 25 30
Met Ser Asp Met Ser Met Pro Arg Arg Ala Ala Pro Glu Asp Asp Thr
35 40 45
Asp Leu Ala Asp Ala Ala Arg Ser Trp Arg Arg Tyr Leu Ile Leu Val
50 55 60
Ile Cys Gly Val Ile Val Ala Val Leu Gly Leu Gly Ile Phe Gly Tyr
65 70 75 80
Leu Ala Trp Trp Ser Leu Cys Asp Gln Ala Ala Gly Val Cys Gln Arg
85 90 95
Gly Glu Pro Val Met Tyr Trp Cys Ser Val Val Ser Leu Ala Ile Leu
100 105 110
Gly Leu Ile Ile Gly Val Leu Thr Gln Ile Trp Leu Glu Lys Arg Trp
115 120 125
Trp His Met Leu Ala Ile Val Ile Pro Ala Val Phe Ile Val Ala Gly
130 135 140
Ile Phe Phe Trp Leu Ala Val
145 150

<210> 147
<211> 368
<212> DNA
<213> Homo sapiens

<400> 147

acgcgtgaaa acggtatgac tcttctggcc ttagtagatc tgtctaaaaa acccgatgag
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tttacacagt gggcattagt agcccgcgat gttcatgaca ttcctggtct acgaaaagtt
120
attggtcaga aagtaccttg tgttgcagtg acggggtcgg aaaaggtgct tcataaaaag
180
gattactggg atctagcaac acctatgcca attgcgtggg gtacaacgga ccgaacagtt
240
attgctgatg cacgacgtac aatccccacc acggagtggg atatccttgc aagactacgt
300
ccacgcctag aagaggttcg caagcaacgt aatgatgtat tgctcctcaa cgaggaggat
360
ccccccta
368

<210> 148
<211> 117
<212> PRT
<213> Homo sapiens

<400> 148
Met Thr Leu Leu Ala Leu Val Asp Leu Ser Lys Lys Pro Asp Glu Phe
1 5 10 15
Thr Gln Trp Ala Leu Val Ala Arg Asp Val His Asp Ile Pro Gly Leu
20 25 30
Arg Lys Val Ile Gly Gln Lys Val Pro Cys Val Ala Val Thr Gly Ser
35 40 45
Glu Lys Val Leu His Lys Lys Asp Tyr Trp Asp Leu Ala Thr Pro Met
50 55 60
Pro Ile Ala Trp Gly Thr Thr Asp Arg Thr Val Ile Ala Asp Ala Arg
65 70 75 80
Arg Thr Ile Pro Thr Thr Glu Trp Asp Ile Leu Ala Arg Leu Arg Pro
85 90 95
Arg Leu Glu Glu Val Arg Lys Gln Arg Asn Asp Val Leu Leu Leu Asn
100 105 110
Glu Glu Asp Pro Pro
115

<210> 149
<211> 407
<212> DNA
<213> Homo sapiens

<400> 149
nngctagcat ggaccctagt cacacaggca gccatacccg aggtcaaagt gacccatttt
60
cctaatatgg ccgctcagat ccaatacttt gaagattcgt ccgtggttat atggcacgat
120
gcggtggatg gtatcgtgta ccgaagtgcg gatgaaggca agtcgtgggc cccaattaag
180
gggcctgaac agggtcaggc gcacctttтc gtgctccatc cctacgacaa gactcaagcg
240
tatattctga cgcgcagcac tcagcattgg cgcacgtcga accgtggcga gacgtggcag
300

tcattctcaa cgcctcatcc gcctacgacc ttgaaagcta tgcctctgga ctttcatccg
360
acgcatcatg actggatcct tttcacgggc caggcttgca cggtaaa
407

<210> 150
<211> 135
<212> PRT
<213> Homo sapiens

<400> 150
Xaa Leu Ala Trp Thr Leu Val Thr Gln Ala Ala Ile Pro Glu Val Lys
1 5 10 15
Val Thr His Phe Pro Asn Met Ala Ala Gln Ile Gln Tyr Phe Glu Asp
20 25 30
Ser Ser Val Val Ile Trp His Asp Ala Val Asp Gly Ile Val Tyr Arg
35 40 45
Ser Ala Asp Glu Gly Lys Ser Trp Ala Pro Ile Lys Gly Pro Glu Gln
50 55 60
Gly Gln Ala His Leu Phe Val Leu His Pro Tyr Asp Lys Thr Gln Ala
65 70 75 80
Tyr Ile Leu Thr Arg Ser Thr Gln His Trp Arg Thr Ser Asn Arg Gly
85 90 95
Glu Thr Trp Gln Ser Phe Ser Thr Pro His Pro Pro Thr Thr Leu Lys
100 105 110
Ala Met Pro Leu Asp Phe His Pro Thr His His Asp Trp Ile Leu Phe
115 120 125
Thr Gly Gln Ala Cys Thr Val
130 135

<210> 151
<211> 448
<212> DNA
<213> Homo sapiens

<400> 151
accggtgtcc gtggctattg ccccgaatgg tccccatccg cgtccccggg aactccctcg
60
gcttttcgcg catccaggtc cccagcccca gctactggtg cgccccgagc ccctaggtgc
120
cagagcggtg gtcggccggg ctcctgccca gtctcggctc ctccctcctc cccaccagaa
180
ggaaaaactt gggcccttcg agaaccctgt ggaatgttct ttgtaatcaa ctgtacatcc
240
gcttccacgg cacggcctcg tgcaaaatcg cgggtttcgg ggccttggag caaattgcgc
300
ttgtcagcgg cgacgtcagg aggacaaggg gaggggttcg cggctgaaac tgcagcttcg
360
cagcacagag ccattttagg ctgctcccca cctcgcgggg cccatgggaa gccggccccg
420
ggagggcgcg gctgcatgga tattcgac
448

<210> 152

<211> 149
<212> PRT
<213> Homo sapiens

<400> 152
Thr Gly Val Arg Gly Tyr Cys Pro Glu Trp Ser Pro Ser Ala Ser Pro
1 5 10 15
Gly Thr Pro Ser Ala Phe Arg Ala Ser Arg Ser Pro Ala Pro Ala Thr
20 25 30
Gly Ala Pro Arg Ala Pro Arg Cys Gln Ser Gly Gly Arg Pro Gly Ser
35 40 45
Cys Pro Val Ser Ala Pro Pro Ser Ser Pro Pro Glu Gly Lys Thr Trp
50 55 60
Ala Leu Arg Glu Pro Cys Gly Met Phe Phe Val Ile Asn Cys Thr Ser
65 70 75 80
Ala Ser Thr Ala Arg Pro Arg Ala Lys Ser Arg Val Ser Gly Pro Trp
85 90 95
Ser Lys Leu Arg Leu Ser Ala Ala Thr Ser Gly Gly Gln Gly Glu Gly
100 105 110
Phe Ala Ala Glu Thr Ala Ala Ser Gln His Arg Ala Ile Leu Gly Cys
115 120 125
Ser Pro Pro Arg Gly Ala His Gly Lys Pro Ala Pro Gly Gly Arg Gly
130 135 140
Cys Met Asp Ile Arg
145

<210> 153
<211> 440
<212> DNA
<213> Homo sapiens

<400> 153
nnntgggtcc atgtatgtgt gtgtatatga gggagacacg caggtgtgtg tccgagtgtg
60
tgtccatggg tccatgtatg tgtgtgtata tgtgggggaa caggtgtgtg tccgagtgtg
120
tgcatgggtc cgtgtatatg cgtgtatata tgcggggata tgtatatgtg tgtgtgtatg
180
aacaggtgta agtggggagc actcaggtgt gtctgtgtgt gttcgtgtac acgtgtgtaa
240
gtgggtgacc atgaaggggt gtgtgtgtcc gtgtgtaggt ttgcgtgcat gcacacatgc
300
atgtgtgtac tggggcatcc aagcccctgg tctccactcc attccaccct acgcctacct
360
ccttgatctc tgcgcccagc cttggctgtg ctcccctgct gtatgcacgt gggtgtctgc
420
acgtgggtgt ctgcacgcgt
440

<210> 154
<211> 69
<212> PRT
<213> Homo sapiens

<400> 154
Gly Arg His Ala Gly Val Cys Pro Ser Val Cys Pro Trp Val His Val
1 5 10 15
Cys Val Cys Ile Cys Gly Gly Thr Gly Val Cys Pro Ser Val Cys Met
20 25 30
Gly Pro Cys Ile Cys Val Tyr Ile Cys Gly Asp Met Tyr Met Cys Val
35 40 45
Cys Met Asn Arg Cys Lys Trp Gly Ala Leu Arg Cys Val Cys Val Cys
50 55 60
Ser Cys Thr Arg Val
65

<210> 155
<211> 344
<212> DNA
<213> Homo sapiens

<400> 155
acgcgtatcg accaccatgt cgtcgtcacc acggcaagcg ctctcggcgg gcgagaacga
60
gtgaacatgg ccgagttgat ggccgatgcc gcgaccggca cgaaaccgtc ctacctacag
120
cgatcttcct cctcgatcac ctcgtttgaa gtggacaggg aacaaagaca ctcagacaac
180
gcgccgcagg aagtaaaaag ttcgctctcc gatcacggcc gtcgcgcgag tgcacaggga
240
gaactgggca cctcgcaagc tacgccaccg cgatccatgc ccccgcccgt atcttccgcc
300
tcctctacct ccccccttacc gatcagcatt atatccgatc taga
344

<210> 156
<211> 92
<212> PRT
<213> Homo sapiens

<400> 156
Met Ala Glu Leu Met Ala Asp Ala Ala Thr Gly Thr Lys Pro Ser Tyr
1 5 10 15
Leu Gln Arg Ser Ser Ser Ser Ile Thr Ser Phe Glu Val Asp Arg Glu
20 25 30
Gln Arg His Ser Asp Asn Ala Pro Gln Glu Val Lys Ser Ser Leu Ser
35 40 45
Asp His Gly Arg Arg Ala Ser Ala Gln Gly Glu Leu Gly Thr Ser Gln
50 55 60
Ala Thr Pro Pro Arg Ser Met Pro Pro Pro Val Ser Ser Ala Ser Ser
65 70 75 80
Thr Ser Pro Leu Pro Ile Ser Ile Ile Ser Asp Leu
85 90

<210> 157
<211> 6816
<212> DNA
<213> Homo sapiens

<400> 157
nnagatctcc aaagaaccaa aaggatcaat atttctggat tcctgtatgg gtgtcgttca
60
gaacaacaaa gtcaggcgtt ttgcttttga gctcaagatg caggacaaaa gtagttatct
120
cttggcagca gacagtgaag tggaaatgga agaatggatc acaattctaa ataagatcct
180
ccagctcaac tttgaagctg caatgcaaga aaagcgaaat ggcgactctc acgaagatga
240
tgaacaaagc aaattggaag gttctggttc cggtttagat agctacctgc cggaacttgc
300
caagagtgca agagaagcag aaatcaaact gaaaagtgaa agcagagtca aacttttta
360
tttggaccca gatgcccaga agcttgactt ctcatcagct gagccagaag tgaagtcatt
420
tgaagagaag tttggaaaaa ggatccttgt caagtgcaat gatttatctt tcaatttgca
480
atgctgtgtt gccgaaaatg aagaaggacc cactacaaat gttgaacctt tctttgttac
540
tctatccctg tttgacataa aatacaaccg gaagatttct gccgatttcc acgtagacct
600
gaaccatttc tcagtgaggc aaatgatcgc caccacgtcc ccggcgctga tgaatggcag
660
tgggccgaaa cccaatctgc cctcaggggc atccttcatg aagccgccat gcagtatccg
720
aagcagggaa tattttcagt cacttgtcct catccagata tatttcttgt ggccagaatt
780
gaaaaagtcc ttcaggggag catcacacat tgcgctgagc catatatgaa aagttcagac
840
tcttctaagg tggcccagaa ggtgctgaag aatgccaagc aggcatgcca aagactagga
900
cagtatagaa tgccatttgc ttgggcagca aggacattgt ttaaggatgc atctggaaat
960
cttgacaaaa atgccagatt ttctgccatc tacaggcaag acagcaataa gctatccaat
1020
gatgacatgc tcaagttact tgcagacttt cggaaacctg agaagatggc taagctccca
1080
gtgattttag gcaatctaga cattacaatt gataatgttt cctcagactt ccctaattat
1140
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1200
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1260
accaatcacc tttacgttta tcctaagtac ttgaaatacg acagtcagaa gtcttttgcc
1320
aaggctagaa atattgcgat ttgcattgaa ttcaaagatt cagatgagga agactctcag
1380
ccccttaagt gcatttatgg cagacctggt gggccagttt tcacaagaag cgcctttgct
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1500
actcagctgc atgaaaagca ccacctgttg ctcacattct tccatgtcag ctgtgacaac
1560

tcaagtaaag gaagcacgaa gaagagggat gtcgttgaaa cccaagttgg ctactcctgg
1620
cttcccctcc tgaaagacgg aagggtggtg acaagcgagc agcacatccc ggtctcggcg
1680
aaccttcctt cgggctatct tggctaccag gagcttggga tgggcaggca ttatggtccg
1740
gaaattaaat gggtagatgg aggcaagcca ctgctgaaaa tttccactca tctggtttct
1800
acagtgtata ctcaggatca gcatttacat aatttttttcc agtactgtca gaaaaccgaa
1860
tctggagccc aagccttagg aaacgaactt gtaaagtacc ttaagagtct gcatgcgatg
1920
gaaggccacg tgatgatcgc cttcttgccc actatcctaa accagctgtt ccgagtcctc
1980
accagagcca cacaggaaga agtcgcggtt aacgtgactc gggtcattat tcatgtggtt
2040
gcccagtgcc atgaggaagg attggagagc cacttgaggt catatgttaa gtacgcgtat
2100
aaggctgagc catatgttgc ctctgaatac aagacagtgc atgaagaact gaccaaatcc
2160
atgaccacga ttctcaagcc ttctgccgat ttcctcacca gcaacaaact actgaagtac
2220
tcatggtttt tctttgatgt actgatcaaa tctatggctc agcatttgat agagaactcc
2280
aaagttaagt tgctgcgaaa ccagagattt cctgcatcct atcatcatgc agtggaaacc
2340
gttgtaaata tgctgatgcc acacatcact cagaagtttc gagataatcc agaggcatct
2400
aagaacgcga atcatagcct tgctgtcttc atcaagagat gtttcacctt catggacagg
2460
ggctttgtct tcaagcagat caacaactac attagctgtt ttgctcctgg agacccaaag
2520
accctctttg aatacaagtt tgaatttctc cgtgtagtgt gcaaccatga acattatatt
2580
ccgttgaact taccaatgcc atttggaaaa ggcaggattc aaagatacca agacctccag
2640
cttgactact cattaacaga tgagttctgc agaaaccact tcttggtggg actgttactg
2700
agggaggtgg ggacagccct ccaggagttc cgggaggtcc gtctgatcgc catcagtgtg
2760
ctcaagaacc tgctgataaa gcattctttt gatgacagat atgcttcaag gagccatgag
2820
gcaaggatag ccaccctcta cctgcctctg tttggtctgc tgattgaaaa cgtccagcgg
2880
atcaatgtga gggatgtgtc acccttccct gtgaacgcgg gcatgactgt gaaggatgaa
2940
tccctggctc taccagctgt gaatccgctg gtgacgccgc agaagggaag caccctggac
3000
aacagcctgc acaaggacct gctgggcgcc atctccggca ttgcttctcc atatacaacc
3060
tcaactccaa acatcaacag tgtgagaaat gctgattcga gaggatctct cataagcaca
3120
gattcgggta acagccttcc agaaaggaat agtgagaaga gcaattccct ggataagcac
3180

caacaaagta gcacattggg aaattccgtg gttcgctgtg ataaacttga ccagtctgag
3240
attaagagcc tactgatgtg tttcctctac atcttaaaga gcatgtctga tgatgctttg
3300
tttacatatt ggaacaaggc ttcaacatct gaacttatgg atttttttac aatatctgaa
3360
gtctgcctgc accagttcca gtacatgggg aagcgataca tagccagaac aggaatgatg
3420
catgccagat tgcagcagct gggcagcctg gataactctc tcacttttaa ccacagctat
3480
ggccactcgg acgcagatgt tctgcaccag tcattacttg aagccaacat tgctactgag
3540
gtttgcctga cagctctgga cacgctttct ctatttacat tggcgtttaa gaaccagctc
3600
ctggccgacc atggacataa tcctctcatg aaaaaagttt ttgatgtcta cctgtgtttt
3660
cttcaaaaac atcagtctga aacggcttta aaaaatgtct tcactgcctt aaggtcctta
3720
atttataagt ttccctcaac attctatgaa gggagagcgg acatgtgtgc ggctctgtgt
3780
tacgagattc tcaagtgctg taactccaag ctgagctcca tcaggacgga ggcctcccag
3840
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3900
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4140
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4380
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4500
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4680
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4740
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4800

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5640
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5760
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6360
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6420

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6600
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6660
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6720
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6816

<210> 158
<211> 1572
<212> PRT
<213> Homo sapiens

<400> 158
Ala Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg
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Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala
20 25 30
Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly
35 40 45
Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr
50 55 60
Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys
65 70 75 80
Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys
85 90 95
His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro
100 105 110
Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn
115 120 125
Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln
130 135 140
Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg
145 150 155 160
Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr
165 170 175
Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His
180 185 190
Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly
195 200 205
Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp
210 215 220
Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile
225 230 235 240
Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu
245 250 255
Gly Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly

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            260                 265                 270
Lys Pro Leu Leu Lys Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr
        275                 280                 285
Gln Asp Gln His Leu His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu
    290                 295                 300
Ser Gly Ala Gln Ala Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser
305                 310                 315                 320
Leu His Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile
                325                 330                 335
Leu Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val
            340                 345                 350
Ala Val Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His
        355                 360                 365
Glu Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr
    370                 375                 380
Lys Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu
385                 390                 395                 400
Leu Thr Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu
                405                 410                 415
Thr Ser Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Asp Val Leu
            420                 425                 430
Ile Lys Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu
        435                 440                 445
Leu Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Val Glu Thr
    450                 455                 460
Val Val Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Arg Asp Asn
465                 470                 475                 480
Pro Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys
                485                 490                 495
Arg Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn
            500                 505                 510
Asn Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu
        515                 520                 525
Tyr Lys Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile
    530                 535                 540
Pro Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr
545                 550                 555                 560
Gln Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn
                565                 570                 575
His Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln
            580                 585                 590
Glu Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu
        595                 600                 605
Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Glu
    610                 615                 620
Ala Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu
625                 630                 635                 640
Asn Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn
                645                 650                 655
Ala Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn
            660                 665                 670
Pro Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His
        675                 680                 685
Lys Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr
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     690                 695                 700
Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser
705                 710                 715                 720
Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu
                725                 730                 735
Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn
            740                 745                 750
Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu
        755                 760                 765
Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu
    770                 775                 780
Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe
785                 790                 795                 800
Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg
                805                 810                 815
Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly
            820                 825                 830
Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp
        835                 840                 845
Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu
    850                 855                 860
Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe
865                 870                 875                 880
Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys
                885                 890                 895
Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr
            900                 905                 910
Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe
        915                 920                 925
Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys
    930                 935                 940
Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr
945                 950                 955                 960
Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr
                965                 970                 975
Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser
            980                 985                 990
Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe
        995                 1000                1005
Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu
    1010                1015                1020
Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg
1025                1030                1035                1040
Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn
                1045                1050                1055
Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
            1060                1065                1070
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg
        1075                1080                1085
Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val
    1090                1095                1100
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val
1105                1110                1115                1120
Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg
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                1125                1130                1135
Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val
            1140                1145                1150
Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly
        1155                1160                1165
Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu
    1170                1175                1180
Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala
1185                1190                1195                1200
Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe
                1205                1210                1215
Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
            1220                1225                1230
Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
        1235                1240                1245
Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser
    1250                1255                1260
Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
1265                1270                1275                1280
Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
                1285                1290                1295
Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
            1300                1305                1310
Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr
        1315                1320                1325
Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
    1330                1335                1340
Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg
1345                1350                1355                1360
Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
                1365                1370                1375
Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
            1380                1385                1390
Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
        1395                1400                1405
Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
    1410                1415                1420
Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
1425                1430                1435                1440
Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
                1445                1450                1455
Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
            1460                1465                1470
Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
        1475                1480                1485
Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
    1490                1495                1500
Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
1505                1510                1515                1520
Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu
                1525                1530                1535
Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His Ile Phe Asn Ala
            1540                1545                1550
Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly Met Thr Ser Ser
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        1555                1560                1565
Ser Ser Val Val
    1570

<210> 159
<211> 540
<212> DNA
<213> Homo sapiens

<400> 159
gccggctctg ccatgtgctt actctgagcc acctaacctc ggcgtgcttc agtttactca
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tccgctcatc tgcagaatgg gtgatgctgt cggtacttcg tggcatacag gaaagtgccc
120
agcatggtca gcctcagtga gaggtggcca gtggggagtg gtggccactg tacacctggc
180
acagcccaga gatgcatgtg ccactctgtt gtgtgcttca accaaggggc gctctggcag
240
ggcttgggtg ggacttccca aagggcatgg aaaagttccc agtcaatgag atccatggag
300
acccatggga gtgggggtca gccccagcct aagaggaccc ccagccctgc cctgtgcccc
360
aggacacacc aggcactgtc ccttgtcgcc ttcccagaca acctgtaccc tccaggccac
420
cagttctcgt ccatgacaaa gaaaggagcc ttctaaataa gtgcccgcca gaggctgcac
480
gcttccctgc cccttccggg tggacctggg tttcaaagag aagctgccag tgcaacgcgt
540

<210> 160
<211> 110
<212> PRT
<213> Homo sapiens

<400> 160
Met Val Ser Leu Ser Glu Arg Trp Pro Val Gly Ser Gly Gly His Cys
 1               5                  10                  15
Thr Pro Gly Thr Ala Gln Arg Cys Met Cys His Ser Val Val Cys Phe
            20                  25                  30
Asn Gln Gly Ala Leu Trp Gln Gly Leu Gly Gly Thr Ser Gln Arg Ala
        35                  40                  45
Trp Lys Ser Ser Gln Ser Met Arg Ser Met Glu Thr His Gly Ser Gly
    50                  55                  60
Gly Gln Pro Gln Pro Lys Arg Thr Pro Ser Pro Ala Leu Cys Pro Arg
65                  70                  75                  80
Thr His Gln Ala Leu Ser Leu Val Ala Phe Pro Asp Asn Leu Tyr Pro
                85                  90                  95
Pro Gly His Gln Phe Ser Ser Met Thr Lys Lys Gly Ala Phe
            100                 105                 110

<210> 161
<211> 351
<212> DNA
<213> Homo sapiens
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<400> 161
nnacgcgtac gtctttcggc cgaagaagga acgtgggcag gggcctcctt cgctggccgc
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cgcgcttggc tcgcagcgac gatgaagggc gacgacagca gcaagatcac ccacaagatc
120
gcccgggcga agcgcgaggg ccgcgtatgg tggagctttg agtacttccc gccgcgcacg
180
ccgcagggca tgcagaattt gtatgaccgt atcgagcgca tgagtcagct gggccccgag
240
tttgtggaca ttacgtggaa tgccgggggc cggacgtcgg atatgacgac gcagctggtc
300
aagacggtgc atgcgtactt tggtgtcgag acgtgcatgc atctgacgtg c
351

<210> 162
<211> 117
<212> PRT
<213> Homo sapiens

<400> 162
Xaa Arg Val Arg Leu Ser Ala Glu Glu Gly Thr Trp Ala Gly Ala Ser
1 5 10 15
Phe Ala Gly Arg Arg Ala Trp Leu Ala Ala Thr Met Lys Gly Asp Asp
20 25 30
Ser Ser Lys Ile Thr His Lys Ile Ala Arg Ala Lys Arg Glu Gly Arg
35 40 45
Val Trp Trp Ser Phe Glu Tyr Phe Pro Pro Arg Thr Pro Gln Gly Met
50 55 60
Gln Asn Leu Tyr Asp Arg Ile Glu Arg Met Ser Gln Leu Gly Pro Glu
65 70 75 80
Phe Val Asp Ile Thr Trp Asn Ala Gly Gly Arg Thr Ser Asp Met Thr
85 90 95
Thr Gln Leu Val Lys Thr Val His Ala Tyr Phe Gly Val Glu Thr Cys
100 105 110
Met His Leu Thr Cys
115

<210> 163
<211> 360
<212> DNA
<213> Homo sapiens

<400> 163
gcgtgctcca tcggcacctt gcagatgggc gaattcgctg aaaacgtcgc cggtggcgtc
60
gacacctaca ccctgcgtca gcccatcggc gtatgcgcag gcatcactcc gttcaacttc
120
ccggcgatga ttccactgtg gatgttcccg atggcgattg cctgcggtaa cactttcgtg
180
ctcaaaccgt ccgaacaaga ccctctgtcg acgatgctgc tggtagaact ggcgctggaa
240
gccggtgtgc cggccggcgt gctcaacgtg gtgcacggcg gcaaggatgt ggtggatgcg
300

ctgtgcaccc ataaagatat caaggcagtt tctttcgtcg gttcgaccgc cgttggtacc
360

<210> 164
<211> 120
<212> PRT
<213> Homo sapiens

<400> 164
Ala Cys Ser Ile Gly Thr Leu Gln Met Gly Glu Phe Ala Glu Asn Val
1 5 10 15
Ala Gly Gly Val Asp Thr Tyr Thr Leu Arg Gln Pro Ile Gly Val Cys
20 25 30
Ala Gly Ile Thr Pro Phe Asn Phe Pro Ala Met Ile Pro Leu Trp Met
35 40 45
Phe Pro Met Ala Ile Ala Cys Gly Asn Thr Phe Val Leu Lys Pro Ser
50 55 60
Glu Gln Asp Pro Leu Ser Thr Met Leu Leu Val Glu Leu Ala Leu Glu
65 70 75 80
Ala Gly Val Pro Ala Gly Val Leu Asn Val Val His Gly Gly Lys Asp
85 90 95
Val Val Asp Ala Leu Cys Thr His Lys Asp Ile Lys Ala Val Ser Phe
100 105 110
Val Gly Ser Thr Ala Val Gly Thr
115 120

<210> 165
<211> 728
<212> DNA
<213> Homo sapiens

<400> 165
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tcccagcgag ggacgcccgg ggctgggggt gccggtcgag cccggggcaa cagcttcacc
120
aagtttggca accgcaacgt cttcatgaag gacaacagct cttcttccag cacagactcc
180
cgctcccgct cctcctccag gtccccgacg cgccacttcc gcagaagtga ctcccactca
240
gactccgaca gctcctactc agggaatgag tgtcaccctg tgggccgcag gaacccgccc
300
cctaagggcc ggggcggtcg aggggcccat atggatcggg gccgaggcag ggcgcagcgt
360
gggaagaggc acgatctggc gcccaccaag cgcagtcgaa agaagatggc ggcgctggag
420
tgtgaggacc cggagcgaga gctgaagaag cagaagcggg cagcccgctt ccagcacgga
480
cactcccgcc gcctgcgcct cgagcccctg gtgctgcaga tgagcagcct ggagagcagt
540
ggggctgacc ctgactggca ggagctgcag atcgtgggca cctgccctga catcaccaag
600
cactacctgc gcctcacctg tgcccccgac ccgtccaccg tgcgccctgt ggcattccct
660

gtggcaggtt ttgaaaaagt cgctgtgcat ggtcaagtgc cactggaaag agaagcagga
720
ctacgcgt
728

<210> 166
<211> 242
<212> PRT
<213> Homo sapiens

<400> 166
Ala Ser Ser Leu His Pro Pro Arg Gly Ala Gly Ser Ala Thr Arg Gly
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Gly Gly Ala Pro Ser Gln Arg Gly Thr Pro Gly Ala Gly Gly Ala Gly
20 25 30
Arg Ala Arg Gly Asn Ser Phe Thr Lys Phe Gly Asn Arg Asn Val Phe
35 40 45
Met Lys Asp Asn Ser Ser Ser Ser Ser Thr Asp Ser Arg Ser Arg Ser
50 55 60
Ser Ser Arg Ser Pro Thr Arg His Phe Arg Arg Ser Asp Ser His Ser
65 70 75 80
Asp Ser Asp Ser Ser Tyr Ser Gly Asn Glu Cys His Pro Val Gly Arg
85 90 95
Arg Asn Pro Pro Pro Lys Gly Arg Gly Gly Arg Gly Ala His Met Asp
100 105 110
Arg Gly Arg Gly Arg Ala Gln Arg Gly Lys Arg His Asp Leu Ala Pro
115 120 125
Thr Lys Arg Ser Arg Lys Lys Met Ala Ala Leu Glu Cys Glu Asp Pro
130 135 140
Glu Arg Glu Leu Lys Lys Gln Lys Arg Ala Ala Arg Phe Gln His Gly
145 150 155 160
His Ser Arg Arg Leu Arg Leu Glu Pro Leu Val Leu Gln Met Ser Ser
165 170 175
Leu Glu Ser Ser Gly Ala Asp Pro Asp Trp Gln Glu Leu Gln Ile Val
180 185 190
Gly Thr Cys Pro Asp Ile Thr Lys His Tyr Leu Arg Leu Thr Cys Ala
195 200 205
Pro Asp Pro Ser Thr Val Arg Pro Val Ala Phe Pro Val Ala Gly Phe
210 215 220
Glu Lys Val Ala Val His Gly Gln Val Pro Leu Glu Arg Glu Ala Gly
225 230 235 240
Leu Arg

<210> 167
<211> 510
<212> DNA
<213> Homo sapiens

<400> 167
nnacgcgtgg aaccagaact caggcccgtg tgaggagtct ggtttggaac acacggggcc
60
gcaacacaga attgtcaggt cctgtgccgt gaccaccacc cctcgggcca tgccaggtgc
120

tggtgagggg caggtggctc ccgccaggcg cctgctggcc tgaccgcact ccgtccacag
180
gtcctcatgg gcgtcctccg gctgggcttc gtgtccgcct acctctcaca gccactgctc
240
gatggctttg ccatgggggc ctccgtgacc atcctgacct cgcagctcaa acacctgctg
300
ggcgtgcgga tcccgcggca ccaggggccc ggcatggtgg tcctcacatg gctgagcctg
360
ctgcgcggcg ccgggcaggc caacgtgtgc gacgtggtca ccagcacggt gtgcctggcg
420
gtgctgctag ccgcgaagga gctctcagac cgctaccgac accgcctgag ggtgccgctg
480
cccacggagc tgctggtcat cgtggtggcc
510

<210> 168
<211> 128
<212> PRT
<213> Homo sapiens

<400> 168
Gly Ala Gly Gly Ser Arg Gln Ala Pro Ala Gly Leu Thr Ala Leu Arg
1 5 10 15
Pro Gln Val Leu Met Gly Val Leu Arg Leu Gly Phe Val Ser Ala Tyr
20 25 30
Leu Ser Gln Pro Leu Leu Asp Gly Phe Ala Met Gly Ala Ser Val Thr
35 40 45
Ile Leu Thr Ser Gln Leu Lys His Leu Leu Gly Val Arg Ile Pro Arg
50 55 60
His Gln Gly Pro Gly Met Val Val Leu Thr Trp Leu Ser Leu Leu Arg
65 70 75 80
Gly Ala Gly Gln Ala Asn Val Cys Asp Val Val Thr Ser Thr Val Cys
85 90 95
Leu Ala Val Leu Leu Ala Ala Lys Glu Leu Ser Asp Arg Tyr Arg His
100 105 110
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Val His Leu Ala Ser Val His Pro Ala Gly Arg His Ser Ile Asp Pro
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Arg Val Arg Ile His Leu Ala Pro His Gly Gly Lys Ala Lys Tyr Val
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85 90 95
Ile Val Asn Val His Tyr Ala Thr Gly Tyr Gly Leu Leu Ala Arg Leu
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Ala His Ile Asp Ala Pro Thr Leu Leu Ser Val Trp Gly Ser Asp Val
115 120 125
Tyr Asp Ser Pro Arg Ala Asn Pro Leu Met Arg His Met Val Arg Ser
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Asn Leu Val Ser Ala Thr Arg Ile Ala Ser Thr Ser His Cys Met Ala
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Arg Val Thr Arg

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<211> 391
<212> DNA
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35 40 45
Lys Gly Phe Ile Lys Ala Gln Val Val Ser Phe Gly Asp Leu Val Glu
50 55 60
Phe Gly Gly Glu Lys Glu Ala Gln Ala Ala Gly Lys Leu Arg Leu Glu
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Gly Lys Glu Tyr Val Met Gln Asp Gly Asp Val Val Glu Phe Arg Phe
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Asn Val

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<212> DNA
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<211> 102
<212> PRT
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Thr Gln Pro Thr Ser Pro Pro Cys Leu Gly Leu Cys Phe Leu Phe Asp
    50                  55                  60
Thr Gly Lys Gln Gly Gly Ala Asp Gln Arg Leu Arg Pro Val Gly Cys
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Gly Gly Val Pro Cys Val Ser Gly Lys Pro Arg Thr Leu Gly Cys Thr
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Phe Val Ser Lys Leu Ala Trp Tyr Met Met Glu Glu Gly Gly Gly Ser
50 55 60
Met His Gly Cys Trp Ser Gly Arg Gly Ser Ser Ser Ser Arg Ser Thr
65 70 75 80
Leu Asp Arg Ala Ser Ser Arg Val Thr Cys Val Val Met Ala Ala Val
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Ser Val Phe Cys Thr Gly Ser Ala Ala Gly Pro Gly Glu Gly Pro Glu
100 105 110
Ala Thr Ala Gly Pro Arg Ala Gly Ala Gln Asp Ala Leu Pro Arg Ser

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Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp Leu Leu Glu Glu Leu
145                 150                 155                 160
Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro Pro Pro Ser Ser Ile
                165                 170                 175
Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu Asp Arg Asn Ala Phe
            180                 185                 190
Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala Thr Val His Ser Ser
        195                 200                 205
Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr Ala Val Met Leu Tyr
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Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln Val Lys Cys Asn Glu
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Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr Val Glu Val Leu Glu
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Pro Glu Val Thr Lys Leu Met Asn Phe Met Tyr Phe Gln Arg Asn Ala
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Ile Glu Arg Phe Cys Gly Glu Val Arg Arg Leu Cys His Ala Glu Arg
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Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Ile Thr Leu Gly Lys Phe
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Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala Ala Gln Phe Leu Arg
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Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser Gln Asn Leu Ser Met
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Phe Leu Ala Asn His Asn Lys Ile Thr Gln Ser Leu Gln Gln Gln Leu
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Cys Val Asp Tyr Tyr Glu Asn Arg Met Tyr Leu Thr Pro Ser Glu Lys
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His Met Leu Leu Lys Val Met Gly Phe Gly Leu Tyr Leu Met Asp Gly
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Ser Val Ser Asn Ile Tyr Lys Leu Asp Ala Lys Lys Arg Ile Asn Leu
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Ser Lys Ile Asp Lys Tyr Phe Lys Gln Leu Gln Val Val Pro Leu Phe
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Tyr Glu Glu Asn Lys Ser Arg Trp Thr Cys Thr Ser Ser Gly Ser Ser
465                 470                 475                 480
Pro Gln Tyr Asn Ile Cys Glu Gln Met Ile Gln Ile Arg Glu Asp His
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Thr Gly Ser Gly Arg Gln Glu Ala Gln Lys Thr Asp Ala Glu Tyr Arg
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Lys Leu Phe Asp Leu Ala Leu Gln Gly Leu Gln Leu Leu Ser Gln Trp
    530                 535                 540
Ser Ala His Val Met Glu Val Tyr Ser Trp Lys Leu Val His Pro Thr
```

```
545                 550                 555                 560
Asp Lys Tyr Ser Asn Lys Asp Cys Pro Asp Ser Ala Glu Glu Tyr Glu
                565                 570                 575
Arg Ala Thr Arg Tyr Asn Tyr Thr Ser Glu Glu Lys Phe Ala Leu Val
            580                 585                 590
Glu Val Ile Ala Met Ile Lys Gly Leu Gln Val Leu Met Gly Arg Met
        595                 600                 605
Glu Ser Val Phe Asn His Ala Ile Arg His Thr Val Tyr Ala Ala Leu
    610                 615                 620
Gln Asp Phe Ser Gln Val Thr Leu Arg Glu Pro Leu Arg Gln Ala Ile
625                 630                 635                 640
Lys Lys Lys Lys Asn Val Ile Gln Ser Val Leu Gln Ala Ile Arg Lys
                645                 650                 655
Thr Val Cys Asp Trp Glu Thr Gly His Glu Pro Phe Asn Asp Pro Ala
            660                 665                 670
Leu Arg Gly Glu Lys Asp Pro Lys Ser Gly Phe Asp Ile Lys Val Pro
        675                 680                 685
Arg Arg Ala Val Gly Pro Ser Ser Thr Gln Leu Tyr Met Val Arg Thr
    690                 695                 700
Met Leu Glu Ser Leu Ile Ala Asp Lys Ser Gly Ser Lys Lys Thr Leu
705                 710                 715                 720
Arg Ser Ser Leu Glu Gly Pro Thr Ile Leu Asp Ile Glu Lys Phe His
                725                 730                 735
Arg Glu Ser Phe Phe Tyr Thr His Leu Ile Asn Phe Ser Glu Thr Leu
            740                 745                 750
Gln Gln Cys Cys Asp Leu Ser Gln Leu Trp Phe Arg Glu Phe Phe Leu
        755                 760                 765
Glu Leu Thr Met Gly Arg Arg Ile Gln Phe Pro Ile Glu Met Ser Met
    770                 775                 780
Pro Trp Ile Leu Thr Asp His Ile Leu Glu Thr Lys Glu Ala Ser Met
785                 790                 795                 800
Met Glu Tyr Val Leu Tyr Ser Leu Asp Leu Tyr Asn Asp Ser Ala His
                805                 810                 815
Tyr Ala Leu Thr Arg Phe Asn Lys Gln Phe Leu Tyr Asp Glu Ile Glu
            820                 825                 830
Ala Glu Val Asn Leu Cys Phe Asp Gln Phe Val Tyr Lys Leu Ala Asp
        835                 840                 845
Gln Ile Phe Ala Tyr Tyr Lys Val Met Ala Gly Ser Leu Leu Leu Asp
    850                 855                 860
Lys Arg Leu Arg Ser Glu Cys Lys Asn Gln Gly Ala Thr Ile His Leu
865                 870                 875                 880
Pro Pro Ser Asn Arg Tyr Glu Thr Leu Leu Lys Gln Arg His Val Gln
                885                 890                 895
Leu Leu Gly Arg Ser Ile Asp Leu Asn Arg Leu Ile Thr Gln Arg Val
            900                 905                 910
Ser Ala Ala Met Tyr Lys Ser Leu Glu Leu Ala Ile Gly Arg Phe Glu
        915                 920                 925
Ser Glu Asp Leu Thr Ser Ile Val Glu Leu Asp Gly Leu Leu Glu Ile
    930                 935                 940
Asn Arg Met Thr His Lys Leu Leu Ser Arg Tyr Leu Thr Leu Asp Gly
945                 950                 955                 960
Phe Asp Ala Met Phe Arg Glu Ala Asn His Asn Val Ser Ala Pro Tyr
                965                 970                 975
Gly Arg Ile Thr Leu His Val Phe Trp Glu Leu Asn Tyr Asp Phe Leu
```

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            980                 985                 990
Pro Asn Tyr Cys Tyr Asn Gly Ser Thr Asn Arg Phe Val Arg Thr Val
        995                 1000                1005
Leu Pro Phe Ser Gln Glu Phe Gln Arg Asp Lys Gln Pro Asn Ala Gln
    1010                1015                1020
Pro Gln Tyr Leu His Gly Ser Lys Ala Leu Asn Leu Ala Tyr Ser Ser
1025                1030                1035                1040
Ile Tyr Gly Ser Tyr Arg Asn Phe Val Gly Pro Pro His Phe Gln Val
                1045                1050                1055
Ile Cys Arg Leu Leu Gly Tyr Gln Gly Ile Ala Val Val Met Glu Glu
            1060                1065                1070
Leu Leu Lys Val Val Lys Ser Leu Leu Gln Gly Thr Ile Leu Gln Tyr
        1075                1080                1085
Val Lys Thr Leu Met Glu Val Met Pro Lys Ile Cys Arg Leu Pro Arg
    1090                1095                1100
His Glu Tyr Gly Ser Pro Gly Ile Leu Glu Phe Phe His His Gln Leu
1105                1110                1115                1120
Lys Asp Ile Val Glu Tyr Ala Glu Leu Lys Thr Val Cys Phe Gln Asn
                1125                1130                1135
Leu Arg Glu Val Gly Asn Ala Ile Leu Phe Cys Leu Leu Ile Glu Gln
            1140                1145                1150
Ser Leu Ser Leu Glu Glu Val Cys Asp Leu Leu His Ala Ala Pro Phe
        1155                1160                1165
Gln Asn Ile Leu Pro Arg Val His Val Lys Glu Gly Glu Arg Leu Asp
    1170                1175                1180
Ala Lys Met Lys Arg Leu Glu Ser Lys Tyr Ala Pro Leu His Leu Val
1185                1190                1195                1200
Pro Leu Ile Glu Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg
                1205                1210                1215
Glu Gly Asp Leu Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met
            1220                1225                1230
Phe Glu Val Ile Leu Thr Arg Ile Arg Ser Phe Leu Asp Asp Pro Ile
        1235                1240                1245
Trp Arg Gly Pro Leu Pro Ser Asn Gly Val Met His Val Asp Glu Cys
    1250                1255                1260
Val Glu Phe His Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile
1265                1270                1275                1280
Pro Val Gly Thr His Glu Phe Thr Val Glu Gln Cys Phe Gly Asp Gly
                1285                1290                1295
Leu His Trp Ala Gly Cys Met Ile Ile Val Leu Leu Gly Gln Gln Arg
            1300                1305                1310
Arg Phe Ala Val Leu Asp Phe Cys Tyr His Leu Leu Lys Val Gln Lys
        1315                1320                1325
His Asp Gly Lys Asp Glu Ile Ile Lys Asn Val Pro Leu Lys Lys Met
    1330                1335                1340
Val Glu Arg Ile Arg Lys Phe Gln Ile Leu Asn Asp Glu Ile Ile Thr
1345                1350                1355                1360
Ile Leu Asp Lys Tyr Leu Lys Ser Gly Asp Gly Glu Gly Thr Pro Val
                1365                1370                1375
Glu His Val Arg Cys Phe Gln Pro Pro Ile His Gln Ser Leu Ala Ser
            1380                1385                1390
Ser
```

<210> 177
<211> 417
<212> DNA
<213> Homo sapiens

<400> 177
acgcgtgatg tcacactgcc tctgccgctg ggtcctaatt cgattgcacg caccatggct
60
gcagttcgtg gcgcgcatag tttctggcat gcttcgcgca tcctggagac cgatcccgcc
120
gctgccgtga aaccgcctaa aaatgtgaag cgattgccca aagccgtgtc cgtggagcaa
180
atgcaaaagc tccttgccat acccagtctt aagactccta ccggcctgcg taatcgagcg
240
atacttgagt tcttatatgc taccggcgcg cgcgtgagcg agatgctggc aacagacctg
300
gacgatatac acctgggcga aaaaccccgc gatgaaaacg gggaatctat tgcacttccc
360
gggtatgtgc gccttttgg aaagggaggt aaagagcgtt tagtcccttt gggatcc
417

<210> 178
<211> 139
<212> PRT
<213> Homo sapiens

<400> 178
Thr Arg Asp Val Thr Leu Pro Leu Pro Leu Gly Pro Asn Ser Ile Ala
1 5 10 15
Arg Thr Met Ala Ala Val Arg Gly Ala His Ser Phe Trp His Ala Ser
20 25 30
Arg Ile Leu Glu Thr Asp Pro Ala Ala Ala Val Lys Pro Pro Lys Asn
35 40 45
Val Lys Arg Leu Pro Lys Ala Val Ser Val Glu Gln Met Gln Lys Leu
50 55 60
Leu Ala Ile Pro Ser Leu Lys Thr Pro Thr Gly Leu Arg Asn Arg Ala
65 70 75 80
Ile Leu Glu Phe Leu Tyr Ala Thr Gly Ala Arg Val Ser Glu Met Leu
85 90 95
Ala Thr Asp Leu Asp Asp Ile His Leu Gly Glu Lys Pro Arg Asp Glu
100 105 110
Asn Gly Glu Ser Ile Ala Leu Pro Gly Tyr Val Arg Leu Phe Gly Lys
115 120 125
Gly Gly Lys Glu Arg Leu Val Pro Leu Gly Ser
130 135

<210> 179
<211> 362
<212> DNA
<213> Homo sapiens

<400> 179
acgcgtcgaa ggtgccggtg ggggcgatca ataacatcgc gcaatccctg gaagagcctc
60

aggtgattgc ccgtgggttg atggtggaag atcccgcatc cccaagaatc cgggaattcg
120
ccattgggcc gggcagcccg aatccaaaat gtcggggcac gcccagtggg agtatggtaa
180
ggggccggca ccgatgttgg nggcagcata cggatggaag tgctgggcga gcgcctgggt
240
ttgccggcag agcaactggg gcagctcaag gcgggcgggg tgatcgagca gttggattga
300
gcaatggcgg ccgcgaagcc cgccatttac cttgatgact gtttagcgcg cggattcttt
360
aa
362

<210> 180
<211> 108
<212> PRT
<213> Homo sapiens

<400> 180
Met Ala Gly Phe Ala Ala Ala Ile Ala Gln Ser Asn Cys Ser Ile Thr
1 5 10 15
Pro Pro Ala Leu Ser Cys Pro Ser Cys Ser Ala Gly Lys Pro Arg Arg
20 25 30
Ser Pro Ser Thr Ser Ile Arg Met Leu Pro Pro Thr Ser Val Pro Ala
35 40 45
Pro Tyr His Thr Pro Thr Gly Arg Ala Pro Thr Phe Trp Ile Arg Ala
50 55 60
Ala Arg Pro Asn Gly Glu Phe Pro Asp Ser Trp Gly Cys Gly Ile Phe
65 70 75 80
His His Gln Pro Thr Gly Asn His Leu Arg Leu Phe Gln Gly Leu Arg
85 90 95
Asp Val Ile Asp Arg Pro His Arg His Leu Arg Arg
100 105

<210> 181
<211> 297
<212> DNA
<213> Homo sapiens

<400> 181
gcgttgatca tgtccgaccc aggcttgatc atgctggtac gccgtcactt cccgtgcatg
60
ccgattcact tgtcggtaca ggccaatacg gtgaattggg ccagcgtcga gttctggcaa
120
cagcaaggta tctgccgggt aatcctgtcg cgggaattgt cactggaaga aatcggcgaa
180
atccgccaac aggtgccggc catggagctg gaagtgtttg tgcacggtgc cctgtacatg
240
gcctattccg ggcgctgttt gttgtccggc tatatgaaca agcgcgatgc caaccaa
297

<210> 182
<211> 99
<212> PRT

<213> Homo sapiens

<400> 182
Ala Leu Ile Met Ser Asp Pro Gly Leu Ile Met Leu Val Arg Arg His
1 5 10 15
Phe Pro Cys Met Pro Ile His Leu Ser Val Gln Ala Asn Thr Val Asn
20 25 30
Trp Ala Ser Val Glu Phe Trp Gln Gln Gln Gly Ile Cys Arg Val Ile
35 40 45
Leu Ser Arg Glu Leu Ser Leu Glu Glu Ile Gly Glu Ile Arg Gln Gln
50 55 60
Val Pro Ala Met Glu Leu Glu Val Phe Val His Gly Ala Leu Tyr Met
65 70 75 80
Ala Tyr Ser Gly Arg Cys Leu Leu Ser Gly Tyr Met Asn Lys Arg Asp
85 90 95
Ala Asn Gln

<210> 183
<211> 351
<212> DNA
<213> Homo sapiens

<400> 183
cgggacgtca ccatgaagcc gaccggctcg ggggatgtgg cgaacaaggt catcacccat
60
attccgttta acatcgtctc ccaggcgact catccattcc ttcgtacctt ggacgatgtc
120
aagcgcatct ctttggcgac cgacgggctc ggccaccagg tcctgctcaa gggctaccag
180
gccgagggcc acgactacgc acaccccgac tacggcggca acgtctccca ccgtgccggc
240
gggatgaagg atctcgagaa gctcaccgag tcgggcaggc agtggaacac cgatttcggc
300
attcacgtca acctggtgga gtcctatcct gaggcgaatc acttcggcga c
351

<210> 184
<211> 117
<212> PRT
<213> Homo sapiens

<400> 184
Arg Asp Val Thr Met Lys Pro Thr Gly Ser Gly Asp Val Ala Asn Lys
1 5 10 15
Val Ile Thr His Ile Pro Phe Asn Ile Val Ser Gln Ala Thr His Pro
20 25 30
Phe Leu Arg Thr Leu Asp Asp Val Lys Arg Ile Ser Leu Ala Thr Asp
35 40 45
Gly Leu Gly His Gln Val Leu Leu Lys Gly Tyr Gln Ala Glu Gly His
50 55 60
Asp Tyr Ala His Pro Asp Tyr Gly Gly Asn Val Ser His Arg Ala Gly
65 70 75 80
Gly Met Lys Asp Leu Glu Lys Leu Thr Glu Ser Gly Arg Gln Trp Asn

```
                85                  90                  95
Thr Asp Phe Gly Ile His Val Asn Leu Val Glu Ser Tyr Pro Glu Ala
            100                 105                 110
Asn His Phe Gly Asp
        115
```

<210> 185
<211> 396
<212> DNA
<213> Homo sapiens

<400> 185
cgcgtgggtc tcagtaaaga aaatttgttg cttagaggat gcaccattag aaacacagag
60
gctgttgtgg gcattgtggt ttatgcaggc catgaaacca aagcaatgct gaacaacagt
120
gggccacggt ataagcgcag caaattagaa agaagagcaa acacagatgt cctctggtgt
180
gtcatgcttc tggtcataat gtgcttaact ggcgcagtag gtcatggaat ctggctgagc
240
aggtatgaaa agatgcattt tttcaatgtt cccgagcctg atggacatat catatcacca
300
ctgttggcag gattttatat gttttggacc gtgatcattt tgttacaggt cttgattcct
360
atttctctct atgtttccat cgaaattgtg aagctt
396

<210> 186
<211> 132
<212> PRT
<213> Homo sapiens

<400> 186

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Arg Val Gly Leu Ser Lys Glu Asn Leu Leu Leu Arg Gly Cys Thr Ile
 1               5                  10                  15
Arg Asn Thr Glu Ala Val Val Gly Ile Val Val Tyr Ala Gly His Glu
            20                  25                  30
Thr Lys Ala Met Leu Asn Asn Ser Gly Pro Arg Tyr Lys Arg Ser Lys
        35                  40                  45
Leu Glu Arg Arg Ala Asn Thr Asp Val Leu Trp Cys Val Met Leu Leu
    50                  55                  60
Val Ile Met Cys Leu Thr Gly Ala Val Gly His Gly Ile Trp Leu Ser
65                  70                  75                  80
Arg Tyr Glu Lys Met His Phe Phe Asn Val Pro Glu Pro Asp Gly His
                85                  90                  95
Ile Ile Ser Pro Leu Leu Ala Gly Phe Tyr Met Phe Trp Thr Val Ile
            100                 105                 110
Ile Leu Leu Gln Val Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu
        115                 120                 125
Ile Val Lys Leu
    130
```

<210> 187
<211> 423

<212> DNA
<213> Homo sapiens

<400> 187
cgagtgctca ccgcgtcagc cgtcatgcgt cccactgagg ctgttgtctc tcggtcggca
60
gaacctcgac gagttcagcg gatcctggac cagcgcgagt gggctggcgt cttcgttgtc
120
gatgagcatc gtcgtttgct tggcacggtc ggcgatcaag aggtcatcga ggctgctcgc
180
cgcggagatc gcagtattgc tgacgcggtg gaaactaacg gcatcctcac ggcgcggacc
240
gacactccgt tgtccgagct cttcgctccg accagcaacg ccagggtgcc gttggccgtt
300
gtcgacgagg acttccacct catgggtgtc atctctcggg tgaccctgct cgacgcgatg
360
tcacgagctc gcgacgaggc aggagaggga tctgtcatgt ccttggagaa caccggaaag
420
ctt
423

<210> 188
<211> 141
<212> PRT
<213> Homo sapiens

<400> 188
Arg Val Leu Thr Ala Ser Ala Val Met Arg Pro Thr Glu Ala Val Val
1 5 10 15
Ser Arg Ser Ala Glu Pro Arg Arg Val Gln Arg Ile Leu Asp Gln Arg
20 25 30
Glu Trp Ala Gly Val Phe Val Val Asp Glu His Arg Arg Leu Leu Gly
35 40 45
Thr Val Gly Asp Gln Glu Val Ile Glu Ala Ala Arg Arg Gly Asp Arg
50 55 60
Ser Ile Ala Asp Ala Val Glu Thr Asn Gly Ile Leu Thr Ala Arg Thr
65 70 75 80
Asp Thr Pro Leu Ser Glu Leu Phe Ala Pro Thr Ser Asn Ala Arg Val
85 90 95
Pro Leu Ala Val Val Asp Glu Asp Phe His Leu Met Gly Val Ile Ser
100 105 110
Arg Val Thr Leu Leu Asp Ala Met Ser Arg Ala Arg Asp Glu Ala Gly
115 120 125
Glu Gly Ser Val Met Ser Leu Glu Asn Thr Gly Lys Leu
130 135 140

<210> 189
<211> 429
<212> DNA
<213> Homo sapiens

<400> 189
ngatggttta ccaacatatg cacggttcga gcggcaatag ctcctcgggg gctggcagtg
60

aaatgtttga agatgccggc gtttccggcc tcaacttgtt tcgatgccgt ggttccaccg
120
atttcgccga tgcggctcat cgcacggtta agaagtttcg tccagataac ccaggacaga
180
gcaaggtata tcaggctcag aaccaggaaa agcagggctt taccccagtg ccccatatag
240
accgcgctag ctacggcaaa aggcgcgccc agtggggtcc aggacagcac tttcatggct
300
gaagggagcg catcccnagc ttcgcctagc cccagagcta acccagcgac cagtggacca
360
gcgcccatca tcagtaggaa ccctacgata atcagccctt gttttacccc tggaatggag
420
ctgatttcn
429

<210> 190
<211> 123
<212> PRT
<213> Homo sapiens

<400> 190
Met Met Gly Ala Gly Pro Leu Val Ala Gly Leu Ala Leu Gly Leu Gly
 1   5   10   15
Glu Ala Xaa Asp Ala Leu Pro Ser Ala Met Lys Val Leu Ser Trp Thr
            20   25   30
Pro Leu Gly Ala Pro Phe Ala Val Ala Ser Ala Val Tyr Met Gly His
        35   40   45
Trp Gly Lys Ala Leu Leu Phe Leu Val Leu Ser Leu Ile Tyr Leu Ala
    50   55   60
Leu Ser Trp Val Ile Trp Thr Lys Leu Leu Asn Arg Ala Met Ser Arg
65   70   75   80
Ile Gly Glu Ile Gly Gly Thr Thr Ala Ser Lys Gln Val Glu Ala Gly
                85   90   95
Asn Ala Gly Ile Phe Lys His Phe Thr Ala Ser Pro Arg Gly Ala Ile
            100   105   110
Ala Ala Arg Thr Val His Met Leu Val Asn His
        115   120

<210> 191
<211> 4845
<212> DNA
<213> Homo sapiens

<400> 191
ccgcccgggg ccatggcgac actcagcttc gtcttcctgc tgctgggggc agtgtcctgg
60
cctccggctt ctgcctccgg ccaggagttc tggcccggac aatcggcggc cgatattctg
120
tcgggggcgg cttcccgcag acggtatctt ctgtatgacg tcaacccccc ggaaggcttc
180
aacctgcgca gggatgtcta tatccgaatc gcctctctcc tgaagactct gctgaagacg
240
gaggagtggg tgcttgtcct gcctccatgg ggccgcctct atcactggca gagtcctgac
300

atccaccagg tccggattcc ctggtctgag ttttttgatc ttccaagtct caataaaaac
360
atccccgtca tcgagtatga gcagttcatc gcagaatctg gtgggccctt tattgaccag
420
gtttacgtcc tgcaaagtta cgcagagggg tggaaagaag ggacctggga agagaaggtg
480
gacgagcggc cgtgtattga tcagctcctg tactcccagg acaagcacga gtactacaga
540
ggatggtttt ggggttatga ggagaccagg ggtctaaacg tctcctgtct gtccgtccag
600
ggctcagcct ccatcgtggc gcccctgctg ctgagaaaca catcagcccg gtccgtgatg
660
ttagacagag ccgagaacct acttcacgac cactatggag ggaaagaata ctgggatacc
720
cgtcgcagca tggtgtttgc caggcacctg cgggaggtgg gagacgagtt caggagcaga
780
catctcaact ccacggacga cgcagacagg atccccttcc aggaggactg gatgaagatg
840
aaggtcaagc tgggctccgc gctaggggge ccctacctgg gagtccacct gagaagaaaa
900
gatttcatct ggggtcacag acaggatgta cccagtctgg aaggggccgt gaggaagatc
960
cgcagcctca tgaagaccca ccggctggac aaggtgtttg tggccacaga tgccgtcaga
1020
aaggaatatg aagagctaaa aaagctgtta cccgagatgg tgaggtttga acccacgtgg
1080
gaggagctgg agctctacaa ggacggaggc gttgcgatta ttgaccagtg gatctgcgca
1140
cacgccaggt gcctgcccac gtcactgtcg gccgagagcg ggtcgggtgg ctttcaaagg
1200
ttcttctgtc ccaagtactc ggtgtcagag cagatggtcg cctgtgttca cagtggtcat
1260
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1320
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1380
aggctgttgg catagctggc ctcgtctcag aacctcttct tgtgtcgcat tttcccatca
1440
ttcccggttt ctgcccctgt ctgcccctg ccctgagagt tgcccgtgcc ctggacttgg
1500
gcatgtcctt gttgctgtgt tgttgagcat ccgtgagcgt ccccgaggcc gggagcgtgg
1560
gccctcgtgt gatcattctc gtggggctgc catgagcgtc cccaaggctg ggagcatggg
1620
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1680
cctcgtgtga tcattctcgt ggggctgccg tgagcgtccc agaggccggg agcgtgggcc
1740
ctgcgtgcag tcattcctct ggggttgctg tgggaggtac gcctgggcct ctgttcctcc
1800
aaagacctgc ctgcccatct gcataggaga tgaaggctgg ggttagggtg aaacggtttg
1860
agttaaatgg aaaatgaaag tagagggaat gatcttcccc gtggttagca ctgtgcacac
1920

gcgtgcgtct ctgtgggtta gtctgtctct ctcctgcccg aggaatgctg agcgccctga
1980
gccggtgcct cttcacacat ctgctatttc ctgtggtgtt ctgggcatgg tgtataagac
2040
ccacagaggc tccgggtgat gctgtctgct gggtgtgggt ccctttccct gttaagcaga
2100
caggatgcag cgctgacttc ttaggtcagg gcggaggtgt gcaggagccc agtcacgagc
2160
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2220
ccgcagccca ggaagcctgc tgtggggagg cttcgcactg agctctcagc ctcctgccct
2280
cagctgcgcg aagcgctcgg cccagctcac tgaagctgcc ctgcctccgg gccggcgcgg
2340
cctgctctgg caggcccctg tgtgtggggt ggtgagggtc tccccaccag tgctgcaccc
2400
cgcagcagca tacaggcctg tgtggcctgc tggccctgtg gctctgtgta cagcgctgtg
2460
catgttacat ttgctctgga aacatctctg gggtttgctt gttcacgaag ttcatgaagt
2520
gccgctggag agccagagac cagctgcgca ggagccggag gaacgggcag gccgctgacc
2580
tgaggtctgg agaaacccct ggagaagggt gtccccacca gcccatacag cgtgtgtgtg
2640
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2700
ggctagacag tgtgtggtta gtaggaatct ctcattgttc accatgtgac ccccaggagg
2760
tattcgacct gcactggcgt gcctggcctg ggatttggtg acggagagga gggctcccag
2820
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2880
cagcaccagg cagagcccct cagggcgccg atgtcgaggg cacctgagcg aggggtgcca
2940
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3000
tggaactcat ttcactcagc tgctcctctc agttctccct gactctggaa cctctgtgac
3060
cccagttctc cctgactctg gaacctctgt gatcctttgc aggtttttt attggcacct
3120
cagtctcaac attttctttt cggattcatg aggaaagaga aatcctgggg ttggacccca
3180
agacgacgta caacaggttc tgcggagacc aagagaaggc gtgtgagcaa cccacccact
3240
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3300
tggatgcagg ttctgtcgcc gtggagtcac cgtctactgc cagccgggag ctgggcggac
3360
aggaccgtcc ctcgcagggt cccaggccca gaagaggccc cacgcctcta gagctgggct
3420
ccgtcctcgg cgttgccagc cgccatggct gatgaagagg ctccgctgct ctcgggggcg
3480
gcggttgttt tcaggcagcg tctgtgaacc cacagctcgg ttgccagcag tgcccgcgtg
3540

gtgacccaga agcaggagtg tttgtcaggc tcccgctctg gcctttccag ccacctttca
3600
tgtcttcata ttttaagtgc attgaggata gatgcaggcg ggtgagctgc cctccgtcag
3660
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3720
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3780
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3840
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3900
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3960
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4020
cccctccctc gccccgactg ccccgcccca ccctcacccc gactgccccg ccctcgcccg
4080
gctggccgtc cctgccctcg ccccggctgg caggtgcaca tggggcctcc aggtctgcca
4140
ttcgctattg agaactagaa atgaggaagg acagttacgc taactccaaa aggctgtcta
4200
ggatgagctg ctttatcagg gagctccttg tacccatttt acagaaatca tttttaggtc
4260
tttgtgccac caccacgagg ggcatctgca aagagggcaa cgctagacac agaatccgtg
4320
gaaggtgcag cagtgcctca ggggtcctca gggtcaggga gccccccctca ccctcttggc
4380
ccgttaccct ttgtgacttt ccaccatggt gtcgtgtgac cctcagtcag gttggtgggg
4440
gctgagtcct cactgagcag ccactttcca catctgctag aggaacagtg acatggacac
4500
ctgtgacaga gagaggacag ttagtgagga gggacagaca gctcttcctt tcggagcctg
4560
gctagtctag gacatcacct tgctgtgtct tctcaagctt ttaaaattga ccctgaacgt
4620cctatggtgt tactcaaagc tgtgcagggt aaatgatgac atatttattc 4680
tttttccatt tgttctagaa acagtgcctt tttcatcagt tgcattttcc aggctgagag
4740
ctgtataaaa cattttggac tgtgaccatg taccttcctt tttaagaaaa ataaactgct
4800
ttatggaagt tggtaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa
4845

<210> 192
<211> 428
<212> PRT
<213> Homo sapiens

<400> 192
Pro Pro Gly Ala Met Ala Thr Leu Ser Phe Val Phe Leu Leu Leu Gly
1 5 10 15
Ala Val Ser Trp Pro Pro Ala Ser Ala Ser Gly Gln Glu Phe Trp Pro
20 25 30
Gly Gln Ser Ala Ala Asp Ile Leu Ser Gly Ala Ala Ser Arg Arg Arg

```
        35                  40                  45
Tyr Leu Leu Tyr Asp Val Asn Pro Pro Glu Gly Phe Asn Leu Arg Arg
    50                  55                  60
Asp Val Tyr Ile Arg Ile Ala Ser Leu Leu Lys Thr Leu Leu Lys Thr
65                  70                  75                  80
Glu Glu Trp Val Leu Val Leu Pro Pro Trp Gly Arg Leu Tyr His Trp
                85                  90                  95
Gln Ser Pro Asp Ile His Gln Val Arg Ile Pro Trp Ser Glu Phe Phe
            100                 105                 110
Asp Leu Pro Ser Leu Asn Lys Asn Ile Pro Val Ile Glu Tyr Glu Gln
        115                 120                 125
Phe Ile Ala Glu Ser Gly Gly Pro Phe Ile Asp Gln Val Tyr Val Leu
    130                 135                 140
Gln Ser Tyr Ala Glu Gly Trp Lys Glu Gly Thr Trp Glu Glu Lys Val
145                 150                 155                 160
Asp Glu Arg Pro Cys Ile Asp Gln Leu Leu Tyr Ser Gln Asp Lys His
                165                 170                 175
Glu Tyr Tyr Arg Gly Trp Phe Trp Gly Tyr Glu Glu Thr Arg Gly Leu
            180                 185                 190
Asn Val Ser Cys Leu Ser Val Gln Gly Ser Ala Ser Ile Val Ala Pro
        195                 200                 205
Leu Leu Leu Arg Asn Thr Ser Ala Arg Ser Val Met Leu Asp Arg Ala
    210                 215                 220
Glu Asn Leu Leu His Asp His Tyr Gly Gly Lys Glu Tyr Trp Asp Thr
225                 230                 235                 240
Arg Arg Ser Met Val Phe Ala Arg His Leu Arg Glu Val Gly Asp Glu
                245                 250                 255
Phe Arg Ser Arg His Leu Asn Ser Thr Asp Asp Ala Asp Arg Ile Pro
            260                 265                 270
Phe Gln Glu Asp Trp Met Lys Met Lys Val Lys Leu Gly Ser Ala Leu
        275                 280                 285
Gly Gly Pro Tyr Leu Gly Val His Leu Arg Arg Lys Asp Phe Ile Trp
    290                 295                 300
Gly His Arg Gln Asp Val Pro Ser Leu Glu Gly Ala Val Arg Lys Ile
305                 310                 315                 320
Arg Ser Leu Met Lys Thr His Arg Leu Asp Lys Val Phe Val Ala Thr
                325                 330                 335
Asp Ala Val Arg Lys Glu Tyr Glu Glu Leu Lys Lys Leu Leu Pro Glu
            340                 345                 350
Met Val Arg Phe Glu Pro Thr Trp Glu Glu Leu Glu Leu Tyr Lys Asp
        355                 360                 365
Gly Gly Val Ala Ile Ile Asp Gln Trp Ile Cys Ala His Ala Arg Cys
    370                 375                 380
Leu Pro Thr Ser Leu Ser Ala Glu Ser Gly Ser Gly Gly Phe Gln Arg
385                 390                 395                 400
Phe Phe Cys Pro Lys Tyr Ser Val Ser Glu Gln Met Val Ala Cys Val
                405                 410                 415
His Ser Gly His Phe His Thr Val Cys Leu Leu Val
            420                 425
```

<210> 193
<211> 350
<212> DNA
<213> Homo sapiens

<400> 193
gccggcgagc tggactgcgc catcatggcc gagcccttcc ccgacaccgg cctggccacg
60
gcgcagctgt acgacgagcc cttcgtcgtc gcgctgcggg cgtcgcaccc gctggccgac
120
cgtgccagca tcagccccga ggaggtcaag ggcgagacca tgttgatgtt gggcacgggc
180
ccctggtttc cccgggcccg cggtgggggt ttggcccgga tttggcgcgt ttctccagcg
240
ccgttaaggg catacgccgc agtttcgagg gctcgtcgct ggagaccatc aagcacatcg
300
tggcttcggg catggcgtga cggtggtgcc gcagctgtcc gtgccgcgcg
350

<210> 194
<211> 116
<212> PRT
<213> Homo sapiens

<400> 194
Ala Gly Glu Leu Asp Cys Ala Ile Met Ala Glu Pro Phe Pro Asp Thr
1 5 10 15
Gly Leu Ala Thr Ala Gln Leu Tyr Asp Glu Pro Phe Val Val Ala Leu
20 25 30
Arg Ala Ser His Pro Leu Ala Asp Arg Ala Ser Ile Ser Pro Glu Glu
35 40 45
Val Lys Gly Glu Thr Met Leu Met Leu Gly Thr Gly Pro Trp Phe Pro
50 55 60
Arg Ala Arg Gly Gly Gly Leu Ala Arg Ile Trp Arg Val Ser Pro Ala
65 70 75 80
Pro Leu Arg Ala Tyr Ala Ala Val Ser Arg Ala Arg Arg Trp Arg Pro
85 90 95
Ser Ser Thr Ser Trp Leu Arg Ala Trp Arg Asp Gly Gly Ala Ala Ala
100 105 110
Val Arg Ala Ala
115

<210> 195
<211> 495
<212> DNA
<213> Homo sapiens

<400> 195
acgcgtgaac gcgacggctt ggcgatcgga ggcgtcggcc ccgtcgttga gtgggccgtt
60
gaaatggttc gcttcgacga aagcgagact ctcgaccgcc ttgcatcggg cgtccttgaa
120
ccagaacttg gcgacgattt ggccgccgtc ctgctcgatt ctcatcgggt tgctgtcatc
180
agcgagggat cgaactggct tgcctcgcta cccgtgatcg taggtcgcaa cacggaacag
240
tttcgcagca taccagacct tgcccgcgac cggatcgaca aactgcacca gttgagccat
300

cgcgaaatag cacgaaatcg cgagctcctg cgtgcccgcg ctgcgtcggg gcaggtgcgg
360
cactgccacg gcgacgcaca cctcggcaac atcgtcatga ttgacggcaa gccggtcctg
420
ttcgacgcga tcgaatttga tcctgatatc gcgacaacgg atgtgctgta cgatttcgcg
480
ttccctctga tggat
495

<210> 196
<211> 165
<212> PRT
<213> Homo sapiens

<400> 196
Thr Arg Glu Arg Asp Gly Leu Ala Ile Gly Gly Val Gly Pro Val Val
1 5 10 15
Glu Trp Ala Val Glu Met Val Arg Phe Asp Glu Ser Glu Thr Leu Asp
20 25 30
Arg Leu Ala Ser Gly Val Leu Glu Pro Glu Leu Gly Asp Asp Leu Ala
35 40 45
Ala Val Leu Leu Asp Ser His Arg Val Ala Val Ile Ser Glu Gly Ser
50 55 60
Asn Trp Leu Ala Ser Leu Pro Val Ile Val Gly Arg Asn Thr Glu Gln
65 70 75 80
Phe Arg Ser Ile Pro Asp Leu Ala Arg Asp Arg Ile Asp Lys Leu His
85 90 95
Gln Leu Ser His Arg Glu Ile Ala Arg Asn Arg Glu Leu Leu Arg Ala
100 105 110
Arg Ala Ala Ser Gly Gln Val Arg His Cys His Gly Asp Ala His Leu
115 120 125
Gly Asn Ile Val Met Ile Asp Gly Lys Pro Val Leu Phe Asp Ala Ile
130 135 140
Glu Phe Asp Pro Asp Ile Ala Thr Thr Asp Val Leu Tyr Asp Phe Ala
145 150 155 160
Phe Pro Leu Met Asp
165

<210> 197
<211> 402
<212> DNA
<213> Homo sapiens

<400> 197
caagcaatgc ttgacgcagt tgttgaatac ttaccagcac cgactgatat tccagcaatc
60
aaaggtatca atccagatga aactgaaggt gaacgtcacg caagcgatga tgagccattc
120
tcttcattag cattcaaaat tgcaactgac ccattcgtag gtaacttaac cttcttccgt
180
gtgtactcag gtgtaattaa ctctggtgat acagtattaa actctgtacg tcaaaaacgt
240
gaacgttttg gtcgtatcgt acagatgcac gctaataaac gtgaagaaat taaagaagtt
300

cgtgcgggcg atatcgctgc agcaatcggc ttaaaagatg taactacggg tgaaccatta
360
tgtgctgtcg atgcaccaat cattcttgag cgtatggaat tc
402

<210> 198
<211> 134
<212> PRT
<213> Homo sapiens

<400> 198
Gln Ala Met Leu Asp Ala Val Val Glu Tyr Leu Pro Ala Pro Thr Asp
1 5 10 15
Ile Pro Ala Ile Lys Gly Ile Asn Pro Asp Glu Thr Glu Gly Glu Arg
20 25 30
His Ala Ser Asp Asp Glu Pro Phe Ser Ser Leu Ala Phe Lys Ile Ala
35 40 45
Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe Arg Val Tyr Ser Gly
50 55 60
Val Ile Asn Ser Gly Asp Thr Val Leu Asn Ser Val Arg Gln Lys Arg
65 70 75 80
Glu Arg Phe Gly Arg Ile Val Gln Met His Ala Asn Lys Arg Glu Glu
85 90 95
Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala Ala Ile Gly Leu Lys
100 105 110
Asp Val Thr Thr Gly Glu Pro Leu Cys Ala Val Asp Ala Pro Ile Ile
115 120 125
Leu Glu Arg Met Glu Phe
130

<210> 199
<211> 507
<212> DNA
<213> Homo sapiens

<400> 199
acgcgtgaag tcgtgcatag atcggtgtga catagagaag cctccgaccc aagctgcgta
60
tatcgcacaa agaccaagcg accctggacg ttctagacag aactctgcta cgaggcctga
120
caatagtgaa atccccgaga acccagctat ggaagggttt ccagatgctc gaaggcctgt
180
cataccagag gttaggttaa actgtatgga gactttcgag gtgaaagttg actcgccggt
240
aaagcctgct cctaaagagg atttagatct gatagatcta tcctcagatt caacctcggg
300
gcctgaaaaa cactctatac tctcaacctc cgacagcgac tctcttgtat ttgagcctct
360
tccctctctc agaatagtcg agagtgacga agaagaggag acgatgaacc aaggcgatga
420
cggccccctcc ggtaaaaatg ctgcctcttc tccctccatc cccagccatc cctccgtcct
480
cagcctgagc acagctccgc ttgtaca
507

<210> 200
<211> 153
<212> PRT
<213> Homo sapiens

<400> 200
Met Glu Gly Glu Glu Ala Ala Phe Leu Pro Glu Gly Pro Ser Ser Pro
1 5 10 15
Trp Phe Ile Val Ser Ser Ser Ser Ser Leu Ser Thr Ile Leu Arg Glu
20 25 30
Gly Arg Gly Ser Asn Thr Arg Glu Ser Leu Ser Glu Val Glu Ser Ile
35 40 45
Glu Cys Phe Ser Gly Pro Glu Val Glu Ser Glu Asp Arg Ser Ile Arg
50 55 60
Ser Lys Ser Ser Leu Gly Ala Gly Phe Thr Gly Glu Ser Thr Phe Thr
65 70 75 80
Ser Lys Val Ser Ile Gln Phe Asn Leu Thr Ser Gly Met Thr Gly Leu
85 90 95
Arg Ala Ser Gly Asn Pro Ser Ile Ala Gly Phe Ser Gly Ile Ser Leu
100 105 110
Leu Ser Gly Leu Val Ala Glu Phe Cys Leu Glu Arg Pro Gly Ser Leu
115 120 125
Gly Leu Cys Ala Ile Tyr Ala Ala Trp Val Gly Gly Phe Ser Met Ser
130 135 140
His Arg Ser Met His Asp Phe Thr Arg
145 150

<210> 201
<211> 527
<212> DNA
<213> Homo sapiens

<400> 201
gatgtggcta ttatccctgt ttcccaggtg agaaacaggg tcagtgatag agctgggatg
60
tgtgcctgca ggctcaccag ccagtcccct cctcaccaag gatgatgttc tccgtggtga
120
gctggtcctt ggtctcctgg aactcgtggc gcacctgggc cagctgcgcc tcgaaggcat
180
ccttctccat ctctttggct agctgcaagt tctggagctg ctcgttgagg tctgtgatct
240
catccacctg ctggttgagc gtgcgcttga ggaaggccac aatctccttc ttgttattgg
300
ccagctgctc aaactcctgg cggaacatct tctcctgcac agccagctca tcccacttcc
360
gctggtaccg ggctagccgg tcctccaggt ctcggatctg gatgtggtag aactccttca
420
tctccttggc cagaggcggc tccacggcca ccaccggctc cttcttgccc cctttcttct
480
tgacttcaag ctccttgcct gccttgctca cactcttttt gggaggc
527

<210> 202

<211> 70
<212> PRT
<213> Homo sapiens

<400> 202
Gly Arg Pro Gln Ser Pro Ser Cys Tyr Trp Pro Ala Ala Gln Thr Pro
1 5 10 15
Gly Gly Thr Ser Ser Pro Ala Gln Pro Ala His Pro Thr Ser Ala Gly
20 25 30
Thr Gly Leu Ala Gly Pro Pro Gly Leu Gly Ser Gly Cys Gly Arg Thr
35 40 45
Pro Ser Ser Pro Trp Pro Glu Ala Ala Pro Arg Pro Pro Pro Ala Pro
50 55 60
Ser Cys Pro Leu Ser Ser
65 70

<210> 203
<211> 304
<212> DNA
<213> Homo sapiens

<400> 203
ngtgcaccgg tggtcatgga caacgccgcc tacgtggtct acacctcggg atccaccggc
60
cgacccaagg gagttgtcgt cacccacacc ggactcgaca gcttcgcact cgaccagcag
120
cgtcgattcc acgcagatca ccactctcga accctgcact tcgccacccc cagcttcgac
180
ggagccgtct tcgagtacct gcaggcattc ggtgtcggag ccaccatggt gatcgtcccg
240
accgacatct acggcggcgc cgaactggca agtctcatcc gccgcgaaca cgtcactcac
300
gcgt
304

<210> 204
<211> 101
<212> PRT
<213> Homo sapiens

<400> 204
Xaa Ala Pro Val Val Met Asp Asn Ala Ala Tyr Val Val Tyr Thr Ser
1 5 10 15
Gly Ser Thr Gly Arg Pro Lys Gly Val Val Val Thr His Thr Gly Leu
20 25 30
Asp Ser Phe Ala Leu Asp Gln Gln Arg Arg Phe His Ala Asp His His
35 40 45
Ser Arg Thr Leu His Phe Ala Thr Pro Ser Phe Asp Gly Ala Val Phe
50 55 60
Glu Tyr Leu Gln Ala Phe Gly Val Gly Ala Thr Met Val Ile Val Pro
65 70 75 80
Thr Asp Ile Tyr Gly Gly Ala Glu Leu Ala Ser Leu Ile Arg Arg Glu
85 90 95
His Val Thr His Ala

100

<210> 205
<211> 356
<212> DNA
<213> Homo sapiens

<400> 205
nngaattcag caatgataac tggctcaatt gaaggtaaga caacaattga gggaattaat
60
gcacaattaa atacagtgtt aactttattt tcaccacaat caaaagataa agatttaatc
120
atgccagatc aacaagaaga aatagatatt ctgattgcaa ccgactgtat ttcagaagga
180
cagaacttac aagattgtga ttacttaata aactatgaca ttcattggaa tccagttcgt
240
atcattcaaa gatttggacg gattgatcga attggttcga agaataaatg tgtacaatta
300
gttaactttt ggccagatat tacattagat gaatatattg atctaaaggg acgcgt
356

<210> 206
<211> 118
<212> PRT
<213> Homo sapiens

<400> 206
Xaa Asn Ser Ala Met Ile Thr Gly Ser Ile Glu Gly Lys Thr Thr Ile
1 5 10 15
Glu Gly Ile Asn Ala Gln Leu Asn Thr Val Leu Thr Leu Phe Ser Pro
20 25 30
Gln Ser Lys Asp Lys Asp Leu Ile Met Pro Asp Gln Gln Glu Glu Ile
35 40 45
Asp Ile Leu Ile Ala Thr Asp Cys Ile Ser Glu Gly Gln Asn Leu Gln
50 55 60
Asp Cys Asp Tyr Leu Ile Asn Tyr Asp Ile His Trp Asn Pro Val Arg
65 70 75 80
Ile Ile Gln Arg Phe Gly Arg Ile Asp Arg Ile Gly Ser Lys Asn Lys
85 90 95
Cys Val Gln Leu Val Asn Phe Trp Pro Asp Ile Thr Leu Asp Glu Tyr
100 105 110
Ile Asp Leu Lys Gly Arg
115

<210> 207
<211> 324
<212> DNA
<213> Homo sapiens

<400> 207
acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
60
catggtgtgt gcacgtgtng cactgtgtgt ggatgcatgg taatgtgcac gtgtgcactg
120

tgtgtggtgt gtatgcatgg tgtgtgcacg tgtgcactgt gtgtgtgtgt atgcatgtgt
180
gtgcacatgt gcactgtgtg gtgtgtatgc atggtgtgtg cacgtgtgca ctgtgtatgc
240
atgngtgtgt gcatgtgtgc actgtgtatg catagtgtgc acgtgtgcac tgtgtggtgt
300
gtatgcatgg taatgtgcac gtgt
324

<210> 208
<211> 108
<212> PRT
<213> Homo sapiens

<400> 208
Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
1 5 10 15
Val Val Cys Met His Gly Val Cys Thr Cys Xaa Thr Val Cys Gly Cys
20 25 30
Met Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val
35 40 45
Cys Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Met Cys
50 55 60
Thr Val Trp Cys Val Cys Met Val Cys Ala Arg Val His Cys Val Cys
65 70 75 80
Met Xaa Val Cys Met Cys Ala Leu Cys Met His Ser Val His Val Cys
85 90 95
Thr Val Trp Cys Val Cys Met Val Met Cys Thr Cys
100 105

<210> 209
<211> 168
<212> DNA
<213> Homo sapiens

<400> 209
nnctccagag gttatgaggt tggaagcccg gttttttttca ggtgcagaaa aggctaccat
60
attcaaggtt ccacgactcg cacctgcctt gccaatttaa catggagtgg gatacagacc
120
gaatgtatac ctcatgcctg cagacagcca gaaaccccgg cacacgcg
168

<210> 210
<211> 56
<212> PRT
<213> Homo sapiens

<400> 210
Xaa Ser Arg Gly Tyr Glu Val Gly Ser Pro Val Phe Phe Arg Cys Arg
1 5 10 15
Lys Gly Tyr His Ile Gln Gly Ser Thr Thr Arg Thr Cys Leu Ala Asn
20 25 30
Leu Thr Trp Ser Gly Ile Gln Thr Glu Cys Ile Pro His Ala Cys Arg

```
        35                  40                  45
Gln Pro Glu Thr Pro Ala His Ala
    50                  55

<210> 211
<211> 354
<212> DNA
<213> Homo sapiens

<400> 211
tacatgggct ttgacacagt ggtggctgaa gctgcactaa gggtgtttgg aggcaatgtc
60
cagctggcag ctcagaccct tgcacaccat ggaggaagcc tcccacccga cctgcagttc
120
tcaggagagg actcctcccc cacaccgtcc acatccccat ctgactctgc agggacctct
180
agtgcctcga cagatgaaga catggagacg gaggctgtca acgaaatcct ggaggacatt
240
ccggagcacg aggaggacta cctggactcc acgctggagg atgaagaagt cattattgct
300
gaatacttgt cctgcgttga aagtataagt tctgccngca aagaacaact gatc
354

<210> 212
<211> 118
<212> PRT
<213> Homo sapiens

<400> 212
Tyr Met Gly Phe Asp Thr Val Val Ala Glu Ala Ala Leu Arg Val Phe
 1               5                  10                  15
Gly Gly Asn Val Gln Leu Ala Ala Gln Thr Leu Ala His His Gly Gly
            20                  25                  30
Ser Leu Pro Pro Asp Leu Gln Phe Ser Gly Glu Asp Ser Ser Pro Thr
        35                  40                  45
Pro Ser Thr Ser Pro Ser Asp Ser Ala Gly Thr Ser Ser Ala Ser Thr
    50                  55                  60
Asp Glu Asp Met Glu Thr Glu Ala Val Asn Glu Ile Leu Glu Asp Ile
65                  70                  75                  80
Pro Glu His Glu Glu Asp Tyr Leu Asp Ser Thr Leu Glu Asp Glu Glu
                85                  90                  95
Val Ile Ile Ala Glu Tyr Leu Ser Cys Val Glu Ser Ile Ser Ser Ala
            100                 105                 110
Xaa Lys Glu Gln Leu Ile
        115

<210> 213
<211> 669
<212> DNA
<213> Homo sapiens

<400> 213
attgcccaat ctcagagtgt ccaggaaagc ctggagagcc tgttgcagtc tattggggaa
60
```

gttgaacaaa acctggaagg gaaacaggtg tcatcactct catcaggagt catccaggaa
120
gccttagcca caaatatgaa attgaagcag gacattgctc ggcaaaagag cagcttggag
180
gccacccgtg agatggtgac ccgattcatg gagacagcag acagtactac agcagcagtg
240
ctgcagggca aactggcaga ggtgagccag cggttcgaac agctctgtct acagcagcaa
300
gaaaaggaga gctccctaaa gaagcttcta ccccaggcag agatgtttga acacctctct
360
ggtaagctgc agcagttcat ggaaaacaaa agtcggatgc tggcctctgg aaatcagcca
420
gatcaagata ttacacattt cttccaacag atccaggagc tcaatttgga aatggaagac
480
caacaggaga acctagatac tcttgagcac ctggtcactg aactgagctc ttgtggcttt
540
gcgctggact tgtgccagca tcaggacagg gtacagaatc taagaaaaga cttcacagag
600
ctacagaaga cagttaaaga gagagagaaa gatgcatcat cttgccagga acagttggat
660
gaattccgg
669

<210> 214
<211> 223
<212> PRT
<213> Homo sapiens

<400> 214
Ile Ala Gln Ser Gln Ser Val Gln Glu Ser Leu Glu Ser Leu Leu Gln
1 5 10 15
Ser Ile Gly Glu Val Glu Gln Asn Leu Glu Gly Lys Gln Val Ser Ser
20 25 30
Leu Ser Ser Gly Val Ile Gln Glu Ala Leu Ala Thr Asn Met Lys Leu
35 40 45
Lys Gln Asp Ile Ala Arg Gln Lys Ser Ser Leu Glu Ala Thr Arg Glu
50 55 60
Met Val Thr Arg Phe Met Glu Thr Ala Asp Ser Thr Thr Ala Ala Val
65 70 75 80
Leu Gln Gly Lys Leu Ala Glu Val Ser Gln Arg Phe Glu Gln Leu Cys
85 90 95
Leu Gln Gln Gln Glu Lys Glu Ser Ser Leu Lys Lys Leu Leu Pro Gln
100 105 110
Ala Glu Met Phe Glu His Leu Ser Gly Lys Leu Gln Gln Phe Met Glu
115 120 125
Asn Lys Ser Arg Met Leu Ala Ser Gly Asn Gln Pro Asp Gln Asp Ile
130 135 140
Thr His Phe Phe Gln Gln Ile Gln Glu Leu Asn Leu Glu Met Glu Asp
145 150 155 160
Gln Gln Glu Asn Leu Asp Thr Leu Glu His Leu Val Thr Glu Leu Ser
165 170 175
Ser Cys Gly Phe Ala Leu Asp Leu Cys Gln His Gln Asp Arg Val Gln
180 185 190
Asn Leu Arg Lys Asp Phe Thr Glu Leu Gln Lys Thr Val Lys Glu Arg

```
        195                 200                 205
Glu Lys Asp Ala Ser Ser Cys Gln Glu Gln Leu Asp Glu Phe Arg
    210                 215                 220
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<210> 215
<211> 814
<212> DNA
<213> Homo sapiens

<400> 215
aaatttcgta cccgctccgg cacagtacga gcccttgacg atgtgagcct ggctattaag
60
agaggttcca tctcagccgt tatcgggcac tccggagccg gcaaatccac cctggttcgc
120
ctcatcaacg gattagagac tcccacgcgt ggccgcgtct tggtagacgg caccgacgtc
180
tcgcagctct cggacaaagc gatgcgcccg ctacgcgcag acatcgggat gatcttccaa
240
cagttcaacc tattcggctc aaggaccatc tacgacaacg ttgcctatcc actcaagctg
300
gctcattgga agaaagcaga cgagaagaag cgcgtcaccg aattgctgag cttcgtcggg
360
ttgacgagca aagcctggga ccatccagac cagctctcgg gcggacagaa acagcgggtt
420
ggtattgccc gagcgctagc aactaaacca tcgattttgt tggctgacga gtccacctcg
480
gcgctggatc cagaaacgac agctgatgtc ctatccctgc tcaagcgggt caatgcggaa
540
ctaggggtga cggtcgtcgt catcacccac gagatggagg tcgtccgctc gattgcccag
600
caggtctcgg tactagcagc tggccatctc gtcgagtctg gaagcgcccg ccaggtcttc
660
gctcatccac agtcagagac cacccagcgt ttcctggcga cgattatcgg ccagcacccg
720
agtggggagg aacaggcacg gttgcagtcg gaaaacccag atgcacgact cgtcgacgtc
780
agttcggtgg ccagtcactc gttcggtgac gcgt
814

<210> 216
<211> 271
<212> PRT
<213> Homo sapiens

<400> 216

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Lys Phe Arg Thr Arg Ser Gly Thr Val Arg Ala Leu Asp Asp Val Ser
 1               5                  10                  15
Leu Ala Ile Lys Arg Gly Ser Ile Ser Ala Val Ile Gly His Ser Gly
            20                  25                  30
Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Glu Thr Pro
        35                  40                  45
Thr Arg Gly Arg Val Leu Val Asp Gly Thr Asp Val Ser Gln Leu Ser
    50                  55                  60
Asp Lys Ala Met Arg Pro Leu Arg Ala Asp Ile Gly Met Ile Phe Gln
```

65 70 75 80
Gln Phe Asn Leu Phe Gly Ser Arg Thr Ile Tyr Asp Asn Val Ala Tyr
85 90 95
Pro Leu Lys Leu Ala His Trp Lys Lys Ala Asp Glu Lys Lys Arg Val
100 105 110
Thr Glu Leu Leu Ser Phe Val Gly Leu Thr Ser Lys Ala Trp Asp His
115 120 125
Pro Asp Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg
130 135 140
Ala Leu Ala Thr Lys Pro Ser Ile Leu Leu Ala Asp Glu Ser Thr Ser
145 150 155 160
Ala Leu Asp Pro Glu Thr Thr Ala Asp Val Leu Ser Leu Leu Lys Arg
165 170 175
Val Asn Ala Glu Leu Gly Val Thr Val Val Val Ile Thr His Glu Met
180 185 190
Glu Val Val Arg Ser Ile Ala Gln Gln Val Ser Val Leu Ala Ala Gly
195 200 205
His Leu Val Glu Ser Gly Ser Ala Arg Gln Val Phe Ala His Pro Gln
210 215 220
Ser Glu Thr Thr Gln Arg Phe Leu Ala Thr Ile Ile Gly Gln His Pro
225 230 235 240
Ser Gly Glu Glu Gln Ala Arg Leu Gln Ser Glu Asn Pro Asp Ala Arg
245 250 255
Leu Val Asp Val Ser Ser Val Ala Ser His Ser Phe Gly Asp Ala
260 265 270

<210> 217
<211> 500
<212> DNA
<213> Homo sapiens

<400> 217
nnacgcgtcg cgatgaaaga ggcgctgaaa ggtgccatcc agattccaac agtgactttt
60
agctctgaga agtccaatac tacagccctg gctgagttcg gaaaatacat tcataaagtc
120
tttcctacag tggtcagcac cagctttatc cagcatgaag tcgtggaaga gtatagccac
180
ctgttcacta tccaaggctc ggaccccagc ttgcagccct acctgctgat ggctcacttt
240
gatgtggtgc ctgcccctga agaaggctgg gaggtgcccc cattctctgg gttggagcgt
300
gatggcgtca tctatggttg gggcacactg gacgacaaga actctgtgat ggcattactg
360
caggccttgg agctcctgct gatcaggaag tacatccccc gaagatcttt cttcatttct
420
ctgggccatg atgaggagtc atcagggaca ggggctcaga ggatctcagc cctgctacag
480
tcaaggggcg tccagctagc
500

<210> 218
<211> 166
<212> PRT

<213> Homo sapiens

<400> 218
Xaa Arg Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro
1 5 10 15
Thr Val Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu
20 25 30
Phe Gly Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser
35 40 45
Phe Ile Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile
50 55 60
Gln Gly Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe
65 70 75 80
Asp Val Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser
85 90 95
Gly Leu Glu Arg Asp Gly Val Ile Tyr Gly Trp Gly Thr Leu Asp Asp
100 105 110
Lys Asn Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Leu Ile
115 120 125
Arg Lys Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp
130 135 140
Glu Glu Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln
145 150 155 160
Ser Arg Gly Val Gln Leu
165

<210> 219
<211> 361
<212> DNA
<213> Homo sapiens

<400> 219
acgcgttgaa acgggtatat tggggatgac gccgctgtgc aatatgcgca aggccataca
60
caaggtccgc acgctcccat gtccctcgtt ttcgacagtt cttttgcgcc gcattatggc
120
gaagccgtcg agattgcgcc tgatatcaag cgcatcacgg tcaacaaccc cagccccttc
180
actttttttcg gcaccaacag ttatctgatc ggccgcgata cgctggcatt gatcgatccc
240
ggtccgcttg acgaggccca tcacgcggcg ctgctgcgtg ccattgccgg ccggccggtc
300
agccatatct ttgtcagcca cacacaccgg gaccactcgc cagtcgcgac ggttttgaaa
360
g
361

<210> 220
<211> 102
<212> PRT
<213> Homo sapiens

<400> 220
Met Ala Asp Arg Pro Ala Gly Asn Gly Thr Gln Gln Arg Arg Val Met

```
 1               5                  10                  15
Gly Leu Val Lys Arg Thr Gly Ile Asp Gln Cys Gln Arg Ile Ala Ala
            20                  25                  30
Asp Gln Ile Thr Val Gly Ala Glu Lys Ser Glu Gly Ala Gly Val Val
        35                  40                  45
Asp Arg Asp Ala Leu Asp Ile Arg Arg Asn Leu Asp Gly Phe Ala Ile
    50                  55                  60
Met Arg Arg Lys Arg Thr Val Glu Asn Glu Gly His Gly Ser Val Arg
65                  70                  75                  80
Thr Leu Cys Met Ala Leu Arg Ile Leu His Ser Gly Val Ile Pro Asn
                85                  90                  95
Ile Pro Val Ser Thr Arg
            100
```

<210> 221
<211> 401
<212> DNA
<213> Homo sapiens

<400> 221
agatctctgt gtcgtcggct gcaaagagga tgagcccaga tgcatatcag gggctccctc
60
ccacatccca cctgctcggg cagcccacgg cagccccaca ctgctgcagc acacctcgct
120
gcagctctgg ttcctcctca gaaatatccc tgccaccctg ctaagccttg gccaacactg
180
caccctgtcc caatgcggct ccagtgacca cacccccagg gcataccctc ctacagagca
240
ttcccaaaaa aggctagagt agacaccagc ctgctccgta gggggcctcc accccattct
300
ccaaggcctc cacccaggga cgcctggtga accagcatcc aggcctggcc cacctccctg
360
ctcagagtcc atgttctgtg acaagggtgg caactgggat t
401

<210> 222
<211> 124
<212> PRT
<213> Homo sapiens

<400> 222
```
Met Asp Ser Glu Gln Gly Gly Gly Pro Gly Leu Asp Ala Gly Ser Pro
 1               5                  10                  15
Gly Val Pro Gly Trp Arg Pro Trp Arg Met Gly Trp Arg Pro Pro Thr
            20                  25                  30
Glu Gln Ala Gly Val Tyr Ser Ser Leu Phe Trp Glu Cys Ser Val Gly
        35                  40                  45
Gly Tyr Ala Leu Gly Val Trp Ser Leu Glu Pro His Trp Asp Arg Val
    50                  55                  60
Gln Cys Trp Pro Arg Leu Ser Arg Val Ala Gly Ile Phe Leu Arg Arg
65                  70                  75                  80
Asn Gln Ser Cys Ser Glu Val Cys Cys Ser Ser Val Gly Leu Pro Trp
                85                  90                  95
Ala Ala Arg Ala Gly Gly Met Trp Glu Gly Ala Pro Asp Met His Leu
```

100 105 110
Gly Ser Ser Ser Leu Gln Pro Thr Thr Gln Arg Ser
115 120

<210> 223
<211> 331
<212> DNA
<213> Homo sapiens

<400> 223
tcatgaaatc tgtgggcagt gacccaggag ggtatgggca ggcccaacca ggttggtgtg
60
cccttgaagc cccacagacc tgccagggca gcagggcagt tgggagccgg agaacctgag
120
aaccaagcca ggctgcatgc aggaggctgg cacgtgaacg ctgcaggtgt tgccggcagc
180
cgtggtgcct ggcagatagt gttcgacccc cnaggacctt cttgctgggc agcccagtcc
240
aaaagctgtt cccgcttaag ccacccccac cgccttggcc acacctggca catgggtgaa
300
gcaagggcat ttcccggggc ttcctgttcc c
331

<210> 224
<211> 103
<212> PRT
<213> Homo sapiens

<400> 224
Met Pro Leu Leu His Pro Cys Ala Arg Cys Gly Gln Gly Gly Gly Gly
1 5 10 15
Gly Leu Ser Gly Asn Ser Phe Trp Thr Gly Leu Pro Ser Lys Lys Val
20 25 30
Leu Gly Gly Arg Thr Leu Ser Ala Arg His His Gly Cys Arg Gln His
35 40 45
Leu Gln Arg Ser Arg Ala Ser Leu Leu His Ala Ala Trp Leu Gly Ser
50 55 60
Gln Val Leu Arg Leu Pro Thr Ala Leu Leu Pro Trp Gln Val Cys Gly
65 70 75 80
Ala Ser Arg Ala His Gln Pro Gly Trp Ala Cys Pro Tyr Pro Pro Gly
85 90 95
Ser Leu Pro Thr Asp Phe Met
100

<210> 225
<211> 339
<212> DNA
<213> Homo sapiens

<400> 225
tgatcacggg cgtgagccac cagcccagca tcccttgcct ttcattcgca cctccacctc
60
cagaatgacc ctcattccct cctgcacaga cggtgacagc agtaactcct acaaacacca
120

ccagactgat cttcaagagc agaggaactc ccaatcacga ttccaccccc gccgggctct
180
caaatcctcc agggctgcct gctatggggg agggaggcac actttgcttg gctctcaagg
240
cctcagccag ccgggtccaa accaactccc agcctggcct caccatccca ccgccaaacc
300
tttgctcaca ctggcccctc ttcctggaac atgggcctn
339

<210> 226
<211> 91
<212> PRT
<213> Homo sapiens

<400> 226
Met Thr Leu Ile Pro Ser Cys Thr Asp Gly Asp Ser Ser Asn Ser Tyr
1 5 10 15
Lys His His Gln Thr Asp Leu Gln Glu Gln Arg Asn Ser Gln Ser Arg
20 25 30
Phe His Pro Arg Arg Ala Leu Lys Ser Ser Arg Ala Ala Cys Tyr Gly
35 40 45
Gly Gly Arg His Thr Leu Leu Gly Ser Gln Gly Leu Ser Gln Pro Gly
50 55 60
Pro Asn Gln Leu Pro Ala Trp Pro His His Pro Thr Ala Lys Pro Leu
65 70 75 80
Leu Thr Leu Ala Pro Leu Pro Gly Thr Trp Ala
85 90

<210> 227
<211> 353
<212> DNA
<213> Homo sapiens

<400> 227
gtcgacccct tcgattgtgg cgaactccat ggctgctgcg ggcctgcgta ggctctcgag
60
tagctcgacg tcgggttcgc gagggctcgc agcgtggcca tgctgcttct tggatggttc
120
gggcaactcc tcgggggatt cgagcagttc ttggcgcacc tgctctggcg tcatcccgga
180
ggccaggccg acaagtgctg cctcctgcca cccgctgagc gacgctgcca tgttgagtac
240
ggcgtcttca ctggtcaggg cgagcgcggt atcgaccagg ttggcgtcca ggccgagaga
300
cagcatgtct gctcagtcgc ggtgatgact ggagtggcgg tctcctgcac ggg
353

<210> 228
<211> 102
<212> PRT
<213> Homo sapiens

<400> 228
Met Leu Ser Leu Gly Leu Asp Ala Asn Leu Val Asp Thr Ala Leu Ala

```
 1               5                  10                  15
Leu Thr Ser Glu Asp Ala Val Leu Asn Met Ala Ala Ser Leu Ser Gly
            20                  25                  30
Trp Gln Glu Ala Ala Leu Val Gly Leu Ala Ser Gly Met Thr Pro Glu
        35                  40                  45
Gln Val Arg Gln Glu Leu Leu Glu Ser Pro Glu Glu Leu Pro Glu Pro
    50                  55                  60
Ser Lys Lys Gln His Gly His Ala Ala Ser Pro Arg Glu Pro Asp Val
65                  70                  75                  80
Glu Leu Leu Glu Ser Leu Arg Arg Pro Ala Ala Ala Met Glu Phe Ala
                85                  90                  95
Thr Ile Glu Gly Val Asp
            100
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<210> 229
<211> 743
<212> DNA
<213> Homo sapiens

<400> 229
nnggctaggg acacggcctc ctcctcaaca ggcagtgcct gtgcaggctc aggggcatca
60
tcaaagataa cacagggctg gtcaggggct gctggctgct cctgccccag gactggctcc
120
aggatgggca aggctgcctc cctggtagcc agggggagag gggaagggag caccagggag
180
tgggccagca ggtgtggcat cggccaggag gagatggagg ccagcagcag ccaagaccag
240
agtaaagtgt ctgccccagg ggtgctcaca gcccaggacc gggtagttgg aaagccagcc
300
cagcttggca ctcagcggag ccaggaggca gatgttcagg actgggagtt cagaaagagg
360
gattcccagg gcacttactc cagccgggat gcagaactcc aggaccagga attcggaaag
420
agagattcac tgggtaccta cagtagtcga gatgtaagcc ttggggactg ggaatttggg
480
aagagagatt ctctgggtgc ttatgccagc caagatgcca acgagcaggg ccaagatttg
540
gggaagaggg accaccatgg taggtacagc agccaggatg ccgatgagca ggactgggag
600
tttcagaaga gagatgtgtc actcggcacc tatggcagcc gggctgcgga gccacaggaa
660
caggagtttg ggaagagcgc ttggataagg gactacagca gtggtggcag ctccaggacc
720
cttgacgccc aggacagaag ctt
743

<210> 230
<211> 247
<212> PRT
<213> Homo sapiens

<400> 230
Xaa Ala Arg Asp Thr Ala Ser Ser Ser Thr Gly Ser Ala Cys Ala Gly

```
 1               5                  10                  15
Ser Gly Ala Ser Ser Lys Ile Thr Gln Gly Trp Ser Gly Ala Ala Gly
            20                  25                  30
Cys Ser Cys Pro Arg Thr Gly Ser Arg Met Gly Lys Ala Ala Ser Leu
        35                  40                  45
Val Ala Arg Gly Arg Gly Glu Gly Ser Thr Arg Glu Trp Ala Ser Arg
    50                  55                  60
Cys Gly Ile Gly Gln Glu Glu Met Glu Ala Ser Ser Ser Gln Asp Gln
65                  70                  75                  80
Ser Lys Val Ser Ala Pro Gly Val Leu Thr Ala Gln Asp Arg Val Val
                85                  90                  95
Gly Lys Pro Ala Gln Leu Gly Thr Gln Arg Ser Gln Glu Ala Asp Val
            100                 105                 110
Gln Asp Trp Glu Phe Arg Lys Arg Asp Ser Gln Gly Thr Tyr Ser Ser
        115                 120                 125
Arg Asp Ala Glu Leu Gln Asp Gln Glu Phe Gly Lys Arg Asp Ser Leu
    130                 135                 140
Gly Thr Tyr Ser Ser Arg Asp Val Ser Leu Gly Asp Trp Glu Phe Gly
145                 150                 155                 160
Lys Arg Asp Ser Leu Gly Ala Tyr Ala Ser Gln Asp Ala Asn Glu Gln
                165                 170                 175
Gly Gln Asp Leu Gly Lys Arg Asp His His Gly Arg Tyr Ser Ser Gln
            180                 185                 190
Asp Ala Asp Glu Gln Asp Trp Glu Phe Gln Lys Arg Asp Val Ser Leu
        195                 200                 205
Gly Thr Tyr Gly Ser Arg Ala Ala Glu Pro Gln Glu Gln Glu Phe Gly
    210                 215                 220
Lys Ser Ala Trp Ile Arg Asp Tyr Ser Ser Gly Gly Ser Ser Arg Thr
225                 230                 235                 240
Leu Asp Ala Gln Asp Arg Ser
                245
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<210> 231
<211> 431
<212> DNA
<213> Homo sapiens

<400> 231
acgcgttggc caccgagagg ctggcgaggg tgtgcagcac ggcgcagtgt ggcagggtcc
60
cagggtgcag cctgcgcagc agctcctcca tcaccttgct gatgaactgt cttcccacgg
120
ccaccaggac gccactcgcc gcctgctgcc agtcccagac caggtccttc gtcttggtca
180
tctcgctgga ggccaggagg atgatggtgc tggctgtgtc cttgtccagc tcactggcgc
240
gactgctcag gaccctctcc atggccctca ggaccgctgc tcggtatggg tgtgccagct
300
tgtcatgctg ccgcagatac tcctcgcagg cacggagcgt ctccaccctg ctggacgcca
360
tcaccgataa ggacccccctg gtgcaggagc aggtctgcag tgccctgtgc tccctcgggg
420
aggtgcggcc g
431

<210> 232
<211> 120
<212> PRT
<213> Homo sapiens

<400> 232
Met Ala Ser Ser Arg Val Glu Thr Leu Arg Ala Cys Glu Glu Tyr Leu
1 5 10 15
Arg Gln His Asp Lys Leu Ala His Pro Tyr Arg Ala Ala Val Leu Arg
20 25 30
Ala Met Glu Arg Val Leu Ser Ser Arg Ala Ser Glu Leu Asp Lys Asp
35 40 45
Thr Ala Ser Thr Ile Ile Leu Leu Ala Ser Ser Glu Met Thr Lys Thr
50 55 60
Lys Asp Leu Val Trp Asp Trp Gln Gln Ala Ala Ser Gly Val Leu Val
65 70 75 80
Ala Val Gly Arg Gln Phe Ile Ser Lys Val Met Glu Glu Leu Leu Arg
85 90 95
Arg Leu His Pro Gly Thr Leu Pro His Cys Ala Val Leu His Thr Leu
100 105 110
Ala Ser Leu Ser Val Ala Asn Ala
115 120

<210> 233
<211> 606
<212> DNA
<213> Homo sapiens

<400> 233
acgcgttcag ggatgccaga aatctaactg ggtaataaaa agctgggaga acattccaga
60
aaggtgggca cccttagcat tcccaaaaag caccagccct cctcatcctt cccagcttct
120
gtgctggaat gcacccccat cggaaaggct cgaaaactca ggacacatta ggatcacctg
180
gaaagcattt gtcaaaacgc atctccctgc gggtcagggt ccaagttaaa atcaaacttc
240
aggtgatgct gactcaggtg gctccagaaa cacctgggga agcagcactt tggaggctgc
300
ctctcacatc caccccacag caagtgggca gggagctagg taaatctcct tcccagttga
360
gaaggggctc ggagcaggca cagagaagag ataccccttag aatgcaagtt gttcagctgc
420
gaaagtccag cctgcaggct tcctgggcaa gctagtgggc tgaagtatgc cacagcaaca
480
ggcttctaga gccggctgcc cagctcctac tctgcctctg ccactcactg actgtgtggt
540
cttgagcagg tcacctgtct gacttggtga gagctgacag gcatcacctg ttagaggctt
600
acgcgt
606

<210> 234

<211> 108
<212> PRT
<213> Homo sapiens

<400> 234
Met His Pro His Arg Lys Gly Ser Lys Thr Gln Asp Thr Leu Gly Ser
1 5 10 15
Pro Gly Lys His Leu Ser Lys Arg Ile Ser Leu Arg Val Arg Val Gln
20 25 30
Val Lys Ile Lys Leu Gln Val Met Leu Thr Gln Val Ala Pro Glu Thr
35 40 45
Pro Gly Glu Ala Ala Leu Trp Arg Leu Pro Leu Thr Ser Thr Pro Gln
50 55 60
Gln Val Gly Arg Glu Leu Gly Lys Ser Pro Ser Gln Leu Arg Arg Gly
65 70 75 80
Ser Glu Gln Ala Gln Arg Arg Asp Thr Leu Arg Met Gln Val Val Gln
85 90 95
Leu Arg Lys Ser Ser Leu Gln Ala Ser Trp Ala Ser
100 105

<210> 235
<211> 328
<212> DNA
<213> Homo sapiens

<400> 235
cgaccgttga ctattctcta caaaccacaa agacaatgat tgatttaact gaatttagaa
60
atagcaaaca cttaaaacag cagcagtaca gagctgaaaa ccagattctt ttgaaagaga
120
ttgaaagtct agaggaagaa cgacttgatc tgaaaaaaaa aattcgccaa atggctcaag
180
aaagaggaaa aagaagggca acttcaggat taaccactgg ggacctgaac ctaactgaaa
240
acatttctca aggagataga ataagtgaaa gaaaattgga tttattgagc ctcaaaaata
300
tgagtgaagc acaatcaaag aatgaatt
328

<210> 236
<211> 97
<212> PRT
<213> Homo sapiens

<400> 236
Met Ile Asp Leu Thr Glu Phe Arg Asn Ser Lys His Leu Lys Gln Gln
1 5 10 15
Gln Tyr Arg Ala Glu Asn Gln Ile Leu Leu Lys Glu Ile Glu Ser Leu
20 25 30
Glu Glu Glu Arg Leu Asp Leu Lys Lys Lys Ile Arg Gln Met Ala Gln
35 40 45
Glu Arg Gly Lys Arg Arg Ala Thr Ser Gly Leu Thr Thr Gly Asp Leu
50 55 60
Asn Leu Thr Glu Asn Ile Ser Gln Gly Asp Arg Ile Ser Glu Arg Lys

65 70 75 80
Leu Asp Leu Leu Ser Leu Lys Asn Met Ser Glu Ala Gln Ser Lys Asn
85 90 95
Glu

<210> 237
<211> 2059
<212> DNA
<213> Homo sapiens

<400> 237
ggccataagg gcacgacgca ttcctagccg atgcaccaac acgggcatga agcctgccga
60
gagcacgaag ccggcgtcca tagctacggc ccatacggtc atgtctgcca tggctccgtt
120
gatgtcagac tgcacatgaa atcggttacg gtaccccagg atcatcgcta ccgagtacac
180
cccgaacagc acccgctggg cgccgatcag cgtgagggag tgccccacca gtggcacttt
240
tcttagatag cggaacccat ccaccacatc cccagtcacc gttctcatcg tccgggaacg
300
atccaccagt ggcggcccaa gctcccgacg tgaaaactgc agcccctagg cgaccgagac
360
tgcgaagagg gctgcggaga tgcagaaaat gatcgtgtcg gcgtggtgca caggaatatg
420
gcgtccggca atcatgcgca ctgctgcagc aacaaccgca ccgatcatga gccctagcgg
480
ccaatcgttg gcatgattga cgatgccgtc aggtagtcgc gcttgtcgat ggtgtattcc
540
aacccagcga ccaaggcggt gagcaaaaac cggttcaggc tcatcgcgat gagcaaccca
600
atgagcaagg ccaggtggga gggcttatcg cgcgcaccac cccagaccaa gatccccagc
660
ccgacccagg tgacggcacg cattcatctg cgtattgtcc cgactacacc gtgagggcgc
720
tctctgatct gcagctcatc aaggttacgc gactgcagta cctcaatgca ctcctggcta
780
cccgagccca gaacctgcca cagtcccctg agaacaccga cctgcaggtt attccaggca
840
gccagaccag gctccttggt gagaagacca ccacagcggc agctttccca gtagcccttt
900
ccctctttgg cacagttgga acctccagtt gataaatgac tgtggactag cgcgcgtttt
960
ttgttttcag agcacacgta agggtccagc cacagcaggc ccggcgtccc ggtggaaggc
1020
agccctgggc ggaacccagg cgtttaacgg ctcactaggc agccccagat ctggggaagc
1080
agatgagcac gtggggagct ggagtgagct gagcagaagt tttgtgcccg cctgccccca
1140
tcccctccag gccacgtttt agatggccct tgtagttgcg ggtcctgggt gtcctcagaa
1200
ctagacatca atgcctggat ccttcagccg gccctgccct cctttaggag acaggagtca
1260

ccagggcaca gccctccagg cccgcctcag gaaggaatga aaggaatgcc atcatctcta
1320
gttcccaggg cccagccttc cccttctccc ccggggcagg gacagtgcgg catattcaga
1380
ttcagacctc tttgggctga gccaccttgt gagtgcagtt actgcctttg tgtggccgtg
1440
acctctattt gtttgctttt aatttgccaa cctatcgctg ctggcagcac tttttgagca
1500
agccgagagc acccattttg gctggggatt cagatcgatg gccttgtcca tgttgtcctt
1560
tctggcttcc ctgatggtgt catgtttcag cgcatgcgcc ccagcctttc ccatgtgcca
1620
aaccagaagc tccactgccc gtaggctgtc cctgtagccc tgctccctcc ctggaggctg
1680
ctcttctgat tctgagagct ggcctagtgg tgctgagggc ccctttctgc ttctctgccc
1740
acctgctgag ttgccactcg cagtgttgtc agttcccgtg ttctgagaag aggtcatgcc
1800
tgggaggaag ggatcgtcat gctgcatcga atcctctctc cgccgtgtgg cccccaggag
1860
agtagctgcc tgttgcacct gctccacacc tccccacagc ctccctgcag gtgctgtgtg
1920
gccgtgatgt gcagagagca gtgagggagg gttcatgaac caggtggatc ctctttaaaa
1980
aaaaaaaaag tttttgttat atctctaaaa tcccatagct aggaacagaa aaaaaggaaa
2040
agacttgaaa tgttctaga
2059

<210> 238
<211> 129
<212> PRT
<213> Homo sapiens

<400> 238
Ala Glu Gln Lys Phe Cys Ala Arg Leu Pro Pro Ser Pro Pro Gly His
1 5 10 15
Val Leu Asp Gly Pro Cys Ser Cys Gly Ser Trp Val Ser Ser Glu Leu
20 25 30
Asp Ile Asn Ala Trp Ile Leu Gln Pro Ala Leu Pro Ser Phe Arg Arg
35 40 45
Gln Glu Ser Pro Gly His Ser Pro Pro Gly Pro Pro Gln Glu Gly Met
50 55 60
Lys Gly Met Pro Ser Ser Leu Val Pro Arg Ala Gln Pro Ser Pro Ser
65 70 75 80
Pro Pro Gly Gln Gly Gln Cys Gly Ile Phe Arg Phe Arg Pro Leu Trp
85 90 95
Ala Glu Pro Pro Cys Glu Cys Ser Tyr Cys Leu Cys Val Ala Val Thr
100 105 110
Ser Ile Cys Leu Leu Leu Ile Cys Gln Pro Ile Ala Ala Gly Ser Thr
115 120 125
Phe

<210> 239
<211> 388
<212> DNA
<213> Homo sapiens

<400> 239
ntctagatca ctctgtagcg catggttaaa tgctgacaca atagaaaagt gcgaggacat
60
cctcgaatta atgagatggt ggactggatg agtcaagttc tcgtcgttgc ggcggctgtc
120
ggtcagctgc ccctcctcca cttctgcttc tcggcgttac cccataccgt attggccgcg
180
tgttcacctt tgaatgcagc catgtcgtcg tctccgtatc gaaatgatgt gccatcgaag
240
atgccgacct cagcatcggc atctgcagtg atgagtgcgt atcgcgccac acgaaacgcc
300
cagcgcaacc gtgtcctcgc acgatacgaa gtgcttgggt atctcagctc tggtacctat
360
ggtcgtgtat ataaagcaaa ggaacttn
388

<210> 240
<211> 104
<212> PRT
<213> Homo sapiens

<400> 240
Met Val Asp Trp Met Ser Gln Val Leu Val Val Ala Ala Ala Val Gly
 1   5   10   15
Gln Leu Pro Leu Leu His Phe Cys Phe Ser Ala Leu Pro His Thr Val
            20   25   30
Leu Ala Ala Cys Ser Pro Leu Asn Ala Ala Met Ser Ser Ser Pro Tyr
        35   40   45
Arg Asn Asp Val Pro Ser Lys Met Pro Thr Ser Ala Ser Ala Ser Ala
    50   55   60
Val Met Ser Ala Tyr Arg Ala Thr Arg Asn Ala Gln Arg Asn Arg Val
65   70   75   80
Leu Ala Arg Tyr Glu Val Leu Gly Tyr Leu Ser Ser Gly Thr Tyr Gly
                85   90   95
Arg Val Tyr Lys Ala Lys Glu Leu
            100

<210> 241
<211> 330
<212> DNA
<213> Homo sapiens

<400> 241
ncgggggcc gagttgaaag ctgccggcac actggctgtg ctgcttgctt cacttctcgg
60
gatgctgctt ccagggcggg cctgggggaa acatcggcct tcccaggcac ccttagcccg
120
tcccatctgg gggcccttag cacagtccct gggaccccac atgctgcctt tcaggctgat
180

gtgggcaaac tcggcagccc agcctactcc cgggccatgg gccaccatct cagcttccct
240
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330

<210> 242
<211> 100
<212> PRT
<213> Homo sapiens

<400> 242
Met Ala Pro Val Pro Pro Met Pro Leu Leu Leu Leu Ile Gln Ser Thr
1 5 10 15
Arg Leu Ser Pro Arg Glu Ala Glu Met Val Ala His Gly Pro Gly Val
20 25 30
Gly Trp Ala Ala Glu Phe Ala His Ile Ser Leu Lys Gly Ser Met Trp
35 40 45
Gly Pro Arg Asp Cys Ala Lys Gly Pro Gln Met Gly Arg Ala Lys Gly
50 55 60
Ala Trp Glu Gly Arg Cys Phe Pro Gln Ala Arg Pro Gly Ser Ser Ile
65 70 75 80
Pro Arg Ser Glu Ala Ser Ser Thr Ala Ser Val Pro Ala Ala Phe Asn
85 90 95
Ser Ala Pro Arg
100

<210> 243
<211> 330
<212> DNA
<213> Homo sapiens

<400> 243
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cacacaggcc accccgcccc cactgcgctc gtcgctaatc ttccctataa cgttgcggta
120
cccgtactgc tacacatgct agatattctc ccctccttgc ggactacagt ggtgatggtg
180
caggcagaag tagccgatcg attggctgcc acaccaggca gccgcattta cggtgtcccc
240
agcgtcaaag tcaactttta cgggactgtc tcgcgtgcgg gagcaattgg acgcaatgtc
300
ttctggccgg ctcccaatgt tgattctggn
330

<210> 244
<211> 110
<212> PRT
<213> Homo sapiens

<400> 244
Xaa Pro Ser Leu Arg Val Ile Thr Lys Asp Ala Met His Val Thr Ala

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 1               5                  10                  15
Glu Glu Ile Leu His Thr Gly His Pro Ala Pro Thr Ala Leu Val Ala
            20                  25                  30
Asn Leu Pro Tyr Asn Val Ala Val Pro Val Leu Leu His Met Leu Asp
        35                  40                  45
Ile Leu Pro Ser Leu Arg Thr Thr Val Val Met Val Gln Ala Glu Val
    50                  55                  60
Ala Asp Arg Leu Ala Ala Thr Pro Gly Ser Arg Ile Tyr Gly Val Pro
65                  70                  75                  80
Ser Val Lys Val Asn Phe Tyr Gly Thr Val Ser Arg Ala Gly Ala Ile
                85                  90                  95
Gly Arg Asn Val Phe Trp Pro Ala Pro Asn Val Asp Ser Gly
            100                 105                 110
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<210> 245
<211> 355
<212> DNA
<213> Homo sapiens

<400> 245
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120
gcgtgttgca gaaacagaag ttgaccgtcg gaggtaggcg gcattcgctt cggatcgaag
180
cgtcccgagg catccatctc gagttgacga cgaaaatctt tccagtccac gccgtagggg
240
ganttggcaa ccacagcatc gaatttgtcc agaaggaagt ggtcgttggt gagggtattg
300
ccccattcaa tacgcgcatc ttcccggaag cgcgcctcta ttgcggccaa cgcgt
355

<210> 246
<211> 101
<212> PRT
<213> Homo sapiens

<400> 246
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Met Arg Val Leu Asn Gly Ala Ile Pro Ser Pro Thr Thr Thr Ser Phe
 1               5                  10                  15
Trp Thr Asn Ser Met Leu Trp Leu Pro Xaa Pro Pro Thr Ala Trp Thr
            20                  25                  30
Gly Lys Ile Phe Val Val Asn Ser Arg Trp Met Pro Arg Asp Ala Ser
        35                  40                  45
Ile Arg Ser Glu Cys Arg Leu Pro Pro Thr Val Asn Phe Cys Phe Cys
    50                  55                  60
Asn Thr Leu His Ser Thr Phe Pro Arg Trp Val Trp Leu Pro Ser Ser
65                  70                  75                  80
Ile Arg Ala Arg His Cys Phe Gln Val Thr Pro Ala Glu Val Asn Pro
                85                  90                  95
Lys Leu Gly Gly Gly
            100
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<210> 247
<211> 333
<212> DNA
<213> Homo sapiens

<400> 247
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gcctgggaca ccagcgtcgt gtccgagatc aagatgggag acaggtacga gacggtcagg
120
ttcttccact gctacaagcg cggagtggac cgcgtgttcg ttgaccaccc actgttcctg
180
gagagggttt ggggaaagac cgaggagaag atctacgggc ctgacgctgg aacggactac
240
agggacaacc agctgcggtt cagcctgcta tgccaggcag cacttgaagc tccaaggatc
300
ctgagcctca acaacaaccc atacttctcc gga
333

<210> 248
<211> 111
<212> PRT
<213> Homo sapiens

<400> 248
Met Ala Ala Asn Gly His Arg Val Met Val Val Ser Pro Arg Tyr Asp
1 5 10 15
Gln Tyr Lys Asp Ala Trp Asp Thr Ser Val Val Ser Glu Ile Lys Met
20 25 30
Gly Asp Arg Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys Arg Gly
35 40 45
Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg Val Trp
50 55 60
Gly Lys Thr Glu Glu Lys Ile Tyr Gly Pro Asp Ala Gly Thr Asp Tyr
65 70 75 80
Arg Asp Asn Gln Leu Arg Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu
85 90 95
Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser Gly
100 105 110

<210> 249
<211> 5503
<212> DNA
<213> Homo sapiens

<400> 249
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120
tcgccacgca ccgcatgcca cctgaacccc agccccgatg gtgaggccta cacactggct
180
tcgagaccac ccgtccgcct caatgatgtc atgctcaggc tggtgacgga gctgcgctgg
240

cagaagttcg tcatgttcta cgacagcgag tatgatatcc gtgggcttca aagctttctg
300
gaccaggcct cgcggctggg ccttgacgtc tctttacaaa aggtggacaa gaacattagc
360
cacgtattca ccagcctgtt caccacgatg aagacagagg agctgaatcg ctaccgggac
420
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480
gccgtggaga ccaacctggc ttccaaggac agccactggg tctttgtgaa tgaggaaatc
540
agtgacccgg agatcctgga tctggtccat agtgcccttg gaaggatgac cgtggtccgg
600
caaatctttc cgtctgcaaa ggacaatcag aaatgcacga ggaacaacca ccgcatctcc
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720
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780
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840
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1140
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1200
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1320
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1380
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1980
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2580
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2700
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2880
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3480

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3660
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3780
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4560
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4620
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4680
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gcctgtgtgt gtgtgtttgt gtgtgtgtgt gtgtgtgaga gagagagaga gagagagaga
5160
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5503

<210> 250
<211> 927
<212> PRT
<213> Homo sapiens

<400> 250
Met Thr Gln Gly Ile Leu Ala Leu Val Thr Ser Thr Gly Cys Ala Ser
1 5 10 15
Ala Asn Ala Leu Gln Ser Leu Thr Asp Ala Met His Ile Pro His Leu
20 25 30
Phe Val Gln Arg Asn Pro Gly Gly Ser Pro Arg Thr Ala Cys His Leu
35 40 45
Asn Pro Ser Pro Asp Gly Glu Ala Tyr Thr Leu Ala Ser Arg Pro Pro
50 55 60
Val Arg Leu Asn Asp Val Met Leu Arg Leu Val Thr Glu Leu Arg Trp
65 70 75 80
Gln Lys Phe Val Met Phe Tyr Asp Ser Glu Tyr Asp Ile Arg Gly Leu
85 90 95
Gln Ser Phe Leu Asp Gln Ala Ser Arg Leu Gly Leu Asp Val Ser Leu
100 105 110
Gln Lys Val Asp Lys Asn Ile Ser His Val Phe Thr Ser Leu Phe Thr
115 120 125
Thr Met Lys Thr Glu Glu Leu Asn Arg Tyr Arg Asp Thr Leu Arg Arg
130 135 140
Ala Ile Leu Leu Leu Ser Pro Gln Gly Ala His Ser Phe Ile Asn Glu
145 150 155 160
Ala Val Glu Thr Asn Leu Ala Ser Lys Asp Ser His Trp Val Phe Val
165 170 175
Asn Glu Glu Ile Ser Asp Pro Glu Ile Leu Asp Leu Val His Ser Ala
180 185 190
Leu Gly Arg Met Thr Val Val Arg Gln Ile Phe Pro Ser Ala Lys Asp
195 200 205
Asn Gln Lys Cys Thr Arg Asn Asn His Arg Ile Ser Ser Leu Leu Cys
210 215 220
Asp Pro Gln Glu Gly Tyr Leu Gln Met Leu Gln Ile Ser Asn Leu Tyr
225 230 235 240
Leu Tyr Asp Ser Val Leu Met Leu Ala Asn Ala Phe His Arg Lys Leu
245 250 255
Glu Asp Arg Lys Trp His Ser Met Ala Ser Leu Asn Cys Ile Arg Lys

```
            260                 265                 270
Ser Thr Lys Pro Trp Asn Gly Gly Arg Ser Met Leu Asp Thr Ile Lys
        275                 280                 285
Lys Gly His Ile Thr Gly Leu Thr Gly Val Met Glu Phe Arg Glu Asp
    290                 295                 300
Ser Ser Asn Pro Tyr Val Gln Phe Glu Ile Leu Gly Thr Thr Tyr Ser
305                 310                 315                 320
Glu Thr Phe Gly Lys Asp Met Arg Lys Leu Ala Thr Trp Asp Ser Glu
                325                 330                 335
Lys Gly Leu Asn Gly Ser Leu Gln Glu Arg Pro Met Gly Ser Arg Leu
            340                 345                 350
Gln Gly Leu Thr Leu Lys Val Val Thr Val Leu Glu Glu Pro Phe Val
        355                 360                 365
Met Val Ala Glu Asn Ile Leu Gly Gln Pro Lys Arg Tyr Lys Gly Phe
    370                 375                 380
Ser Ile Asp Val Leu Asp Ala Leu Ala Lys Ala Leu Gly Phe Lys Tyr
385                 390                 395                 400
Glu Ile Tyr Gln Ala Pro Asp Gly Arg Tyr Gly His Gln Leu His Asn
                405                 410                 415
Thr Ser Trp Asn Gly Met Ile Gly Glu Leu Ile Ser Lys Arg Ala Asp
            420                 425                 430
Leu Ala Ile Ser Ala Ile Thr Ile Thr Pro Glu Arg Glu Ser Val Val
        435                 440                 445
Asp Phe Ser Lys Arg Tyr Met Asp Tyr Ser Val Gly Ile Leu Ile Lys
    450                 455                 460
Lys Pro Glu Glu Lys Ile Ser Ile Phe Ser Leu Phe Ala Pro Phe Asp
465                 470                 475                 480
Phe Ala Val Trp Ala Cys Ile Ala Ala Ala Ile Pro Val Val Gly Val
                485                 490                 495
Leu Ile Phe Val Leu Asn Arg Ile Gln Ala Val Arg Ala Gln Ser Ala
            500                 505                 510
Ala Gln Pro Arg Pro Ser Ala Ser Ala Thr Leu His Ser Ala Ile Trp
        515                 520                 525
Ile Val Tyr Gly Ala Phe Val Gln Gln Gly Gly Glu Ser Ser Val Asn
    530                 535                 540
Ser Met Ala Met Arg Ile Val Met Gly Ser Trp Trp Leu Phe Thr Leu
545                 550                 555                 560
Ile Val Cys Ser Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Thr Val
                565                 570                 575
Ser Arg Met Asp Asn Pro Ile Arg Thr Phe Gln Asp Leu Ser Lys Gln
            580                 585                 590
Val Glu Met Ser Tyr Gly Thr Val Arg Asp Ser Ala Val Tyr Glu Tyr
        595                 600                 605
Phe Arg Ala Lys Gly Thr Asn Pro Leu Glu Gln Asp Ser Thr Phe Ala
    610                 615                 620
Glu Leu Trp Arg Thr Ile Ser Lys Asn Gly Gly Ala Asp Asn Cys Val
625                 630                 635                 640
Ser Ser Pro Ser Glu Gly Ile Arg Lys Ala Lys Lys Gly Asn Tyr Ala
                645                 650                 655
Phe Leu Trp Asp Val Ala Val Val Glu Tyr Ala Ala Leu Thr Asp Asp
            660                 665                 670
Asp Cys Ser Val Thr Val Ile Gly Asn Ser Ile Ser Ser Lys Gly Tyr
        675                 680                 685
Gly Ile Ala Leu Gln His Gly Ser Pro Tyr Arg Asp Leu Phe Ser Gln
```

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    690                 695                 700
Arg Ile Leu Glu Leu Gln Asp Thr Gly Asp Leu Asp Val Leu Lys Gln
705                 710                 715                 720
Lys Trp Trp Pro His Met Gly Arg Cys Asp Leu Thr Ser His Ala Ser
                725                 730                 735
Ala Gln Ala Asp Gly Lys Ser Leu Lys Leu His Ser Phe Ala Gly Val
            740                 745                 750
Phe Cys Ile Leu Ala Ile Gly Leu Leu Leu Ala Cys Leu Val Ala Ala
        755                 760                 765
Leu Glu Leu Trp Trp Asn Ser Asn Arg Cys His Gln Glu Thr Pro Lys
    770                 775                 780
Glu Asp Lys Glu Val Asn Leu Glu Gln Val His Arg Arg Met Asn Ser
785                 790                 795                 800
Leu Met Asp Glu Asp Ile Ala His Lys Gln Ile Ser Pro Ala Ser Ile
                805                 810                 815
Glu Leu Ser Ala Leu Glu Met Gly Gly Leu Ala Pro Thr Gln Thr Leu
            820                 825                 830
Glu Pro Thr Arg Glu Tyr Gln Asn Thr Gln Leu Ser Val Ser Thr Phe
        835                 840                 845
Leu Pro Glu Gln Ser Ser His Gly Thr Ser Arg Thr Leu Ser Ser Gly
    850                 855                 860
Pro Ser Ser Asn Leu Pro Leu Pro Leu Ser Ser Ser Ala Thr Met Pro
865                 870                 875                 880
Ser Met Gln Cys Lys His Arg Ser Pro Asn Gly Gly Leu Phe Arg Gln
                885                 890                 895
Ser Pro Val Lys Thr Pro Ile Pro Met Ser Phe Gln Pro Val Pro Gly
            900                 905                 910
Gly Val Leu Pro Glu Ala Leu Asp Thr Ser His Gly Thr Ser Ile
        915                 920                 925
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<210> 251
<211> 291
<212> DNA
<213> Homo sapiens

<400> 251
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gacgtcaacg cgctcgaacg gctgcggttg gccgtgcgcg ccagcgtggt catcctcatc
120
gagtaccacc attcggtgac cctgctgctg cgggtgcgcg ggaactcacc tctggaacga
180
gaggccctcg aggcccgccg ccgtatcgat gcgaaggttc ccgctctcgt cgagagcgcc
240
atcgccgagg gtggtctgcg ctcggatttc actcccgggc tcatcacgcg t
291

<210> 252
<211> 97
<212> PRT
<213> Homo sapiens

<400> 252
Xaa Ile Ser Arg Gly Val Arg Ala Leu Asp Ser Ala Val Glu Thr Glu

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 1               5                  10                  15
Ser Leu Arg Glu Asp Val Asn Ala Leu Glu Arg Leu Arg Leu Ala Val
            20                  25                  30
Arg Ala Ser Val Val Ile Leu Ile Glu Tyr His His Ser Val Thr Leu
        35                  40                  45
Leu Leu Arg Val Arg Gly Asn Ser Pro Leu Glu Arg Glu Ala Leu Glu
    50                  55                  60
Ala Arg Arg Arg Ile Asp Ala Lys Val Pro Ala Leu Val Glu Ser Ala
65                  70                  75                  80
Ile Ala Glu Gly Gly Leu Arg Ser Asp Phe Thr Pro Gly Leu Ile Thr
                85                  90                  95
Arg
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<210> 253
<211> 327
<212> DNA
<213> Homo sapiens

<400> 253
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cgctcacggt cctgtaccga ccgatctcgc aaccttccgc agaccgatcc accaaccgcg
120
cccacatgtc ggcagtgatg gcgggcacct tgcgggagaa ggccgggaag gtcgagcgag
180
ccaatgaccg tcgcacggtc ggcacgctcc acgagcggga cgagaagctc gcggcaggac
240
gctcactcgt cgcggtgtcc tccgcggtct ccatcaccgt ccctgcgaca tggaacgccc
300
acgacttcgg acggcgactc gacgcgt
327

<210> 254
<211> 106
<212> PRT
<213> Homo sapiens

<400> 254

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Met Gly Ala Leu Ala Arg Val Leu Val Pro Ser Gln Pro Gly Glu Arg
 1               5                  10                  15
Arg Ala Leu Thr Val Leu Tyr Arg Pro Ile Ser Gln Pro Ser Ala Asp
            20                  25                  30
Arg Ser Thr Asn Arg Ala His Met Ser Ala Val Met Ala Gly Thr Leu
        35                  40                  45
Arg Glu Lys Ala Gly Lys Val Glu Arg Ala Asn Asp Arg Arg Thr Val
    50                  55                  60
Gly Thr Leu His Glu Arg Asp Glu Lys Leu Ala Ala Gly Arg Ser Leu
65                  70                  75                  80
Val Ala Val Ser Ser Ala Val Ser Ile Thr Val Pro Ala Thr Trp Asn
                85                  90                  95
Ala His Asp Phe Gly Arg Arg Leu Asp Ala
            100                 105
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<210> 255
<211> 372
<212> DNA
<213> Homo sapiens

<400> 255
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atcgtggacc atagacctga cttaatctta tgtgattgga tgatgccagg agggagtggc
120
atcgagctaa ctcgtcgctt aaagaaagac agcacgacag cagaaatccc tgttatttta
180
ctaacggcca aaagtgaaga agacaataaa attcaaggct tagaagtcgg tgcagatgac
240
tacatcacta aacctttctc tcctcgtgaa ctagtagcac gcctcaaggc ggtattacgc
300
cgagcgactc cacaaggtat tgatgatcct attgaaattg atggtttaac gcttgatccc
360
attagccaac gc
372

<210> 256
<211> 124
<212> PRT
<213> Homo sapiens

<400> 256
Leu Glu Met Ala Gly Tyr Glu Tyr Met Glu Ala Glu Asn Ser Gln Gln
 1   5   10   15
Ala His Glu Ile Ile Val Asp His Arg Pro Asp Leu Ile Leu Cys Asp
            20   25   30
Trp Met Met Pro Gly Gly Ser Gly Ile Glu Leu Thr Arg Arg Leu Lys
        35   40   45
Lys Asp Ser Thr Thr Ala Glu Ile Pro Val Ile Leu Leu Thr Ala Lys
    50   55   60
Ser Glu Glu Asp Asn Lys Ile Gln Gly Leu Glu Val Gly Ala Asp Asp
65   70   75   80
Tyr Ile Thr Lys Pro Phe Ser Pro Arg Glu Leu Val Ala Arg Leu Lys
                85   90   95
Ala Val Leu Arg Arg Ala Thr Pro Gln Gly Ile Asp Asp Pro Ile Glu
            100   105   110
Ile Asp Gly Leu Thr Leu Asp Pro Ile Ser Gln Arg
        115   120

<210> 257
<211> 639
<212> DNA
<213> Homo sapiens

<400> 257
nnacgcgtag cggtcgaggt tgcggacacc atgcccgaac ccggcctgct cgccatcgag
60
gcacccatgg gacacggcaa gaccgaggcc gccctcatgt gcgcacaggt gctcgccgaa
120

cggttcgggc tcggcggcat cttcttcggt ctaccgacga tggccacgtc caatcccatg
180
ttcggtcgag ttcgggaatg gctggacgct gtgccagcca aggacccgtc aagcatttcc
240
ctggctcact cgaaagctgg actcaacgag gagtaccagc agctcatgcc gtggaacgcc
300
accatggccg tctacgacga aggtgccggc acgcagcgtg aagcttcggc gatcgtccat
360
gagtggttct tgggccgcaa gcgcgcgatc ctggccgacc acgtcgtcgg gaccatcgac
420
caggcactgt tcaccggtct caaagccaag catgtggtgt tacgccacct cggtctggcg
480
agcaaggtcg tcatcattga tgaggtccac gccgccgacg tctatatgcg cgaatacctc
540
aaggtcgtcc tcgaatggct cggcgcctac cgcacgccag tcatcctcat gtccgcgacg
600
ctgccaccgg cccaacgtca tgaactcgcg ctagcgtac
639

<210> 258
<211> 213
<212> PRT
<213> Homo sapiens

<400> 258
Xaa Arg Val Ala Val Glu Val Ala Asp Thr Met Pro Glu Pro Gly Leu
1 5 10 15
Leu Ala Ile Glu Ala Pro Met Gly His Gly Lys Thr Glu Ala Ala Leu
20 25 30
Met Cys Ala Gln Val Leu Ala Glu Arg Phe Gly Leu Gly Gly Ile Phe
35 40 45
Phe Gly Leu Pro Thr Met Ala Thr Ser Asn Pro Met Phe Gly Arg Val
50 55 60
Arg Glu Trp Leu Asp Ala Val Pro Ala Lys Asp Pro Ser Ser Ile Ser
65 70 75 80
Leu Ala His Ser Lys Ala Gly Leu Asn Glu Glu Tyr Gln Gln Leu Met
85 90 95
Pro Trp Asn Ala Thr Met Ala Val Tyr Asp Glu Gly Ala Gly Thr Gln
100 105 110
Arg Glu Ala Ser Ala Ile Val His Glu Trp Phe Leu Gly Arg Lys Arg
115 120 125
Ala Ile Leu Ala Asp His Val Val Gly Thr Ile Asp Gln Ala Leu Phe
130 135 140
Thr Gly Leu Lys Ala Lys His Val Val Leu Arg His Leu Gly Leu Ala
145 150 155 160
Ser Lys Val Val Ile Ile Asp Glu Val His Ala Ala Asp Val Tyr Met
165 170 175
Arg Glu Tyr Leu Lys Val Val Leu Glu Trp Leu Gly Ala Tyr Arg Thr
180 185 190
Pro Val Ile Leu Met Ser Ala Thr Leu Pro Pro Ala Gln Arg His Glu
195 200 205
Leu Ala Leu Ala Tyr
210

<210> 259
<211> 252
<212> DNA
<213> Homo sapiens

<400> 259
acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
60
ncatggtgtg tgcacgtgtg cnactgtgta tgcatggtaa tgtgcacgtg tgcanctgtg
120
tgtnggtgtg tatgcatgng tgtgtgcacg tgtgcactgn agtgtggggt gtatgcatgg
180
tgtgtgcaca tgagcactgt gtggtgtgta tgcatggtgn ggtgcacgtg tgcactgtgt
240
atgcaatggt gt
252

<210> 260
<211> 84
<212> PRT
<213> Homo sapiens

<400> 260
Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1   5   10   15
Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
            20   25   30
Val Met Cys Thr Cys Ala Xaa Val Cys Xaa Cys Val Cys Met Xaa Val
        35   40   45
Cys Thr Cys Ala Leu Xaa Cys Gly Val Tyr Ala Trp Cys Val His Met
    50   55   60
Ser Thr Val Trp Cys Val Cys Met Val Xaa Cys Thr Cys Ala Leu Cys
65   70   75   80
Met Gln Trp Cys

<210> 261
<211> 1202
<212> DNA
<213> Homo sapiens

<400> 261
gctagcccgg tcgcgttcgt cgtcgatttg ctggcggcag tcccctcgat cgtcttcggt
60
ctgtggggcg gcatcgtctt cggatcgtcg ggaatcatca acggttacgc gggggcctta
120
ttcaaagcgc tcggctggat tccgatcttt tccgaagatc cgtcgtggtc ctcggctact
180
ggcacggtct accttgccag tctcgtcctg gccatcatga tcctgccaat tatcactgct
240
gttagccgcg acgtcatgcc ccgaacgccc catgatcaag tcgaggccgc gctcgccctc
300
ggatcgacgc gctgggaggt catcaagctt gcagtgttcc cccactcgcg gtccggcatc
360

atttccggat ccatgttggg tctaggacgc gccctcggcg agaccctggc tgtcaccctc
420
atcctgcaga cgatgagccc catggcgctc aaacagaacc tcaacctgtc gatcttcgtc
480
ggtggtgaga cattcgcgtc gaagattgcc ggtaacttct ccgaggccat tagcgatccc
540
acctcgctgg gtgccctcgt ggcgtcggcc ctggccctgt tcgtcattac cttcgtggtc
600
aacgcgactg cccggttgat tgcggcgaag ggggttaagc gatgagcgcc accacccctg
660
accacatcac ccaccatggc gacaacacgc ccggacagct agatctctcc cgcccgtctg
720
gtaaacggac tatcaagagc ggctgcgcct caacattcat gatcgtggcc accgtactgg
780
ctgttatccc actggcctgg ctgctcttcg cggccgtccg gcgcggcatc ggatcactat
840
tccacgcgtc gtggtggacc cactcgatgg atccctcctt cgacttggcc gagcagggcg
900
ccatccacgc tatcgtcgga acccttgaaa ttggccttat tacatcgatt atctcggtac
960
cgatcgctct gatgaccgcg atcttcctag tcgagtacgc ccgcggaact aagatcgcca
1020
aggtcattag cttcgccgtc gacgtgctaa ccggtgtacc ttcaatcgtc gcggccctct
1080
tcgtcttcgc cgtagtcgtt accaccttcg gtggcaccca atccgcgtgg gcctcctcgt
1140
tggccctcat gatcctcatg gttccgacgg tgctgcgatc aaccgaggaa atgctcaagc
1200
tt
1202

<210> 262
<211> 214
<212> PRT
<213> Homo sapiens

<400> 262
Ala Ser Pro Val Ala Phe Val Val Asp Leu Leu Ala Ala Val Pro Ser
 1   5   10   15
Ile Val Phe Gly Leu Trp Gly Gly Ile Val Phe Gly Ser Ser Gly Ile
            20   25   30
Ile Asn Gly Tyr Ala Gly Ala Leu Phe Lys Ala Leu Gly Trp Ile Pro
        35   40   45
Ile Phe Ser Glu Asp Pro Ser Trp Ser Ser Ala Thr Gly Thr Val Tyr
    50   55   60
Leu Ala Ser Leu Val Leu Ala Ile Met Ile Leu Pro Ile Ile Thr Ala
65   70   75   80
Val Ser Arg Asp Val Met Pro Arg Thr Pro His Asp Gln Val Glu Ala
                85   90   95
Ala Leu Ala Leu Gly Ser Thr Arg Trp Glu Val Ile Lys Leu Ala Val
            100   105   110
Phe Pro His Ser Arg Ser Gly Ile Ile Ser Gly Ser Met Leu Gly Leu
        115   120   125
Gly Arg Ala Leu Gly Glu Thr Leu Ala Val Thr Leu Ile Leu Gln Thr

```
    130                 135                 140
Met Ser Pro Met Ala Leu Lys Gln Asn Leu Asn Leu Ser Ile Phe Val
145                 150                 155                 160
Gly Gly Glu Thr Phe Ala Ser Lys Ile Ala Gly Asn Phe Ser Glu Ala
                165                 170                 175
Ile Ser Asp Pro Thr Ser Leu Gly Ala Leu Val Ala Ser Ala Leu Ala
            180                 185                 190
Leu Phe Val Ile Thr Phe Val Val Asn Ala Thr Ala Arg Leu Ile Ala
        195                 200                 205
Ala Lys Gly Val Lys Arg
    210
```

<210> 263
<211> 424
<212> DNA
<213> Homo sapiens

<400> 263
acgcgtgagt gctctgcgct ggaaacaacg gtgatagagc ccatccgccg tgaactttcc
60
gacgtggtgc tcgtgaacaa gctcgaaaag tatgtacgcg aacgtacctc ggaagacgtt
120
gcgcacatgg aagaggatgc ggaccagacg ggcaacgaca tcctcacgac gatcctgctg
180
tcgaactggg atccactatt ggatatgacg acgcaggatc atgtgctggc catgcaaaag
240
gcttatatgg cctcgccatt ccgtgccaat ttggacctgg catacccatc ttcgacgcca
300
caggcccagt cccagccggc gatgccgccg tgggagacag ggacctcagc cagtagcatg
360
gcggatgctc gtgaatttgc gctgctgaag ctgtacctgc gtagcttgct gcagaagcac
420
gann
424

<210> 264
<211> 99
<212> PRT
<213> Homo sapiens

<400> 264
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Met Glu Glu Asp Ala Asp Gln Thr Gly Asn Asp Ile Leu Thr Thr Ile
 1               5                  10                  15
Leu Leu Ser Asn Trp Asp Pro Leu Leu Asp Met Thr Thr Gln Asp His
            20                  25                  30
Val Leu Ala Met Gln Lys Ala Tyr Met Ala Ser Pro Phe Arg Ala Asn
        35                  40                  45
Leu Asp Leu Ala Tyr Pro Ser Ser Thr Pro Gln Ala Gln Ser Gln Pro
    50                  55                  60
Ala Met Pro Pro Trp Glu Thr Gly Thr Ser Ala Ser Ser Met Ala Asp
65                  70                  75                  80
Ala Arg Glu Phe Ala Leu Leu Lys Leu Tyr Leu Arg Ser Leu Leu Gln
                85                  90                  95
Lys His Xaa
```

<210> 265
<211> 360
<212> DNA
<213> Homo sapiens

<400> 265
ncgtacggcc ctggcgtccg catggacgag ggataccatt ccggcatgac ggtgccgggt
60
gccttcgact ccctcatcgg caagctcatc atcactggtg atagccgtga gcaagccctg
120
gctcgagctg cccgcgccct cgacgaaatc gtcatcgacg gcatgccgac ggtcattccc
180
tttcaccagg cggtggttca cgacccggct ttcactgccg ccgacggctg cttcggcgtc
240
tttaccgact ggatcgaaac cgagttcgac aacaagatcg agccatacac cgggtctctg
300
ggcgagtctg ccaattccga gcctcctcgt gaggtcgtcg tcgaggtcaa cggtaaacgc
360

<210> 266
<211> 120
<212> PRT
<213> Homo sapiens

<400> 266
Xaa Tyr Gly Pro Gly Val Arg Met Asp Glu Gly Tyr His Ser Gly Met
 1   5   10   15
Thr Val Pro Gly Ala Phe Asp Ser Leu Ile Gly Lys Leu Ile Ile Thr
            20   25   30
Gly Asp Ser Arg Glu Gln Ala Leu Ala Arg Ala Ala Arg Ala Leu Asp
        35   40   45
Glu Ile Val Ile Asp Gly Met Pro Thr Val Ile Pro Phe His Gln Ala
    50   55   60
Val Val His Asp Pro Ala Phe Thr Ala Ala Asp Gly Cys Phe Gly Val
65   70   75   80
Phe Thr Asp Trp Ile Glu Thr Glu Phe Asp Asn Lys Ile Glu Pro Tyr
                85   90   95
Thr Gly Ser Leu Gly Glu Ser Ala Asn Ser Glu Pro Pro Arg Glu Val
            100   105   110
Val Val Glu Val Asn Gly Lys Arg
        115   120

<210> 267
<211> 471
<212> DNA
<213> Homo sapiens

<400> 267
natcctcaac gtgtgttcag ttccacgcga aagatcatgt tcgtcatcgg atcgatgccg
60
ttaacgcatc ctagtcaatc caccgatggc gaccctggca aaaaatacga ggtgacttgg
120

ctagatctcg ggcaccttca ccctagtcgg ccgggactcg tcactatcac cacaactgtc
180
gatgatgacg tcatcacctc ttcccaggta aatgtcggca acctccaccg cggggatgaa
240
aaacttttcg aagctcgcga ttaccgccag attccgatgc ttgcatcacg tcatggctgg
300
acagctccat tcattggtga gaccggcgca gcccatgcca tcgaggatgc gatgggcatt
360
accatcccaa ctcgcgtggc atggatacga accctgctcg ctgagttcag cagaatcacc
420
tcacacttca cattttgtc atgggtaggc catcactgtg atgatgccgg c
471

<210> 268
<211> 157
<212> PRT
<213> Homo sapiens

<400> 268
Xaa Pro Gln Arg Val Phe Ser Ser Thr Arg Lys Ile Met Phe Val Ile
1 5 10 15
Gly Ser Met Pro Leu Thr His Pro Ser Gln Ser Thr Asp Gly Asp Pro
20 25 30
Gly Lys Lys Tyr Glu Val Thr Trp Leu Asp Leu Gly His Leu His Pro
35 40 45
Ser Arg Pro Gly Leu Val Thr Ile Thr Thr Thr Val Asp Asp Asp Val
50 55 60
Ile Thr Ser Ser Gln Val Asn Val Gly Asn Leu His Arg Gly Asp Glu
65 70 75 80
Lys Leu Phe Glu Ala Arg Asp Tyr Arg Gln Ile Pro Met Leu Ala Ser
85 90 95
Arg His Gly Trp Thr Ala Pro Phe Ile Gly Glu Thr Gly Ala Ala His
100 105 110
Ala Ile Glu Asp Ala Met Gly Ile Thr Ile Pro Thr Arg Val Ala Trp
115 120 125
Ile Arg Thr Leu Leu Ala Glu Phe Ser Arg Ile Thr Ser His Phe Thr
130 135 140
Phe Leu Ser Trp Val Gly His His Cys Asp Asp Ala Gly
145 150 155

<210> 269
<211> 387
<212> DNA
<213> Homo sapiens

<400> 269
acgcgtgtcg tgtttccaga aaaaaccaat aaattagagt ttatggtaga agtgattgct
60
gatatgacgg taatcaatcc atttgatttc tttgtggaaa gctacgcaga agactaccca
120
tttgcttatg acaaagctct taaaaaagag ttagaacctt atttacaggt ttctgaacct
180
tgttcgttac tcgacaaatg gctgtctggt gttgatcgtg aaaaaacacc gatcaatgat
240

tttctagtcg caataaacag tcgccttgcc ggtgatattg gctatggtat tcgcttagaa
300
ccgggcgttc agtcacctga agaaacgctc acattaatga aaggctcttg tcgcgatacc
360
tcggggttat tggttcaaat actacgc
387

<210> 270
<211> 129
<212> PRT
<213> Homo sapiens

<400> 270
Thr Arg Val Val Phe Pro Glu Lys Thr Asn Lys Leu Glu Phe Met Val
1 5 10 15
Glu Val Ile Ala Asp Met Thr Val Ile Asn Pro Phe Asp Phe Phe Val
20 25 30
Glu Ser Tyr Ala Glu Asp Tyr Pro Phe Ala Tyr Asp Lys Ala Leu Lys
35 40 45
Lys Glu Leu Glu Pro Tyr Leu Gln Val Ser Glu Pro Cys Ser Leu Leu
50 55 60
Asp Lys Trp Leu Ser Gly Val Asp Arg Glu Lys Thr Pro Ile Asn Asp
65 70 75 80
Phe Leu Val Ala Ile Asn Ser Arg Leu Ala Gly Asp Ile Gly Tyr Gly
85 90 95
Ile Arg Leu Glu Pro Gly Val Gln Ser Pro Glu Glu Thr Leu Thr Leu
100 105 110
Met Lys Gly Ser Cys Arg Asp Thr Ser Gly Leu Leu Val Gln Ile Leu
115 120 125
Arg

<210> 271
<211> 443
<212> DNA
<213> Homo sapiens

<400> 271
gccggcacca acggaaagtc ctctaccgcg cgcatggtcg attcgctttt gcgtgccttc
60
caccgccgag tgggtttggt aaccagccca cacctgcagc gcgttactga gcgcatcggc
120
attgatggcc agcccattca cccgcgcgat tatgtacgca tctggcacga gattaagcca
180
tttgtggaaa tggtcgatgc cgaatcggac atgcctatgt ctaagttcga ggtcttcgtg
240
ggcctgtcct atgctgcgtt tgccgacgcc cccggggacg tcgctgtcgt cgaagtcggc
300
cttggcggac gttgggacgc taccaatgtg gtcaacgcgg atgtctctgt cattaccccg
360
gtgggcatgg accacacgga ttacctgggg gagacgatca ctgaaatcgc aggcgagaaa
420
gctggcatta ttaagccacg cgt
443

<210> 272
<211> 147
<212> PRT
<213> Homo sapiens

<400> 272
Ala Gly Thr Asn Gly Lys Ser Ser Thr Ala Arg Met Val Asp Ser Leu
1 5 10 15
Leu Arg Ala Phe His Arg Arg Val Gly Leu Val Thr Ser Pro His Leu
20 25 30
Gln Arg Val Thr Glu Arg Ile Gly Ile Asp Gly Gln Pro Ile His Pro
35 40 45
Arg Asp Tyr Val Arg Ile Trp His Glu Ile Lys Pro Phe Val Glu Met
50 55 60
Val Asp Ala Glu Ser Asp Val Pro Met Ser Lys Phe Glu Val Phe Val
65 70 75 80
Gly Leu Ser Tyr Ala Ala Phe Ala Asp Ala Pro Gly Asp Val Ala Val
85 90 95
Val Glu Val Gly Leu Gly Gly Arg Trp Asp Ala Thr Asn Val Val Asn
100 105 110
Ala Asp Val Ser Val Ile Thr Pro Val Gly Met Asp His Thr Asp Tyr
115 120 125
Leu Gly Glu Thr Ile Thr Glu Ile Ala Gly Glu Lys Ala Gly Ile Ile
130 135 140
Lys Pro Arg
145

<210> 273
<211> 864
<212> DNA
<213> Homo sapiens

<400> 273
caaagtaaga ctgcttcaaa ttttgtgttc tgctctgcag ctcgctcccc cctgctgtcg
60
aagagaagcc aaagcccccc ccccccacct caaaggctcg gaagtctggc atccctactt
120
ccgagcctgg atcccagtaa ggatcttgcc ctccctgcaa caccgagtgc cttagacagc
180
tgctgcctga gaactggcct ccagccggtg tcctcattcc atggggctcc ctgctgactg
240
catttcctga tctgggatga tgtttaccag cccaaaacca gtcatgttct tccaaaagct
300
tctctttgat agaattttga ggccatgcca cctcccttcc agtccacatg gaattccaga
360
atcagtcaca gcctctgatt ttttccaaga agagattgcc ttcaccattg ttaaatgtca
420
gcctgtacgg cagagacatg gtggtctgca caagcctgga caagttcttc catattgatg
480
gtgggagcaa cccctgtaat ctactccttg gaaggatttt ttgctttgct tatgaaaagc
540
tgtgcttgag acttaggtac ttttctcacg tggacacact gatcccatcc catattgcat
600

ctttgaagag atggatatca agtacacttt ggtagctgaa ataatcatat ctttctgatg
660
tctattgtat ctcctttgag gaaaagaaca cacattttta atggagattg gctgctttca
720
ggtatgtgtg tctatcattg aaagagcatg gactcaaaca tcagccctga gttcttgagt
780
ccacccaact cccatcttct tgtggcacag gaaagctgcc ctctccctct cccaccacac
840
tcctgactaa tgcccttcac gcgt
864

<210> 274
<211> 116
<212> PRT
<213> Homo sapiens

<400> 274
Met Trp Thr Gly Arg Glu Val Ala Trp Pro Gln Asn Ser Ile Lys Glu
1 5 10 15
Lys Leu Leu Glu Glu His Asp Trp Phe Trp Ala Gly Lys His His Pro
20 25 30
Arg Ser Gly Asn Ala Val Ser Arg Glu Pro His Gly Met Arg Thr Pro
35 40 45
Ala Gly Gly Gln Phe Ser Gly Ser Ser Cys Leu Arg His Ser Val Leu
50 55 60
Gln Gly Gly Gln Asp Pro Tyr Trp Asp Pro Gly Ser Glu Val Gly Met
65 70 75 80
Pro Asp Phe Arg Ala Phe Glu Val Gly Gly Gly Gly Phe Gly Phe Ser
85 90 95
Ser Thr Ala Gly Gly Ser Glu Leu Gln Ser Arg Thr Gln Asn Leu Lys
100 105 110
Gln Ser Tyr Phe
115

<210> 275
<211> 911
<212> DNA
<213> Homo sapiens

<400> 275
naaatttaaa ggaacctccc ttctataacg gagagtattt attgcagctt tcctttctgt
60
ttattttcag gaatgaaagg aattacccag ccttctgctt ttatacctac agctgaaagt
120
aattcctttc agcctcaggt gaagactttg ccatctccaa ttgatgctaa acagcagttg
180
caacggaaaa tccagaagaa gcagcaagaa cagaaactac aatccccttt gccaggagaa
240
tctgcagcaa aaaagtcaga aagtgctaca agcaatggag tgactaatct tcctaatgga
300
aatccttcaa tcctttctcc tcaacctatt ggtatcgttg tggcagctgt ccctagtccc
360
attccggtcc agcggactag gcaattggta acttcaccga gtccaatgag ttcttctnga
420

cggcaaagtt cttcccctca atgtacaggt ggtcactcag cacatgcagt ctgtgaaaca
480
ggcaccaaag actccccaga acgttccagc agtcctggtg ggaatcgttc tgcccggcac
540
cgttaccctc agatcttacc caaaccagcg aacaccagtg cactcaccat tcgctctcca
600
actactgtcc tctttactag tagtcccatc aaaactgctg ttgtacccgc ttcacacatg
660
agttctctaa atgtggtgaa aatgacaaca atatccctca cacccagcaa cagtaacacc
720
cctcttaaac attctgcctc agtcagcagt gctacaggaa caacagaaga atcaaggagt
780
gttccacaga tcaagaatgg ttctgtcgtg tcgcttcagt ctcctgggtc caggagcagc
840
agtgcggggg gaacatctgc tgtggaagtc aaagtggaac ccgaaacatc atcagatgag
900
catcctgtac a
911

<210> 276
<211> 279
<212> PRT
<213> Homo sapiens

<400> 276
Met Lys Gly Ile Thr Gln Pro Ser Ala Phe Ile Pro Thr Ala Glu Ser
 1   5   10   15
Asn Ser Phe Gln Pro Gln Val Lys Thr Leu Pro Ser Pro Ile Asp Ala
            20   25   30
Lys Gln Gln Leu Gln Arg Lys Ile Gln Lys Lys Gln Gln Glu Gln Lys
        35   40   45
Leu Gln Ser Pro Leu Pro Gly Glu Ser Ala Ala Lys Lys Ser Glu Ser
    50   55   60
Ala Thr Ser Asn Gly Val Thr Asn Leu Pro Asn Gly Asn Pro Ser Ile
65   70   75   80
Leu Ser Pro Gln Pro Ile Gly Ile Val Val Ala Ala Val Pro Ser Pro
                85   90   95
Ile Pro Val Gln Arg Thr Arg Gln Leu Val Thr Ser Pro Ser Pro Met
            100   105   110
Ser Ser Ser Xaa Arg Gln Ser Ser Ser Pro Gln Cys Thr Gly Gly His
        115   120   125
Ser Ala His Ala Val Cys Glu Thr Gly Thr Lys Asp Ser Pro Glu Arg
    130   135   140
Ser Ser Ser Pro Gly Gly Asn Arg Ser Ala Arg His Arg Tyr Pro Gln
145   150   155   160
Ile Leu Pro Lys Pro Ala Asn Thr Ser Ala Leu Thr Ile Arg Ser Pro
                165   170   175
Thr Thr Val Leu Phe Thr Ser Ser Pro Ile Lys Thr Ala Val Val Pro
            180   185   190
Ala Ser His Met Ser Ser Leu Asn Val Val Lys Met Thr Thr Ile Ser
        195   200   205
Leu Thr Pro Ser Asn Ser Asn Thr Pro Leu Lys His Ser Ala Ser Val
    210   215   220
Ser Ser Ala Thr Gly Thr Thr Glu Glu Ser Arg Ser Val Pro Gln Ile

```
225                 230                 235                 240
Lys Asn Gly Ser Val Val Ser Leu Gln Ser Pro Gly Ser Arg Ser Ser
                245                 250                 255
Ser Ala Gly Gly Thr Ser Ala Val Glu Val Lys Val Glu Pro Glu Thr
            260                 265                 270
Ser Ser Asp Glu His Pro Val
        275
```

<210> 277
<211> 652
<212> DNA
<213> Homo sapiens

<400> 277
nnaccggtgg ggactctcgc tgaggtcctt aatggccctt ctcgtgtccc ggacggcacc
60
atgaaccttg ttggtgggct gcgtcaggca atggccacca ctggttactc ggaggtcaaa
120
gagttccagc gcatcgagct gacgattcgc taaccgttcc accacgcaga atggtgttcc
180
ggtgagcggg tggatagcta gccttcggcc atgagtgaag tgcccgatga attggtcgtg
240
ttgcgtggcg cgattgacaa catggacgcc gccctcatcc atctgcttgc cgaaaggttc
300
cggattactc gcgaggtagg ccgcctcaag gcggagtgcg gtttacctcc ggccgacccc
360
gcccgtgagg ctgagcagat cgcgcggttg cggcagttag cggtcgagtc gaacctcgac
420
cccgaattcg cgcagaaggt catcacgttc atcgtggccg aggtggtgcg tcaccacgaa
480
gctattgctg acgattctgg cgacgactct ggagtggcgg atacggggga ggcggatgtc
540
cctgggtcgg gcagctgagt tacagatcag gcgatgacgt cgccctggtg caccttcgac
600
gggattccga cgacgactgt gccgggggcg acatccttga cgaccaacgc gt
652

<210> 278
<211> 115
<212> PRT
<213> Homo sapiens

<400> 278
```
Met Ser Glu Val Pro Asp Glu Leu Val Val Leu Arg Gly Ala Ile Asp
 1               5                  10                  15
Asn Met Asp Ala Ala Leu Ile His Leu Leu Ala Glu Arg Phe Arg Ile
            20                  25                  30
Thr Arg Glu Val Gly Arg Leu Lys Ala Glu Cys Gly Leu Pro Pro Ala
        35                  40                  45
Asp Pro Ala Arg Glu Ala Glu Gln Ile Ala Arg Leu Arg Gln Leu Ala
    50                  55                  60
Val Glu Ser Asn Leu Asp Pro Glu Phe Ala Gln Lys Val Ile Thr Phe
65                  70                  75                  80
Ile Val Ala Glu Val Val Arg His His Glu Ala Ile Ala Asp Asp Ser
```

85 90 95
Gly Asp Asp Ser Gly Val Ala Asp Thr Gly Glu Ala Asp Val Pro Gly
100 105 110
Ser Gly Ser
115

<210> 279
<211> 348
<212> DNA
<213> Homo sapiens

<400> 279
cgggaggtca cacaagcatt caaaccatag cagatggtaa atgttatgtt atgtgtattt
60
taccacaatc cttaaaaaga aaagaaagaa aggcatatgg aacccctagt tacctctcat
120
ccagcttcaa aattgtcagt gcatggtcaa tcttgtctta tctgcccctc acccacccctt
180
ttccagaaag aagacccaga ggattccaca tctgcctgga aaccacgacc agtctcgact
240
ggaagttgtt gttaatgttg catgtattca taaaacctct aggcatttct agtgtccctc
300
agaatttttc caaattcagg caaacacaga aattacttcc aaaaattt
348

<210> 280
<211> 99
<212> PRT
<213> Homo sapiens

<400> 280
Met Cys Ile Leu Pro Gln Ser Leu Lys Arg Lys Glu Arg Lys Ala Tyr
1 5 10 15
Gly Thr Pro Ser Tyr Leu Ser Ser Ser Phe Lys Ile Val Ser Ala Trp
20 25 30
Ser Ile Leu Ser Tyr Leu Pro Leu Thr His Pro Phe Pro Glu Arg Arg
35 40 45
Pro Arg Gly Phe His Ile Cys Leu Glu Thr Thr Thr Ser Leu Asp Trp
50 55 60
Lys Leu Leu Leu Met Leu His Val Phe Ile Lys Pro Leu Gly Ile Ser
65 70 75 80
Ser Val Pro Gln Asn Phe Ser Lys Phe Arg Gln Thr Gln Lys Leu Leu
85 90 95
Pro Lys Ile

<210> 281
<211> 384
<212> DNA
<213> Homo sapiens

<400> 281
agatctgcgc agatcgataa tggattaaag actcttgacg ctggagtcac cgagatgaac
60

aacaaggtgt tgggggcaac gaaggctgtc ggtgattcca ccactaccgt caaccaggtg
120
aattctgcgt taggaantgc cgactcagcg gcagagaaga cgtcgagcgc cgttactcag
180
acgcgcgtgg gtgcccaggc gattaccggc gctgctcaaa atgtcatggc tgattcccaa
240
gctgtcaact cagccatggt tccgcttatt aataacgtga caaagaatct tcctaccttg
300
caaaaacagg ccaggaatct cgtgtcagtg aacggtaccc tgcagaaccc caacggtgat
360
tctgtcatta agattcaaca gacc
384

<210> 282
<211> 110
<212> PRT
<213> Homo sapiens

<400> 282
Met Asn Asn Lys Val Leu Gly Ala Thr Lys Ala Val Gly Asp Ser Thr
1 5 10 15
Thr Thr Val Asn Gln Val Asn Ser Ala Leu Gly Xaa Ala Asp Ser Ala
20 25 30
Ala Glu Lys Thr Ser Ser Ala Val Thr Gln Thr Arg Val Gly Ala Gln
35 40 45
Ala Ile Thr Gly Ala Ala Gln Asn Val Met Ala Asp Ser Gln Ala Val
50 55 60
Asn Ser Ala Met Val Pro Leu Ile Asn Asn Val Thr Lys Asn Leu Pro
65 70 75 80
Thr Leu Gln Lys Gln Ala Arg Asn Leu Val Ser Val Asn Gly Thr Leu
85 90 95
Gln Asn Pro Asn Gly Asp Ser Val Ile Lys Ile Gln Gln Thr
100 105 110

<210> 283
<211> 426
<212> DNA
<213> Homo sapiens

<400> 283
cgcgtagacc aatgtgagac ggccgtcacc aagggcatgc gcgacaagtc ggttggtagc
60
ggaccggata ttgtgcgtcg cgagctgcgc catgtcgtga cgagcggcac gattgtcgat
120
ggaagcgtac tggctgacga attgagcagc tactgcatga gtatcaagga gcacgtccgc
180
tctgatggcc tatccgagtt tggcatctgc accctcgacg ccgccaccgc cgagttccga
240
tacatgacat tcgtcgacga tgccgtgctg tcacaactcg agacattgct gcgttctcta
300
cgcatcaagg aagtcttgca tgaaaaaggg gtcatgttgc cttccacgct gcgcttgatc
360
cgcaacgcgg tgcccaccac ctgccaaatt accatgctca agcctgatac cgaattgtcg
420

gagaga
426

<210> 284
<211> 142
<212> PRT
<213> Homo sapiens

<400> 284
Arg Val Asp Gln Cys Glu Thr Ala Val Thr Lys Gly Met Arg Asp Lys
1 5 10 15
Ser Val Gly Ser Gly Pro Asp Ile Val Arg Arg Glu Leu Arg His Val
20 25 30
Val Thr Ser Gly Thr Ile Val Asp Gly Ser Val Leu Ala Asp Glu Leu
35 40 45
Ser Ser Tyr Cys Met Ser Ile Lys Glu His Val Arg Ser Asp Gly Leu
50 55 60
Ser Glu Phe Gly Ile Cys Thr Leu Asp Ala Ala Thr Ala Glu Phe Arg
65 70 75 80
Tyr Met Thr Phe Val Asp Asp Ala Val Leu Ser Gln Leu Glu Thr Leu
85 90 95
Leu Arg Ser Leu Arg Ile Lys Glu Val Leu His Glu Lys Gly Val Met
100 105 110
Leu Pro Ser Thr Leu Arg Leu Ile Arg Asn Ala Val Pro Thr Thr Cys
115 120 125
Gln Ile Thr Met Leu Lys Pro Asp Thr Glu Leu Ser Glu Arg
130 135 140

<210> 285
<211> 345
<212> DNA
<213> Homo sapiens

<400> 285
acgcgtgcag tcccttaccg acatgctggc agatgagctc gacggcagcc gcttcaccgg
60
cgatttctca gaaatctaca aacgtcagaa ctcgatcttc ggcgatgtaa ggaataactt
120
ttacaaaaaa ggataccgca tcatcaacgt agcgaatggt gtattgcgca agatttcact
180
ggtaagcgca ggcaatgcag acaatgtgaa aggtcaggcc ctgttcttcc gcggtgtggc
240
gcatttcgaa ctcgtgcgtt tgtttgcaca accctggggt tatacttcgg acaattcaca
300
ctacggcatc ccgctccgca atgaaatcgt aattggttct attcn
345

<210> 286
<211> 107
<212> PRT
<213> Homo sapiens

<400> 286
Met Leu Ala Asp Glu Leu Asp Gly Ser Arg Phe Thr Gly Asp Phe Ser

```
 1               5                  10                  15
Glu Ile Tyr Lys Arg Gln Asn Ser Ile Phe Gly Asp Val Arg Asn Asn
            20                  25                  30
Phe Tyr Lys Lys Gly Tyr Arg Ile Ile Asn Val Ala Asn Gly Val Leu
        35                  40                  45
Arg Lys Ile Ser Leu Val Ser Ala Gly Asn Ala Asp Asn Val Lys Gly
    50                  55                  60
Gln Ala Leu Phe Phe Arg Gly Val Ala His Phe Glu Leu Val Arg Leu
65                  70                  75                  80
Phe Ala Gln Pro Trp Gly Tyr Thr Ser Asp Asn Ser His Tyr Gly Ile
                85                  90                  95
Pro Leu Arg Asn Glu Ile Val Ile Gly Ser Ile
            100                 105
```

<210> 287
<211> 1379
<212> DNA
<213> Homo sapiens

<400> 287
nnttaactgc ccctttgcag tctttattct gggacattag cactgtctgg ttatcttgct
60
tcagttgagg gattcgggac aatagcagtg ctgatggtaa tgttggcgat ttccctgttt
120
gttttgcagg tcacggccag gggctttggg ccgctgttac agtttgccta cactgccaag
180
ctgttactca gcagagaaaa catccgcgag gtcatccgct gtgctgagtt cctgcgcatg
240
cacaacctgg aggactcctg cttcagcttc ctgcagaccc agctcctgaa cagtgaggat
300
ggcctgtttg tgtgccggaa ggatgctgcg tgccagcgcc cacacgagga ctgcgagaac
360
tctgcaggag aggaggagga tgaagaggag gagacgatgg attcagagac ggccaagatg
420
gcttgcccca gggaccagat gcttccagag cccatcagct ttgaggccgc cgccatcccc
480
gtagcagaga aggaagaagc cctgctgccc gagcctgacg tgcccacaga caccaaggag
540
agctcagaaa aggacgcgtt aacgcagtac cccagataca agaaatacca gcttgcatgt
600
accaagaatg tctataatgc atcatcacac agtacctcag gttttgcaag cacattccgg
660
gaagataact ctagcaacag cctcaagccg gggcttgcca gggggcagat taaaagtgag
720
ccgcccagtg aagagaatga ggaagagagc atcacgctct gcctgtctgg agatgagcct
780
gacgccaagg acagagcggg ggatgtcgag atggaccgga aacagcccag ccctgccccc
840
acccccacgg ccccagctgg ggccgcctgc ctggagagat ccaggagcgt ggcctcgccc
900
tcctgcttaa ggtctctgtt cagcataacg aaaagtgtgg agctgtctgg cctgcccagt
960
acatctcagc agcactttgc caggagtcca gcctgccctt ttgacaaggg gatcactcag
1020

ggtgacctta aaactgacta cacccctttc acagggaatt atggacagcc ccacgtgggc
1080
cagaaggagg tgtccaactt caccatgggg tcgcccctca gggggcctgg gttggaggct
1140
ctctgtaaac aggagggaga gctggaccgg aggagcgtga tcttctcctc cagcgcttgt
1200
gaccaagtga gcacctcggt gcattcttat tctggggtga gcagtttgga caaagacctc
1260
tctgagccgg tgccaaaggg tctgtgggtg ggagccggcc agtcctccc cagctcgcag
1320
gcctactccc acggtgggct gatggccgac cacttgccag gaaggatgcg gcccaacac
1379

<210> 288
<211> 428
<212> PRT
<213> Homo sapiens

<400> 288
Met Val Met Leu Ala Ile Ser Leu Phe Val Leu Gln Val Thr Ala Arg
1 5 10 15
Gly Phe Gly Pro Leu Leu Gln Phe Ala Tyr Thr Ala Lys Leu Leu Leu
20 25 30
Ser Arg Glu Asn Ile Arg Glu Val Ile Arg Cys Ala Glu Phe Leu Arg
35 40 45
Met His Asn Leu Glu Asp Ser Cys Phe Ser Phe Leu Gln Thr Gln Leu
50 55 60
Leu Asn Ser Glu Asp Gly Leu Phe Val Cys Arg Lys Asp Ala Ala Cys
65 70 75 80
Gln Arg Pro His Glu Asp Cys Glu Asn Ser Ala Gly Glu Glu Glu Asp
85 90 95
Glu Glu Glu Glu Thr Met Asp Ser Glu Thr Ala Lys Met Ala Cys Pro
100 105 110
Arg Asp Gln Met Leu Pro Glu Pro Ile Ser Phe Glu Ala Ala Ala Ile
115 120 125
Pro Val Ala Glu Lys Glu Glu Ala Leu Leu Pro Glu Pro Asp Val Pro
130 135 140
Thr Asp Thr Lys Glu Ser Ser Glu Lys Asp Ala Leu Thr Gln Tyr Pro
145 150 155 160
Arg Tyr Lys Lys Tyr Gln Leu Ala Cys Thr Lys Asn Val Tyr Asn Ala
165 170 175
Ser Ser His Ser Thr Ser Gly Phe Ala Ser Thr Phe Arg Glu Asp Asn
180 185 190
Ser Ser Asn Ser Leu Lys Pro Gly Leu Ala Arg Gly Gln Ile Lys Ser
195 200 205
Glu Pro Pro Ser Glu Glu Asn Glu Glu Glu Ser Ile Thr Leu Cys Leu
210 215 220
Ser Gly Asp Glu Pro Asp Ala Lys Asp Arg Ala Gly Asp Val Glu Met
225 230 235 240
Asp Arg Lys Gln Pro Ser Pro Ala Pro Thr Pro Thr Ala Pro Ala Gly
245 250 255
Ala Ala Cys Leu Glu Arg Ser Arg Ser Val Ala Ser Pro Ser Cys Leu
260 265 270
Arg Ser Leu Phe Ser Ile Thr Lys Ser Val Glu Leu Ser Gly Leu Pro

```
        275                 280                 285
Ser Thr Ser Gln Gln His Phe Ala Arg Ser Pro Ala Cys Pro Phe Asp
    290                 295                 300
Lys Gly Ile Thr Gln Gly Asp Leu Lys Thr Asp Tyr Thr Pro Phe Thr
305                 310                 315                 320
Gly Asn Tyr Gly Gln Pro His Val Gly Gln Lys Glu Val Ser Asn Phe
                325                 330                 335
Thr Met Gly Ser Pro Leu Arg Gly Pro Gly Leu Glu Ala Leu Cys Lys
            340                 345                 350
Gln Glu Gly Glu Leu Asp Arg Arg Ser Val Ile Phe Ser Ser Ser Ala
        355                 360                 365
Cys Asp Gln Val Ser Thr Ser Val His Ser Tyr Ser Gly Val Ser Ser
    370                 375                 380
Leu Asp Lys Asp Leu Ser Glu Pro Val Pro Lys Gly Leu Trp Val Gly
385                 390                 395                 400
Ala Gly Gln Ser Leu Pro Ser Ser Gln Ala Tyr Ser His Gly Gly Leu
                405                 410                 415
Met Ala Asp His Leu Pro Gly Arg Met Arg Pro Asn
            420                 425
```

<210> 289
<211> 822
<212> DNA
<213> Homo sapiens

<400> 289
ngcattaccg ggctgaagac gggtgctcat gacctcaacg atataggcta ttgctagaac
60
cacgccggcc cacgccgcgc aaagcgcaga cacggcacca ggaggggtca catggctgat
120
agcaagtcga aggcgaagga cgagcgcact gccgatgaga tcaggcggga tattgcagcg
180
acccgtgctt gcctggcagc cggggtggag aacctcgtgg aggaggtgca tccggcaacc
240
ctcaagcgtg aagcatctga tcgtgcccgt gattttgtgc agggtgagtt tgatcaggtc
300
aagagccagg tcaaagatga gaaatggtgg cgcgtgcagc ggatcgcgat ggccgcagga
360
gtgctcgctg ccggcgtcgt cagcattatt gtgctgcgcg cgatagtcgg tcgcgcaacg
420
ggcgctaccg ctcgtcgcaa gcttgagaag ctgcagcttt ctcaggcgaa gcgggttcga
480
aaagatgcca agcagcgtag taaggaagat gaaaaggcag ccaagaaaaa tgccaagctc
540
ggcaagaaga acgctaagaa gtacggcaag ctcgataccg atgactcgtc ggtaagcaac
600
cttgccgaga aaatgctcaa acaggccgcc gtgctgcgtg cacaggcggc tgccggggcg
660
tgagaacagt gccgcctagc aaacagcggt cacagcgcaa aacaggtttg gctccgaccc
720
atggtggacc ggagccaaac tgtgttaccg catcatttga taccgccagc agccaggcct
780
gcgacaatgc gacgctggaa taccagcacc atgatgacta gt
822

<210> 290
<211> 183
<212> PRT
<213> Homo sapiens

<400> 290
Met Ala Asp Ser Lys Ser Lys Ala Lys Asp Glu Arg Thr Ala Asp Glu
1 5 10 15
Ile Arg Arg Asp Ile Ala Ala Thr Arg Ala Cys Leu Ala Ala Gly Val
20 25 30
Glu Asn Leu Val Glu Glu Val His Pro Ala Thr Leu Lys Arg Glu Ala
35 40 45
Ser Asp Arg Ala Arg Asp Phe Val Gln Gly Glu Phe Asp Gln Val Lys
50 55 60
Ser Gln Val Lys Asp Glu Lys Trp Trp Arg Val Gln Arg Ile Ala Met
65 70 75 80
Ala Ala Gly Val Leu Ala Ala Gly Val Val Ser Ile Ile Val Leu Arg
85 90 95
Ala Ile Val Gly Arg Ala Thr Gly Ala Thr Ala Arg Arg Lys Leu Glu
100 105 110
Lys Leu Gln Leu Ser Gln Ala Lys Arg Val Arg Lys Asp Ala Lys Gln
115 120 125
Arg Ser Lys Glu Asp Glu Lys Ala Ala Lys Lys Asn Ala Lys Leu Gly
130 135 140
Lys Lys Asn Ala Lys Lys Tyr Gly Lys Leu Asp Thr Asp Asp Ser Ser
145 150 155 160
Val Ser Asn Leu Ala Glu Lys Met Leu Lys Gln Ala Ala Val Leu Arg
165 170 175
Ala Gln Ala Ala Ala Gly Ala
180

<210> 291
<211> 351
<212> DNA
<213> Homo sapiens

<400> 291
ctccacgccg acaagactta cgacgggcgt cgctgccggg ctgagtgccg ggcccgctcc
60
atcacccccc gcatcgctcg ccgcggcgtg gagaccagcg agcgcttggg ccggtatcgc
120
tgggtcgtcg agcgcacctt cgcctggctc aaccgctttc ggcgcctcgc catccgctac
180
gagcggcgtg ctgacatcca cgaagccttc gtgatcctcg gctgcgccct catctgcctc
240
aaccagatca gacggttttg ttaggtgctg taaagggaga atggctgcag ctgggctatc
300
tgctccctcg tcaaccagaa acaggctgct catcctcact caacaacgcg t
351

<210> 292
<211> 87
<212> PRT

<213> Homo sapiens

<400> 292
Leu His Ala Asp Lys Thr Tyr Asp Gly Arg Arg Cys Arg Ala Glu Cys
1 5 10 15
Arg Ala Arg Ser Ile Thr Pro Arg Ile Ala Arg Arg Gly Val Glu Thr
20 25 30
Ser Glu Arg Leu Gly Arg Tyr Arg Trp Val Val Glu Arg Thr Phe Ala
35 40 45
Trp Leu Asn Arg Phe Arg Arg Leu Ala Ile Arg Tyr Glu Arg Arg Ala
50 55 60
Asp Ile His Glu Ala Phe Val Ile Leu Gly Cys Ala Leu Ile Cys Leu
65 70 75 80
Asn Gln Ile Arg Arg Phe Cys
85

<210> 293
<211> 716
<212> DNA
<213> Homo sapiens

<400> 293
nncttcacca caccggccat caacgcacct cctcgtgata acttgacctt ctgccgaacc
60
ggttaatcag tttagtggcg aggcatgaca cgttgacgag tcagctgtgg tacatgtgcg
120
gaacactcac aatgccacgg cggcatgttg ctgtcggtca cgacccttat ggtgatcgct
180
gtgagaaccc gaacggcaga tgcgattctg gcggcactgg atctgaacag gtttaaggtt
240
gcgaagactt tcgatgttcc agtgtgcgtc atagctggtg ccgggacagg taaaactcgt
300
gctgtcactc atcgcattgc ctacggtgca gcgacaggca agcttgatcc gcgtcgtacc
360
ctcgcggtca cttttacgac taaggcagct ggcacgatga gaggtcgact cgccgatctg
420
ggggttgttg gtgtgcaggc tcgcactatt cattctgcgg cgttgcggca gatcaagttt
480
ttctggcctc gtgcatataa ctgtgagttg ccaccggtga gtgattctcg tttctcgatg
540
gtggcggaga cgacccatcg cattggtctg ggcaatgaca aggcgctgct gcgcgacttg
600
tccgccgaga tctcgtgggc gaaggtctca aatgtgccga ctgatcaata cgcatccctg
660
gctagggcgg aaggtcgggt ggtggcggga gtttcggcaa ctgacgtagg acgcgt
716

<210> 294
<211> 190
<212> PRT
<213> Homo sapiens

<400> 294
Met Leu Leu Ser Val Thr Thr Leu Met Val Ile Ala Val Arg Thr Arg

```
 1               5                  10                  15
Thr Ala Asp Ala Ile Leu Ala Ala Leu Asp Leu Asn Arg Phe Lys Val
            20                  25                  30
Ala Lys Thr Phe Asp Val Pro Val Cys Val Ile Ala Gly Ala Gly Thr
        35                  40                  45
Gly Lys Thr Arg Ala Val Thr His Arg Ile Ala Tyr Gly Ala Ala Thr
    50                  55                  60
Gly Lys Leu Asp Pro Arg Arg Thr Leu Ala Val Thr Phe Thr Thr Lys
65                  70                  75                  80
Ala Ala Gly Thr Met Arg Gly Arg Leu Ala Asp Leu Gly Val Val Gly
                85                  90                  95
Val Gln Ala Arg Thr Ile His Ser Ala Ala Leu Arg Gln Ile Lys Phe
            100                 105                 110
Phe Trp Pro Arg Ala Tyr Asn Cys Glu Leu Pro Pro Val Ser Asp Ser
        115                 120                 125
Arg Phe Ser Met Val Ala Glu Thr Thr His Arg Ile Gly Leu Gly Asn
    130                 135                 140
Asp Lys Ala Leu Leu Arg Asp Leu Ser Ala Glu Ile Ser Trp Ala Lys
145                 150                 155                 160
Val Ser Asn Val Pro Thr Asp Gln Tyr Ala Ser Leu Ala Arg Ala Glu
                165                 170                 175
Gly Arg Val Val Ala Gly Val Ser Ala Thr Asp Val Gly Arg
            180                 185                 190
```

<210> 295
<211> 417
<212> DNA
<213> Homo sapiens

<400> 295
ttcatatcag gcagtacccg agtccatgcg atcaacaacg tcagcgtatc tttcacccat
60
tctggagtgc accttctcat gggagaaagc ggatcaggaa aaagcaccct catcaatctc
120
ctagctggtc tggatacccc agattcgggg tccgtctacg cagaaggcgt caccgtatct
180
gatcagagcg aggcgagcag agcccaattt cgattacgcc acatcgccgt catcttccag
240
gacgacaacc tcatcgctga gttgaccaat accgagaata ttgcgctacc cctgtgggcg
300
cagggcacat cgaagtccga tgccactgaa atcgcccacg aagccatgcg aaaactagga
360
atcgagtcat tgggcagacg ctaccccggc gaggtctcgg gtggccaacg gcaacgc
417

<210> 296
<211> 139
<212> PRT
<213> Homo sapiens

<400> 296
```
Phe Ile Ser Gly Ser Thr Arg Val His Ala Ile Asn Asn Val Ser Val
 1               5                  10                  15
Ser Phe Thr His Ser Gly Val His Leu Leu Met Gly Glu Ser Gly Ser
```

```
            20                  25                  30
Gly Lys Ser Thr Leu Ile Asn Leu Leu Ala Gly Leu Asp Thr Pro Asp
        35                  40                  45
Ser Gly Ser Val Tyr Ala Glu Gly Val Thr Val Ser Asp Gln Ser Glu
    50                  55                  60
Ala Ser Arg Ala Gln Phe Arg Leu Arg His Ile Ala Val Ile Phe Gln
65                  70                  75                  80
Asp Asp Asn Leu Ile Ala Glu Leu Thr Asn Thr Glu Asn Ile Ala Leu
                85                  90                  95
Pro Leu Trp Ala Gln Gly Thr Ser Lys Ser Asp Ala Thr Glu Ile Ala
            100                 105                 110
His Glu Ala Met Arg Lys Leu Gly Ile Glu Ser Leu Gly Arg Arg Tyr
        115                 120                 125
Pro Gly Glu Val Ser Gly Gly Gln Arg Gln Arg
    130                 135
```

<210> 297
<211> 378
<212> DNA
<213> Homo sapiens

<400> 297
tacaccatcg gtgaccagat tgtcgaagct ctgcaggtgc actcgaagat gtccgacaag
60
gacgcttggg cgcgtgccat cgagctgctc gacttggtgg ggattccgaa tcccgaggtg
120
cgtgccaaag cttttccgca cgagttttcc ggtggcatga ggcaacgagt cgtcatcgcc
180
atggccatcg cgaacgaccc tgacctcatc atcgccgacg agccgacgac ggccctcgac
240
gtgaccatcc aggcccagat tctcgatttg ctgcgcgtag cccagcgtga aacccatgcg
300
ggcgtcgtta tgatcaccca cgacctcggt gtggtagctg gtctggctga cagggttgcc
360
gtgatgtatg ccggacgc
378

<210> 298
<211> 126
<212> PRT
<213> Homo sapiens

<400> 298

```
Tyr Thr Ile Gly Asp Gln Ile Val Glu Ala Leu Gln Val His Ser Lys
 1               5                  10                  15
Met Ser Asp Lys Asp Ala Trp Ala Arg Ala Ile Glu Leu Leu Asp Leu
            20                  25                  30
Val Gly Ile Pro Asn Pro Glu Val Arg Ala Lys Ala Phe Pro His Glu
        35                  40                  45
Phe Ser Gly Gly Met Arg Gln Arg Val Val Ile Ala Met Ala Ile Ala
    50                  55                  60
Asn Asp Pro Asp Leu Ile Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp
65                  70                  75                  80
Val Thr Ile Gln Ala Gln Ile Leu Asp Leu Leu Arg Val Ala Gln Arg
```

```
                85                  90                  95
Glu Thr His Ala Gly Val Val Met Ile Thr His Asp Leu Gly Val Val
            100                 105                 110
Ala Gly Leu Ala Asp Arg Val Ala Val Met Tyr Ala Gly Arg
        115                 120                 125
```

<210> 299
<211> 368
<212> DNA
<213> Homo sapiens

<400> 299
gtgcacggtt tcgttggcat gcgcaatgac cgggagaact tgcgttttga tccgagactt
60
ccagcccaat ggacgtcgat caaacaccac atgctcattg gcgactctca catgctcgtt
120
ttcctggaac gtgacgccat tacgttccag attctgtcgg gccatgaccg cgacgtgaca
180
gtgcgcggtg agctctacca cattggggtt gagccggtga gggtgccgtt gtccgatcag
240
gggccgttgc gtcctagcct gcgcgttacc catccgatct cggggttgcg tcgagctgac
300
ggttctctta tcactgcaga agttcccggc agcattgctg agacgattgg gtcttctccg
360
atctcgac
368

<210> 300
<211> 122
<212> PRT
<213> Homo sapiens

<400> 300
```
Val His Gly Phe Val Gly Met Arg Asn Asp Arg Glu Asn Leu Arg Phe
 1               5                  10                  15
Asp Pro Arg Leu Pro Ala Gln Trp Thr Ser Ile Lys His His Met Leu
            20                  25                  30
Ile Gly Asp Ser His Met Leu Val Phe Leu Glu Arg Asp Ala Ile Thr
        35                  40                  45
Phe Gln Ile Leu Ser Gly His Asp Arg Asp Val Thr Val Arg Gly Glu
    50                  55                  60
Leu Tyr His Ile Gly Val Glu Pro Val Arg Val Pro Leu Ser Asp Gln
65                  70                  75                  80
Gly Pro Leu Arg Pro Ser Leu Arg Val Thr His Pro Ile Ser Gly Leu
                85                  90                  95
Arg Arg Ala Asp Gly Ser Leu Ile Thr Ala Glu Val Pro Gly Ser Ile
            100                 105                 110
Ala Glu Thr Ile Gly Ser Ser Pro Ile Ser
        115                 120
```

<210> 301
<211> 456
<212> DNA
<213> Homo sapiens

<400> 301
ggccgggtta ttgcccgccc gtttgtcggg gaaacccggc agaccttcga gcgcaccggc
60
aaccggcgcg actattccgt accgccgccc gaaccgacct tgctcgacag gcttacggac
120
gcgggccgga cggtgatcgc aatcggcaag attggtgata tctacgcgca caaaggcgtg
180
tctcaggtgc gtaaggcaat ggcaatattg gccttgttcg atgaaacact cattgccatg
240
gacgacgcgc aggacggcga tctggtcttc accaacttcg tggatttcga catgctctac
300
gggcatcgca gggatgtgcc cggctatgcc gccgcgctcg aggctttcga ccggaggctg
360
ccggaagcca tggcgaaatt gcggacgggc gatcttctga tcctgacagc cgatcatggc
420
tgcgacccga ccctcaaggg aaccgaccac acgcgt
456

<210> 302
<211> 152
<212> PRT
<213> Homo sapiens

<400> 302
Gly Arg Val Ile Ala Arg Pro Phe Val Gly Glu Thr Arg Gln Thr Phe
1 5 10 15
Glu Arg Thr Gly Asn Arg Arg Asp Tyr Ser Val Pro Pro Pro Glu Pro
20 25 30
Thr Leu Leu Asp Arg Leu Thr Asp Ala Gly Arg Thr Val Ile Ala Ile
35 40 45
Gly Lys Ile Gly Asp Ile Tyr Ala His Lys Gly Val Ser Gln Val Arg
50 55 60
Lys Ala Met Ala Ile Leu Ala Leu Phe Asp Glu Thr Leu Ile Ala Met
65 70 75 80
Asp Asp Ala Gln Asp Gly Asp Leu Val Phe Thr Asn Phe Val Asp Phe
85 90 95
Asp Met Leu Tyr Gly His Arg Arg Asp Val Pro Gly Tyr Ala Ala Ala
100 105 110
Leu Glu Ala Phe Asp Arg Arg Leu Pro Glu Ala Met Ala Lys Leu Arg
115 120 125
Thr Gly Asp Leu Leu Ile Leu Thr Ala Asp His Gly Cys Asp Pro Thr
130 135 140
Leu Lys Gly Thr Asp His Thr Arg
145 150

<210> 303
<211> 402
<212> DNA
<213> Homo sapiens

<400> 303
nncgtgggca tcgaggagtt cctcgacatg aagtatcacg cgacgccgat tcatcgtcgc
60

tgacagcggt tttccggaac acatcagcgt tcagacagga gcgaggagac catgtacctg
120
ggtgctcagc tgttcagtga cagcgagtac gagcagcgcc tgagacgtgt ccgtgagctc
180
atggaccgtc agggtctgtc ggcgatcatc gtcaccgatc cggccaacat cttctatctg
240
atcggttaca acgcctggtc gttctacacc ccgcagatgc tgttcgtgcc gatcgacgga
300
gagatggtcc tctacgctcg cgagatggat cgcatggcgc acatcngcac gacgtcgttg
360
cccgccgatc agatcgtcgg ttacccggag agttatgtgc ac
402

<210> 304
<211> 97
<212> PRT
<213> Homo sapiens

<400> 304
Met Tyr Leu Gly Ala Gln Leu Phe Ser Asp Ser Glu Tyr Glu Gln Arg
1 5 10 15
Leu Arg Arg Val Arg Glu Leu Met Asp Arg Gln Gly Leu Ser Ala Ile
20 25 30
Ile Val Thr Asp Pro Ala Asn Ile Phe Tyr Leu Ile Gly Tyr Asn Ala
35 40 45
Trp Ser Phe Tyr Thr Pro Gln Met Leu Phe Val Pro Ile Asp Gly Glu
50 55 60
Met Val Leu Tyr Ala Arg Glu Met Asp Arg Met Ala His Ile Xaa Thr
65 70 75 80
Thr Ser Leu Pro Ala Asp Gln Ile Val Gly Tyr Pro Glu Ser Tyr Val
85 90 95
His

<210> 305
<211> 375
<212> DNA
<213> Homo sapiens

<400> 305
nnacgcgtcg gttccgcatc gagcgaccgg atcgcatcga cgagcacgct gcaccagtgc
60
gtgtcgtcct ggcgaatatg ggcgatcagc cggtacagtt cgggatcgtc gctcacctcg
120
gccgccattt cggatgcgac acgcgcgcct gcgcgctcgg cctccagcaa ctcgtcgagc
180
gtcgccacca gcgcggcgcg atcttcatgc ggagtcagat cggcgcgggc gtcaggcccg
240
tcgccatgcg tcggaatcga catgcagcac cctcctgcca ggatcgatgg cgtaatacgt
300
gcgacggtac acggcgcgtg ttgcacgaac gtgcaaatca gcgcgtgcct cgtgccatat
360
acgtcacatc atatg
375

<210> 306
<211> 125
<212> PRT
<213> Homo sapiens

<400> 306
Xaa Arg Val Gly Ser Ala Ser Ser Asp Arg Ile Ala Ser Thr Ser Thr
 1   5   10   15
Leu His Gln Cys Val Ser Ser Trp Arg Ile Trp Ala Ile Ser Arg Tyr
            20   25   30
Ser Ser Gly Ser Ser Leu Thr Ser Ala Ala Ile Ser Asp Ala Thr Arg
        35   40   45
Ala Pro Ala Arg Ser Ala Ser Ser Asn Ser Ser Ser Val Ala Thr Ser
    50   55   60
Ala Ala Arg Ser Ser Cys Gly Val Arg Ser Ala Arg Ala Ser Gly Pro
65   70   75   80
Ser Pro Cys Val Gly Ile Asp Met Gln His Pro Pro Ala Arg Ile Asp
                85   90   95
Gly Val Ile Arg Ala Thr Val His Gly Ala Cys Cys Thr Asn Val Gln
            100   105   110
Ile Ser Ala Cys Leu Val Pro Tyr Thr Ser His His Met
        115   120   125

<210> 307
<211> 685
<212> DNA
<213> Homo sapiens

<400> 307
actagttctg gccgctcccc tggggctttg ggtaacaatt gtcagcccca cccatcctag
60
ggttaggaag gctattctct ttggccactc tcatcctaag acctatttgg agaacctctg
120
gggtttgagt ctttttttca gcagaatgag gcttgatccc gcattatagc acctcgcaca
180
tttgatgtct cttcttctca cccactcacc ccaccctggg ggttggggca aaaaagtggc
240
tcaaagctgc ggttcagagt tccttgtaaa caaggctcct ccctcactgt cctcaccctg
300
ctccagcaga gggagcagcg gaaggaccac tctgctgcag ccatgcttgt ttctaaccca
360
gcagaactgg acataatggg aacagggtct gaagacaatc aatccagggc tgcagtgggt
420
gctgagtctg gggaagcctc cacctggagg ggcagctggg cagtggcagc tcccttggaa
480
tggctcagcc tctggacatc accccaccca accagagccc tggctcttgc tggatgtcca
540
cagatgagtg cctgggattg gtctcagcca ctatgggggg gatgtgcagg gagaggtgat
600
gagggagtga gcaggactgt ctatgtgcct ctgtcctcat cctgaggctt gggtctgaaa
660
ttggtgctgc agcactggca cgcgt
685

<210> 308
<211> 100
<212> PRT
<213> Homo sapiens

<400> 308
Met Leu Val Ser Asn Pro Ala Glu Leu Asp Ile Met Gly Thr Gly Ser
1 5 10 15
Glu Asp Asn Gln Ser Arg Ala Ala Val Gly Ala Glu Ser Gly Glu Ala
20 25 30
Ser Thr Trp Arg Gly Ser Trp Ala Val Ala Ala Pro Leu Glu Trp Leu
35 40 45
Ser Leu Trp Thr Ser Pro His Pro Thr Arg Ala Leu Ala Leu Ala Gly
50 55 60
Cys Pro Gln Met Ser Ala Trp Asp Trp Ser Gln Pro Leu Trp Gly Gly
65 70 75 80
Cys Ala Gly Arg Gly Asp Glu Gly Val Ser Arg Thr Val Tyr Val Pro
85 90 95
Leu Ser Ser Ser
100

<210> 309
<211> 432
<212> DNA
<213> Homo sapiens

<400> 309
caggctcgta ctattcgtat ccctgtgcat atggtcgagg tcatcaataa gctggctcgc
60
gtccagcgtc agatgctcca ggacctaggt cgtgagccca ccccggaaga gcttgccaac
120
gaactcgata tgaccgcaga gaaggtcatt gaggtgcaga aatacggtcg cgagccgatc
180
tcgctgcata ccccactggg tgaggatggc gattctgagt tcggtgacct tattgaggat
240
tccgaggcca tcgtgccagc agacgccgtc aacttcaccc tgttgcagga gcagctgcat
300
gatgtcctcg ataccttgtc cgagcgagag gccggtgtcg tgtcgatgcg attcggcttg
360
accgacggac agcccaagac cctggatgag atcggcaaag tctacggtgt tactcgggag
420
cgcatccgcc ag
432

<210> 310
<211> 144
<212> PRT
<213> Homo sapiens

<400> 310
Gln Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn
1 5 10 15
Lys Leu Ala Arg Val Gln Arg Gln Met Leu Gln Asp Leu Gly Arg Glu

```
            20                  25                  30
Pro Thr Pro Glu Glu Leu Ala Asn Glu Leu Asp Met Thr Ala Glu Lys
        35                  40                  45
Val Ile Glu Val Gln Lys Tyr Gly Arg Glu Pro Ile Ser Leu His Thr
    50                  55                  60
Pro Leu Gly Glu Asp Gly Asp Ser Glu Phe Gly Asp Leu Ile Glu Asp
65                  70                  75                  80
Ser Glu Ala Ile Val Pro Ala Asp Ala Val Asn Phe Thr Leu Leu Gln
                85                  90                  95
Glu Gln Leu His Asp Val Leu Asp Thr Leu Ser Glu Arg Glu Ala Gly
            100                 105                 110
Val Val Ser Met Arg Phe Gly Leu Thr Asp Gly Gln Pro Lys Thr Leu
        115                 120                 125
Asp Glu Ile Gly Lys Val Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln
    130                 135                 140
```

<210> 311
<211> 358
<212> DNA
<213> Homo sapiens

<400> 311
acgcgtatcg aaaatatccc tcccattatt accgctcgcc ctgaactgat ggctcatgaa
60
ctgacgccag aatctcttga tgcgagcctg gagtgggccg atgtggtggt cattggtcct
120
ggactgggac aacaagcgtg gggcaaaaaa gcgctacaaa aggtcgagaa ttgtcgtaaa
180
ccgatgctgt gggatgccga cgcgcttaac cttctggcaa tcaatcctga taaacgtcac
240
aatcgcatcc tgacgccaca ccccggcgag gccgcgcggc tgcttagctg cagcgtcgca
300
gaaattgaaa acgatcgctt acttntctgc gcacgtctgg taaaacggta acccgagt
358

<210> 312
<211> 116
<212> PRT
<213> Homo sapiens

<400> 312
```
Thr Arg Ile Glu Asn Ile Pro Pro Ile Ile Thr Ala Arg Pro Glu Leu
 1               5                  10                  15
Met Ala His Glu Leu Thr Pro Glu Ser Leu Asp Ala Ser Leu Glu Trp
            20                  25                  30
Ala Asp Val Val Val Ile Gly Pro Gly Leu Gly Gln Gln Ala Trp Gly
        35                  40                  45
Lys Lys Ala Leu Gln Lys Val Glu Asn Cys Arg Lys Pro Met Leu Trp
    50                  55                  60
Asp Ala Asp Ala Leu Asn Leu Leu Ala Ile Asn Pro Asp Lys Arg His
65                  70                  75                  80
Asn Arg Ile Leu Thr Pro His Pro Gly Glu Ala Ala Arg Leu Leu Ser
                85                  90                  95
Cys Ser Val Ala Glu Ile Glu Asn Asp Arg Leu Leu Xaa Cys Ala Arg
```

100 105 110
Leu Val Lys Arg
115

<210> 313
<211> 347
<212> DNA
<213> Homo sapiens

<400> 313
ncaactgaaa gcattgagat gagcgacgtg ctgtcccccc tccaccccac caaggccaac
60
acccctggtg gcgaaccgcg caccatccgc acctcgaacg cgcacatcat tgccgtcacc
120
agtggcaaag gcggcgtggg caagaccttt gtctccgcca acctggccgc cgcgctgacc
180
cgcctgggac tgcgcgtgct ggtactggac gccgacctgg gcctggccaa cttggacgtg
240
gtgctgaacc tctaccccaa ggtgacgctg cacgatgtgt tcaccggcaa ggcctcgctg
300
caagacgcgg tggtcacggc ccccggcggc ttccatgtgc tgctagc
347

<210> 314
<211> 115
<212> PRT
<213> Homo sapiens

<400> 314
Xaa Thr Glu Ser Ile Glu Met Ser Asp Val Leu Ser Pro Phe His Pro
1 5 10 15
Thr Lys Ala Asn Thr Pro Gly Gly Glu Pro Arg Thr Ile Arg Thr Ser
20 25 30
Asn Ala His Ile Ile Ala Val Thr Ser Gly Lys Gly Gly Val Gly Lys
35 40 45
Thr Phe Val Ser Ala Asn Leu Ala Ala Ala Leu Thr Arg Leu Gly Leu
50 55 60
Arg Val Leu Val Leu Asp Ala Asp Leu Gly Leu Ala Asn Leu Asp Val
65 70 75 80
Val Leu Asn Leu Tyr Pro Lys Val Thr Leu His Asp Val Phe Thr Gly
85 90 95
Lys Ala Ser Leu Gln Asp Ala Val Val Thr Ala Pro Gly Gly Phe His
100 105 110
Val Leu Leu
115

<210> 315
<211> 544
<212> DNA
<213> Homo sapiens

<400> 315
nnacgcgttc gtcaacagga aaacaacaac ggcttctcgc tggagggaac catgcttgcc
60

gaagatatct acgcgatcat gctgttttca tcgctcatcc tggtcgtccc ggggccatcc
120
aacaccttgc tgctcagcgc ccgtttccat ttcggctcgc tgcgggcggc gcccttcatc
180
ctgcttgagg cgttgggcta ctcgctatcc atttcggcat ggggctgggt attggcgcgc
240
ctgtccgaga gcaatccatg gatcatcagt ctgaccaagg cactctgcgc gctatatgtg
300
gcgcttctgg cggtgaagac ctggaatgcc ntcgatccgc agtgcggggc cggtaacttc
360
cgccatgggc ccctgcccct gttcgtggca accctgtcga acccgaaggc gctgatcttc
420
gccagcgtga tctttcccgg caaggcgttc ctcgacttct ggaacaacta cacgatctcg
480
ctgctggcct tcctggttgt gctggcgccc atcgggatgc tttgggtcgg gctgggggcc
540
ggta
544

<210> 316
<211> 159
<212> PRT
<213> Homo sapiens

<400> 316
Ile Tyr Ala Ile Met Leu Phe Ser Ser Leu Ile Leu Val Val Pro Gly
1 5 10 15
Pro Ser Asn Thr Leu Leu Leu Ser Ala Arg Phe His Phe Gly Ser Leu
20 25 30
Arg Ala Ala Pro Phe Ile Leu Leu Glu Ala Leu Gly Tyr Ser Leu Ser
35 40 45
Ile Ser Ala Trp Gly Trp Val Leu Ala Arg Leu Ser Glu Ser Asn Pro
50 55 60
Trp Ile Ile Ser Leu Thr Lys Ala Leu Cys Ala Leu Tyr Val Ala Leu
65 70 75 80
Leu Ala Val Lys Thr Trp Asn Ala Xaa Asp Pro Gln Cys Gly Ala Gly
85 90 95
Asn Phe Arg His Gly Pro Leu Pro Leu Phe Val Ala Thr Leu Ser Asn
100 105 110
Pro Lys Ala Leu Ile Phe Ala Ser Val Ile Phe Pro Gly Lys Ala Phe
115 120 125
Leu Asp Phe Trp Asn Asn Tyr Thr Ile Ser Leu Leu Ala Phe Leu Val
130 135 140
Val Leu Ala Pro Ile Gly Met Leu Trp Val Gly Leu Gly Ala Gly
145 150 155

<210> 317
<211> 343
<212> DNA
<213> Homo sapiens

<400> 317
nggtcagcct ctcgcccagg caattctctt aagatacatg agctgctatg agtaccaaag
60

ccagaggttt gtccactgag agaagcacat tggaaagggg ggcgtgggcc tgggactgtg
120
tggcacttta tgcacggggg gggcctaagg ggggnggtcc accaaccatg cactgngggt
180
ggggtgtggg taacatgccg tgcattttgg gggtgtgcca tgagtggcac accatggggg
240
tggcatgtgg ggcatgtatg catgtggtgt tggcgcagca aactcagctc ttacctggct
300
ggggccagcc tctaaaactt ctcacattgg gctcccttct gac
343

<210> 318
<211> 98
<212> PRT
<213> Homo sapiens

<400> 318

Met	Ser	Thr	Lys	Ala	Arg	Gly	Leu	Ser	Thr	Glu	Arg	Ser	Thr	Leu	Glu
1				5				10					15		
Arg	Gly	Ala	Trp	Ala	Trp	Asp	Cys	Val	Ala	Leu	Tyr	Ala	Arg	Gly	Gly
		20					25					30			
Pro	Lys	Gly	Gly	Gly	Pro	Pro	Thr	Met	His	Xaa	Gly	Trp	Gly	Val	Gly
	35					40					45				
Asn	Met	Pro	Cys	Ile	Leu	Gly	Val	Cys	His	Glu	Trp	His	Thr	Met	Gly
50					55					60					
Val	Ala	Cys	Gly	Ala	Cys	Met	His	Val	Val	Leu	Ala	Gln	Gln	Thr	Gln
65				70					75						80
Leu	Leu	Pro	Gly	Trp	Gly	Gln	Pro	Leu	Lys	Leu	Leu	Thr	Leu	Gly	Ser
			85					90					95		
Leu	Leu														

<210> 319
<211> 429
<212> DNA
<213> Homo sapiens

<400> 319
gaattctcga tgtaccccct cccggcagtc ctattctcga gctgagcggg cacagtggcc
60
ccgttaacag tgtggcttgg ggtccaccca gccagagcac gttgcgaaat ggacctagta
120
agggcatgat atgtacagga ggcgacgatg ctcagtgcct cgtatatgat ctgactagct
180
caactcttcg aacagcatct gctcaaggac ggcgctctcg aaacagtcca tataaacaaa
240
gccattcacc gggaatagac ggatggcgtg tcggcgcaga agtgccggtg ctcgcttata
300
cggccccgtc tatggtcaac aatgctagct ggctcggcat gcctgcgcca tcaaaacgca
360
catcgctaca gagcaaacac cgcagccttt accgcagctt actcagtgag tggactgagt
420
atacgtccn
429

<210> 320
<211> 101
<212> PRT
<213> Homo sapiens

<400> 320
Met Ile Cys Thr Gly Gly Asp Asp Ala Gln Cys Leu Val Tyr Asp Leu
1 5 10 15
Thr Ser Ser Thr Leu Arg Thr Ala Ser Ala Gln Gly Arg Arg Ser Arg
20 25 30
Asn Ser Pro Tyr Lys Gln Ser His Ser Pro Gly Ile Asp Gly Trp Arg
35 40 45
Val Gly Ala Glu Val Pro Val Leu Ala Tyr Thr Ala Pro Ser Met Val
50 55 60
Asn Asn Ala Ser Trp Leu Gly Met Pro Ala Pro Ser Lys Arg Thr Ser
65 70 75 80
Leu Gln Ser Lys His Arg Ser Leu Tyr Arg Ser Leu Leu Ser Glu Trp
85 90 95
Thr Glu Tyr Thr Ser
100

<210> 321
<211> 530
<212> DNA
<213> Homo sapiens

<400> 321
ngtgcacgac gtgctcgcca agtccctcgg gtcctctaat gcgatcaacg tggttcacgc
60
caccgtcgat gcgttgcagc agctcgagga gcccgaagag gtcgcccgtc gccgcggcaa
120
gtccgttgag gagatcgccc cagcagccat gctgcgtgcg cgcaaggagg ccgacgaggc
180
cgccgctgct gcccgcatgg aggaaaaggc gggggttaac tgatgagcaa gctgaagatc
240
acccagatca agtctggcat cgctaccaag ccaaatcatc gtgagaccct gcgcagcctc
300
ggactgaagc gtattggtga cacggtcatc aaggaggacc gcccggagtt ccgcggcatg
360
gtccggaccg ttcgtcacct cgtcaccatg gaagaggtgg actgacatgg ctattgagct
420
ccatgacctc aagcccgctc ctggtgccca caaggccaag acccgcgttg gtcgtggtga
480
gggttccaag ggtaagaccg ctggtcgcgg taccaagggc accggtgcac
530

<210> 322
<211> 60
<212> PRT
<213> Homo sapiens

<400> 322
Met Ser Lys Leu Lys Ile Thr Gln Ile Lys Ser Gly Ile Ala Thr Lys

```
 1               5                  10                  15
Pro Asn His Arg Glu Thr Leu Arg Ser Leu Gly Leu Lys Arg Ile Gly
            20                  25                  30
Asp Thr Val Ile Lys Glu Asp Arg Pro Glu Phe Arg Gly Met Val Arg
        35                  40                  45
Thr Val Arg His Leu Val Thr Met Glu Glu Val Asp
    50                  55                  60
```

<210> 323
<211> 468
<212> DNA
<213> Homo sapiens

<400> 323
ntccggaccc gctgtggcca cgtattctgc cgttcctgta ttgctaccag tctaaagaac
60
aacaagtgga cctgtcctta ttgccgggca tatcttcctt cagaaggagt tccagcaact
120
gatgtagcca aaagaatgaa atcagagtat aagaactgcg ctgagtgtga caccctggtt
180
tgcctcagtg aaatgagggc acatattcgg acttgtcaga agtacataga taagtatgga
240
ccactacaag aacttgagga gacagcagca aggtgtgtat gtccctttg tcagagggaa
300
ctgtatgaag acagcttgct ggatcattgt attactcatc acagatcgga acggaggcct
360
gtgttctgtc cactttgcca tttaataccc gatgagaatc caagcagctt cagtggcagt
420
ttaataagac atctgcaagt tagtcacact ttggtttatg atgatttc
468

<210> 324
<211> 156
<212> PRT
<213> Homo sapiens

<400> 324
```
Xaa Arg Thr Arg Cys Gly His Val Phe Cys Arg Ser Cys Ile Ala Thr
 1               5                  10                  15
Ser Leu Lys Asn Asn Lys Trp Thr Cys Pro Tyr Cys Arg Ala Tyr Leu
            20                  25                  30
Pro Ser Glu Gly Val Pro Ala Thr Asp Val Ala Lys Arg Met Lys Ser
        35                  40                  45
Glu Tyr Lys Asn Cys Ala Glu Cys Asp Thr Leu Val Cys Leu Ser Glu
    50                  55                  60
Met Arg Ala His Ile Arg Thr Cys Gln Lys Tyr Ile Asp Lys Tyr Gly
65                  70                  75                  80
Pro Leu Gln Glu Leu Glu Glu Thr Ala Ala Arg Cys Val Cys Pro Phe
                85                  90                  95
Cys Gln Arg Glu Leu Tyr Glu Asp Ser Leu Leu Asp His Cys Ile Thr
            100                 105                 110
His His Arg Ser Glu Arg Arg Pro Val Phe Cys Pro Leu Cys His Leu
        115                 120                 125
Ile Pro Asp Glu Asn Pro Ser Ser Phe Ser Gly Ser Leu Ile Arg His
```

```
    130                 135                 140
Leu Gln Val Ser His Thr Leu Val Tyr Asp Asp Phe
145                 150                 155

<210> 325
<211> 374
<212> DNA
<213> Homo sapiens

<400> 325
acgcgtgaag ggaggacgag gaagtaacgg gaagcacaag gccgctgctg gggagatggc
60
actggagccc cctaggaagc atctcacagg ctgtggccct tggcacgggg atctggggcc
120
aggtcgagcg caggtctggg tatcatgcga gtgcgggctc gctggggcgg gaaagagttt
180
ggagctctgc tcccagggaa tccccactcc cgcagatgac ttgcccgaga gagttctgct
240
ggtggatttt gatggaaatt ctatttgatc gcacccactt ggttcactgt gtgcttccgg
300
gtccccaggt tttaggtgct tcatgccctg ctgggaacga gacacgctcc tgccctcagt
360
gaatcttcag tcta
374

<210> 326
<211> 108
<212> PRT
<213> Homo sapiens

<400> 326
Met Lys His Leu Lys Pro Gly Asp Pro Glu Ala His Ser Glu Pro Ser
 1               5                  10                  15
Gly Cys Asp Gln Ile Glu Phe Pro Ser Lys Ser Thr Ser Arg Thr Leu
            20                  25                  30
Ser Gly Lys Ser Ser Ala Gly Val Gly Ile Pro Trp Glu Gln Ser Ser
        35                  40                  45
Lys Leu Phe Pro Ala Pro Ala Ser Pro His Ser His Asp Thr Gln Thr
    50                  55                  60
Cys Ala Arg Pro Gly Pro Arg Ser Pro Cys Gln Gly Pro Gln Pro Val
65                  70                  75                  80
Arg Cys Phe Leu Gly Gly Ser Ser Ala Ile Ser Pro Ala Ala Ala Leu
                85                  90                  95
Cys Phe Pro Leu Leu Pro Arg Pro Pro Phe Thr Arg
            100                 105

<210> 327
<211> 538
<212> DNA
<213> Homo sapiens

<400> 327
cactataaaa tccagtttgg ggcccgtgtt ctttcctatt ggtctgtcag gtgaaaaact
60
```

ccggctgggg gaaaagcgtc cggtggtttg ttggtaaaga gggtgcgtga tgggctctgg
120
ggaatggagg atggcgcacc ggctgtgggt ggactgtgga aacgggggt ggcagtgccg
180
gggtagttgt cctgctggtc tggttttggg atcctgggct ggagaaatgc gatccaaaag
240
agctcgggat gggctcagag cgacccacga aaataccagg ggccaagtaa aatgaaccca
300
ccctttaaca gtgcacaaag cgctggcaca cggtccacgt ctggtgacgc aggctgcccg
360
aagcgctcca accattttgc aaacctggga gagcaagagg ggctctgcag gtctagccgc
420
cgcccctgtc ccactctggc cagccggagt ttttcaccta cagaccaata ggaaagaaca
480
cgggccccaa actggatttt atagtctgag ctctcagcat ctaaggaatg atatgccc
538

<210> 328
<211> 125
<212> PRT
<213> Homo sapiens

<400> 328
Met Val Gly Ala Leu Arg Ala Ala Cys Val Thr Arg Arg Gly Pro Cys
 1   5   10   15
Ala Ser Ala Leu Cys Thr Val Lys Gly Trp Val His Phe Thr Trp Pro
            20   25   30
Leu Val Phe Ser Trp Val Ala Leu Ser Pro Ser Arg Ala Leu Leu Asp
        35   40   45
Arg Ile Ser Pro Ala Gln Asp Pro Lys Thr Arg Pro Ala Gly Gln Leu
    50   55   60
Pro Arg His Cys His Pro Pro Phe Pro Gln Ser Thr His Ser Arg Cys
65   70   75   80
Ala Ile Leu His Ser Pro Glu Pro Ile Thr His Pro Leu Tyr Gln Gln
                85   90   95
Thr Thr Gly Arg Phe Ser Pro Ser Arg Ser Phe Ser Pro Asp Arg Pro
            100   105   110
Ile Gly Lys Asn Thr Gly Pro Lys Leu Asp Phe Ile Val
        115   120   125

<210> 329
<211> 407
<212> DNA
<213> Homo sapiens

<400> 329
tccggagagt tccctcccca ggaattcctt ctaagaatcc atgtggaaat agagcctgaa
60
gctcttcagt ctttctgctc cactgagcag tgttttcctg ataccttgg tatcctgcca
120
gcagcctcgt tatgactcct aactccattg ccctccatgg cccctgggcg ctctctctct
180
ctttctctcc aggtagtaga gcactgcttc tggcttcttg tgcacagaag ggtttcccac
240

agctgagagc tgggctccta ctgacatagt tatttccttt atatcctgcc ccaccttctt
300
ctggtagcac acagcaacct tgcatagtag ctggtatcat taccttccca atcaacaggc
360
cttgatttct tataggactt tttctctcag atttacattg cttcttt
407

<210> 330
<211> 113
<212> PRT
<213> Homo sapiens

<400> 330
Met Ile Pro Ala Thr Met Gln Gly Cys Cys Val Leu Pro Glu Glu Gly
 1   5   10   15
Gly Ala Gly Tyr Lys Gly Asn Asn Tyr Val Ser Arg Ser Pro Ala Leu
            20   25   30
Ser Cys Gly Lys Pro Phe Cys Ala Gln Glu Ala Arg Ser Ser Ala Leu
        35   40   45
Leu Pro Gly Glu Lys Glu Arg Glu Ser Ala Gln Gly Pro Trp Arg Ala
    50   55   60
Met Glu Leu Gly Val Ile Thr Arg Leu Leu Ala Gly Tyr Gln Gly Tyr
65   70   75   80
Gln Glu Asn Thr Ala Gln Trp Ser Arg Lys Thr Glu Glu Leu Gln Ala
                85   90   95
Leu Phe Pro His Gly Phe Leu Glu Gly Ile Pro Gly Glu Gly Thr Leu
            100   105   110
Arg

<210> 331
<211> 523
<212> DNA
<213> Homo sapiens

<400> 331
tgtaccgaac ctgctggtct cgagggcctt gctgggctcg tcgtacgcac agctgacgaa
60
tccaccggcc cccatcccgg cgccactttc gctgaggcca tggagtcgat cggagccagc
120
tacgacggat cggccgggtt ggccggaagt cacgtcggcg tcgatgtgcc cgtgacaagg
180
ttcgacgcag cggctgaact cttcgtcgaa ttgttgaaca ccacgagcct ggttgaagag
240
gacatcgccc gtcagatcga cgcggcgcga gcctccctgg cccagaccag ccagcgcgga
300
tcggccctag ccgagatggc agcagcacgt gcgctatggc cagtggggtc acggtcgtcc
360
ctgcccacga tcggtaccct ctcgtcggtg gaaaagctca acgccgcagc cgcacgagaa
420
ttctgggccg cgcactggac gatctccgat gccgtgctgg tggttgccgg agagggagtc
480
gaggacctcg acttgtcaat attcaaggag tggacgacca gct
523

<210> 332
<211> 174
<212> PRT
<213> Homo sapiens

<400> 332
Cys Thr Glu Pro Ala Gly Leu Glu Gly Leu Ala Gly Leu Val Val Arg
1 5 10 15
Thr Ala Asp Glu Ser Thr Gly Pro His Pro Gly Ala Thr Phe Ala Glu
20 25 30
Ala Met Glu Ser Ile Gly Ala Ser Tyr Asp Gly Ser Ala Gly Leu Ala
35 40 45
Gly Ser His Val Gly Val Asp Val Pro Val Thr Arg Phe Asp Ala Ala
50 55 60
Ala Glu Leu Phe Val Glu Leu Leu Asn Thr Thr Ser Leu Val Glu Glu
65 70 75 80
Asp Ile Ala Arg Gln Ile Asp Ala Ala Arg Ala Ser Leu Ala Gln Thr
85 90 95
Ser Gln Arg Gly Ser Ala Leu Ala Glu Met Ala Ala Ala Arg Ala Leu
100 105 110
Trp Pro Val Gly Ser Arg Ser Ser Leu Pro Thr Ile Gly Thr Leu Ser
115 120 125
Ser Val Glu Lys Leu Asn Ala Ala Ala Ala Arg Glu Phe Trp Ala Ala
130 135 140
His Trp Thr Ile Ser Asp Ala Val Leu Val Val Ala Gly Glu Gly Val
145 150 155 160
Glu Asp Leu Asp Leu Ser Ile Phe Lys Glu Trp Thr Thr Ser
165 170

<210> 333
<211> 372
<212> DNA
<213> Homo sapiens

<400> 333
nntgttcgtc gtgtcgaccc ggaactcaag gcccaggcga tgacggtgaa ggtgccaacc
60
gatccccatc accgcccggg agttccattg aagtctgcga aggaccgtat ggacatcatt
120
tctgcttacc gagaactcgg aagctatcgc gccgcagccg aggtgtgcgg caccacccac
180
aagaccgtca agcgggtggt cgatcggttt gaagccggcg atccacccac cggtggcaag
240
gaacgggccc gcaactacga tgcggtggcc cagctcgtcg cgcagcgagt cgcgcggtca
300
cacggccgga tcactgccaa acggctgcta ccggtagcgc gagcggcagg atatgagggg
360
tcggcgcgga at
372

<210> 334
<211> 88
<212> PRT

<213> Homo sapiens

<400> 334
Met Asp Ile Ile Ser Ala Tyr Arg Glu Leu Gly Ser Tyr Arg Ala Ala
1 5 10 15
Ala Glu Val Cys Gly Thr Thr His Lys Thr Val Lys Arg Val Val Asp
20 25 30
Arg Phe Glu Ala Gly Asp Pro Pro Thr Gly Gly Lys Glu Arg Ala Arg
35 40 45
Asn Tyr Asp Ala Val Ala Gln Leu Val Ala Gln Arg Val Ala Arg Ser
50 55 60
His Gly Arg Ile Thr Ala Lys Arg Leu Leu Pro Val Ala Arg Ala Ala
65 70 75 80
Gly Tyr Glu Gly Ser Ala Arg Asn
85

<210> 335
<211> 356
<212> DNA
<213> Homo sapiens

<400> 335
gtgcacgcct tgctgggcga gggcgatgcg cctgcgcgca ccttcgtgga cggtaccttt
60
ggcaggggag ggcattcgcg gctcatcctg cagcggttgg ggccgcaagg ccgcctggtg
120
gcgttcgaca aggacaccga agccattcaa gcagcggcgc gcatcacgga tgcgcgcttt
180
tccatcnggc accaggggtt cagccatctc ggggaactgc ccgccgccag cgtgtccggt
240
gtgctgctgg acctgggcgt gagctccccg cagatcgacg acccccagcg cgggttcagt
300
tttcgtttcg atggtccgct ggacatgcgc atggacacca ctccgatgca tggatg
356

<210> 336
<211> 118
<212> PRT
<213> Homo sapiens

<400> 336
Val His Ala Leu Leu Gly Glu Gly Asp Ala Pro Ala Arg Thr Phe Val
1 5 10 15
Asp Gly Thr Phe Gly Arg Gly Gly His Ser Arg Leu Ile Leu Gln Arg
20 25 30
Leu Gly Pro Gln Gly Arg Leu Val Ala Phe Asp Lys Asp Thr Glu Ala
35 40 45
Ile Gln Ala Ala Ala Arg Ile Thr Asp Ala Arg Phe Ser Ile Xaa His
50 55 60
Gln Gly Phe Ser His Leu Gly Glu Leu Pro Ala Ala Ser Val Ser Gly
65 70 75 80
Val Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Ile Asp Asp Pro Gln
85 90 95
Arg Gly Phe Ser Phe Arg Phe Asp Gly Pro Leu Asp Met Arg Met Asp

100 105 110
Thr Thr Pro Met His Gly
115

<210> 337
<211> 447
<212> DNA
<213> Homo sapiens

<400> 337
cagcctctct ccgaccgcgc cggtgtgaag cacgggcatg ccggtgtgca agtggcacca
60
cagccaaaac agcgagctca cacttcaaac tccttcaaag accccaggcc tctgtaagaa
120
ccgctcatct ctgtgcccac agctcccccg cttccatgtg acccagaaat ggaaccacgc
180
agcagaggcg gggatcacag gtgaagcagc tgtgaacatt tgcttcaggc ttctgtgcaa
240
acaggcgcca tcatgtcagc cggtgagcag gagcaacgtg cgtgggtcag ggggtggcca
300
cacgtccaac tttataagaa atgacagatt ccctgatggc catagggatc tgcagggcca
360
gcagcaggca taggacttcc ggtggccctg cgtcttcatc aacactgagt attgtcaggg
420
tttctgtact gtttttacag ccaattg
447

<210> 338
<211> 111
<212> PRT
<213> Homo sapiens

<400> 338
Met Pro Val Cys Lys Trp His His Ser Gln Asn Ser Glu Leu Thr Leu
1 5 10 15
Gln Thr Pro Ser Lys Thr Pro Gly Leu Cys Lys Asn Arg Ser Ser Leu
20 25 30
Cys Pro Gln Leu Pro Arg Phe His Val Thr Gln Lys Trp Asn His Ala
35 40 45
Ala Glu Ala Gly Ile Thr Gly Glu Ala Ala Val Asn Ile Cys Phe Arg
50 55 60
Leu Leu Cys Lys Gln Ala Pro Ser Cys Gln Pro Val Ser Arg Ser Asn
65 70 75 80
Val Arg Gly Ser Gly Gly Gly His Thr Ser Asn Phe Ile Arg Asn Asp
85 90 95
Arg Phe Pro Asp Gly His Arg Asp Leu Gln Gly Gln Gln Gln Ala
100 105 110

<210> 339
<211> 588
<212> DNA
<213> Homo sapiens

<400> 339

tctagaatga agcgctgtat cctagcaccg gcagacgtac caagactatc aagggcgtca
60
gatcgtttat cctgcagttg ccattcatca gacaaatcca gtggaaccca atggaagaca
120
ccgacctgca agcgctgatg gccagactcg aattgctaat tgatcgggtc gagcaactta
180
agagtcaaaa cggactccta ttagctcagg aaaagacctg ggcgcganaa cgcgctcacc
240
tcattgaaaa aaacgaaatc gcccggcgta aggtcgaatc gatgatttcg cgcctgaagg
300
ccctggagca agactatgag ttaagcaata gcgttacgtg cagatcctcg acaaagaata
360
ttcgatcatc tgcccccagg aagaacgcag cacctggtga gtgctgcccg ctacctggaa
420
ggccaaaagg cgtgaaatcc gcagcagcgg caaagtcatc ggtgccgacc gcatcgccgt
480
gatggccgcg ctgaacatca cccacgatct gctgcataag caggaacggc ctgacgttca
540
ggccagcggc tcaacgcgcg agcaagtgcg tgacctgctg gaacgcgt
588

<210> 340
<211> 123
<212> PRT
<213> Homo sapiens

<400> 340
Met Glu Asp Thr Asp Leu Gln Ala Leu Met Ala Arg Leu Glu Leu Leu
1 5 10 15
Ile Asp Arg Val Glu Gln Leu Lys Ser Gln Asn Gly Leu Leu Leu Ala
20 25 30
Gln Glu Lys Thr Trp Ala Arg Xaa Arg Ala His Leu Ile Glu Lys Asn
35 40 45
Glu Ile Ala Arg Arg Lys Val Glu Ser Met Ile Ser Arg Leu Lys Ala
50 55 60
Leu Glu Gln Asp Tyr Glu Leu Ser Asn Ser Val Thr Cys Arg Ser Ser
65 70 75 80
Thr Lys Asn Ile Arg Ser Ser Ala Pro Arg Lys Asn Ala Ala Pro Gly
85 90 95
Glu Cys Cys Pro Leu Pro Gly Arg Pro Lys Gly Val Lys Ser Ala Ala
100 105 110
Ala Ala Lys Ser Ser Val Pro Thr Ala Ser Pro
115 120

<210> 341
<211> 401
<212> DNA
<213> Homo sapiens

<400> 341
ngccgcgcgg cctacctgct gtacctggcc tatgccacct ggcgtgaccg ctcggccttt
60
gcaatgaacg acacgccgac agttgcgacc gcgcgcagcc tgatcctgcg tggcttcttg
120

ctgaacattc ttaaccccaa gctgacaatt ttcttcctgg ccttcctgcc tcaattcgta
180
acgccaggcg gcaccgcgcc ggccttgcag atgctggtac tgagcggcgt gttcatggcg
240
atgacgcttg cagtgtttgt gctgtatggc ctgttggcga atgtgtttcg tcgtgcagtg
300
gtcgagtcgc cacgtgtgca gaactggctg cgacgcagtt ttgccacggc ctttgccggg
360
ctggggttga acctggcgtt tgcgcagcgc tgaggacgcg t
401

<210> 342
<211> 130
<212> PRT
<213> Homo sapiens

<400> 342
Xaa Arg Ala Ala Tyr Leu Leu Tyr Leu Ala Tyr Ala Thr Trp Arg Asp
 1   5   10   15
Arg Ser Ala Phe Ala Met Asn Asp Thr Pro Thr Val Ala Thr Ala Arg
            20   25   30
Ser Leu Ile Leu Arg Gly Phe Leu Leu Asn Ile Leu Asn Pro Lys Leu
        35   40   45
Thr Ile Phe Phe Leu Ala Phe Leu Pro Gln Phe Val Thr Pro Gly Gly
    50   55   60
Thr Ala Pro Ala Leu Gln Met Leu Val Leu Ser Gly Val Phe Met Ala
65   70   75   80
Met Thr Leu Ala Val Phe Val Leu Tyr Gly Leu Leu Ala Asn Val Phe
                85   90   95
Arg Arg Ala Val Val Glu Ser Pro Arg Val Gln Asn Trp Leu Arg Arg
            100   105   110
Ser Phe Ala Thr Ala Phe Ala Gly Leu Gly Leu Asn Leu Ala Phe Ala
        115   120   125
Gln Arg
    130

<210> 343
<211> 389
<212> DNA
<213> Homo sapiens

<400> 343
gtgttgcgca actacatggc gtccctgccg ttcagcgtgg tcgagtcggc gcgcatcgac
60
gggtgctcca acttccagat cttctggaag ctgatcgccc cgatggcgat gccggcgatg
120
gcggcgttcg cgaccctgca gttcctgtgg gtgtggaacg acctgctcat cgccaagctc
180
ttcctcacca acgacaaccc cacggtgatc gtcaagctcc aacagctttc cnngggcccc
240
aaggcccagg gtgcggagct gctgacggcg ggcgccttca tctccatcgt gctacccatg
300
atcgtcttct tcgtgctcca gaacttcctg gtgcgcggta tgacgtcggg tgccgtcaag
360

gggtgaccgc tcaactgcag tggcccggg
389

<210> 344
<211> 121
<212> PRT
<213> Homo sapiens

<400> 344
Val Leu Arg Asn Tyr Met Ala Ser Leu Pro Phe Ser Val Val Glu Ser
1 5 10 15
Ala Arg Ile Asp Gly Cys Ser Asn Phe Gln Ile Phe Trp Lys Leu Ile
20 25 30
Ala Pro Met Ala Met Pro Ala Met Ala Ala Phe Ala Thr Leu Gln Phe
35 40 45
Leu Trp Val Trp Asn Asp Leu Leu Ile Ala Lys Leu Phe Leu Thr Asn
50 55 60
Asp Asn Pro Thr Val Ile Val Lys Leu Gln Gln Leu Ser Xaa Gly Pro
65 70 75 80
Lys Ala Gln Gly Ala Glu Leu Leu Thr Ala Gly Ala Phe Ile Ser Ile
85 90 95
Val Leu Pro Met Ile Val Phe Phe Val Leu Gln Asn Phe Leu Val Arg
100 105 110
Gly Met Thr Ser Gly Ala Val Lys Gly
115 120

<210> 345
<211> 360
<212> DNA
<213> Homo sapiens

<400> 345
ctagtacttt atgctgatgg tgaacgtcgt tacatccttg cccctaaagg catggttgct
60
ggtgatgtga tccaatctgg tgaagatgca tcaattaaag taggtaactg cttaccgatg
120
cgtaatattc cagttggtac aacagtacac gctgtagaaa tgaaacctgc taaaggtgca
180
caaattgcac gttctgctgg ttcttacagc caaattatag ctcgtgatgg tgcttacgtt
240
actctacgtt tacgtagtgg tgaaatgcgt aaaatccctg ctgagtgtcg tgcaacaatc
300
ggtgaagttg gtaatgcaga acatatgcta cgtcaactag gtaaagctgg tgctacgcgt
360

<210> 346
<211> 120
<212> PRT
<213> Homo sapiens

<400> 346
Leu Val Leu Tyr Ala Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys
1 5 10 15
Gly Met Val Ala Gly Asp Val Ile Gln Ser Gly Glu Asp Ala Ser Ile

```
            20                  25                  30
Lys Val Gly Asn Cys Leu Pro Met Arg Asn Ile Pro Val Gly Thr Thr
        35                  40                  45
Val His Ala Val Glu Met Lys Pro Ala Lys Gly Ala Gln Ile Ala Arg
    50                  55                  60
Ser Ala Gly Ser Tyr Ser Gln Ile Ile Ala Arg Asp Gly Ala Tyr Val
65                  70                  75                  80
Thr Leu Arg Leu Arg Ser Gly Glu Met Arg Lys Ile Pro Ala Glu Cys
                85                  90                  95
Arg Ala Thr Ile Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Gln
            100                 105                 110
Leu Gly Lys Ala Gly Ala Thr Arg
        115                 120
```

<210> 347
<211> 565
<212> DNA
<213> Homo sapiens

<400> 347
accggtgatg ccaaaggtgc tgtgacaagg ggattcatcg gttcgggcaa ggtcgtcacg
60
gcagctgccg tcatcatgat ttcggtgttc gtcttcttca tccccgaggg catgaacgcc
120
atcaaggaaa tcgccctggc cctggccgtc gggatcctca cggatgcctt cttggtgcgg
180
atgaccctcg tcccggccgt gatggccctg ctaggtgaca aggcatggtg gttgcccggg
240
tggctggatc gacgcctacc ccgcctcgac atcgagggag aagggatcac ccacgaggaa
300
aagctggccg cctggcccac agcggatcac accgaggccc tgcacgccga ggggatcggg
360
gtggaggggc tcttcgaagg cctcgatctg cacgtcgaac cgcgtcaggt gcaagccgtc
420
gtcggatcgc agaacagtgt ctcggccgtc ctgctggcga tcgggggacg gctgcccttg
480
gatcacggcc ggatgaggtc gggaggattg ctgctacccg agcgggcttc cagagtgcgt
540
cgggtgacgt ggttcctcga cgcgt
565

<210> 348
<211> 188
<212> PRT
<213> Homo sapiens

<400> 348
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Thr Gly Asp Ala Lys Gly Ala Val Thr Arg Gly Phe Ile Gly Ser Gly
 1               5                  10                  15
Lys Val Val Thr Ala Ala Ala Val Ile Met Ile Ser Val Phe Val Phe
            20                  25                  30
Phe Ile Pro Glu Gly Met Asn Ala Ile Lys Glu Ile Ala Leu Ala Leu
        35                  40                  45
Ala Val Gly Ile Leu Thr Asp Ala Phe Leu Val Arg Met Thr Leu Val
```

```
    50                  55                  60
Pro Ala Val Met Ala Leu Leu Gly Asp Lys Ala Trp Trp Leu Pro Gly
65                  70                  75                  80
Trp Leu Asp Arg Arg Leu Pro Arg Leu Asp Ile Glu Gly Glu Gly Ile
                85                  90                  95
Thr His Glu Glu Lys Leu Ala Ala Trp Pro Thr Ala Asp His Thr Glu
            100                 105                 110
Ala Leu His Ala Glu Gly Ile Gly Val Glu Gly Leu Phe Glu Gly Leu
        115                 120                 125
Asp Leu His Val Glu Pro Arg Gln Val Gln Ala Val Val Gly Ser Gln
    130                 135                 140
Asn Ser Val Ser Ala Val Leu Leu Ala Ile Gly Gly Arg Leu Pro Leu
145                 150                 155                 160
Asp His Gly Arg Met Arg Ser Gly Gly Leu Leu Leu Pro Glu Arg Ala
                165                 170                 175
Ser Arg Val Arg Arg Val Thr Trp Phe Leu Asp Ala
            180                 185
```

<210> 349
<211> 339
<212> DNA
<213> Homo sapiens

<400> 349
ntgctggcca cggataatga ccgtactctg cgtgatgtcg ttgccgctga ccctacccat
60
gagctcggtt cggctaccgc tcatacgttt gcggacaatt tgccgttcct tcttaaactg
120
ctcgcggcag aagagccact atcgttgcag gctcatccca gtttggcgca agcacaggaa
180
gggtacgggc gggagaatcg caaaggggtg ccattagatg ccccagaccg gaattaccac
240
gatcccaacc ataaaccgga gcttattgtt gggctgacgc gattccacgc actagccggc
300
ttccgtgaac cacaacgcac acttgagctt tttgacgcg
339

<210> 350
<211> 113
<212> PRT
<213> Homo sapiens

<400> 350
```
Xaa Leu Ala Thr Asp Asn Asp Arg Thr Leu Arg Asp Val Val Ala Ala
 1               5                  10                  15
Asp Pro Thr His Glu Leu Gly Ser Ala Thr Ala His Thr Phe Ala Asp
            20                  25                  30
Asn Leu Pro Phe Leu Leu Lys Leu Leu Ala Ala Glu Glu Pro Leu Ser
        35                  40                  45
Leu Gln Ala His Pro Ser Leu Ala Gln Ala Gln Glu Gly Tyr Gly Arg
    50                  55                  60
Glu Asn Arg Lys Gly Val Pro Leu Asp Ala Pro Asp Arg Asn Tyr His
65                  70                  75                  80
Asp Pro Asn His Lys Pro Glu Leu Ile Val Gly Leu Thr Arg Phe His
```

85 90 95
Ala Leu Ala Gly Phe Arg Glu Pro Gln Arg Thr Leu Glu Leu Phe Asp
100 105 110
Ala

<210> 351
<211> 354
<212> DNA
<213> Homo sapiens

<400> 351
gcgcgcccca gtgccgagac ccggggcttc aggagccggc cccgggagag aagagtgcgg
60
cggcggacgg agaaaacaac tccaaagttg gcgaaaggca ccgcccctac tcccgggctg
120
ccgccgcctc cccgccccca gccctggcat ccagagtacg ggtcgagccc gnggccatgg
180
agccccccctg gggaggcggc accagggagc ctgggccccg gggctccgcc gcgaccccat
240
cgggtagacc acagaagctc cgggaccctt ccggcacctc tggacagccc aggatgctgt
300
tggccacccn ntcctcctcc tcctccttgg aggcgctctg gcccatccag accg
354

<210> 352
<211> 118
<212> PRT
<213> Homo sapiens

<400> 352
Ala Arg Pro Ser Ala Glu Thr Arg Gly Phe Arg Ser Arg Pro Arg Glu
1 5 10 15
Arg Arg Val Arg Arg Arg Thr Glu Lys Thr Thr Pro Lys Leu Ala Lys
20 25 30
Gly Thr Ala Pro Thr Pro Gly Leu Pro Pro Pro Arg Pro Gln Pro
35 40 45
Trp His Pro Glu Tyr Gly Ser Ser Pro Xaa Pro Trp Ser Pro Pro Gly
50 55 60
Glu Ala Ala Pro Gly Ser Leu Gly Pro Gly Ala Pro Pro Arg Pro His
65 70 75 80
Arg Val Asp His Arg Ser Ser Gly Thr Leu Pro Ala Pro Leu Asp Ser
85 90 95
Pro Gly Cys Cys Trp Pro Pro Xaa Pro Pro Pro Pro Pro Trp Arg Arg
100 105 110
Ser Gly Pro Ser Arg Pro
115

<210> 353
<211> 1469
<212> DNA
<213> Homo sapiens

<400> 353

nntcatgaag gcttgaactt gcgtgatctt cagcctgcgg acctggcggt tgacggcgtt
60
attgagccgg tggacctcgt ggtcggagat gtctctttta tctccttgac gatgatcctt
120
gaacccattt cagctgttgt cagcccacac ggcctcatgc tgttgctggt gaagcctcaa
180
tttgaggttg gttgcaaggc tttgggagcc catggcgttg tcacggaccc ggccctgcgc
240
ttgcaggcca tcgcgggtgt catggcagca gcggtagatt tgggttggcg tatgcgtgac
300
gagtgcgata gcccgttgcc cgggcaggat ggaaacgttg agcacttcgt cttgctggaa
360
cgtacgggtc ggtgacagac gtccgggcat atcatgggcc gctactgtgg tcttgtgaac
420
gacacgagcc cttcgagata cgttgtcgtc gtcacccatg ccacgcggga cgacgctttt
480
gacgcggctg ccgaattcat ctctgaaatg gcggggcgag acattggttg cgcggttccg
540
gatgatcagg tgaagccgat gtcaagcaag ctgccaggga tcgatcttga aagcttggga
600
gagttcgccc acgaggcgga ggtggtcgtc gtctttggcg gcgacggcac gatcttgcga
660
gctgctgaat ggtcattacc tcgccacgtt cccatgattg gcgtcaacct tggccatgtc
720
ggttttctgg ctgagctgga gcgctccgat atggcggatc tagtgaacaa ggtgtgttcg
780
cgcgactaca ccgttgagga tcgcctcgtg cttaaaacca ccgtcaccga gcattccgga
840
caacaccgtt ggagttcttt tgccgtcaac gagttgtctc tggaaaaggc agcccggcgg
900
cgcatgctcg acgttctggc gtctgtcgac gagttgccgg tgcaacgctg gagttgcgac
960
gggatcctgg tctcgacccc gaccggatcg acggcctacg cgttctcagc tggcggcccg
1020
gtcatgtggc ccgatctcga cgccatgctc atggtgccgt tgagcgctca cgctctcttt
1080
gctcgaccgc tggtcatgag cccagctgct cgagtggacc ttgacatcca gccagacggt
1140
tcagaatcgg cggttctgtg gtgcgacggg cgccgatcgt gcaccgtacg accgggggaa
1200
agaatcaccg tcgtccgcca tcccgaccgt ctgcgcattg ctcgtctggc cgcgcagccc
1260
ttcacatcgc gtctggtcaa gaagtttgag ctcccggtca gcgggtggcg tcagggtcgt
1320
gaccgtcatc acctagagga gacttcgtga tacgtagtgt gcgaattcgt ggactcggcg
1380
tcatcgatga gacggtcctc gaaccctcat ccgcgctgac ggcagtcacc ggcgagaccg
1440
gcgccggaaa gaccatggtg gtcaccggt
1469

<210> 354
<211> 318
<212> PRT

<213> Homo sapiens

<400> 354

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Met Gly Arg Tyr Cys Gly Leu Val Asn Asp Thr Ser Pro Ser Arg Tyr
 1               5                  10                  15
Val Val Val Val Thr His Ala Thr Arg Asp Asp Ala Phe Asp Ala Ala
            20                  25                  30
Ala Glu Phe Ile Ser Glu Met Ala Gly Arg Asp Ile Gly Cys Ala Val
        35                  40                  45
Pro Asp Asp Gln Val Lys Pro Met Ser Ser Lys Leu Pro Gly Ile Asp
    50                  55                  60
Leu Glu Ser Leu Gly Glu Phe Ala His Glu Ala Glu Val Val Val Val
65                  70                  75                  80
Phe Gly Gly Asp Gly Thr Ile Leu Arg Ala Ala Glu Trp Ser Leu Pro
                85                  90                  95
Arg His Val Pro Met Ile Gly Val Asn Leu Gly His Val Gly Phe Leu
            100                 105                 110
Ala Glu Leu Glu Arg Ser Asp Met Ala Asp Leu Val Asn Lys Val Cys
        115                 120                 125
Ser Arg Asp Tyr Thr Val Glu Asp Arg Leu Val Leu Lys Thr Thr Val
    130                 135                 140
Thr Glu His Ser Gly Gln His Arg Trp Ser Ser Phe Ala Val Asn Glu
145                 150                 155                 160
Leu Ser Leu Glu Lys Ala Ala Arg Arg Arg Met Leu Asp Val Leu Ala
                165                 170                 175
Ser Val Asp Glu Leu Pro Val Gln Arg Trp Ser Cys Asp Gly Ile Leu
            180                 185                 190
Val Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
        195                 200                 205
Pro Val Met Trp Pro Asp Leu Asp Ala Met Leu Met Val Pro Leu Ser
    210                 215                 220
Ala His Ala Leu Phe Ala Arg Pro Leu Val Met Ser Pro Ala Ala Arg
225                 230                 235                 240
Val Asp Leu Asp Ile Gln Pro Asp Gly Ser Glu Ser Ala Val Leu Trp
                245                 250                 255
Cys Asp Gly Arg Arg Ser Cys Thr Val Arg Pro Gly Glu Arg Ile Thr
            260                 265                 270
Val Val Arg His Pro Asp Arg Leu Arg Ile Ala Arg Leu Ala Ala Gln
        275                 280                 285
Pro Phe Thr Ser Arg Leu Val Lys Lys Phe Glu Leu Pro Val Ser Gly
    290                 295                 300
Trp Arg Gln Gly Arg Asp Arg His His Leu Glu Glu Thr Ser
305                 310                 315
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<210> 355
<211> 558
<212> DNA
<213> Homo sapiens

<400> 355

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nggatcccac ctcctggaat ggaaacccac ataccagttc tcttcctcga tttgaatgcg
60
gatgacctca gtgccaatga gcagcttgtt ggcccccatg catccggcgt gaactccatc
120
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ctgcccaagg agcatggcag ccagtttttc tacctgccca tcataaagca cagtgatgat
180
gaggtttcag ccacagcctc ttgggattcc tcggtgcatg attctgttca cttgaatggg
240
gtcacaccac agaatgaaag gatttaccta attgtgaaaa ccacagttca actcagccac
300
cctgctgcta tggagttagt attacgaaaa cgaattgcag ccaatattta caacaaacag
360
agtttcacgc agagtttgaa gaggagaata tccctgaaaa atatatttta ttcctgtggt
420
gtaacctatg aaatagtatc caatatacca aaggcaactg aggagataga ggaccgggaa
480
acgctggctc tcctggcagc aaggagtgaa aacgaaggca catcagatgg gaagacgtac
540
attgagaagt acactcga
558

<210> 356
<211> 186
<212> PRT
<213> Homo sapiens

<400> 356
Xaa Ile Pro Pro Pro Gly Met Glu Thr His Ile Pro Val Leu Phe Leu
 1   5   10   15
Asp Leu Asn Ala Asp Asp Leu Ser Ala Asn Glu Gln Leu Val Gly Pro
            20   25   30
His Ala Ser Gly Val Asn Ser Ile Leu Pro Lys Glu His Gly Ser Gln
        35   40   45
Phe Phe Tyr Leu Pro Ile Ile Lys His Ser Asp Asp Glu Val Ser Ala
    50   55   60
Thr Ala Ser Trp Asp Ser Ser Val His Asp Ser Val His Leu Asn Gly
65   70   75   80
Val Thr Pro Gln Asn Glu Arg Ile Tyr Leu Ile Val Lys Thr Thr Val
                85   90   95
Gln Leu Ser His Pro Ala Ala Met Glu Leu Val Leu Arg Lys Arg Ile
            100   105   110
Ala Ala Asn Ile Tyr Asn Lys Gln Ser Phe Thr Gln Ser Leu Lys Arg
        115   120   125
Arg Ile Ser Leu Lys Asn Ile Phe Tyr Ser Cys Gly Val Thr Tyr Glu
    130   135   140
Ile Val Ser Asn Ile Pro Lys Ala Thr Glu Glu Ile Glu Asp Arg Glu
145   150   155   160
Thr Leu Ala Leu Leu Ala Ala Arg Ser Glu Asn Glu Gly Thr Ser Asp
                165   170   175
Gly Lys Thr Tyr Ile Glu Lys Tyr Thr Arg
            180   185

<210> 357
<211> 323
<212> DNA
<213> Homo sapiens

<400> 357

acgcgtgcgt gtgttgtgtg agtcgggtgt gtgcatgcgt gtgggtgtgc agcaggtggg
60
gtacgatcag gctgaaggct gatcaggcac aaggctctgg gggagagccc tggttccagc
120
cctggggtca gagcagcagg ggccagaaag acggcagggg tgagcactgc acccgctggg
180
cagggcaggg ccacagaagg cagggcatgg aggccacgtg aagggcttga cagagtggat
240
ggatgtctcc ggaagcacct gcgtggccca gtcagcagga tcagactcgc atgtgtcagg
300
gtcaccatgg gtcagcgagg atn
323

<210> 358
<211> 102
<212> PRT
<213> Homo sapiens

<400> 358
Met Val Thr Leu Thr His Ala Ser Leu Ile Leu Leu Thr Gly Pro Arg
1 5 10 15
Arg Cys Phe Arg Arg His Pro Ser Thr Leu Ser Ser Pro Ser Arg Gly
20 25 30
Leu His Ala Leu Pro Ser Val Ala Leu Pro Cys Pro Ala Gly Ala Val
35 40 45
Leu Thr Pro Ala Val Phe Leu Ala Pro Ala Ala Leu Thr Pro Gly Leu
50 55 60
Glu Pro Gly Leu Ser Pro Arg Ala Leu Cys Leu Ile Ser Leu Gln Pro
65 70 75 80
Asp Arg Thr Pro Pro Ala Ala His Pro His Ala Cys Thr His Pro Thr
85 90 95
His Thr Thr His Ala Arg
100

<210> 359
<211> 265
<212> DNA
<213> Homo sapiens

<400> 359
acgcgtaccg acaagcgccc ggtgatggcc gaccttcgcg aatcgggcgc aatcgagcag
60
gatgcggaca tgatcgtctt catctaccgc gacgattact acaacaagga aaattcgccg
120
gacaaggggc tggccgagat catcatcggc aagcatcggg ggggccccac cggctcgtgc
180
aagctgaagt tcttcggcga gtacacccgt ttcgacaacc tggcccacaa ctcggttggt
240
tcgttcgaat aacggatgat tccgg
265

<210> 360
<211> 83
<212> PRT

<213> Homo sapiens

<400> 360
Thr Arg Thr Asp Lys Arg Pro Val Met Ala Asp Leu Arg Glu Ser Gly
1 5 10 15
Ala Ile Glu Gln Asp Ala Asp Met Ile Val Phe Ile Tyr Arg Asp Asp
20 25 30
Tyr Tyr Asn Lys Glu Asn Ser Pro Asp Lys Gly Leu Ala Glu Ile Ile
35 40 45
Ile Gly Lys His Arg Gly Gly Pro Thr Gly Ser Cys Lys Leu Lys Phe
50 55 60
Phe Gly Glu Tyr Thr Arg Phe Asp Asn Leu Ala His Asn Ser Val Gly
65 70 75 80
Ser Phe Glu

<210> 361
<211> 453
<212> DNA
<213> Homo sapiens

<400> 361
gctttgcagg aggaaatctc tatctctggc tgcaagatga ggctgagcta cctgagcagc
60
cggacccctg gctacaaatc tgtcctgagg atcagcctca cccacccgac catccccttc
120
aacctcatga aggtgcacct catggtagcg gtggagggcc gcctcttcag gaagtggttc
180
gctgcagccc cagacctgtc ctattatttc atttgggaca agacagacgt ctacaaccag
240
aaggtgtttg ggctttcaga agcctttgtt tccgtgggtt atgaatatga atcctgccca
300
gatctaatcc tgtgggaaaa aagaacaaca gtgctgcagg gctatgaaat tgacgcgtcc
360
aagcttggag gatggagcct agacaaacat catgccctca acattcaaag tggcatcctg
420
cacaaaggga atggngagaa ccagtttgtg tct
453

<210> 362
<211> 151
<212> PRT
<213> Homo sapiens

<400> 362
Ala Leu Gln Glu Glu Ile Ser Ile Ser Gly Cys Lys Met Arg Leu Ser
1 5 10 15
Tyr Leu Ser Ser Arg Thr Pro Gly Tyr Lys Ser Val Leu Arg Ile Ser
20 25 30
Leu Thr His Pro Thr Ile Pro Phe Asn Leu Met Lys Val His Leu Met
35 40 45
Val Ala Val Glu Gly Arg Leu Phe Arg Lys Trp Phe Ala Ala Ala Pro
50 55 60
Asp Leu Ser Tyr Tyr Phe Ile Trp Asp Lys Thr Asp Val Tyr Asn Gln

65 70 75 80
Lys Val Phe Gly Leu Ser Glu Ala Phe Val Ser Val Gly Tyr Glu Tyr
85 90 95
Glu Ser Cys Pro Asp Leu Ile Leu Trp Glu Lys Arg Thr Thr Val Leu
100 105 110
Gln Gly Tyr Glu Ile Asp Ala Ser Lys Leu Gly Gly Trp Ser Leu Asp
115 120 125
Lys His His Ala Leu Asn Ile Gln Ser Gly Ile Leu His Lys Gly Asn
130 135 140
Gly Glu Asn Gln Phe Val Ser
145 150

<210> 363
<211> 502
<212> DNA
<213> Homo sapiens

<400> 363
ggtaccaaaa aagtttgcca cagtattcac actccaggtc tccataaacc ttccagatcc
60
gctcacacaa gctggtgttc atttgcttct tctgtaaact gttcaggacc ttcatgaaag
120
cggtgatgcc tgaccggtgc tcaggggcag ctttgcaaga gtcaggctga tgtgtgatgg
180
tgtccccacc accagctact ggagggagga ggtctgaggc ctcagctggg tttgacctga
240
gacacctgct gggatctggg tcaccagctg aaagcacagc catgttctgc ccttccccta
300
gggggctctg ggcgccatgg ctttcctgat ctgacccagc actctgggcc ttggacagca
360
gtagtgtgat cacttcacct tgcgtctgga ctgagcttct gtgctgcatg tctgggggct
420
tctcaggagc agcatgagcc tctgcggagg aggtatcatt tttcaacaaa aaatcatctg
480
aaaccacctc ttgagaatgc ag
502

<210> 364
<211> 136
<212> PRT
<213> Homo sapiens

<400> 364
Met Gln His Arg Ser Ser Val Gln Thr Gln Gly Glu Val Ile Thr Leu
1 5 10 15
Leu Leu Ser Lys Ala Gln Ser Ala Gly Ser Asp Gln Glu Ser His Gly
20 25 30
Ala Gln Ser Pro Leu Gly Glu Gly Gln Asn Met Ala Val Leu Ser Ala
35 40 45
Gly Asp Pro Asp Pro Ser Arg Cys Leu Arg Ser Asn Pro Ala Glu Ala
50 55 60
Ser Asp Leu Leu Pro Pro Val Ala Gly Gly Gly Asp Thr Ile Thr His
65 70 75 80
Gln Pro Asp Ser Cys Lys Ala Ala Pro Glu His Arg Ser Gly Ile Thr

```
                85                  90                  95
Ala Phe Met Lys Val Leu Asn Ser Leu Gln Lys Lys Gln Met Asn Thr
            100                 105                 110
Ser Leu Cys Glu Arg Ile Trp Lys Val Tyr Gly Asp Leu Glu Cys Glu
        115                 120                 125
Tyr Cys Gly Lys Leu Phe Trp Tyr
    130                 135
```

<210> 365
<211> 333
<212> DNA
<213> Homo sapiens

<400> 365
atctcaacgg atgcatccat caaggagatg atccccccag gtgctcttgt tatgctcaca
60
ccactgatcg ttgggattct atttggggtt gagaccctct ctggagtcct tgctggtgcc
120
cttgtctctg gtgttcagat tgccatttct gcatccaaca ctggtggtgc ctgggacaac
180
gccaagaagt acattgaggc tggagtttca gagcatgcca ggacccttgg cccaaaaggt
240
tctgaccctc acaaggcggc tgtcattggt gacaccattg gagatcctct caaggacacg
300
tctggccctt ccctcaacat cctcatcaag ctt
333

<210> 366
<211> 111
<212> PRT
<213> Homo sapiens

<400> 366
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Ile Ser Thr Asp Ala Ser Ile Lys Glu Met Ile Pro Pro Gly Ala Leu
 1               5                  10                  15
Val Met Leu Thr Pro Leu Ile Val Gly Ile Leu Phe Gly Val Glu Thr
            20                  25                  30
Leu Ser Gly Val Leu Ala Gly Ala Leu Val Ser Gly Val Gln Ile Ala
        35                  40                  45
Ile Ser Ala Ser Asn Thr Gly Gly Ala Trp Asp Asn Ala Lys Lys Tyr
    50                  55                  60
Ile Glu Ala Gly Val Ser Glu His Ala Arg Thr Leu Gly Pro Lys Gly
65                  70                  75                  80
Ser Asp Pro His Lys Ala Ala Val Ile Gly Asp Thr Ile Gly Asp Pro
                85                  90                  95
Leu Lys Asp Thr Ser Gly Pro Ser Leu Asn Ile Leu Ile Lys Leu
            100                 105                 110
```

<210> 367
<211> 381
<212> DNA
<213> Homo sapiens

<400> 367

gcgttcgtcg cactacccgg cggcggcgga acccttgacg agctactcga agcatggaca
60
tggcagcagc tcggtgtaca cagcaaaccc gtgngccttg tacgactcga cnncttctgg
120
gcaccgctga ccgcgctact caaccacatg accatcgaaa gcttcattcg ccctgaggac
180
cgcgcctcgc tcgtgatcgc cgataccata catcagctga tggccgatct tgagggatgg
240
accccaccac caccgaagtg gcgctcgtga catagaacaa atgattctga ctatggctca
300
ttgacatctg cgcagcggct actagctcca ttgacttcaa atcgggcctt ggccgaggct
360
cngttcaggt ggcccggaat g
381

<210> 368
<211> 89
<212> PRT
<213> Homo sapiens

<400> 368
Ala Phe Val Ala Leu Pro Gly Gly Gly Gly Thr Leu Asp Glu Leu Leu
 1   5   10   15
Glu Ala Trp Thr Trp Gln Gln Leu Gly Val His Ser Lys Pro Val Xaa
            20   25   30
Leu Val Arg Leu Asp Xaa Phe Trp Ala Pro Leu Thr Ala Leu Leu Asn
        35   40   45
His Met Thr Ile Glu Ser Phe Ile Arg Pro Glu Asp Arg Ala Ser Leu
    50   55   60
Val Ile Ala Asp Thr Ile His Gln Leu Met Ala Asp Leu Glu Gly Trp
65   70   75   80
Thr Pro Pro Pro Pro Lys Trp Arg Ser
                85

<210> 369
<211> 313
<212> DNA
<213> Homo sapiens

<400> 369
gatacatgat cctctcatac cgcacacaca ccgctcccct ctgccgcaat tcgcagacaa
60
acttgcgcag gcttcacagc aagccgtcaa ggctgcttcc tgtgggctac cgatagtctc
120
gtacgcgagt tctcggacat caacgccaac gtcgggcaag atactgtcaa cgccatctac
180
acattctacg agcagcaagc gaccagtttc cttcgccagc tgaacgacct cccacccgaa
240
gagcttcccg acgtcatcga ggacttcttc cgcctgtcca ctgatgtcct tctttaccat
300
ttccagcaag ctt
313

<210> 370

<211> 101
<212> PRT
<213> Homo sapiens

<400> 370
Ser Ser His Thr Ala His Thr Pro Leu Pro Ser Ala Ala Ile Arg Arg
1 5 10 15
Gln Thr Cys Ala Gly Phe Thr Ala Ser Arg Gln Gly Cys Phe Leu Trp
20 25 30
Ala Thr Asp Ser Leu Val Arg Glu Phe Ser Asp Ile Asn Ala Asn Val
35 40 45
Gly Gln Asp Thr Val Asn Ala Ile Tyr Thr Phe Tyr Glu Gln Gln Ala
50 55 60
Thr Ser Phe Leu Arg Gln Leu Asn Asp Leu Pro Pro Glu Glu Leu Pro
65 70 75 80
Asp Val Ile Glu Asp Phe Phe Arg Leu Ser Thr Asp Val Leu Leu Tyr
85 90 95
His Phe Gln Gln Ala
100

<210> 371
<211> 380
<212> DNA
<213> Homo sapiens

<400> 371
atgacgggtc acgtcatcct ggcgattcca caggtggtga cgtcatggat cggcctcatc
60
tgcatcgcca ttggcacggg ctttatcaag ccgaacctct ccacggtggt aggaggtctt
120
tacgatgacg gtgacccccg ccgcgatcag ggtttcctgt acttctacat gtcgatcagt
180
attggatctc tcttcgcgcc gatcgtcacc ggcctcctca aggaccatta cggctaccac
240
gtaggtttca ttgccgctgc tatcggtatg gctctgggtc tgatcgcctt cttccacggt
300
cgttccaaac tgcgtgagct cgccttcgac atccccaatc cgctggcccc cggcgagggt
360
cgccggatgg tgctccgcgg
380

<210> 372
<211> 126
<212> PRT
<213> Homo sapiens

<400> 372
Met Thr Gly His Val Ile Leu Ala Ile Pro Gln Val Val Thr Ser Trp
1 5 10 15
Ile Gly Leu Ile Cys Ile Ala Ile Gly Thr Gly Phe Ile Lys Pro Asn
20 25 30
Leu Ser Thr Val Val Gly Gly Leu Tyr Asp Asp Gly Asp Pro Arg Arg
35 40 45
Asp Gln Gly Phe Leu Tyr Phe Tyr Met Ser Ile Ser Ile Gly Ser Leu

```
    50                  55                  60
Phe Ala Pro Ile Val Thr Gly Leu Leu Lys Asp His Tyr Gly Tyr His
65                  70                  75                  80
Val Gly Phe Ile Ala Ala Ala Ile Gly Met Ala Leu Gly Leu Ile Ala
                85                  90                  95
Phe Phe His Gly Arg Ser Lys Leu Arg Glu Leu Ala Phe Asp Ile Pro
            100                 105                 110
Asn Pro Leu Ala Pro Gly Glu Gly Arg Arg Met Val Leu Arg
        115                 120                 125
```

<210> 373
<211> 475
<212> DNA
<213> Homo sapiens

<400> 373
acatgttgga aaaattgcct cccactctgg tgctacaggt atgaatctca gccacagtga
60
tgactgtggc agctacaggc ctgatgaaca ccccaccaag aaaaggagca tcatgtgcct
120
gcttctctct ggttcctaaa tcctttggcc aaacattttc cccacaaccc tccactccag
180
ttggctggtc actgcctctc agaaagaagt cccaggtccc tgtcagcccc agagcgcctg
240
catggactct gcccactgtc cctttccaac acggaggccc ccaattctgg ggacccctac
300
accctaccct gtaccaccac atccccatgc ctgctccaga cagcactaac ctcccatgac
360
agtgggacca aagcagttct taaaggtcca atccactcag ttcttaaatg aaaaacagtt
420
gcccatgagt caccccccaaa gacgtccgca catatgccaa acattcggtg tgcac
475

<210> 374
<211> 109
<212> PRT
<213> Homo sapiens

<400> 374
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Met Gly Met Trp Trp Tyr Arg Val Gly Cys Arg Gly Pro Gln Asn Trp
 1               5                  10                  15
Gly Pro Pro Cys Trp Lys Gly Thr Val Gly Arg Val His Ala Gly Ala
            20                  25                  30
Leu Gly Leu Thr Gly Thr Trp Asp Phe Phe Leu Arg Gly Ser Asp Gln
        35                  40                  45
Pro Thr Gly Val Glu Gly Cys Gly Glu Asn Val Trp Pro Lys Asp Leu
    50                  55                  60
Gly Thr Arg Glu Lys Gln Ala His Asp Ala Pro Phe Leu Gly Gly Val
65                  70                  75                  80
Phe Ile Arg Pro Val Ala Ala Thr Val Ile Thr Val Ala Glu Ile His
                85                  90                  95
Thr Cys Ser Thr Arg Val Gly Gly Asn Phe Ser Asn Met
            100                 105
```

<210> 375
<211> 332
<212> DNA
<213> Homo sapiens

<400> 375
nnacgcgtcg cctccacctc gaaacccgcc ggcggtcgtt ttttcaccat ggccgaccgc
60
aaggcccaag ttgcgacggt cacggacacg ctgtatttca cgccgtcgca atgggatgga
120
tgcatggcac ggatgcgtgg ggataagata tcagcactga agtggaatca gatgcagatg
180
gcggcatgct ccttcatagc ggcagtgggt gcgaagctgg gctgcccgca gcgcactatg
240
ggcacggcgc agctgctgta ccagcgtttc catctatttc atgcgccgac tgagttttcg
300
ttacatgagg tggctttgac gtgtctcttc ac
332

<210> 376
<211> 110
<212> PRT
<213> Homo sapiens

<400> 376
Xaa Arg Val Ala Ser Thr Ser Lys Pro Ala Gly Gly Arg Phe Phe Thr
 1   5   10   15
Met Ala Asp Arg Lys Ala Gln Val Ala Thr Val Thr Asp Thr Leu Tyr
            20   25   30
Phe Thr Pro Ser Gln Trp Asp Gly Cys Met Ala Arg Met Arg Gly Asp
        35   40   45
Lys Ile Ser Ala Leu Lys Trp Asn Gln Met Gln Met Ala Ala Cys Ser
    50   55   60
Phe Ile Ala Ala Val Gly Ala Lys Leu Gly Cys Pro Gln Arg Thr Met
65   70   75   80
Gly Thr Ala Gln Leu Leu Tyr Gln Arg Phe His Leu Phe His Ala Pro
                85   90   95
Thr Glu Phe Ser Leu His Glu Val Ala Leu Thr Cys Leu Phe
            100   105   110

<210> 377
<211> 369
<212> DNA
<213> Homo sapiens

<400> 377
cgcgtgccag gtatgtcaac tgatctgtcg gatatttccg aggttgagta ccgtcaactg
60
aggctggaac gagtggtgct gtgttcggtg tggactcagg gaactgccgc agacgccgag
120
aacgctatgg cggagctgaa agcccttgct gaaacggcgg gatctcaggt actcgaagct
180
gtcatgcaac gtcggactac cccggatccg gcgacgtaca ttggttcggg caaggtggct
240

gagcttgccg aggtggtgcg ggcgactggt gccgatactg tcatttgtga cggtgaactt
300
gacgccgctc agttgcgcaa cctcgaggat cgggtcaagn gcaaagttgt ggaccggtcg
360
gtctgattc
369

<210> 378
<211> 121
<212> PRT
<213> Homo sapiens

<400> 378
Arg Val Pro Gly Met Ser Thr Asp Leu Ser Asp Ile Ser Glu Val Glu
1 5 10 15
Tyr Arg Gln Leu Arg Leu Glu Arg Val Val Leu Cys Ser Val Trp Thr
20 25 30
Gln Gly Thr Ala Ala Asp Ala Glu Asn Ala Met Ala Glu Leu Lys Ala
35 40 45
Leu Ala Glu Thr Ala Gly Ser Gln Val Leu Glu Ala Val Met Gln Arg
50 55 60
Arg Thr Thr Pro Asp Pro Ala Thr Tyr Ile Gly Ser Gly Lys Val Ala
65 70 75 80
Glu Leu Ala Glu Val Val Arg Ala Thr Gly Ala Asp Thr Val Ile Cys
85 90 95
Asp Gly Glu Leu Asp Ala Ala Gln Leu Arg Asn Leu Glu Asp Arg Val
100 105 110
Lys Xaa Lys Val Val Asp Arg Ser Val
115 120

<210> 379
<211> 408
<212> DNA
<213> Homo sapiens

<400> 379
acgcgttact taaacttatc tgtaaataat aaattcatta tttctagttg gttaggtact
60
atgggctgtg gtttaccagg tgctatggca gctaaaattg cttatccaaa ccgtcaagca
120
gtagctatca caggcgacgg tgcgttccaa atggtaatgc aagactttgc tacagctgtt
180
caatataact taccaatgac aatctttgta ttaaataaca aacaattgtc attcattaaa
240
tatgaacaac aagctgctgg tgaattagag tatgccattg atttctctga tatggatcat
300
gctaaatttg ctgaagctgc tggtggtaaa ggctatgttg tgagagatgt aagtcgtctt
360
gacgacatcg ttgaagaggc aatggctcaa gatgttccaa caatcgtt
408

<210> 380
<211> 136
<212> PRT

<213> Homo sapiens

<400> 380
Thr Arg Tyr Leu Asn Leu Ser Val Asn Asn Lys Phe Ile Ile Ser Ser
1 5 10 15
Trp Leu Gly Thr Met Gly Cys Gly Leu Pro Gly Ala Met Ala Ala Lys
20 25 30
Ile Ala Tyr Pro Asn Arg Gln Ala Val Ala Ile Thr Gly Asp Gly Ala
35 40 45
Phe Gln Met Val Met Gln Asp Phe Ala Thr Ala Val Gln Tyr Asn Leu
50 55 60
Pro Met Thr Ile Phe Val Leu Asn Asn Lys Gln Leu Ser Phe Ile Lys
65 70 75 80
Tyr Glu Gln Gln Ala Ala Gly Glu Leu Glu Tyr Ala Ile Asp Phe Ser
85 90 95
Asp Met Asp His Ala Lys Phe Ala Glu Ala Ala Gly Gly Lys Gly Tyr
100 105 110
Val Val Arg Asp Val Ser Arg Leu Asp Asp Ile Val Glu Glu Ala Met
115 120 125
Ala Gln Asp Val Pro Thr Ile Val
130 135

<210> 381
<211> 613
<212> DNA
<213> Homo sapiens

<400> 381
nacgcgtcat aggcgggccc agtggaagac cacgccaaca cagttggttg agatccgcgt
60
tgagggcaag gtcctgcgcg tcccgcgaaa tctggtcaag gcctaccact ctgggctgat
120
cgacgtcgag gactgaaccc tgggagcctg ggcggtccag catgactgct caggctcatt
180
accaaaacgc gtcgatcccg tagggttgtc gtcatgagca agcccgaagt gaccctgccc
240
gattccgccc ccgacgacct cgtcgttgag gacatcacca tcggcgacgg ccctgaagcg
300
tccgctggca acctcgtcga agtgcactac gtcggcgtgg ccttaagcaa tggtcgtgag
360
ttcgattctt cctggaaccg cggggagccg ctgaccttcc aactaggggc tggccaggtg
420
atccccgagt gggatgaagg tgtccaaggt atgaaggtcg gtggacgacg caaactcgtc
480
atccccccacc accttgctta cggtccgcaa ggaatctccg gtgtgatcgc tggcggtgag
540
acgctggtct tcgtctgcga ccttgtcaac atcatctgac gtgacccccg ctcaagcagt
600
cttcgcgccc ggg
613

<210> 382
<211> 137
<212> PRT

<213> Homo sapiens

<400> 382
Leu Leu Arg Leu Ile Thr Lys Thr Arg Arg Ser Arg Arg Val Val Val
1 5 10 15
Met Ser Lys Pro Glu Val Thr Leu Pro Asp Ser Ala Pro Asp Asp Leu
20 25 30
Val Val Glu Asp Ile Thr Ile Gly Asp Gly Pro Glu Ala Ser Ala Gly
35 40 45
Asn Leu Val Glu Val His Tyr Val Gly Val Ala Leu Ser Asn Gly Arg
50 55 60
Glu Phe Asp Ser Ser Trp Asn Arg Gly Glu Pro Leu Thr Phe Gln Leu
65 70 75 80
Gly Ala Gly Gln Val Ile Pro Glu Trp Asp Glu Gly Val Gln Gly Met
85 90 95
Lys Val Gly Gly Arg Arg Lys Leu Val Ile Pro His His Leu Ala Tyr
100 105 110
Gly Pro Gln Gly Ile Ser Gly Val Ile Ala Gly Gly Glu Thr Leu Val
115 120 125
Phe Val Cys Asp Leu Val Asn Ile Ile
130 135

<210> 383
<211> 352
<212> DNA
<213> Homo sapiens

<400> 383
nggagcaaca cctggtcctt gggaatgaag tgtaggagtt gcatttgctg aggttggtgt
60
ttgccaaaga gatgccagct tcttcgaact actgctgtgc aactcttcat gttcaaaacc
120
cagttttctg tttttcacac ctgaacatac acccccctgc agttgggtgg ctcccccgtt
180
accagctggg ctctatctac agagagagca atggcttccc ttcccttgaa ggaagtctca
240
ccctcacaag gacacttgat ccgctgcaaa gcagaaagtg tgcggaccct ttgggaaggg
300
cgttcttttc ttgtttagaa cctaggattc tgtttttccc aaacaggatc an
352

<210> 384
<211> 93
<212> PRT
<213> Homo sapiens

<400> 384
Met Pro Ala Ser Ser Asn Tyr Cys Cys Ala Thr Leu His Val Gln Asn
1 5 10 15
Pro Val Phe Cys Phe Ser His Leu Asn Ile His Pro Pro Ala Val Gly
20 25 30
Trp Leu Pro Arg Tyr Gln Leu Gly Ser Ile Tyr Arg Glu Ser Asn Gly
35 40 45
Phe Pro Ser Leu Glu Gly Ser Leu Thr Leu Thr Arg Thr Leu Asp Pro

```
    50                  55                  60
Leu Gln Ser Arg Lys Cys Ala Asp Pro Leu Gly Arg Ala Phe Phe Ser
65                  70                  75                  80
Cys Leu Glu Pro Arg Ile Leu Phe Phe Pro Asn Arg Ile
                85                  90
```

<210> 385
<211> 342
<212> DNA
<213> Homo sapiens

<400> 385
gccggcgcca cgaaatgcaa aatgcgccct tcaccggacg ccaggttgat cgagccgcca
60
gcacctcggg caatgtcctg ggcctgactg gcacacgcaa tcaaagcgag caacaacaca
120
caaaaacgca tcatgaggca gacgccaggg aagtgacaga agccgcagca ggcgcgcggc
180
gattggaaat atcggtgagg ctaatggtca ccagcgcttg caggttgtat tcggtggcca
240
attcgcggaa cgacagcacc gccagttcca gctcgccgcg cagcaccagg cgacgcaagc
300
tgcggcgcaa ctccgggtgc accaacaaca ccgcactgtt ca
342

<210> 386
<211> 109
<212> PRT
<213> Homo sapiens

<400> 386

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Met Gln Asn Ala Pro Phe Thr Gly Arg Gln Val Asp Arg Ala Ala Ser
 1               5                  10                  15
Thr Ser Gly Asn Val Leu Gly Leu Thr Gly Thr Arg Asn Gln Ser Glu
            20                  25                  30
Gln Gln His Thr Lys Thr His His Glu Ala Asp Ala Arg Glu Val Thr
        35                  40                  45
Glu Ala Ala Ala Gly Ala Arg Arg Leu Glu Ile Ser Val Arg Leu Met
    50                  55                  60
Val Thr Ser Ala Cys Arg Leu Tyr Ser Val Ala Asn Ser Arg Asn Asp
65                  70                  75                  80
Ser Thr Ala Ser Ser Ser Ser Pro Arg Ser Thr Arg Arg Arg Lys Leu
                85                  90                  95
Arg Arg Asn Ser Gly Cys Thr Asn Asn Thr Ala Leu Phe
            100                 105
```

<210> 387
<211> 379
<212> DNA
<213> Homo sapiens

<400> 387
acgcgtgacg cgccggcatc ggaagcgttg actgcagaga agaccgcgca cgtggctgtg
60

ggacgtgctg gcacgtctga catggtgcgt ggacccgcct tctcttcgcc tgcgcatgcc
120
atgcaagagg agcttgacaa tgtgcgtgat ctcgcccatg cgcggcagca agcgctcgat
180
gctgttcgtt ccgagctgct cgaagcgcag caagcatgtg cctcgtgcca gctgcagctg
240
cagcatgtgc cagatgatcg tgtgcgagcg catcccatat accaggcgct ccatgcggac
300
gttgcttaca tgcagcaaga acttgatcac gtacgagacg cattggcttc ggcagaatct
360
gagaatgcga gcctgcgcg
379

<210> 388
<211> 114
<212> PRT
<213> Homo sapiens

<400> 388
Met Arg Leu Val Arg Asp Gln Val Leu Ala Ala Cys Lys Gln Arg Pro
1 5 10 15
His Gly Ala Pro Gly Ile Trp Asp Ala Leu Ala His Asp His Leu Ala
20 25 30
His Ala Ala Ala Ala Ala Gly Thr Arg His Met Leu Ala Ala Leu Arg
35 40 45
Ala Ala Arg Asn Glu Gln His Arg Ala Leu Ala Ala Ala His Gly Arg
50 55 60
Asp His Ala His Cys Gln Ala Pro Leu Ala Trp His Ala Gln Ala Lys
65 70 75 80
Arg Arg Arg Val His Ala Pro Cys Gln Thr Cys Gln His Val Pro Gln
85 90 95
Pro Arg Ala Arg Ser Ser Leu Gln Ser Thr Leu Pro Met Pro Ala Arg
100 105 110
His Ala

<210> 389
<211> 382
<212> DNA
<213> Homo sapiens

<400> 389
ngatggccga ctgtcccact gtcagtacgc gaagctcgcc gtcgagtcgg tccacgtccg
60
ggcctcccac gtgctccgca accctccgaa gcgatgacct ggcccggggg cggcaacgag
120
gtattgcgtt tggagacgct tggggtcaat tacggccagg tgcgcgccgt cgatgccctg
180
acgaccaccg tagagcgcgg caccatcacc tgcctcatgg gtcgaaatgg atcaggcaag
240
tcgtctctga tgtgggcgat ccaaggggca acaaagtcct cagggagggt actggtcaac
300
cacgagggtt cttgggctga cccccgcaaa gccgacgccg cgaccgctcg acgaatggtg
360

agcttagtcc cgcagtcagc cn
382

<210> 390
<211> 127
<212> PRT
<213> Homo sapiens

<400> 390
Xaa Trp Pro Thr Val Pro Leu Ser Val Arg Glu Ala Arg Arg Arg Val
 1   5   10   15
Gly Pro Arg Pro Gly Leu Pro Arg Ala Pro Gln Pro Ser Glu Ala Met
            20   25   30
Thr Trp Pro Gly Gly Gly Asn Glu Val Leu Arg Leu Glu Thr Leu Gly
        35   40   45
Val Asn Tyr Gly Gln Val Arg Ala Val Asp Ala Leu Thr Thr Thr Val
    50   55   60
Glu Arg Gly Thr Ile Thr Cys Leu Met Gly Arg Asn Gly Ser Gly Lys
65   70   75   80
Ser Ser Leu Met Trp Ala Ile Gln Gly Ala Thr Lys Ser Ser Gly Arg
                85   90   95
Val Leu Val Asn His Glu Gly Ser Trp Ala Asp Pro Arg Lys Ala Asp
            100   105   110
Ala Ala Thr Ala Arg Arg Met Val Ser Leu Val Pro Gln Ser Ala
        115   120   125

<210> 391
<211> 456
<212> DNA
<213> Homo sapiens

<400> 391
nnacgcgttg ccgctctgtg aggcgcctat cacggtgaca ctctcggtgc tatgagcgtg
60
tgcgacccta tcggtggcat gcacgccntg ttcagcgact ctattcccca gcagatcttc
120
ctgcccgcgc cctccttctt tcgccgccga cgaggccgac gtggagacgt ggtgcagcga
180
ggccgatgaa tcctggacac ccaccgcgac gacctggccg ggatcattgt cgagcccatc
240
ttgcaaggag ccggaggcat gtggccgtgg tctccgtcct gtctgaagca cctgcgccgt
300
cgtgctgatg aacttgacct agttcttatc gccgacgagg tcgctactgg atttgggcgg
360
actggcaaac ttttcgcatg cgagtgggcc gatatcgttc ctgacatcat ggtggttggg
420
aaatccatga ctggcggata cctgacccag tcggcc
456

<210> 392
<211> 55
<212> PRT
<213> Homo sapiens

<400> 392
Gly Ala Tyr His Gly Asp Thr Leu Gly Ala Met Ser Val Cys Asp Pro
1 5 10 15
Ile Gly Gly Met His Ala Xaa Phe Ser Asp Ser Ile Pro Gln Gln Ile
20 25 30
Phe Leu Pro Ala Pro Ser Phe Phe Arg Arg Arg Arg Gly Arg Arg Gly
35 40 45
Asp Val Val Gln Arg Gly Arg
50 55

<210> 393
<211> 371
<212> DNA
<213> Homo sapiens

<400> 393
nacgcgttgc tcgtcattgg tggctactcg gcctacgaag gtatctacac catgatgact
60
gagcgggacc ggtacccggc tttccgtatt ccgacggtgt gcatcccggc ttctatcgac
120
aacaacctcc ccggttcgga actgtccatc ggcaccgaca ccgctctcaa cgtcatcgtc
180
gaggcgatgg acaagattaa ggagtcgggt atcgcgtcca gacgctgctt cgtcgtcgag
240
acgatgggtc gtgactgcgg atacctcgcg ttgatgtcgg gtatcgcagc tggcgctgag
300
cggatctata ccaacgagga cggtatctcc ctggacgatc tagccaacga cgtccattgg
360
ttgcgggagt c
371

<210> 394
<211> 123
<212> PRT
<213> Homo sapiens

<400> 394
Xaa Ala Leu Leu Val Ile Gly Gly Tyr Ser Ala Tyr Glu Gly Ile Tyr
1 5 10 15
Thr Met Met Thr Glu Arg Asp Arg Tyr Pro Ala Phe Arg Ile Pro Thr
20 25 30
Val Cys Ile Pro Ala Ser Ile Asp Asn Asn Leu Pro Gly Ser Glu Leu
35 40 45
Ser Ile Gly Thr Asp Thr Ala Leu Asn Val Ile Val Glu Ala Met Asp
50 55 60
Lys Ile Lys Glu Ser Gly Ile Ala Ser Arg Arg Cys Phe Val Val Glu
65 70 75 80
Thr Met Gly Arg Asp Cys Gly Tyr Leu Ala Leu Met Ser Gly Ile Ala
85 90 95
Ala Gly Ala Glu Arg Ile Tyr Thr Asn Glu Asp Gly Ile Ser Leu Asp
100 105 110
Asp Leu Ala Asn Asp Val His Trp Leu Arg Glu
115 120

<210> 395
<211> 351
<212> DNA
<213> Homo sapiens

<400> 395
gaattctagt tgggagattc attgaccaga cttttggaat aaacactagt catcatgcta
60
gcgacaggtg gtcttgtgca tggtagaaag gcagtccaag cctatgtctc tgaaacctgc
120
tctcatttct gttttctact ttacgattta tgttatctca tactccccat gttgcctgtt
180
ctccagtttt tttacttgtg ttatttccat tcttctattc ctgctcaatt tctgcctcag
240
ggcagaattg tgtccaacag ctcttaaatg cagcgcagaa actgtgatgt taaaaacatc
300
ttgttatccg gccccaaaac atgttgtcct tggtaactct tactggtttg t
351

<210> 396
<211> 90
<212> PRT
<213> Homo sapiens

<400> 396
Met Val Glu Arg Gln Ser Lys Pro Met Ser Leu Lys Pro Ala Leu Ile
1 5 10 15
Ser Val Phe Tyr Phe Thr Ile Tyr Val Ile Ser Tyr Ser Pro Cys Cys
20 25 30
Leu Phe Ser Ser Phe Phe Thr Cys Val Ile Ser Ile Leu Leu Phe Leu
35 40 45
Leu Asn Phe Cys Leu Arg Ala Glu Leu Cys Pro Thr Ala Leu Lys Cys
50 55 60
Ser Ala Glu Thr Val Met Leu Lys Thr Ser Cys Tyr Pro Ala Pro Lys
65 70 75 80
His Val Val Leu Gly Asn Ser Tyr Trp Phe
85 90

<210> 397
<211> 483
<212> DNA
<213> Homo sapiens

<400> 397
gccgtcatta aagagatcac ccctctcctc caacctggtg atgtcctcgt cgacggtggt
60
aatgcttatt ttggtgatac ccgccgccgt gaggaggaaa tacgtcccac cggcattcac
120
tatgttggta ctggcatctc cggtgggggа gtcggggccc tgagggtccc atcaattatg
180
cctggcgggg ttaaggaatc ttacgaaatc atcggaccgg tcttagaaaa aatctccgcc
240
cacgtcgacg gtgaaccctg ctgcgcatgg atgggtactg acggcgccgg acacttcgtc
300

aagatggtcc ataatggcat cgagtacgcc gatatgcagt tcattggcga ggcgcccttc
360
ctttttgcgn tgcccgccgg tttgaccaat gctgaggccg ccgatgcctt cgagtcgtgg
420
aaccatggcg acctcaattc ctacctcgtc gaaatcactt ctcgggtact gcgtgccaag
480
gat
483

<210> 398
<211> 161
<212> PRT
<213> Homo sapiens

<400> 398
Ala Val Ile Lys Glu Ile Thr Pro Leu Leu Gln Pro Gly Asp Val Leu
1 5 10 15
Val Asp Gly Gly Asn Ala Tyr Phe Gly Asp Thr Arg Arg Arg Glu Glu
20 25 30
Glu Ile Arg Pro Thr Gly Ile His Tyr Val Gly Thr Gly Ile Ser Gly
35 40 45
Gly Gly Val Gly Ala Leu Arg Val Pro Ser Ile Met Pro Gly Gly Val
50 55 60
Lys Glu Ser Tyr Glu Ile Ile Gly Pro Val Leu Glu Lys Ile Ser Ala
65 70 75 80
His Val Asp Gly Glu Pro Cys Cys Ala Trp Met Gly Thr Asp Gly Ala
85 90 95
Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp Met
100 105 110
Gln Phe Ile Gly Glu Ala Pro Phe Leu Phe Ala Xaa Pro Ala Gly Leu
115 120 125
Thr Asn Ala Glu Ala Ala Asp Ala Phe Glu Ser Trp Asn His Gly Asp
130 135 140
Leu Asn Ser Tyr Leu Val Glu Ile Thr Ser Arg Val Leu Arg Ala Lys
145 150 155 160
Asp

<210> 399
<211> 314
<212> DNA
<213> Homo sapiens

<400> 399
nngggaatga agaccaccca gcccttcctt tcctcaaatc ttctccaggc ttctgtgcat
60
ggctcatcca cccatccact cattcaccca tctatccatc cactcatcca cccatccagt
120
cattcactca tttgtccatc cactcatgta cccatccact cattcgccca tttatccatc
180
cactcaacca tccactcatc cacccatcca nctcatcatc cgtccagtca cccatctatc
240
cacccatgta tccatccact catccaccca tccactcatc tgtccatcca cttatccacc
300

catctactca ccca
314

<210> 400
<211> 104
<212> PRT
<213> Homo sapiens

<400> 400
Xaa Gly Met Lys Thr Thr Gln Pro Phe Leu Ser Ser Asn Leu Leu Gln
 1   5   10   15
Ala Ser Val His Gly Ser Ser Thr His Pro Leu Ile His Pro Ser Ile
            20   25   30
His Pro Leu Ile His Pro Ser Ser His Ser Leu Ile Cys Pro Ser Thr
        35   40   45
His Val Pro Ile His Ser Phe Ala His Leu Ser Ile His Ser Thr Ile
    50   55   60
His Ser Ser Thr His Pro Xaa His His Pro Ser Ser His Pro Ser Ile
65   70   75   80
His Pro Cys Ile His Pro Leu Ile His Pro Ser Thr His Leu Ser Ile
                85   90   95
His Leu Ser Thr His Leu Leu Thr
            100

<210> 401
<211> 2165
<212> DNA
<213> Homo sapiens

<400> 401
gagaaaatgg aactacctgt atataaatta ggtgagcaaa cagtgataca ggtagtttta
60
agaagcaaat atatacagtc aatttaacag tgtttacttc tctggattgt ttaatggtgt
120
caaaatgaaa gatctattga agtttcacta tacattgcat tgattgaacc ttggagagtt
180
ttatgaaaaa gaggggcatc ccttgccatc tgtttgccag tcttccttgc cccttccttt
240
gaaatgcctg cctctttttt gcccagattg tttcctgacc atccgaactc agatggggtc
300
ctctaagttc ttcctggata ttcacaaatc ccttcacaag gcccacgtgc gaagtgaatg
360
atctggaggt gcctgggcat ctgtgttgga agggagtcaa gactcaccag ccagtcagtt
420
tgtgggctac agttgtccca caaaaatcag gcatgttcac ctccccctctg ggcccctaca
480
gctgggactg atcatagcct cagattagaa gaaatactga cttctaactc tataagccag
540
cactcctggg taaggagtga agctctgttg gccatgccgc tttggactgc tgggcagagc
600
tgagcctaca gttttgtact ggggtgcacg gatgacagct gggaagatgg aaaggcagct
660
tgaggattta tagcagctaa agggtaaatg ctgttatgca aaaggtcccc atatgaactt
720

cctacaggtg tagccgcagc caagtgtctg tacagctgct gagaatttgt cggtgatgta
780
aaaattcctc tttgcatcac aagcgagtgg aaagccaggg gctgcatgag tggagaaagc
840
acagtctggt ttttcaagta ctgcagagaa tgagaatacc cagccgggag cctggagttg
900
aggcccgagt tacacaggct cccggaatac agacctggga agatagggga ggagagggga
960
agcttgtggc cttttgatcc gccccggaa tgcccaccgt gcgctgcttt gctgccttca
1020
tctcctgctc agaggccttc tccttcccag agacctcctt ggatgggtct aagggagaca
1080
ctgcccgggc ctttttccct gcaatcacaa ggtccaaatc ctccaggctg cgcttgatcg
1140
gccgcgccgc cccaatgttc tacgggctca ttttccggtg caggattggg tggaccatgc
1200
cttccatctt cctgaaattc tccagtctca catggtgagg ttttcctgat cttgaaagcg
1260
attcagggta ttttttaggg cctgacatgg tcatgggtga tacccgacag gctttggggt
1320
gacagtctcg actctggctg cctaagacct ggaactggga gatgcctttg ctctcctggg
1380
gccctgtggt ggaatgagcc aggcccagga ccttgccggt aggtttgtgc gggttcttgg
1440
gaaggctcag atctgtaggc tgatcatccg taggggcttc tgctgccgcc gacttttttgt
1500
cttgcaggtg cagggacgtg agataattta catggagctt ttcttggtgt ctgtgggaag
1560
gaaaagaact gttttccgat tccctgtaca tgtccctgga agggtatttg gatgtctgtt
1620
cattatgaag atggtgctcg gtgtgtctgt agaggctatg gagatgaggg gacgagtaga
1680
agtcagccag gaagctaggc atgtgggaat gggggagggc ccttttctct aagagtttat
1740
ccttgccctc ctgaatttct tgcttcagga cgtaggagtc agcaaggggg ttaaggtgat
1800
gcttggagaa gctgcagcgg tggggatctg atcgactcag tttctcatgc ttaaagatgt
1860
cattgatggt ctttctctct tccgagggct tgcttctgaa actctggacg tgctgaatca
1920
ctgatggccg gctgaccgcc atatggtcag tgctttggcc atggtgggtc tgggacaaac
1980
tggaacacaa gtcatcccta gcaatcagtt tctttttgct gatcaaaggg ggtggggagc
2040
cataagggta gctgctggag aggctggccc cactcacttg ggacaaaagc tttttcttgg
2100
ccagtgggga catcatgcct gggttgcccc tagagtagag caggggcgtg taattaagtc
2160
catgg
2165

<210> 402
<211> 87
<212> PRT

<213> Homo sapiens

<400> 402
Glu Tyr Pro Ala Gly Ser Leu Glu Leu Arg Pro Glu Leu His Arg Leu
1 5 10 15
Pro Glu Tyr Arg Pro Gly Lys Ile Gly Glu Glu Arg Gly Ser Leu Trp
20 25 30
Pro Phe Asp Pro Pro Pro Glu Cys Pro Pro Cys Ala Ala Leu Leu Pro
35 40 45
Ser Ser Pro Ala Gln Arg Pro Ser Pro Ser Gln Arg Pro Pro Trp Met
50 55 60
Gly Leu Arg Glu Thr Leu Pro Gly Pro Phe Ser Leu Gln Ser Gln Gly
65 70 75 80
Pro Asn Pro Pro Gly Cys Ala
85

<210> 403
<211> 369
<212> DNA
<213> Homo sapiens

<400> 403
cccatgggtg tgtcccagga cggcgtcatg aagcgtcagg taaatgacaa ggaaacggtc
60
gcgcacttgt tcgaatacac gacgcaagtg tctgtcgact cgacgccgca actcgtccag
120
ccttcgccca cgtcgcacga caacctcgtg cctgtccaga tgatcttttg cttcaagcag
180
cgcaacgcga aaaagatcaa tagccaccgc tgggtatttc atgcactggg ccgcatgcta
240
cagcccgaca tggtcgtctt ggtggacgtc ggcacgaagc ccggccacct cgccctatac
300
catctatggc aggcattcta tcaccgacct accttgggcg gtgcttgcgg cgaaattcat
360
gctatgatc
369

<210> 404
<211> 123
<212> PRT
<213> Homo sapiens

<400> 404
Pro Met Gly Val Ser Gln Asp Gly Val Met Lys Arg Gln Val Asn Asp
1 5 10 15
Lys Glu Thr Val Ala His Leu Phe Glu Tyr Thr Thr Gln Val Ser Val
20 25 30
Asp Ser Thr Pro Gln Leu Val Gln Pro Ser Pro Thr Ser His Asp Asn
35 40 45
Leu Val Pro Val Gln Met Ile Phe Cys Phe Lys Gln Arg Asn Ala Lys
50 55 60
Lys Ile Asn Ser His Arg Trp Val Phe His Ala Leu Gly Arg Met Leu
65 70 75 80
Gln Pro Asp Met Val Val Leu Val Asp Val Gly Thr Lys Pro Gly His

```
                85                  90                  95
Leu Ala Leu Tyr His Leu Trp Gln Ala Phe Tyr His Arg Pro Thr Leu
            100                 105                 110
Gly Gly Ala Cys Gly Glu Ile His Ala Met Ile
        115                 120
```

<210> 405
<211> 840
<212> DNA
<213> Homo sapiens

<400> 405
gaattcccgc gcaccagctc gaagctggag cactttgtgt ctatcctgct gaagtgcttc
60
gactcgccct ggaccacgag ggccctgtcg gagacagtgg tggaggagag cgaccccaag
120
ccggccttca gcaagatgaa tgggtccatg gacaaaaagt catcgaccgt cagtgaggac
180
gtggaggcca ccgtgcccat gctgcagcgg accaagtcac ggatcgagca gggtatcgtg
240
gaccgctcag agacgggcgt gctggacaag aaggaggggg agcaagccaa ggcgctgttt
300
gagaaggtga agaagttccg gacccatgtg gaggaggggg acattgtgta ccgcctctac
360
atgcggcaga ccatcatcaa ggtgatcaag ttcatcctca tcatctgcta caccgtctac
420
tacgtgcaca acatcaagtt cgacgtggac tgcaccgtgg acattgagag cctgacgggc
480
taccgcacct accgctgtgc ccacccccctg gccacactct tcaagatcct ggcgtccttc
540
tacatcagcc tagtcatctt ctacggcctc atctgcatgt atacactgtg gtggatgcta
600
cggcgctccc tcaagaagta ctcgtttgag tcgatccgtg aggagagcag ctacagcgac
660
atccccgacg tcaagaacga cttcgccttc atgctgcacc tcattgacca atacgacccg
720
ctctactcca agcgcttcgc cgtcttcctg tcggaggtga gtgagaacaa gctgcggcag
780
ctgaacctca acaacgagtg gacgctggac aagctccggt acggagagaa gacaacgcgt
840

<210> 406
<211> 91
<212> PRT
<213> Homo sapiens

<400> 406
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Leu Ile Cys Met Tyr Thr Leu Trp Trp Met Leu Arg Arg Ser Leu Lys
 1               5                  10                  15
Lys Tyr Ser Phe Glu Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile
            20                  25                  30
Pro Asp Val Lys Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln
        35                  40                  45
Tyr Asp Pro Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val
```

```
    50                  55                  60
Ser Glu Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu
65                  70                  75                  80
Asp Lys Leu Arg Tyr Gly Glu Lys Thr Thr Arg
                85                  90
```

<210> 407
<211> 535
<212> DNA
<213> Homo sapiens

<400> 407
gcctattgta ccagctctcc agggctgggg acttgctaga gcagggttcc cagtgccccc
60
aggctctact ttgctctgcc tggtctcagg gtgtagggga tggagagctg gacttccagc
120
ctgcttcttg gctgtctagg ggccaggggc tcgggacaca gagctcctgg aggccgagca
180
caagccttgg gcagaggtga ggcagagctc tgactgtttc attcgactac gttgccaagg
240
agatgctcgc tcggagtggt tgctctggct ctgggattcc aaaccaagct gccttctctg
300
atgtggcctt agtgctctgg gcggatgtac cttggctctg cctggaccct ctctctcttc
360
caggcctctg tcccaccagg atgatgccta tccagagctc attgtcctct cccacttcct
420
ccccgagctt cccattccgt gtctctctgg agggcccatc atcatcctgg tggaggtgtt
480
gcactgagga ccacagcagc cctcgcattc ccacgggcaa aggggtatgt gtagg
535

<210> 408
<211> 97
<212> PRT
<213> Homo sapiens

<400> 408
```
Met Leu Ala Arg Ser Gly Cys Ser Gly Ser Gly Ile Pro Asn Gln Ala
 1               5                  10                  15
Ala Phe Ser Asp Val Ala Leu Val Leu Trp Ala Asp Val Pro Trp Leu
            20                  25                  30
Cys Leu Asp Pro Leu Ser Leu Pro Gly Leu Cys Pro Thr Arg Met Met
        35                  40                  45
Pro Ile Gln Ser Ser Leu Ser Ser Pro Thr Ser Ser Pro Ser Phe Pro
    50                  55                  60
Phe Arg Val Ser Leu Glu Gly Pro Ser Ser Ser Trp Trp Arg Cys Cys
65                  70                  75                  80
Thr Glu Asp His Ser Ser Pro Arg Ile Pro Thr Gly Lys Gly Val Cys
                85                  90                  95
Val
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<210> 409
<211> 375

<212> DNA
<213> Homo sapiens

<400> 409
ngtgtcatgg gtgtctatac cagcgatgag gccaagactg ccaagacttt tggtattggt
60
ggacttccga ttacgactaa tatttctctt gccaacaact tcaatatgga tgaaatttct
120
gatattgtct tccgtgtcaa tgataccagt ttgacaccaa ctgtgggacc agaattagct
180
agaaaattga ccgaaattgc tggtcttcag caaggggagt atcaggtgtc agatgcgact
240
gcagccttcc aagaagtgca acaattgttc ggctttataa ctacgattat tagtgccatt
300
gcaggaattt ccctttttgt tggagggact ggtgttatga acatcatgct ggtttcggtg
360
acggagcgta cgcgt
375

<210> 410
<211> 125
<212> PRT
<213> Homo sapiens

<400> 410
Xaa Val Met Gly Val Tyr Thr Ser Asp Glu Ala Lys Thr Ala Lys Thr
 1   5   10   15
Phe Gly Ile Gly Gly Leu Pro Ile Thr Thr Asn Ile Ser Leu Ala Asn
            20   25   30
Asn Phe Asn Met Asp Glu Ile Ser Asp Ile Val Phe Arg Val Asn Asp
        35   40   45
Thr Ser Leu Thr Pro Thr Val Gly Pro Glu Leu Ala Arg Lys Leu Thr
    50   55   60
Glu Ile Ala Gly Leu Gln Gln Gly Glu Tyr Gln Val Ser Asp Ala Thr
65   70   75   80
Ala Ala Phe Gln Glu Val Gln Gln Leu Phe Gly Phe Ile Thr Thr Ile
                85   90   95
Ile Ser Ala Ile Ala Gly Ile Ser Leu Phe Val Gly Gly Thr Gly Val
            100   105   110
Met Asn Ile Met Leu Val Ser Val Thr Glu Arg Thr Arg
        115   120   125

<210> 411
<211> 409
<212> DNA
<213> Homo sapiens

<400> 411
ccacatactt caccctcctc acccccctcca cctactccac cacctggcag tcgccatcga
60
ggatgggacg caactccacg tccacatgct ccggaccacg cggcgtgtgg tggatgtgca
120
gcacgcggtc ggggcccctt gagctcgaag gcgcggcgca tcgggcagtg ctcgccggcc
180

tggtcgcagg gcacgtcgta ctggtgcgag acgcggaagc acttgtggcc gatgtaggcg
240
cgatcggctg tcccgaactg gcgctgatag gccgtgtaca caacacaaac tgttgtactc
300
ccggtccacc acgatcatgg gctgggactc gtgttccagg tgggggggcca gggcttgggc
360
ctgcggtgag cgcgtggggt ggatggggca tagcgtcggt gaggaggtg
409

<210> 412
<211> 119
<212> PRT
<213> Homo sapiens

<400> 412
Met Pro His Pro Pro His Ala Leu Thr Ala Gly Pro Ser Pro Gly Pro
 1   5   10   15
Pro Pro Gly Thr Arg Val Pro Ala His Asp Arg Gly Gly Pro Gly Val
            20   25   30
Gln Gln Phe Val Leu Cys Thr Arg Pro Ile Ser Ala Ser Ser Gly Gln
        35   40   45
Pro Ile Ala Pro Thr Ser Ala Thr Ser Ala Ser Ala Ser Arg Thr Ser
    50   55   60
Thr Thr Cys Pro Ala Thr Arg Pro Ala Ser Thr Ala Arg Cys Ala Ala
65   70   75   80
Pro Ser Ser Ser Arg Gly Pro Asp Arg Val Leu His Ile His His Thr
                85   90   95
Pro Arg Gly Pro Glu His Val Asp Val Glu Leu Arg Pro Ile Leu Asp
            100   105   110
Gly Asp Cys Gln Val Val Glu
        115

<210> 413
<211> 357
<212> DNA
<213> Homo sapiens

<400> 413
ccgggcatcc caccaccggg tgtcatgaac caagtagtgg cccctatggt agggactcca
60
gcaccgggtg gaagtccata tggacaacag gtgggagttt tggggcctcc agggcagcag
120
gcaccacctc catatcccgg cccacatcca gctggacccc ctgtcataca gcagccaaca
180
acacccatgt ttgtagctcc ccccccaaag acccagcggc ttcttcactc agaggcctac
240
ctgaaataca ttgaaggact cagtgcggag tccaacagca ttagcaagtg ggatcagaca
300
ctggcagctc ggagacgcga cgtccatttg tcgaaagaac aggagagccg cctaccc
357

<210> 414
<211> 119
<212> PRT

<213> Homo sapiens

<400> 414
Pro Gly Ile Pro Pro Pro Gly Val Met Asn Gln Val Val Ala Pro Met
1 5 10 15
Val Gly Thr Pro Ala Pro Gly Gly Ser Pro Tyr Gly Gln Gln Val Gly
20 25 30
Val Leu Gly Pro Pro Gly Gln Gln Ala Pro Pro Pro Tyr Pro Gly Pro
35 40 45
His Pro Ala Gly Pro Pro Val Ile Gln Gln Pro Thr Thr Pro Met Phe
50 55 60
Val Ala Pro Pro Pro Lys Thr Gln Arg Leu Leu His Ser Glu Ala Tyr
65 70 75 80
Leu Lys Tyr Ile Glu Gly Leu Ser Ala Glu Ser Asn Ser Ile Ser Lys
85 90 95
Trp Asp Gln Thr Leu Ala Ala Arg Arg Arg Asp Val His Leu Ser Lys
100 105 110
Glu Gln Glu Ser Arg Leu Pro
115

<210> 415
<211> 332
<212> DNA
<213> Homo sapiens

<400> 415
tctagagcca acttggttat cgtaatgaat agagagacta catctatatc aattattacg
60
ctctatagta atcatgaagc ttgggttata tgtatgacaa aaattgcaga aaaatcgaaa
120
caagaatatg gcgacttact aaaagaaaaa gaccatttac aagatatgga acagcttgag
180
atgactatcg tctcgatcca tacgccgtat ccgtccattg tcagaattca aggaaaaatc
240
aacacattac agccagagct ttggcaagct cccaatttag caattcggtt aattgtgagc
300
aatccgccag agggacaacc catctcacgc gt
332

<210> 416
<211> 102
<212> PRT
<213> Homo sapiens

<400> 416
Met Asn Arg Glu Thr Thr Ser Ile Ser Ile Ile Thr Leu Tyr Ser Asn
1 5 10 15
His Glu Ala Trp Val Ile Cys Met Thr Lys Ile Ala Glu Lys Ser Lys
20 25 30
Gln Glu Tyr Gly Asp Leu Leu Lys Glu Lys Asp His Leu Gln Asp Met
35 40 45
Glu Gln Leu Glu Met Thr Ile Val Ser Ile His Thr Pro Tyr Pro Ser
50 55 60
Ile Val Arg Ile Gln Gly Lys Ile Asn Thr Leu Gln Pro Glu Leu Trp

65 70 75 80
Gln Ala Pro Asn Leu Ala Ile Arg Leu Ile Val Ser Asn Pro Pro Glu
85 90 95
Gly Gln Pro Ile Ser Arg
100

<210> 417
<211> 483
<212> DNA
<213> Homo sapiens

<400> 417
gaattcctcg ccgtctctga ggtgggcgag gacacctttg tgcgctccac cgagggagac
60
tacgcggcca acgtcgaggc cgtggtgacc ccagcaccgg cggagaaaga tattgagggc
120
cagccagaag cacaggaaca tgacaccccg ggtacagaga ccattgagaa gctggtcgaa
180
tgggcccagg gcgcaggcat tactgtaaac ccccgcgttg tttgttatta taccctcaag
240
tgcatgatga tcaagctcca ccacccggcc gcggagagcg aagagcgcga gtccgagttg
300
gcggcggttc tcatccctgg cgatcgagag ctggatgaaa agcgccttga ggccgcactc
360
gagccggtgg agtttgagtt ggcaggggat aaggactttg cagacaatga cttcctagtc
420
aagggctatg ttggcccgcg cgctttgaac gccaatggca tcaaggtctt ggccgatcca
480
cgc
483

<210> 418
<211> 161
<212> PRT
<213> Homo sapiens

<400> 418
Glu Phe Leu Ala Val Ser Glu Val Gly Glu Asp Thr Phe Val Arg Ser
1 5 10 15
Thr Glu Gly Asp Tyr Ala Ala Asn Val Glu Ala Val Val Thr Pro Ala
20 25 30
Pro Ala Glu Lys Asp Ile Glu Gly Gln Pro Glu Ala Gln Glu His Asp
35 40 45
Thr Pro Gly Thr Glu Thr Ile Glu Lys Leu Val Glu Trp Ala Gln Gly
50 55 60
Ala Gly Ile Thr Val Asn Pro Arg Val Val Cys Tyr Tyr Thr Leu Lys
65 70 75 80
Cys Met Met Ile Lys Leu His His Pro Ala Ala Glu Ser Glu Glu Arg
85 90 95
Glu Ser Glu Leu Ala Ala Val Leu Ile Pro Gly Asp Arg Glu Leu Asp
100 105 110
Glu Lys Arg Leu Glu Ala Ala Leu Glu Pro Val Glu Phe Glu Leu Ala
115 120 125
Gly Asp Lys Asp Phe Ala Asp Asn Asp Phe Leu Val Lys Gly Tyr Val

130 135 140
Gly Pro Arg Ala Leu Asn Ala Asn Gly Ile Lys Val Leu Ala Asp Pro
145 150 155 160
Arg

<210> 419
<211> 797
<212> DNA
<213> Homo sapiens

<400> 419
atttcacccc aggaaaacca gtaaggacca atgattaagc ccaaggttgg gtaccgagtt
60
cggatccata agtaccggcc gcccagggtg ctggaatttg ggctcccccc ggtgaaaata
120
tccatgcagc cgcgttgtct taggtagaaa agggagactg gggtggggtg ggctgagctc
180
aagcccctgc ctacatactt tagtagtaac gactcccgat ctgcatccaa cacatttacc
240
gaacttctag taagcgcccc ccgctgcaag cgaaagcact cccctgccaa gaaacagatc
300
ttttccactt aaaattccca aactcagacc ttccactttt tactgaacaa aaagcgtgta
360
catgatctga agggttgaca tgacattttc taaattgggc gaatcaggaa gaggttgatg
420
aaaatccttg acgttttctg gggataggac atttgtgtgt gataacgttc ttaagtcgaa
480
tttcagtgtg gcagtgcacg cagattcttc attggtgtta gtgtatttcc atacggtatg
540
tattagtaca agaaatagtg ttccctttga cactcgaacc caaggagtgg tccgaggctt
600
tttgaggcaa cgtaggatca atgtctctga agcagatttg gtgaaggatg caggtctcat
660
aatttacaga gcaatcacag ccttctttga aacggagaaa ttagattcta tgaaattttg
720
tcagtgcaga tagatatgat gtggagaaac ggggaaaatt gagtacaaaa agatgaggct
780
tgaatgatgg ctggcca
797

<210> 420
<211> 106
<212> PRT
<213> Homo sapiens

<400> 420
Met Arg Pro Ala Ser Phe Thr Lys Ser Ala Ser Glu Thr Leu Ile Leu
1 5 10 15
Arg Cys Leu Lys Lys Pro Arg Thr Thr Pro Trp Val Arg Val Ser Lys
20 25 30
Gly Thr Leu Phe Leu Val Leu Ile His Thr Val Trp Lys Tyr Thr Asn
35 40 45
Thr Asn Glu Glu Ser Ala Cys Thr Ala Thr Leu Lys Phe Asp Leu Arg

```
    50                  55                  60
Thr Leu Ser His Thr Asn Val Leu Ser Pro Glu Asn Val Lys Asp Phe
65                  70                  75                  80
His Gln Pro Leu Pro Asp Ser Pro Asn Leu Glu Asn Val Met Ser Thr
                85                  90                  95
Leu Gln Ile Met Tyr Thr Leu Phe Val Gln
            100                 105

<210> 421
<211> 406
<212> DNA
<213> Homo sapiens

<400> 421
ggatccacca tgatggagcc cacccaccca tcctcagtcc acctgctgca gcttctccat
60
aacccaacac aggtcaatct tgtctcccta aacacaccat gtgctctcat gctgccatgg
120
tttgcctggg gccctctcta cctcctctgc tttctggaga acccttgcac tcctcccaag
180
ccttcaagtt ggaaagtgaa cagtcagcat atgtctctag ctcagccctt actgcgtgga
240
ttcatgaaga ttggttcact gtcagcccct gaccagaacg tgtgttttag gaaagcagga
300
accaagtctt accaatgtct gtagtcccag cctccaccct ggcatacagt aggtgctcat
360
tgaatgtggg agggaaagag gagacacatg gaagggaatg tcattc
406

<210> 422
<211> 104
<212> PRT
<213> Homo sapiens

<400> 422
Met Met Glu Pro Thr His Pro Ser Ser Val His Leu Leu Gln Leu Leu
 1               5                  10                  15
His Asn Pro Thr Gln Val Asn Leu Val Ser Leu Asn Thr Pro Cys Ala
            20                  25                  30
Leu Met Leu Pro Trp Phe Ala Trp Gly Pro Leu Tyr Leu Leu Cys Phe
        35                  40                  45
Leu Glu Asn Pro Cys Thr Pro Pro Lys Pro Ser Ser Trp Lys Val Asn
    50                  55                  60
Ser Gln His Met Ser Leu Ala Gln Pro Leu Leu Arg Gly Phe Met Lys
65                  70                  75                  80
Ile Gly Ser Leu Ser Ala Pro Asp Gln Asn Val Cys Phe Arg Lys Ala
                85                  90                  95
Gly Thr Lys Ser Tyr Gln Cys Leu
            100

<210> 423
<211> 628
<212> DNA
<213> Homo sapiens
```

<400> 423
ngccacccta cgcctcgcct gcaatggcaa cttcagatcc ccggtggcac cgtagtctta
60
gagccaccgg ttctgagcgg ggaggacgac ggggttgggg cggaggaagg agagggagaa
120
ggagatgggg atttgctgac gcagacccaa gcccaaacgc cgactccagc acccgcttgg
180
ccggcgcccc cagccacacc gcgcttcctg gccctcgcaa atggctccct gttggtgccc
240
ctcctgagtg ccaaggaggc gggcgtctac acttgccgtg cacacaatga gctgggcgcc
300
aactctacgt caatacgcgt ggcggtggca gcaaccgggc ccccaaaaca cgcgcctggc
360
gccgggggag aacccgacgg acaggccccg acctctgagc gcaagtccac agccaagggc
420
cggggcaaca gcgtcctgcc ttccaaaccc gagggcaaaa tcaaaggcca aggcctggcc
480
aaggtcagca ttctcgggga gaccgagacg gagccggagg aggacacaag tgagggagag
540
gaggccgaag accagatcct cgcggacccg gcggaggagc agcgctgtgg caacggggac
600
ccctctcggt acgtttctaa ccacgcgt
628

<210> 424
<211> 209
<212> PRT
<213> Homo sapiens

<400> 424
Xaa His Pro Thr Pro Arg Leu Gln Trp Gln Leu Gln Ile Pro Gly Gly
 1   5   10   15
Thr Val Val Leu Glu Pro Pro Val Leu Ser Gly Glu Asp Asp Gly Val
            20   25   30
Gly Ala Glu Glu Gly Glu Gly Glu Gly Asp Gly Asp Leu Leu Thr Gln
        35   40   45
Thr Gln Ala Gln Thr Pro Thr Pro Ala Pro Ala Trp Pro Ala Pro Pro
    50   55   60
Ala Thr Pro Arg Phe Leu Ala Leu Ala Asn Gly Ser Leu Leu Val Pro
65   70   75   80
Leu Leu Ser Ala Lys Glu Ala Gly Val Tyr Thr Cys Arg Ala His Asn
                85   90   95
Glu Leu Gly Ala Asn Ser Thr Ser Ile Arg Val Ala Val Ala Ala Thr
            100   105   110
Gly Pro Pro Lys His Ala Pro Gly Ala Gly Gly Glu Pro Asp Gly Gln
        115   120   125
Ala Pro Thr Ser Glu Arg Lys Ser Thr Ala Lys Gly Arg Gly Asn Ser
    130   135   140
Val Leu Pro Ser Lys Pro Glu Gly Lys Ile Lys Gly Gln Gly Leu Ala
145   150   155   160
Lys Val Ser Ile Leu Gly Glu Thr Glu Thr Glu Pro Glu Glu Asp Thr
                165   170   175
Ser Glu Gly Glu Glu Ala Glu Asp Gln Ile Leu Ala Asp Pro Ala Glu

```
            180                 185                 190
Glu Gln Arg Cys Gly Asn Gly Asp Pro Ser Arg Tyr Val Ser Asn His
        195                 200                 205
Ala
```

<210> 425
<211> 471
<212> DNA
<213> Homo sapiens

<400> 425
ccggccgtcg aagactttga ggacgatgta gctcgcagcg cagcgttacg agccctggag
60
tacgtggatt tgaccccagg cactnaagtg cgcgtcatcg ccattgacac cgtgttccta
120
ggatcgtgca cgaatggccg tgaggactta cggctggctg ctgaggttcc caaaggacga
180
catatcgcag cgggcacccg gatgctcgtc gcccctggat ctgctcgtgt ccgtctgcag
240
gctatggagg aaggcctcga cgagatcggt tcccggtttg ctgacatctt tcgcaataac
300
tctgcgaaca atggcttgtt actggctcag gttgaccccg aggtcgtcga agagttgtgg
360
gactttgccg agcagcatcc tggtgagcag ctcaccgtct ccctcgagaa tcggacgatc
420
aaccttccgg gtcgcacgac ctacccgttc catattgatg acgtcacgcg t
471

<210> 426
<211> 157
<212> PRT
<213> Homo sapiens

<400> 426
```
Pro Ala Val Glu Asp Phe Glu Asp Asp Val Ala Arg Ser Ala Ala Leu
 1               5                  10                  15
Arg Ala Leu Glu Tyr Val Asp Leu Thr Pro Gly Thr Xaa Val Arg Val
            20                  25                  30
Ile Ala Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Gly Arg Glu
        35                  40                  45
Asp Leu Arg Leu Ala Ala Glu Val Pro Lys Gly Arg His Ile Ala Ala
    50                  55                  60
Gly Thr Arg Met Leu Val Ala Pro Gly Ser Ala Arg Val Arg Leu Gln
65                  70                  75                  80
Ala Met Glu Glu Gly Leu Asp Glu Ile Gly Ser Arg Phe Ala Asp Ile
                85                  90                  95
Phe Arg Asn Asn Ser Ala Asn Asn Gly Leu Leu Leu Ala Gln Val Asp
            100                 105                 110
Pro Glu Val Val Glu Glu Leu Trp Asp Phe Ala Glu Gln His Pro Gly
        115                 120                 125
Glu Gln Leu Thr Val Ser Leu Glu Asn Arg Thr Ile Asn Leu Pro Gly
    130                 135                 140
Arg Thr Thr Tyr Pro Phe His Ile Asp Asp Val Thr Arg
```

145 150 155

<210> 427
<211> 546
<212> DNA
<213> Homo sapiens

<400> 427
ctagcggtag tagaaggtat gcagtttgat cgcggctact tgtctccgta tttcatcaac
60
aatcaagaaa caatgaatgc agagctagaa aacccattta ttcttcttgt tgataagaaa
120
atttctaata tccgtgactt gctaccaatt ttggaaggtg ttgctaaagc atcgcgccca
180
ttgttgatca ttgcggaaga cgttgaaggc gaagcgttgg caaccttggt tgttaacact
240
atgcgcggca tcgtaaaagt agcggcagcg aaagcgccag gttttggtga tcgccgtaaa
300
gcaatgcttc aagacattgc tgtgctaacg ggttcaactg ttatttcaga agaaattggc
360
attaagcttg aagaagcgac aattgaacag ttgggtacag cgaagcgcgt tacattgaca
420
aaagaaagta caacgattgt tgatggtgcg ggtgttgcag ctaatattac tggtcgtgtt
480
gagcaaattc gtgcagaaat tgctaactct tcttctggct acgataaaga gaaattgcaa
540
gaacgc
546

<210> 428
<211> 182
<212> PRT
<213> Homo sapiens

<400> 428
Leu Ala Val Val Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro
1 5 10 15
Tyr Phe Ile Asn Asn Gln Glu Thr Met Asn Ala Glu Leu Glu Asn Pro
20 25 30
Phe Ile Leu Leu Val Asp Lys Lys Ile Ser Asn Ile Arg Asp Leu Leu
35 40 45
Pro Ile Leu Glu Gly Val Ala Lys Ala Ser Arg Pro Leu Leu Ile Ile
50 55 60
Ala Glu Asp Val Glu Gly Glu Ala Leu Ala Thr Leu Val Val Asn Thr
65 70 75 80
Met Arg Gly Ile Val Lys Val Ala Ala Ala Lys Ala Pro Gly Phe Gly
85 90 95
Asp Arg Arg Lys Ala Met Leu Gln Asp Ile Ala Val Leu Thr Gly Ser
100 105 110
Thr Val Ile Ser Glu Glu Ile Gly Ile Lys Leu Glu Glu Ala Thr Ile
115 120 125
Glu Gln Leu Gly Thr Ala Lys Arg Val Thr Leu Thr Lys Glu Ser Thr
130 135 140
Thr Ile Val Asp Gly Ala Gly Val Ala Ala Asn Ile Thr Gly Arg Val

145 150 155 160
Glu Gln Ile Arg Ala Glu Ile Ala Asn Ser Ser Ser Gly Tyr Asp Lys
165 170 175
Glu Lys Leu Gln Glu Arg
180

<210> 429
<211> 425
<212> DNA
<213> Homo sapiens

<400> 429
gctagcagcc cttacaggag acgggctaat aataatgcag cagtggctcc gacaacttgc
60
ccgttgcagc cggtcacgga tccatttgct tttagtagac aggcgctcca aagtacacca
120
ctgggcagtt cgtccaaaag cagtccacct gtcttgcaag gcccagcccc cgcagggttt
180
tctcaacacc ccggtttgct tgtgccttac acacaatgca aaaaatagct ctcagggacc
240
ctgtgagccc ctgcctggac ctctgacaca gcccagagca catgccagtc cgttttctgg
300
tgcattgaca ccttcagcac ctcctgggcc tgagatgaac aggagtgcag aggtcggtcc
360
cagttcagag cctgaagttc agactctgcc atatcttcct cactacattc caggagtgga
420
tcctg
425

<210> 430
<211> 130
<212> PRT
<213> Homo sapiens

<400> 430
Met Gln Gln Trp Leu Arg Gln Leu Ala Arg Cys Ser Arg Ser Arg Ile
1 5 10 15
His Leu Leu Leu Val Asp Arg Arg Ser Lys Val His His Trp Ala Val
20 25 30
Arg Pro Lys Ala Val His Leu Ser Cys Lys Ala Gln Pro Pro Gln Gly
35 40 45
Phe Leu Asn Thr Pro Val Cys Leu Cys Leu Thr His Asn Ala Lys Asn
50 55 60
Ser Ser Gln Gly Pro Cys Glu Pro Leu Pro Gly Pro Leu Thr Gln Pro
65 70 75 80
Arg Ala His Ala Ser Pro Phe Ser Gly Ala Leu Thr Pro Ser Ala Pro
85 90 95
Pro Gly Pro Glu Met Asn Arg Ser Ala Glu Val Gly Pro Ser Ser Glu
100 105 110
Pro Glu Val Gln Thr Leu Pro Tyr Leu Pro His Tyr Ile Pro Gly Val
115 120 125
Asp Pro
130

<210> 431
<211> 192
<212> DNA
<213> Homo sapiens

<400> 431
ctagccatcc accagcgtac acacacggga gagaggccct acactggcct cgggtgcaac
60
cgccgcttcc gccagcgcac ggccctcgtc atccaccagc gcatccacac gggcgagaag
120
cctnacccgt gcccggactg cgagcggcgc ttctcctcct cctctcgcct ggtcagtcac
180
cggcgtgtgc ac
192

<210> 432
<211> 64
<212> PRT
<213> Homo sapiens

<400> 432
Leu Ala Ile His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Thr Gly
1 5 10 15
Leu Gly Cys Asn Arg Arg Phe Arg Gln Arg Thr Ala Leu Val Ile His
20 25 30
Gln Arg Ile His Thr Gly Glu Lys Pro Xaa Pro Cys Pro Asp Cys Glu
35 40 45
Arg Arg Phe Ser Ser Ser Ser Arg Leu Val Ser His Arg Arg Val His
50 55 60

<210> 433
<211> 635
<212> DNA
<213> Homo sapiens

<400> 433
nngccggcgg ctgcgttggg atacgacgtc gctgcgattg ggcgtgagta tctttggtac
60
ctcatggagg agcgtggcgc gtatgcggag gccgccgcgc tcatgccgct gctgctccgg
120
accgaccgag gcgcgtggga cacgtttgtg tgctgctacc tcgagcggca ccaaagggat
180
gcgatactcc cgcacattcc gacgcaggac ccccagctga gtgagatggt gtacgatctc
240
gtgctggtgc atctgctgca gcacgatccc acgcagctgt tggcgacgct ccgcgcatgg
300
ccgagtcaca tctactcgaa gcaggcggtg gctgcggcga tcggcgatca cgcacgaacc
360
agccgcacgc tgctcgagtg cctcgcacag ctgtacatgg ccgcacatca gcccggcaag
420
gctctgacat actacatgcg cctgcgtgat ccatgcgtgt ttgatctcat tcgcgagtac
480
gatctgctga tcgatgtgca gcaccacatc ggcacgctcg tcgagctcga tcaggaatgc
540

gccggctcca ctgagccgcg ctccagcgcg cttatgccgc tgctcgtgcc atatacccac
600
tcgattccca tccagcgcgc catggcgcag ctcga
635

<210> 434
<211> 211
<212> PRT
<213> Homo sapiens

<400> 434
Xaa Pro Ala Ala Ala Leu Gly Tyr Asp Val Ala Ala Ile Gly Arg Glu
1 5 10 15
Tyr Leu Trp Tyr Leu Met Glu Glu Arg Gly Ala Tyr Ala Glu Ala Ala
20 25 30
Ala Leu Met Pro Leu Leu Leu Arg Thr Asp Arg Gly Ala Trp Asp Thr
35 40 45
Phe Val Cys Cys Tyr Leu Glu Arg His Gln Arg Asp Ala Ile Leu Pro
50 55 60
His Ile Pro Thr Gln Asp Pro Gln Leu Ser Glu Met Val Tyr Asp Leu
65 70 75 80
Val Leu Val His Leu Leu Gln His Asp Pro Thr Gln Leu Leu Ala Thr
85 90 95
Leu Arg Ala Trp Pro Ser His Ile Tyr Ser Lys Gln Ala Val Ala Ala
100 105 110
Ala Ile Gly Asp His Ala Arg Thr Ser Arg Thr Leu Leu Glu Cys Leu
115 120 125
Ala Gln Leu Tyr Met Ala Ala His Gln Pro Gly Lys Ala Leu Thr Tyr
130 135 140
Tyr Met Arg Leu Arg Asp Pro Cys Val Phe Asp Leu Ile Arg Glu Tyr
145 150 155 160
Asp Leu Leu Ile Asp Val Gln His His Ile Gly Thr Leu Val Glu Leu
165 170 175
Asp Gln Glu Cys Ala Gly Ser Thr Glu Pro Arg Ser Ser Ala Leu Met
180 185 190
Pro Leu Leu Val Pro Tyr Thr His Ser Ile Pro Ile Gln Arg Ala Met
195 200 205
Ala Gln Leu
210

<210> 435
<211> 493
<212> DNA
<213> Homo sapiens

<400> 435
nncgtacgtt cgcgtatttt ccgcgcccgg gaagctatcg ataataaagt tcaaccgctg
60
atccagcgtt agcaatggcg ggcacaggaa gggtacttag gcatgcagaa agaaaagctt
120
tccgctctga tggatggtga atcgttcgac agcgagctgt tgagttctct gtcgcaagat
180
cgaacgcttc aacaaagctg gcagggctat cacctgatac gtgacacact gcgaggtgat
240

gtcgggcaag tgatgcatct cgacatcgcc gatcgcgtag ccgctgcact tgagaaagaa
300
cccgcccggc tggtgccttc cgccgttcag gaatctcagc cgcagcctca cacctggcag
360
aaaatgccgt tctgggacaa agtgcgtccc tgggcgagcc agattacgca aatcggtatg
420
gcggcctgcg tgtcgctggc ggtgatcgtc ggcgtgcagc agtacaacca gccttctgcg
480
ccatcgaacg cgt
493

<210> 436
<211> 130
<212> PRT
<213> Homo sapiens

<400> 436
Met Gln Lys Glu Lys Leu Ser Ala Leu Met Asp Gly Glu Ser Phe Asp
1 5 10 15
Ser Glu Leu Leu Ser Ser Leu Ser Gln Asp Arg Thr Leu Gln Gln Ser
20 25 30
Trp Gln Gly Tyr His Leu Ile Arg Asp Thr Leu Arg Gly Asp Val Gly
35 40 45
Gln Val Met His Leu Asp Ile Ala Asp Arg Val Ala Ala Ala Leu Glu
50 55 60
Lys Glu Pro Ala Arg Leu Val Pro Ser Ala Val Gln Glu Ser Gln Pro
65 70 75 80
Gln Pro His Thr Trp Gln Lys Met Pro Phe Trp Asp Lys Val Arg Pro
85 90 95
Trp Ala Ser Gln Ile Thr Gln Ile Gly Met Ala Ala Cys Val Ser Leu
100 105 110
Ala Val Ile Val Gly Val Gln Gln Tyr Asn Gln Pro Ser Ala Pro Ser
115 120 125
Asn Ala
130

<210> 437
<211> 447
<212> DNA
<213> Homo sapiens

<400> 437
ntggtaaccg gtgtccctga tatggaccct gctgtgttag agcgtaaatt atttatttta
60
cgtaattatg taacacgcat ctgtttggag tctgttaatg gaattaagga caacttttac
120
attaatacat tctcatacaa aacaatcgtt tataaaggtc agttaaccac tgaacaagtg
180
ccacaatatt tcttagattt acaaaatcca agtatggtaa cggcattagc gcttgttcat
240
tcacgtttct caacaaatac atttcctcgt tggcgtttag cacaaccatt ccgttacatc
300
gctcataatg gcgaaatcaa tacggttcgc ggtaatatca attggatgaa agcacgtgaa
360

gcgttacttg aagctgaatt tttcactcgc tcagaattag atatgttaat gccaatctgt
420
acggatggta tgtctgactc ggcaagg
447

<210> 438
<211> 149
<212> PRT
<213> Homo sapiens

<400> 438
Xaa Val Thr Gly Val Pro Asp Met Asp Pro Ala Val Leu Glu Arg Lys
 1   5   10   15
Leu Phe Ile Leu Arg Asn Tyr Val Thr Arg Ile Cys Leu Glu Ser Val
            20   25   30
Asn Gly Ile Lys Asp Asn Phe Tyr Ile Asn Thr Phe Ser Tyr Lys Thr
        35   40   45
Ile Val Tyr Lys Gly Gln Leu Thr Thr Glu Gln Val Pro Gln Tyr Phe
    50   55   60
Leu Asp Leu Gln Asn Pro Ser Met Val Thr Ala Leu Ala Leu Val His
65   70   75   80
Ser Arg Phe Ser Thr Asn Thr Phe Pro Arg Trp Arg Leu Ala Gln Pro
                85   90   95
Phe Arg Tyr Ile Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn
            100   105   110
Ile Asn Trp Met Lys Ala Arg Glu Ala Leu Leu Glu Ala Glu Phe Phe
        115   120   125
Thr Arg Ser Glu Leu Asp Met Leu Met Pro Ile Cys Thr Asp Gly Met
    130   135   140
Ser Asp Ser Ala Arg
145

<210> 439
<211> 395
<212> DNA
<213> Homo sapiens

<400> 439
nacgcgtgaa gggagagtgg ggccgagccc caggaggctg tcctgcagca gctgcaccag
60
cttcccaggg gccggctgga cctggccacg caaagcctga cggtggagac ctgcagggcc
120
ctgggcaagc tgctgccgag ggagacgctg tgcacggagc tggtcctgag tgactgcatg
180
ctcagcgagg aaggggccac actgctgctc cgaggcctgt gtgccaacac cgtgctgcgc
240
tttctggact taaagggcaa caaccttcgg gctgcagggg ccgaggctct gggaaaactc
300
ctccaacaga acaagtccat tcagagcctc acgctggagt ggaacagcct gggcacgtgg
360
gacgatgcct tcgccacctt ctgcgggggc ctggc
395

<210> 440

<211> 128
<212> PRT
<213> Homo sapiens

<400> 440
Arg Glu Ser Gly Ala Glu Pro Gln Glu Ala Val Leu Gln Gln Leu His
1 5 10 15
Gln Leu Pro Arg Gly Arg Leu Asp Leu Ala Thr Gln Ser Leu Thr Val
20 25 30
Glu Thr Cys Arg Ala Leu Gly Lys Leu Leu Pro Arg Glu Thr Leu Cys
35 40 45
Thr Glu Leu Val Leu Ser Asp Cys Met Leu Ser Glu Glu Gly Ala Thr
50 55 60
Leu Leu Leu Arg Gly Leu Cys Ala Asn Thr Val Leu Arg Phe Leu Asp
65 70 75 80
Leu Lys Gly Asn Asn Leu Arg Ala Ala Gly Ala Glu Ala Leu Gly Lys
85 90 95
Leu Leu Gln Gln Asn Lys Ser Ile Gln Ser Leu Thr Leu Glu Trp Asn
100 105 110
Ser Leu Gly Thr Trp Asp Asp Ala Phe Ala Thr Phe Cys Gly Gly Leu
115 120 125

<210> 441
<211> 364
<212> DNA
<213> Homo sapiens

<400> 441
gcccagtact acgtgaacat gttcgatgcc gagcagggct tcttcgacag gcgcagcccg
60
ggcggcgagt tccaagccgg cttggatccg gaatcctggg gcggtctgtt cactgagacc
120
gacggttgga acttcgcctt ccacgctcca caggacggcc gggggctggc cgcgctctac
180
ggcggtccga aaggcttgga gaacaagctc gatgcctttt tcgcgacgcc ggaaaacgcg
240
gacaagccgg cgtacggcgg aatccacgaa atggtcgagg ccagagcggt ccggatgggc
300
caattgggca tgtccaacga gccctcgcac catattccct acatctacaa ctatgccggc
360
gcgc
364

<210> 442
<211> 121
<212> PRT
<213> Homo sapiens

<400> 442
Ala Gln Tyr Tyr Val Asn Met Phe Asp Ala Glu Gln Gly Phe Phe Asp
1 5 10 15
Arg Arg Ser Pro Gly Gly Glu Phe Gln Ala Gly Leu Asp Pro Glu Ser
20 25 30
Trp Gly Gly Leu Phe Thr Glu Thr Asp Gly Trp Asn Phe Ala Phe His

```
        35                  40                  45
Ala Pro Gln Asp Gly Arg Gly Leu Ala Ala Leu Tyr Gly Gly Pro Lys
    50                  55                  60
Gly Leu Glu Asn Lys Leu Asp Ala Phe Phe Ala Thr Pro Glu Asn Ala
65                  70                  75                  80
Asp Lys Pro Ala Tyr Gly Gly Ile His Glu Met Val Glu Ala Arg Ala
                85                  90                  95
Val Arg Met Gly Gln Leu Gly Met Ser Asn Glu Pro Ser His His Ile
            100                 105                 110
Pro Tyr Ile Tyr Asn Tyr Ala Gly Ala
        115                 120
```

<210> 443
<211> 430
<212> DNA
<213> Homo sapiens

<400> 443
accggttacg gctcagtgca acaagagatg ttcgccaaca acctcgtgcg gatgccgctg
60
ctcatggtgc tggcaatccc cttcgccaag atcctctcga cgaccctgtc catcggatcg
120
ggcggtccgg cggcgtcttc cggccctggc atggtcatcg gcggagccac tggcgcggca
180
ctgtggcgcc tcctcgaggg gctgccaggt atcccatcct caccgatgag tttcgtcatt
240
gtcggcatga tcgcctgctt cggtgcggtt gcccatgccc cactcggcgt gctgctcatg
300
gttggcgaga tgaccggaaa cctgtcgctg ctcgctcctg gcatgatcgc cgtcgccgtc
360
gctggccgag ttgtcgggga cacttcgatc tacacctctc agctcaagga tcgcctggag
420
ggcgacgcgt
430

<210> 444
<211> 143
<212> PRT
<213> Homo sapiens

<400> 444

```
Thr Gly Tyr Gly Ser Val Gln Gln Glu Met Phe Ala Asn Asn Leu Val
 1               5                  10                  15
Arg Met Pro Leu Leu Met Val Leu Ala Ile Pro Phe Ala Lys Ile Leu
            20                  25                  30
Ser Thr Thr Leu Ser Ile Gly Ser Gly Gly Pro Ala Ala Ser Ser Gly
        35                  40                  45
Pro Gly Met Val Ile Gly Gly Ala Thr Gly Ala Ala Leu Trp Arg Leu
    50                  55                  60
Leu Glu Gly Leu Pro Gly Ile Pro Ser Ser Pro Met Ser Phe Val Ile
65                  70                  75                  80
Val Gly Met Ile Ala Cys Phe Gly Ala Val Ala His Ala Pro Leu Gly
                85                  90                  95
Val Leu Leu Met Val Gly Glu Met Thr Gly Asn Leu Ser Leu Leu Ala
```

```
            100                 105                 110
Pro Gly Met Ile Ala Val Ala Val Ala Gly Arg Val Val Gly Asp Thr
        115                 120                 125
Ser Ile Tyr Thr Ser Gln Leu Lys Asp Arg Leu Glu Gly Asp Ala
    130                 135                 140
```

<210> 445
<211> 360
<212> DNA
<213> Homo sapiens

<400> 445
ccatggggct gcctagcctc tggggaggcc cctcagctgg tgacaccagc agggcagatt
60
tcttgcttta ttgctcaccc tgtccagggt tccctctgtt tgtgagggag ctgctgccac
120
cttgggtcca ggaagcatga agctccgcag gtcagcctcc tggtgggagg acttttcctt
180
agttttcttt gctcttctgc tctgagtcca gccctggctg gacctttgat ccctttctctc
240
tttatcagga aattttctga ctttcttctt ttgccttttc aagatctgtg atgccatctc
300
caagtgggaa caagccatga aggagctgca ccccggaaag tctgagggtg ggacacgcgt
360

<210> 446
<211> 101
<212> PRT
<213> Homo sapiens

<400> 446
```
Met Ala Cys Ser His Leu Glu Met Ala Ser Gln Ile Leu Lys Arg Gln
 1               5                  10                  15
Lys Lys Lys Val Arg Lys Phe Pro Asp Lys Glu Arg Arg Asp Gln Arg
            20                  25                  30
Ser Ser Gln Gly Trp Thr Gln Ser Arg Arg Ala Lys Lys Thr Lys Glu
        35                  40                  45
Lys Ser Ser His Gln Glu Ala Asp Leu Arg Ser Phe Met Leu Pro Gly
    50                  55                  60
Pro Lys Val Ala Ala Ala Pro Ser Gln Thr Glu Gly Thr Leu Asp Arg
65                  70                  75                  80
Val Ser Asn Lys Ala Arg Asn Leu Pro Cys Trp Cys His Gln Leu Arg
                85                  90                  95
Gly Leu Pro Arg Gly
            100
```

<210> 447
<211> 487
<212> DNA
<213> Homo sapiens

<400> 447
acgcgtgaag ggggaaattg ctcgtgccac ctgaggatta atcattaccc tggaacccctt
60

cccaaggcca tcaaggaaca cgcacccctt accagacctt ccagctgctg ggggctctcc
120
gagtgaggct gaggtcatgg agaagggaat ggggggcccc catggccagc tggacctgat
180
cactgcctcc ccactcagcc acagccctca gggccctgtg ccagtccaga agcccattca
240
gggacacctt tggccaatgt tctgtttcat ctgcgaggca accttcccca gtgccccaac
300
catagcgttt tcccccaaac accctcagga aggagggacc actacctgtg caggggggc
360
caggagcctc ctgagagcct catatgggga ggaagtggta ccatctcacc cccattgcct
420
ttctctccta cttccacctg gccagcttcc ctcagtgccc ctcctgcctc agtgcccctt
480
cacgcgt
487

<210> 448
<211> 117
<212> PRT
<213> Homo sapiens

<400> 448
Met Glu Lys Gly Met Gly Gly Pro His Gly Gln Leu Asp Leu Ile Thr
1 5 10 15
Ala Ser Pro Leu Ser His Ser Pro Gln Gly Pro Val Pro Val Gln Lys
20 25 30
Pro Ile Gln Gly His Leu Trp Pro Met Phe Cys Phe Ile Cys Glu Ala
35 40 45
Thr Phe Pro Ser Ala Pro Thr Ile Ala Phe Ser Pro Lys His Pro Gln
50 55 60
Glu Gly Gly Thr Thr Thr Cys Ala Gly Gly Ala Arg Ser Leu Leu Arg
65 70 75 80
Ala Ser Tyr Gly Glu Glu Val Val Pro Ser His Pro His Cys Leu Ser
85 90 95
Leu Leu Leu Pro Pro Gly Gln Leu Pro Ser Val Pro Leu Leu Pro Gln
100 105 110
Cys Pro Phe Thr Arg
115

<210> 449
<211> 353
<212> DNA
<213> Homo sapiens

<400> 449
gagctcagcc agttggagtt tgagaagcgg cagctgcaca gggacttgga gcaggccaag
60
gagaaggggg agcgggcaga gaagctggag agggagctac agcgactcca ggaggagaac
120
gggaggctgg ccaggaaggt gacctccctg gagacagcca ccgagaaagt cgaggccctg
180
gagcatgaga gccagggcct gcagctggag aaccggactc tgaggaagtc tctggacacc
240

ttgcagaacg tgtccctgca gcttgagggc ctggagcgtg acaacaagca gctggacgca
300
gagaacctgg agctgcgcag gctggtggag accatgcgga gacgacaacg cgt
353

<210> 450
<211> 117
<212> PRT
<213> Homo sapiens

<400> 450
Glu Leu Ser Gln Leu Glu Phe Glu Lys Arg Gln Leu His Arg Asp Leu
1 5 10 15
Glu Gln Ala Lys Glu Lys Gly Glu Arg Ala Glu Lys Leu Glu Arg Glu
20 25 30
Leu Gln Arg Leu Gln Glu Glu Asn Gly Arg Leu Ala Arg Lys Val Thr
35 40 45
Ser Leu Glu Thr Ala Thr Glu Lys Val Glu Ala Leu Glu His Glu Ser
50 55 60
Gln Gly Leu Gln Leu Glu Asn Arg Thr Leu Arg Lys Ser Leu Asp Thr
65 70 75 80
Leu Gln Asn Val Ser Leu Gln Leu Glu Gly Leu Glu Arg Asp Asn Lys
85 90 95
Gln Leu Asp Ala Glu Asn Leu Glu Leu Arg Arg Leu Val Glu Thr Met
100 105 110
Arg Arg Arg Gln Arg
115

<210> 451
<211> 444
<212> DNA
<213> Homo sapiens

<400> 451
gtgatgcggc tgactaagcc tactttattc accaatatcc cagtaacatg tgaagagaaa
60
gacttacctg gagatctctt taaccagctg atgagagatg atccttcaac cgttaatggt
120
gcagaagttt taatgttggg agaaatgctg actttaccac agaattttgg gaatatattt
180
ttgggagaga ccttttccag ttatatcagc gttcataatg atagcaatca agttgtaaaa
240
gacatattag taaaagctga tcttcagaca agttctcagc gtttaaatct ttcagcctcc
300
aatgctgcag tggctgaact taaaccggat tgttgtattg atgatgtcat acatcatgaa
360
gtcaaagaaa ttggaacaca catcttggta tgtgctgtga gttatacaac tcaggctgga
420
gaaaaaatgt atttcagaaa attt
444

<210> 452
<211> 148
<212> PRT

<213> Homo sapiens

<400> 452
Val Met Arg Leu Thr Lys Pro Thr Leu Phe Thr Asn Ile Pro Val Thr
1 5 10 15
Cys Glu Glu Lys Asp Leu Pro Gly Asp Leu Phe Asn Gln Leu Met Arg
20 25 30
Asp Asp Pro Ser Thr Val Asn Gly Ala Glu Val Leu Met Leu Gly Glu
35 40 45
Met Leu Thr Leu Pro Gln Asn Phe Gly Asn Ile Phe Leu Gly Glu Thr
50 55 60
Phe Ser Ser Tyr Ile Ser Val His Asn Asp Ser Asn Gln Val Val Lys
65 70 75 80
Asp Ile Leu Val Lys Ala Asp Leu Gln Thr Ser Ser Gln Arg Leu Asn
85 90 95
Leu Ser Ala Ser Asn Ala Ala Val Ala Glu Leu Lys Pro Asp Cys Cys
100 105 110
Ile Asp Asp Val Ile His His Glu Val Lys Glu Ile Gly Thr His Ile
115 120 125
Leu Val Cys Ala Val Ser Tyr Thr Thr Gln Ala Gly Glu Lys Met Tyr
130 135 140
Phe Arg Lys Phe
145

<210> 453
<211> 373
<212> DNA
<213> Homo sapiens

<400> 453
gctagctctg accccacctt tgccaagtgg cactagggtg gccaatgggg actagggttg
60
tataattgga aaatacagtc tcccctgttg tccaagaaag gccccagatg acctggggct
120
tgaaaggcac tcccgctggg tgcttcctgg gagcaggtgg ggggcagcgg ggcggcgggg
180
cctgtctgtg ctgagcatcc ccagctccag ggcaggtgct gggctctgag ccccactggt
240
gcgttttggg atgggctggc ctgcgcggct gtcgtttcag agcacacaga agagaccctg
300
ccacaggagg agtgggagga gaagctgttg atgttcctgc gagacaccct ggccatcatt
360
tctgacaacg cgt
373

<210> 454
<211> 108
<212> PRT
<213> Homo sapiens

<400> 454
Met Met Ala Arg Val Ser Arg Arg Asn Ile Asn Ser Phe Ser Ser His
1 5 10 15
Ser Ser Cys Gly Arg Val Ser Ser Val Cys Ser Glu Thr Thr Ala Ala

```
            20                  25                  30
Gln Ala Ser Pro Ser Gln Asn Ala Pro Val Gly Leu Arg Ala Gln His
        35                  40                  45
Leu Pro Trp Ser Trp Gly Cys Ser Ala Gln Thr Gly Pro Ala Ala Pro
    50                  55                  60
Leu Pro Pro Thr Cys Ser Gln Glu Ala Pro Ser Gly Ser Ala Phe Gln
65                  70                  75                  80
Ala Pro Gly His Leu Gly Pro Phe Leu Asp Asn Arg Gly Asp Cys Ile
                85                  90                  95
Phe Gln Leu Tyr Asn Pro Ser Pro His Trp Pro Pro
            100                 105
```

<210> 455
<211> 602
<212> DNA
<213> Homo sapiens

<400> 455
cctaggcaaa gcatgcccac cctacctccc cttaccctta cccttcattt tcccctaagc
60
acccatcacc accgatgtta ctgtatgtgt ttgcttacgc tgacagccca ccacccacac
120
tggaatgtcc gcacgacaaa ggcaggactc ttggctgcct tagccacagc tggatcccca
180
gagctttgta gggtgttggg cacagagtgg agtgggtact taataagtat ctgtggaatg
240
aacatgtaca gagtgaagcc ctgtgcccag aacaggctca aaataagctc aattcctttc
300
cttgccactt actaagtcct ttttctctcg ccccctctca ctgacctggt tttgatgcca
360
gacagcacag atgggctagg gaggcaggtg gggaagcaga gatctgcgtc tcttggagct
420
ggagctggtg ggtggggctc cttcctggtg ctgcggaggc tcattgggga ggtggcagcg
480
acccccctcag gagcctctgt cgcctgcact cagatctgtg cctttccaca gcgcccggag
540
gaagacttgc tcaggagata aattcaaaga caacaggaag ctggacgtgg tggctcacgc
600
gt
602

<210> 456
<211> 100
<212> PRT
<213> Homo sapiens

<400> 456
```
Met Pro Thr Leu Pro Pro Leu Thr Leu Thr Leu His Phe Pro Leu Ser
 1               5                  10                  15
Thr His His His Arg Cys Tyr Cys Met Cys Leu Leu Thr Leu Thr Ala
            20                  25                  30
His His Pro His Trp Asn Val Arg Thr Thr Lys Ala Gly Leu Leu Ala
        35                  40                  45
Ala Leu Ala Thr Ala Gly Ser Pro Glu Leu Cys Arg Val Leu Gly Thr
```

```
    50                  55                  60
Glu Trp Ser Gly Tyr Leu Ile Ser Ile Cys Gly Met Asn Met Tyr Arg
65                  70                  75                  80
Val Lys Pro Cys Ala Gln Asn Arg Leu Lys Ile Ser Ser Ile Pro Phe
                85                  90                  95
Leu Ala Thr Tyr
            100
```

<210> 457
<211> 324
<212> DNA
<213> Homo sapiens

<400> 457
acgcgtcatg tggatattcc tgggaggttc ccaggaacgt ttctggacgg gcccccgacc
60
agaggtcagg gaacttttct tattattctg cacgtgccca gggatagtca aaccaggtct
120
tccccttctg ctggccgcaa cacgccagcc gccgccacga ccgcacgctg aattcatgac
180
ccgacacgcg acgtggcagc gagcacaccc accgctagga gaaagagcgc tcatcgaaga
240
tcgttttctg tccactggcc agcgccacta tgatcaggtg gggtatccgc ccggcggcgg
300
gagcaccggg acgccggggc gccg
324

<210> 458
<211> 105
<212> PRT
<213> Homo sapiens

<400> 458
```
Met Trp Ile Phe Leu Gly Gly Ser Gln Glu Arg Phe Trp Thr Gly Pro
 1               5                  10                  15
Arg Pro Glu Val Arg Glu Leu Phe Leu Leu Phe Cys Thr Cys Pro Gly
            20                  25                  30
Ile Val Lys Pro Gly Leu Pro Leu Leu Leu Ala Ala Thr Arg Gln Pro
        35                  40                  45
Pro Pro Arg Pro His Ala Glu Phe Met Thr Arg His Ala Thr Trp Gln
    50                  55                  60
Arg Ala His Pro Pro Leu Gly Glu Arg Ala Leu Ile Glu Asp Arg Phe
65                  70                  75                  80
Leu Ser Thr Gly Gln Arg His Tyr Asp Gln Val Gly Tyr Pro Pro Gly
                85                  90                  95
Gly Gly Ser Thr Gly Thr Pro Gly Arg
            100                 105
```

<210> 459
<211> 415
<212> DNA
<213> Homo sapiens

<400> 459

acgcgttcat tcggcatctg cttccatgga tttcctgcgg ggaggcgcgg ccgagagtgc
60
gggtgtcgaa cacgacactt cagtgatcgt ttcaaccacc ggccgagatg ggtcctgacg
120
ctgggcttca agccgcttgc gctcgcgctc ctgatctcgg gcagcgcgat tccggtggtt
180
tatgctgccg gcagacgact gcgcacgccc ctcacgaggt atctgcacat gcttaaaggg
240
agaggcctca cccgacagct gggcatcgga tttacgaagc ccacgacgaa tcttcctcgc
300
ctcctcaaag ccgatcatcg gcatgccagg tttgtggttg aatgcttcga tcaacacact
360
aggatcgttg gggtccacca catacaccga gcggcaatcg agcggatacg acctc
415

<210> 460
<211> 105
<212> PRT
<213> Homo sapiens

<400> 460

Met	Pro	Met	Ile	Gly	Phe	Glu	Glu	Ala	Arg	Lys	Ile	Arg	Arg	Gly	Leu
1				5					10					15	
Arg	Lys	Ser	Asp	Ala	Gln	Leu	Ser	Gly	Glu	Ala	Ser	Pro	Phe	Lys	His
			20					25					30		
Val	Gln	Ile	Pro	Arg	Glu	Gly	Arg	Ala	Gln	Ser	Ser	Ala	Gly	Ser	Ile
		35					40					45			
Asn	His	Arg	Asn	Arg	Ala	Ala	Arg	Asp	Gln	Glu	Arg	Glu	Arg	Lys	Arg
	50					55					60				
Leu	Glu	Ala	Gln	Arg	Gln	Asp	Pro	Ser	Arg	Pro	Val	Val	Glu	Thr	Ile
65					70					75					80
Thr	Glu	Val	Ser	Cys	Ser	Thr	Pro	Ala	Leu	Ser	Ala	Ala	Pro	Pro	Arg
				85					90					95	
Arg	Lys	Ser	Met	Glu	Ala	Asp	Ala	Glu							
			100					105							

<210> 461
<211> 357
<212> DNA
<213> Homo sapiens

<400> 461
acgcgttcga ggtcggctaa atttatcatg cgcacgacaa agagagtagt ggctcacaac
60
cgggtcacat gcatgatgac aaaaactggc agaatagagt tgatgtcatc ccgtctacca
120
gctcctagaa ccagctcaga gagtcccggt gtcggtaccg tcgagactca gtacacaact
180
gtcgcgatac cggacgaccc tcttcatctg gttgcagatg ggcgtctcaa tcacgtcact
240
gtcgcttacg aaacctacgg gaagctcaat acgtccagcg acaatgcggt ctatacctgt
300
catgcgctta ctggtgatgc ccatgcagcc ggatttcacc ccggtgtagt ccgtccg
357

<210> 462
<211> 119
<212> PRT
<213> Homo sapiens

<400> 462
Thr Arg Ser Arg Ser Ala Lys Phe Ile Met Arg Thr Thr Lys Arg Val
1 5 10 15
Val Ala His Asn Arg Val Thr Cys Met Met Thr Lys Thr Gly Arg Ile
20 25 30
Glu Leu Met Ser Ser Arg Leu Pro Ala Pro Arg Thr Ser Ser Glu Ser
35 40 45
Pro Gly Val Gly Thr Val Glu Thr Gln Tyr Thr Thr Val Ala Ile Pro
50 55 60
Asp Asp Pro Leu His Leu Val Ala Asp Gly Arg Leu Asn His Val Thr
65 70 75 80
Val Ala Tyr Glu Thr Tyr Gly Lys Leu Asn Thr Ser Ser Asp Asn Ala
85 90 95
Val Tyr Thr Cys His Ala Leu Thr Gly Asp Ala His Ala Ala Gly Phe
100 105 110
His Pro Gly Val Val Arg Pro
115

<210> 463
<211> 434
<212> DNA
<213> Homo sapiens

<400> 463
gtgcacgggg tatgcgaggg atgcggcatt gccaccaatg ccgctgacct gcgcagatac
60
gaggcagctg gtgacgatga agtggtgcga tgcgaggaat gcgatcgtat cctggtgcgt
120
accggagagt ccatctgagc ccttcttgtg gcggtgatgc cgggatatcc gtagaattag
180
cggtcggacg agccatccgg gtgatcgcgg cagcggtgag ttgtcgagga aagtccgggc
240
tccatagagc agggtggtgg gtaacgccca cccggggtga cccgcgggaa agtgccacag
300
agaacagact gccggtttcg agccggtgag ggtgaaacgg tggagtaagt gcccaccgcg
360
tcatcggtga cggtgacggc atggcaaacc ccacctggag caaggccaag aagaccgtga
420
ggtcgcggac gcgt
434

<210> 464
<211> 127
<212> PRT
<213> Homo sapiens

<400> 464
Met Pro Ser Pro Ser Pro Met Thr Arg Trp Ala Leu Thr Pro Pro Phe

```
 1               5                  10                  15
His Pro His Arg Leu Glu Thr Gly Ser Leu Phe Ser Val Ala Leu Ser
            20                  25                  30
Arg Gly Ser Pro Arg Val Gly Val Thr His His Pro Ala Leu Trp Ser
        35                  40                  45
Pro Asp Phe Pro Arg Gln Leu Thr Ala Ala Ala Ile Thr Arg Met Ala
    50                  55                  60
Arg Pro Thr Ala Asn Ser Thr Asp Ile Pro Ala Ser Pro Pro Gln Glu
65                  70                  75                  80
Gly Leu Arg Trp Thr Leu Arg Tyr Ala Pro Gly Tyr Asp Arg Ile Pro
                85                  90                  95
Arg Ile Ala Pro Leu His Arg His Gln Leu Pro Arg Ile Cys Ala Gly
            100                 105                 110
Gln Arg His Trp Trp Gln Cys Arg Ile Pro Arg Ile Pro Arg Ala
        115                 120                 125
```

<210> 465
<211> 438
<212> DNA
<213> Homo sapiens

<400> 465
gatcatttag aatttatgga agaagctgat gtgaaagcta tggtcaaatc tggcactgtg
60
gctgtattgc taccaggagc attttacacc ttgaaagaaa ctcaacttcc accgatgaat
120
ttgttacgtc agtacggagt agacattgct atttcgacgg atgctaatcc agggacgtcg
180
ccagcgttat cattacggtt aatgatgaat atggcatgta ccttgtttgg tatgacacct
240
gaaaccgccc ttgcaggggt aacaattcat gcggcaaaag cgttggggat tagcgattct
300
catggcactt tagaagttgg caaggtagct gattttgtct gctgggatgt ggaaagcccc
360
ggtgaacttt gttattggtt aggagagcag ttagtaaagc aacgtattca gcacggagta
420
tcccatgaat aatctaga
438

<210> 466
<211> 143
<212> PRT
<213> Homo sapiens

<400> 466
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Asp His Leu Glu Phe Met Glu Glu Ala Asp Val Lys Ala Met Val Lys
 1               5                  10                  15
Ser Gly Thr Val Ala Val Leu Leu Pro Gly Ala Phe Tyr Thr Leu Lys
            20                  25                  30
Glu Thr Gln Leu Pro Pro Met Asn Leu Leu Arg Gln Tyr Gly Val Asp
        35                  40                  45
Ile Ala Ile Ser Thr Asp Ala Asn Pro Gly Thr Ser Pro Ala Leu Ser
    50                  55                  60
Leu Arg Leu Met Met Asn Met Ala Cys Thr Leu Phe Gly Met Thr Pro
```

65 70 75 80
Glu Thr Ala Leu Ala Gly Val Thr Ile His Ala Ala Lys Ala Leu Gly
85 90 95
Ile Ser Asp Ser His Gly Thr Leu Glu Val Gly Lys Val Ala Asp Phe
100 105 110
Val Cys Trp Asp Val Glu Ser Pro Gly Glu Leu Cys Tyr Trp Leu Gly
115 120 125
Glu Gln Leu Val Lys Gln Arg Ile Gln His Gly Val Ser His Glu
130 135 140

<210> 467
<211> 460
<212> DNA
<213> Homo sapiens

<400> 467
ntttccctgg ctattggcca tgtgggacac aacgttccgc ctaccccaga gcggttaagc
60
tgcatccctg caccttcttc tcccaccgct tcaaagccac agtgaggaac ttcggagctt
120
ctcgcagtga agatggcgtt ggaggaatgg atgccctggc tagaagaggc ggaatatctg
180
ttgattgtgt ggaccgacca caaaaacctg gagtatctcc acacaaccaa gtgcctcaac
240
tccaggcaag caagaagggc ccagctgttt acctggttcc acttttccct ctcctaccgg
300
ccggggtcca agaacatcag gctggatgcc ctttcttgcc actttatggg catgggccca
360
ttcctccagg cttgcctgtc acccgggctc ccgtcaaacc ctggccttcg tgcgacaaca
420
ctcttggtgc cttctatggt tctgtatgtt gccgcaattg
460

<210> 468
<211> 118
<212> PRT
<213> Homo sapiens

<400> 468
Gly Thr Ser Glu Leu Leu Ala Val Lys Met Ala Leu Glu Glu Trp Met
1 5 10 15
Pro Trp Leu Glu Glu Ala Glu Tyr Leu Leu Ile Val Trp Thr Asp His
20 25 30
Lys Asn Leu Glu Tyr Leu His Thr Thr Lys Cys Leu Asn Ser Arg Gln
35 40 45
Ala Arg Arg Ala Gln Leu Phe Thr Trp Phe His Phe Ser Leu Ser Tyr
50 55 60
Arg Pro Gly Ser Lys Asn Ile Arg Leu Asp Ala Leu Ser Cys His Phe
65 70 75 80
Met Gly Met Gly Pro Phe Leu Gln Ala Cys Leu Ser Pro Gly Leu Pro
85 90 95
Ser Asn Pro Gly Leu Arg Ala Thr Thr Leu Leu Val Pro Ser Met Val
100 105 110
Leu Tyr Val Ala Ala Ile

115

<210> 469
<211> 381
<212> DNA
<213> Homo sapiens

<400> 469
cttgtgcaca cgttattttt ccaatacaaa tagtttaaaa agtaaactcc aaatacctat
60
aagccccctc aaagcacctt ccaaatatga accttgttaa tgcccaaggt ccagaggggt
120
cccccagaaa ggcccaggag cctggggcat gggaaagctg tcggggtccc catgctgact
180
ccctggactc caagcgatat tccataaagc cagggcctcc tggctgcggg agggaggcct
240
tgacccaaaa tccattcggc cctggatact ggagaggcag aggcctctgc tgatgagaag
300
ccctgagttc ctggctagct gtggttaacc acaaaaaatg cgggggggtga tgattttcga
360
agtccatcgg caaagaaaga c
381

<210> 470
<211> 110
<212> PRT
<213> Homo sapiens

<400> 470
Met Asp Phe Glu Asn His His Pro Pro His Phe Leu Trp Leu Thr Thr
1 5 10 15
Ala Ser Gln Glu Leu Arg Ala Ser His Gln Gln Arg Pro Leu Pro Leu
20 25 30
Gln Tyr Pro Gly Pro Asn Gly Phe Trp Val Lys Ala Ser Leu Pro Gln
35 40 45
Pro Gly Gly Pro Gly Phe Met Glu Tyr Arg Leu Glu Ser Arg Glu Ser
50 55 60
Ala Trp Gly Pro Arg Gln Leu Ser His Ala Pro Gly Ser Trp Ala Phe
65 70 75 80
Leu Gly Asp Pro Ser Gly Pro Trp Ala Leu Thr Arg Phe Ile Phe Gly
85 90 95
Arg Cys Phe Glu Gly Ala Tyr Arg Tyr Leu Glu Phe Thr Phe
100 105 110

<210> 471
<211> 378
<212> DNA
<213> Homo sapiens

<400> 471
accggtgact acctgcagca ctggattgac atgggtaaaa agggcggcga ccgcatgcca
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gaggtcttcc tggttaactg gttccgccgc ggcgacgatg gccgcttcct gtggccgngg
120

cttggcgaaa acttcccggt cctanagtgg atcatcgacc gcattgaagg caacgtagag
180
gccgaggaca cggtggtcgg acgcaccgcc cgcgccgagg acatcgactt gcaaggcctt
240
gacttcgatg tcgacgacgt tcgcgccgca ctcgccgttg acccgaagga atgggaaggc
300
gatatgcaag acaacgccga gtacctgaac ttcctgggct cccgcgtgcc cgaggaagtg
360
tggaaccagt tccgcgcc
378

<210> 472
<211> 126
<212> PRT
<213> Homo sapiens

<400> 472
Thr Gly Asp Tyr Leu Gln His Trp Ile Asp Met Gly Lys Lys Gly Gly
1 5 10 15
Asp Arg Met Pro Glu Val Phe Leu Val Asn Trp Phe Arg Arg Gly Asp
20 25 30
Asp Gly Arg Phe Leu Trp Pro Xaa Leu Gly Glu Asn Phe Pro Val Leu
35 40 45
Xaa Trp Ile Ile Asp Arg Ile Glu Gly Asn Val Glu Ala Glu Asp Thr
50 55 60
Val Val Gly Arg Thr Ala Arg Ala Glu Asp Ile Asp Leu Gln Gly Leu
65 70 75 80
Asp Phe Asp Val Asp Asp Val Arg Ala Ala Leu Ala Val Asp Pro Lys
85 90 95
Glu Trp Glu Gly Asp Met Gln Asp Asn Ala Glu Tyr Leu Asn Phe Leu
100 105 110
Gly Ser Arg Val Pro Glu Glu Val Trp Asn Gln Phe Arg Ala
115 120 125

<210> 473
<211> 339
<212> DNA
<213> Homo sapiens

<400> 473
accggttggt gggggaaggg acccatccca tgccacctgt cctagaaaat gtttcccctt
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gttgagcagc tgctggatct agggctgctg ggtctaagtc caaaaaggga aaaaggaaaa
120
aggcaccaag taaaagaagg gggaagctgc caaaaccccc cctgccaaaa ctctcccacc
180
ctgcttccat ttccctctcc agggaacagg tgtacctccc ctcctccctg tcctcctcag
240
atgccccagg ggctctctac ttcattcctg ccgaccctgc caggagtggc ctcaggggta
300
gaggctccta gttggagaat ttgcttgcag gaaggtgaa
339

<210> 474

<211> 97
<212> PRT
<213> Homo sapiens

<400> 474
Met Phe Pro Leu Val Glu Gln Leu Leu Asp Leu Gly Leu Leu Gly Leu
1 5 10 15
Ser Pro Lys Arg Glu Lys Gly Lys Arg His Gln Val Lys Glu Gly Gly
20 25 30
Ser Cys Gln Asn Pro Pro Cys Gln Asn Ser Pro Thr Leu Leu Pro Phe
35 40 45
Pro Ser Pro Gly Asn Arg Cys Thr Ser Pro Pro Pro Cys Pro Pro Gln
50 55 60
Met Pro Gln Gly Leu Ser Thr Ser Phe Leu Pro Thr Leu Pro Gly Val
65 70 75 80
Ala Ser Gly Val Glu Ala Pro Ser Trp Arg Ile Cys Leu Gln Glu Gly
85 90 95
Glu

<210> 475
<211> 345
<212> DNA
<213> Homo sapiens

<400> 475
acgcgtgaag ggtcccctcc aaactctgag cctccttcca agccttgctg ggagctcccc
60
agcgcctgcc ggagaggcct ctcctccagg cgggcttccc gcgccgatgt gaaggagagg
120
ctgccccaga ggggtctgga tcgtaatcca gaaagggaca gtcccacagc cataatcccg
180
aatgctggga ctcttcagta aaggaagaga tggctttttc gttcatctgc ctttctgaaa
240
ggtaaaatat ctccagatcc gggctctctg ggcgactgcg tatgtggggg tccctgaagc
300
ctttgatgga tcttgttaga agtgggttgt tcatcttggg gtttt
345

<210> 476
<211> 111
<212> PRT
<213> Homo sapiens

<400> 476
Met Asn Asn Pro Leu Leu Thr Arg Ser Ile Lys Gly Phe Arg Asp Pro
1 5 10 15
His Ile Arg Ser Arg Pro Glu Ser Pro Asp Leu Glu Ile Phe Tyr Leu
20 25 30
Ser Glu Arg Gln Met Asn Glu Lys Ala Ile Ser Ser Phe Thr Glu Glu
35 40 45
Ser Gln His Ser Gly Leu Trp Leu Trp Asp Cys Pro Phe Leu Asp Tyr
50 55 60
Asp Pro Asp Pro Ser Gly Ala Ala Ser Pro Ser His Arg Arg Gly Lys

65 70 75 80
Pro Ala Trp Arg Arg Gly Leu Ser Gly Arg Arg Trp Gly Ala Pro Ser
85 90 95
Lys Ala Trp Lys Glu Ala Gln Ser Leu Glu Gly Thr Leu His Ala
100 105 110

<210> 477
<211> 422
<212> DNA
<213> Homo sapiens

<400> 477
acgcgtggcc gagccagcgt gctcaaggaa atggtcaacg gcactcttat taacggctgg
60
gactctcccg aggtggaacg ggcactggac ctgtgcatgg cgtgcaaagg gtgcgcccga
120
gattgcccca ccggaatcga catggccagc taccgcagca cggttcttga cgaaaaatac
180
cgtcaccgtc tccgccctcg ctcccacctg acgatggggc tgctgcccat gtgggaacgt
240
ttgctcaatc ggaccccagg agcgccgtcg ctggctaacg cagtgctttc gatgccggtc
300
ttcgcacgtc ttgctagatg gacagccggg gtggatcagc gtcgtccccc cccccgattc
360
cagccctcgg ccagattggc cagtccgcag gccgccccgg ttaaggagat tgtggcggat
420
cc
422

<210> 478
<211> 140
<212> PRT
<213> Homo sapiens

<400> 478
Thr Arg Gly Arg Ala Ser Val Leu Lys Glu Met Val Asn Gly Thr Leu
1 5 10 15
Ile Asn Gly Trp Asp Ser Pro Glu Val Glu Arg Ala Leu Asp Leu Cys
20 25 30
Met Ala Cys Lys Gly Cys Ala Arg Asp Cys Pro Thr Gly Ile Asp Met
35 40 45
Ala Ser Tyr Arg Ser Thr Val Leu Asp Glu Lys Tyr Arg His Arg Leu
50 55 60
Arg Pro Arg Ser His Leu Thr Met Gly Leu Leu Pro Met Trp Glu Arg
65 70 75 80
Leu Leu Asn Arg Thr Pro Gly Ala Pro Ser Leu Ala Asn Ala Val Leu
85 90 95
Ser Met Pro Val Phe Ala Arg Leu Ala Arg Trp Thr Ala Gly Val Asp
100 105 110
Gln Arg Arg Pro Leu Pro Arg Phe Gln Pro Ser Ala Arg Leu Ala Ser
115 120 125
Pro Gln Ala Ala Pro Val Lys Glu Ile Val Ala Asp
130 135 140

<210> 479
<211> 348
<212> DNA
<213> Homo sapiens

<400> 479
cgcgtggcca ttggccgggc gctggtgcgg cacccgcgac tggtgattgc cgatgagccg
60
atctcggcgt tggacatgac catccagaag cagattcttg agctgttcga gcgcctgcag
120
gcgcagtacg gctttgcctg cctgttcatc tcccacgacc tggcagcggt ggaacgcatc
180
gcccaccggg tggcggtgat gagcgagggc agggtggtgg aaatgggtgc ccgcgacgag
240
atcttcgacc gcccgcagca cccctacacc cgcaagctgc tggccgccgc cagccccttg
300
gagaaacttg aaaacggtgg ctaccgcatc cgccagggcc ccgtaccg
348

<210> 480
<211> 116
<212> PRT
<213> Homo sapiens

<400> 480
Arg Val Ala Ile Gly Arg Ala Leu Val Arg His Pro Arg Leu Val Ile
1 5 10 15
Ala Asp Glu Pro Ile Ser Ala Leu Asp Met Thr Ile Gln Lys Gln Ile
20 25 30
Leu Glu Leu Phe Glu Arg Leu Gln Ala Gln Tyr Gly Phe Ala Cys Leu
35 40 45
Phe Ile Ser His Asp Leu Ala Ala Val Glu Arg Ile Ala His Arg Val
50 55 60
Ala Val Met Ser Glu Gly Arg Val Val Glu Met Gly Ala Arg Asp Glu
65 70 75 80
Ile Phe Asp Arg Pro Gln His Pro Tyr Thr Arg Lys Leu Leu Ala Ala
85 90 95
Ala Ser Pro Leu Glu Lys Leu Glu Asn Gly Gly Tyr Arg Ile Arg Gln
100 105 110
Gly Pro Val Pro
115

<210> 481
<211> 441
<212> DNA
<213> Homo sapiens

<400> 481
aagcttctga ctgtggcatt ctccctgctt aatatgtcct caatatcccc tacttactgg
60
gcaaaatcct gcttatgctt tgggactagc tcaaagacca ctcccttgga tggtgccttc
120
cctgccctgc cggcttgcgc tggcttcctc agtgttagga ttaccatcac attgcatcat
180

gagagcagaa gaccatctcc atgtgactgc tgcccctgct cccagcaggg cccacaanca
240
cccagtccag gacctggctc acgctgggtg gcggatgccc aggaatgggg ctctggatct
300
gcctcttctc ctgcaggacc aggaaaccgc tgccctgtcc ctgccccagg aaaccctcag
360
taaatcccca gtcatttgag tttcccctca gcgccagaga ccaataacac atctccacca
420
acctgaaaaa ccttcacgcg t
441

<210> 482
<211> 120
<212> PRT
<213> Homo sapiens

<400> 482
Lys Leu Leu Thr Val Ala Phe Ser Leu Leu Asn Met Ser Ser Ile Ser
1 5 10 15
Pro Thr Tyr Trp Ala Lys Ser Cys Leu Cys Phe Gly Thr Ser Ser Lys
20 25 30
Thr Thr Pro Leu Asp Gly Ala Phe Pro Ala Leu Pro Ala Cys Ala Gly
35 40 45
Phe Leu Ser Val Arg Ile Thr Ile Thr Leu His His Glu Ser Arg Arg
50 55 60
Pro Ser Pro Cys Asp Cys Cys Pro Cys Ser Gln Gln Gly Pro Gln Xaa
65 70 75 80
Pro Ser Pro Gly Pro Gly Ser Arg Trp Val Ala Asp Ala Gln Glu Trp
85 90 95
Gly Ser Gly Ser Ala Ser Ser Pro Ala Gly Pro Gly Asn Arg Cys Pro
100 105 110
Val Pro Ala Pro Gly Asn Pro Gln
115 120

<210> 483
<211> 330
<212> DNA
<213> Homo sapiens

<400> 483
acgcgttcat tccctgatgg ccacgcacga gctaacggag ggatggggcg aagggaaggc
60
caaggttgcc tcgaagacca aggagtgtgc agggcaggac ctcgttttaa aggaatatcc
120
tctcaccaga gacacgcggc ggccaggcag ggccggagcg gggcctgtgc ccaggctccg
180
agcgtctgcc cagcccagca tccctgtccc cagccaggaa tatgtcttcg tggcatagag
240
ggagctcttg gagccacacc tgcgtgtgca catgtgtcac cccactgctg ggaggggctc
300
tcccgggacc ctgcagcgtg ggctgggccc
330

<210> 484

<211> 96
<212> PRT
<213> Homo sapiens

<400> 484
Met Gly Arg Arg Glu Gly Gln Gly Cys Leu Glu Asp Gln Gly Val Cys
1 5 10 15
Arg Ala Gly Pro Arg Phe Lys Gly Ile Ser Ser His Gln Arg His Ala
20 25 30
Ala Ala Arg Gln Gly Arg Ser Gly Ala Cys Ala Gln Ala Pro Ser Val
35 40 45
Cys Pro Ala Gln His Pro Cys Pro Gln Pro Gly Ile Cys Leu Arg Gly
50 55 60
Ile Glu Gly Ala Leu Gly Ala Thr Pro Ala Cys Ala His Val Ser Pro
65 70 75 80
His Cys Trp Glu Gly Leu Ser Arg Asp Pro Ala Ala Trp Ala Gly Pro
85 90 95

<210> 485
<211> 377
<212> DNA
<213> Homo sapiens

<400> 485
acgcgtgctc gcgcggacga agtcggcgct gatcgcccag tcatgcgccc tgcccgtgcc
60
gcccagttcg gcgatcgccg cattcggccg gccggaatcg agaaggaatg cgtggacgta
120
cgggggatac caaaggaatc ttgtcgaggg cttcgcggcc ctcgacgtgg atcacctgta
180
cccgacggac gtggggaagc cgtcccgcaa gctcacggga ctccgcgaca tcgatgtgcg
240
atacgatttg caccgtcgtc ggctgcgtgc gcgacacatg ctccgcgatc gcctcagcgg
300
tggtttccga cgtcagcagg aacgtggcga cgggtggcat ggcggtcgcc gttatgtcgg
360
cattcccatt cctcggg
377

<210> 486
<211> 111
<212> PRT
<213> Homo sapiens

<400> 486
Met Arg Pro Ala Arg Ala Ala Gln Phe Gly Asp Arg Arg Ile Arg Pro
1 5 10 15
Ala Gly Ile Glu Lys Glu Cys Val Asp Val Arg Gly Ile Pro Lys Glu
20 25 30
Ser Cys Arg Gly Leu Arg Gly Pro Arg Arg Gly Ser Pro Val Pro Asp
35 40 45
Gly Arg Gly Glu Ala Val Pro Gln Ala His Gly Thr Pro Arg His Arg
50 55 60
Cys Ala Ile Arg Phe Ala Pro Ser Ser Ala Ala Cys Ala Thr His Ala

65 70 75 80
Pro Arg Ser Pro Gln Arg Trp Phe Pro Thr Ser Ala Gly Thr Trp Arg
85 90 95
Arg Val Ala Trp Arg Ser Pro Leu Cys Arg His Ser His Ser Ser
100 105 110

<210> 487
<211> 459
<212> DNA
<213> Homo sapiens

<400> 487
nnacgcgtaa gatcgattgt ggatcagcac cgatgctggt ccccccgacg ttgttgttgg
60
cgggtgttgt tgtaaggagt gtgtgtgatg cgtgttggtg ttcctactga ggttaagaat
120
agtgagtttc gtgtggctgt gacgccggcg ggtgttcatg cgttggttgg tcgtggtcat
180
gaggtgttgg ttcaggctgg tgctggtgtg ggttcgggta ttccggattc ggattttgtg
240
ggtgctggtg cgcgggttgt gggtgatgtg gagtcggtgt ggggtgatgc tgatttggtg
300
ttgaaggtga aggagcctgt tgcggaggag tatgggcggt tgcatgaggg tttggttctt
360
tttacgtatc ttcatttggc tgctgatgag gcgttgactc gtgagctttt ggggcgtggg
420
gtgacgtcga ttgcgtatga gacggtggag ttggccgat
459

<210> 488
<211> 124
<212> PRT
<213> Homo sapiens

<400> 488
Met Arg Val Gly Val Pro Thr Glu Val Lys Asn Ser Glu Phe Arg Val
1 5 10 15
Ala Val Thr Pro Ala Gly Val His Ala Leu Val Gly Arg Gly His Glu
20 25 30
Val Leu Val Gln Ala Gly Ala Gly Val Gly Ser Gly Ile Pro Asp Ser
35 40 45
Asp Phe Val Gly Ala Gly Ala Arg Val Val Gly Asp Val Glu Ser Val
50 55 60
Trp Gly Asp Ala Asp Leu Val Leu Lys Val Lys Glu Pro Val Ala Glu
65 70 75 80
Glu Tyr Gly Arg Leu His Glu Gly Leu Val Leu Phe Thr Tyr Leu His
85 90 95
Leu Ala Ala Asp Glu Ala Leu Thr Arg Glu Leu Leu Gly Arg Gly Val
100 105 110
Thr Ser Ile Ala Tyr Glu Thr Val Glu Leu Ala Asp
115 120

<210> 489
<211> 542

<212> DNA
<213> Homo sapiens

<400> 489
nacgcgtttg gcgtactgag tgcggtggtg gatggcgacg acagtggcaa gccgctgctc
60
aaccagcacg gttgctacaa agtgcgcttt ccatttaccc gcgatcaaaa gcccagcact
120
cggggttcgg catggctgcg cagggtgtcg ttgtctgccg gttccagcca tggcatgcac
180
tttccgctgc tcaaaggcag tgaagtgttg gtgtcatttc tgggggggcga ccccgaccgg
240
ccgattatcg ttggctgcgt accaaactcg gaaaccccga gcatggtcgt tgagcgtaac
300
gccacccaga gcggcttctc cacggccgga gggcacttcc tggcgatgga agaccacccc
360
ggggctgccc atctgaagct gggtgcgcct ggcggcaaca gcgtcttcac actgggcaat
420
ggcaaagtcg ccggcgcgca actgcgcacc aacgccccac atgcaattga catcgtcttc
480
gctcaaacac gaagtgcccg gcgtgtactc attgtcgatg ggcaccgggg acccggcggc
540
cg
542

<210> 490
<211> 180
<212> PRT
<213> Homo sapiens

<400> 490
Xaa Ala Phe Gly Val Leu Ser Ala Val Val Asp Gly Asp Asp Ser Gly
 1   5   10   15
Lys Pro Leu Leu Asn Gln His Gly Cys Tyr Lys Val Arg Phe Pro Phe
            20   25   30
Thr Arg Asp Gln Lys Pro Ser Thr Arg Gly Ser Ala Trp Leu Arg Arg
        35   40   45
Val Ser Leu Ser Ala Gly Ser Ser His Gly Met His Phe Pro Leu Leu
    50   55   60
Lys Gly Ser Glu Val Leu Val Ser Phe Leu Gly Gly Asp Pro Asp Arg
65   70   75   80
Pro Ile Ile Val Gly Cys Val Pro Asn Ser Glu Thr Pro Ser Met Val
                85   90   95
Val Glu Arg Asn Ala Thr Gln Ser Gly Phe Ser Thr Ala Gly Gly His
            100   105   110
Phe Leu Ala Met Glu Asp His Pro Gly Ala Ala His Leu Lys Leu Gly
        115   120   125
Ala Pro Gly Gly Asn Ser Val Phe Thr Leu Gly Asn Gly Lys Val Ala
    130   135   140
Gly Ala Gln Leu Arg Thr Asn Ala Pro His Ala Ile Asp Ile Val Phe
145   150   155   160
Ala Gln Thr Arg Ser Ala Arg Arg Val Leu Ile Val Asp Gly His Arg
                165   170   175
Gly Pro Gly Gly

180

<210> 491
<211> 825
<212> DNA
<213> Homo sapiens

<400> 491
nacgcgtcga ggcgacggtc ggcgccgtca tggcgactgt tctcgagggc acatgggaac
60
gcatcggtgc cggattccgg actgccttaa ccacagcctt ggaacgcacc gatgaatggg
120
tgggcggccc tgacagcaag cccctcaacg aagtcgagac actgcgccgg tgcgccgatg
180
aactcatcgg cgggcccgtc ggcgcggttg ccgcgatgca cggagggtca atcgaattgg
240
tcgacgtgtc ggtcggtgac gaagagcgca gagtcgacgt caccatgaag ggagcatgcc
300
gaggttgccc ggcagccatc agaccctaca tcagcgcctg gaacatcaac tgagtctgcg
360
nattgcgcga gccggtcacc gtgcgggaaa tctgacacct actccgacag ctccacctcg
420
acgagcacct ccacgacgag gccaagccac tcgtagacgc attcctcctc ggcatccaat
480
tcctcccggg ccgcccgagc gacttcgtcg gcagtaacct ggtcgatgat ccctagcctg
540
gcggccatca tgccacgcag cgcattgaca gtacgaagcc aacgttgcgt catcacaggg
600
ttcatggaga tacagccggt tcggtgcaac gtctccacat cagcacttaa ggactgagcg
660
tcttcccagc gcgccgcgac atcctcggcg tcatggtcga catggaattg cgcgtcagct
720
gagtcgtcgt cacgataggc gctgggcagg atcaatcgac gcacctcgtc gtcctcctgg
780
agtccagaaa actggctctc ccaaaaagcg aacgggtccc cctcc
825

<210> 492
<211> 58
<212> PRT
<213> Homo sapiens

<400> 492
Met Asn Gly Trp Ala Ala Leu Thr Ala Ser Pro Ser Thr Lys Ser Arg
 1   5   10   15
His Cys Ala Gly Ala Pro Met Asn Ser Ser Ala Gly Pro Ser Ala Arg
            20   25   30
Leu Pro Arg Cys Thr Glu Gly Gln Ser Asn Trp Ser Thr Cys Arg Ser
        35   40   45
Val Thr Lys Ser Ala Glu Ser Thr Ser Pro
    50   55

<210> 493
<211> 863

<212> DNA
<213> Homo sapiens

<400> 493
nacgcgttcc aacctcgtca aaacggctat cgcaggaaat gaccccaact ggggtcgcat
60
cctcgcggcg atcggatgtg ttcctgagaa tatagctccc ttcgatcccg accaggtgga
120
tgtgtccatc aatgacattc agatctgtaa ggccgggggt atcggggagg accgcaacct
180
cgtcgatatg aggccacgag aggttcacat cgatattgag ctgcatgcgg gtgatgccga
240
agctgcggta tggactaatg atctgaccca ccaatacgtc gaagagaata gcgcgtatac
300
atcatgaccc ttgctcttga catccccctc aacgactccc agttctcggc tcagcggaaa
360
tctgaggtcc tggtagaagc gctgccttgg atcaggcggt ttcagggccg cactgtcgtc
420
gtgaaatatg gcggcaacgc gatggttgat cccggtctgc agcaggcctt cgccgacgac
480
attgtgttta tggcctctgt ggggattcgc cctattgtcg tccacggtgg tggccctcag
54:
atcaatgcca tgcttgctga atccgctacc ccggtggagt tccgtaatgg tttgcgggtg
600
acatctccgg aggtcatgga ggttgtccgg atggtgctcg tcgggcaggt gggccgtcag
660
ctcgttaacc gaatcaacgc ctatgcgccg ctagcagctg gcatgtcagg cgaggacttt
720
ggccttttt cggcccggaa gtcgcgggta attgttgatg gcgagcaaat agacatgggt
780
ttagtgggag acatcgttga cgtcaacatc gatctcgtta tctctatgct tgatcgcggt
840
cagattccgg tcattgcacc ggt
863

<210> 494
<211> 186
<212> PRT
<213> Homo sapiens

<400> 494
Met Thr Leu Ala Leu Asp Ile Pro Leu Asn Asp Ser Gln Phe Ser Ala
 1   5   10   15
Gln Arg Lys Ser Glu Val Leu Val Glu Ala Leu Pro Trp Ile Arg Arg
            20   25   30
Phe Gln Gly Arg Thr Val Val Val Lys Tyr Gly Gly Asn Ala Met Val
        35   40   45
Asp Pro Gly Leu Gln Gln Ala Phe Ala Asp Asp Ile Val Phe Met Ala
    50   55   60
Ser Val Gly Ile Arg Pro Ile Val Val His Gly Gly Gly Pro Gln Ile
65   70   75   80
Asn Ala Met Leu Ala Glu Ser Ala Thr Pro Val Glu Phe Arg Asn Gly
                85   90   95
Leu Arg Val Thr Ser Pro Glu Val Met Glu Val Val Arg Met Val Leu

```
            100                 105                 110
Val Gly Gln Val Gly Arg Gln Leu Val Asn Arg Ile Asn Ala Tyr Ala
        115                 120                 125
Pro Leu Ala Ala Gly Met Ser Gly Glu Asp Phe Gly Leu Phe Ser Ala
    130                 135                 140
Arg Lys Ser Arg Val Ile Val Asp Gly Glu Gln Ile Asp Met Gly Leu
145                 150                 155                 160
Val Gly Asp Ile Val Asp Val Asn Ile Asp Leu Val Ile Ser Met Leu
                165                 170                 175
Asp Arg Gly Gln Ile Pro Val Ile Ala Pro
            180                 185
```

<210> 495
<211> 514
<212> DNA
<213> Homo sapiens

<400> 495
gcgcgcgaca ccggtgcccc gattagcgtg ccagtgggtg acgtcactaa gggtcacgtc
60
tggaatgtga caggtgacgt tcttaacgcc ngatccctcc acaatcgagg tgacnntgag
120
cgttggccga tccaccggga tccccccggcc ttcgatgacc ttgagcccga gaccgagatg
180
ctggagaccg gtattaaggt ccttgacttg ctgactcctt acgtcaaggg cggcaagatt
240
ggcctctttg gcggcgctgg tgtgggtaag acggtgctca ttcaggagat gatttaccgt
300
atcgcccaca acttcggcgg tacttcggtt ttcgccggtg tcggtgagcg tacccgcgag
360
ggtaacgacc tcatcaacga gatggacgag gccggtgtgc tcaaagacac cgccctggta
420
ttcggccaga tggacgagcc cccgggcacg cggtacgagc tgtcgcgctg gcagccctgc
480
ggcccatgcc tggtcaactg ctgtgggacc ttgg
514

<210> 496
<211> 171
<212> PRT
<213> Homo sapiens

<400> 496
```
Ala Arg Asp Thr Gly Ala Pro Ile Ser Val Pro Val Gly Asp Val Thr
 1               5                  10                  15
Lys Gly His Val Trp Asn Val Thr Gly Asp Val Leu Asn Ala Xaa Ser
            20                  25                  30
Leu His Asn Arg Gly Asp Xaa Glu Arg Trp Pro Ile His Arg Asp Pro
        35                  40                  45
Pro Ala Phe Asp Asp Leu Glu Pro Glu Thr Glu Met Leu Glu Thr Gly
    50                  55                  60
Ile Lys Val Leu Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
65                  70                  75                  80
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu
```

```
                85                  90                  95
Met Ile Tyr Arg Ile Ala His Asn Phe Gly Gly Thr Ser Val Phe Ala
            100                 105                 110
Gly Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Leu Ile Asn Glu Met
        115                 120                 125
Asp Glu Ala Gly Val Leu Lys Asp Thr Ala Leu Val Phe Gly Gln Met
    130                 135                 140
Asp Glu Pro Pro Gly Thr Arg Tyr Glu Leu Ser Arg Trp Gln Pro Cys
145                 150                 155                 160
Gly Pro Cys Leu Val Asn Cys Cys Gly Thr Leu
                165                 170
```

<210> 497
<211> 662
<212> DNA
<213> Homo sapiens

<400> 497
acgcgtcctg ggatctcaac cccagcagtc tggcttgttt ctcattccca caatttcctg
60
ggttccacca agcagcgaaa actgccagga tgaatgagga aaaaacccag ccccacaaac
120
gagacacacg ctggcgggga gagacgcagc agagctcctt cctgtctgtg gactcggagc
180
aaagacgtgg ggccccatct tttgtgtttt cctcaagcgg ggaaagaatg gactgtttgc
240
atgcttcgtg ccacacgccc gcggtgatcc cagccagggc cccgagcgca gaggcggagc
300
tgtgctcagc acaggcctgg gacctccccc ggcaggcacc tgtgggggggt gcagcccccg
360
ggaaggaggc aactgcctca cttaacatcc tccgctgcaa ggtggtggcg ccgagaggcg
420
tgtctgtgaa gacaggtacc aggatggcag gacccgcacg cctcttccca cacctgtcag
480
cttcggaagc atctctcgag gactctggtc ccaggatgtc tcccaggaca agccagtctg
540
cctcttcctc ctacttctgc tgtagcctgg gaccagacct ggccaaggtc agccagcggg
600
gagggccgag gtctgagctc tcgtcctgcc gtggcccccg cgatggcttg gggtgcaagc
660
tt
662

<210> 498
<211> 191
<212> PRT
<213> Homo sapiens

<400> 498
```
Met Asn Glu Glu Lys Thr Gln Pro His Lys Arg Asp Thr Arg Trp Arg
 1               5                  10                  15
Gly Glu Thr Gln Gln Ser Ser Phe Leu Ser Val Asp Ser Glu Gln Arg
            20                  25                  30
Arg Gly Ala Pro Ser Phe Val Phe Ser Ser Ser Gly Glu Arg Met Asp
```

```
         35                  40                  45
Cys Leu His Ala Ser Cys His Thr Pro Ala Val Ile Pro Ala Arg Ala
     50                  55                  60
Pro Ser Ala Glu Ala Glu Leu Cys Ser Ala Gln Ala Trp Asp Leu Pro
65                  70                  75                  80
Arg Gln Ala Pro Val Gly Gly Ala Ala Pro Gly Lys Glu Ala Thr Ala
                85                  90                  95
Ser Leu Asn Ile Leu Arg Cys Lys Val Val Ala Pro Arg Gly Val Ser
            100                 105                 110
Val Lys Thr Gly Thr Arg Met Ala Gly Pro Ala Arg Leu Phe Pro His
        115                 120                 125
Leu Ser Ala Ser Glu Ala Ser Leu Glu Asp Ser Gly Pro Arg Met Ser
    130                 135                 140
Pro Arg Thr Ser Gln Ser Ala Ser Ser Ser Tyr Phe Cys Cys Ser Leu
145                 150                 155                 160
Gly Pro Asp Leu Ala Lys Val Ser Gln Arg Gly Gly Pro Arg Ser Glu
                165                 170                 175
Leu Ser Ser Cys Arg Gly Pro Arg Asp Gly Leu Gly Cys Lys Leu
            180                 185                 190
```

<210> 499
<211> 444
<212> DNA
<213> Homo sapiens

<400> 499
acgcgtgaag ggtgggcagt gttgagctga gtgagccctc ctccctgcaa tgctggagcc
60
ctgccttctg cctgaccctc tggcttccta agcagtctat acgtgagaag ccctttcttc
120
aagtgaaagc ttctgagctc actacgagag cactggagct ggaacctctc tgggttcaaa
180
tcctcaactg gggggttgga ggaggttact tcacttctca aaacctcaat ttccttatct
240
gcaaaatggg gtaataggag cccctcttca tcaatgcttg gagggaatgc ctggcacagt
300
agggcagtta ccgtcatgga gaacagaaag gccccgagct atcctggatg tggtgagaat
360
gggtcctgga tcctgcctgc tcggcctttt cattctcttc ttcacctaca ggctcccaca
420
aagggcctct gaaaacacag ggtg
444

<210> 500
<211> 105
<212> PRT
<213> Homo sapiens

<400> 500
```
Met Thr Val Thr Ala Leu Leu Cys Gln Ala Phe Pro Pro Ser Ile Asp
 1               5                  10                  15
Glu Glu Gly Leu Leu Leu Pro His Phe Ala Asp Lys Glu Ile Glu Val
            20                  25                  30
Leu Arg Ser Glu Val Thr Ser Ser Asn Pro Pro Val Glu Asp Leu Asn
```

35 40 45
Pro Glu Arg Phe Gln Leu Gln Cys Ser Arg Ser Glu Leu Arg Ser Phe
50 55 60
His Leu Lys Lys Gly Leu Leu Thr Tyr Arg Leu Leu Arg Lys Pro Glu
65 70 75 80
Gly Gln Ala Glu Gly Arg Ala Pro Ala Leu Gln Gly Gly Gly Leu Thr
85 90 95
Gln Leu Asn Thr Ala His Pro Ser Arg
100 105

<210> 501
<211> 800
<212> DNA
<213> Homo sapiens

<400> 501
agatctgatc cgagaagtgg ctgctcaggg aaatgactac tccatggctt tcttaactca
60
ggtactcctt attcaatgag aggcctgagg tgagacccgc catgcggcgc gtggatcgca
120
tggtgttagt gcacactagc aaggggctta ggtctccagc tgaggtcaga tgcacacttg
180
gaccttgtac tggggagtaa cacacatctc tgtgttcagc gaaccatcca ggagctgttt
240
gaagtttatt ctcccatgga tgatgctggc ttcccggtca aagctgagga gtttgtggtg
300
ctttctcagg aaccttctgt cacggaaacc attgcaccca aaattgcaag acctttcata
360
gaggccctca agagtattga gtatctggag gaggatgccc agaagtccgc acaggagggg
420
gtgctgggac cacacactga tgctctgtca tcagactctg agaacatgcc gtgtgatgaa
480
gaaccatccc aattagagga gctagctgac ttcatggagc agcttacacc aattgaaaaa
540
tatgctttaa attacctgga atcttgaggc agggcctgag agagcacgct gcgccgtact
600
tccagcagct gcggcagacc acggctccac gcctgctgca gttccctgag ctgaggctgg
660
tgcagttcga ctcaggtatg cggcagttgg gggcgtggcc cgtgcgggag ctgcactggc
720
cctggatgat gaggcgctct tgatgtgatt cgtttcccag ggaagttgga agctttagct
780
atcttgcttc agaaactgaa
800

<210> 502
<211> 103
<212> PRT
<213> Homo sapiens

<400> 502
Met Asp Asp Ala Gly Phe Pro Val Lys Ala Glu Glu Phe Val Val Leu
1 5 10 15
Ser Gln Glu Pro Ser Val Thr Glu Thr Ile Ala Pro Lys Ile Ala Arg

```
            20                  25                  30
Pro Phe Ile Glu Ala Leu Lys Ser Ile Glu Tyr Leu Glu Glu Asp Ala
        35                  40                  45
Gln Lys Ser Ala Gln Glu Gly Val Leu Gly Pro His Thr Asp Ala Leu
    50                  55                  60
Ser Ser Asp Ser Glu Asn Met Pro Cys Asp Glu Glu Pro Ser Gln Leu
65                  70                  75                  80
Glu Glu Leu Ala Asp Phe Met Glu Gln Leu Thr Pro Ile Glu Lys Tyr
                85                  90                  95
Ala Leu Asn Tyr Leu Glu Ser
            100
```

<210> 503
<211> 538
<212> DNA
<213> Homo sapiens

<400> 503
nnacgcgttg tcgtctctcc gatcattgat tttgttgtat tctgcaatga tgtaaaggaa
60
gatgatgaca cggagaagtt taaagaagcc attgtgaaat ttcataggct gtttgggatg
120
ccagaggaag agaaactcgt caactattac tcttgcagct attggaaggg gaaggtcccc
180
cgtcagggtt ggatgtacct cagcattaac caccttgct tttattcttt tcttatggga
240
agggaagcga aactggtcat ccggtgggta gacatcactc agcttgagaa gaatgccccc
300
ctgcttctgc ctgatgtgat caaagtgagc acacggtcca gtgagcattt cttctctgta
360
ttcctcaaca tcaacgagac cttcaagtta atggagcagc ttgccaacat agccatgagg
420
caactcttag acaatgaggg atttgaacaa gatcgatccc tgcccaaact caaaaggaaa
480
tctcctaaaa aagtgtctgc tctaaaacgt gatcttgatg cctgggccct tcacgcgt
538

<210> 504
<211> 179
<212> PRT
<213> Homo sapiens

<400> 504
```
Xaa Arg Val Val Val Ser Pro Ile Ile Asp Phe Val Val Phe Cys Asn
 1               5                  10                  15
Asp Val Lys Glu Asp Asp Asp Thr Glu Lys Phe Lys Glu Ala Ile Val
            20                  25                  30
Lys Phe His Arg Leu Phe Gly Met Pro Glu Glu Glu Lys Leu Val Asn
        35                  40                  45
Tyr Tyr Ser Cys Ser Tyr Trp Lys Gly Lys Val Pro Arg Gln Gly Trp
    50                  55                  60
Met Tyr Leu Ser Ile Asn His Leu Cys Phe Tyr Ser Phe Leu Met Gly
65                  70                  75                  80
Arg Glu Ala Lys Leu Val Ile Arg Trp Val Asp Ile Thr Gln Leu Glu
```

```
                85                  90                  95
Lys Asn Ala Pro Leu Leu Leu Pro Asp Val Ile Lys Val Ser Thr Arg
            100                 105                 110
Ser Ser Glu His Phe Phe Ser Val Phe Leu Asn Ile Asn Glu Thr Phe
        115                 120                 125
Lys Leu Met Glu Gln Leu Ala Asn Ile Ala Met Arg Gln Leu Leu Asp
    130                 135                 140
Asn Glu Gly Phe Glu Gln Asp Arg Ser Leu Pro Lys Leu Lys Arg Lys
145                 150                 155                 160
Ser Pro Lys Lys Val Ser Ala Leu Lys Arg Asp Leu Asp Ala Trp Ala
                165                 170                 175
Leu His Ala
```

<210> 505
<211> 381
<212> DNA
<213> Homo sapiens

<400> 505
gtgcacgaca ccgaacggta cgaacgtatc tcccaggcac gtcgcgagga acagcaggcc
60
atgctcggct acgacngctc aagaacctgt cgcatgacct tgctcaccgg gcagctggac
120
gacccctcca cgactccttg cggacgctgc gacgtctgtg ctggcccgtg gtactcagtc
180
gaggtcgatc agtcagccgc tgtgagagcc gtccaatccc tcaaccgggt gggagttccg
240
gtggaaccac gcgccgcctg gcccgcaggg atggacgccc tccaggttgc gctcaagggt
300
cgcatcagtg ccgaggagat cgctgcagag ggccgcgtca tcgccagact ctccgatctg
360
ggttggggag gggcgctgcg c
381

<210> 506
<211> 127
<212> PRT
<213> Homo sapiens

<400> 506
```
Val His Asp Thr Glu Arg Tyr Glu Arg Ile Ser Gln Ala Arg Arg Glu
 1               5                  10                  15
Glu Gln Gln Ala Met Leu Gly Tyr Asp Xaa Ser Arg Thr Cys Arg Met
            20                  25                  30
Thr Leu Leu Thr Gly Gln Leu Asp Asp Pro Ser Thr Thr Pro Cys Gly
        35                  40                  45
Arg Cys Asp Val Cys Ala Gly Pro Trp Tyr Ser Val Glu Val Asp Gln
    50                  55                  60
Ser Ala Ala Val Arg Ala Val Gln Ser Leu Asn Arg Val Gly Val Pro
65                  70                  75                  80
Val Glu Pro Arg Ala Ala Trp Pro Ala Gly Met Asp Ala Leu Gln Val
                85                  90                  95
Ala Leu Lys Gly Arg Ile Ser Ala Glu Glu Ile Ala Ala Glu Gly Arg
```

```
            100                 105                 110
Val Ile Ala Arg Leu Ser Asp Leu Gly Trp Gly Gly Ala Leu Arg
        115                 120                 125

<210> 507
<211> 499
<212> DNA
<213> Homo sapiens

<400> 507
gccggcgtgt tcaacctcat ggtgtgggcc ttcattaccg acgtcatcga tgcccaggag
60
gtcatgtccg gggagcgtga agacggtgtc atctatggcg tgaactcctt cgcccgcaaa
120
cttgcccagg ccattgccgg tggaatcggc ggagccatgc tgacgatgat cggctaccag
180
tcctcctccc aaggtggtgc cgttcagtcg gagtccgtcg tcaatcacct gtacacgctc
240
gccaccgcca tcccgacgat ctgctgcctc ggcgctgccc tgctcatgct gggctacccg
300
ctcacccgcg acaaggtggt cgccaacgcc gacgagttgg ctcgtcgcca cgcagtacag
360
gccgagcaaa actcctgacc cataacggag gcacatcatg gacacgctca tgcggatcac
420
cgaccacttg acaacctcgc cgggtatcca attgaaaatt gacaagcgat ggggtgcctc
480
cgtcacattt gtgacgcgt
499

<210> 508
<211> 125
<212> PRT
<213> Homo sapiens

<400> 508
Ala Gly Val Phe Asn Leu Met Val Trp Ala Phe Ile Thr Asp Val Ile
 1               5                  10                  15
Asp Ala Gln Glu Val Met Ser Gly Glu Arg Glu Asp Gly Val Ile Tyr
            20                  25                  30
Gly Val Asn Ser Phe Ala Arg Lys Leu Ala Gln Ala Ile Ala Gly Gly
        35                  40                  45
Ile Gly Gly Ala Met Leu Thr Met Ile Gly Tyr Gln Ser Ser Ser Gln
    50                  55                  60
Gly Gly Ala Val Gln Ser Glu Ser Val Val Asn His Leu Tyr Thr Leu
65                  70                  75                  80
Ala Thr Ala Ile Pro Thr Ile Cys Cys Leu Gly Ala Ala Leu Leu Met
                85                  90                  95
Leu Gly Tyr Pro Leu Thr Arg Asp Lys Val Val Ala Asn Ala Asp Glu
            100                 105                 110
Leu Ala Arg Arg His Ala Val Gln Ala Glu Gln Asn Ser
        115                 120                 125

<210> 509
<211> 360
```

<212> DNA
<213> Homo sapiens

<400> 509
ttggccatgg atttggctcg caagttcagt cccaaagatg tcacgctcta tctaatggac
60
ttcgggacca atggtgtggc accactaggc caattaccac aggtggccga caccttgctt
120
ttggatcata cggagaagat tgccaagttt gtacgcatca tggagcggga gctcaaccgg
180
cgtaagaagc tcttgtccga ctacggtgtt ggtacactag agctctaccg tcaggctagc
240
ggtcagcaag agccggccat cgtcatcctg ctggacagtt atgagtccat gaaggaagag
300
gcctatgaag cggagctctt cacgctcttg gtgcggatct cccgggaagg tctcagcatc
360

<210> 510
<211> 120
<212> PRT
<213> Homo sapiens

<400> 510
Leu Ala Met Asp Leu Ala Arg Lys Phe Ser Pro Lys Asp Val Thr Leu
1 5 10 15
Tyr Leu Met Asp Phe Gly Thr Asn Gly Val Ala Pro Leu Gly Gln Leu
20 25 30
Pro Gln Val Ala Asp Thr Leu Leu Leu Asp His Thr Glu Lys Ile Ala
35 40 45
Lys Phe Val Arg Ile Met Glu Arg Glu Leu Asn Arg Arg Lys Lys Leu
50 55 60
Leu Ser Asp Tyr Gly Val Gly Thr Leu Glu Leu Tyr Arg Gln Ala Ser
65 70 75 80
Gly Gln Gln Glu Pro Ala Ile Val Ile Leu Leu Asp Ser Tyr Glu Ser
85 90 95
Met Lys Glu Glu Ala Tyr Glu Ala Glu Leu Phe Thr Leu Leu Val Arg
100 105 110
Ile Ser Arg Glu Gly Leu Ser Ile
115 120

<210> 511
<211> 361
<212> DNA
<213> Homo sapiens

<400> 511
ntcgcgaacc gcggctatgc ggtgctccag cccaatttcc gcggatcggg cggttatggc
60
actgcgttcg gcgatgccgg catcggccag atcgggcgca agatgcagga cgatctcgac
120
gacgggatgg actggctggt caaggagggc atcgtcgaca agggccgggt gtgcatcgtc
180
ggggcctcct atggcggcta tgccgcgatg tggggcgcga tccgcaatcc cgaacgctat
240

cgctgcgcgg cgagcctggc gggggttgcc gattaaggcc atgctcaaat ataaccggcg
300
ctatctcgac aaggaggcgg gcaagcgctg gccgccccgn tcaaccggcg aacccgaatt
360
c
361

<210> 512
<211> 91
<212> PRT
<213> Homo sapiens

<400> 512
Xaa Ala Asn Arg Gly Tyr Ala Val Leu Gln Pro Asn Phe Arg Gly Ser
 1   5   10   15
Gly Gly Tyr Gly Thr Ala Phe Gly Asp Ala Gly Ile Gly Gln Ile Gly
            20   25   30
Arg Lys Met Gln Asp Asp Leu Asp Asp Gly Met Asp Trp Leu Val Lys
        35   40   45
Glu Gly Ile Val Asp Lys Gly Arg Val Cys Ile Val Gly Ala Ser Tyr
    50   55   60
Gly Gly Tyr Ala Ala Met Trp Gly Ala Ile Arg Asn Pro Glu Arg Tyr
65   70   75   80
Arg Cys Ala Ala Ser Leu Ala Gly Val Ala Asp
                85   90

<210> 513
<211> 369
<212> DNA
<213> Homo sapiens

<400> 513
nnatgcagac tagaagatgg catgacggtt ttggctggcg gtttcgggct atgcggcatt
60
ccagaaaatc tgattcaaga gatcaaacga cgccagactt gtgatttgac catagtgtca
120
aataactgtg gtgtagatgg ttttggttta ggggttttgc tagaagataa gcaagtacgc
180
aaaatggtgt cttcttatgt gggtgaaaat gcactgtttg agaagcaatt attacaaggt
240
gagttggaag tcgagctcac tcctcaaggc actcttgccg aaaaactacg cgctggcggc
300
gcgggaattc ctgccttttt cacagcaacg ggtgtaggta cacctattgg tgagggtaaa
360
gacacgcgt
369

<210> 514
<211> 123
<212> PRT
<213> Homo sapiens

<400> 514
Xaa Cys Arg Leu Glu Asp Gly Met Thr Val Leu Ala Gly Gly Phe Gly

```
 1               5                  10                  15
Leu Cys Gly Ile Pro Glu Asn Leu Ile Gln Glu Ile Lys Arg Arg Gln
            20                  25                  30
Thr Cys Asp Leu Thr Ile Val Ser Asn Asn Cys Gly Val Asp Gly Phe
        35                  40                  45
Gly Leu Gly Val Leu Leu Glu Asp Lys Gln Val Arg Lys Met Val Ser
    50                  55                  60
Ser Tyr Val Gly Glu Asn Ala Leu Phe Glu Lys Gln Leu Leu Gln Gly
65                  70                  75                  80
Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Lys Leu
                85                  90                  95
Arg Ala Gly Gly Ala Gly Ile Pro Ala Phe Phe Thr Ala Thr Gly Val
            100                 105                 110
Gly Thr Pro Ile Gly Glu Gly Lys Asp Thr Arg
        115                 120
```

<210> 515
<211> 387
<212> DNA
<213> Homo sapiens

<400> 515
gcgtgggacg agaaggccgc cggcaactgc gcgatcgact acgggttcca ccagatcctc
60
tccgacgtgc aggactcgtc gctgaccgcg atggacgagc tgatcaccga gggcgtgaca
120
tccttcaagc tcttcgtggc ctacaagggc gtcttcctct cggacgacgg gcagatcctg
180
cgggcgttcc agaagggcgc cgacaacggc gcgatgatga tgatgcacgc cgagaacggc
240
gcgatcatcg acgtgctcgt gcagcaggcg ctcgaggccg ggaagaccac cccgtactac
300
cacggcatca gccggccgtg gcaggccgag gaggaggcca cccaccgcgc gatcatgatc
360
gccgacctga ccggtgcgcc gttgtac
387

<210> 516
<211> 129
<212> PRT
<213> Homo sapiens

<400> 516
```
Ala Trp Asp Glu Lys Ala Ala Gly Asn Cys Ala Ile Asp Tyr Gly Phe
 1               5                  10                  15
His Gln Ile Leu Ser Asp Val Gln Asp Ser Ser Leu Thr Ala Met Asp
            20                  25                  30
Glu Leu Ile Thr Glu Gly Val Thr Ser Phe Lys Leu Phe Val Ala Tyr
        35                  40                  45
Lys Gly Val Phe Leu Ser Asp Asp Gly Gln Ile Leu Arg Ala Phe Gln
    50                  55                  60
Lys Gly Ala Asp Asn Gly Ala Met Met Met Met His Ala Glu Asn Gly
65                  70                  75                  80
Ala Ile Ile Asp Val Leu Val Gln Gln Ala Leu Glu Ala Gly Lys Thr
```

```
                85                  90                  95
Thr Pro Tyr Tyr His Gly Ile Ser Arg Pro Trp Gln Ala Glu Glu Glu
            100                 105                 110
Ala Thr His Arg Ala Ile Met Ile Ala Asp Leu Thr Gly Ala Pro Leu
        115                 120                 125
Tyr
```

<210> 517
<211> 377
<212> DNA
<213> Homo sapiens

<400> 517
acgcgtgaag ggctggtggg caggccttgc gccccctctg gggacagctc tcctccaccc
60
agacccccttc gggccaacag tggggagggg ctgccgtctg agccactgtt ccgacagggg
120
attcgcgagt tccgggggag ctggggactg agctgcgggc ctcctgggct ggggctcttc
180
tccgaggttg gaggcagctt tagaaacttg agacccctag ctggagaggg cagaaggggt
240
ccctgagctt ccccaggaga agggggggca atttggagct tgcttttcac ctgagatgag
300
gaatgggggt ggccaggccg agagcccagt ggggcatccc cagcacccat gaacatgcta
360
aggaagggga ggggccc
377

<210> 518
<211> 118
<212> PRT
<213> Homo sapiens

<400> 518
```
Met Phe Met Gly Ala Gly Asp Ala Pro Leu Gly Ser Arg Pro Gly His
 1               5                  10                  15
Pro His Ser Ser Ser Gln Val Lys Ser Lys Leu Gln Ile Gly Pro Pro
            20                  25                  30
Ser Pro Gly Glu Ala Gln Gly Pro Leu Leu Pro Ser Pro Ala Arg Gly
        35                  40                  45
Leu Lys Phe Leu Lys Leu Pro Pro Thr Ser Glu Lys Ser Pro Ser Pro
    50                  55                  60
Gly Gly Pro Gln Leu Ser Pro Gln Leu Pro Arg Asn Ser Arg Ile Pro
65                  70                  75                  80
Cys Arg Asn Ser Gly Ser Asp Gly Ser Pro Ser Pro Leu Leu Ala Arg
                85                  90                  95
Arg Gly Leu Gly Gly Gly Glu Leu Ser Pro Glu Gly Ala Gln Gly Leu
            100                 105                 110
Pro Thr Ser Pro Ser Arg
        115
```

<210> 519
<211> 311

<212> DNA
<213> Homo sapiens

<400> 519
gcgcgccagg gggaagggag agaaaacaca gaaaaatgag ggggaaatac cagatactga
60
agaatttaaa ttattataaa ggaacctttt ctgcaactct gaaaaatgtt agaatatcca
120
aagaaattga taattttcta ggaaaacatg acttaccaaa attaactcta gaaaagaatc
180
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Asn Phe Leu Gly Lys His Asp Leu Pro Lys Leu Thr Leu Glu Lys Asn
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Arg Tyr Thr Ser Val Thr Thr Glu Val Glu Lys Val Val Asn Ile Leu
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35 40 45
Val Ile Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu Cys Thr Gly
50 55 60
Arg Thr Gly Val Arg Pro Val Val Val Glu Thr Tyr Ala Lys Ala Leu
65 70 75 80
Asn Ala Gly Ile Val Pro Gly Val Arg Glu Tyr Gly Ser Leu Gly Cys
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Ser Gly Asp Leu Ala Pro Leu Ala His Cys Ala Leu Ala Leu Leu Gly
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Glu Gly Glu Val Arg
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Phe Pro Leu Asp Phe Gln Val Ile Leu Ala Gly Ser Gln Arg Phe Arg
50 55 60
Glu Lys Phe Pro Pro Val Phe Phe Ser Ser Phe Arg Asn Thr Val Gln
65 70 75 80
Ser Ser Asn Asn Lys Phe Arg Arg Asn Phe Thr Met Thr Tyr His Leu
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Ser Pro Gly Asn Tyr Val Val Val Ala Gln Thr Arg Arg Lys Ser Ala
100 105 110
Glu Phe Leu Leu Arg Ile Phe Leu Lys Met Pro Asp Ser Asp Arg His
115 120 125
Leu Ser Ser His Phe Asn Leu Arg Met Lys Gly Ser Pro Ser Glu His
130 135 140
Gly Ser Gln Gln Ser Ile Phe Asn Arg Tyr Ala Gln Gln Arg Leu Asp
145 150 155 160
Ile Asp Ala Thr Gln Leu Gln Gly Leu Leu Asn Gln Glu Leu Leu Thr
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        35   40   45
His Thr Glu Glu Glu Val Glu Val Asp Ser His Ala Tyr Ser His Arg
    50   55   60
Trp Lys Arg Asn Leu Asp Phe Leu Lys Ala Val Asp Thr Asn Arg Ala
65   70   75   80
Ser Val Gly Gln Asp Ser Leu Glu Pro Arg Ser Phe Thr Asp Leu Leu
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Leu Asp Asp Gly Gln Asp Asn Asn Thr Gln Ile Glu Glu Asp Thr Asp
            100   105   110
His Asn Tyr Tyr Ile Ser Arg Ile Tyr Gly Pro Ser Asp Ser Ala Ser
        115   120   125
Arg Asp Leu Trp Val Asn Ile Asp Gln Met Glu Lys Asp Lys Val Lys
    130   135   140
Ile His Gly Ile Leu Ser Asn Thr His Arg Gln Ala Ala Arg Val Asn
145   150   155   160
Leu Ser Phe Asp Phe Pro Phe Tyr Gly His Phe Leu Arg Glu Ile Thr
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Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile
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Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr
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Asp Met Val His Arg Pro Pro Ala Met Ser Gln Ala Cys Asn Thr Glu
            100                 105                 110
Pro Cys Pro Pro Arg Trp His Val Gly Ser Trp Gly Pro Cys Ser Ala
        115                 120                 125
Thr Cys Gly Val Gly Ile Gln Thr Arg Asp Val Tyr Cys Leu His Pro
    130                 135                 140
Gly Glu Thr Pro Ala Pro Pro Glu Glu Cys Arg Asp Glu Lys Pro His
145                 150                 155                 160
Ala Leu Gln Ala Cys Asn Gln Phe Asp Cys Pro Pro Gly Trp His Ile
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Glu Glu Trp Gln Gln Cys Ser Arg Thr Cys Gly Gly Gly Thr Gln Asn
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Arg Arg Val Thr Cys Arg Gln Leu Leu Thr Asp Gly Ser Phe Leu Asn
        195                 200                 205
Leu Ser Asp Glu Leu Cys Gln Gly Pro Lys Ala Ser Ser His Lys Ser
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Cys Ala Arg Thr Asp Cys Pro Pro His Leu Ala Val Gly Asp Trp Ser
225                 230                 235                 240
Lys Cys Ser Val Ser Cys Gly Val Gly Ile Gln Arg Arg Lys Gln Val
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Cys Gln Arg Leu Ala Ala Lys Gly Arg Arg Ile Pro Leu Ser Glu Met
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Met Cys Arg Asp Leu Pro Gly Leu Pro Leu Val Arg Ser Cys Gln Met
        275                 280                 285
Pro Glu Cys Ser Lys Ile Lys Ser Glu Met Lys Thr Lys Leu Gly Glu
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Gln Gly Pro Gln Ile Leu Ser Val Gln Arg Val Tyr Ile Gln Thr Arg
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Glu Glu Lys Arg Ile Asn Leu Thr Ile Gly Ser Arg Ala Tyr Leu Leu
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Pro Asn Thr Ser Val Ile Ile Lys Cys Pro Val Arg Arg Phe Gln Lys
            340                 345                 350
Ser Leu Ile Gln Trp Glu Lys Asp Gly Arg Cys Leu Gln Asn Ser Lys
        355                 360                 365
Arg Leu Gly Ile Thr Lys Ser Gly Ser Leu Lys Ile His Gly Leu Ala
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Pro Ala Leu Arg Glu Pro Met Arg Glu Tyr Pro Gly Met Asp His Ser
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Glu Ala Asn Ser Leu Gly Val Thr Trp His Lys Met Arg Gln Met Trp
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Glu Ala Ala Leu Gly Ala Asn Val Thr Ile Arg Cys Pro Val Lys Gly
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Val Pro Gln Pro Asn Ile Thr Trp Leu Lys Arg Gly Gly Ser Leu Ser
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Pro Glu Ser Arg Ile Val Phe Leu Gln Gly His Lys Lys Tyr Ile Leu
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<212> DNA
<213> Homo sapiens

<400> 529
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<210> 530
<211> 802
<212> PRT

<213> Homo sapiens

<400> 530

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Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro Glu Gly Cys
        35                  40                  45
Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly Ala Arg Gly Asp
    50                  55                  60
Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser Asp Pro Asp Gly Gly
65                  70                  75                  80
Pro Arg Asp Arg Asn Phe Leu Phe Val Gly Val Met Thr Ala Gln Lys
                85                  90                  95
Tyr Leu Gln Thr Arg Ala Val Ala Ala Tyr Arg Thr Trp Ser Lys Thr
            100                 105                 110
Ile Pro Gly Lys Val Gln Phe Phe Ser Ser Glu Gly Ser Asp Thr Ser
        115                 120                 125
Val Pro Ile Pro Val Val Pro Leu Arg Gly Val Asp Asp Ser Tyr Pro
    130                 135                 140
Pro Gln Lys Lys Ser Phe Met Met Leu Lys Tyr Met His Asp His Tyr
145                 150                 155                 160
Leu Asp Lys Tyr Glu Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile
                165                 170                 175
Lys Gly Asp Arg Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu
            180                 185                 190
Pro Leu Phe Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly
        195                 200                 205
Lys Leu Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly
    210                 215                 220
Val Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
225                 230                 235                 240
Lys Cys Leu Arg Glu Met Tyr Thr Thr His Glu Asp Val Glu Val Gly
                245                 250                 255
Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser Tyr Glu
            260                 265                 270
Met Gln Gln Leu Phe Tyr Glu Asn Tyr Glu Gln Asn Lys Lys Gly Tyr
        275                 280                 285
Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala Ile Thr Leu His
    290                 295                 300
Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu His Ser Tyr Met Leu
305                 310                 315                 320
Ser Arg Lys Ile Ser Glu Leu Arg His Arg Thr Ile Gln Leu His Arg
                325                 330                 335
Glu Ile Val Leu Met Ser Lys Tyr Ser Asn Thr Glu Ile His Lys Glu
            340                 345                 350
Asp Leu Gln Leu Gly Ile Pro Pro Ser Phe Met Arg Phe Gln Pro Arg
        355                 360                 365
Gln Arg Glu Glu Ile Leu Glu Trp Glu Phe Leu Thr Gly Lys Tyr Leu
    370                 375                 380
Tyr Ser Ala Val Asp Gly Gln Pro Pro Arg Arg Gly Met Asp Ser Ala
385                 390                 395                 400
Gln Arg Glu Ala Leu Asp Asp Ile Val Met Gln Val Met Glu Met Ile
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                405                 410                 415
Asn Ala Asn Ala Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile
            420                 425                 430
Gln Tyr Gly Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile
        435                 440                 445
Leu Asp Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr
    450                 455                 460
Val Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile
465                 470                 475                 480
Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys Arg
                485                 490                 495
Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser Leu Lys
            500                 505                 510
Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu His Lys Glu
        515                 520                 525
Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu Ser Gly Arg Phe
    530                 535                 540
Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu Lys Thr Cys Leu Ile
545                 550                 555                 560
Pro Asn Gln Asn Val Lys Leu Val Val Leu Leu Phe Asn Ser Asp Ser
                565                 570                 575
Asn Pro Asp Lys Ala Lys Gln Val Glu Leu Met Thr Asp Tyr Arg Ile
            580                 585                 590
Lys Tyr Pro Lys Ala Asp Met Gln Ile Leu Pro Val Ser Gly Glu Phe
        595                 600                 605
Ser Arg Ala Leu Ala Leu Glu Val Gly Ser Ser Gln Phe Asn Asn Glu
    610                 615                 620
Ser Leu Leu Phe Phe Cys Asp Val Asp Leu Val Phe Thr Thr Glu Phe
625                 630                 635                 640
Leu Gln Arg Cys Arg Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe
                645                 650                 655
Pro Ile Ile Phe Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys
            660                 665                 670
Val Pro Ser Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp
        675                 680                 685
Arg Asn Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val
    690                 695                 700
Arg Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp
705                 710                 715                 720
Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe Arg
                725                 730                 735
Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe Cys Asp
            740                 745                 750
Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly Ser Lys Ala
        755                 760                 765
Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met Trp Leu Glu Lys
    770                 775                 780
Asn Asp Pro Ser Tyr Ser Lys Ser Ser Asn Asn Asn Gly Ser Val Arg
785                 790                 795                 800
Thr Ala
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<210> 531
<211> 321

<212> DNA
<213> Homo sapiens

<400> 531
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120
aggaagaagc gtgaaacgct gtaggaccag cgtttcgaac gcccccgagg tgaaccctcg
180
ggggcgtctg aatcaggcca gttgggcctg ggacgacagc ggttgcagcg gcagcaatgg
240
cgcgtgcgga tcagccttga tcgattcacg ccaggcgccg agccactcgg cgtggccttc
300
gttccacacc tgctggtgca g
321

<210> 532
<211> 96
<212> PRT
<213> Homo sapiens

<400> 532
Met Gly Gly Phe Leu Pro Gln Gln Lys Ala Arg Gln Tyr Val Ser Asn
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Lys Gly Leu Leu Phe Arg Asn Asn Lys Gly Leu Glu Leu Arg Gly Arg
            20   25   30
Ser Val Lys Arg Cys Arg Thr Ser Val Ser Asn Ala Pro Glu Val Asn
        35   40   45
Pro Arg Gly Arg Leu Asn Gln Ala Ser Trp Ala Trp Asp Asp Ser Gly
    50   55   60
Cys Ser Gly Ser Asn Gly Ala Cys Gly Ser Ala Leu Ile Asp Ser Arg
65   70   75   80
Gln Ala Pro Ser His Ser Ala Trp Pro Ser Phe His Thr Cys Trp Cys
                85   90   95

<210> 533
<211> 335
<212> DNA
<213> Homo sapiens

<400> 533
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120
gagacgtggt cgagtcaggt ccggcatttc attagccttt tacacccaaa agtcaccctc
180
accaacattg acaacgtcct caacaaagat cacctgcgtt ggctacactt tcttttggag
240
ggtcgcctgg agccaaacgt gcgcctgatt gtccagggct actgttcgcc tggcaagctg
300
taccgcaagc ttgaggagct atatgcccct tctgc
335

<210> 534
<211> 103
<212> PRT
<213> Homo sapiens

<400> 534
Met Pro Arg Asp Ile Asp Phe Ser Glu Ala Asn Arg Ser Ile Ile Asp
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Asn Met Ala Thr Ala Ser Ile Pro Leu Phe Arg Thr His Lys Asn Trp
20 25 30
Glu Thr Trp Ser Ser Gln Val Arg His Phe Ile Ser Leu Leu His Pro
35 40 45
Lys Val Thr Leu Thr Asn Ile Asp Asn Val Leu Asn Lys Asp His Leu
50 55 60
Arg Trp Leu His Phe Leu Leu Glu Gly Arg Leu Glu Pro Asn Val Arg
65 70 75 80
Leu Ile Val Gln Gly Tyr Cys Ser Pro Gly Lys Leu Tyr Arg Lys Leu
85 90 95
Glu Glu Leu Tyr Ala Pro Ser
100

<210> 535
<211> 402
<212> DNA
<213> Homo sapiens

<400> 535
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ggttatcagc cgaggaatcc acggcgaaat gaccagtagc ggccctaata caactatgct
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gccgagcagc agacgtcgag gtcgggtcat gaggatgccg acggccaccg cgaccgggta
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<210> 536
<211> 114
<212> PRT
<213> Homo sapiens

<400> 536
Met Ala Leu His Thr Trp Arg Leu Val Asn Pro Glu Thr Val Asp Val
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Val Glu Leu Arg Gly Ala Asp Thr Gly Ser His Gln Val Gly Gly Val
20 25 30
Ser Ser Ala Gly Gly Leu Ala Leu Trp Ser Ala Leu Ala Ile Ser Leu

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        35                  40                  45
Val Pro Ala Leu Trp Val Tyr Pro Val Ala Val Ala Val Gly Ile Leu
    50                  55                  60
Met Thr Arg Pro Arg Arg Leu Leu Leu Gly Ser Ile Val Val Leu Gly
65                  70                  75                  80
Pro Leu Leu Val Ile Ser Pro Trp Ile Pro Arg Leu Ile Thr Glu Pro
                85                  90                  95
Gly Arg Met Ala Thr Gly Ala Glu Pro Val Leu Ser Pro Ala Val Glu
            100                 105                 110
Thr Arg
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<210> 537
<211> 404
<212> DNA
<213> Homo sapiens

<400> 537
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ttcggctacg gcagccgcat gaagagcggc gcctacatgc ccaccagcca ccacatgaac
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ctggcgacct ggcacaccat caactcggtg tactcgcaaa aatcccagct ggccctgggc
180
agcatgcgct acgacatcga agacaccggc ggcatcgacc gcctgttcaa gctgatcgaa
240
cagcgtgctg ggcactggct tgccatggaa gtggaagaaa ccaagatcca gctcacccat
300
caagacagcc gccacgtgcc gctggaccgc atcgaagcgg gcctgagcgt agacctgagc
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404

<210> 538
<211> 118
<212> PRT
<213> Homo sapiens

<400> 538
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Met Pro Thr Ser His His Met Asn Leu Ala Thr Trp His Thr Ile Asn
            20                  25                  30
Ser Val Tyr Ser Gln Lys Ser Gln Leu Ala Leu Gly Ser Met Arg Tyr
        35                  40                  45
Asp Ile Glu Asp Thr Gly Gly Ile Asp Arg Leu Phe Lys Leu Ile Glu
    50                  55                  60
Gln Arg Ala Gly His Trp Leu Ala Met Glu Val Glu Glu Thr Lys Ile
65                  70                  75                  80
Gln Leu Thr His Gln Asp Ser Arg His Val Pro Leu Asp Arg Ile Glu
                85                  90                  95
Ala Gly Leu Ser Val Asp Leu Ser Arg Ala Leu Phe Glu Ser Ser Ile
            100                 105                 110
Asp Asn Leu Leu Glu Arg
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115

<210> 539
<211> 534
<212> DNA
<213> Homo sapiens

<400> 539
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120
ttacttgcca tttatggaaa aaaggggat acaagcaaca tcatcacagt aagagtggct
180
gatgggcaaa cagtgcaagg ggaagtctgg aaaacaacgc cttaccaagt ggctgctgaa
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360
gctcaagctg tgagtatttt aaaaccagac agccaaactt tgggtagtta tgttgtaaac
420
tacattatat aagaggccac atattgaatt cacgaatgtt gagtttttg ggggtttcta
480
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534

<210> 540
<211> 143
<212> PRT
<213> Homo sapiens

<400> 540
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20 25 30
Ile Leu Lys Lys Asp His Gln Leu Leu Leu Ala Ile Tyr Gly Lys Lys
35 40 45
Gly Asp Thr Ser Asn Ile Ile Thr Val Arg Val Ala Asp Gly Gln Thr
50 55 60
Val Gln Gly Glu Val Trp Lys Thr Thr Pro Tyr Gln Val Ala Ala Glu
65 70 75 80
Ile Ser Gln Glu Leu Ala Glu Ser Thr Val Ile Ala Lys Val Asn Gly
85 90 95
Glu Leu Trp Asp Leu Asp Arg Pro Leu Glu Gly Asp Ser Ser Leu Glu
100 105 110
Leu Leu Thr Phe Asp Asn Glu Glu Ala Gln Ala Val Ser Ile Leu Lys
115 120 125
Pro Asp Ser Gln Thr Leu Gly Ser Tyr Val Val Asn Tyr Ile Ile
130 135 140

<210> 541
<211> 551

<212> DNA
<213> Homo sapiens

<400> 541
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ctgaagcagg ccggctctgg cgtccacgct gcaggcaccc cagaaaacag cgcccccgtg
120
gagtcggagc ccagccagtg ggcgtgtaaa gtgtgttctg ccaccttcct ggagctgcag
180
ctcctcaatg gtaaggagga cgtgtgggga gccccagttg taaaactcct gtgtcgattt
240
ctctctgact tacgctgtca cctgtctgcg gctgtcgggg gtgtcccaga ctttgtcctg
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360
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420
ttgggaagtt gcatttcagc tgggcgcctt gactctggag cactggcagg ggccaggggc
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540
ccctcacgcg t
551

<210> 542
<211> 168
<212> PRT
<213> Homo sapiens

<400> 542
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Gly Thr Pro Glu Asn Ser Ala Pro Val Glu Ser Glu Pro Ser Gln Trp
            20   25   30
Ala Cys Lys Val Cys Ser Ala Thr Phe Leu Glu Leu Gln Leu Leu Asn
        35   40   45
Gly Lys Glu Asp Val Trp Gly Ala Pro Val Val Lys Leu Leu Cys Arg
    50   55   60
Phe Leu Ser Asp Leu Arg Cys His Leu Ser Ala Ala Val Gly Gly Val
65   70   75   80
Pro Asp Phe Val Leu Ser Ala Pro Leu Pro His Asn Val Val Ala Arg
                85   90   95
Thr Lys Ala Phe Ser Gly Phe Lys Ala Ser Gly Gln Ser Arg Phe Pro
            100   105   110
Pro Pro Thr Pro Ala Gly Leu Thr Pro His Ser Ser Trp Leu Gly Ser
        115   120   125
Cys Ile Ser Ala Gly Arg Leu Asp Ser Gly Ala Leu Ala Gly Ala Arg
    130   135   140
Gly Gln Glu Pro Ala Val Ala Cys Val Val His Ser Cys Leu Cys Cys
145   150   155   160
Leu Tyr Leu Thr Ala Pro Ser Arg
                165

<210> 543
<211> 349
<212> DNA
<213> Homo sapiens

<400> 543
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gggggcaaag gcagccgcct ggccccgatg accgatcagg tggccaaacc agccgtgccg
120
tttatgggga cgtaccgcct gattgacttt tcgctgtcca acattgtcca cagcggcttg
180
caggacgtct ggatcattga gcaaaacctg ccccatagct taaacgagca cctggctggg
240
gggcgctcct gggatctgga ccgcacccgc ggtggcctga aggtcatgcc gccctttcc
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349

<210> 544
<211> 116
<212> PRT
<213> Homo sapiens

<400> 544
Xaa Lys Pro Asp Met Asn Thr Arg Ile Ala Gly Lys Thr Val Leu Thr
1 5 10 15
Ile Ile Leu Ala Gly Gly Lys Gly Ser Arg Leu Ala Pro Met Thr Asp
20 25 30
Gln Val Ala Lys Pro Ala Val Pro Phe Met Gly Thr Tyr Arg Leu Ile
35 40 45
Asp Phe Ser Leu Ser Asn Ile Val His Ser Gly Leu Gln Asp Val Trp
50 55 60
Ile Ile Glu Gln Asn Leu Pro His Ser Leu Asn Glu His Leu Ala Gly
65 70 75 80
Gly Arg Ser Trp Asp Leu Asp Arg Thr Arg Gly Gly Leu Lys Val Met
85 90 95
Pro Pro Phe Ser Gly Pro Ala Asp Glu Asp Gly Gly Phe Ser Glu Gly
100 105 110
Asn Ala His Ala
115

<210> 545
<211> 390
<212> DNA
<213> Homo sapiens

<400> 545
catgatgcaa aaacagacat gcttatttca aaatataaaa gtgaaaaaga tcgtttagca
60
caagaaattg ttggtgtcat cacaggttct gcaatgccgg gtggttcagc aaaccgtatc
120
ccaaataaag caggctcaaa tccagaaggt tctattgcaa cgcgttttat tgcagaaaca
180

atgtataacg aactcaaaac agtggattta actattcaaa atgctggcgg tgtacgcgca
240
gatattttac cggggaatgt aacctttaac gatgcttata ctttcttacc tttcgggaat
300
acgttatata cctataaaat ggaaagttca ttagtgaaac aagtgcttga agatgcaatg
360
ctatttgctt tgggtccccc ccccccccc
390

<210> 546
<211> 130
<212> PRT
<213> Homo sapiens

<400> 546
His Asp Ala Lys Thr Asp Met Leu Ile Ser Lys Tyr Lys Ser Glu Lys
 1   5   10   15
Asp Arg Leu Ala Gln Glu Ile Val Gly Val Ile Thr Gly Ser Ala Met
            20   25   30
Pro Gly Gly Ser Ala Asn Arg Ile Pro Asn Lys Ala Gly Ser Asn Pro
        35   40   45
Glu Gly Ser Ile Ala Thr Arg Phe Ile Ala Glu Thr Met Tyr Asn Glu
    50   55   60
Leu Lys Thr Val Asp Leu Thr Ile Gln Asn Ala Gly Gly Val Arg Ala
65   70   75   80
Asp Ile Leu Pro Gly Asn Val Thr Phe Asn Asp Ala Tyr Thr Phe Leu
                85   90   95
Pro Phe Gly Asn Thr Leu Tyr Thr Tyr Lys Met Glu Ser Ser Leu Val
            100   105   110
Lys Gln Val Leu Glu Asp Ala Met Leu Phe Ala Leu Gly Pro Pro Pro
        115   120   125
Pro Pro
    130

<210> 547
<211> 306
<212> DNA
<213> Homo sapiens

<400> 547
aagcttgttt ttctgatttt tattcaaatc tctatcatgg atgaagcatg cagtttcaga
60
atcagttcag tgttgacaac atatcaagat attctgcagt caatctcaat gtatgttcat
120
gaagcctcca acatattttg tgggatacca tctttgtcag gcattgtgct aggcactgtc
180
cctgcagtga ataagaaaga caggatttct gtatttatgg ggcttagtac caagttgttc
240
tcaaactttc atgtttgtgt atacaaatca gctgaggcct tcactaaact cnnnnnccnn
300
nnccnn
306

<210> 548

<211> 90
<212> PRT
<213> Homo sapiens

<400> 548
Met Asp Glu Ala Cys Ser Phe Arg Ile Ser Ser Val Leu Thr Thr Tyr
1 5 10 15
Gln Asp Ile Leu Gln Ser Ile Ser Met Tyr Val His Glu Ala Ser Asn
20 25 30
Ile Phe Cys Gly Ile Pro Ser Leu Ser Gly Ile Val Leu Gly Thr Val
35 40 45
Pro Ala Val Asn Lys Lys Asp Arg Ile Ser Val Phe Met Gly Leu Ser
50 55 60
Thr Lys Leu Phe Ser Asn Phe His Val Cys Val Tyr Lys Ser Ala Glu
65 70 75 80
Ala Phe Thr Lys Leu Xaa Xaa Xaa Xaa Xaa
85 90

<210> 549
<211> 780
<212> DNA
<213> Homo sapiens

<400> 549
nnacgcgtac ttccaacacc tatgctccag tatggaggac gggtaaagtc tcttgttaat
60
gttttaatca tacacatatt gtctgtaagt atgaagagaa aggcatatca gaaatatttc
120
aattcagcga tttgaaatgt ttacttttctg tttattgaaa atttttgttc tttttcacca
180
tgttattttt ttctcctcgt gtagaatcgg acagtagcaa caccgagcca tggagtatgg
240
gacatgcgag ggaaacaatt ccacacagga gttgaaatca aaatgtgggc tatcgcttgt
300
tttgccacac agaggcagtg cagagaagaa atattgaagg gtttcacaga ccagctgcgt
360
aagatttcta aggatgcagg gatgcccatc cagggccagc catgcttctg caaatatgca
420
caggggcag acagcgtaga gcccatgttc cggcatctca agaacacata ttctggccta
480
cagcttatta tcgtcatcct gccggggaag acaccagtgt atgcggaagt gaaacgtgta
540
ggagacacac ttttgggtat ggctacacaa tgtgttcaag tcaagaatgt aataaaaaca
600
tctcctcaaa ctctgtcaaa cttgtgccta aagataaatg ttaaactcgg agggatcaat
660
aatattcttg tacctcatca aagaccttct gtgttccagc aaccagtgat ctttttggga
720
gccgatgtca ctcatccacc tgctggtgat ggaaagaagc cttctattgc tgctgttgta
780

<210> 550
<211> 192
<212> PRT

<213> Homo sapiens

<400> 550
Asn Arg Thr Val Ala Thr Pro Ser His Gly Val Trp Asp Met Arg Gly
1 5 10 15
Lys Gln Phe His Thr Gly Val Glu Ile Lys Met Trp Ala Ile Ala Cys
20 25 30
Phe Ala Thr Gln Arg Gln Cys Arg Glu Glu Ile Leu Lys Gly Phe Thr
35 40 45
Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro Ile Gln Gly
50 55 60
Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro
65 70 75 80
Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln Leu Ile Ile
85 90 95
Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val
100 105 110
Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln Val Lys Asn
115 120 125
Val Ile Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile
130 135 140
Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro His Gln Arg
145 150 155 160
Pro Ser Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr
165 170 175
His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala Ala Val Val
180 185 190

<210> 551
<211> 291
<212> DNA
<213> Homo sapiens

<400> 551
nnggatccgg attatggggc tattgctaac aggtcaacgg ccatcaaggt gctcgttgcc
60
gtggcaccgc cagccccgga gcctactcgc gagccaccga cgaactccgc tccttccgag
120
gaaccgtcct cgtcgtcaat cgcaccggtc ccgccggccc cgacgactgc agtacccacg
180
actagttcgt cgtcgggccg ctgaccgatg cgcccatcgg cgggctcatc tggctggcgc
240
tagcgggggc ttcgatgtcc ccataccaca gcgtccgcta aattgcccnc c
291

<210> 552
<211> 67
<212> PRT
<213> Homo sapiens

<400> 552
Xaa Asp Pro Asp Tyr Gly Ala Ile Ala Asn Arg Ser Thr Ala Ile Lys
1 5 10 15
Val Leu Val Ala Val Ala Pro Pro Ala Pro Glu Pro Thr Arg Glu Pro

```
            20                  25                  30
Pro Thr Asn Ser Ala Pro Ser Glu Glu Pro Ser Ser Ser Ser Ile Ala
        35                  40                  45
Pro Val Pro Pro Ala Pro Thr Thr Ala Val Pro Thr Thr Ser Ser Ser
    50                  55                  60
Ser Gly Arg
65
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<210> 553
<211> 471
<212> DNA
<213> Homo sapiens

<400> 553
ctagccgatg taggattagt aggttttccg agcgtgggta aatctacctt actctcaata
60
gtatctaaag ccaaaccgaa aattggtgca tatcatttca ctacaattaa acctaactta
120
ggtgttgttt ccacaaaaga tcaacgtagt tttgttatgg cagatttacc aggtttaatt
180
gaaggtgcat ctgatggcgt tggattagga catcaatttt taagacatgt agagagaaca
240
aaagttattg ttcacatgat tgatatgagc ggttctgaag gtagagaacc tattgaagat
300
tataaagtca ttaatcaaga attagctgcg tacgagcaac gtttagaaga tagacctcaa
360
atcgtagtag ctaacaagat ggatttacct gaatcacaag ataatttaaa cttgtttaaa
420
gaagaaattg gcgaagatgt gccagttatt ccagtttcaa caataacgcg t
471

<210> 554
<211> 157
<212> PRT
<213> Homo sapiens

<400> 554

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Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr
 1               5                  10                  15
Leu Leu Ser Ile Val Ser Lys Ala Lys Pro Lys Ile Gly Ala Tyr His
            20                  25                  30
Phe Thr Thr Ile Lys Pro Asn Leu Gly Val Val Ser Thr Lys Asp Gln
        35                  40                  45
Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala Ser
    50                  55                  60
Asp Gly Val Gly Leu Gly His Gln Phe Leu Arg His Val Glu Arg Thr
65                  70                  75                  80
Lys Val Ile Val His Met Ile Asp Met Ser Gly Ser Glu Gly Arg Glu
                85                  90                  95
Pro Ile Glu Asp Tyr Lys Val Ile Asn Gln Glu Leu Ala Ala Tyr Glu
            100                 105                 110
Gln Arg Leu Glu Asp Arg Pro Gln Ile Val Val Ala Asn Lys Met Asp
        115                 120                 125
Leu Pro Glu Ser Gln Asp Asn Leu Asn Leu Phe Lys Glu Glu Ile Gly
```

```
    130                 135                 140
Glu Asp Val Pro Val Ile Pro Val Ser Thr Ile Thr Arg
145                 150                 155

<210> 555
<211> 300
<212> DNA
<213> Homo sapiens

<400> 555
tctagagatt gagaacaatt atggatacag aaatggttga ttccgtcaaa tatattcgag
60
attcggaatc atgtgaggct cgcgtgctgg agatcttagc cagaaggccg tccatgatgg
120
tgcagatctt gcgtggcgac ggcttaatta acgaagacca gagattagtc agattatggc
180
ttaataaagt acctagaatt gttcgcctgc ttctccggct tagtgtgttc gtcgctgcgg
240
caataggtgc ccgtgcggta tgggcggcgg cttccggtaa tcccgatctt gttcacgcgt
300

<210> 556
<211> 93
<212> PRT
<213> Homo sapiens

<400> 556
Met Asp Thr Glu Met Val Asp Ser Val Lys Tyr Ile Arg Asp Ser Glu
 1               5                  10                  15
Ser Cys Glu Ala Arg Val Leu Glu Ile Leu Ala Arg Arg Pro Ser Met
            20                  25                  30
Met Val Gln Ile Leu Arg Gly Asp Gly Leu Ile Asn Glu Asp Gln Arg
        35                  40                  45
Leu Val Arg Leu Trp Leu Asn Lys Val Pro Arg Ile Val Arg Leu Leu
    50                  55                  60
Leu Arg Leu Ser Val Phe Val Ala Ala Ala Ile Gly Ala Arg Ala Val
65                  70                  75                  80
Trp Ala Ala Ala Ser Gly Asn Pro Asp Leu Val His Ala
                85                  90

<210> 557
<211> 678
<212> DNA
<213> Homo sapiens

<400> 557
atcttcccgg tttatgagga gaatgcgctg cgtgtcgagt ttttcggcga cgaaattgag
60
gccctcacga cgatgcaccc gctcaccggg gaggtcatca gcgaggacga gcaggtctac
120
gtgttcccgg ctacccacta tgtcgccggc ccggaacgta tggagcgggc catagcgtcc
180
atccagcagg agctcgagga gcgcctggcc gttctagagc gtgatgggaa actgttggag
240
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gcccaacggt tacgtatgcg tactacctac gatatcgaga tgatgcagca ggtcggtgcc
300
tgtgctggca tcgaaaacta ttcgcggcac atcgacggac gcgctcccgg ctcagccccg
360
aactgtctgc ttgactactt tccggaagat tttgtgctcg tcattgatga atcccacgtg
420
accgtcccgc agattggcgg gatgtatgag ggggacatga gccgcaagcg gacattggta
480
gaacatggtt tccgactgcc cagcgcgatg gacaaccgtc ctctcaaatt cgacgagttc
540
acccagcgga tcggccagac tgtctacctg tccgccacgc ccggttcgta cgagaccgaa
600
cgagctcacg gcgtcgtcga acaaatcatt cgtccgacag gtctggtgga tccggagatt
660
atcgtcaagc ctacgcgt
678

<210> 558
<211> 226
<212> PRT
<213> Homo sapiens

<400> 558
Ile Phe Pro Val Tyr Glu Glu Asn Ala Leu Arg Val Glu Phe Phe Gly
1 5 10 15
Asp Glu Ile Glu Ala Leu Thr Thr Met His Pro Leu Thr Gly Glu Val
20 25 30
Ile Ser Glu Asp Glu Gln Val Tyr Val Phe Pro Ala Thr His Tyr Val
35 40 45
Ala Gly Pro Glu Arg Met Glu Arg Ala Ile Ala Ser Ile Gln Gln Glu
50 55 60
Leu Glu Glu Arg Leu Ala Val Leu Glu Arg Asp Gly Lys Leu Leu Glu
65 70 75 80
Ala Gln Arg Leu Arg Met Arg Thr Thr Tyr Asp Ile Glu Met Met Gln
85 90 95
Gln Val Gly Ala Cys Ala Gly Ile Glu Asn Tyr Ser Arg His Ile Asp
100 105 110
Gly Arg Ala Pro Gly Ser Ala Pro Asn Cys Leu Leu Asp Tyr Phe Pro
115 120 125
Glu Asp Phe Val Leu Val Ile Asp Glu Ser His Val Thr Val Pro Gln
130 135 140
Ile Gly Gly Met Tyr Glu Gly Asp Met Ser Arg Lys Arg Thr Leu Val
145 150 155 160
Glu His Gly Phe Arg Leu Pro Ser Ala Met Asp Asn Arg Pro Leu Lys
165 170 175
Phe Asp Glu Phe Thr Gln Arg Ile Gly Gln Thr Val Tyr Leu Ser Ala
180 185 190
Thr Pro Gly Ser Tyr Glu Thr Glu Arg Ala His Gly Val Val Glu Gln
195 200 205
Ile Ile Arg Pro Thr Gly Leu Val Asp Pro Glu Ile Ile Val Lys Pro
210 215 220
Thr Arg
225

<210> 559
<211> 335
<212> DNA
<213> Homo sapiens

<400> 559
ggatcctatg gagctcaagt tcaagaaaag aaactgtaaa catggaggtt ttgtgataaa
60
tggaatgcag tcagagggaa ggaactgccn gcttaaagtg tcctatgctg cgctttccag
120
agcaatacag tacacagtgg agggcgctac catggagtct ctgggtgaaa gttaggatgg
180
tatggtggca ccagccaaac ttctcagggt tcataggcag acagcagctc tggagtggaa
240
ctaaagtgta tccaggagct gaagcccctta atcagctagg gctcacacag agtcaaggta
300
gggtcaaaaa cattcagtct gggaccatat ctaga
335

<210> 560
<211> 92
<212> PRT
<213> Homo sapiens

<400> 560
Met Glu Cys Ser Gln Arg Glu Gly Thr Ala Xaa Leu Lys Cys Pro Met
 1   5   10   15
Leu Arg Phe Pro Glu Gln Tyr Ser Thr Gln Trp Arg Ala Leu Pro Trp
            20   25   30
Ser Leu Trp Val Lys Val Arg Met Val Trp Trp His Gln Pro Asn Phe
        35   40   45
Ser Gly Phe Ile Gly Arg Gln Gln Leu Trp Ser Gly Thr Lys Val Tyr
    50   55   60
Pro Gly Ala Glu Ala Leu Asn Gln Leu Gly Leu Thr Gln Ser Gln Gly
65   70   75   80
Arg Val Lys Asn Ile Gln Ser Gly Thr Ile Ser Arg
                85   90

<210> 561
<211> 477
<212> DNA
<213> Homo sapiens

<400> 561
ngcgcgcccc ctcctccgat ggcggcggag atccagccca agcctctgac ccgcaagccg
60
atcctgctgc agcggatgga ggggtcccag gaggtggtga atatggccgt gatcgtgccc
120
aaagaggagg gcgtcatcag cgtctccgag gacaggacag ttcgtgtttg gttaaagaga
180
gacagtggac agtattggcc aagcgtatac catgcaatgc cttgagttta tattgtcaga
240
agattataac aagatgactc ctgtgaaaaa ctatcaagcg catcagagca gagtgacgat
300

gatcctgttt gtcctggagc tggagtgggt gctgagcaca ggacaggaca agcaatttgc
360
ctggcactgc tctgagagtg ggcagcgcct gggaggttat cggaccagtg ctgtggcctc
420
aggcctgcaa tttgatgttg aaacccggca tgtgtttatc ggtgaccact caggcca
477

<210> 562
<211> 74
<212> PRT
<213> Homo sapiens

<400> 562
Xaa Ala Pro Pro Pro Pro Met Ala Ala Glu Ile Gln Pro Lys Pro Leu
 1   5   10   15
Thr Arg Lys Pro Ile Leu Leu Gln Arg Met Glu Gly Ser Gln Glu Val
            20   25   30
Val Asn Met Ala Val Ile Val Pro Lys Glu Glu Gly Val Ile Ser Val
        35   40   45
Ser Glu Asp Arg Thr Val Arg Val Trp Leu Lys Arg Asp Ser Gly Gln
    50   55   60
Tyr Trp Pro Ser Val Tyr His Ala Met Pro
65   70

<210> 563
<211> 403
<212> DNA
<213> Homo sapiens

<400> 563
ccatggcaga cagggagctg agcggcctgc ggacccaggt gcaccagagc atggtgcccc
60
tgctcctaca cctgaaggac caatgcccaa ctgtcgccac gggcaatgcc caccccaaga
120
aaaggaaggg aaaaggcctc aaccttggcc agggctggaa cccacaggag gccagggtac
180
ggggcagacg gatggcagca gcactgcctg agagttgggg gagctcccac ggggcagcaa
240
gtggcgggca gagggtctgg ccatctgcac tggtttctgt gaccacagtt ggcctgcccg
300
ctcccccact gcaccactga cgaagcgaga ccctgcctca aaaaaaaaaa caaaaacaaa
360
aacaaaaaca aaactcaaac ttcacactgg agatctgtgc aat
403

<210> 564
<211> 105
<212> PRT
<213> Homo sapiens

<400> 564
Met Ala Asp Arg Glu Leu Ser Gly Leu Arg Thr Gln Val His Gln Ser
 1   5   10   15
Met Val Pro Leu Leu Leu His Leu Lys Asp Gln Cys Pro Thr Val Ala

```
            20                  25                  30
Thr Gly Asn Ala His Pro Lys Lys Arg Lys Gly Lys Gly Leu Asn Leu
        35                  40                  45
Gly Gln Gly Trp Asn Pro Gln Glu Ala Arg Val Arg Gly Arg Arg Met
    50                  55                  60
Ala Ala Ala Leu Pro Glu Ser Trp Gly Ser Ser His Gly Ala Ala Ser
65                  70                  75                  80
Gly Gly Gln Arg Val Trp Pro Ser Ala Leu Val Ser Val Thr Thr Val
                85                  90                  95
Gly Leu Pro Ala Pro Pro Leu His His
            100                 105
```

<210> 565
<211> 311
<212> DNA
<213> Homo sapiens

<400> 565
ncctctccat ggagcagccc catcttcact cttcacctgg ggccaggcct tccacagcag
60
ccaccaccca gcgaccacag agaggctgcg cggaggacac aggagagagg gagcccacgg
120
gcacgatctc caccggcttt cccagctccc tgggtcagcc ccacgggacc tctcctcctc
180
tctcccacat ctccaagcca gccttgcata tagtaagagc tgtgatcagg atggaaagag
240
gcttgggccg cacagacctg gacaatgtcc cagtgagggc tggaggtgct agaagggcac
300
aggaggcccc n
311

<210> 566
<211> 101
<212> PRT
<213> Homo sapiens

<400> 566
```
Met Glu Gln Pro His Leu His Ser Ser Pro Gly Ala Arg Pro Ser Thr
 1               5                  10                  15
Ala Ala Thr Thr Gln Arg Pro Gln Arg Gly Cys Ala Glu Asp Thr Gly
            20                  25                  30
Glu Arg Glu Pro Thr Gly Thr Ile Ser Thr Gly Phe Pro Ser Ser Leu
        35                  40                  45
Gly Gln Pro His Gly Thr Ser Pro Pro Leu Ser His Ile Ser Lys Pro
    50                  55                  60
Ala Leu His Ile Val Arg Ala Val Ile Arg Met Glu Arg Gly Leu Gly
65                  70                  75                  80
Arg Thr Asp Leu Asp Asn Val Pro Val Arg Ala Gly Gly Ala Arg Arg
                85                  90                  95
Ala Gln Glu Ala Pro
            100
```

<210> 567
<211> 929

<212> DNA
<213> Homo sapiens

<400> 567
atcacatcgg tcgctgaacc ccgacgagcc tcaccttgtc gaaatattca tccttgagat
60
cagcccacgt gccgtcgacc tctacctcgg tgagggtcgc gggcgggtac caacagccga
120
cctcgtcctc ggctccactc atggcggcaa gttccgctgc cagtccgggg atcgtcgggg
180
catgggcgat gatgagcagg ttatccacat cgtcgtcgat ttctccgatg cgccgacgca
240
cggtatcagt gccgcagtaa tagagggctc gcatgaattc gaccggacaa tccagttgga
300
ggcagtccca ggtctggcgg gtgcgtaggg catcggagac cagagcatgt ccaacattgc
360
gcagtcctaa acgcgtgccg acctcacggg cctgacggcg ccccacgtcg gtgagcggac
420
gctcccgatc cccgcccgga gcatgggatg cgggctgtgc atgtctcatg aggaacagag
480
tgtgcatgga tccatcgttg cacttcgcgg tcgccgcggt tctacgatgt tggcatgccg
540
ttgacggatt tgggcattga tgaggcgcgt acctaccgcc cgaacgtccc tgaacccgat
600
ggtttcgact ctttttgggc cgagaccctc gatgagtatt ccggcgttcc ccaagatctg
660
acggcggtgc ctttcgataa ccgtcaggct ctgatagata cctgggattt gtcgtgggtg
720
gggtatcaca actctcgggt gagcgggtga ttacatgccc cagccgctgt gaacggccca
780
ttccccccttg tcatcgagta cctcgggtac tcgagttcgc gtggtgtgcc gattggatca
840
gtcttcgctg ctgctggcta tgcacatatc gtcgtcgatc cacgtggtca ggggtggggc
900
cacccaacct tgacggaaaa ctgtccgga
929

<210> 568
<211> 71
<212> PRT
<213> Homo sapiens

<400> 568
Met Pro Leu Thr Asp Leu Gly Ile Asp Glu Ala Arg Thr Tyr Arg Pro
1 5 10 15
Asn Val Pro Glu Pro Asp Gly Phe Asp Ser Phe Trp Ala Glu Thr Leu
20 25 30
Asp Glu Tyr Ser Gly Val Pro Gln Asp Leu Thr Ala Val Pro Phe Asp
35 40 45
Asn Arg Gln Ala Leu Ile Asp Thr Trp Asp Leu Ser Trp Val Gly Tyr
50 55 60
His Asn Ser Arg Val Ser Gly
65 70

<210> 569
<211> 371
<212> DNA
<213> Homo sapiens

<400> 569
ncgcaaactt caacggtgcc atctgccata ttccagggat gccagatttg gatggaaaat
60
accatatcac tctcgattca gaattcgtac ttgatttagt ggcctttaac aaaacgctac
120
ctgtcgatta cttaatggtc gaaggaacgg aacttgtgta ttcaaacatg gaagaactac
180
ctgaatgccc atattatcca aaagatcaaa agccaatcgt gattgggaaa aacacaaaac
240
tcaaggaaca accaacagcc gttgctctct tctcggatgt tgataaacgg ccagagatta
300
aatcaaaaat cttagaccgc tatgataatg atattgaaat ccgtacttgg ggcggtactt
360
cccatgtcta n
371

<210> 570
<211> 111
<212> PRT
<213> Homo sapiens

<400> 570
Met Pro Asp Leu Asp Gly Lys Tyr His Ile Thr Leu Asp Ser Glu Phe
 1   5   10   15
Val Leu Asp Leu Val Ala Phe Asn Lys Thr Leu Pro Val Asp Tyr Leu
            20   25   30
Met Val Glu Gly Thr Glu Leu Val Tyr Ser Asn Met Glu Glu Leu Pro
        35   40   45
Glu Cys Pro Tyr Tyr Pro Lys Asp Gln Lys Pro Ile Val Ile Gly Lys
    50   55   60
Asn Thr Lys Leu Lys Glu Gln Pro Thr Ala Val Ala Leu Phe Ser Asp
65   70   75   80
Val Asp Lys Arg Pro Glu Ile Lys Ser Lys Ile Leu Asp Arg Tyr Asp
                85   90   95
Asn Asp Ile Glu Ile Arg Thr Trp Gly Gly Thr Ser His Val Xaa
            100   105   110

<210> 571
<211> 407
<212> DNA
<213> Homo sapiens

<400> 571
nacgcgtatc ttcgctggtc cacaccagac gtggcattaa acgacgtcac aagaacgaca
60
ccgggccttg acgggcccac gcacgaagag gccaagacac tgaccgagac tactgtttcc
120
gttcccacct ccttcgccga cctcggcgtc cgagaagata tctgccaggc gctggaaggg
180

gtgggaattg tctccccgtt cccgatccag gccatgtcga tcccgattgc cgtcgagggc
240
acggatctta ttgggcaggc gcgtactggc actggcaaaa cactcgcctt cggcatcacc
300
atcttgcagc gcatcaccct gcccggtgac gaaggttggg aagaactcac caccaaaggc
360
aagcccccaa gcactcgtga tgtgccccta cccgggagct aggtcgg
407

<210> 572
<211> 100
<212> PRT
<213> Homo sapiens

<400> 572
Leu Thr Glu Thr Thr Val Ser Val Pro Thr Ser Phe Ala Asp Leu Gly
1 5 10 15
Val Arg Glu Asp Ile Cys Gln Ala Leu Glu Gly Val Gly Ile Val Ser
20 25 30
Pro Phe Pro Ile Gln Ala Met Ser Ile Pro Ile Ala Val Glu Gly Thr
35 40 45
Asp Leu Ile Gly Gln Ala Arg Thr Gly Thr Gly Lys Thr Leu Ala Phe
50 55 60
Gly Ile Thr Ile Leu Gln Arg Ile Thr Leu Pro Gly Asp Glu Gly Trp
65 70 75 80
Glu Glu Leu Thr Thr Lys Gly Lys Pro Pro Ser Thr Arg Asp Val Pro
85 90 95
Leu Pro Gly Ser
100

<210> 573
<211> 393
<212> DNA
<213> Homo sapiens

<400> 573
acgcgtctac cgtaggatcc atgaccttcc gcaagaccga ccaccacaag aacgccattg
60
actacgaggt cgccggacta atgtggctcg ctgctgcccg gccagatggg gccggcatcg
120
tcgaggtgct cgaccacggc aagggatggc tcaccgaacc cgaattgtcc actgggcacc
180
ccacccgcga ggcagccgag gactttggcc gccgactggc tcacacccac gcagccgggg
240
cctcacacct gggggctgca cctgacgggt ttgttcccga cgatgggtat atcggccgtg
300
ctcccctgcc actgccgtcc gaaccaatct cctcctgggg agagttttac gctcagtgcc
360
gcatcgaacc atatatggac agtctcgacg ctg
393

<210> 574
<211> 124
<212> PRT

<213> Homo sapiens

<400> 574
Met Thr Phe Arg Lys Thr Asp His His Lys Asn Ala Ile Asp Tyr Glu
1 5 10 15
Val Ala Gly Leu Met Trp Leu Ala Ala Ala Arg Pro Asp Gly Ala Gly
20 25 30
Ile Val Glu Val Leu Asp His Gly Lys Gly Trp Leu Thr Glu Pro Glu
35 40 45
Leu Ser Thr Gly His Pro Thr Arg Glu Ala Ala Glu Asp Phe Gly Arg
50 55 60
Arg Leu Ala His Thr His Ala Ala Gly Ala Ser His Leu Gly Ala Ala
65 70 75 80
Pro Asp Gly Phe Val Pro Asp Asp Gly Tyr Ile Gly Arg Ala Pro Leu
85 90 95
Pro Leu Pro Ser Glu Pro Ile Ser Ser Trp Gly Glu Phe Tyr Ala Gln
100 105 110
Cys Arg Ile Glu Pro Tyr Met Asp Ser Leu Asp Ala
115 120

<210> 575
<211> 372
<212> DNA
<213> Homo sapiens

<400> 575
nntatccatg cagacatggg accagggtct ctgagggcag gaagcaaagt gggtgagggg
60
gatgggacaa gatgccctgg tgctaaggcc tctggagctg gagctggtta tagggatgat
120
accaggcacc ctgagtcact cgcacctcac aatggggccg cttctgggag ccagtgggct
180
tatggggctg gcaatgtgct gggttatgag gatggatcag aacttccagg gcctcaggga
240
actggggtca gaacagccta tggagaaagg tcaaggggcc ttgggcctag gagtacaggg
300
ccaggggtg aggcaggctt tagagatggt tcaggaggcc tccaaggaat gggatcagca
360
gatgggcccg gt
372

<210> 576
<211> 124
<212> PRT
<213> Homo sapiens

<400> 576
Xaa Ile His Ala Asp Met Gly Pro Gly Ser Leu Arg Ala Gly Ser Lys
1 5 10 15
Val Gly Glu Gly Asp Gly Thr Arg Cys Pro Gly Ala Lys Ala Ser Gly
20 25 30
Ala Gly Ala Gly Tyr Arg Asp Asp Thr Arg His Pro Glu Ser Leu Ala
35 40 45
Pro His Asn Gly Ala Ala Ser Gly Ser Gln Trp Ala Tyr Gly Ala Gly

```
    50                  55                  60
Asn Val Leu Gly Tyr Glu Asp Gly Ser Glu Leu Pro Gly Pro Gln Gly
65                  70                  75                  80
Thr Gly Val Arg Thr Ala Tyr Gly Glu Arg Ser Arg Gly Leu Gly Pro
                85                  90                  95
Arg Ser Thr Gly Pro Gly Gly Glu Ala Gly Phe Arg Asp Gly Ser Gly
            100                 105                 110
Gly Leu Gln Gly Met Gly Ser Ala Asp Gly Pro Gly
        115                 120
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<210> 577
<211> 432
<212> DNA
<213> Homo sapiens

<400> 577
nagcgcaatg tcatgatgtc ggatttgtca atgtcggatt tctcatccca gccatcaccc
60
ccgcagcgcc gggcgcggat gaccagcggc cagcgccgtg aacagctcat cagcgtggcc
120
cgtcgcctct tcgcagacaa tggcatggca gggacctccg tcgaggagat cgccgctacc
180
gcgggagtct ccaaacccgt catctacgag catttcgggt ccaaggatgg gctgtacgcc
240
gtcgtcgtag accgcgaggt acgccaccta caagattccc tcaacgccgc catgacccgc
300
ccaaagcaag gcccgaaacg caccctggag tcagcggtac tggccctgct ggactacatc
360
gacgaccgtc cagacggttt tcggatcatc tcgcgagact cctcggtcgg ttcagccacc
420
ggttcgtacg cg
432

<210> 578
<211> 118
<212> PRT
<213> Homo sapiens

<400> 578
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Met Thr Ser Gly Gln Arg Arg Glu Gln Leu Ile Ser Val Ala Arg Arg
 1               5                  10                  15
Leu Phe Ala Asp Asn Gly Met Ala Gly Thr Ser Val Glu Glu Ile Ala
            20                  25                  30
Ala Thr Ala Gly Val Ser Lys Pro Val Ile Tyr Glu His Phe Gly Ser
        35                  40                  45
Lys Asp Gly Leu Tyr Ala Val Val Val Asp Arg Glu Val Arg His Leu
    50                  55                  60
Gln Asp Ser Leu Asn Ala Ala Met Thr Arg Pro Lys Gln Gly Pro Lys
65                  70                  75                  80
Arg Thr Leu Glu Ser Ala Val Leu Ala Leu Leu Asp Tyr Ile Asp Asp
                85                  90                  95
Arg Pro Asp Gly Phe Arg Ile Ile Ser Arg Asp Ser Ser Val Gly Ser
            100                 105                 110
Ala Thr Gly Ser Tyr Ala
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115

<210> 579
<211> 320
<212> DNA
<213> Homo sapiens

<400> 579
ggccccaaac actccgacct cagctggtcc agcatgctgg gcaccgtgct gctgctggcc
60
ctgctcccag ggatcaccac cttacccagc gggccacctg ctcccccgtt ccccgcggcg
120
cccggccccc ggctgcgcag acccctcttc agcctgaagc tgtccgacac agaggacgtc
180
tttcctcgcc gcgcggggcc gctcgaggtc ccggccgaca gccgcgtgtt cgtgcaggcg
240
gccttggccc gtccctcccc gcgctggggc ctggccctgc accgctgctc agtgacgccg
300
tcctcacgcc cggccccggg
320

<210> 580
<211> 95
<212> PRT
<213> Homo sapiens

<400> 580
Met Leu Gly Thr Val Leu Leu Leu Ala Leu Leu Pro Gly Ile Thr Thr
1 5 10 15
Leu Pro Ser Gly Pro Pro Ala Pro Pro Phe Pro Ala Ala Pro Gly Pro
20 25 30
Trp Leu Arg Arg Pro Leu Phe Ser Leu Lys Leu Ser Asp Thr Glu Asp
35 40 45
Val Phe Pro Arg Arg Ala Gly Pro Leu Glu Val Pro Ala Asp Ser Arg
50 55 60
Val Phe Val Gln Ala Ala Leu Ala Arg Pro Ser Pro Arg Trp Gly Leu
65 70 75 80
Ala Leu His Arg Cys Ser Val Thr Pro Ser Ser Arg Pro Ala Pro
85 90 95

<210> 581
<211> 419
<212> DNA
<213> Homo sapiens

<400> 581
nacgacggca accattcgct gtggaaggag ctgaacggcc agctcgacgt gcagtttttc
60
cacgtcggca tgggcttcaa gacgccagta cgcatgcaca gcgtcgaccc caagacccgc
120
gaagcccgcg aggtgcattt ccgcccgtcg ctgttcaact atgccaagac cacggtggac
180
accaagcagc tgaccggcga cctgggtttc tccggtttca agctgttcaa ggcgccggaa
240

ctggatcgcc atgacgtgct gtcgtttctc ggcgccagtt acttccgtgc ggtggacgca
300
acccgccagt acggcctctc cgcacgcggc ctggcgattg atacctacgc gaaaaaacgc
360
gaggaattcc ccgacttcac gcagttctgg ttcgaaaccc cgagcaagga cccacgcgt
419

<210> 582
<211> 139
<212> PRT
<213> Homo sapiens

<400> 582
Xaa Asp Gly Asn His Ser Leu Trp Lys Glu Leu Asn Gly Gln Leu Asp
 1   5   10   15
Val Gln Phe Phe His Val Gly Met Gly Phe Lys Thr Pro Val Arg Met
            20   25   30
His Ser Val Asp Pro Lys Thr Arg Glu Ala Arg Glu Val His Phe Arg
        35   40   45
Pro Ser Leu Phe Asn Tyr Ala Lys Thr Thr Val Asp Thr Lys Gln Leu
    50   55   60
Thr Gly Asp Leu Gly Phe Ser Gly Phe Lys Leu Phe Lys Ala Pro Glu
65   70   75   80
Leu Asp Arg His Asp Val Leu Ser Phe Leu Gly Ala Ser Tyr Phe Arg
                85   90   95
Ala Val Asp Ala Thr Arg Gln Tyr Gly Leu Ser Ala Arg Gly Leu Ala
            100   105   110
Ile Asp Thr Tyr Ala Lys Lys Arg Glu Glu Phe Pro Asp Phe Thr Gln
        115   120   125
Phe Trp Phe Glu Thr Pro Ser Lys Asp Pro Arg
    130   135

<210> 583
<211> 407
<212> DNA
<213> Homo sapiens

<400> 583
cttttgatca atgctgatgg cacgaagcta tcgaaaaggt cgggtgatgt ccgcgtagct
60
gattatatgg agcagggatg ggagccggag acgctggtga acctagttgc cctcacgggc
120
tatagctatg cgaatttgga gcatgctgat catgatgtca agacgatgaa cgaactcatc
180
cgtgactttg agcttactcg tatctcccat acgcgagcca cactccccat ggacaagctt
240
gtgtttttga acaagcatca cttgacaaat aagctggcgc tcgccacgac gtgtgagcag
300
accaaacaag acctattgtc gcgtatccgg ccgatcacta cctcgtggta cggcgattat
360
tcagatgatt atatcctgcg cgtcgtaaca ctgggacccc aacgcgt
407

<210> 584

<211> 135
<212> PRT
<213> Homo sapiens

<400> 584
Leu Leu Ile Asn Ala Asp Gly Thr Lys Leu Ser Lys Arg Ser Gly Asp
1 5 10 15
Val Arg Val Ala Asp Tyr Met Glu Gln Gly Trp Glu Pro Glu Thr Leu
20 25 30
Val Asn Leu Val Ala Leu Thr Gly Tyr Ser Tyr Ala Asn Leu Glu His
35 40 45
Ala Asp His Asp Val Lys Thr Met Asn Glu Leu Ile Arg Asp Phe Glu
50 55 60
Leu Thr Arg Ile Ser His Thr Arg Ala Thr Leu Pro Met Asp Lys Leu
65 70 75 80
Val Phe Leu Asn Lys His His Leu Thr Asn Lys Leu Ala Leu Ala Thr
85 90 95
Thr Cys Glu Gln Thr Lys Gln Asp Leu Leu Ser Arg Ile Arg Pro Ile
100 105 110
Thr Thr Ser Trp Tyr Gly Asp Tyr Ser Asp Asp Tyr Ile Leu Arg Val
115 120 125
Val Thr Leu Gly Pro Gln Arg
130 135

<210> 585
<211> 502
<212> DNA
<213> Homo sapiens

<400> 585
nnacgcgtcc tcgctggata tgaggctgtg aagagggaac gctgcgtcat tgatctggac
60
gatattttgt tgtgcgcggt gggattgttg gttcagcacc gtgacatcac tgaggagatt
120
cgggctcggt accgacattt cgttgtcgac gaataccagg acgtttctcc gctgcagcat
180
aggttgcttg aactgtggtt tggcgatcga aatgatgtat gcgtcgtggg agatccgcac
240
caggccattc actcttatgc aggcgcacga gctgactacc tcctcgactt cgttgccgat
300
catcctggcg ctaaacgcat cgatttggtt cgcaactacc gctccactcc cgagatcgtt
360
cagttggcca atgaagttct tgtcaaccgt atgactccag aggaggcttt ggaacatggc
420
aggggagtca cattggtttc gcggggtcga tccggtcccg agcccatcta tcaggctctc
480
ggggacgatg cctccgaagc tt
502

<210> 586
<211> 167
<212> PRT
<213> Homo sapiens

<400> 586
Xaa Arg Val Leu Ala Gly Tyr Glu Ala Val Lys Arg Glu Arg Cys Val
1 5 10 15
Ile Asp Leu Asp Asp Ile Leu Leu Cys Ala Val Gly Leu Leu Val Gln
20 25 30
His Arg Asp Ile Thr Glu Glu Ile Arg Ala Arg Tyr Arg His Phe Val
35 40 45
Val Asp Glu Tyr Gln Asp Val Ser Pro Leu Gln His Arg Leu Leu Glu
50 55 60
Leu Trp Phe Gly Asp Arg Asn Asp Val Cys Val Val Gly Asp Pro His
65 70 75 80
Gln Ala Ile His Ser Tyr Ala Gly Ala Arg Ala Asp Tyr Leu Leu Asp
85 90 95
Phe Val Ala Asp His Pro Gly Ala Lys Arg Ile Asp Leu Val Arg Asn
100 105 110
Tyr Arg Ser Thr Pro Glu Ile Val Gln Leu Ala Asn Glu Val Leu Val
115 120 125
Asn Arg Met Thr Pro Glu Glu Ala Leu Glu His Gly Arg Gly Val Thr
130 135 140
Leu Val Ser Arg Gly Arg Ser Gly Pro Glu Pro Ile Tyr Gln Ala Leu
145 150 155 160
Gly Asp Asp Ala Ser Glu Ala
165

<210> 587
<211> 746
<212> DNA
<213> Homo sapiens

<400> 587
gcgtcctgcc tcgagggcct cgggagcttc cgctgcctct gttggccagg ctacagcggc
60
gagctgtgcg aggtggacga ggacgagtgt gcatcgagcc cctgccagca tgggggccga
120
tgcctgcagc gctctgaccc ggccctctac gggggtgtcc aggccgcctt ccctggcgcc
180
ttcagcttcc gccatgctgc gggtttcctg tgccactgcc ctcctggctt tgagggagcc
240
gactgcggtg tggaggtgga cgagtgtgcc tcacggccat gcctcaatgg aggccactgc
300
caggacctgc ccaatggctt ccagtgtcac tgcccagatg gctacgcagg gccgacatgt
360
gaggaagatg tggatgaatg cctgtccgat ccctgcctgc acggcggaac ctgcagtgac
420
actgtggcag gctatatctg caggtgccca gagacctggg gtgggcgcga ctgttctgtg
480
cagctcactg gctgccaggg ccacacctgc ccgctggctg ccacctgcat ccctatcttc
540
gagtctgggg tccacagtta cgtctgccac tgcccacctg gtacccatgg accgttctgt
600
ggccagaata ccaccttctc tgtgatggct gggagcccca ttcaggcatc agtgccagct
660
ggtggccccc tgggtctggc actgaggttt cgcaccacac tgcccgctgg gaccttggcc
720

actcgcaatg acaccaagga aagctt
746

<210> 588
<211> 248
<212> PRT
<213> Homo sapiens

<400> 588
Ala Ser Cys Leu Glu Gly Leu Gly Ser Phe Arg Cys Leu Cys Trp Pro
1 5 10 15
Gly Tyr Ser Gly Glu Leu Cys Glu Val Asp Glu Asp Glu Cys Ala Ser
20 25 30
Ser Pro Cys Gln His Gly Gly Arg Cys Leu Gln Arg Ser Asp Pro Ala
35 40 45
Leu Tyr Gly Gly Val Gln Ala Ala Phe Pro Gly Ala Phe Ser Phe Arg
50 55 60
His Ala Ala Gly Phe Leu Cys His Cys Pro Pro Gly Phe Glu Gly Ala
65 70 75 80
Asp Cys Gly Val Glu Val Asp Glu Cys Ala Ser Arg Pro Cys Leu Asn
85 90 95
Gly Gly His Cys Gln Asp Leu Pro Asn Gly Phe Gln Cys His Cys Pro
100 105 110
Asp Gly Tyr Ala Gly Pro Thr Cys Glu Glu Asp Val Asp Glu Cys Leu
115 120 125
Ser Asp Pro Cys Leu His Gly Gly Thr Cys Ser Asp Thr Val Ala Gly
130 135 140
Tyr Ile Cys Arg Cys Pro Glu Thr Trp Gly Gly Arg Asp Cys Ser Val
145 150 155 160
Gln Leu Thr Gly Cys Gln Gly His Thr Cys Pro Leu Ala Ala Thr Cys
165 170 175
Ile Pro Ile Phe Glu Ser Gly Val His Ser Tyr Val Cys His Cys Pro
180 185 190
Pro Gly Thr His Gly Pro Phe Cys Gly Gln Asn Thr Thr Phe Ser Val
195 200 205
Met Ala Gly Ser Pro Ile Gln Ala Ser Val Pro Ala Gly Gly Pro Leu
210 215 220
Gly Leu Ala Leu Arg Phe Arg Thr Thr Leu Pro Ala Gly Thr Leu Ala
225 230 235 240
Thr Arg Asn Asp Thr Lys Glu Ser
245

<210> 589
<211> 381
<212> DNA
<213> Homo sapiens

<400> 589
atctcacaag tacaattaca gtctcaagaa ctgagctatc agcaaaagca aggtcttcag
60
ccagtacctc tgcaagccac tatgagtgct gcaactggta tccagccatc gcctgtaaat
120
gtggttggtg taacttcagc tttaggtcag cagccttcca tttccagttt ggctcaaccc
180

cagctaccat attctcaggc ggctcctcca gtgcaaactc cccttccagg ggcaccacca
240
ccccaacagt tacagtatgg acaacagcaa ccaatggttt ctacacagat ggccccaggc
300
catgtcaaat cagtgactca aaatcctgct tcagagtatg tacaacagca gccaattctt
360
caaacagcaa tgtcctccgg a
381

<210> 590
<211> 127
<212> PRT
<213> Homo sapiens

<400> 590
Ile Ser Gln Val Gln Leu Gln Ser Gln Glu Leu Ser Tyr Gln Gln Lys
1 5 10 15
Gln Gly Leu Gln Pro Val Pro Leu Gln Ala Thr Met Ser Ala Ala Thr
20 25 30
Gly Ile Gln Pro Ser Pro Val Asn Val Val Gly Val Thr Ser Ala Leu
35 40 45
Gly Gln Gln Pro Ser Ile Ser Ser Leu Ala Gln Pro Gln Leu Pro Tyr
50 55 60
Ser Gln Ala Ala Pro Pro Val Gln Thr Pro Leu Pro Gly Ala Pro Pro
65 70 75 80
Pro Gln Gln Leu Gln Tyr Gly Gln Gln Gln Pro Met Val Ser Thr Gln
85 90 95
Met Ala Pro Gly His Val Lys Ser Val Thr Gln Asn Pro Ala Ser Glu
100 105 110
Tyr Val Gln Gln Gln Pro Ile Leu Gln Thr Ala Met Ser Ser Gly
115 120 125

<210> 591
<211> 684
<212> DNA
<213> Homo sapiens

<400> 591
tcgaccatgg atcatctgcg ccacggcatc cacctgcgtg gttatgcgca gaagaacccg
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aagcaggaat acaagcgcga gtcgttcacc ctgttctccg agctgctgga ctcgatcaag
120
cgcgattcga ttcgggtcct cttccacgtc caggggccgg gggaaaaatc cgtatcgaaa
180
naaaaagcgc gcctgcgtca ggaagccgaa gccctggccc agcgcatgca gttcgagcac
240
gctgaagccc caggcctgga cgcgccggaa atcctcggtg aagaagtcga tgtcgccctg
300
gccaccgcgc cggtacgcaa cgagcagaag ctgggccgta acgaactgtg ctactgcggt
360
tcgggcaaga agtacaagca ctgccacggt cagatcagct aaggtcttta ccggatactg
420
aaatacctgc gccgcgaccg gcattagccg tcgcggcgtt tttccatttg aaacactgcc
480

cttgtgacgg cagtgcagat atcacattaa aaggagggca ttcatgggtg ttggttctgg
540
gtccttggcc tacgttgcac ccggttgccg gttttgaact cggtatcgcc tcggccggta
600
tcaagcgccc tgggcgcaag gatgtggtgg cgatgcgctg cgccgaaggt tccacggtgg
660
cgggggtgtt taccctcaac gcgt
684

<210> 592
<211> 133
<212> PRT
<213> Homo sapiens

<400> 592
Ser Thr Met Asp His Leu Arg His Gly Ile His Leu Arg Gly Tyr Ala
1 5 10 15
Gln Lys Asn Pro Lys Gln Glu Tyr Lys Arg Glu Ser Phe Thr Leu Phe
20 25 30
Ser Glu Leu Leu Asp Ser Ile Lys Arg Asp Ser Ile Arg Val Leu Phe
35 40 45
His Val Gln Gly Pro Gly Glu Lys Ser Val Ser Lys Xaa Lys Ala Arg
50 55 60
Leu Arg Gln Glu Ala Glu Ala Leu Ala Gln Arg Met Gln Phe Glu His
65 70 75 80
Ala Glu Ala Pro Gly Leu Asp Ala Pro Glu Ile Leu Gly Glu Glu Val
85 90 95
Asp Val Ala Leu Ala Thr Ala Pro Val Arg Asn Glu Gln Lys Leu Gly
100 105 110
Arg Asn Glu Leu Cys Tyr Cys Gly Ser Gly Lys Lys Tyr Lys His Cys
115 120 125
His Gly Gln Ile Ser
130

<210> 593
<211> 615
<212> DNA
<213> Homo sapiens

<400> 593
nnacgcgtgc agaccgcgcg gagtctcgct ccggtgcgga tagcgttagg ctcccaaacc
60
tgtgaaaccg tcacggtaga gcgtcgtggc gggctaccac ttagagcggc ccgattcacc
120
gataccatcc ccgcgccgct aggccagcca cgatggtcga cggccaccat ccagacccca
180
gtcataccta ctacacgtgg tcgattcgtg atcggccccg tcatgatgcg caccatcgac
240
ccgtttggca tggcccgcca tcacaccgat ctcggtcagg ttgccgaagt cattgtcacg
300
ccaaggatcg tcgatttggg cgcctccggg gagctcgggg gtcagggatt cgacacaagg
360
tcctcagcga tccatgccgg acgacgtggt cccgacgatg ccatggtgcg cgattggcac
420

accggagact cggtgcgacg cattcactgg cgctccaccg ctcaccgcgg ggacctcatg
480
gtccgatgcg aggagcaggc ctggaaccca tccgtcgtca tcgtgttgga ttctcgggct
540
cggcgtcacg ctggaactgg ccccgacgca tcctttgaat gggccgtcaa cgcggtggca
600
tccatctcga cgcgt
615

<210> 594
<211> 205
<212> PRT
<213> Homo sapiens

<400> 594
Xaa Arg Val Gln Thr Ala Arg Ser Leu Ala Pro Val Arg Ile Ala Leu
1 5 10 15
Gly Ser Gln Thr Cys Glu Thr Val Thr Val Glu Arg Arg Gly Gly Leu
20 25 30
Pro Leu Arg Ala Ala Arg Phe Thr Asp Thr Ile Pro Ala Pro Leu Gly
35 40 45
Gln Pro Arg Trp Ser Thr Ala Thr Ile Gln Thr Pro Val Ile Pro Thr
50 55 60
Thr Arg Gly Arg Phe Val Ile Gly Pro Val Met Met Arg Thr Ile Asp
65 70 75 80
Pro Phe Gly Met Ala Arg His His Thr Asp Leu Gly Gln Val Ala Glu
85 90 95
Val Ile Val Thr Pro Arg Ile Val Asp Leu Gly Ala Ser Gly Glu Leu
100 105 110
Gly Gly Gln Gly Phe Asp Thr Arg Ser Ser Ala Ile His Ala Gly Arg
115 120 125
Arg Gly Pro Asp Asp Ala Met Val Arg Asp Trp His Thr Gly Asp Ser
130 135 140
Val Arg Arg Ile His Trp Arg Ser Thr Ala His Arg Gly Asp Leu Met
145 150 155 160
Val Arg Cys Glu Glu Gln Ala Trp Asn Pro Ser Val Val Ile Val Leu
165 170 175
Asp Ser Arg Ala Arg Arg His Ala Gly Thr Gly Pro Asp Ala Ser Phe
180 185 190
Glu Trp Ala Val Asn Ala Val Ala Ser Ile Ser Thr Arg
195 200 205

<210> 595
<211> 303
<212> DNA
<213> Homo sapiens

<400> 595
acgcgtccta gccgcagtga atgttgctga accccggtga cctcacagtg gaggggcggc
60
cccatggggc catcggaccg cgccgcgcgg gggcgttcgc cagggcctcc gcagaagccc
120
gcctgtgccc gcaaccgccc cgaaattctc tccctggcac cgtgtccgct ttacggagcc
180

cggagcaagg ctcagaaaaa tgtcccagcc aaaaacatgg tacatgcctg tcatcaggca
240
agtcttcaaa gagcggctgg gaccaggggc cgagggacct cgtttagagg cggcttaggg
300
gga
303

<210> 596
<211> 88
<212> PRT
<213> Homo sapiens

<400> 596
Met Leu Leu Asn Pro Gly Asp Leu Thr Val Glu Gly Arg Pro His Gly
1 5 10 15
Ala Ile Gly Pro Arg Arg Ala Gly Ala Phe Ala Arg Ala Ser Ala Glu
20 25 30
Ala Arg Leu Cys Pro Gln Pro Pro Arg Asn Ser Leu Pro Gly Thr Val
35 40 45
Ser Ala Leu Arg Ser Pro Glu Gln Gly Ser Glu Lys Cys Pro Ser Gln
50 55 60
Lys His Gly Thr Cys Leu Ser Ser Gly Lys Ser Ser Lys Ser Gly Trp
65 70 75 80
Asp Gln Gly Pro Arg Asp Leu Val
85

<210> 597
<211> 2709
<212> DNA
<213> Homo sapiens

<400> 597
nacgcgtgca cgcagtgcgg caaagccttc cgctggaagt ccaactttaa tttgcacaag
60
aagaaccaca tggtggagaa gacctacgaa tgtaaagaat gcgggaaatc ctttggcgat
120
ctcgtgtccc ggaggaaaca catgaggatt cacatcgtca agaaacccgt ggaatgtcgg
180
cagtgcggga agaccttccg aaaccagtcc atccttaaga ctcacatgaa ctctcacact
240
ggagagaaac catacgggtg cgatctctgc gggaaagctt tcagcgcgag ttcaaacctc
300
accgcacaca ggaagataca cacgcaagag agacgctacg aatgcgccgc ctgcgggaaa
360
gtcttcggtg actatttatc ccggcggagg cacatgagcg ttcaccttgt aaagaaacga
420
gttgagtgta ggcattgtgg caaggccttc aggaaccagt caacgctgaa gacgcacatg
480
cgaagccaca cgggggagaa accgtacgaa tgcgatcact gtgggaaggc cttcagcata
540
ggctccaacc tgaatgtgca caggcggatc cacaccgggg agaagcccta cgaatgcctt
600
gtctgcggga aagccttcag cgaccactca tccctcagga gccacgtgaa aactcaccgg
660

ggagagaagc tctttnngtg tcatccgtgt ggaaaaggct ccagtgagcg cgccntgctt
720
tagagacaca ggatgattca gaccggaaac agacctcgtg ggtgtaagag gaagcctctg
780
tgagctcgca ccttactggg tgcaaaagaa tccacggaac ttgggagaag tccagttcct
840
gtaaaaactg ggaagacgag gcgttctcat cccataggag gtttgtgaga actcacgccg
900
ggggtgaaaa tgtacgtctg tagcatggag aagccttcag gtacattcag ctcttaacaa
960
acacaggaag acttaatggc agcttggcat ttaatgtcaa aatccaagcc gtggcattta
1020
atgtcaaaat gacttcagac cacttctagc cttctgggcc catgagtaat aatgagcaca
1080
ctagggagca tctctgtaaa cacagtggct ggggaaaccc ttcctagtct cacttgattc
1140
ctcatgacgg aaatcacact aaagagagaa atcagtgaag taaggaacgt ggaaggtcat
1200
gaatgggccg caaaccacgg ccagctgctt gtctttgtat ggcttgccag ctaacaatag
1260
tggttccatc tttaaggaag aagaatgttt gatggagaaa atttgtggcc aatgaagtct
1320
gaaatacttc ctgtcatctg ccccttttcca gaaaaacttg gccgaccctt ggtctacagc
1380
acgggttctc agtcgggcga cgatttggct gtctaggcgt catttggcaa tgtctagaga
1440
catttttggt agttagaatg gggggaagat actcctgact tgtaataaga agacatcaga
1500
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1560
aaacgtcact gttgctgagg ttgaaaataa tcatgcagtc attcctcaat tactgcctgc
1620
agcaattcct ccatttttat gaatcttgtg agcacttacg ctaggagaaa tttcttttac
1680
aaaactttta aaatacaatt agtgctgata attcctatgt ggaaatgatt ccagccatgg
1740
tcccctcact tgagcatgtg aatattctca cggagagaag ccccagcgag attttccggt
1800
gaatacggga ttgcacttac tctttcatca cggaaacaga ccccccgaga gaagccccaa
1860
cgagattttc cggtgaatac gggactgcac gtactctctc atcatgaaaa cagagccccg
1920
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1980
atcaagaaag gtttgtttat agtattttta ctatagcttc atccttgata acgtcctaat
2040
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2100
ttctcagtac cactttgtta ctggtacctg atgcacacgg attgcgacca gagcatgatg
2160
cctccatcaa gtggtaatat gtttgcagcc tgctgtccag ccaagagtga cagatacttc
2220
tagtgacttc cccggtatcc actctcatct tcttccaata tcaagagaat ccaggttctg
2280

tcagattagt aaggtgtgct aatctaaatt ttaaaaaatc tcttacaggt tttcttgcag
2340
ctggtaccat ccatgtctca cagccctggc cactgacaga tcagcagatg tcaccacgtg
2400
ggcttctgag aaagctcttg aatggggatc gttcttaaac atgaattcct ccctgtatgt
2460
tttgttcttt gctttacttt tcaccttgca aagagatcca gtacctagta ttggaagatc
2520
caccttaacg accgtgcata tgaaaaccac agtctaagga agtgactgca gaaagctcac
2580
agcgaccctg gcctcccctg tggcctcttt gagtgtctgc agcagccctg gacttccaga
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2700
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2709

<210> 598
<211> 240
<212> PRT
<213> Homo sapiens

<400> 598
Xaa Ala Cys Thr Gln Cys Gly Lys Ala Phe Arg Trp Lys Ser Asn Phe
1 5 10 15
Asn Leu His Lys Lys Asn His Met Val Glu Lys Thr Tyr Glu Cys Lys
20 25 30
Glu Cys Gly Lys Ser Phe Gly Asp Leu Val Ser Arg Arg Lys His Met
35 40 45
Arg Ile His Ile Val Lys Lys Pro Val Glu Cys Arg Gln Cys Gly Lys
50 55 60
Thr Phe Arg Asn Gln Ser Ile Leu Lys Thr His Met Asn Ser His Thr
65 70 75 80
Gly Glu Lys Pro Tyr Gly Cys Asp Leu Cys Gly Lys Ala Phe Ser Ala
85 90 95
Ser Ser Asn Leu Thr Ala His Arg Lys Ile His Thr Gln Glu Arg Arg
100 105 110
Tyr Glu Cys Ala Ala Cys Gly Lys Val Phe Gly Asp Tyr Leu Ser Arg
115 120 125
Arg Arg His Met Ser Val His Leu Val Lys Lys Arg Val Glu Cys Arg
130 135 140
His Cys Gly Lys Ala Phe Arg Asn Gln Ser Thr Leu Lys Thr His Met
145 150 155 160
Arg Ser His Thr Gly Glu Lys Pro Tyr Glu Cys Asp His Cys Gly Lys
165 170 175
Ala Phe Ser Ile Gly Ser Asn Leu Asn Val His Arg Arg Ile His Thr
180 185 190
Gly Glu Lys Pro Tyr Glu Cys Leu Val Cys Gly Lys Ala Phe Ser Asp
195 200 205
His Ser Ser Leu Arg Ser His Val Lys Thr His Arg Gly Glu Lys Leu
210 215 220
Phe Xaa Cys His Pro Cys Gly Lys Gly Ser Ser Glu Arg Ala Xaa Leu
225 230 235 240

<210> 599
<211> 340
<212> DNA
<213> Homo sapiens

<400> 599
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120
caggcatgtt tgccgggccg catcccttgc acttgcagtc cgtggcctat cggccgaggc
180
gcaggcctgc agttggagcc gtgcgtgggt gtcccgcgcg aggagcgtgt tggcagacta
240
tggggctcgt cggaggacga ggatgtgagt ggcgatggct ttgcgcgact gggcgtattc
300
cacccggcga tggtgctcca gatcgtccag ggcatgatca
340

<210> 600
<211> 111
<212> PRT
<213> Homo sapiens

<400> 600
Met Pro Trp Thr Ile Trp Ser Thr Ile Ala Gly Trp Asn Thr Pro Ser
1 5 10 15
Arg Ala Lys Pro Ser Pro Leu Thr Ser Ser Ser Ser Asp Glu Pro His
20 25 30
Ser Leu Pro Thr Arg Ser Ser Arg Gly Thr Pro Thr His Gly Ser Asn
35 40 45
Cys Arg Pro Ala Pro Arg Pro Ile Gly His Gly Leu Gln Val Gln Gly
50 55 60
Met Arg Pro Gly Lys His Ala Trp Ala Lys Arg Cys Arg Leu Arg Cys
65 70 75 80
Thr Ala Thr Pro Ser Thr Cys Ala Met Thr Pro Asn Lys Arg Ser Asp
85 90 95
Thr Thr Glu Arg Ser His His Asp Val Lys Ser Arg Glu Ala Arg
100 105 110

<210> 601
<211> 421
<212> DNA
<213> Homo sapiens

<400> 601
gccggcggca gcgacatctc gctcaacgtc ggcgtgcgcg gcctgacttc gcgtctttct
60
ccgcgctcca ccattttgat ggacggcgtc ccgctggcgg tcgcgcctta cggccagccg
120
cagctgtcga tggccccgct gtctatcggt aatctgcaat cggtggacgt ggtgcgcggc
180
ggcggcgcgg tgcgctacgg gccgcagaac gtcggcggcg tgatcaactt cgttacccga
240

gacattccca aaacgtttgg cggtgccgcc agcgtacaaa cccagggtgc cagccacggc
300
ggcctgaaga ccctgaccag cgcctccgtg ggcggcaccg cagacaacgg cctcggcgcc
360
gagctgctct actccggcct gcacggccag ggctaccgcg acaacaacga caacaccgac
420
n
421

<210> 602
<211> 140
<212> PRT
<213> Homo sapiens

<400> 602
Ala Gly Gly Ser Asp Ile Ser Leu Asn Val Gly Val Arg Gly Leu Thr
1 5 10 15
Ser Arg Leu Ser Pro Arg Ser Thr Ile Leu Met Asp Gly Val Pro Leu
20 25 30
Ala Val Ala Pro Tyr Gly Gln Pro Gln Leu Ser Met Ala Pro Leu Ser
35 40 45
Ile Gly Asn Leu Gln Ser Val Asp Val Val Arg Gly Gly Gly Ala Val
50 55 60
Arg Tyr Gly Pro Gln Asn Val Gly Gly Val Ile Asn Phe Val Thr Arg
65 70 75 80
Asp Ile Pro Lys Thr Phe Gly Gly Ala Ala Ser Val Gln Thr Gln Gly
85 90 95
Ala Ser His Gly Gly Leu Lys Thr Leu Thr Ser Ala Ser Val Gly Gly
100 105 110
Thr Ala Asp Asn Gly Leu Gly Ala Glu Leu Leu Tyr Ser Gly Leu His
115 120 125
Gly Gln Gly Tyr Arg Asp Asn Asn Asp Asn Thr Asp
130 135 140

<210> 603
<211> 309
<212> DNA
<213> Homo sapiens

<400> 603
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ttcgacggcc tggccatcgg cggtctgtcg gtgggcgagc ccaagcacga gatgatcaag
120
gtgctggatt acctgccggg cctgatgccg gctgacaaac ctcgttacct tatgggcgtt
180
ggcaaaccgg aagacctcgt agagggtgtg cgccgcggtg tggacatgtt cgattgcgtg
240
atgccaaccc gtaatgcccg caatgggcat ctgttcatcg atacaggcgt gctgaagatc
300
cgtaacgcg
309

<210> 604

<211> 103
<212> PRT
<213> Homo sapiens

<400> 604
Xaa Gly Gly Met His Glu Ser Leu Arg Lys Arg Ser Leu Glu Gly Leu
1 5 10 15
Asp Lys Ile Gly Phe Asp Gly Leu Ala Ile Gly Gly Leu Ser Val Gly
20 25 30
Glu Pro Lys His Glu Met Ile Lys Val Leu Asp Tyr Leu Pro Gly Leu
35 40 45
Met Pro Ala Asp Lys Pro Arg Tyr Leu Met Gly Val Gly Lys Pro Glu
50 55 60
Asp Leu Val Glu Gly Val Arg Arg Gly Val Asp Met Phe Asp Cys Val
65 70 75 80
Met Pro Thr Arg Asn Ala Arg Asn Gly His Leu Phe Ile Asp Thr Gly
85 90 95
Val Leu Lys Ile Arg Asn Ala
100

<210> 605
<211> 428
<212> DNA
<213> Homo sapiens

<400> 605
acgcgttcac gatagggtag ttgcctattt caacgcggtc ggtattttcc tgcacaacaa
60
actggcccaa ggctgggcta tagtcaggtg catagtactt ggtgaagtag cgtacgtccg
120
cacccacatc acatttcagt accttggcta tcttcaatcg gaaaaaaaga ttggagtaaa
180
tgttgagttt tggtaatggc aacgccgttt gactggaaga gttttggaag gtaatgaccg
240
attcccagtg caaaggtccc catgctacat cctgcgacaa tgaggccgtt agcacgttta
300
ttgcctcgct gctttgccga acgccaacct ctgtaccgat acgctgatac tgattgttga
360
tggtataggc ttgcgccagg taggtataat tggtcaattc gtccatggca atgcgcagtg
420
aagtcttg
428

<210> 606
<211> 135
<212> PRT
<213> Homo sapiens

<400> 606
Met Asp Glu Leu Thr Asn Tyr Thr Tyr Leu Ala Gln Ala Tyr Thr Ile
1 5 10 15
Asn Asn Gln Tyr Gln Arg Ile Gly Thr Glu Val Gly Val Arg Gln Ser
20 25 30
Ser Glu Ala Ile Asn Val Leu Thr Ala Ser Leu Ser Gln Asp Val Ala

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        35                  40                  45
Trp Gly Pro Leu His Trp Glu Ser Val Ile Thr Phe Gln Asn Ser Ser
    50                  55                  60
Ser Gln Thr Ala Leu Pro Leu Pro Lys Leu Asn Ile Tyr Ser Asn Leu
65                  70                  75                  80
Phe Phe Arg Leu Lys Ile Ala Lys Val Leu Lys Cys Asp Val Gly Ala
                85                  90                  95
Asp Val Arg Tyr Phe Thr Lys Tyr Tyr Ala Pro Asp Tyr Ser Pro Ala
            100                 105                 110
Leu Gly Gln Phe Val Val Gln Glu Asn Thr Asp Arg Val Glu Ile Gly
        115                 120                 125
Asn Tyr Pro Ile Val Asn Ala
    130                 135
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<210> 607
<211> 366
<212> DNA
<213> Homo sapiens

<400> 607
gatcacgatg aattgtgggc gtacacgtac gagaatgtga tggcgctaaa cttgccgcct
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gacattgtgt gtaaaggatt ctttagaaaa ttggaaaacg tagtgaccgg agtcaatttg
120
gttttcaacg gcaaacatta tcaaattgta aagaaagagg atgacctatt caaattgacc
180
aaaagcaatt gttacaagtt gagcaacata aaatttaaca attggaaata cttgtacttg
240
acaacgcacg gtgtgtacaa cgtgttcacc aacagctttc attcgagctg tccatttttg
300
ttgggcacca cgttgccgca gacattcaag aagcccaccg acgaaaagta tttgcccgag
360
gacgcg
366

<210> 608
<211> 122
<212> PRT
<213> Homo sapiens

<400> 608
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Asp His Asp Glu Leu Trp Ala Tyr Thr Tyr Glu Asn Val Met Ala Leu
 1               5                  10                  15
Asn Leu Pro Pro Asp Ile Val Cys Lys Gly Phe Phe Arg Lys Leu Glu
            20                  25                  30
Asn Val Val Thr Gly Val Asn Leu Val Phe Asn Gly Lys His Tyr Gln
        35                  40                  45
Ile Val Lys Lys Glu Asp Asp Leu Phe Lys Leu Thr Lys Ser Asn Cys
    50                  55                  60
Tyr Lys Leu Ser Asn Ile Lys Phe Asn Asn Trp Lys Tyr Leu Tyr Leu
65                  70                  75                  80
Thr Thr His Gly Val Tyr Asn Val Phe Thr Asn Ser Phe His Ser Ser
                85                  90                  95
Cys Pro Phe Leu Leu Gly Thr Thr Leu Pro Gln Thr Phe Lys Lys Pro
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            100                 105                 110
Thr Asp Glu Lys Tyr Leu Pro Glu Asp Ala
        115                 120

<210> 609
<211> 291
<212> DNA
<213> Homo sapiens

<400> 609
nacgcgttat gacacggcct cctccaaggt cagtgtcatc gagtcacgta actcgtcggt
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tgggtcggtt ggaacgagtc cgtcatgagc ccggtcgcca tggacgactc cagcagtccg
120
tacccagcct ggaagcagga cccccacgcg acggaatcgc cggcttccaa gtcgtcgccc
180
ccgaagcctc aaacttcccc cgccccgtac gccgggccgg ctccgaagac accggccaca
240
cctggaccat ctggggcggg ggcgccgccg tggtggtggc gggtggagcc g
291

<210> 610
<211> 69
<212> PRT
<213> Homo sapiens

<400> 610
Met Ser Pro Val Ala Met Asp Asp Ser Ser Ser Pro Tyr Pro Ala Trp
 1               5                  10                  15
Lys Gln Asp Pro His Ala Thr Glu Ser Pro Ala Ser Lys Ser Ser Pro
            20                  25                  30
Pro Lys Pro Gln Thr Ser Pro Ala Pro Tyr Ala Gly Pro Ala Pro Lys
        35                  40                  45
Thr Pro Ala Thr Pro Gly Pro Ser Gly Ala Gly Ala Pro Pro Trp Trp
    50                  55                  60
Trp Arg Val Glu Pro
65

<210> 611
<211> 393
<212> DNA
<213> Homo sapiens

<400> 611
nnnatcttgt gtcgattttc ggtcgcatat actatggggg agtattgtat aatgcggcgg
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tgtacccaag tagagaggtg ttcgatgcca cacagtccgg aagaaaagaa gcaagcactg
120
acgcgcatca ggcgcatcaa aggtcaggta gcgactcttg agcaagcgct tgatgcaggt
180
gcgaaatgtc ctgcaattct tcagcagctt gcggccgttc gtggcgcagt caacggattg
240
atggcaacgg ttctggagag ctatctgcgg gaagagtttc ccagtagcga aatcaggagc
300
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gattcgcaga acaagtccat tgacgagacc atctctatcg tccgctccta tctgcggtag
360
aggcaccagg gtgtcctcgg tgagggcaaa ttt
393

<210> 612
<211> 119
<212> PRT
<213> Homo sapiens

<400> 612
Xaa Ile Leu Cys Arg Phe Ser Val Ala Tyr Thr Met Gly Glu Tyr Cys
 1   5   10   15
Ile Met Arg Arg Cys Thr Gln Val Glu Arg Cys Ser Met Pro His Ser
            20   25   30
Pro Glu Glu Lys Lys Gln Ala Leu Thr Arg Ile Arg Arg Ile Lys Gly
        35   40   45
Gln Val Ala Thr Leu Glu Gln Ala Leu Asp Ala Gly Ala Lys Cys Pro
    50   55   60
Ala Ile Leu Gln Gln Leu Ala Ala Val Arg Gly Ala Val Asn Gly Leu
65   70   75   80
Met Ala Thr Val Leu Glu Ser Tyr Leu Arg Glu Glu Phe Pro Ser Ser
                85   90   95
Glu Ile Arg Ser Asp Ser Gln Asn Lys Ser Ile Asp Glu Thr Ile Ser
            100   105   110
Ile Val Arg Ser Tyr Leu Arg
        115

<210> 613
<211> 567
<212> DNA
<213> Homo sapiens

<400> 613
gaaaatgctc ctggcgcctc agggaaggtc cttctcaaag aaaaggatgg ggctgaatcg
60
ctggaaacgg ttcacaagga agccgagtcc caagcctact tttggtcctg acagtgtgga
120
acactggata aagagagtgg agaaagcctc agagtttgca gtgtcaaatg catttttac
180
tagaaattca gatttaccta gaagtccctg gggccaaatc acagatttga aaacatctga
240
gcaaatagag gatcatgatg aaatctatgc agaagctcag gagctggtca atgactggtt
300
agacaccaaa cttaagcaag aattagcaag tgaggaagaa ggtgatgcta aaaacactgt
360
gtcaagtgtc actattatgc cggaagccaa tggccatttg aaatatgaca agtttgatga
420
tttatgtggc tatttggagg aagaagagga aagtaccacc gttcaaaaat ttatagacca
480
tctgctccat aaaaatgtgg tagattctgc aatgatggaa gatcttggaa ggaaggaaaa
540
ccaagacaag aagcagcaga aggatcc
567

<210> 614
<211> 187
<212> PRT
<213> Homo sapiens

<400> 614
Met Leu Leu Ala Pro Gln Gly Arg Ser Phe Ser Lys Lys Arg Met Gly
1 5 10 15
Leu Asn Arg Trp Lys Arg Phe Thr Arg Lys Pro Ser Pro Lys Pro Thr
20 25 30
Phe Gly Pro Asp Ser Val Glu His Trp Ile Lys Arg Val Glu Lys Ala
35 40 45
Ser Glu Phe Ala Val Ser Asn Ala Phe Phe Thr Arg Asn Ser Asp Leu
50 55 60
Pro Arg Ser Pro Trp Gly Gln Ile Thr Asp Leu Lys Thr Ser Glu Gln
65 70 75 80
Ile Glu Asp His Asp Glu Ile Tyr Ala Glu Ala Gln Glu Leu Val Asn
85 90 95
Asp Trp Leu Asp Thr Lys Leu Lys Gln Glu Leu Ala Ser Glu Glu Glu
100 105 110
Gly Asp Ala Lys Asn Thr Val Ser Ser Val Thr Ile Met Pro Glu Ala
115 120 125
Asn Gly His Leu Lys Tyr Asp Lys Phe Asp Asp Leu Cys Gly Tyr Leu
130 135 140
Glu Glu Glu Glu Glu Ser Thr Thr Val Gln Lys Phe Ile Asp His Leu
145 150 155 160
Leu His Lys Asn Val Val Asp Ser Ala Met Met Glu Asp Leu Gly Arg
165 170 175
Lys Glu Asn Gln Asp Lys Lys Gln Gln Lys Asp
180 185

<210> 615
<211> 685
<212> DNA
<213> Homo sapiens

<400> 615
nnacgcgtgc tgccctaagt gacggattcc atgtcggtgc gagtcgggtc ggggccgatg
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ggccatgaac gggccctagc gagggccgga ctcggccccg tggccggatg cgacgaggcg
120
gggcggggcg cgtgtgcagg gccattggta gccgcagctg tcattcttga tgatcgcaga
180
tccggcagga ttgcggggct agcagattcc aagacactat ctgcggccaa gagagaggcc
240
ctgtttaacg tcatcatgga taaagctttg gcagtgtcgt gggtacgtgt agaagccgac
300
gaatgcgatc ggttggggat gcaggaggca gatatcagcg gcttgaggcg tgccgtggtg
360
aggctgggag ttgaaccggg ctacgtgctg tcggacggtt tcccggtcga cggactgacg
420
gttcccgatc tgggaatgtg gaagggcgat tcagtgtgtg cgtgtgtggc agctgcctcc
480

atcgtggcca aagtggccag ggatcgcatc atgatcgcta tggacgccga gattcctggt
540
tacgattttg cggtgcacaa ggggtacgcg acagccttac accagcgtcg tctgaaggag
600
ttaggaccgt ctcgtcagca ccggatgagc tacgccaatg tgcgacgagc ggctaggctt
660
cattcatcat gagtgccgaa gatct
685

<210> 616
<211> 213
<212> PRT
<213> Homo sapiens

<400> 616
Met Ser Val Arg Val Gly Ser Gly Pro Met Gly His Glu Arg Ala Leu
 1   5   10   15
Ala Arg Ala Gly Leu Gly Pro Val Ala Gly Cys Asp Glu Ala Gly Arg
            20   25   30
Gly Ala Cys Ala Gly Pro Leu Val Ala Ala Ala Val Ile Leu Asp Asp
        35   40   45
Arg Arg Ser Gly Arg Ile Ala Gly Leu Ala Asp Ser Lys Thr Leu Ser
    50   55   60
Ala Ala Lys Arg Glu Ala Leu Phe Asn Val Ile Met Asp Lys Ala Leu
65   70   75   80
Ala Val Ser Trp Val Arg Val Glu Ala Asp Glu Cys Asp Arg Leu Gly
                85   90   95
Met Gln Glu Ala Asp Ile Ser Gly Leu Arg Arg Ala Val Val Arg Leu
            100   105   110
Gly Val Glu Pro Gly Tyr Val Leu Ser Asp Gly Phe Pro Val Asp Gly
        115   120   125
Leu Thr Val Pro Asp Leu Gly Met Trp Lys Gly Asp Ser Val Cys Ala
    130   135   140
Cys Val Ala Ala Ala Ser Ile Val Ala Lys Val Ala Arg Asp Arg Ile
145   150   155   160
Met Ile Ala Met Asp Ala Glu Ile Pro Gly Tyr Asp Phe Ala Val His
                165   170   175
Lys Gly Tyr Ala Thr Ala Leu His Gln Arg Arg Leu Lys Glu Leu Gly
            180   185   190
Pro Ser Arg Gln His Arg Met Ser Tyr Ala Asn Val Arg Arg Ala Ala
        195   200   205
Arg Leu His Ser Ser
    210

<210> 617
<211> 337
<212> DNA
<213> Homo sapiens

<400> 617
nncacctgtt tggctcgggg cactcgcgga tcatggtcga ggaaatgtgg ccgcgctacg
60
gctcgtttcc cggcttcaac cccatcgtcg agctgtcgct gtcgttccac aacctcgtcg
120

tcggcgccaa cggccagcgc caggccatgt tcctcgaaaa cgtttccggc cttcccggag
180
cgaatcctcc gaaacttcga cctgtcccaa caagactctg cactcgtgat ttcatcaagc
240
gctgcaacgt cgtgccaatc gagatggccg aggagttcca gcgtcgcggc gtccgcgtcg
300
tctcgatcat ctcgctggcg cactcgcagg cgtcgac
337

<210> 618
<211> 112
<212> PRT
<213> Homo sapiens

<400> 618
Xaa Thr Cys Leu Ala Arg Gly Thr Arg Gly Ser Trp Ser Arg Lys Cys
1 5 10 15
Gly Arg Ala Thr Ala Arg Phe Pro Ala Ser Thr Pro Ser Ser Ser Cys
20 25 30
Arg Cys Arg Ser Thr Thr Ser Ser Ser Ala Pro Thr Ala Ser Ala Arg
35 40 45
Pro Cys Ser Ser Lys Thr Phe Pro Ala Phe Pro Glu Arg Ile Leu Arg
50 55 60
Asn Phe Asp Leu Ser Gln Gln Asp Ser Ala Leu Val Ile Ser Ser Ser
65 70 75 80
Ala Ala Thr Ser Cys Gln Ser Arg Trp Pro Arg Ser Ser Ser Val Ala
85 90 95
Ala Ser Ala Ser Ser Arg Ser Ser Arg Trp Arg Thr Arg Arg Arg Arg
100 105 110

<210> 619
<211> 425
<212> DNA
<213> Homo sapiens

<400> 619
acgcgttttt tatgccgatc ttatgctcta acctagaaac aatatcagct acaaacctaa
60
tagctataag ataatattcg aaagcatcaa taggagtttt gatcatttcc gcatacctaa
120
gttttatagc atctttgtca gaaggcaaac ctgccaaacc agatgaatcg atgccactct
180
caaacttgct caaatgttca attaaatcat ccaagttgtg gccatgctta ccgcttccag
240
attttgaatg aatcattact ttaattgatt tttcaatcgc taaatggaat tcccagcaag
300
caatagaagc ccgctcattt ttaaagctca gtatgtcact aatgcctttt tcgaagtggc
360
tccatattcc ctgcgccata ttagaagctg actggttgga atggcttgcc atgttcaaat
420
ctaga
425

<210> 620

<211> 137
<212> PRT
<213> Homo sapiens

<400> 620
Met Ala Ser His Ser Asn Gln Ser Ala Ser Asn Met Ala Gln Gly Ile
1 5 10 15
Trp Ser His Phe Glu Lys Gly Ile Ser Asp Ile Leu Ser Phe Lys Asn
20 25 30
Glu Arg Ala Ser Ile Ala Cys Trp Glu Phe His Leu Ala Ile Glu Lys
35 40 45
Ser Ile Lys Val Met Ile His Ser Lys Ser Gly Ser Gly Lys His Gly
50 55 60
His Asn Leu Asp Asp Leu Ile Glu His Leu Ser Lys Phe Glu Ser Gly
65 70 75 80
Ile Asp Ser Ser Gly Leu Ala Gly Leu Pro Ser Asp Lys Asp Ala Ile
85 90 95
Lys Leu Arg Tyr Ala Glu Met Ile Lys Thr Pro Ile Asp Ala Phe Glu
100 105 110
Tyr Tyr Leu Ile Ala Ile Arg Phe Val Ala Asp Ile Val Ser Arg Leu
115 120 125
Glu His Lys Ile Gly Ile Lys Asn Ala
130 135

<210> 621
<211> 453
<212> DNA
<213> Homo sapiens

<400> 621
cccggcaagg gagccatctt gacgaatatg tccttgtggt ggttcgacca attggccgac
60
atcgtcgata accatctcgt gagcgtggat gtccccgccg aggtcgcagg gcgcgccatg
120
gtcgttgagg aactcgacat gttcccggtc gaatgcgtcg tgcggggcta cctcaccggt
180
tcagggtggg ccgaatatca gcgcaaccag gccgtgtgcg gaatccgcct tcccgagggg
240
ctgcagaatg ggtcccggct cgaagagccc attttcaccc cggcaattaa ggccccgcag
300
ggagaacatg acgagaacat cgactatcta cgcctggtag aactcgtcgg tcccngatgn
360
tcagcgcagc tgcatgacct ttcgctgcgg gtctaccagc gtgcagagga gatcgctcgg
420
aagcgaggca tcctcctggc ggataccaag ctt
453

<210> 622
<211> 151
<212> PRT
<213> Homo sapiens

<400> 622
Pro Gly Lys Gly Ala Ile Leu Thr Asn Met Ser Leu Trp Trp Phe Asp

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 1               5                  10                  15
Gln Leu Ala Asp Ile Val Asp Asn His Leu Val Ser Val Asp Val Pro
            20                  25                  30
Ala Glu Val Ala Gly Arg Ala Met Val Val Glu Glu Leu Asp Met Phe
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Gln Asp Ile Asn Ser Ser Arg Pro Val Leu Leu Asn Gly Thr Tyr Asp
305                 310                 315                 320
Val Gln Val Thr Ser Gly Gly Thr Phe Ile Gly Ile Gly Arg Lys Thr
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Pro Asp Cys Gln Gly Asn Thr Lys Tyr Phe Arg Cys Lys Phe Cys Asn
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Phe Thr Tyr Met Gly Asn Ser Ser Thr Glu Leu Glu Gln His Phe Leu
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Gln Thr His Pro Asn Lys Ile Lys Ala Ser Leu Pro Ser Ser Glu Val
    370                 375                 380
Ala Lys Pro Ser Glu Lys Asn Ser Asn Lys Ser Ile Pro Ala Leu Gln
385                 390                 395                 400
Ser Ser Asp Ser Gly Asp Leu Gly Lys Trp Gln Asp Lys Ile Thr Val
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Lys Ala Gly Asp Asp Thr Pro Val Gly Tyr Ser Val Pro Ile Lys Pro
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Leu Asp Ser Ser Arg Gln Asn Gly Thr Glu Ala Thr Ser Tyr Tyr Trp
        435                 440                 445
Cys Lys Phe Cys Ser Phe Ser Cys Glu Ser Ser Ser Ser Leu Lys Leu
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Leu Glu His Tyr Gly Lys Gln His Gly Ala Val Gln Ser Gly Gly Leu
465                 470                 475                 480
Asn Pro Glu Leu Asn Asp Lys Leu Ser Arg Gly Ser Val Ile Asn Gln
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Asn Asp Leu Ala Lys Ser Ser Glu Gly Glu Thr Met Thr Lys Thr Asp
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Lys Ser Ser Ser Gly Ala Lys Lys Lys Asp Phe Ser Ser Lys Gly Ala
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Glu Asp Asn Met Val Thr Ser Tyr Asn Cys Gln Phe Cys Asp Phe Arg
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Tyr Ser Lys Ser His Gly Pro Asp Val Ile Val Val Gly Pro Leu Leu
545                 550                 555                 560
Arg His Tyr Gln Gln Leu His Asn Ile His Lys Cys Thr Ile Lys His
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Cys Pro Phe Cys Pro Arg Gly Leu Cys Ser Pro Glu Lys His Leu Gly
            580                 585                 590
Glu Ile Thr Tyr Pro Phe Ala Cys Arg Lys Ser Asn Cys Ser His Cys
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Ala Leu Leu Leu Leu His Leu Ser Pro Gly Ala Ala Gly Ser Ser Arg
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Val Lys His Gln Cys His Gln Cys Ser Phe Thr Thr Pro Asp Val Asp
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Val Leu Leu Phe His Tyr Glu Ser Val His Glu Ser Gln Ala Ser Asp
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Val Lys Gln Glu Ala Asn His Leu Gln Gly Ser Asp Gly Gln Gln Ser
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Val Lys Glu Ser Lys Glu His Ser Cys Thr Lys Cys Asp Phe Ile Thr
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Gln Val Glu Glu Glu Ile Ser Arg His Tyr Arg Arg Ala His Ser Cys
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Tyr Lys Cys Arg Gln Cys Ser Phe Thr Ala Ala Asp Thr Gln Ser Leu
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Leu Glu His Phe Asn Thr Val His Cys Gln Glu Gln Asp Ile Thr Thr
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Ala Asn Gly Glu Glu Asp Gly His Ala Ile Ser Thr Ile Lys Glu Glu
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Pro Lys Ile Asp Phe Arg Val Tyr Asn Leu Leu Thr Pro Asp Ser Lys
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Met Gly Glu Pro Val Ser Glu Ser Val Val Lys Arg Glu Lys Leu Glu
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Glu Lys Asp Gly Leu Lys Glu Lys Val Trp Thr Glu Ser Ser Ser Asp
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Asp Leu Arg Asn Val Thr Trp Arg Gly Ala Asp Ile Leu Arg Gly Ser
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Pro Ser Tyr Thr Gln Ala Ser Leu Gly Leu Leu Thr Pro Val Ser Gly
            820                 825                 830
Thr Gln Glu Gln Thr Lys Thr Leu Arg Asp Ser Pro Asn Val Glu Ala
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Ala His Leu Ala Arg Pro Ile Tyr Gly Leu Ala Val Glu Thr Lys Gly
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Phe Leu Gln Gly Ala Pro Ala Gly Gly Glu Lys Ser Gly Ala Leu Pro
865                 870                 875                 880
Gln Gln Tyr Pro Ala Ser Gly Glu Asn Lys Ser Lys Asp Glu Ser Gln
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Ser Leu Leu Arg Arg Arg Arg Gly Ser Gly Val Phe Cys Ala Asn Cys
            900                 905                 910
Leu Thr Thr Lys Thr Ser Leu Trp Arg Lys Asn Ala Asn Gly Gly Tyr
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Val Cys Asn Ala Tyr Gly Leu Tyr Gln Lys Leu His Ser Thr Pro Arg
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Pro Leu Asn Ile Ile Lys Gln Asn Asn Gly Glu Gln Ile Ile Arg Arg
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Arg Thr Arg Lys Arg Leu Asn Pro Glu Ala Leu Gln Ala Glu Gln Leu
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Asn Lys Gln Gln Arg Gly Ser Asn Glu Glu Gln Val Asn Gly Ser Pro
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Leu Glu Arg Arg Ser Glu Asp His Leu Thr Glu Ser His Gln Arg Glu
        995                 1000                1005
Ile Pro Leu Pro Ser Leu Ser Lys Tyr Glu Ala Gln Gly Ser Leu Thr
    1010                1015                1020
Lys Ser His Ser Ala Gln Gln Pro Val Leu Val Ser Gln Thr Leu Asp
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Ile His Lys Arg Met Gln Pro Leu His Ile Gln Ile Lys Ser Pro Gln
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Glu Ser Thr Gly Asp Pro Gly Asn Ser Ser Ser Val Ser Glu Gly Lys
            1060                1065                1070
Gly Ser Ser Glu Arg Gly Ser Pro Ile Glu Lys Tyr Met Arg Pro Ala
        1075                1080                1085
Lys His Pro Asn Tyr Ser Pro Pro Gly Ser Pro Ile Glu Lys Tyr Gln
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Tyr Pro Leu Phe Gly Leu Pro Phe Val His Asn Asp Phe Gln Ser Glu
1105                1110                1115                1120
Ala Asp Trp Leu Arg Phe Trp Ser Lys Tyr Lys Leu Ser Val Pro Gly
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Asn Pro His Tyr Leu Ser His Val Pro Gly Leu Pro Asn Pro Cys Gln
            1140                1145                1150
Asn Tyr Val Pro Tyr Pro Thr Phe Asn Leu Pro Pro His Phe Ser Ala
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Val Gly Ser Asp Asn Asp Ile Pro Leu Asp Leu Ala Ile Lys His Ser
    1170                1175                1180
Arg Pro Gly Pro Thr Ala Asn Gly Ala Ser Lys Glu Lys Thr Lys Ala
1185                1190                1195                1200
Pro Pro Asn Val Lys Asn Glu Gly Pro Leu Asn Val Val Lys Thr Glu
                1205                1210                1215
Lys Val Asp Arg Ser Thr Gln Asp Glu Leu Ser Thr Lys Cys Val His
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Cys Gly Ile Val Phe Leu Asp Glu Val Met Tyr Ala Leu His Met Ser
        1235                1240                1245
Cys His Gly Asp Ser Gly Pro Phe Gln Cys Ser Ile Cys Gln His Leu
    1250                1255                1260
Cys Thr Asp Lys Tyr Asp Phe Thr Thr His Ile Gln Arg Gly Leu His
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Arg Asn Asn Ala Gln Val Glu Lys Asn Gly Lys Pro Lys Glu
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<211> 411
<212> DNA
<213> Homo sapiens

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300
atcggtggcg cggatatgcc agtcgtcatt tcgatgctga acagctactc cggttgggca
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411

<210> 630
<211> 137
<212> PRT
<213> Homo sapiens

<400> 630
Xaa Ala Phe Ala Glu Glu Gly Thr Gly Ala Ser Thr Phe Gln Leu Ser

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Glu Ile Trp Ile Gly Ile Phe Ile Gly Ala Leu Thr Phe Thr Gly Ser
            20                  25                  30
Leu Val Ala Trp Gly Lys Leu Ser Gly Lys Val Ala Ser Lys Pro Leu
        35                  40                  45
Thr Leu Pro Gly Arg Asn Trp Ile Asn Leu Gly Leu Leu Val Val Ile
    50                  55                  60
Ile Ala Cys Gly Ile Trp Phe Ser Asn Val Ser Gly Gly Ile Ala Trp
65                  70                  75                  80
Leu Pro Leu Ala Leu Leu Thr Leu Ala Ser Leu Phe Leu Gly Phe His
                85                  90                  95
Phe Val Ala Ala Ile Gly Gly Ala Asp Met Pro Val Val Ile Ser Met
            100                 105                 110
Leu Asn Ser Tyr Ser Gly Trp Ala Ala Ala Phe Ser Gly Phe Ser Leu
        115                 120                 125
His Ile Pro Val Leu Ile Val Thr Gly
    130                 135
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<211> 275
<212> DNA
<213> Homo sapiens

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275

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Gly Leu Val Ser Glu Tyr Leu Val Cys Lys Arg Lys Leu Glu Ser Lys
            20                  25                  30
Lys Glu Ala Leu Leu Ile Leu Ser Lys Glu Leu Asp Thr Cys Gln Gln
        35                  40                  45
Glu Arg Asp Gln Tyr Lys Leu Met Ala Asn Gln Leu Arg Glu Arg His
    50                  55                  60
Gln Ser Leu Lys Lys Lys Tyr Arg Glu Leu Ile Asp Gly Asp Pro Ser
65                  70                  75                  80
Leu Pro Pro Glu Lys Arg Lys
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Glu Trp Arg Leu Ser Gly Gln Pro Phe Leu Thr Ala Arg Ala Xaa Leu
            20   25   30
Val Asp Ala Val Val Asn Ala Val Glu His Tyr Ser Glu Leu Thr Pro
        35   40   45
Gln Leu Leu Thr Thr Gly Gly Thr Ser Asp Gly Arg Phe Ile Ala Gln
    50   55   60
Met Gly Xaa Gln Val Val Glu Leu Gly Pro Val Asn Ala Thr Ile His
65   70   75   80
Lys Val Asn Glu Cys Val His Ala Ala Asp Leu Gln Leu Leu Ser Arg
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Met Tyr Gln Arg Ile Met Glu Gln Leu Val Ala
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<210> 636
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Tyr Leu Leu Asp Val Val Asp Ser Glu Glu Gln Asp Met Ala Leu Asn
35 40 45
Ile His Ala Phe Ser Ala Gly Leu Gly Gly Ala Ile Gly Tyr Val Leu
50 55 60
Gly Gly Leu Asp Trp Thr Gln Thr Phe Leu Gly Ser Trp Phe Arg Thr
65 70 75 80
Gln Asn Gln Val Leu Phe Phe Phe Ala Ala Ile Ile Phe Thr Val Ser
85 90 95
Val Ala Leu His Leu Phe Ser Ile Asp Glu Glu Gln Tyr Ser Pro Gln
100 105 110
Gln Glu Arg Ser Ala Glu Glu Pro Gly Ala Leu Asp Gly Gly Glu Pro
115 120 125
His Gly Val Pro Ala Phe Pro Asp Glu Val Gln Ser Glu His Glu Leu
130 135 140
Ala Leu Asp Tyr Pro Asp Val Asp Ile Met Arg Ser Lys Ser Asp Ser
145 150 155 160
Ala Leu His Val Pro Asp Thr Ala Leu Asp Leu Glu Pro Glu Leu Leu
165 170 175
Phe Leu His Asp Ile Glu Pro Ser Ile Phe His Asp Ala Ser Tyr Pro
180 185 190
Ala Thr Pro Arg Ser Thr Ser Gln Glu Leu Ala Lys Thr Lys Leu Pro
195 200 205
Arg Leu Ala Thr Phe Leu Lys Glu Ala Ala Lys Glu Asp Glu Thr Leu
210 215 220
Leu Asp Asn His Leu Asn Glu Ala Lys Val Pro Asn Gly Ser Gly Ser
225 230 235 240
Pro Thr Lys Asp Ala Leu Gly Gly Tyr Thr Arg Val Asp Thr Lys Pro
245 250 255
Ser Ala Thr Ser Ser Ser Met Arg Arg Arg Arg His Ala Phe Arg Arg
260 265 270
Gln Ala Ser Ser Thr Phe Ser Tyr Tyr Gly Lys Leu Gly Ser His Cys
275 280 285
Tyr Arg Tyr Arg Arg Ala Asn Ala Val Val Leu Ile Lys Pro Ser Arg

```
    290                 295                 300
Ser Met Ser Asp Leu Tyr Asp Met Gln Lys Arg Gln Arg Gln His Arg
305                 310                 315                 320
His Arg Asn Gln Ser Gly Ala Thr Thr Ser Ser Gly Asp Thr Glu Ser
                325                 330                 335
Glu Glu Gly Glu Gly Glu Thr Thr Val Arg Leu Leu Trp Leu Ser Met
            340                 345                 350
Leu Lys Met Pro Arg Glu Leu Met Arg Leu Cys Leu Cys His Leu Leu
        355                 360                 365
Thr Trp Phe Ser Val Ile Ala Glu Ala Val Phe Tyr Thr Asp Phe Met
    370                 375                 380
Gly Gln Val Ile Phe Glu Gly Asp Pro Lys Ala Pro Ser Asn Ser Thr
385                 390                 395                 400
Ala Trp Gln Ala Tyr Asn Ala Gly Val Lys Met Gly Cys Trp Gly Leu
                405                 410                 415
Val Ile Tyr Ala Ala Thr Gly Ala Ile Cys Ser Ala Leu Leu Gln Lys
            420                 425                 430
Tyr Leu Asp Asn Tyr Asp Leu Ser Val Arg Val Ile Tyr Val Leu Gly
        435                 440                 445
Thr Leu Gly Phe Ser Val Gly Thr Ala Val Met Ala Met Phe Pro Asn
    450                 455                 460
Val Tyr Val Ala Met Val Thr Ile Ser Thr Met Gly Ile Val Ser Met
465                 470                 475                 480
Ser Ile Ser Tyr Cys Pro Tyr Ala Leu Leu Gly Gln Tyr His Asp Ile
                485                 490                 495
Lys Gln Tyr Ile His His Ser Pro Gly Asn Ser Lys Arg Gly Phe Gly
            500                 505                 510
Ile Asp Cys Ala Ile Leu Ser Cys Gln Val Tyr Ile Ser Gln Ile Leu
        515                 520                 525
Val Ala Ser Ala Leu Gly Gly Val Val Asp Ala Val Gly Thr Val Arg
    530                 535                 540
Val Ile Pro Met Val Ala Ser Val Gly Ser Phe Leu Gly Phe Leu Thr
545                 550                 555                 560
Ala Thr Phe Leu Val Ile Tyr Pro Asp Val Ser Glu Glu Ala Lys Glu
                565                 570                 575
Glu Gln Lys Gly Leu Ser Ser Pro Leu Ala Gly Glu Gly Arg Ala Gly
            580                 585                 590
Gly Asn Ser Glu Lys Pro Thr Val Leu Lys Leu Thr Arg Lys Glu Gly
        595                 600                 605
Leu Gln Gly Pro Val Glu Thr Glu Ser Val Val
    610                 615
```

<210> 637
<211> 370
<212> DNA
<213> Homo sapiens

<400> 637
ngaaaaacag gatgaatccc gtatcattct taagcccgaa aagtactgaa tgtcgtcttc
60
tctcgatcgg tgatgatctg gaaaggaaaa atcatcgtga ctactacatc acccgctact
120
acgcaaagac cgtcagttgg caggaaagtt ggttcctggt cccttaatcc atggtgtttt
180

tgtaggccct tattattttt cggaatggtt cggtttattg cgattccagt attcctcact
240
gtgccgaata tcattaatat cggaatccaa gccgcggtgg tggcgattat ggccttcggt
300
atgaccttcg tcatcgttac ctccggcatt gatttgtctg tgggttcggt cgcagctctt
360
tcagccatgg
370

<210> 638
<211> 99
<212> PRT
<213> Homo sapiens

<400> 638
Met Ile Trp Lys Gly Lys Ile Ile Val Thr Thr Thr Ser Pro Ala Thr
 1   5   10   15
Thr Gln Arg Pro Ser Val Gly Arg Lys Val Gly Ser Trp Ser Leu Asn
            20   25   30
Pro Trp Cys Phe Cys Arg Pro Leu Leu Phe Phe Gly Met Val Arg Phe
        35   40   45
Ile Ala Ile Pro Val Phe Leu Thr Val Pro Asn Ile Ile Asn Ile Gly
    50   55   60
Ile Gln Ala Ala Val Val Ala Ile Met Ala Phe Gly Met Thr Phe Val
65   70   75   80
Ile Val Thr Ser Gly Ile Asp Leu Ser Val Gly Ser Val Ala Ala Leu
                85   90   95
Ser Ala Met

<210> 639
<211> 330
<212> DNA
<213> Homo sapiens

<400> 639
nacgcgtcga tgggcaacta catcttcagt cgggatgccc tggtcgaggc actcttcgca
60
gactcccagt ccgctgagtc gcgtcatgac atgggtggcg acatcatccc gagattcgtc
120
gaggccgggg acgcgcaggt ctacgacttc tgtgacaacc aggtgcccgg aaccaccgag
180
aaggatcggg actactggcg ggacgtggga actatcgatg cctaccacga cgcgcacatg
240
gacctcgtgt cggtggaacc ggagttcaac ctctacaacc ccgactggcc gatctggagc
300
atccaggaac aggcaccggg agcgaaattt
330

<210> 640
<211> 110
<212> PRT
<213> Homo sapiens

<400> 640
Xaa Ala Ser Met Gly Asn Tyr Ile Phe Ser Arg Asp Ala Leu Val Glu
1 5 10 15
Ala Leu Phe Ala Asp Ser Gln Ser Ala Glu Ser Arg His Asp Met Gly
20 25 30
Gly Asp Ile Ile Pro Arg Phe Val Glu Ala Gly Asp Ala Gln Val Tyr
35 40 45
Asp Phe Cys Asp Asn Gln Val Pro Gly Thr Thr Glu Lys Asp Arg Asp
50 55 60
Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Tyr His Asp Ala His Met
65 70 75 80
Asp Leu Val Ser Val Glu Pro Glu Phe Asn Leu Tyr Asn Pro Asp Trp
85 90 95
Pro Ile Trp Ser Ile Gln Glu Gln Ala Pro Gly Ala Lys Phe
100 105 110

<210> 641
<211> 491
<212> DNA
<213> Homo sapiens

<400> 641
cgcgtgaccg gcgcggagaa cgtgcgcaag atcctcatgg gcgagcacca cctcgtgagc
60
accgagtggc ctcgcagcac ccgcatgttg ctgggcccca acacggtgtc caattccatt
120
ggcgacatcc accgcaacaa gcgcaaggtc ttctccaaga tcttcagcca cgaggccctg
180
gagagttacc tgcccaagat ccagctggtg atccaggaca cactgcgcgc ctggagcagc
240
caccccgagg ccatcaacgt gtaccaggag gcgcagaagc tgaccttccg catggccatc
300
cgggtgctgc tgggcttcag catccctgag gaggaccttg ggcacctctt tgaggtctac
360
cagcagtttg tggacaatgt cttctccctg cctgtcgacc tgcccttcag tggctaccgg
420
cggggcattc aggctcggca gatcctgcag aaggggctgg agaaggccat ccgggagaag
480
ctgcagtgca c
491

<210> 642
<211> 163
<212> PRT
<213> Homo sapiens

<400> 642
Arg Val Thr Gly Ala Glu Asn Val Arg Lys Ile Leu Met Gly Glu His
1 5 10 15
His Leu Val Ser Thr Glu Trp Pro Arg Ser Thr Arg Met Leu Leu Gly
20 25 30
Pro Asn Thr Val Ser Asn Ser Ile Gly Asp Ile His Arg Asn Lys Arg
35 40 45
Lys Val Phe Ser Lys Ile Phe Ser His Glu Ala Leu Glu Ser Tyr Leu

```
    50                  55                  60
Pro Lys Ile Gln Leu Val Ile Gln Asp Thr Leu Arg Ala Trp Ser Ser
65                  70                  75                  80
His Pro Glu Ala Ile Asn Val Tyr Gln Glu Ala Gln Lys Leu Thr Phe
                85                  90                  95
Arg Met Ala Ile Arg Val Leu Leu Gly Phe Ser Ile Pro Glu Glu Asp
            100                 105                 110
Leu Gly His Leu Phe Glu Val Tyr Gln Gln Phe Val Asp Asn Val Phe
        115                 120                 125
Ser Leu Pro Val Asp Leu Pro Phe Ser Gly Tyr Arg Arg Gly Ile Gln
    130                 135                 140
Ala Arg Gln Ile Leu Gln Lys Gly Leu Glu Lys Ala Ile Arg Glu Lys
145                 150                 155                 160
Leu Gln Cys
```

<210> 643
<211> 628
<212> DNA
<213> Homo sapiens

<400> 643
nagatctttg acatctacgt ggtcaccgct gactacctgc ccctaggggc tgagcaggat
60
gccatcacgc tgcgggaagg ccagtatgtg gaggtcctgg atgcagccca cccactgcgc
120
tggcttgtcc gcaccaagcc caccaagtcc agcccctcac ggcagggctg ggtgtcacca
180
gcctacctgg acaggaggct caagctgtca cctgagtggg gggccgctga ggcccctgag
240
ttccctgggg aggctgtgtc tgaagacgaa tacaaggcaa ggctgagctc tgtgatccag
300
gagctgctga gttctgagca ggccttcgtg gaggagctgc agttcctgca gagccaccac
360
ctgcagcacc tggagcgctg cccccacgtg cccatagctg tggccggcca gaaggcagtc
420
atcttccgca atgtgcggga catcggccgc ttccacagca gcttcctgca ggagttgcag
480
cagtgcgaca cggacgacga cgtggccatg tgcttcatca agaaccaggc ggcctttgag
540
cagtacctgg agttcctggt gggacgtgtg caggctgagt cggtggtcgt cagcacggcc
600
atccaggagt tctacaagaa atacgcgt
628

<210> 644
<211> 209
<212> PRT
<213> Homo sapiens

<400> 644
```
Xaa Ile Phe Asp Ile Tyr Val Val Thr Ala Asp Tyr Leu Pro Leu Gly
 1               5                  10                  15
Ala Glu Gln Asp Ala Ile Thr Leu Arg Glu Gly Gln Tyr Val Glu Val
```

```
            20                  25                  30
Leu Asp Ala Ala His Pro Leu Arg Trp Leu Val Arg Thr Lys Pro Thr
        35                  40                  45
Lys Ser Ser Pro Ser Arg Gln Gly Trp Val Ser Pro Ala Tyr Leu Asp
    50                  55                  60
Arg Arg Leu Lys Leu Ser Pro Glu Trp Gly Ala Ala Glu Ala Pro Glu
65                  70                  75                  80
Phe Pro Gly Glu Ala Val Ser Glu Asp Glu Tyr Lys Ala Arg Leu Ser
                85                  90                  95
Ser Val Ile Gln Glu Leu Leu Ser Ser Glu Gln Ala Phe Val Glu Glu
            100                 105                 110
Leu Gln Phe Leu Gln Ser His His Leu Gln His Leu Glu Arg Cys Pro
        115                 120                 125
His Val Pro Ile Ala Val Ala Gly Gln Lys Ala Val Ile Phe Arg Asn
    130                 135                 140
Val Arg Asp Ile Gly Arg Phe His Ser Ser Phe Leu Gln Glu Leu Gln
145                 150                 155                 160
Gln Cys Asp Thr Asp Asp Asp Val Ala Met Cys Phe Ile Lys Asn Gln
                165                 170                 175
Ala Ala Phe Glu Gln Tyr Leu Glu Phe Leu Val Gly Arg Val Gln Ala
            180                 185                 190
Glu Ser Val Val Val Ser Thr Ala Ile Gln Glu Phe Tyr Lys Lys Tyr
        195                 200                 205
Ala
```

<210> 645
<211> 417
<212> DNA
<213> Homo sapiens

<400> 645
atccataggc attgccagag tattcacttc ctgttggagg cacacagggg agaggcctgt
60
gaggggaagg gcatcaatgc agggctgggg tgtgggaagg tctgcagggc tggcaatggg
120
caagctcagg aatggtgggg gagacagttg gagccacggc agggacaatg gagctcagaa
180
ggtccctctg tcatcccttt tggaacccat tgatctggaa aatttggggc agtgtccttt
240
tccgtaggta ctggaggcac tggcttgaca tactacagcc ctcccaggag gcccagaagg
300
tagatgttat aactaccccc attttccaga tgaagaaact gagcctctgg gatctgcgga
360
agctcccaga gctggagcag ttagtccctg ggccctacac tcacagcaca gtttccc
417

<210> 646
<211> 95
<212> PRT
<213> Homo sapiens

<400> 646
Met Val Gly Glu Thr Val Gly Ala Thr Ala Gly Thr Met Glu Leu Arg

```
 1               5                  10                  15
Arg Ser Leu Cys His Pro Phe Trp Asn Pro Leu Ile Trp Lys Ile Trp
            20                  25                  30
Gly Ser Val Leu Phe Arg Arg Tyr Trp Arg His Trp Leu Asp Ile Leu
        35                  40                  45
Gln Pro Ser Gln Glu Ala Gln Lys Val Asp Val Ile Thr Thr Pro Ile
    50                  55                  60
Phe Gln Met Lys Lys Leu Ser Leu Trp Asp Leu Arg Lys Leu Pro Glu
65                  70                  75                  80
Leu Glu Gln Leu Val Pro Gly Pro Tyr Thr His Ser Thr Val Ser
                85                  90                  95
```

<210> 647
<211> 421
<212> DNA
<213> Homo sapiens

<400> 647
acgcgtttcg gttcttgagc gcttccacca attcagcggt ggtgagcggc ccctgtgcat
60
cgcgcagcag ggtgatcaga taggcgatat ccgcctcgtt cagttgcacg gtgtcgttat
120
cggtagccat gcgtggcgaa ctcctttggc atgggaaaat cgggtgaggc caacgggcac
180
agcaacagga cgtgtccctt gcggcacgtg gcaacacgtc agtatagcgc gtttccgccg
240
ggatttccgt tgaatgaagg caagaagtcg ggcacgcatc cacctgctac cgctcggtgg
300
tacgatagcc gcggcgccac caggttggct acattccaaa cgcaacgcag gaacccgcat
360
gaacagcgtt tttcgcaaca aaccccttat gacgctggct ctcgggcatt tcagtgtcga
420
c
421

<210> 648
<211> 90
<212> PRT
<213> Homo sapiens

<400> 648
```
Met Gly Lys Ser Gly Glu Ala Asn Gly His Ser Asn Arg Thr Cys Pro
 1               5                  10                  15
Leu Arg His Val Ala Thr Arg Gln Tyr Ser Ala Phe Pro Pro Gly Phe
            20                  25                  30
Pro Leu Asn Glu Gly Lys Lys Ser Gly Thr His Pro Pro Ala Thr Ala
        35                  40                  45
Arg Trp Tyr Asp Ser Arg Gly Ala Thr Arg Leu Ala Thr Phe Gln Thr
    50                  55                  60
Gln Arg Arg Asn Pro His Glu Gln Arg Phe Ser Gln Gln Thr Pro Tyr
65                  70                  75                  80
Asp Ala Gly Ser Arg Ala Phe Gln Cys Arg
                85                  90
```

<210> 649
<211> 563
<212> DNA
<213> Homo sapiens

<400> 649
cgcaacatgc ataaacacat gtgctcctcc gagactcagc tacttccttt gccctctctg
60
gacctcagtg tccaggcttg tgcatttagg ggctcaggtt tgggctctgt gcctatgagc
120
cagtctatgt gtgcactgtc tgtctgtctg tccgtctgcc agcaaccttc aaggccccag
180
gaggggaagg caccaatgga aggtgggggc agggaaggag gtagcgttga caagttccaa
240
tgtctggctt tccctcctgg aaaccccgag ctggggctgg ccccccccttc ccttcctgtc
300
tctctcgctc aagcacgtcc cttctaagag cccctctctg cagacgcccc cagtggaacc
360
aagcctagat tcgctgccaa gaaggccgac atttttttaga cttgccacgt taaaggggcc
420
tgcacaggca cgcactcaaa tccccccctc catgtcctcc gcctgtgcac attcaggcaa
480
cccgaaacac acaaagacac ggttggacac agcggccacc tgtgcacaca ggaggtagca
540
catggagcgc atctgacccc ggg
563

<210> 650
<211> 106
<212> PRT
<213> Homo sapiens

<400> 650
Met His Lys His Met Cys Ser Ser Glu Thr Gln Leu Leu Pro Leu Pro
 1   5   10   15
Ser Leu Asp Leu Ser Val Gln Ala Cys Ala Phe Arg Gly Ser Gly Leu
            20   25   30
Gly Ser Val Pro Met Ser Gln Ser Met Cys Ala Leu Ser Val Cys Leu
        35   40   45
Ser Val Cys Gln Gln Pro Ser Arg Pro Gln Glu Gly Lys Ala Pro Met
    50   55   60
Glu Gly Gly Gly Arg Glu Gly Gly Ser Val Asp Lys Phe Gln Cys Leu
65   70   75   80
Ala Phe Pro Pro Gly Asn Pro Glu Leu Gly Leu Ala Pro Pro Ser Leu
                85   90   95
Pro Val Ser Leu Ala Gln Ala Arg Pro Phe
            100   105

<210> 651
<211> 351
<212> DNA
<213> Homo sapiens

<400> 651

gaattcttca acaagctctc ctgctctagg atcaaggata gacctataca aggtccaaac
60
cataatggag tccatggggt caaagttatc tcctggagct cagcagttga tggatatggt
120
taggtgtcag cagcggaatt gtattcccat tggagagcag cttcagtcgg tgttgggcaa
180
ttctggatac aagcatatga ttggactaca atcctcatct accttaggaa ccttaaacaa
240
gtcgtcctcc acacctttc cttttagaac tggattgaca tctgggaacg tgactgaaaa
300
cttacaagcg tacattgata aaagtacaca actgcctggt ggagagaatt c
351

<210> 652
<211> 95
<212> PRT
<213> Homo sapiens

<400> 652
Met Glu Ser Met Gly Ser Lys Leu Ser Pro Gly Ala Gln Gln Leu Met
1 5 10 15
Asp Met Val Arg Cys Gln Gln Arg Asn Cys Ile Pro Ile Gly Glu Gln
20 25 30
Leu Gln Ser Val Leu Gly Asn Ser Gly Tyr Lys His Met Ile Gly Leu
35 40 45
Gln Ser Ser Ser Thr Leu Gly Thr Leu Asn Lys Ser Ser Ser Thr Pro
50 55 60
Phe Pro Phe Arg Thr Gly Leu Thr Ser Gly Asn Val Thr Glu Asn Leu
65 70 75 80
Gln Ala Tyr Ile Asp Lys Ser Thr Gln Leu Pro Gly Gly Glu Asn
85 90 95

<210> 653
<211> 399
<212> DNA
<213> Homo sapiens

<400> 653
nncccgggtg gggctggggt ggggccagca tcagaggagg acatgaccaa gctgtgcaac
60
caccggcgga aagctgttgc tatggcaact ctgtaccgca gcatggagac cacctgctca
120
cactcttctc ctggagaggg agcgagcccc caaatgttcc acactgtgtc cccagggccc
180
ccctctgccc gccctccctg tcgagttcct cctacaactc cacttaatgg gggtcctggc
240
tcccttcccc cagaaccacc ctcagtttcc caggcctttc ccactctagc aggccctggg
300
gggcttttcc ccccaaggct tgctgaccca gtcccttctg ggggcagtag cagcccccgt
360
ttcctcccaa ggggcaatgc ccccctctcca gccccacct
399

<210> 654

<211> 133
<212> PRT
<213> Homo sapiens

<400> 654
Xaa Pro Gly Gly Ala Gly Val Gly Pro Ala Ser Glu Glu Asp Met Thr
1 5 10 15
Lys Leu Cys Asn His Arg Arg Lys Ala Val Ala Met Ala Thr Leu Tyr
20 25 30
Arg Ser Met Glu Thr Thr Cys Ser His Ser Ser Pro Gly Glu Gly Ala
35 40 45
Ser Pro Gln Met Phe His Thr Val Ser Pro Gly Pro Pro Ser Ala Arg
50 55 60
Pro Pro Cys Arg Val Pro Pro Thr Thr Pro Leu Asn Gly Gly Pro Gly
65 70 75 80
Ser Leu Pro Pro Glu Pro Pro Ser Val Ser Gln Ala Phe Pro Thr Leu
85 90 95
Ala Gly Pro Gly Gly Leu Phe Pro Pro Arg Leu Ala Asp Pro Val Pro
100 105 110
Ser Gly Gly Ser Ser Ser Pro Arg Phe Leu Pro Arg Gly Asn Ala Pro
115 120 125
Ser Pro Ala Pro Pro
130

<210> 655
<211> 368
<212> DNA
<213> Homo sapiens

<400> 655
tgaaggaaat tctctatggc ttgtgttcat catgtagaac agcccatgag gagaatagga
60
gatgaggtgg gaagtgcact gggatctggg ggaagaagcc cggggttcaa gactcagcta
120
ctgactgcat ggtgtcaaag gattcgggca tcctctctga ggctgagtct tcagatgaca
180
gtgagaacag ggacacctgc cctgcccttc tcacggggcg tgtgggcacc catgagcatg
240
cttgacaaat gcaaggtgcc atacaaacag gaactgcaca atctcaccgc ccggcctact
300
cagcattgtt atttttacct ttacatctat atgaagatgt agttccattc cttttaactg
360
ttgttttc
368

<210> 656
<211> 108
<212> PRT
<213> Homo sapiens

<400> 656
Met Ala Cys Val His His Val Glu Gln Pro Met Arg Arg Ile Gly Asp
1 5 10 15
Glu Val Gly Ser Ala Leu Gly Ser Gly Gly Arg Ser Pro Gly Phe Lys

```
            20                  25                  30
Thr Gln Leu Leu Thr Ala Trp Cys Gln Arg Ile Arg Ala Ser Ser Leu
        35                  40                  45
Arg Leu Ser Leu Gln Met Thr Val Arg Thr Gly Thr Pro Ala Leu Pro
    50                  55                  60
Phe Ser Arg Gly Val Trp Ala Pro Met Ser Met Leu Asp Lys Cys Lys
65                  70                  75                  80
Val Pro Tyr Lys Gln Glu Leu His Asn Leu Thr Ala Arg Pro Thr Gln
                85                  90                  95
His Cys Tyr Phe Tyr Leu Tyr Ile Tyr Met Lys Met
            100                 105
```

<210> 657
<211> 330
<212> DNA
<213> Homo sapiens

<400> 657
gtcgaccacg gcatgaaaaa gccggggatg atcctcatca acaacccctg gggcgagtcc
60
aacgaggcgg gcttcaagcg cgccctcgaa gagcgtggca tggccaacgc cggtgtcgag
120
cgtattcagg acagcgacct ggacgtggtg ccgcaattga ccccgcctga aaaacgccgg
180
tgccgacacc ttgctgatgg tcggcaacgt cggcccttcg gcacaggtgg tcaagtccct
240
ggaccgcatg ggttgggacg tgcctgtggt gtctcactgg gggccggccg gnggtcgctt
300
tggcgagctg gcggggccta acgcttctcg
330

<210> 658
<211> 102
<212> PRT
<213> Homo sapiens

<400> 658
```
Met Lys Lys Pro Gly Met Ile Leu Ile Asn Asn Pro Trp Gly Glu Ser
 1               5                  10                  15
Asn Glu Ala Gly Phe Lys Arg Ala Leu Glu Glu Arg Gly Met Ala Asn
            20                  25                  30
Ala Gly Val Glu Arg Ile Gln Asp Ser Asp Leu Asp Val Val Pro Gln
        35                  40                  45
Leu Thr Pro Pro Glu Lys Arg Arg Cys Arg His Leu Ala Asp Gly Arg
    50                  55                  60
Gln Arg Arg Pro Phe Gly Thr Gly Gly Gln Val Pro Gly Pro His Gly
65                  70                  75                  80
Leu Gly Arg Ala Cys Gly Val Ser Leu Gly Ala Gly Arg Xaa Ser Leu
                85                  90                  95
Trp Arg Ala Gly Gly Ala
            100
```

<210> 659
<211> 1505

<212> DNA
<213> Homo sapiens

<400> 659
gccaggatca tgtccaccac cacatgccaa gtggtggcgt tcctcctgtc catcctgggg
60
ctggccggct gcatcgcggc caccgggatg gacatgtgga gcacccagga cctgtacgac
120
aaccccgtca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt gaggcagagt
180
tcaggcttca ccgaatgcag gccctatttc accatcctgg gacttccagc catgctgcag
240
gcagtgcgag ccctgatgat cgtaggcatc gtcctgggtg ccattggcct cctggtatcc
300
atctttgccc tgaaatgcat ccgcattggc agcatggagg actctgccaa agccaacatg
360
acactgacct ccgggatcat gttcattgtc tcaggtcttt gtgcaattgc tggagtgtct
420
gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat gtacaccggc
480
atgggtggga tggtgcagac tgttcagacc aggtacacat ttggtgcggc tctgttcgtg
540
ggctgggtcg ctggaggcct cacactaatt gggggtgtga tgatgtgcat cgcctgccgg
600
ggcctggcac cagaagaaac caactacaaa gccgtttctt atcatgcctc aggccacagt
660
gttgcctaca agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac
720
aagaagatat acgatggagg tgcccgcaca gaggacgagg tacaatctta tccttccaag
780
cacgactatg tgtaatgctc taagacctct cagcacgggc ggaagaaact cccggagagc
840
tcacccaaaa aacaaggaga tcccatctag atttcttctt gcttttgact cacagctgga
900
agttagaaaa gcctcgattt catctttgga gaggccaagt ggtcttagcc tcagtctctg
960
tctctaaata ttccaccata aaacagctga gttatttatg aattagaagc tatagctcac
1020
attttcaatc ctctatttct ttttttaaat ataactttct actctgatga gagaatgtgg
1080
ttttaatctc tctctcacat tttgatgatt tagacagact ccccctcttc ctcctagtca
1140
ataaacccat tgatgatcta tttcccagct tatccccaag aaaacttttg aaaggaaaga
1200
gtagacccaa agatgttatt ttctgctgtt tgaattttgt ctccccaccc ccaacttggc
1260
tagtaataaa cacttactga agaagaagca ataagagaaa gatatttgta atctctccag
1320
cccatgatct cggttttctt acactgtgat cttaaaagtt accaaaccaa agtcattttc
1380
agtttgaggc aaccaaacct ttctactgct gttgacatct tcttattaca gcaacaccat
1440
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1500

taccc
1505

<210> 660
<211> 261
<212> PRT
<213> Homo sapiens

<400> 660
Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
1 5 10 15
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
20 25 30
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
35 40 45
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
50 55 60
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
65 70 75 80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
85 90 95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
100 105 110
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
115 120 125
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
130 135 140
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145 150 155 160
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
165 170 175
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
180 185 190
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
195 200 205
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
210 215 220
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
225 230 235 240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
245 250 255
Lys His Asp Tyr Val
260

<210> 661
<211> 451
<212> DNA
<213> Homo sapiens

<400> 661
nnacgcgtgt agtttgtgta tcggcgcgga actcgccgcg tctgatctcg aggagcttcc
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cccatggacg agattttaac cttgcttgcc ggaggcggtg acgacgagcc agagtggcat
120

gacaaggcat tatgtgccca gactgatccg gaggcattct tccctgaaaa gggtggatcc
180
acccgtgagg ccaagcgcat ctgtgagtcc tgtgaggtcc gccaggagtg cttggagtac
240
gcccttgcga atgacgagag gttcggaatc tggggcggat tgtccgagat ggagaggcgt
300
cggctgcgca agcgggcgtg acctgacgtc ggagcgcggt tattgacacg gcccggtaaa
360
atgccctgtc tgcccgggat ggctgtctgc acgatgcggc atatgcgatg atcgcagacg
420
tggtgtgcat cccgtgctcc atgacgtcga c
451

<210> 662
<211> 85
<212> PRT
<213> Homo sapiens

<400> 662
Met Asp Glu Ile Leu Thr Leu Leu Ala Gly Gly Gly Asp Asp Glu Pro
1 5 10 15
Glu Trp His Asp Lys Ala Leu Cys Ala Gln Thr Asp Pro Glu Ala Phe
20 25 30
Phe Pro Glu Lys Gly Gly Ser Thr Arg Glu Ala Lys Arg Ile Cys Glu
35 40 45
Ser Cys Glu Val Arg Gln Glu Cys Leu Glu Tyr Ala Leu Ala Asn Asp
50 55 60
Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu Met Glu Arg Arg Arg
65 70 75 80
Leu Arg Lys Arg Ala
85

<210> 663
<211> 552
<212> DNA
<213> Homo sapiens

<400> 663
ctcgagcgtc tcgacgccga cgccgcccag ggagccaagg aagacctctc gcagcgcgac
60
ccctacgacg tgctcgtcgt aggggcgggt cccgccggtg ccgcggccgc cgtgtacgcg
120
gctcgtaagg gcattcgcac cgccatggtc gggtctcgga tcggcggcca ggtactcgat
180
accgaggcca tcgacaacct catctcggtg ccgcacacca ccggtccgcg tctggccgac
240
gccctccgca gccacgtcaa cgactacaac attgacgtta ttgagcgtca gaccgccagc
300
gccatagaga ccaccggcgg tatgaccacc gtgcatctga ccgacggcga cctgcgggcg
360
cgctcagtca tcgtggccac cggtgcccgc tggcgcaacc ttggcgtacc tggcgaggag
420
gaataccgca ccaagggtgt gacctactgc ccgcactgcg atggcccgct attcacaggc
480

aaaaaggtgg ccgtcgtcgg aggtggaaac tccggtattg aggccgctat cgacctcgcc
540
ggcgtcgtcg ac
552

<210> 664
<211> 184
<212> PRT
<213> Homo sapiens

<400> 664
Leu Glu Arg Leu Asp Ala Asp Ala Ala Gln Gly Ala Lys Glu Asp Leu
1 5 10 15
Ser Gln Arg Asp Pro Tyr Asp Val Leu Val Val Gly Ala Gly Pro Ala
20 25 30
Gly Ala Ala Ala Ala Val Tyr Ala Ala Arg Lys Gly Ile Arg Thr Ala
35 40 45
Met Val Gly Ser Arg Ile Gly Gly Gln Val Leu Asp Thr Glu Ala Ile
50 55 60
Asp Asn Leu Ile Ser Val Pro His Thr Thr Gly Pro Arg Leu Ala Asp
65 70 75 80
Ala Leu Arg Ser His Val Asn Asp Tyr Asn Ile Asp Val Ile Glu Arg
85 90 95
Gln Thr Ala Ser Ala Ile Glu Thr Thr Gly Gly Met Thr Thr Val His
100 105 110
Leu Thr Asp Gly Asp Leu Arg Ala Arg Ser Val Ile Val Ala Thr Gly
115 120 125
Ala Arg Trp Arg Asn Leu Gly Val Pro Gly Glu Glu Glu Tyr Arg Thr
130 135 140
Lys Gly Val Thr Tyr Cys Pro His Cys Asp Gly Pro Leu Phe Thr Gly
145 150 155 160
Lys Lys Val Ala Val Val Gly Gly Gly Asn Ser Gly Ile Glu Ala Ala
165 170 175
Ile Asp Leu Ala Gly Val Val Asp
180

<210> 665
<211> 352
<212> DNA
<213> Homo sapiens

<400> 665
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acacgctctt catttcgccc ggcagcagtt cggcgccggc gcagacaaag gtccaggcct
120
cgctcacgcg gtggccccgg ccagcggctt ttccaggatc tcgaaacgca ggtcgtcgcg
180
cttggggatg ccgaatcgtt cgtcgccata cgggaacggc ttcttgatgc cggtgcgcag
240
gtagccgcgg cgctcgtaga agcgatcaga tcgcgcgcac gtcgatcact gtcatctgca
300
ttaccggcac gttccattcg cgcgcggcgt gggcttcggc ggcgtccatc aa
352

<210> 666
<211> 105
<212> PRT
<213> Homo sapiens

<400> 666
Met Glu Arg Ala Gly Asn Ala Asp Asp Ser Asp Arg Arg Ala Arg Asp
1 5 10 15
Leu Ile Ala Ser Thr Ser Ala Ala Ala Thr Cys Ala Pro Ala Ser Arg
20 25 30
Ser Arg Ser Arg Met Ala Thr Asn Asp Ser Ala Ser Pro Ser Ala Thr
35 40 45
Thr Cys Val Ser Arg Ser Trp Lys Ser Arg Trp Pro Gly Pro Pro Arg
50 55 60
Glu Arg Gly Leu Asp Leu Cys Leu Arg Arg Arg Arg Thr Ala Ala Gly
65 70 75 80
Arg Asn Glu Glu Arg Val Arg Arg Ser Asp Arg Tyr Thr Asp Arg Gly
85 90 95
Val Gln Pro Arg Arg Arg Thr Val Arg
100 105

<210> 667
<211> 391
<212> DNA
<213> Homo sapiens

<400> 667
nacgcgtacg aatcggtgtt gcgtcgcaac ccaggggagg ccgagttcca ccaggctgtg
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cgggagatct ttgaatctct cggcccggtg ctcgacaaga atccgcagta cgtggaggca
120
gccgtgttgt cgcgcatctg cgaaccggaa cgccagatca ttttccgggt gccgtgggtt
180
gacgacgagg gcaagatccg tatcaaccgt ggcttccgcg ttgaatattc gtcggtactg
240
gggccgtata agggtggatt gcgattccac ccctcggtgt acttaggaac gattaagttc
300
cttggttttg agcagatctt caaaaatgct ctgactggca tgccgatcgg tggcgcgaag
360
ggtgggtcgg actttgatcc ccatgacgcg t
391

<210> 668
<211> 130
<212> PRT
<213> Homo sapiens

<400> 668
Xaa Ala Tyr Glu Ser Val Leu Arg Arg Asn Pro Gly Glu Ala Glu Phe
1 5 10 15
His Gln Ala Val Arg Glu Ile Phe Glu Ser Leu Gly Pro Val Leu Asp
20 25 30
Lys Asn Pro Gln Tyr Val Glu Ala Ala Val Leu Ser Arg Ile Cys Glu

```
        35                  40                  45
Pro Glu Arg Gln Ile Ile Phe Arg Val Pro Trp Val Asp Asp Glu Gly
    50                  55                  60
Lys Ile Arg Ile Asn Arg Gly Phe Arg Val Glu Tyr Ser Ser Val Leu
65                  70                  75                  80
Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Tyr Leu Gly
                85                  90                  95
Thr Ile Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn Ala Leu Thr
            100                 105                 110
Gly Met Pro Ile Gly Gly Ala Lys Gly Gly Ser Asp Phe Asp Pro His
        115                 120                 125
Asp Ala
    130
```

<210> 669
<211> 707
<212> DNA
<213> Homo sapiens

<400> 669
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attgagaaca cccttgctgc cttcggccac gcggtcgagg tgggatgcac ctaccttgaa
120
actgacgttc acgcgaccag cgacggggtg ctagtggcct tccacgatcc gatactcgat
180
cgcgtcactg aatcaggcgg agtcatcgcc gccatgccgt ggcacaaggt caaacaagcc
240
aaggttggtg gcgaaccgat ccccacctta gatgagattt tcgacgcctt tcccgacgcg
300
ttcatcaata tcgacatcaa gcatgatggc gccaccatgc cgctcatcga cgttctttcc
360
cgtcaccggg cttggagtcg ggtttgcgtc gggtcgttca gcagtaaacg catccagacc
420
ttccgtcgcc tggttcaggg acgcactgcg actgcagtgg ggtcggtggg agtcnnggct
480
gggctgtcat cagccctcat agcatgcaga tggcacagtc ccatgggaat gcgtaccagg
540
tgccgcaccg cttgacccgg tnatggggtg ccccttgtga caccgacctt cattaaagct
600
gcccatcgtc aggggcgagc tgttcatgtc tggacggtta atgagatctc tgaggctcga
660
gaactgatgg atatgggggt cgacggcatc gtcacagatc gtccgga
707

<210> 670
<211> 170
<212> PRT
<213> Homo sapiens

<400> 670
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Met Ala Val Asn Lys Gly Ile Glu Asn Thr Leu Ala Ala Phe Gly His
 1               5                  10                  15
Ala Val Glu Val Gly Cys Thr Tyr Leu Glu Thr Asp Val His Ala Thr
```

```
            20                  25                  30
Ser Asp Gly Val Leu Val Ala Phe His Asp Pro Ile Leu Asp Arg Val
        35                  40                  45
Thr Glu Ser Gly Gly Val Ile Ala Ala Met Pro Trp His Lys Val Lys
    50                  55                  60
Gln Ala Lys Val Gly Gly Glu Pro Ile Pro Thr Leu Asp Glu Ile Phe
65                  70                  75                  80
Asp Ala Phe Pro Asp Ala Phe Ile Asn Ile Asp Ile Lys His Asp Gly
                85                  90                  95
Ala Thr Met Pro Leu Ile Asp Val Leu Ser Arg His Arg Ala Trp Ser
            100                 105                 110
Arg Val Cys Val Gly Ser Phe Ser Ser Lys Arg Ile Gln Thr Phe Arg
        115                 120                 125
Arg Leu Val Gln Gly Arg Thr Ala Thr Ala Val Gly Ser Val Gly Val
    130                 135                 140
Xaa Ala Gly Leu Ser Ser Ala Leu Ile Ala Cys Arg Trp His Ser Pro
145                 150                 155                 160
Met Gly Met Arg Thr Arg Cys Arg Thr Ala
                165                 170
```

<210> 671
<211> 444
<212> DNA
<213> Homo sapiens

<400> 671
acgcgtgggc cttcgggttg atgggatcag aaggggacgg gacctgtaga aaggggcctg
60
cagctcagag catggggcgg ccttggctca ctacgcctgc agctgtgaat tcgttctccg
120
gtgctggaga gggatctggt tatctccatt ctcttgtctc cacgtggaaa ggaaggacgt
180
gcgctctcat cctacgtgtt ttgagaaatc gcattgtccc cagctctgcg ggaggatctg
240
gggacgcagt ggggaaccag acaggcagtt ggaggtctag tgcgcgccag aagccagttc
300
ccacccaggg tgccatttgc tgggcgccct agggagctgc gtgggcatcc agaggagtga
360
gtcgcccccc gctctgctca gtgcccactt ccccgggcag ggcaggcgtt attaacgtag
420
agggagaaca cccatgcaca caac
444

<210> 672
<211> 103
<212> PRT
<213> Homo sapiens

<400> 672
```
Met Gly Ser Glu Gly Asp Gly Thr Cys Arg Lys Gly Pro Ala Ala Gln
 1               5                  10                  15
Ser Met Gly Arg Pro Trp Leu Thr Thr Pro Ala Ala Val Asn Ser Phe
            20                  25                  30
Ser Gly Ala Gly Glu Gly Ser Gly Tyr Leu His Ser Leu Val Ser Thr
```

```
        35                  40                  45
Trp Lys Gly Arg Thr Cys Ala Leu Ile Leu Arg Val Leu Arg Asn Arg
    50                  55                  60
Ile Val Pro Ser Ser Ala Gly Gly Ser Gly Asp Ala Val Gly Asn Gln
65                  70                  75                  80
Thr Gly Ser Trp Arg Ser Ser Ala Arg Gln Lys Pro Val Pro Thr Gln
                85                  90                  95
Gly Ala Ile Cys Trp Ala Pro
            100
```

<210> 673
<211> 452
<212> DNA
<213> Homo sapiens

<400> 673
acgcgtccct gcagaaatcc tctcggccta ggtcatccgc aagatgtggc agggcatgca
60
ccgtgaaagc cttcaagtct gccgcagcaa gaccgcacgc ctgctgaaat tcgcagttgt
120
gccgcggtcc ctgatgcgga caaactcggc caccacgatc agcctgacgc ttgcggacca
180
acgttcaaat actgtgcact tgaaacgtcc gggccgcatc acctgggtga ctttgtgcga
240
ccgacattac ttatgttcac gctctttcag ttcttgtcaa taccgtattt ttcgtcgacg
300
tctccatcag aaaaatgtcg gtgttaccgc accgcagacg atgcgtaccc ttgcgctgac
360
gatggaggcc ttgaaaagtg cattagccac tactgggcga atctacggca aaaagctgtt
420
actaggcggt gattggggag gcccgtagtg gc
452

<210> 674
<211> 134
<212> PRT
<213> Homo sapiens

<400> 674
```
Met Trp Gln Gly Met His Arg Glu Ser Leu Gln Val Cys Arg Ser Lys
 1               5                  10                  15
Thr Ala Arg Leu Leu Lys Phe Ala Val Val Pro Arg Ser Leu Met Arg
            20                  25                  30
Thr Asn Ser Ala Thr Thr Ile Ser Leu Thr Leu Ala Asp Gln Arg Ser
        35                  40                  45
Asn Thr Val His Leu Lys Arg Pro Gly Arg Ile Thr Trp Val Thr Leu
    50                  55                  60
Cys Asp Arg His Tyr Leu Cys Ser Arg Ser Phe Ser Ser Cys Gln Tyr
65                  70                  75                  80
Arg Ile Phe Arg Arg Arg Leu His Gln Lys Asn Val Gly Val Thr Ala
                85                  90                  95
Pro Gln Thr Met Arg Thr Leu Ala Leu Thr Met Glu Ala Leu Lys Ser
            100                 105                 110
Ala Leu Ala Thr Thr Gly Arg Ile Tyr Gly Lys Lys Leu Leu Leu Gly
```

115 120 125
Gly Asp Trp Gly Gly Pro
130

<210> 675
<211> 8564
<212> DNA
<213> Homo sapiens

<400> 675
atgtcgggct ccacacagct tgtggcacag acgtggaggg ccactgagcc ccgctacccg
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ccccacagcc tttcctaccc agtgcagatc gcccggacgc acacggacgt cgggctcctg
120
gagtaccagc accactcccg cgactatgcc tcccacctgt cgccgggctc catcatccag
180
ccccagcggc ggaggccctc cctgctgtct gagttccagc ccgggaatga acggtcccag
240
gagctccacc tgcggccaga gtcccactca tacctgcccg agctggggaa gtcagagatg
300
gagttcattg aaagcaagcg ccctcggcta gagctgctgc ctgacccccc gctgcgaccg
360
tcacccctgc tggccacggg ccagcctgcg ggatctgaag acctcaccaa ggaccgtagc
420
ctgacgggca agctggaacc ggtgtctccc cccagccccc cgcacactga ccctgagctg
480
gagctggtgc cgccacggct gtccaaggag gagctgatcc agaacatgga ccgcgtggac
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cgagagatca ccatggtaga gcagcagatc tctaagctga agaagaagca gcaacagctg
600
gaggaggagg ctgccaagcc gcccgagcct gagaagcccg tgtcaccgcc gcccatcgag
660
tcgaagcacc gcagcctggt gcagatcatc tacgacgaga accggaagaa ggctgaagct
720
gcacatcgga ttctggaagg cctggggccc caggtggagc tgccgctgta caaccagccc
780
tccgacaccc ggcagtatca tgagaacatc aaaataaacc aggcgatgcg gaagaagcta
840
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900
cgctatgacc agctcatgga ggcctgggaa aaaaaggtgg agcgcatcga gaacaacccc
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cggcggcggg ccaaggagag caaggtgcgc gagtactacg aaaagcagtt ccctgagatc
1020
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1260
aaggtgtaca aagaccgcca ggtcatgaac atgtggagtg agcaggagaa ggagaccttc
1320

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1380
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1740
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1800
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1860
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1920
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3120
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4980
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35 40 45
Tyr Ala Ser His Leu Ser Pro Gly Ser Ile Ile Gln Pro Gln Arg Arg
50 55 60
Arg Pro Ser Leu Leu Ser Glu Phe Gln Pro Gly Asn Glu Arg Ser Gln
65 70 75 80
Glu Leu His Leu Arg Pro Glu Ser His Ser Tyr Leu Pro Glu Leu Gly
85 90 95
Lys Ser Glu Met Glu Phe Ile Glu Ser Lys Arg Pro Arg Leu Glu Leu
100 105 110
Leu Pro Asp Pro Leu Leu Arg Pro Ser Pro Leu Leu Ala Thr Gly Gln
115 120 125
Pro Ala Gly Ser Glu Asp Leu Thr Lys Asp Arg Ser Leu Thr Gly Lys
130 135 140
Leu Glu Pro Val Ser Pro Pro Ser Pro Pro His Thr Asp Pro Glu Leu
145 150 155 160
Glu Leu Val Pro Pro Arg Leu Ser Lys Glu Glu Leu Ile Gln Asn Met

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Asp Arg Val Asp Arg Glu Ile Thr Met Val Glu Gln Gln Ile Ser Lys
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Leu Lys Lys Lys Gln Gln Gln Leu Glu Glu Glu Ala Ala Lys Pro Pro
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Glu Pro Glu Lys Pro Val Ser Pro Pro Pro Ile Glu Ser Lys His Arg
    210                 215                 220
Ser Leu Val Gln Ile Ile Tyr Asp Glu Asn Arg Lys Lys Ala Glu Ala
225                 230                 235                 240
Ala His Arg Ile Leu Glu Gly Leu Gly Pro Gln Val Glu Leu Pro Leu
                245                 250                 255
Tyr Asn Gln Pro Ser Asp Thr Arg Gln Tyr His Glu Asn Ile Lys Ile
            260                 265                 270
Asn Gln Ala Met Arg Lys Lys Leu Ile Leu Tyr Phe Lys Arg Arg Asn
        275                 280                 285
His Ala Arg Lys Gln Trp Glu Gln Lys Phe Cys Gln Arg Tyr Asp Gln
    290                 295                 300
Leu Met Glu Ala Trp Glu Lys Lys Val Glu Arg Ile Glu Asn Asn Pro
305                 310                 315                 320
Arg Arg Arg Ala Lys Glu Ser Lys Val Arg Glu Tyr Tyr Glu Lys Gln
                325                 330                 335
Phe Pro Glu Ile Arg Lys Gln Arg Glu Leu Gln Glu Arg Met Gln Gly
            340                 345                 350
Arg Val Gly Gln Arg Gly Ser Gly Leu Ser Met Ser Ala Ala Arg Ser
        355                 360                 365
Glu His Glu Val Ser Glu Ile Ile Asp Gly Leu Ser Glu Gln Glu Asn
    370                 375                 380
Leu Glu Lys Gln Met Arg Gln Leu Ala Val Ile Pro Pro Met Leu Tyr
385                 390                 395                 400
Asp Ala Asp Gln Gln Arg Ile Lys Phe Ile Asn Met Asn Gly Leu Met
                405                 410                 415
Ala Asp Pro Met Lys Val Tyr Lys Asp Arg Gln Val Met Asn Met Trp
            420                 425                 430
Ser Glu Gln Glu Lys Glu Thr Phe Arg Glu Lys Phe Met Gln His Pro
        435                 440                 445
Lys Asn Phe Gly Leu Ile Ala Ser Phe Leu Glu Arg Lys Thr Val Ala
    450                 455                 460
Glu Cys Val Leu Tyr Tyr Tyr Leu Thr Lys Lys Asn Glu Asn Tyr Lys
465                 470                 475                 480
Ser Leu Val Arg Arg Ser Tyr Arg Arg Arg Gly Lys Ser Gln Gln Gln
                485                 490                 495
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro
            500                 505                 510
Met Pro Arg Ser Ser Gln Glu Glu Lys Asp Glu Lys Glu Lys Glu Lys
        515                 520                 525
Glu Ala Glu Lys Glu Glu Glu Lys Pro Glu Val Glu Asn Asp Lys Glu
    530                 535                 540
Asp Leu Leu Lys Glu Lys Thr Asp Asp Thr Ser Gly Glu Asp Asn Asp
545                 550                 555                 560
Glu Lys Glu Ala Val Ala Ser Lys Gly Arg Lys Thr Ala Asn Ser Gln
                565                 570                 575
Gly Arg Arg Lys Gly Arg Ile Thr Arg Ser Met Ala Asn Glu Ala Asn
            580                 585                 590
Ser Glu Glu Ala Ile Thr Pro Gln Gln Ser Ala Glu Leu Ala Ser Met
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595 600 605
Glu Leu Asn Glu Ser Ser Arg Trp Thr Glu Glu Glu Met Glu Thr Ala
610 615 620
Lys Lys Gly Leu Leu Glu His Gly Arg Asn Trp Ser Ala Ile Ala Arg
625 630 635 640
Met Val Gly Ser Lys Thr Val Ser Gln Cys Lys Asn Phe Tyr Phe Asn
645 650 655
Tyr Lys Lys Arg Gln Asn Leu Asp Glu Ile Leu Gln Gln His Lys Leu
660 665 670
Lys Met Glu Lys Glu Arg Asn Ala Arg Arg Lys Lys Lys Lys Ala Pro
675 680 685
Ala Ala Ala Ser Glu Glu Ala Ala Phe Pro Pro Val Val Glu Asp Glu
690 695 700
Glu Met Glu Ala Ser Gly Val Ser Gly Asn Glu Glu Glu Met Val Glu
705 710 715 720
Glu Ala Glu Ala Leu His Ala Ser Gly Asn Glu Val Pro Arg Gly Glu
725 730 735
Cys Ser Gly Pro Ala Thr Val Asn Asn Ser Ser Asp Thr Glu Ser Ile
740 745 750
Pro Ser Pro His Thr Glu Ala Ala Lys Asp Thr Gly Gln Asn Gly Pro
755 760 765
Lys Pro Pro Ala Thr Leu Gly Ala Asp Gly Pro Pro Pro Gly Pro Pro
770 775 780
Thr Pro Pro Arg Arg Thr Ser Arg Ala Pro Ile Glu Pro Thr Pro Ala
785 790 795 800
Ser Glu Ala Thr Gly Ala Pro Thr Pro Pro Pro Ala Pro Pro Ser Pro
805 810 815
Ser Ala Pro Pro Pro Val Val Pro Lys Glu Glu Lys Glu Glu Glu Thr
820 825 830
Ala Ala Ala Pro Pro Val Glu Glu Gly Glu Glu Gln Lys Pro Pro Ala
835 840 845
Ala Glu Glu Leu Ala Val Asp Thr Gly Lys Ala Glu Glu Pro Val Lys
850 855 860
Ser Glu Cys Thr Glu Glu Ala Glu Glu Gly Pro Ala Lys Gly Lys Asp
865 870 875 880
Ala Glu Ala Ala Glu Ala Thr Ala Glu Gly Ala Leu Lys Ala Glu Lys
885 890 895
Lys Glu Gly Gly Ser Gly Arg Ala Thr Thr Ala Lys Ser Ser Gly Ala
900 905 910
Pro Gln Asp Ser Asp Ser Ser Ala Thr Cys Ser Ala Asp Glu Val Asp
915 920 925
Glu Ala Glu Gly Gly Asp Lys Asn Arg Leu Leu Ser Pro Arg Pro Ser
930 935 940
Leu Leu Thr Pro Thr Gly Asp Pro Arg Ala Asn Ala Ser Pro Gln Lys
945 950 955 960
Pro Leu Asp Leu Lys Gln Leu Lys Gln Arg Ala Ala Ala Ile Pro Pro
965 970 975
Ile Gln Val Thr Lys Val His Glu Pro Pro Arg Glu Asp Ala Ala Pro
980 985 990
Thr Lys Pro Ala Pro Pro Ala Pro Pro Pro Pro Gln Asn Leu Gln Pro
995 1000 1005
Glu Ser Asp Ala Pro Gln Gln Pro Gly Ser Ser Pro Arg Gly Lys Ser
1010 1015 1020
Arg Ser Pro Ala Pro Pro Ala Asp Lys Glu Ala Phe Ala Ala Glu Ala

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Gln Lys Leu Pro Gly Asp Pro Pro Cys Trp Thr Ser Gly Leu Pro Phe
                1045                1050                1055
Pro Val Pro Pro Arg Glu Val Ile Lys Ala Ser Pro His Ala Pro Asp
            1060                1065                1070
Pro Ser Ala Phe Ser Tyr Ala Pro Pro Gly His Pro Leu Pro Leu Gly
        1075                1080                1085
Leu His Asp Thr Ala Arg Pro Val Leu Pro Arg Pro Pro Thr Ile Ser
    1090                1095                1100
Asn Pro Pro Pro Leu Ile Ser Ser Ala Lys His Pro Ser Val Leu Glu
1105                1110                1115                1120
Arg Gln Ile Gly Ala Ile Ser Gln Gly Met Ser Val Gln Leu His Val
                1125                1130                1135
Pro Tyr Ser Glu His Ala Lys Ala Pro Val Gly Pro Val Thr Met Gly
            1140                1145                1150
Leu Pro Leu Pro Met Asp Pro Lys Lys Leu Ala Pro Phe Ser Gly Val
        1155                1160                1165
Lys Gln Glu Gln Leu Ser Pro Arg Gly Gln Ala Gly Pro Pro Glu Ser
    1170                1175                1180
Leu Gly Val Pro Thr Ala Gln Glu Ala Ser Val Leu Arg Gly Thr Ala
1185                1190                1195                1200
Leu Gly Ser Val Pro Gly Gly Ser Ile Thr Lys Gly Ile Pro Ser Thr
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Arg Val Pro Ser Asp Ser Ala Ile Thr Tyr Arg Gly Ser Ile Thr His
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Gly Thr Pro Ala Asp Val Leu Tyr Lys Gly Thr Ile Thr Arg Ile Ile
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Gly Glu Asp Ser Pro Ser Arg Leu Asp Arg Gly Arg Glu Asp Ser Leu
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Pro Lys Gly His Val Ile Tyr Glu Gly Lys Lys Gly His Val Leu Ser
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Tyr Glu Gly Gly Met Ser Val Thr Gln Cys Ser Lys Glu Asp Gly Arg
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Ser Ser Ser Gly Pro Pro His Glu Thr Ala Ala Pro Lys Arg Thr Tyr
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Asp Met Met Glu Gly Arg Val Gly Arg Ala Ile Ser Ser Ala Ser Ile
        1315                1320                1325
Glu Gly Leu Met Gly Arg Ala Ile Pro Pro Glu Arg His Ser Pro His
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His Leu Lys Glu Gln His His Ile Arg Gly Ser Ile Thr Gln Gly Ile
1345                1350                1355                1360
Pro Arg Ser Tyr Val Glu Ala Gln Glu Asp Tyr Leu Arg Arg Glu Ala
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Lys Leu Leu Lys Arg Glu Gly Thr Pro Pro Pro Pro Pro Pro Ser Arg
            1380                1385                1390
Asp Leu Thr Glu Ala Tyr Lys Thr Gln Ala Leu Gly Pro Leu Lys Leu
        1395                1400                1405
Lys Pro Ala His Glu Gly Leu Val Ala Thr Val Lys Glu Ala Gly Arg
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Ser Ile His Glu Ile Pro Arg Glu Glu Leu Arg His Thr Pro Glu Leu
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Pro Leu Ala Pro Arg Pro Leu Lys Glu Gly Ser Ile Thr Gln Gly Thr
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Pro Leu Lys Tyr Asp Thr Gly Ala Ser Thr Thr Gly Ser Lys Lys His
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1475 1480 1485
His Pro Leu Asp Val Met Ala Asp Ala Arg Ala Leu Glu Arg Ala Cys
1490 1495 1500
Tyr Glu Glu Ser Leu Lys Ser Arg Pro Gly Thr Ala Ser Ser Ser Gly
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1585 1590 1595 1600
Val Pro Glu His His Pro His Pro Ile Ser Pro Tyr Glu His Leu Leu
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Arg Gly Val Ser Gly Val Asp Leu Tyr Arg Ser His Ile Pro Leu Ala
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Phe Asp Pro Thr Ser Ile Pro Arg Gly Ile Pro Leu Asp Ala Ala Ala
1635 1640 1645
Ala Tyr Tyr Leu Pro Arg His Leu Ala Pro Asn Pro Thr Tyr Pro His
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1665 1670 1675 1680
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1685 1690 1695
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1715 1720 1725
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1745 1750 1755 1760
Tyr Leu Pro Thr Ala Pro Gln Pro Phe Ser Ser Arg His Ser Ser Ser
1765 1770 1775
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1780 1785 1790
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1795 1800 1805
Arg Glu Arg Glu Lys Ser Ile Leu Thr Ser Thr Thr Thr Val Glu His
1810 1815 1820
Ala Pro Ile Trp Arg Pro Gly Thr Glu Gln Ser Ser Gly Ser Ser Gly
1825 1830 1835 1840
Ser Ser Gly Gly Gly Gly Gly Ser Ser Ser Arg Pro Ala Ser His Ser
1845 1850 1855
His Ala His Gln His Ser Pro Ile Ser Pro Arg Thr Gln Asp Ala Leu
1860 1865 1870
Gln Gln Arg Pro Ser Val Leu His Asn Thr Gly Met Lys Gly Ile Ile
1875 1880 1885
Thr Ala Val Glu Pro Ser Thr Pro Thr Val Leu Arg Ser Thr Ser Thr

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Ser Ser Pro Val Arg Pro Ala Ala Thr Phe Pro Pro Ala Thr His Cys
1905                1910                1915                1920
Pro Leu Gly Gly Thr Leu Asp Gly Val Tyr Pro Thr Leu Met Glu Pro
                1925                1930                1935
Val Leu Leu Pro Lys Glu Ala Pro Arg Val Ala Arg Pro Glu Arg Pro
            1940                1945                1950
Arg Ala Asp Thr Gly His Ala Phe Leu Ala Lys Pro Pro Ala Arg Ser
        1955                1960                1965
Gly Leu Glu Pro Ala Ser Ser Pro Ser Lys Gly Ser Glu Pro Arg Pro
    1970                1975                1980
Leu Val Pro Pro Val Ser Gly His Ala Thr Ile Ala Arg Thr Pro Ala
1985                1990                1995                2000
Lys Asn Leu Ala Pro His His Ala Ser Pro Asp Pro Pro Ala Pro Pro
                2005                2010                2015
Ala Ser Ala Ser Asp Pro His Arg Glu Lys Thr Gln Ser Lys Pro Phe
            2020                2025                2030
Ser Ile Gln Glu Leu Glu Leu Arg Ser Leu Gly Tyr His Gly Ser Ser
        2035                2040                2045
Tyr Ser Pro Glu Gly Val Glu Pro Val Ser Pro Val Ser Ser Pro Ser
    2050                2055                2060
Leu Thr His Asp Lys Gly Leu Pro Lys His Leu Glu Glu Leu Asp Lys
2065                2070                2075                2080
Ser His Leu Glu Gly Glu Leu Arg Pro Lys Gln Pro Gly Pro Val Lys
                2085                2090                2095
Leu Gly Gly Glu Ala Ala His Leu Pro His Leu Arg Pro Leu Pro Glu
            2100                2105                2110
Ser Gln Pro Ser Ser Ser Pro Leu Leu Gln Thr Ala Pro Gly Val Lys
        2115                2120                2125
Gly His Gln Arg Val Val Thr Leu Ala Gln His Ile Ser Glu Val Ile
    2130                2135                2140
Thr Gln Asp Tyr Thr Arg His His Pro Gln Gln Leu Ser Ala Pro Leu
2145                2150                2155                2160
Pro Ala Pro Leu Tyr Ser Phe Pro Gly Ala Ser Cys Pro Val Leu Asp
                2165                2170                2175
Leu Arg Arg Pro Pro Ser Asp Leu Tyr Leu Pro Pro Pro Asp His Gly
            2180                2185                2190
Ala Pro Ala Arg Gly Ser Pro His Ser Glu Gly Gly Lys Arg Ser Pro
        2195                2200                2205
Glu Pro Asn Lys Thr Ser Val Leu Gly Gly Gly Glu Asp Gly Ile Glu
    2210                2215                2220
Pro Val Ser Pro Pro Glu Gly Met Thr Glu Pro Gly His Ser Arg Ser
2225                2230                2235                2240
Ala Val Tyr Pro Leu Leu Tyr Arg Asp Gly Glu Gln Thr Glu Pro Ser
                2245                2250                2255
Arg Met Gly Ser Lys Ser Pro Gly Asn Thr Ser Gln Pro Pro Ala Phe
            2260                2265                2270
Phe Ser Lys Leu Thr Glu Ser Asn Ser Ala Met Val Lys Ser Lys Lys
        2275                2280                2285
Gln Glu Ile Asn Lys Lys Leu Asn Thr His Asn Arg Asn Glu Pro Glu
    2290                2295                2300
Tyr Asn Ile Ser Gln Pro Gly Thr Glu Ile Phe Asn Met Pro Ala Ile
2305                2310                2315                2320
Thr Gly Thr Gly Leu Met Thr Tyr Arg Ser Gln Ala Val Gln Glu His
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2325 2330 2335
Ala Ser Thr Asn Met Gly Leu Glu Ala Ile Ile Arg Lys Ala Leu Met
2340 2345 2350
Gly Lys Tyr Asp Gln Trp Glu Glu Ser Pro Pro Leu Ser Ala Asn Ala
2355 2360 2365
Phe Asn Pro Leu Asn Ala Ser Ala Ser Leu Pro Ala Ala Met Pro Ile
2370 2375 2380
Thr Ala Ala Asp Gly Arg Ser Asp His Thr Leu Thr Ser Pro Gly Gly
2385 2390 2395 2400
Gly Gly Lys Ala Lys Val Ser Gly Arg Pro Ser Ser Arg Lys Ala Lys
2405 2410 2415
Ser Pro Ala Pro Gly Leu Ala Ser Gly Asp Arg Pro Pro Ser Val Ser
2420 2425 2430
Ser Val His Ser Glu Gly Asp Cys Asn Arg Arg Thr Pro Leu Thr Asn
2435 2440 2445
Arg Val Trp Glu Asp Arg Pro Ser Ser Ala Gly Ser Thr Pro Phe Pro
2450 2455 2460
Tyr Asn Pro Leu Ile Met Arg Leu Gln Ala Gly Val Met Ala Ser Pro
2465 2470 2475 2480
Pro Pro Pro Gly Leu Pro Ala Gly Ser Gly Pro Leu Ala Gly Pro His
2485 2490 2495
His Ala Trp Asp Glu Glu Pro Lys Pro Leu Leu Cys Ser Gln Tyr Glu
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Thr Leu Ser Asp Ser Glu
2515

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<211> 345
<212> DNA
<213> Homo sapiens

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120
gccaacggta tcttgaatgt gagcgcaaag gataaggcta ccggtaagga acagaagatt
180
cgcatcgaag cttcaagtgg tttgagtcag gaagaaatcg acagaatgaa agctgaggca
240
gaacagaatg cagcagcagg caaggctgaa cgcgaaaaga ttgataagct gaaccaagct
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gactcaatga tttccccccc cgaaaactcc tgaaagacaa cgatn
345

<210> 678
<211> 110
<212> PRT
<213> Homo sapiens

<400> 678
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Gln Phe Thr Leu Glu Gly Ile Ala Pro Ala Arg Arg Gly Val Pro Gln

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Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Ser
        35                  40                  45
Ala Lys Asp Lys Ala Thr Gly Lys Glu Gln Lys Ile Arg Ile Glu Ala
    50                  55                  60
Ser Ser Gly Leu Ser Gln Glu Glu Ile Asp Arg Met Lys Ala Glu Ala
65                  70                  75                  80
Glu Gln Asn Ala Ala Ala Gly Lys Ala Glu Arg Glu Lys Ile Asp Lys
                85                  90                  95
Leu Asn Gln Ala Asp Ser Met Ile Ser Pro Pro Glu Asn Ser
            100                 105                 110
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<212> DNA
<213> Homo sapiens

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120
ggtacaggcc tggatttcaa gcgtgccatt gctgacgtca cgcatgtgcc acccgaacgc
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caaaaagtac tcatcaaggg aggattgcta aaagacgata ccccattagg taaagtgggt
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gaaaaacctg tgctgttcct ggaggatttg ccggaagacg agctcaacaa ggctaaggat
360
cc
362

<210> 680
<211> 100
<212> PRT
<213> Homo sapiens

<400> 680
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            20                  25                  30
Val Thr His Val Pro Pro Glu Arg Gln Lys Val Leu Ile Lys Gly Gly
        35                  40                  45
Leu Leu Lys Asp Asp Thr Pro Leu Gly Lys Val Gly Ala Arg Ala Gly
    50                  55                  60
Gln Gln Phe Met Val Leu Gly Ala Val Gly Glu Leu Pro Lys Ala Pro
65                  70                  75                  80
Glu Lys Pro Val Leu Phe Leu Glu Asp Leu Pro Glu Asp Glu Leu Asn
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Lys Ala Lys Asp
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<210> 681
<211> 357
<212> DNA
<213> Homo sapiens

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120
ggttttgatt ttatcggaag tactttagta ggatatacaa aacaaagtaa aggtgacaaa
180
atcgaagaaa atgactttga aatcttgaga acagttttag aacgaattaa acatccacta
240
attgcagaag gcaatatcga tacacctgaa aaggtgaaac gtgtgcttga gttaggcgcg
300
tatagtgtcg ttgtagggtc agcgattact cgtccacaac tcatcacgaa aaaattt
357

<210> 682
<211> 119
<212> PRT
<213> Homo sapiens

<400> 682
Thr Arg Pro Asn Gly Gln Thr Leu Asp Asp Phe Tyr His Glu Ile Arg
1 5 10 15
Ala Lys Tyr Pro Glu Gln Leu Leu Met Ala Asp Cys Ser Thr Val Glu
20 25 30
Glu Met Ile His Ala Asp Glu Leu Gly Phe Asp Phe Ile Gly Ser Thr
35 40 45
Leu Val Gly Tyr Thr Lys Gln Ser Lys Gly Asp Lys Ile Glu Glu Asn
50 55 60
Asp Phe Glu Ile Leu Arg Thr Val Leu Glu Arg Ile Lys His Pro Leu
65 70 75 80
Ile Ala Glu Gly Asn Ile Asp Thr Pro Glu Lys Val Lys Arg Val Leu
85 90 95
Glu Leu Gly Ala Tyr Ser Val Val Val Gly Ser Ala Ile Thr Arg Pro
100 105 110
Gln Leu Ile Thr Lys Lys Phe
115

<210> 683
<211> 411
<212> DNA
<213> Homo sapiens

<400> 683
ntctccgacc gcgtggtaaa actggcgacc ttaattgctg aagatgagca agctgaaatg
60
aatattgttt tgcccgcagc gtggttgcat gattgcgtca gttaccctaa aaaccatgta
120
ttaagagcac aaagtgcatt acatgcagca gataaagcga ttgtattttt gcgcagtatt
180

aattacccca aacaatactt attagcaatt catcatgcaa tttcagcgca cagtgtcagt
240
ggtaaaatac aggcaatgag tttagaagct caaatagtgc aagatgcaga tagattggat
300
gcgctagggg caattggcgt ggctcgttgc attcaagtaa gtagccagtt acagcgccca
360
ctatattctg aagttgaccc cttcagcgag acacgatctc tagtctgcat g
411

<210> 684
<211> 137
<212> PRT
<213> Homo sapiens

<400> 684
Xaa Ser Asp Arg Val Val Lys Leu Ala Thr Leu Ile Ala Glu Asp Glu
1 5 10 15
Gln Ala Glu Met Asn Ile Val Leu Pro Ala Ala Trp Leu His Asp Cys
20 25 30
Val Ser Tyr Pro Lys Asn His Val Leu Arg Ala Gln Ser Ala Leu His
35 40 45
Ala Ala Asp Lys Ala Ile Val Phe Leu Arg Ser Ile Asn Tyr Pro Lys
50 55 60
Gln Tyr Leu Leu Ala Ile His His Ala Ile Ser Ala His Ser Val Ser
65 70 75 80
Gly Lys Ile Gln Ala Met Ser Leu Glu Ala Gln Ile Val Gln Asp Ala
85 90 95
Asp Arg Leu Asp Ala Leu Gly Ala Ile Gly Val Ala Arg Cys Ile Gln
100 105 110
Val Ser Ser Gln Leu Gln Arg Pro Leu Tyr Ser Glu Val Asp Pro Phe
115 120 125
Ser Glu Thr Arg Ser Leu Val Cys Met
130 135

<210> 685
<211> 417
<212> DNA
<213> Homo sapiens

<400> 685
acgcgttgcg ttgcggagtg aacccggaac gatggatgga ttgacactat tcggcctgtt
60
cgccgtcact gcgatgctgg tctgctatgc catggaggac cgcagccact ggttcgtgct
120
gctgttcgcg gccgcttggc gctcggttcg gcctacggct tcctccaagg cgcctggccg
180
ttcggcttcg tcgaggcgat atgggcgctc gttgcctgcg gcgtggtgga cgatcaggcc
240
gcgatgaccg catcgtccgg cttaagcccg gaaacgaaac cgaccagtgc gctggtttga
300
tgggcggcgc gtcgctggat gcacagcgtc tcgacgcgag cgtgatgatg gcctcagcgc
360
gtgcatgccg acgctgtcgc tcatcgcgct acgctcgacc acggcgcgcg gcaatag
417

<210> 686
<211> 110
<212> PRT
<213> Homo sapiens

<400> 686
Met Pro Trp Arg Thr Ala Ala Thr Gly Ser Cys Cys Cys Ser Arg Pro
1 5 10 15
Leu Gly Ala Arg Phe Gly Leu Arg Leu Pro Pro Arg Arg Leu Ala Val
20 25 30
Arg Leu Arg Arg Gly Asp Met Gly Ala Arg Cys Leu Arg Arg Gly Gly
35 40 45
Arg Ser Gly Arg Asp Asp Arg Ile Val Arg Leu Lys Pro Gly Asn Glu
50 55 60
Thr Asp Gln Cys Ala Gly Leu Met Gly Gly Ala Ser Leu Asp Ala Gln
65 70 75 80
Arg Leu Asp Ala Ser Val Met Met Ala Ser Ala Arg Ala Cys Arg Arg
85 90 95
Cys Arg Ser Ser Arg Tyr Ala Arg Pro Arg Arg Ala Ala Ile
100 105 110

<210> 687
<211> 412
<212> DNA
<213> Homo sapiens

<400> 687
nnacgcgtga ccgaccaact gcgagccacc ctgctcgcca tggctgctat ggggttgcac
60
gacggcatcg atattccgtc tggggcgatt attgaaagct gccgcacctt atcagccgtt
120
ctcgatgaaa cccacggtgg tcgcacgatc gagcttcggg taccacctgc gtgcgcggtt
180
caattggcgg ccattgagtc gggccccaac caccaccggg gcactccgcc caatgtggcc
240
gagaccgacc ctgtcacctt cctgcagttg gcaactggct tctcacactg gccagaaatg
300
cgctcagcag gacgggttca ggcgtctgga tcccacgtcg acgacgttgc tggcgtgttc
360
ccagtcgttg atatggccgg ggttttccgc gacatttttg ccgacgacta ga
412

<210> 688
<211> 136
<212> PRT
<213> Homo sapiens

<400> 688
Xaa Arg Val Thr Asp Gln Leu Arg Ala Thr Leu Leu Ala Met Ala Ala
1 5 10 15
Met Gly Leu His Asp Gly Ile Asp Ile Pro Ser Gly Ala Ile Ile Glu
20 25 30
Ser Cys Arg Thr Leu Ser Ala Val Leu Asp Glu Thr His Gly Gly Arg

```
        35                  40                  45
Thr Ile Glu Leu Arg Val Pro Pro Ala Cys Ala Val Gln Leu Ala Ala
    50                  55                  60
Ile Glu Ser Gly Pro Asn His His Arg Gly Thr Pro Pro Asn Val Ala
65                  70                  75                  80
Glu Thr Asp Pro Val Thr Phe Leu Gln Leu Ala Thr Gly Phe Ser His
                85                  90                  95
Trp Pro Glu Met Arg Ser Ala Gly Arg Val Gln Ala Ser Gly Ser His
            100                 105                 110
Val Asp Asp Val Ala Gly Val Phe Pro Val Val Asp Met Ala Gly Val
        115                 120                 125
Phe Arg Asp Ile Phe Ala Asp Asp
    130                 135
```

<210> 689
<211> 499
<212> DNA
<213> Homo sapiens

<400> 689
cgcgtcgcgg tactcgacgt cgattttcat cacggtaacg gcacccagaa catttttac
60
ccgcgcaatg acgtgatgtt catatcgctg cacggcgagc cggccgtgtc ctatccctac
120
tattcggggt tcagcgatga agtcggcgca ggtgttggcg aagggttcaa cctcaactac
180
ccgctgccga aaaacaccgc ctgggatacc taccgcgacg ccctgctgca tgcctgcagg
240
aaactccagc aattctcgcc gcaggtattg gtgatctcac tgggggtcga caccttcaag
300
gacgacccga tcagtcactt cctgctggaa ggcgaggatt tcatcgggat cggcgagctg
360
atagcgagtg tgggttgccc caccctgttt gtgatggaag gcggctatat ggtcgatgaa
420
atcggaatca acgcggtgaa cgtactgcat ggcttcgaga gcaagcgcgc ttgagcatcc
480
gcccgaagac ggcgtgata
499

<210> 690
<211> 157
<212> PRT
<213> Homo sapiens

<400> 690
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Arg Val Ala Val Leu Asp Val Asp Phe His His Gly Asn Gly Thr Gln
 1               5                  10                  15
Asn Ile Phe Tyr Pro Arg Asn Asp Val Met Phe Ile Ser Leu His Gly
            20                  25                  30
Glu Pro Ala Val Ser Tyr Pro Tyr Tyr Ser Gly Phe Ser Asp Glu Val
        35                  40                  45
Gly Ala Gly Val Gly Glu Gly Phe Asn Leu Asn Tyr Pro Leu Pro Lys
    50                  55                  60
Asn Thr Ala Trp Asp Thr Tyr Arg Asp Ala Leu Leu His Ala Cys Arg
```

65 70 75 80
Lys Leu Gln Gln Phe Ser Pro Gln Val Leu Val Ile Ser Leu Gly Val
85 90 95
Asp Thr Phe Lys Asp Asp Pro Ile Ser His Phe Leu Leu Glu Gly Glu
100 105 110
Asp Phe Ile Gly Ile Gly Glu Leu Ile Ala Ser Val Gly Cys Pro Thr
115 120 125
Leu Phe Val Met Glu Gly Gly Tyr Met Val Asp Glu Ile Gly Ile Asn
130 135 140
Ala Val Asn Val Leu His Gly Phe Glu Ser Lys Arg Ala
145 150 155

<210> 691
<211> 336
<212> DNA
<213> Homo sapiens

<400> 691
ntgctgcgtg aaaacgtgca gcgcggcgca tcagcgactg gcgagcgctt tggctggagt
60
tcgcaaaggc aaggcccctg ggagttggcc tgcgacatcg cgctgccgtg cgccacccag
120
aacgaactgg acgccgacgc cgcccgcacg ctgctgcgca acggctgcct ttgcgtggct
180
ggaggcgcga atatgccgcc cgcgcttgag gctgtggata tctttatcga ggcgggcatt
240
ctgttcgcgc ccggcaaggc atccaatgcc ggcggcgtgg ccgtgagtgg cctggaaatg
300
tcgcagaacg ccatgcgcct gctgtggacc gccggc
336

<210> 692
<211> 112
<212> PRT
<213> Homo sapiens

<400> 692
Xaa Leu Arg Glu Asn Val Gln Arg Gly Ala Ser Ala Thr Gly Glu Arg
1 5 10 15
Phe Gly Trp Ser Ser Gln Arg Gln Gly Pro Trp Glu Leu Ala Cys Asp
20 25 30
Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu Leu Asp Ala Asp Ala Ala
35 40 45
Arg Thr Leu Leu Arg Asn Gly Cys Leu Cys Val Ala Gly Gly Ala Asn
50 55 60
Met Pro Pro Ala Leu Glu Ala Val Asp Ile Phe Ile Glu Ala Gly Ile
65 70 75 80
Leu Phe Ala Pro Gly Lys Ala Ser Asn Ala Gly Gly Val Ala Val Ser
85 90 95
Gly Leu Glu Met Ser Gln Asn Ala Met Arg Leu Leu Trp Thr Ala Gly
100 105 110

<210> 693
<211> 580

<212> DNA
<213> Homo sapiens

<400> 693
ngggcaaccc ggaaggtccg gcgtcccagc cgcctacctc gctgggaccc tggtcttgct
60
gtcccccgct ggcctcctgc ccaagcgact gcggccagga tgggccggaa ggtgaccgtg
120
gccacctgcg cactcaacca gtgggccctg gacttcgagg gcaatttgca aagaatttta
180
aagagtattg aaattgccaa aaacagagga gcaagataca ggcttggacc agagctggaa
240
atatgcggct gcggatgttg ggatcattat tacgagtcgg acaccctctt gcactcgttt
300
caagtcctag cggcccttgt ggagtctccc gtcactcagg acatcatctg cgacgtgggg
360
atacctgtaa tgcaccgaaa cgtccgctac aactgcagag tgatattcct caacaggaag
420
atcctgctca tcagacccaa gatggccttg gccaatgaag gcaactaccg cgagctgcgc
480
tggttcaccc cgtggtcgag gagtcggtga gtcgggtgcc tgaccactcc tgggatgtgc
540
gttaagcacc tccgctgtgt gtagccttgg gtcctgatca
580

<210> 694
<211> 136
<212> PRT
<213> Homo sapiens

<400> 694
Met Gly Arg Lys Val Thr Val Ala Thr Cys Ala Leu Asn Gln Trp Ala
 1   5   10   15
Leu Asp Phe Glu Gly Asn Leu Gln Arg Ile Leu Lys Ser Ile Glu Ile
            20   25   30
Ala Lys Asn Arg Gly Ala Arg Tyr Arg Leu Gly Pro Glu Leu Glu Ile
        35   40   45
Cys Gly Cys Gly Cys Trp Asp His Tyr Tyr Glu Ser Asp Thr Leu Leu
    50   55   60
His Ser Phe Gln Val Leu Ala Ala Leu Val Glu Ser Pro Val Thr Gln
65   70   75   80
Asp Ile Ile Cys Asp Val Gly Ile Pro Val Met His Arg Asn Val Arg
                85   90   95
Tyr Asn Cys Arg Val Ile Phe Leu Asn Arg Lys Ile Leu Leu Ile Arg
            100   105   110
Pro Lys Met Ala Leu Ala Asn Glu Gly Asn Tyr Arg Glu Leu Arg Trp
        115   120   125
Phe Thr Pro Trp Ser Arg Ser Arg
    130   135

<210> 695
<211> 439
<212> DNA
<213> Homo sapiens

<400> 695
ntggtgactc aggcgtccaa tggcacgatg gctgacgtcg tcaatatgcc gtcctcgacc
60
atcatggctc tgtcgagggc tgattacctg ctcgatatcg agacttcggt gcccggtatc
120
ggcgacaagt tcgtcccgga cgtctggggc aaactcaaac tcggcaagga caacgagcac
180
accgctctgc cctggtactt cggcccgttc gtcgtgacgt acaacaagga cattttcaag
240
gatgttggcc tcgatcccga aatcccgccg aagacgatga ccgagtacct cgacttcgcc
300
aagaaaatca ccgctgccgg caagcaggcg gtctatggca acacgtcgtg gtacatgctc
360
gcggaatggc gtgccctcgg cgtcaaggtc atgaatgacg acttcaccaa gttcactttt
420
gcctcggaat ccaacgcgt
439

<210> 696
<211> 146
<212> PRT
<213> Homo sapiens

<400> 696
Xaa Val Thr Gln Ala Ser Asn Gly Thr Met Ala Asp Val Val Asn Met
1 5 10 15
Pro Ser Ser Thr Ile Met Ala Leu Ser Arg Ala Asp Tyr Leu Leu Asp
20 25 30
Ile Glu Thr Ser Val Pro Gly Ile Gly Asp Lys Phe Val Pro Asp Val
35 40 45
Trp Gly Lys Leu Lys Leu Gly Lys Asp Asn Glu His Thr Ala Leu Pro
50 55 60
Trp Tyr Phe Gly Pro Phe Val Val Thr Tyr Asn Lys Asp Ile Phe Lys
65 70 75 80
Asp Val Gly Leu Asp Pro Glu Ile Pro Pro Lys Thr Met Thr Glu Tyr
85 90 95
Leu Asp Phe Ala Lys Lys Ile Thr Ala Ala Gly Lys Gln Ala Val Tyr
100 105 110
Gly Asn Thr Ser Trp Tyr Met Leu Ala Glu Trp Arg Ala Leu Gly Val
115 120 125
Lys Val Met Asn Asp Asp Phe Thr Lys Phe Thr Phe Ala Ser Glu Ser
130 135 140
Asn Ala
145

<210> 697
<211> 368
<212> DNA
<213> Homo sapiens

<400> 697
nggcaataac gccgtcgtcg aaatccgttc ccttgatctc gaacatgccg atgaagcggt
60

tgtcggtgat ggggtcggag atgtcgccct cccacaactt gaacttgatc ggaccaaccc
120
tttccaccct ggagagactc gcctgccttg aaagtcttct tgcccttctt gggcaactga
180
tcgccctccc gaacgagata atccaagctc aagcgaccgc ccaccttgtc gcgcgcctcc
240
acaccgacgg aatgcgatgc cgggatcgca tcgatgctag cggcggtgcg tgcaatgaca
300
atcttgtctt cacgcagcga tacgggcccg ccgttggaat cgaacacaaa caccttgaag
360
gcgttgtn
368

<210> 698
<211> 108
<212> PRT
<213> Homo sapiens

<400> 698
Met Pro Met Lys Arg Leu Ser Val Met Gly Ser Glu Met Ser Pro Ser
1 5 10 15
His Asn Leu Asn Leu Ile Gly Pro Thr Leu Ser Thr Leu Glu Arg Leu
20 25 30
Ala Cys Leu Glu Ser Leu Leu Ala Leu Leu Gly Gln Leu Ile Ala Leu
35 40 45
Pro Asn Glu Ile Ile Gln Ala Gln Ala Thr Ala His Leu Val Ala Arg
50 55 60
Leu His Thr Asp Gly Met Arg Cys Arg Asp Arg Ile Asp Ala Ser Gly
65 70 75 80
Gly Ala Cys Asn Asp Asn Leu Val Phe Thr Gln Arg Tyr Gly Pro Ala
85 90 95
Val Gly Ile Glu His Lys His Leu Glu Gly Val Val
100 105

<210> 699
<211> 363
<212> DNA
<213> Homo sapiens

<400> 699
nacgcgtaca caaatagtat cggaatcatt tcctatcatg ctgctatgac gagatttctc
60
cacacctcag attggcaact ggggatgact cggcactacc tgtcgaagcg cggcgacgac
120
gacccacagg cacggtttac tgccgatcga atcgagacgg tgcgcaggct gggcgacgtt
180
gcccggaagg agggctgcga gtttgtcgtc gtcgccggag atgtcttcga aacccacaat
240
gtctccactc agatcattgc ccgcgcgtgt gaggcgatag cctccattga tctccccgtg
300
tacctgctgc ccggaaatca cgacagctta gagccggggt gtctctggga tgggccagaa
360
ttc
363

<210> 700
<211> 121
<212> PRT
<213> Homo sapiens

<400> 700
Xaa Ala Tyr Thr Asn Ser Ile Gly Ile Ile Ser Tyr His Ala Ala Met
1 5 10 15
Thr Arg Phe Leu His Thr Ser Asp Trp Gln Leu Gly Met Thr Arg His
20 25 30
Tyr Leu Ser Lys Arg Gly Asp Asp Asp Pro Gln Ala Arg Phe Thr Ala
35 40 45
Asp Arg Ile Glu Thr Val Arg Arg Leu Gly Asp Val Ala Arg Lys Glu
50 55 60
Gly Cys Glu Phe Val Val Val Ala Gly Asp Val Phe Glu Thr His Asn
65 70 75 80
Val Ser Thr Gln Ile Ile Ala Arg Ala Cys Glu Ala Ile Ala Ser Ile
85 90 95
Asp Leu Pro Val Tyr Leu Leu Pro Gly Asn His Asp Ser Leu Glu Pro
100 105 110
Gly Cys Leu Trp Asp Gly Pro Glu Phe
115 120

<210> 701
<211> 585
<212> DNA
<213> Homo sapiens

<400> 701
nacgcgtccg ggcacaccgt caccgaggcg acgttccacg gccaccccac gctgatctat
60
ttcggctacg tccattgcgc ggatgtctgc ccgctgacac tgggcaacat ggtctcggcc
120
ctcgatcgcc tgggctcccg ggcggacggc atcgttccga tcttcatctc cgtcgatccg
180
gcccgcgaca cacccgcgct ggtcggacag tatgtcgcgc atttctcgcc gcggatcgtc
240
gggctgaccg gcaccgcagc gcagctggcg ccggtactgg cggagttcca catcaccgcg
300
cgcgccgaac ctgcggcaca cgacatggcc gccgacatgt atgccgtcga ccacagcgcc
360
ctcctctatc tgatggacgg caacaaccgc ctgttgcggg tgatggcggt cagcgccgac
420
gctgcctcgc tgacgcacca gctggcggcc ggcctggccg gggcaagaat gagaccatga
480
aagcgatcgg accgacggac gcccccgaac aggcagcgcc gggctggtcg ttcggcatca
540
tcctgctgct cggcatcgcc ggcatgctcg atttcgtcga ccggt
585

<210> 702
<211> 159
<212> PRT

<213> Homo sapiens

<400> 702
Xaa Ala Ser Gly His Thr Val Thr Glu Ala Thr Phe His Gly His Pro
1 5 10 15
Thr Leu Ile Tyr Phe Gly Tyr Val His Cys Ala Asp Val Cys Pro Leu
20 25 30
Thr Leu Gly Asn Met Val Ser Ala Leu Asp Arg Leu Gly Ser Arg Ala
35 40 45
Asp Gly Ile Val Pro Ile Phe Ile Ser Val Asp Pro Ala Arg Asp Thr
50 55 60
Pro Ala Leu Val Gly Gln Tyr Val Ala His Phe Ser Pro Arg Ile Val
65 70 75 80
Gly Leu Thr Gly Thr Ala Ala Gln Leu Ala Pro Val Leu Ala Glu Phe
85 90 95
His Ile Thr Ala Arg Ala Glu Pro Ala Ala His Asp Met Ala Ala Asp
100 105 110
Met Tyr Ala Val Asp His Ser Ala Leu Leu Tyr Leu Met Asp Gly Asn
115 120 125
Asn Arg Leu Leu Arg Val Met Ala Val Ser Ala Asp Ala Ala Ser Leu
130 135 140
Thr His Gln Leu Ala Ala Gly Leu Ala Gly Ala Arg Met Arg Pro
145 150 155

<210> 703
<211> 390
<212> DNA
<213> Homo sapiens

<400> 703
ttctctgctc catacacacc tcagcagaat ggcatcgccg agcgcaagaa cataactctt
60
attgagatgg cccgaacgat gcttgatgag tacaagactc cgcggaagtt ctggcctgaa
120
gccattgata ctgcttgtca caccatcaac cgcgtttatc ttcacaaggt tttggagaaa
180
acctcttatg agttcctaac tggtaagaaa cccaatgtaa gctatttcag agtatttggt
240
gctaggtgct ggatcaagga tcctcatcac acttcaaaat ttgcaccgaa agcacatgaa
300
ggttttatgc ttggttacgg aaaggattcg cactcctaca gagtcttcaa cctctttcac
360
tataaagtgg ttcaaactgt ggatgtgcgn
390

<210> 704
<211> 130
<212> PRT
<213> Homo sapiens

<400> 704
Phe Ser Ala Pro Tyr Thr Pro Gln Gln Asn Gly Ile Ala Glu Arg Lys
1 5 10 15
Asn Ile Thr Leu Ile Glu Met Ala Arg Thr Met Leu Asp Glu Tyr Lys

```
            20                  25                  30
Thr Pro Arg Lys Phe Trp Pro Glu Ala Ile Asp Thr Ala Cys His Thr
        35                  40                  45
Ile Asn Arg Val Tyr Leu His Lys Val Leu Glu Lys Thr Ser Tyr Glu
    50                  55                  60
Phe Leu Thr Gly Lys Lys Pro Asn Val Ser Tyr Phe Arg Val Phe Gly
65                  70                  75                  80
Ala Arg Cys Trp Ile Lys Asp Pro His His Thr Ser Lys Phe Ala Pro
                85                  90                  95
Lys Ala His Glu Gly Phe Met Leu Gly Tyr Gly Lys Asp Ser His Ser
            100                 105                 110
Tyr Arg Val Phe Asn Leu Phe His Tyr Lys Val Val Gln Thr Val Asp
        115                 120                 125
Val Arg
    130
```

<210> 705
<211> 513
<212> DNA
<213> Homo sapiens

<400> 705
acgcgtattt cgtccaaatg attcaaatca aaacgccgcc gttaaaaacg atgcaggcga
60
agacaatgcg aataaaaaag gtggtaaata agcatgagtt ttaaaatgac acaatctcaa
120
tacacaagtc tttatggacc aactgtagga gactccgtga gattaggaga tacgaacttg
180
tttgcacaag ttgagaaaga ctatgcaaat tatggggatg aagctacttt cggtggcgga
240
aaatcaattc gtgatggtat ggctcaaaat cctaatgtga caagagatga taaaaatgta
300
gccgatttag ttttaactaa cgcattaatt attgattatg acaagattgt taaagcagat
360
atcggtatta aaaatggtta tatttttaag attggtaaag ctggaaaccc agatataatg
420
gataacgttg acatcatcat tggtgcaaca actgatatta ttgctgctga aggtaaaatt
480
gttactgccg gcggtatcga tacacacgtg cac
513

<210> 706
<211> 140
<212> PRT
<213> Homo sapiens

<400> 706
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Met Ser Phe Lys Met Thr Gln Ser Gln Tyr Thr Ser Leu Tyr Gly Pro
 1               5                  10                  15
Thr Val Gly Asp Ser Val Arg Leu Gly Asp Thr Asn Leu Phe Ala Gln
            20                  25                  30
Val Glu Lys Asp Tyr Ala Asn Tyr Gly Asp Glu Ala Thr Phe Gly Gly
        35                  40                  45
Gly Lys Ser Ile Arg Asp Gly Met Ala Gln Asn Pro Asn Val Thr Arg
```

```
    50                  55                  60
Asp Asp Lys Asn Val Ala Asp Leu Val Leu Thr Asn Ala Leu Ile Ile
65                  70                  75                  80
Asp Tyr Asp Lys Ile Val Lys Ala Asp Ile Gly Ile Lys Asn Gly Tyr
                85                  90                  95
Ile Phe Lys Ile Gly Lys Ala Gly Asn Pro Asp Ile Met Asp Asn Val
            100                 105                 110
Asp Ile Ile Ile Gly Ala Thr Thr Asp Ile Ile Ala Ala Glu Gly Lys
        115                 120                 125
Ile Val Thr Ala Gly Gly Ile Asp Thr His Val His
    130                 135                 140
```

<210> 707
<211> 409
<212> DNA
<213> Homo sapiens

<400> 707
acgcgtggca tcctcagacc accaaagaca atcctgtcct gggaggcagg gagaaagccg
60
gcacactaca cagtgcacag gtgaagccct caggggtcc tggagcaggg ccacctccct
120
gggggatccc caggtgccat tttcatggca gtgtctatgg acggctcccc ttggcatggt
180
gctgggtggc aatcctggct gtagctgcca ccccctgccc tttttgcttc cctccgaggg
240
cattgtgatc atcagtgtga gtctgttggg aaggagagcc aggtccccag gtttgggaaa
300
ggagtagggt ttcccagcct gtctggccat caccccccag cccagcccct cctgctgggt
360
gacgtgctca gttcggcccc tgctgtactg ggaggggggct aggagcata
409

<210> 708
<211> 136
<212> PRT
<213> Homo sapiens

<400> 708
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Met Leu Leu Ala Pro Ser Gln Tyr Ser Arg Gly Arg Thr Glu His Val
 1               5                  10                  15
Thr Gln Gln Glu Gly Leu Gly Trp Gly Val Met Ala Arg Gln Ala Gly
            20                  25                  30
Lys Pro Tyr Ser Phe Pro Lys Pro Gly Asp Leu Ala Leu Leu Pro Asn
        35                  40                  45
Arg Leu Thr Leu Met Ile Thr Met Pro Ser Glu Gly Ser Lys Lys Gly
    50                  55                  60
Arg Gly Trp Gln Leu Gln Pro Gly Leu Pro Pro Ser Thr Met Pro Arg
65                  70                  75                  80
Gly Ala Val His Arg His Cys His Glu Asn Gly Thr Trp Gly Ser Pro
                85                  90                  95
Arg Glu Val Ala Leu Leu Gln Asp Pro Leu Arg Ala Ser Pro Val His
            100                 105                 110
Cys Val Val Cys Arg Leu Ser Pro Cys Leu Pro Gly Gln Asp Cys Leu
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```
        115                 120                 125
Trp Trp Ser Glu Asp Ala Thr Arg
    130                 135

<210> 709
<211> 771
<212> DNA
<213> Homo sapiens

<400> 709
acgcgtctga cggagagcct cctgagtctc cccacgcaga ggactcagaa agggaatcgg
60
tgaccacacc tgggccagcg acgtgtggtg cgccagcctc cccagcggat cacctcctcc
120
tcccctccca ggaggagagt ttctccgaag tccccatgag tgaagcaagc tcagcgaaag
180
acactccact ctttaggatg gagggagagg atgcccttgt gactcagtat cagagcaaag
240
ccagtgacca cgaaggttta ttgtctgacc ccttgagtga ccttcagttg gtctcagatt
300
ttaaatctcc aatcatggcc gatctgaact taagccttcc ttccattcct gaagtcgcat
360
cggatgatga aagaatagat caggttgaag atgacggaga tcaggttgaa gatgatggag
420
agacagcaaa gtcgtcaact ctggacatag gagctttgtc cttgggcttg gtagtcccct
480
gtcctgagag gggaaagggg cccagtggcg aggcagatag gttggtactg ggggagggcc
540
tgtgtgattt caggctgcaa gcaccccagg catctgtgac agctccttca gagcagacca
600
cagagttcgg aattcacaaa ccacatcttg gcaagagctc aagcttggat aaacagctgc
660
caggccccag tggtggtgag gaagaaaaac cgatgggaaa tgggagtcca agcccgcctc
720
ctggcacatc cctggacaat cctgtaccca gcccctcccc ttctgagatc t
771

<210> 710
<211> 205
<212> PRT
<213> Homo sapiens

<400> 710
Met Ser Glu Ala Ser Ser Ala Lys Asp Thr Pro Leu Phe Arg Met Glu
 1               5                  10                  15
Gly Glu Asp Ala Leu Val Thr Gln Tyr Gln Ser Lys Ala Ser Asp His
            20                  25                  30
Glu Gly Leu Leu Ser Asp Pro Leu Ser Asp Leu Gln Leu Val Ser Asp
        35                  40                  45
Phe Lys Ser Pro Ile Met Ala Asp Leu Asn Leu Ser Leu Pro Ser Ile
    50                  55                  60
Pro Glu Val Ala Ser Asp Asp Glu Arg Ile Asp Gln Val Glu Asp Asp
65                  70                  75                  80
Gly Asp Gln Val Glu Asp Asp Gly Glu Thr Ala Lys Ser Ser Thr Leu
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                85                  90                  95
Asp Ile Gly Ala Leu Ser Leu Gly Leu Val Val Pro Cys Pro Glu Arg
            100                 105                 110
Gly Lys Gly Pro Ser Gly Glu Ala Asp Arg Leu Val Leu Gly Glu Gly
        115                 120                 125
Leu Cys Asp Phe Arg Leu Gln Ala Pro Gln Ala Ser Val Thr Ala Pro
    130                 135                 140
Ser Glu Gln Thr Thr Glu Phe Gly Ile His Lys Pro His Leu Gly Lys
145                 150                 155                 160
Ser Ser Ser Leu Asp Lys Gln Leu Pro Gly Pro Ser Gly Gly Glu Glu
                165                 170                 175
Glu Lys Pro Met Gly Asn Gly Ser Pro Ser Pro Pro Pro Gly Thr Ser
            180                 185                 190
Leu Asp Asn Pro Val Pro Ser Pro Ser Pro Ser Glu Ile
        195                 200                 205
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<210> 711
<211> 432
<212> DNA
<213> Homo sapiens

<400> 711
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attctcctgt tttatatcta ctccccccta ggttcatcct actccctcat cttctgagct
120
aatgtgcccg ctttatttgc acttgcatgg aatatgatta tgaacacagt ttttatcatt
180
gatgaccacc ccgttatcag gttggcgatt cgtatgttgt tggaacacga gggttataag
240
gtcgttggtg aaacggacaa cggttgtgac gcgatccaaa tggttcgcga atgcctgccg
300
gacctgatca tcctggatat cagcatcccg aaactcgacg gcctcgaagt gctctgccga
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ttcaacgcca tgaacacatc catgaaaacc ctgattctta ccgcccagag tccgacgttg
420
ttcgccacgc gt
432

<210> 712
<211> 93
<212> PRT
<213> Homo sapiens

<400> 712
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Met Ile Met Asn Thr Val Phe Ile Ile Asp Asp His Pro Val Ile Arg
 1               5                  10                  15
Leu Ala Ile Arg Met Leu Leu Glu His Glu Gly Tyr Lys Val Val Gly
            20                  25                  30
Glu Thr Asp Asn Gly Cys Asp Ala Ile Gln Met Val Arg Glu Cys Leu
        35                  40                  45
Pro Asp Leu Ile Ile Leu Asp Ile Ser Ile Pro Lys Leu Asp Gly Leu
    50                  55                  60
Glu Val Leu Cys Arg Phe Asn Ala Met Asn Thr Ser Met Lys Thr Leu
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65 70 75 80
Ile Leu Thr Ala Gln Ser Pro Thr Leu Phe Ala Thr Arg
85 90

<210> 713
<211> 465
<212> DNA
<213> Homo sapiens

<400> 713
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atgcgcatgg aaatgaccga cttcgccgcg gtgatcttca acccggtggc gcaggccaag
120
ttcgtgcata cggtcagcgc gggctacgtg gccggcgcca tgttcgtcat gtcgatcagc
180
gcctggtacc tgctcaaggg ccgccacacc gacctggcca agcgctcgat ggcggtcgcc
240
gccagcttcg gcctggcgtc ggcgctgtcg gtcgtcgtgc tgggtgacga aagcggttat
300
ctcaccaccg aacaccagaa gatgaagatc gcggccatgg aatccatgtg gcacaccgag
360
ccggcgcccg cgtccttcaa cctgatcgcg ctgcccaacc aggccgaacg caagaacgac
420
ttcgccatcg agattcccta cgtcatgngc ctcatcggca cgcgt
465

<210> 714
<211> 155
<212> PRT
<213> Homo sapiens

<400> 714
Ile Leu Ile Ala Asn Gly Gly Met Gln Asn Pro Val Gly Ala Val Phe
1 5 10 15
Asn Pro Asp Thr Met Arg Met Glu Met Thr Asp Phe Ala Ala Val Ile
20 25 30
Phe Asn Pro Val Ala Gln Ala Lys Phe Val His Thr Val Ser Ala Gly
35 40 45
Tyr Val Ala Gly Ala Met Phe Val Met Ser Ile Ser Ala Trp Tyr Leu
50 55 60
Leu Lys Gly Arg His Thr Asp Leu Ala Lys Arg Ser Met Ala Val Ala
65 70 75 80
Ala Ser Phe Gly Leu Ala Ser Ala Leu Ser Val Val Val Leu Gly Asp
85 90 95
Glu Ser Gly Tyr Leu Thr Thr Glu His Gln Lys Met Lys Ile Ala Ala
100 105 110
Met Glu Ser Met Trp His Thr Glu Pro Ala Pro Ala Ser Phe Asn Leu
115 120 125
Ile Ala Leu Pro Asn Gln Ala Glu Arg Lys Asn Asp Phe Ala Ile Glu
130 135 140
Ile Pro Tyr Val Met Xaa Leu Ile Gly Thr Arg
145 150 155

<210> 715
<211> 354
<212> DNA
<213> Homo sapiens

<400> 715
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cagaccggcc tgctgcctca ggcactggtg cgtttgcgcc aggcagcgcc gacggtggag
120
tgcaagttgg taccgggggt ttccctggag ttgctcagcc aggtggacgc aggcgagctg
180
gactcggcga tcatcattcg cccgcccttt gatttgccca aggagttgca cgtacaggta
240
ctgcgcaagg agccgtttgt gttgatcgtg ccccaggcgg tcgggggtga tgacccgttg
300
caactgctcg aagctcatcc ccacgtgcgc tacgaccgcg cttcgtttgg cggg
354

<210> 716
<211> 118
<212> PRT
<213> Homo sapiens

<400> 716
Xaa Pro Val Asp Ala Asn Glu Tyr Arg Gly Glu Leu Lys Val Gly Ala
 1   5   10   15
Ile Thr Thr Ala Gln Thr Gly Leu Leu Pro Gln Ala Leu Val Arg Leu
            20   25   30
Arg Gln Ala Ala Pro Thr Val Glu Cys Lys Leu Val Pro Gly Val Ser
        35   40   45
Leu Glu Leu Leu Ser Gln Val Asp Ala Gly Glu Leu Asp Ser Ala Ile
    50   55   60
Ile Ile Arg Pro Pro Phe Asp Leu Pro Lys Glu Leu His Val Gln Val
65   70   75   80
Leu Arg Lys Glu Pro Phe Val Leu Ile Val Pro Gln Ala Val Gly Gly
                85   90   95
Asp Asp Pro Leu Gln Leu Leu Glu Ala His Pro His Val Arg Tyr Asp
            100   105   110
Arg Ala Ser Phe Gly Gly
        115

<210> 717
<211> 401
<212> DNA
<213> Homo sapiens

<400> 717
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ccgttaagtc atctaaatag gccattctgt ggctctccat cagtaagaac caaatccata
120
ggagaagttg agcggatagt aatgcatcaa attgatgctg agaaaccgaa aaatgggaca
180

atataatcaa gctgacaata ctgatcaaac cactcgcatg aaagctacta ccgcttgacc
240
accaagcaga aaaaaccaat gaaatgctta aaaataaaat cgtccaaagt aaaaagctag
300
accaggtggt agccagatta aaaataggcc gctctagaaa atgaaaagaa atccaatgag
360
attcaacggc gtagcaccag cacagcaaca tagccactag t
401

<210> 718
<211> 130
<212> PRT
<213> Homo sapiens

<400> 718
Met Leu Leu Cys Trp Cys Tyr Ala Val Glu Ser His Trp Ile Ser Phe
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His Phe Leu Glu Arg Pro Ile Phe Asn Leu Ala Thr Thr Trp Ser Ser
20 25 30
Phe Leu Leu Trp Thr Ile Leu Phe Leu Ser Ile Ser Leu Val Phe Ser
35 40 45
Ala Trp Trp Ser Ser Gly Ser Ser Phe His A Ser Gly Leu Ile Ser
50 55 60
Ile Val Ser Leu Ile Ile Leu Ser His Phe Ser Val Ser Gln His Gln
65 70 75 80
Phe Asp Ala Leu Leu Ser Ala Gln Leu Leu Leu Trp Ile Trp Phe Leu
85 90 95
Leu Met Glu Ser His Arg Met Ala Tyr Leu Asp Asp Leu Thr Ala Leu
100 105 110
Pro Gly Arg Arg Ala Leu Asn Glu Lys Leu Val Gly Leu Pro Lys Arg
115 120 125
Tyr Ala
130

<210> 719
<211> 685
<212> DNA
<213> Homo sapiens

<400> 719
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ctcttgaagg cggattttca taggcgctgc gcctctcata ttcaagcatc aaggcaatcc
120
aatctccctg cgttggtaac tgggcaaaag aaagacctct gcagtccagc aacctcatcg
180
tgcaaatgcc gtggcgtggt caactctgac ggcctggaag ctgcagacct tgtcaaagga
240
cctcggccga aattcaccct tgatctcttt gtcttgtcca actcttgtcc ctgagaatga
300
aactgtcttc tgagagtcca tcaatgcgac gctgactcgt gagaagtgct gaatcacgtc
360
gccattttgg agacctgcca acgcagctct ggaacctgcc aggacgcctt ccacaacacc
420

agaacgcagc gactttgcgt taaatccaag ctcaaacacc tcttgctcca caggcctgag
480
cataaaaagg tattctgcga cgggaaatgt aaagtctgag cttaggtgca gagtaccgcc
540
atcgatcagt gtctgatact gcttgtccgc gacttctttg ccgagcaatg ggtatagcgt
600
tttcaaccaa gtggaagcag tcgtttgctc accctggcga ttccggcgag ttagggacat
660
gaccacgtca tcgatgggat tttgc
685

<210> 720
<211> 161
<212> PRT
<213> Homo sapiens

<400> 720
Met Ser Leu Thr Arg Arg Asn Arg Gln Gly Glu Gln Thr Thr Ala Ser
1 5 10 15
Thr Trp Leu Lys Thr Leu Tyr Pro Leu Leu Gly Lys Glu Val Ala Asp
20 25 30
Lys Gln Tyr Gln Thr Leu Ile Asp Gly Gly Thr Leu His Leu Ser Ser
35 40 45
Asp Phe Thr Phe Pro Val Ala Glu Tyr Leu Phe Met Leu Arg Pro Val
50 55 60
Glu Gln Glu Val Phe Glu Leu Gly Phe Asn Ala Lys Ser Leu Arg Ser
65 70 75 80
Gly Val Val Glu Gly Val Leu Ala Gly Ser Arg Ala Ala Leu Ala Gly
85 90 95
Leu Gln Asn Gly Asp Val Ile Gln His Phe Ser Arg Val Ser Val Ala
100 105 110
Leu Met Asp Ser Gln Lys Thr Val Ser Phe Ser Gly Thr Arg Val Gly
115 120 125
Gln Asp Lys Glu Ile Lys Gly Glu Phe Arg Pro Arg Ser Phe Asp Lys
130 135 140
Val Cys Ser Phe Gln Ala Val Arg Val Asp His Ala Thr Ala Phe Ala
145 150 155 160
Arg

<210> 721
<211> 579
<212> DNA
<213> Homo sapiens

<400> 721
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attgcccaca ttgagcgagc ccacaagccc tacacagagg acctcaccgc ccatgtccgc
120
aggaacgctc tcagggtggc tgaagtctgg atggatgaat ttaaaagcca cgtctactgg
180
catggaacat accaggagga ctcaggaatt gacattgggg acatcactgc aaggaaggct
240

ctcaggaaac agctgcagtg caagaccttc cggtggtacc tggtcagcgt gtacccagag
300
atgaggatgt actccgacat cattgcctat ggagtgctgc agaattctct gaagactgat
360
ttgtgtcttg accaggggcc agatacagag aatgtcccca tcatgtacat ctgccatggg
420
atgacgcctc agaacgtgta ctacacgagc agtcagcaga tccatgtggg cattctgagc
480
cccaccgtgg atgatgatga caaccgatgc ctggtggacg tcaacagccg gccccggctc
540
atcgaatgca gctacgccaa agccaagagg atgaagctt
579

<210> 722
<211> 193
<212> PRT
<213> Homo sapiens

<400> 722
Lys Leu Gly Ile Arg Val Trp Gln Cys Gly Gly Ser Val Glu Val Leu
1 5 10 15
Pro Cys Ser Arg Ile Ala His Ile Glu Arg Ala His Lys Pro Tyr Thr
20 25 30
Glu Asp Leu Thr Ala His Val Arg Arg Asn Ala Leu Arg Val Ala Glu
35 40 45
Val Trp Met Asp Glu Phe Lys Ser His Val Tyr Trp His Gly Thr Tyr
50 55 60
Gln Glu Asp Ser Gly Ile Asp Ile Gly Asp Ile Thr Ala Arg Lys Ala
65 70 75 80
Leu Arg Lys Gln Leu Gln Cys Lys Thr Phe Arg Trp Tyr Leu Val Ser
85 90 95
Val Tyr Pro Glu Met Arg Met Tyr Ser Asp Ile Ile Ala Tyr Gly Val
100 105 110
Leu Gln Asn Ser Leu Lys Thr Asp Leu Cys Leu Asp Gln Gly Pro Asp
115 120 125
Thr Glu Asn Val Pro Ile Met Tyr Ile Cys His Gly Met Thr Pro Gln
130 135 140
Asn Val Tyr Tyr Thr Ser Ser Gln Gln Ile His Val Gly Ile Leu Ser
145 150 155 160
Pro Thr Val Asp Asp Asp Asp Asn Arg Cys Leu Val Asp Val Asn Ser
165 170 175
Arg Pro Arg Leu Ile Glu Cys Ser Tyr Ala Lys Ala Lys Arg Met Lys
180 185 190
Leu

<210> 723
<211> 384
<212> DNA
<213> Homo sapiens

<400> 723
acgcgtcctc ttacgctcag ttttgacaat gcgtgctggc agccaaccga agccgtaaaa
60

ctcaacgaaa tgctctcgct taaaccgtgc gaaggaaccc caccgcaatg gcgcttattc
120
cgcgaagggg attaccaaat gcgcattgat acgcgctccg gaacgcctac gctgatgctt
180
accgtacaaa gtgtaaccga caaacctgtt acggacgtca ctcgacaatg tcctaaatgg
240
gacggcaagc ccctcaccct tgacgtaacg aatacattcc cggaaggctc cgtcgtacga
300
gacttctaca gcaagcaaac cgctatggtg cagcaaggta aaatcacact tcagcctgcc
360
gctaacagca atggcctgct gctg
384

<210> 724
<211> 128
<212> PRT
<213> Homo sapiens

<400> 724
Thr Arg Pro Leu Thr Leu Ser Phe Asp Asn Ala Cys Trp Gln Pro Thr
1 5 10 15
Glu Ala Val Lys Leu Asn Glu Met Leu Ser Leu Lys Pro Cys Glu Gly
20 25 30
Thr Pro Pro Gln Trp Arg Leu Phe Arg Glu Gly Asp Tyr Gln Met Arg
35 40 45
Ile Asp Thr Arg Ser Gly Thr Pro Thr Leu Met Leu Thr Val Gln Ser
50 55 60
Val Thr Asp Lys Pro Val Thr Asp Val Thr Arg Gln Cys Pro Lys Trp
65 70 75 80
Asp Gly Lys Pro Leu Thr Leu Asp Val Thr Asn Thr Phe Pro Glu Gly
85 90 95
Ser Val Val Arg Asp Phe Tyr Ser Lys Gln Thr Ala Met Val Gln Gln
100 105 110
Gly Lys Ile Thr Leu Gln Pro Ala Ala Asn Ser Asn Gly Leu Leu Leu
115 120 125

<210> 725
<211> 521
<212> DNA
<213> Homo sapiens

<400> 725
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cctggtgaac agcttcccag gtgtgcattt agggcctcct agggatcatc aaagttttta
120
gaaaataggt ttccttcttc cacaggcatg gagaaggaag gaaattttgc actggccttt
180
gggaagctga agaagagctg gggggaggct tgttctgaca aaatagtgac tctctccctg
240
cttgaaatgt cccacagaag gctgtttctg gttcacattt gcccctctag gtccactccc
300
tccccttcat cctgctcact gccagagaga ctatgctggg agtggtgcat cggtggtctc
360

caggcccttt taggctcaag gtgttcattc cctggctcct tccctgccat gtctttgttc
420
cttcctccct ccttcccatc ccagcagcca ccctcctcct tccaccagac ctgggaacca
480
tcatcccaac cacaatcacc ccgtggttct attacacgcg t
521

<210> 726
<211> 124
<212> PRT
<213> Homo sapiens

<400> 726
Met Glu Lys Glu Gly Asn Phe Ala Leu Ala Phe Gly Lys Leu Lys Lys
1 5 10 15
Ser Trp Gly Glu Ala Cys Ser Asp Lys Ile Val Thr Leu Ser Leu Leu
20 25 30
Glu Met Ser His Arg Arg Leu Phe Leu Val His Ile Cys Pro Ser Arg
35 40 45
Ser Thr Pro Ser Pro Ser Ser Cys Ser Leu Pro Glu Arg Leu Cys Trp
50 55 60
Glu Trp Cys Ile Gly Gly Leu Gln Ala Leu Leu Gly Ser Arg Cys Ser
65 70 75 80
Phe Pro Gly Ser Phe Pro Ala Met Ser Leu Phe Leu Pro Pro Ser Phe
85 90 95
Pro Ser Gln Gln Pro Pro Ser Ser Phe His Gln Thr Trp Glu Pro Ser
100 105 110
Ser Gln Pro Gln Ser Pro Arg Gly Ser Ile Thr Arg
115 120

<210> 727
<211> 629
<212> DNA
<213> Homo sapiens

<400> 727
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tctgttgcct gacggcacgg tggctcagga ctcgatctcg ggaaccttgg cgactcgcgg
120
tgccattatc gacgctggtg agttgaaggc tccgacgcat cgggcgtttg cgtcaatcag
180
tgccgcccgc cacgaggtcc aaggagaact cgaatgaatc cgaatgacta cctggtgctc
240
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300
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360
cacgtacacg gctctctcga cggacaggtc ggggttttct tcgtgatgat cgtggcagcc
420
gctgaggtgg ttgtcggttt ggcgatcatc gtcactattt tccgttcccg tcgcaccact
480
tcggtggacg acaccaacct gctgaagttc tgagggaggt accgtgactg tcttggaaac
540

cggcttgttc aacgtggcct ggctcatgat tgcggtgcca ctggtggttg ccgcgctgct
600
attggtgctg ggacgccgca gcgacgcgt
629

<210> 728
<211> 99
<212> PRT
<213> Homo sapiens

<400> 728
Met Asn Pro Asn Asp Tyr Leu Val Leu Ser Ala Ile Leu Phe Ala Ile
1 5 10 15
Gly Ile Val Gly Phe Leu Thr Arg Arg Asn Ala Leu Val Ala Phe Met
20 25 30
Ser Val Glu Leu Met Leu Asn Ala Ala Asn Leu Ala Leu Val Thr Phe
35 40 45
Ala His Val His Gly Ser Leu Asp Gly Gln Val Gly Val Phe Phe Val
50 55 60
Met Ile Val Ala Ala Ala Glu Val Val Val Gly Leu Ala Ile Ile Val
65 70 75 80
Thr Ile Phe Arg Ser Arg Arg Thr Thr Ser Val Asp Asp Thr Asn Leu
85 90 95
Leu Lys Phe

<210> 729
<211> 4716
<212> DNA
<213> Homo sapiens

<400> 729
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ttaaggaaat gctgcaggac agggaatccc aaaatcaaaa gtctacagtt ccgtcaagaa
120
ggagaatgta ttcttttgat gatgtgctgg aggaaggaaa gcgacccccc acaatgactg
180
tgtcagaagc aagttaccag agtgagagag tagaagagaa gggagcaact tattcttcag
240
aaattcccaa agaagattct accacttttg caaaaagaga ggacccgtgt aacaactgaa
300
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360
cgttcacgga gcacacaaat ggaatcaact cgtgtttcag cttctctccc cagaagttac
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480
acaaggggaa tctcatcact ccccagatct tacacgatgg atgatgcttg gaagtataat
540
ggagatgttg aagacattaa gagaactcca aacaatgtgg tcagcacccc tgcaccaagc
600
ccggacgcaa gccaactggc ttcaagctta tctagccaga aagaggtagc agcaacagaa
660

gaagatgtga caaggctgcc ctctcctaca tccccccttct catctctttc ccaagaccag
720
gctgccactt ctaaagccac attgtcttcc acatctggtc ttgatttaat gtctgaatct
780
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840
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960
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1020
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1080
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1140
atttacaact cagaaaaatc ttcaaatcta tctgtaacaa ctgatttctc cgaaagcctt
1200
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1260
gaatcaaaag catctgaatc catttctttg aaaaacttaa aaaggcgatc acaatttttt
1320
gaacaaggaa gctctgattc ggtggttcct gatcttccag ttccaaccat cagtgccccg
1380
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1440
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1560
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1680
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cagcttgtta ttgagagaga gaggaaatgg gagcaacagc ttcaggaaga gcaagagcaa
1800
aagcggcttc aggctgaggc tgaggagcag aagcgtcctg cggaggagca gaagcgccag
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1920
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1980
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2040
ttagaccaaa ttgggaacac gacctcttca cagaggagat ccaagaaaga acaagtacca
2100
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2160
cacaatgaca acagctggat ccgacagcgc agtgccagtg tcaacaaaga gcctgttagt
2220
cttcctggga tcatgagaag aggcgaatct ttagataacc tggactcccc ccgatccaat
2280

tcttggagac agcctccttg gctcaatcag cccacaggat tctatgcttc ttcctctgtg
2340
caagacttta gtcgcccacc acctcagctg gtgtccacat caaaccgtgc ctacatgcgg
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2460
gtggccacca cacagtcccc caccccgaga agccattccc cttcagcttc acagtcaggc
2520
tctcagctgc gtaacaggtc agtcagtggg aagcgcatat gctcctactg caataacatt
2580
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<210> 730
<211> 797
<212> PRT
<213> Homo sapiens

<400> 730
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20 25 30
Ser Gln Thr Arg Gly Ile Ser Ser Leu Pro Arg Ser Tyr Thr Met Asp
35 40 45
Asp Ala Trp Lys Tyr Asn Gly Asp Val Glu Asp Ile Lys Arg Thr Pro
50 55 60
Asn Asn Val Val Ser Thr Pro Ala Pro Ser Pro Asp Ala Ser Gln Leu
65 70 75 80
Ala Ser Ser Leu Ser Ser Gln Lys Glu Val Ala Ala Thr Glu Glu Asp
85 90 95
Val Thr Arg Leu Pro Ser Pro Thr Ser Pro Phe Ser Ser Leu Ser Gln
100 105 110
Asp Gln Ala Ala Thr Ser Lys Ala Thr Leu Ser Ser Thr Ser Gly Leu
115 120 125
Asp Leu Met Ser Glu Ser Gly Glu Gly Glu Ile Ser Pro Gln Arg Glu
130 135 140
Val Ser Arg Ser Gln Asp Gln Phe Ser Asp Met Arg Ile Ser Ile Asn

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145                 150                 155                 160
Gln Thr Pro Gly Lys Ser Leu Asp Phe Gly Phe Thr Ile Lys Trp Asp
                165                 170                 175
Ile Pro Gly Ile Phe Val Ala Ser Val Glu Ala Gly Ser Pro Ala Glu
            180                 185                 190
Phe Ser Gln Leu Gln Val Asp Asp Glu Ile Ile Ala Ile Asn Asn Thr
        195                 200                 205
Lys Phe Ser Tyr Asn Asp Ser Lys Glu Trp Glu Glu Ala Met Ala Lys
    210                 215                 220
Ala Gln Glu Thr Gly His Leu Val Met Asp Val Arg Arg Tyr Gly Lys
225                 230                 235                 240
Ala Gly Ser Pro Glu Thr Lys Trp Ile Asp Ala Thr Ser Gly Ile Tyr
                245                 250                 255
Asn Ser Glu Lys Ser Ser Asn Leu Ser Val Thr Thr Asp Phe Ser Glu
            260                 265                 270
Ser Leu Gln Ser Ser Asn Ile Glu Ser Lys Glu Ile Asn Gly Ile His
        275                 280                 285
Asp Glu Ser Asn Ala Phe Glu Ser Lys Ala Ser Glu Ser Ile Ser Leu
    290                 295                 300
Lys Asn Leu Lys Arg Arg Ser Gln Phe Phe Glu Gln Gly Ser Ser Asp
305                 310                 315                 320
Ser Val Val Pro Asp Leu Pro Val Pro Thr Ile Ser Ala Pro Ser Arg
                325                 330                 335
Trp Val Trp Asp Gln Glu Glu Glu Arg Lys Arg Gln Glu Arg Trp Gln
            340                 345                 350
Lys Glu Gln Asp Arg Leu Leu Gln Glu Lys Tyr Gln Arg Glu Gln Glu
        355                 360                 365
Lys Leu Arg Glu Glu Trp Gln Arg Ala Lys Gln Glu Ala Glu Arg Glu
    370                 375                 380
Asn Ser Lys Tyr Leu Asp Glu Glu Leu Met Val Leu Ser Ser Asn Ser
385                 390                 395                 400
Met Ser Leu Thr Thr Arg Glu Pro Ser Leu Ala Thr Trp Glu Ala Thr
                405                 410                 415
Trp Ser Glu Gly Ser Lys Ser Ser Asp Arg Glu Gly Thr Arg Ala Gly
            420                 425                 430
Glu Glu Glu Arg Arg Gln Pro Gln Glu Glu Val Val His Glu Asp Gln
        435                 440                 445
Gly Lys Lys Pro Gln Asp Gln Leu Val Ile Glu Arg Glu Arg Lys Trp
    450                 455                 460
Glu Gln Gln Leu Gln Glu Glu Gln Glu Gln Lys Arg Leu Gln Ala Glu
465                 470                 475                 480
Ala Glu Glu Gln Lys Arg Pro Ala Glu Glu Gln Lys Arg Gln Ala Glu
                485                 490                 495
Ile Glu Arg Glu Thr Ser Val Arg Ile Tyr Gln Tyr Arg Arg Pro Val
            500                 505                 510
Asp Ser Tyr Asp Ile Pro Lys Thr Glu Glu Ala Ser Ser Gly Phe Leu
        515                 520                 525
Pro Gly Asp Arg Asn Lys Ser Arg Ser Thr Thr Glu Leu Asp Asp Tyr
    530                 535                 540
Ser Thr Asn Lys Asn Gly Asn Asn Lys Tyr Leu Asp Gln Ile Gly Asn
545                 550                 555                 560
Thr Thr Ser Ser Gln Arg Arg Ser Lys Lys Glu Gln Val Pro Ser Gly
                565                 570                 575
Ala Glu Leu Glu Arg Gln Gln Ile Leu Gln Glu Met Arg Lys Arg Thr
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            580                 585                 590
Pro Leu His Asn Asp Asn Ser Trp Ile Arg Gln Arg Ser Ala Ser Val
        595                 600                 605
Asn Lys Glu Pro Val Ser Leu Pro Gly Ile Met Arg Arg Gly Glu Ser
    610                 615                 620
Leu Asp Asn Leu Asp Ser Pro Arg Ser Asn Ser Trp Arg Gln Pro Pro
625                 630                 635                 640
Trp Leu Asn Gln Pro Thr Gly Phe Tyr Ala Ser Ser Ser Val Gln Asp
                645                 650                 655
Phe Ser Arg Pro Pro Pro Gln Leu Val Ser Thr Ser Asn Arg Ala Tyr
            660                 665                 670
Met Arg Asn Pro Ser Ser Ser Val Pro Pro Pro Ser Ala Gly Ser Val
        675                 680                 685
Lys Thr Ser Thr Thr Gly Val Ala Thr Thr Gln Ser Pro Thr Pro Arg
    690                 695                 700
Ser His Ser Pro Ser Ala Ser Gln Ser Gly Ser Gln Leu Arg Asn Arg
705                 710                 715                 720
Ser Val Ser Gly Lys Arg Ile Cys Ser Tyr Cys Asn Asn Ile Leu Gly
                725                 730                 735
Lys Gly Ala Ala Met Ile Ile Glu Ser Leu Gly Leu Cys Tyr His Leu
            740                 745                 750
His Cys Phe Lys Cys Val Ala Cys Glu Cys Asp Leu Gly Gly Ser Ser
        755                 760                 765
Ser Gly Ala Glu Val Arg Ile Arg Asn His Gln Leu Tyr Cys Asn Asp
    770                 775                 780
Cys Tyr Leu Arg Phe Lys Ser Gly Arg Pro Thr Ala Met
785                 790                 795
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<210> 731
<211> 513
<212> DNA
<213> Homo sapiens

<400> 731
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120
tcttcaaatg actgactggg gaaacagatt gttggaaaaa cactttcggg ttgcctcgat
180
ggggtcaata ccttatcagg ccacaggaaa gacaaaggaa aatgcttcct gctggagcat
240
gtgcacatat gttgttcctt taactccaaa tacgtatgca ggggtggtgg taggatcaga
300
aaatgtgtga tcagaaagtg accagttccc caccattttg tgtgggtttt attttctttc
360
tgctccgtgt tgactctttt ccccacaaca cggaagctgc ttaatccaaa gacttggacc
420
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480
cagctccatg actacattta aatattgact agt
513

<210> 732

<211> 113
<212> PRT
<213> Homo sapiens

<400> 732
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Phe Arg Val Val Gly Lys Arg Val Asn Thr Glu Gln Lys Glu Asn Lys
20 25 30
Thr His Thr Lys Trp Trp Gly Thr Gly His Phe Leu Ile Thr His Phe
35 40 45
Leu Ile Leu Pro Pro Pro Leu His Thr Tyr Leu Glu Leu Lys Glu Gln
50 55 60
His Met Cys Thr Cys Ser Ser Arg Lys His Phe Pro Leu Ser Phe Leu
65 70 75 80
Trp Pro Asp Lys Val Leu Thr Pro Ser Arg Gln Pro Glu Ser Val Phe
85 90 95
Pro Thr Ile Cys Phe Pro Ser Gln Ser Phe Glu Glu Ser Arg Glu Ala
100 105 110
Glu

<210> 733
<211> 4366
<212> DNA
<213> Homo sapiens

<400> 733
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120
ggaggcctct tgaagaactc caggcctatc atgctgtctc tccgctaaag cctgaggccc
180
gaggtcagag gattcaggaa ggctctgcag tcggcccagg agggcggggt cccgtggtgg
240
aggcggggag agggaaggac cgcacggagc accaacccct gctcggcccc gtaccaggaa
300
gcgctggggg gcagaggagc ggagttgagg cagaagccag gtgaggctgg agtcctgggg
360
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420
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480
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600
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720
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780

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4366

<210> 734
<211> 364
<212> PRT
<213> Homo sapiens

<400> 734
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Gly Ala Lys Thr Gln Ala Gln Glu Arg Glu Val Ile Gln Lys Glu Cys
20 25 30
Ala His Ile Arg Ala Ser Phe Arg Asp Gly Asp Pro Val His Arg His
35 40 45
Arg Gln Leu Ala Lys Leu Leu Tyr Val His Met Leu Gly Tyr Pro Ala
50 55 60
His Phe Gly Gln Met Glu Cys Leu Lys Leu Ile Ala Ser Ser Arg Phe
65 70 75 80
Thr Asp Lys Arg Val Gly Tyr Leu Gly Ala Met Leu Leu Leu Asp Glu
85 90 95
Arg His Asp Ala His Leu Leu Ile Thr Asn Ser Ile Lys Asn Asp Leu
100 105 110
Ser Gln Gly Ile Gln Pro Val Gln Gly Leu Ala Leu Cys Thr Leu Ser
115 120 125
Thr Met Gly Ser Ala Glu Met Cys Arg Asp Leu Ala Pro Glu Val Glu
130 135 140
Lys Leu Leu Leu Gln Pro Ser Pro Tyr Val Arg Lys Lys Ala Ile Leu
145 150 155 160
Thr Ala Val His Met Ile Arg Lys Val Pro Glu Leu Ser Ser Val Phe
165 170 175
Leu Pro Pro Cys Ala Gln Leu Leu His Glu Arg His His Gly Ile Leu
180 185 190
Leu Gly Thr Ile Thr Leu Ile Thr Glu Leu Cys Glu Arg Ser Pro Ala
195 200 205
Ala Leu Arg His Phe Arg Lys Val Val Pro Gln Leu Val His Ile Leu
210 215 220
Arg Thr Leu Val Thr Met Gly Tyr Ser Thr Glu His Ser Ile Ser Gly
225 230 235 240
Val Ser Asp Pro Phe Leu Gln Val Gln Ile Leu Arg Leu Leu Arg Ile
245 250 255
Leu Gly Arg Asn His Glu Glu Ser Ser Glu Thr Met Asn Asp Leu Leu
260 265 270
Ala Gln Val Ala Thr Asn Thr Asp Thr Ser Arg Asn Ala Gly Asn Ala

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        275                 280                 285
Val Leu Phe Glu Thr Val Leu Thr Ile Met Asp Ile Arg Ser Ala Ala
    290                 295                 300
Gly Leu Arg Val Leu Ala Val Asn Ile Leu Gly Arg Phe Leu Leu Asn
305                 310                 315                 320
Ser Asp Arg Asn Ile Arg Tyr Val Ala Leu Thr Ser Leu Leu Arg Leu
                325                 330                 335
Val Gln Ser Asp His Ser Ala Val Gln Arg His Arg Pro Thr Val Val
            340                 345                 350
Glu Cys Leu Arg Glu Thr Asp Ala Ser Leu Ser Arg
        355                 360
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<210> 735
<211> 597
<212> DNA
<213> Homo sapiens

<400> 735
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120
tgcttggtgt cctcgatccc gctctgaccg cccactggac cgctcaaccc aggacatcct
180
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240
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300
cgtggatttc gccgttgccg tagaacattg gccgcagttc gaaaacatca agcagcacct
360
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420
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480
gccagccacc atcaaatggc cgcccgacat ggctgtcatg atgaatgttg ctggctacgc
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597

<210> 736
<211> 175
<212> PRT
<213> Homo sapiens

<400> 736
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Met Asp Ser Arg Asn Leu Glu Thr Ala Asn Leu Ile Pro Glu Lys Ile
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Ile Ala Trp Cys Pro Arg Ser Arg Ser Asp Arg Pro Leu Asp Arg Ser
            20                  25                  30
Thr Gln Asp Ile Leu Ser Ala Ile His Asp Val Ala Ala Pro Leu Ala
        35                  40                  45
Leu Pro Ile Phe Val Val Gly Ala Thr Ala Arg Asp Ile Leu Leu Thr
    50                  55                  60
His Val Phe Gly Ile Glu Thr Gly Arg Ala Thr Leu Asp Val Asp Phe
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65                  70                  75                  80
Ala Val Ala Val Glu His Trp Pro Gln Phe Glu Asn Ile Lys Gln His
                85                  90                  95
Leu Leu Ala Asn Asp His Phe Asp Ser Ala Ala Ser Ile Thr His Arg
            100                 105                 110
Leu Leu Tyr Arg Thr Ser Asp Asn Thr Ile Ala Arg Pro Ile Asp Leu
        115                 120                 125
Ile Pro Phe Gly Gly Ile Glu Gln Pro Pro Ala Thr Ile Lys Trp Pro
    130                 135                 140
Pro Asp Met Ala Val Met Met Asn Val Ala Gly Tyr Ala Asp Ala Trp
145                 150                 155                 160
Arg Ala Ala Val Glu Val Glu Phe Val Pro Gly Arg Ser Ile Arg
                165                 170                 175
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<210> 737
<211> 497
<212> DNA
<213> Homo sapiens

<400> 737
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120
caccctgccc tgtcctggat cagccacgtc accttcgtta aaactgtcag tgtgggggat
180
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240
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300
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360
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actctgaccg ctgatgacat ggccgaactc ctcggaacca ttagctacga gatcacttgc
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497

<210> 738
<211> 165
<212> PRT
<213> Homo sapiens

<400> 738
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 1               5                  10                  15
Thr Ser Met Val Arg Ala Gly Ile Val Gly Tyr Gly Tyr Asp Pro Asn
            20                  25                  30
Pro His Ala Asp Arg Ala Asp Leu His Pro Ala Leu Ser Trp Ile Ser
        35                  40                  45
His Val Thr Phe Val Lys Thr Val Ser Val Gly Asp Thr Ile Gly Tyr
    50                  55                  60
Gly Arg Thr Trp Thr Ala Ser Glu Thr Thr Lys Ile Ala Thr Val Pro
```

```
65                  70                  75                  80
Val Gly Tyr Ala Asp Gly Leu Ser Arg Gly Leu Ser Asn Lys Gly His
                85                  90                  95
Val Leu Ile Arg Gly Ser Val His Pro Ile Val Gly Arg Ile Cys Met
            100                 105                 110
Asp Gln Phe Met Val Asp Leu Gly Pro Asp Ser Asn Val Thr Val Gly
        115                 120                 125
Asp Glu Val Val Leu Ile Gly Thr Gln Glu Asp Glu Thr Leu Thr Ala
    130                 135                 140
Asp Asp Met Ala Glu Leu Leu Gly Thr Ile Ser Tyr Glu Ile Thr Cys
145                 150                 155                 160
Ala Ile Ser Lys Arg
                165
```

<210> 739
<211> 438
<212> DNA
<213> Homo sapiens

<400> 739
cggctgcggg aagagcgggc gcacgcgctc aagaccaagg aaaagctggc acagaccgcc
60
acggcctcat cagcagctgt gggctcaggc ccccctcccg aggcggagca ggcgtggccg
120
cagagcagcg gggaggagga gctgcagctc cagctggccc tggccatgag caaggaggag
180
gccgaccagc ccccgtcctg cggccccgag gacgacgccc agctccagct ggcccttagt
240
ttgagccgag aagagcatga taaggaggag cggatccgtc gcggggatga cctgcggctg
300
cagatggcaa tcgaggagag caagagggag actgggggca aggaggagtc gtccctcatg
360
gaccttgctg acgtcttcac gcccccagct cctgccccga ccacagaccc ctgggggggc
420
ccagcaccca tggctgct
438

<210> 740
<211> 146
<212> PRT
<213> Homo sapiens

<400> 740
```
Arg Leu Arg Glu Glu Arg Ala His Ala Leu Lys Thr Lys Glu Lys Leu
 1               5                  10                  15
Ala Gln Thr Ala Thr Ala Ser Ser Ala Ala Val Gly Ser Gly Pro Pro
            20                  25                  30
Pro Glu Ala Glu Gln Ala Trp Pro Gln Ser Ser Gly Glu Glu Glu Leu
        35                  40                  45
Gln Leu Gln Leu Ala Leu Ala Met Ser Lys Glu Glu Ala Asp Gln Pro
    50                  55                  60
Pro Ser Cys Gly Pro Glu Asp Asp Ala Gln Leu Gln Leu Ala Leu Ser
65                  70                  75                  80
Leu Ser Arg Glu Glu His Asp Lys Glu Glu Arg Ile Arg Arg Gly Asp
```

```
                85                  90                  95
Asp Leu Arg Leu Gln Met Ala Ile Glu Glu Ser Lys Arg Glu Thr Gly
            100                 105                 110
Gly Lys Glu Glu Ser Ser Leu Met Asp Leu Ala Asp Val Phe Thr Pro
        115                 120                 125
Pro Ala Pro Ala Pro Thr Thr Asp Pro Trp Gly Gly Pro Ala Pro Met
    130                 135                 140
Ala Ala
145
```

<210> 741
<211> 726
<212> DNA
<213> Homo sapiens

<400> 741
gcctctctcc gaccgcgttg ttgtaaggat gtcgcgacgg tgcgcaaaaa tgaatatgtg
60
aatttgccgg tcatctgcct cgtcgggccc actgctagcg gaaaatcagg gctagcggtg
120
cgagtgtgcc gccgcttgta tgtcgatgag caccccgccg aaattattaa tactgactcg
180
atggtggtgt atcgcgggat ggacattggc actgccaccc ctacactgcg cgagcagcgc
240
acggtagtgc atcacctggt gtcgattctt gatgtgactg tgccctcctc gctagtactg
300
atgcagacgc tggcccgtga tgccgtcgag gattgtctgt cgcgtggtgt catccctgtc
360
ttggtgggag ggtctgcgct gtacaccaag gccatcattg acgaaatgtc catcccgcca
420
actgatccgg aagtgagggc tcggtggcag gagaagctag atgccgaggg gccgcgagtt
480
ctgcatgacg agcttgcccg tcgcgatccc aaggcggctg agtcaatctt gcccggcaac
540
ggcaggcgaa tcgtttcgtg ccctcgaagt ttattgaccc tgacagggtc ctttactgcc
600
accgatcccc gacgggaccc tccactggcc aagacggtgc aaatgggctt agaactgtcg
660
cgcaaagaca tagaccagcg tattgccgat cgggttgacc agatgtgggc atacggtttc
720
gtcgac
726

<210> 742
<211> 242
<212> PRT
<213> Homo sapiens

<400> 742
```
Ala Ser Leu Arg Pro Arg Cys Cys Lys Asp Val Ala Thr Val Arg Lys
 1               5                  10                  15
Asn Glu Tyr Val Asn Leu Pro Val Ile Cys Leu Val Gly Pro Thr Ala
            20                  25                  30
Ser Gly Lys Ser Gly Leu Ala Val Arg Val Cys Arg Arg Leu Tyr Val
```

```
        35                  40                  45
Asp Glu His Pro Ala Glu Ile Ile Asn Thr Asp Ser Met Val Val Tyr
    50                  55                  60
Arg Gly Met Asp Ile Gly Thr Ala Thr Pro Thr Leu Arg Glu Gln Arg
65                  70                  75                  80
Thr Val Val His His Leu Val Ser Ile Leu Asp Val Thr Val Pro Ser
                85                  90                  95
Ser Leu Val Leu Met Gln Thr Leu Ala Arg Asp Ala Val Glu Asp Cys
            100                 105                 110
Leu Ser Arg Gly Val Ile Pro Val Leu Val Gly Gly Ser Ala Leu Tyr
        115                 120                 125
Thr Lys Ala Ile Ile Asp Glu Met Ser Ile Pro Pro Thr Asp Pro Glu
    130                 135                 140
Val Arg Ala Arg Trp Gln Glu Lys Leu Asp Ala Glu Gly Pro Arg Val
145                 150                 155                 160
Leu His Asp Glu Leu Ala Arg Arg Asp Pro Lys Ala Ala Glu Ser Ile
                165                 170                 175
Leu Pro Gly Asn Gly Arg Arg Ile Val Ser Cys Pro Arg Ser Leu Leu
            180                 185                 190
Thr Leu Thr Gly Ser Phe Thr Ala Thr Asp Pro Arg Arg Asp Pro Pro
        195                 200                 205
Leu Ala Lys Thr Val Gln Met Gly Leu Glu Leu Ser Arg Lys Asp Ile
    210                 215                 220
Asp Gln Arg Ile Ala Asp Arg Val Asp Gln Met Trp Ala Tyr Gly Phe
225                 230                 235                 240
Val Asp
```

<210> 743
<211> 430
<212> DNA
<213> Homo sapiens

<400> 743
naaaaaagtg atggtttcgg atctgtggcc agtcgtcttg caagaaatca ttatgacgtg
60
gatgagggca acagcancat tcatgttaat caagacattg cgcgcagaac agggacggga
120
aagctattgg tacgagtgtg cccggcgcac gtgtactcag aggagcccga tggcactatt
180
tccgtggagt acgcagcgtg tctggagtgt ggcacttgtc tggcggttgc tgcgccaggg
240
tcgcttgaat ggcactatcc cgcaggtgca atgggtattt cgttcagaga aggatgaagt
300
ccttgtgggc gactgtaaag cgacatggcc gtcgctcggt aggaggaatt gtggtgtccg
360
caccaaatag tgctcaggat gaagttcgtc atggaaatcc ggctccaacc gtttcgggag
420
ctggtcgcga
430

<210> 744
<211> 98
<212> PRT

<213> Homo sapiens

<400> 744
Xaa Lys Ser Asp Gly Phe Gly Ser Val Ala Ser Arg Leu Ala Arg Asn
1 5 10 15
His Tyr Asp Val Asp Glu Gly Asn Ser Xaa Ile His Val Asn Gln Asp
20 25 30
Ile Ala Arg Arg Thr Gly Thr Gly Lys Leu Leu Val Arg Val Cys Pro
35 40 45
Ala His Val Tyr Ser Glu Glu Pro Asp Gly Thr Ile Ser Val Glu Tyr
50 55 60
Ala Ala Cys Leu Glu Cys Gly Thr Cys Leu Ala Val Ala Ala Pro Gly
65 70 75 80
Ser Leu Glu Trp His Tyr Pro Ala Gly Ala Met Gly Ile Ser Phe Arg
85 90 95
Glu Gly

<210> 745
<211> 362
<212> DNA
<213> Homo sapiens

<400> 745
cggccgattg aagcgtcgct gcggtttgag tcggtgatgg atgcggtgga cggtgcttcg
60
gcgtcgtggt ggcgcatggc gcggtatttc atcgccgagc ttgaacgcag cagcgagttg
120
tatgagcagg cggcgtttac ccgcgatctg gaaagctcgc tgatcaaggg cctgatcctc
180
gcccagccga acaactactc cgaagaactg cgcgacgtac tcggcgtgaa gctgccgcat
240
tacttgattc gcgcgcggca gtacatccac gacaacgccc gcgaagccgt gcatctggaa
300
gacctggaaa ccgctgccgg ggtatcgcgg ttcaagttgt tcgatgcgtt tcgcaaatac
360
tt
362

<210> 746
<211> 108
<212> PRT
<213> Homo sapiens

<400> 746
Met Asp Ala Val Asp Gly Ala Ser Ala Ser Trp Trp Arg Met Ala Arg
1 5 10 15
Tyr Phe Ile Ala Glu Leu Glu Arg Ser Ser Glu Leu Tyr Glu Gln Ala
20 25 30
Ala Phe Thr Arg Asp Leu Glu Ser Ser Leu Ile Lys Gly Leu Ile Leu
35 40 45
Ala Gln Pro Asn Asn Tyr Ser Glu Glu Leu Arg Asp Val Leu Gly Val
50 55 60
Lys Leu Pro His Tyr Leu Ile Arg Ala Arg Gln Tyr Ile His Asp Asn

65 70 75 80
Ala Arg Glu Ala Val His Leu Glu Asp Leu Glu Thr Ala Ala Gly Val
85 90 95
Ser Arg Phe Lys Leu Phe Asp Ala Phe Arg Lys Tyr
100 105

<210> 747
<211> 416
<212> DNA
<213> Homo sapiens

<400> 747
nacgcgttga tcgccgccga ccgtttcatc ccgcaatcac ccgacatggc ggcctatttt
60
ctgaatgccg atggcacgcc taaagccacc ggcacgctgc tcaagaaccc agcgctggcc
120
gccgtgttca aacgtatcgc caaggaagga ccggacgcgc tgtaccacgg gccgattgcc
180
gacgagatcg cgcgcaaggt tcagggcaac cgcaatgcgg gcagcctgtc gcaagcggac
240
ctcaaggctt acaccgccaa ggaacgcacg ccgctgtgca ccgactacaa gcaatatcag
300
gtgtgcggca tgccaccgcc gtcgtcaggc gggattgcgg tggcgcagat cctcggcacg
360
ctgcaggccg tggaagcccg cgacccacgc ctggccatcg cccccatgaa accggt
416

<210> 748
<211> 138
<212> PRT
<213> Homo sapiens

<400> 748
Xaa Ala Leu Ile Ala Ala Asp Arg Phe Ile Pro Gln Ser Pro Asp Met
1 5 10 15
Ala Ala Tyr Phe Leu Asn Ala Asp Gly Thr Pro Lys Ala Thr Gly Thr
20 25 30
Leu Leu Lys Asn Pro Ala Leu Ala Ala Val Phe Lys Arg Ile Ala Lys
35 40 45
Glu Gly Pro Asp Ala Leu Tyr His Gly Pro Ile Ala Asp Glu Ile Ala
50 55 60
Arg Lys Val Gln Gly Asn Arg Asn Ala Gly Ser Leu Ser Gln Ala Asp
65 70 75 80
Leu Lys Ala Tyr Thr Ala Lys Glu Arg Thr Pro Leu Cys Thr Asp Tyr
85 90 95
Lys Gln Tyr Gln Val Cys Gly Met Pro Pro Pro Ser Ser Gly Gly Ile
100 105 110
Ala Val Ala Gln Ile Leu Gly Thr Leu Gln Ala Val Glu Ala Arg Asp
115 120 125
Pro Arg Leu Ala Ile Ala Pro Met Lys Pro
130 135

<210> 749
<211> 1211

<212> DNA
<213> Homo sapiens

<400> 749
nagtcctaga cgccagaccc gctcagaccc tcctgccagg tgacagccgc caagatgggg
60
tcttgggccc tgctgtggcc tcccctgctg ttcaccgggc tgctcgtccg acccccgggg
120
accatggccc aggcccagta ctgctctgtg aacaaggaca tctttgaagt agaggagaac
180
acaaatgtca ccgagccgct ggtggacatc cacgtcccgg agggccagga ggtgaccctc
240
ggagccttgt ccacccccct tgcatttcgg atccagggaa accagctgtt tctcaacgtg
300
actcctgatt acgaggagaa gtcactgctt gaggctcagc tgctgtgtca gagcggaggc
360
acattggtga cccagctaag ggtgttcgtg tcagtgctgg acgtcaatga caatgccccc
420
gaattccccc ttaagaccaa ggagataagg gtggaggagg acacgaaagt gaactccacc
480
gtcatccccg agacgcaact gcaggctgag gaccgcgaca aggacgacat tctgttctac
540
accctccagg aaatgacagc aggtgccagt gactacttct ccctggtgag tgtaaaccgt
600
cccgccctga ggctggaccg gcccctggac ttctacgagc ggccgaacat gaccttctgg
660
ctgctggtgc gggacactcc gggggagaat gtggaaccca gccacactgc caccgccaca
720
ctagtgctga acgtggtgcc cgccgacctg cggcccccgt ggttcctgcc ctgcaccttc
780
tcagatggct acgtctgcat tcaagctcag taccacgggg ctgtccccac ggggcacata
840
ctgccatctc ccctcgtcct gcgtcccgga cccatctacg ctgaggacgg agaccgcggc
900
atcaaccagc ccatcatcta cagcatcttt aggggaaacg tgaatggtac attcatcatc
960
cacccagact cgggcaacct caccgtggcc aggagtgtcc ccagccccat gaccttcctt
1020
ctgctggtga agggccaaca ggccgacctt gcccgctact cagtgaccca ggtcaccgtg
1080
gagggctgtg gctgcggccg ggagcccgcc ccgcttcccc cagagcctgt atcgtggcac
1140
cgtggcgcgt ggcgctggag cgggcgttgt ggtcaaggat gcagctgccc cttttcagcc
1200
tctgaggatc c
1211

<210> 750
<211> 385
<212> PRT
<213> Homo sapiens

<400> 750
Met Gly Ser Trp Ala Leu Leu Trp Pro Pro Leu Leu Phe Thr Gly Leu

```
 1               5                  10                  15
Leu Val Arg Pro Pro Gly Thr Met Ala Gln Ala Gln Tyr Cys Ser Val
            20                  25                  30
Asn Lys Asp Ile Phe Glu Val Glu Glu Asn Thr Asn Val Thr Glu Pro
        35                  40                  45
Leu Val Asp Ile His Val Pro Glu Gly Gln Glu Val Thr Leu Gly Ala
    50                  55                  60
Leu Ser Thr Pro Phe Ala Phe Arg Ile Gln Gly Asn Gln Leu Phe Leu
65                  70                  75                  80
Asn Val Thr Pro Asp Tyr Glu Glu Lys Ser Leu Leu Glu Ala Gln Leu
                85                  90                  95
Leu Cys Gln Ser Gly Gly Thr Leu Val Thr Gln Leu Arg Val Phe Val
            100                 105                 110
Ser Val Leu Asp Val Asn Asp Asn Ala Pro Glu Phe Pro Phe Lys Thr
        115                 120                 125
Lys Glu Ile Arg Val Glu Glu Asp Thr Lys Val Asn Ser Thr Val Ile
    130                 135                 140
Pro Glu Thr Gln Leu Gln Ala Glu Asp Arg Asp Lys Asp Asp Ile Leu
145                 150                 155                 160
Phe Tyr Thr Leu Gln Glu Met Thr Ala Gly Ala Ser Asp Tyr Phe Ser
                165                 170                 175
Leu Val Ser Val Asn Arg Pro Ala Leu Arg Leu Asp Arg Pro Leu Asp
            180                 185                 190
Phe Tyr Glu Arg Pro Asn Met Thr Phe Trp Leu Leu Val Arg Asp Thr
        195                 200                 205
Pro Gly Glu Asn Val Glu Pro Ser His Thr Ala Thr Ala Thr Leu Val
    210                 215                 220
Leu Asn Val Val Pro Ala Asp Leu Arg Pro Pro Trp Phe Leu Pro Cys
225                 230                 235                 240
Thr Phe Ser Asp Gly Tyr Val Cys Ile Gln Ala Gln Tyr His Gly Ala
                245                 250                 255
Val Pro Thr Gly His Ile Leu Pro Ser Pro Leu Val Leu Arg Pro Gly
            260                 265                 270
Pro Ile Tyr Ala Glu Asp Gly Asp Arg Gly Ile Asn Gln Pro Ile Ile
        275                 280                 285
Tyr Ser Ile Phe Arg Gly Asn Val Asn Gly Thr Phe Ile Ile His Pro
    290                 295                 300
Asp Ser Gly Asn Leu Thr Val Ala Arg Ser Val Pro Ser Pro Met Thr
305                 310                 315                 320
Phe Leu Leu Leu Val Lys Gly Gln Gln Ala Asp Leu Ala Arg Tyr Ser
                325                 330                 335
Val Thr Gln Val Thr Val Glu Gly Cys Gly Cys Gly Arg Glu Pro Ala
            340                 345                 350
Pro Leu Pro Pro Glu Pro Val Ser Trp His Arg Gly Ala Trp Arg Trp
        355                 360                 365
Ser Gly Arg Cys Gly Gln Gly Cys Ser Cys Pro Phe Ser Ala Ser Glu
    370                 375                 380
Asp
385
```

<210> 751
<211> 345
<212> DNA
<213> Homo sapiens

<400> 751
cgcgtcgcgg tcatcgtcaa cgacatgagc gaggtcaaca tcgacgcggc gctggtggcg
60
gcaggcggcg ggctgtcgcg caccgaggag aagctcgtcg agatgtcgaa cggctgcatc
120
tgctgcacgc tgcgcgacga cctgatgcag gaagtggcga gactggcggg cgaaggccgc
180
ttcgatgcgc tggtcatcga gagcaccggc gtgtccgagc cgatgccggt cgccgccacg
240
ttcgatttcc gtgaccagga cggcgtctcg ctcgccgacg tcgcgcggct ggataccatg
300
gtcaccgtcg tcgacgccgc gtccttcctg cgcgactacg gctcg
345

<210> 752
<211> 115
<212> PRT
<213> Homo sapiens

<400> 752
Arg Val Ala Val Ile Val Asn Asp Met Ser Glu Val Asn Ile Asp Ala
1 5 10 15
Ala Leu Val Ala Ala Gly Gly Gly Leu Ser Arg Thr Glu Glu Lys Leu
20 25 30
Val Glu Met Ser Asn Gly Cys Ile Cys Cys Thr Leu Arg Asp Asp Leu
35 40 45
Met Gln Glu Val Ala Arg Leu Ala Gly Glu Gly Arg Phe Asp Ala Leu
50 55 60
Val Ile Glu Ser Thr Gly Val Ser Glu Pro Met Pro Val Ala Ala Thr
65 70 75 80
Phe Asp Phe Arg Asp Gln Asp Gly Val Ser Leu Ala Asp Val Ala Arg
85 90 95
Leu Asp Thr Met Val Thr Val Val Asp Ala Ala Ser Phe Leu Arg Asp
100 105 110
Tyr Gly Ser
115

<210> 753
<211> 352
<212> DNA
<213> Homo sapiens

<400> 753
gcgcgccagt acgccaagac cgtccgcaag gaccgcaagg gcgaacggcg gcgtcggggc
60
gcgtcggact agtccacgat gcatccgaac cgcgccttcc gctttgccga tgatgtctcg
120
atgctcgatt tcgcggccaa gcgagccttt gcgcacatct tcgtgagcac gcccgagggg
180
cctatggtag cgcatgcccc ggttacgccc ttcgacggag ccttccgctt ccatgtcgcg
240
cgcggcaatc ggatcgcgcg gcacctggat ggcgcgacgc tgctgctcag catcagcgcg
300

accgacggct atatcagccc gagctggtac gccgacccgc agggaccaca gt
352

<210> 754
<211> 91
<212> PRT
<213> Homo sapiens

<400> 754
Met His Pro Asn Arg Ala Phe Arg Phe Ala Asp Asp Val Ser Met Leu
1 5 10 15
Asp Phe Ala Ala Lys Arg Ala Phe Ala His Ile Phe Val Ser Thr Pro
20 25 30
Glu Gly Pro Met Val Ala His Ala Pro Val Thr Pro Phe Asp Gly Ala
35 40 45
Phe Arg Phe His Val Ala Arg Gly Asn Arg Ile Ala Arg His Leu Asp
50 55 60
Gly Ala Thr Leu Leu Leu Ser Ile Ser Ala Thr Asp Gly Tyr Ile Ser
65 70 75 80
Pro Ser Trp Tyr Ala Asp Pro Gln Gly Pro Gln
85 90

<210> 755
<211> 301
<212> DNA
<213> Homo sapiens

<400> 755
tgggatgcag ggtctttctt ctccaaggat ttcattcctg gagggagaaa agggccccag
60
ctgtctgcca tcaaaccggg ttgccgggct ggagctcctc ccaggcccgt gtgaggaaga
120
gcaaaggccg gcaggggctc gatgggacca gtcgctcgct caggcccagg aaaaccacac
180
agctgggggc tgtcaggatt ggaccagggt caggccggcc aggcgatggc gggaaaagca
240
ggcccactct gcagacctca atgtctcagg tgcactgcag ggcaaccccg cctaccccgg
300
g
301

<210> 756
<211> 99
<212> PRT
<213> Homo sapiens

<400> 756
Met Gln Gly Leu Ser Ser Pro Arg Ile Ser Phe Leu Glu Gly Glu Lys
1 5 10 15
Gly Pro Ser Cys Leu Pro Ser Asn Arg Val Ala Gly Leu Glu Leu Leu
20 25 30
Pro Gly Pro Cys Glu Glu Glu Gln Arg Pro Ala Gly Ala Arg Trp Asp
35 40 45
Gln Ser Leu Ala Gln Ala Gln Glu Asn His Thr Ala Gly Gly Cys Gln

```
    50                  55                  60
Asp Trp Thr Arg Val Arg Pro Ala Arg Arg Trp Arg Glu Lys Gln Ala
65                  70                  75                  80
His Ser Ala Asp Leu Asn Val Ser Gly Ala Leu Gln Gly Asn Pro Ala
                85                  90                  95
Tyr Pro Gly
```

<210> 757
<211> 311
<212> DNA
<213> Homo sapiens

<400> 757
actgaggcga tcgccagagg ggtgggcgtg cgagggctgc tcaacatcca gttcgccctg
60
gtctccgatg ttctctacgt catcgaggcc aaccccaggg catcgcgcac agtccccttc
120
gtctcaaagg catccggcgt gcagctcgcc aaagcggcgg ccctcatcat gacaggggag
180
acgatcgcct cgctcaggcg ctccggccac ctgcccgagg ccgacgccgc cgtcaccgat
240
cccgatgacc cgatcgccgt caaggaggcg gtcctaccct tcaaacgatt ccgcaccacc
300
gagggacgcg t
311

<210> 758
<211> 103
<212> PRT
<213> Homo sapiens

<400> 758

```
Thr Glu Ala Ile Ala Arg Gly Val Gly Val Arg Gly Leu Leu Asn Ile
 1               5                  10                  15
Gln Phe Ala Leu Val Ser Asp Val Leu Tyr Val Ile Glu Ala Asn Pro
            20                  25                  30
Arg Ala Ser Arg Thr Val Pro Phe Val Ser Lys Ala Ser Gly Val Gln
        35                  40                  45
Leu Ala Lys Ala Ala Ala Leu Ile Met Thr Gly Glu Thr Ile Ala Ser
    50                  55                  60
Leu Arg Arg Ser Gly His Leu Pro Glu Ala Asp Ala Ala Val Thr Asp
65                  70                  75                  80
Pro Asp Asp Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Lys Arg
                85                  90                  95
Phe Arg Thr Thr Glu Gly Arg
            100
```

<210> 759
<211> 391
<212> DNA
<213> Homo sapiens

<400> 759

gtgcacaccg gcaagctggt gtggaactgg gacagcggca acccggacga cactacgccg
60
attgccgagg gcaagaccta cacccgcaac tcgccgaaca tgtggtccat gttcgccgtc
120
gacgaaaaac tcggcatgct ctacctgccg atgggcaacc agaccccgga ccagttcggg
180
ggctaccgca cgcctgcgtc ggaactgcac gctgccggcc tgacagcgct ggatatcgac
240
actggtaaag tgcgctggca ctaccagttc acccaccatg acctgtggga catggacgtg
300
ggcggccagc cgagcctgat cgacatcaag accgccgccg gcgtgaaaca agccgtgatg
360
gcctcgacca agcaaggcag catctacgcg t
391

<210> 760
<211> 130
<212> PRT
<213> Homo sapiens

<400> 760
Val His Thr Gly Lys Leu Val Trp Asn Trp Asp Ser Gly Asn Pro Asp
 1   5   10   15
Asp Thr Thr Pro Ile Ala Glu Gly Lys Thr Tyr Thr Arg Asn Ser Pro
            20   25   30
Asn Met Trp Ser Met Phe Ala Val Asp Glu Lys Leu Gly Met Leu Tyr
        35   40   45
Leu Pro Met Gly Asn Gln Thr Pro Asp Gln Phe Gly Gly Tyr Arg Thr
    50   55   60
Pro Ala Ser Glu Leu His Ala Ala Gly Leu Thr Ala Leu Asp Ile Asp
65   70   75   80
Thr Gly Lys Val Arg Trp His Tyr Gln Phe Thr His His Asp Leu Trp
                85   90   95
Asp Met Asp Val Gly Gly Gln Pro Ser Leu Ile Asp Ile Lys Thr Ala
            100   105   110
Ala Gly Val Lys Gln Ala Val Met Ala Ser Thr Lys Gln Gly Ser Ile
        115   120   125
Tyr Ala
    130

<210> 761
<211> 324
<212> DNA
<213> Homo sapiens

<400> 761
cctaggtagg cccaaagggg cctaactttc ttgctgccct ggtggagcaa gaaatatctt
60
ctaggagagg ccaatccttc cctgccccac agctccttct ctgcaaagct caggggggcaa
120
tcaggtacct cctgcccaag aggcccccat ggttcctcgc ctaaggaagg cagggcgggg
180
cattgggagc cgttgacagc tgggctcagc tgggggggagg ggtcagtttg ggagcaggtg
240

cagatttcag ggaggggggg gcctaaaggg aagtagggat cttggtaggc tgcaaaattt
300
tcctccccat cccccatcca caga
324

<210> 762
<211> 105
<212> PRT
<213> Homo sapiens

<400> 762
Met Gly Asp Gly Glu Glu Asn Phe Ala Ala Tyr Gln Asp Pro Tyr Phe
1 5 10 15
Pro Leu Gly Pro Pro Leu Pro Glu Ile Cys Thr Cys Ser Gln Thr Asp
20 25 30
Pro Ser Pro Gln Leu Ser Pro Ala Val Asn Gly Ser Gln Cys Pro Ala
35 40 45
Leu Pro Ser Leu Gly Glu Glu Pro Trp Gly Pro Leu Gly Gln Glu Val
50 55 60
Pro Asp Cys Pro Leu Ser Phe Ala Glu Lys Glu Leu Trp Gly Arg Glu
65 70 75 80
Gly Leu Ala Ser Pro Arg Arg Tyr Phe Leu Leu His Gln Gly Ser Lys
85 90 95
Lys Val Arg Pro Leu Trp Ala Tyr Leu
100 105

<210> 763
<211> 301
<212> DNA
<213> Homo sapiens

<400> 763
acgcgttatg ggcggcccgg atgggcgatg cgctatccca cacctcgatg atggcggaca
60
tcctcggcgg tgtgctggaa gtggcggcca atatcgcgat tactgcgggc gcgaccgctg
120
ccgcggtggc cgccaccggc tttaccgagg ccaccggcgg cctcggctgc ttcctgctgg
180
gcgctgcctt gggcaccatt gccggcctgg ccatgagcaa cattggcgcg gacacagggc
240
tgaccaagat atgcaatgcc tttaacaacg ccttatttgc gcccaccgtg catgcgaaca
300
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301

<210> 764
<211> 100
<212> PRT
<213> Homo sapiens

<400> 764
Met Phe Ala Cys Thr Val Gly Ala Asn Lys Ala Leu Leu Lys Ala Leu
1 5 10 15
His Ile Leu Val Ser Pro Val Ser Ala Pro Met Leu Leu Met Ala Arg

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            20                  25                  30
Pro Ala Met Val Pro Lys Ala Ala Pro Ser Arg Lys Gln Pro Arg Pro
        35                  40                  45
Pro Val Ala Ser Val Lys Pro Val Ala Ala Thr Ala Ala Ala Val Ala
    50                  55                  60
Pro Ala Val Ile Ala Ile Leu Ala Ala Thr Ser Ser Thr Pro Pro Arg
65                  70                  75                  80
Met Ser Ala Ile Ile Glu Val Trp Asp Ser Ala Ser Pro Ile Arg Ala
                85                  90                  95
Ala His Asn Ala
            100
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<210> 765
<211> 831
<212> DNA
<213> Homo sapiens

<400> 765
ngcacactcc agcctctgtt ctttctctcc ttgtgccttt gcccttacca cggttcctca
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taacattgtt gttcctgtat ttaaggccct ataaacaggg agatgcgcca cctcatcagt
120
agcctccaga atcacaatca ccagctgaaa ggggaggtcc tgagatataa gcggaaattg
180
agagaagccc agtctgacct gaacaagaca cgcctgcgta gtggtagtgc cctcctgcag
240
tcccagtcta gtactgagga cccgaaggat gagcctgcgg agctaaaacc agattctggg
300
gacttatcct cccagtcctc agcttcaaag gcatctcagg aggatgccaa tgaaatcaag
360
tctaaacggg atgaagaaga acgagaacga gaaaggaggg agaaggagag ggaacgagaa
420
agagaacggg agaaggagaa ggagagagaa cgagagaagc agaagctaaa agagtcagaa
480
aaagagagag attctgctaa ggataaagag aaaggcaaac atgatgatgg acggaaaaag
540
gaagcagaaa ttatcaaaca attgaagatt gaactcaaga aggcacagga gagccaaaag
600
gagatgaaac tattgctgga tatgtaccgt tctgccccaa aggaacagag agacaaagtt
660
cagctgatgg cagctgagaa gaagtctaag gcagagttgg aagatctaag gcaaagactc
720
aaggatctgg aagataaaga gaagaaagag aacaagaaaa tggctgatga ggatgccttg
780
aggaagatcc gggcagtgga ggagcagata gaatacctac agaagaagct a
831

<210> 766
<211> 243
<212> PRT
<213> Homo sapiens

<400> 766
Met Arg His Leu Ile Ser Ser Leu Gln Asn His Asn His Gln Leu Lys

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 1               5                  10                  15
Gly Glu Val Leu Arg Tyr Lys Arg Lys Leu Arg Glu Ala Gln Ser Asp
            20                  25                  30
Leu Asn Lys Thr Arg Leu Arg Ser Gly Ser Ala Leu Leu Gln Ser Gln
        35                  40                  45
Ser Ser Thr Glu Asp Pro Lys Asp Glu Pro Ala Glu Leu Lys Pro Asp
    50                  55                  60
Ser Gly Asp Leu Ser Ser Gln Ser Ser Ala Ser Lys Ala Ser Gln Glu
65                  70                  75                  80
Asp Ala Asn Glu Ile Lys Ser Lys Arg Asp Glu Glu Glu Arg Glu Arg
                85                  90                  95
Glu Arg Arg Glu Lys Glu Arg Glu Arg Glu Arg Glu Arg Glu Lys Glu
            100                 105                 110
Lys Glu Arg Glu Arg Glu Lys Gln Lys Leu Lys Glu Ser Glu Lys Glu
        115                 120                 125
Arg Asp Ser Ala Lys Asp Lys Glu Lys Gly Lys His Asp Asp Gly Arg
    130                 135                 140
Lys Lys Glu Ala Glu Ile Ile Lys Gln Leu Lys Ile Glu Leu Lys Lys
145                 150                 155                 160
Ala Gln Glu Ser Gln Lys Glu Met Lys Leu Leu Leu Asp Met Tyr Arg
                165                 170                 175
Ser Ala Pro Lys Glu Gln Arg Asp Lys Val Gln Leu Met Ala Ala Glu
            180                 185                 190
Lys Lys Ser Lys Ala Glu Leu Glu Asp Leu Arg Gln Arg Leu Lys Asp
        195                 200                 205
Leu Glu Asp Lys Glu Lys Lys Glu Asn Lys Lys Met Ala Asp Glu Asp
    210                 215                 220
Ala Leu Arg Lys Ile Arg Ala Val Glu Glu Gln Ile Glu Tyr Leu Gln
225                 230                 235                 240
Lys Lys Leu
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<210> 767
<211> 431
<212> DNA
<213> Homo sapiens

<400> 767
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ccccggcacc agaagttcct ctgcgcgtcc gacggcgaca tgggcgtccc cacggccccg
120
gaggccggca gctggcgctg gggatccctg ctcttcgctc tcttcctggc tgcgtcccta
180
ggtccggtgg cagccttcaa ggtcgccacg ccgtattccc tgtatgtctg tcccgagggg
240
cagaacgtca ccctcacctg caggctcttg ggccctgtgg acaaagggca cgatgtgacc
300
ttctacaaga cgtggtaccg cagctcgagg ggcgaggtgc agacctgctc agagcgccgg
360
cccatccgca acctcacgtt ccaggacctt cacctgcacc atggaggcca ccaggctgcc
420
aacaccagcc a
431

<210> 768
<211> 110
<212> PRT
<213> Homo sapiens

<400> 768
Met Gly Val Pro Thr Ala Pro Glu Ala Gly Ser Trp Arg Trp Gly Ser
1 5 10 15
Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val Ala Ala
20 25 30
Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
35 40 45
Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
50 55 60
Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val
65 70 75 80
Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
85 90 95
Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser
100 105 110

<210> 769
<211> 422
<212> DNA
<213> Homo sapiens

<400> 769
tgtacacctc gtaatacatg atcgcgatac cgcccgcgat gaccctaagc aactcattct
60
cgacttcgaa ctccatcaag tgatttttgc ggtcgacgaa tctggtttcc gtatgaaaga
120
acggtatgtt ttgtatgtcg cggccctgcc actcaaacct caccgtgtca cccacctcaa
180
aaaaatcccg ggtcggccca caaataaatc aattgcgccg ctcctccgag ttcttccatg
240
tcaacgatct cccctggctg ctcaagccaa ggccctcgcg gccgtgggac tccaaggttg
300
acgttgaccc gactgatttc ggaccagttg gcgtcggtat tgggggcagg gtagttaccg
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cccatgtcga tgatctacat cgccaccggc agcgtgtctt cgtagtcgtc atgcctgatc
420
an
422

<210> 770
<211> 99
<212> PRT
<213> Homo sapiens

<400> 770
Met Phe Cys Met Ser Arg Pro Cys His Ser Asn Leu Thr Val Ser Pro
1 5 10 15
Thr Ser Lys Lys Ser Arg Val Gly Pro Gln Ile Asn Gln Leu Arg Arg

```
            20                  25                  30
Ser Ser Glu Phe Phe His Val Asn Asp Leu Pro Trp Leu Leu Lys Pro
        35                  40                  45
Arg Pro Ser Arg Pro Trp Asp Ser Lys Val Asp Val Asp Pro Thr Asp
    50                  55                  60
Phe Gly Pro Val Gly Val Gly Ile Gly Gly Arg Val Val Thr Ala His
65                  70                  75                  80
Val Asp Asp Leu His Arg His Arg Gln Arg Val Phe Val Val Val Met
                85                  90                  95
Pro Asp Xaa
```

<210> 771
<211> 369
<212> DNA
<213> Homo sapiens

<400> 771
gcctacgcgc aattcctcgc gggtatggcg tttaacaatg cgtctctcgg gtatgtgcat
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gcaatggcgc atcagctggg cggtttttac gatctgccgc acggcgtgtg caatgcgata
120
ctgttgccac acgtgcagac gtttaactgc aaagtggcgg cctcgcgcct gcgtgattgc
180
gcccaggcca tgggtgtcga tgtcagtcaa atgacagcag aacagggcgc acaggcgtgt
240
atcgcagaga ttcgctctct ggcacgtcag gtgaatatcc cggtgggatt gcgtgacctc
300
aacgtgaagg aagcggactt cccgattctg gcgaccaacg cgctaaaaga ccctgtgggt
360
ttgattaat
369

<210> 772
<211> 123
<212> PRT
<213> Homo sapiens

<400> 772
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Ala Tyr Ala Gln Phe Leu Ala Gly Met Ala Phe Asn Asn Ala Ser Leu
 1               5                  10                  15
Gly Tyr Val His Ala Met Ala His Gln Leu Gly Gly Phe Tyr Asp Leu
            20                  25                  30
Pro His Gly Val Cys Asn Ala Ile Leu Leu Pro His Val Gln Thr Phe
        35                  40                  45
Asn Cys Lys Val Ala Ala Ser Arg Leu Arg Asp Cys Ala Gln Ala Met
    50                  55                  60
Gly Val Asp Val Ser Gln Met Thr Ala Glu Gln Gly Ala Gln Ala Cys
65                  70                  75                  80
Ile Ala Glu Ile Arg Ser Leu Ala Arg Gln Val Asn Ile Pro Val Gly
                85                  90                  95
Leu Arg Asp Leu Asn Val Lys Glu Ala Asp Phe Pro Ile Leu Ala Thr
            100                 105                 110
Asn Ala Leu Lys Asp Pro Val Gly Leu Ile Asn
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115 120

<210> 773
<211> 309
<212> DNA
<213> Homo sapiens

<400> 773
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60
ggttacttga tccgcgtgga gccgggcgta caaactccgg aattcaccct ggaaaacgcc
120
tccggttcct gccgggattc ggcgtggttg ctggtgcaac tgctgcgcaa cctgggcctg
180
gcggcgcgat ttgtgtctgg ctatctgatc caactgaccg ccgacgtcaa agccctcgac
240
ggcccgtccg gcaccgaggt ggatttcacc gacctgcatg cctggtgcga agtgtatttg
300
cccggcgcc
309

<210> 774
<211> 103
<212> PRT
<213> Homo sapiens

<400> 774
Pro Pro Leu Pro Ala Val Asp Phe Leu Val Gly Leu Asn Gln Arg Leu
1 5 10 15
Ala Ala Asp Ile Gly Tyr Leu Ile Arg Val Glu Pro Gly Val Gln Thr
20 25 30
Pro Glu Phe Thr Leu Glu Asn Ala Ser Gly Ser Cys Arg Asp Ser Ala
35 40 45
Trp Leu Leu Val Gln Leu Leu Arg Asn Leu Gly Leu Ala Ala Arg Phe
50 55 60
Val Ser Gly Tyr Leu Ile Gln Leu Thr Ala Asp Val Lys Ala Leu Asp
65 70 75 80
Gly Pro Ser Gly Thr Glu Val Asp Phe Thr Asp Leu His Ala Trp Cys
85 90 95
Glu Val Tyr Leu Pro Gly Ala
100

<210> 775
<211> 4125
<212> DNA
<213> Homo sapiens

<400> 775
nncaggatgg gcgcgaacaa tggcaaacag tacggcagtg agggcaaagg cagctcgagc
60
atctcatctg acgtgagttc aagtacagat cacacgccca ctaaagccca gaagaatgtg
120
gctaccagcg aagactccga cctgagcatg cgcacactga gcacgcccag cccagccctg
180

atatgtccac cgaatctccc aggatttcag aatggaaggg gctcgtccac ctcctcgtcc
240
tccatcaccg gggagacggt ggccatggtg cactccccgc ccccgacccg cctcacacac
300
ccgctcatcc ggctcgcctc cagaccccag aaggatcagg ccagcataga ccggctcccg
360
gaccactcca tggtgcagat cttctccttc ctgcccacca accagctgtg ccgctgcgcg
420
cgagtgtgcc gccgctggta caacctggcc tgggacccgc ggctctggag gactatccgc
480
ctgacgggcg agaccatcaa cgtggaccgc gccctcaagg tgctgacccg cagactctgc
540
caggacaccc ccaacgtgtg tctcatgctg gaaaccgtaa ctgtcagtgg ctgcaggcgg
600
ctcacagacc gagggctgta caccatcgcc cagtgctgcc ccgaactgag gcgactggaa
660
gtctcaggct gttacaatat ctccaacgag gccgtctttg atgtggtgtc cctctgccct
720
aatctggagc acctggatgt gtcaggatgc tccaaagtga cctgcatcag cttgacccgg
780
gaggcctcca ttaaactgtc acccttgcat ggcaaacaga tttccatccg ctacctggac
840
atgacggact gcttcgtgct ggaggacgaa ggcctgcaca ccatcgcggc gcactgcacg
900
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1200
aagaactgca ccaaactcaa atccctggat atcggcaaat gccctttggt atccgacacg
1260
ggcctggagt gcctggccct gaactgcttc aacctcaagc ggctcagcct caagtcctgc
1320
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1380
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1440
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1680
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1740
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1800

gccctttccc tcgcacacag gccccacccc cacagttcca cgcccccccc ccaaggccac
1860
accctccctc cctagagcag cagcgaggat ccatcatcag aatcacagtg ctctccagac
1920
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1980
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2040
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2100
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2160
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2280
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2340
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2400
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2520
gcaaagccca gatcccccca tcagttgctt ttactcagtg ttttcaaata ggagtaaagg
2580
cccttgcaat ttttaattaa caagcaaggc ccaagggaac acatgtcctc aaaagttttt
2640
ctgatccctc gccttgcaca cctggcatgc atcaggcaca tctgtcctac agctggcaga
2700
gacagatgcc tcggttcttt gtcattcaga ttgcatttga cctcttctca tctatttatt
2760
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2820
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2880
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2940
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3000
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3300
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3420

caaacatcat ggcctcccat ccaatcaaca tcatcaaatt acatgtgtaa tcaaggctct
3480
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3540
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3600
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3660
gagtgagctg gtttaatact ctgagaatga gcagggagat ccagagaatg aatccctgac
3720
cgcatcacct aaactgtctt ccaaacatga gacaaagctg actgttcaca ctgattgccc
3780
agcacatacc gtcttgccag tttcttcttt tctcccagtc tcctgttcat ccattctgtt
3840
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3900
gagaccaaac caaaggtctc actaggaaat ttatctgttt taaaacattg cttccttcct
3960
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4020
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4080
tgttcgtaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa
4125

<210> 776
<211> 483
<212> PRT
<213> Homo sapiens

<400> 776
Tyr Gly Ser Glu Gly Lys Gly Ser Ser Ser Ile Ser Ser Asp Val Ser
 1   5   10   15
Ser Ser Thr Asp His Thr Pro Thr Lys Ala Gln Lys Asn Val Ala Thr
            20   25   30
Ser Glu Asp Ser Asp Leu Ser Met Arg Thr Leu Ser Thr Pro Ser Pro
        35   40   45
Ala Leu Ile Cys Pro Pro Asn Leu Pro Gly Phe Gln Asn Gly Arg Gly
    50   55   60
Ser Ser Thr Ser Ser Ser Ser Ile Thr Gly Glu Thr Val Ala Met Val
65   70   75   80
His Ser Pro Pro Pro Thr Arg Leu Thr His Pro Leu Ile Arg Leu Ala
                85   90   95
Ser Arg Pro Gln Lys Asp Gln Ala Ser Ile Asp Arg Leu Pro Asp His
            100   105   110
Ser Met Val Gln Ile Phe Ser Phe Leu Pro Thr Asn Gln Leu Cys Arg
        115   120   125
Cys Ala Arg Val Cys Arg Arg Trp Tyr Asn Leu Ala Trp Asp Pro Arg
    130   135   140
Leu Trp Arg Thr Ile Arg Leu Thr Gly Glu Thr Ile Asn Val Asp Arg
145   150   155   160
Ala Leu Lys Val Leu Thr Arg Arg Leu Cys Gln Asp Thr Pro Asn Val
                165   170   175
Cys Leu Met Leu Glu Thr Val Thr Val Ser Gly Cys Arg Arg Leu Thr

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            180                 185                 190
Asp Arg Gly Leu Tyr Thr Ile Ala Gln Cys Cys Pro Glu Leu Arg Arg
        195                 200                 205
Leu Glu Val Ser Gly Cys Tyr Asn Ile Ser Asn Glu Ala Val Phe Asp
    210                 215                 220
Val Val Ser Leu Cys Pro Asn Leu Glu His Leu Asp Val Ser Gly Cys
225                 230                 235                 240
Ser Lys Val Thr Cys Ile Ser Leu Thr Arg Glu Ala Ser Ile Lys Leu
                245                 250                 255
Ser Pro Leu His Gly Lys Gln Ile Ser Ile Arg Tyr Leu Asp Met Thr
            260                 265                 270
Asp Cys Phe Val Leu Glu Asp Glu Gly Leu His Thr Ile Ala Ala His
        275                 280                 285
Cys Thr Gln Leu Thr His Leu Tyr Leu Arg Arg Cys Val Arg Leu Thr
    290                 295                 300
Asp Glu Gly Leu Arg Tyr Leu Val Ile Tyr Cys Ala Ser Ile Lys Glu
305                 310                 315                 320
Leu Ser Val Ser Asp Cys Arg Phe Val Ser Asp Phe Gly Leu Arg Glu
                325                 330                 335
Ile Ala Lys Leu Glu Ser Arg Leu Arg Tyr Leu Ser Ile Ala His Cys
            340                 345                 350
Gly Arg Val Thr Asp Val Gly Ile Arg Tyr Val Ala Lys Tyr Cys Ser
        355                 360                 365
Lys Leu Arg Tyr Leu Asn Ala Arg Gly Cys Glu Gly Ile Thr Asp His
    370                 375                 380
Gly Val Glu Tyr Leu Ala Lys Asn Cys Thr Lys Leu Lys Ser Leu Asp
385                 390                 395                 400
Ile Gly Lys Cys Pro Leu Val Ser Asp Thr Gly Leu Glu Cys Leu Ala
                405                 410                 415
Leu Asn Cys Phe Asn Leu Lys Arg Leu Ser Leu Lys Ser Cys Glu Ser
            420                 425                 430
Ile Thr Gly Gln Gly Leu Gln Ile Val Ala Ala Asn Cys Phe Asp Leu
        435                 440                 445
Gln Thr Leu Asn Val Gln Asp Cys Glu Val Ser Val Glu Ala Leu Arg
    450                 455                 460
Phe Val Lys Arg His Cys Lys Arg Cys Val Ile Glu His Thr Asn Pro
465                 470                 475                 480
Ala Phe Phe
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<210> 777
<211> 705
<212> DNA
<213> Homo sapiens

<400> 777
ggtaccatcg tttttaaacc taattaagat attactcatt cttgttggtg cccaattcca
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caccaatctg ctctttaatg ccagactgat ggctctaaca atccttatta actccttttt
120
gtggcttcaa ggaaaaacaa aaacctcttc tctcattcac cacctctagg ccaggagaaa
180
ttatttttgg ttcaggcttt cacagtgggg gtctgaaagt gaccagtcta gaaaaggatg
240

actcagcaaa aggagagctc tgaaggtccc tgaggcggca cggtccagca ttattaggtc
300
acatggtatg acctgaaaca aatacgttct tcccaaatgt ggcaggaccg ggagagcttc
360
tcaccaggag ggaaccgccg caatgaccgc cggacgtcca gcaacacttg ttggtagtcc
420
ttgctcatct gccgtaggtt cttccctgat ataggaggtg ggtcattggc attgacattg
480
aggagcttgg gccacacttt tcgtctgatc tcatcagtca ggagccctcc ttcactgata
540
gccatgcgtc taagggcagc cacatcagtg ggatcactgt tcagagcctg gtgtatctct
600
aacactttct ttttcctttt ggcgttaaag tctgccttct ccgcgccgcc gtcccagtgg
660
ccggaggtgg gccgtcccct gcgcactccg gaggccatcc ccggg
705

<210> 778
<211> 134
<212> PRT
<213> Homo sapiens

<400> 778
Met Ala Ser Gly Val Arg Arg Gly Arg Pro Thr Ser Gly His Trp Asp
 1   5   10   15
Gly Gly Ala Glu Lys Ala Asp Phe Asn Ala Lys Arg Lys Lys Lys Val
            20   25   30
Leu Glu Ile His Gln Ala Leu Asn Ser Asp Pro Thr Asp Val Ala Ala
        35   40   45
Leu Arg Arg Met Ala Ile Ser Glu Gly Gly Leu Leu Thr Asp Glu Ile
    50   55   60
Arg Arg Lys Val Trp Pro Lys Leu Leu Asn Val Asn Ala Asn Asp Pro
65   70   75   80
Pro Pro Ile Ser Gly Lys Asn Leu Arg Gln Met Ser Lys Asp Tyr Gln
                85   90   95
Gln Val Leu Leu Asp Val Arg Arg Ser Leu Arg Arg Phe Pro Pro Gly
            100   105   110
Glu Lys Leu Ser Arg Ser Cys His Ile Trp Glu Glu Arg Ile Cys Phe
        115   120   125
Arg Ser Tyr His Val Thr
    130

<210> 779
<211> 322
<212> DNA
<213> Homo sapiens

<400> 779
tccggacatg tgcaaacaat tcaatgatgt ggtgcgtcga catggtgtgc atcactctgt
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gactgtgagt gattctgagg ataccgttgc gccgtcccag ctggttcgat cccctcgtaa
120
cgccttgcct ttgaaggaac ccagtgggaa ggctagacca agtaaatatg aatcaccaaa
180

cgccagcaac ttcatcgtca ggcatgtggc aactggcaaa gagggcactg atgatgagta
240
tgctaactca aactactact actcgatgtc tgccaatcga ctaggagacg aggaaacgga
300
ggaaatgata ggtttggcta cc
322

<210> 780
<211> 105
<212> PRT
<213> Homo sapiens

<400> 780
Met Cys Lys Gln Phe Asn Asp Val Val Arg Arg His Gly Val His His
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Ser Val Thr Val Ser Asp Ser Glu Asp Thr Val Ala Pro Ser Gln Leu
20 25 30
Val Arg Ser Pro Arg Asn Ala Leu Pro Leu Lys Glu Pro Ser Gly Lys
35 40 45
Ala Arg Pro Ser Lys Tyr Glu Ser Pro Asn Ala Ser Asn Phe Ile Val
50 55 60
Arg His Val Ala Thr Gly Lys Glu Gly Thr Asp Asp Glu Tyr Ala Asn
65 70 75 80
Ser Asn Tyr Tyr Tyr Ser Met Ser Ala Asn Arg Leu Gly Asp Glu Glu
85 90 95
Thr Glu Glu Met Ile Gly Leu Ala Thr
100 105

<210> 781
<211> 297
<212> DNA
<213> Homo sapiens

<400> 781
nntcgcgtgc ctggaatgtg tgtctgtgta tgtgtgtgta tgtatgtgtg tatggaatgt
60
gtgtgtatgn gaatatgtgt gtgtatgnga atgtgtgtgt gtgtttggaa tgtgtgtatg
120
gaatgtgtgt ctgtgtatgg aatatgtgtg agtatgngaa tgtgtgtgtg tgtttggaat
180
gtatcgaatg tgtgtctgtg tgtaaggaat gtgtgtgtat ggaatgtgtt tacgtgcatg
240
tgtctggaat gtgtgtgtat ggaatgtgtg tgtatgtgta tgngaatgtg tgtgtgt
297

<210> 782
<211> 99
<212> PRT
<213> Homo sapiens

<400> 782
Xaa Arg Val Pro Gly Met Cys Val Cys Val Cys Val Cys Met Tyr Val
1 5 10 15
Cys Met Glu Cys Val Cys Met Xaa Ile Cys Val Cys Met Xaa Met Cys

```
            20                  25                  30
Val Cys Val Trp Asn Val Cys Met Glu Cys Val Ser Val Tyr Gly Ile
        35                  40                  45
Cys Val Ser Met Xaa Met Cys Val Cys Val Trp Asn Val Ser Asn Val
    50                  55                  60
Cys Leu Cys Val Arg Asn Val Cys Val Trp Asn Val Phe Thr Cys Met
65                  70                  75                  80
Cys Leu Glu Cys Val Cys Met Glu Cys Val Cys Met Cys Met Xaa Met
                85                  90                  95
Cys Val Cys
```

<210> 783
<211> 612
<212> DNA
<213> Homo sapiens

<400> 783
accggtgacg taactgctcc cgctggcagc ttcgagggcg atgtcgattt gcgtgcccgg
60
caccgggtcg agtgagctgc ccagcagcaa gcccaccaca tcggtgacca gaccgatcac
120
tttgttgagc acgtcgatga cgggcaactt caaggaaatc caggtgcgga cttgcgcggt
180
ccgcacaaaa atcggctggg tgtcgatcaa ctgcgggttg ccaatcgcag aatttgcgcg
240
gttcgatgac acgtgtcttc accgtgatat tcagcagccc cagtacgtcc accggcaact
300
cgacggccac cgcgctggct ttgttggaca gctgcacaaa gccctgaatc aggttgaaca
360
gttgcaggtt gacgtccagg gcgctcttgt ccgtgccgtt ttgtatattg atcaggtcgc
420
ccaggtgcag gatctgcgtg cctggggcaa tcagcttgat tgcttcgagg ttattgatca
480
ccacctggac cgcattaccg cccagcttga gcacatcgat ggcggcctgg atcaactggc
540
cgacggtcgc gtcggtcttg agcaactggt cgtagttgcc ggcgctgacg ttgaggcgga
600
tggccgacgc gt
612

<210> 784
<211> 190
<212> PRT
<213> Homo sapiens

<400> 784
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Met Ser Ile Cys Val Pro Gly Thr Gly Ser Ser Glu Leu Pro Ser Ser
 1               5                  10                  15
Lys Pro Thr Thr Ser Val Thr Arg Pro Ile Thr Leu Leu Ser Thr Ser
            20                  25                  30
Met Thr Gly Asn Phe Lys Glu Ile Gln Val Arg Thr Cys Ala Val Arg
        35                  40                  45
Thr Lys Ile Gly Trp Val Ser Ile Asn Cys Gly Leu Pro Ile Ala Glu
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```
    50                  55                  60
Phe Ala Arg Phe Asp Asp Thr Cys Leu His Arg Asp Ile Gln Gln Pro
65                  70                  75                  80
Gln Tyr Val His Arg Gln Leu Asp Gly His Arg Ala Gly Phe Val Gly
                85                  90                  95
Gln Leu His Lys Ala Leu Asn Gln Val Glu Gln Leu Gln Val Asp Val
            100                 105                 110
Gln Gly Ala Leu Val Arg Ala Val Leu Tyr Ile Asp Gln Val Ala Gln
        115                 120                 125
Val Gln Asp Leu Arg Ala Trp Gly Asn Gln Leu Asp Cys Phe Glu Val
    130                 135                 140
Ile Asp His His Leu Asp Arg Ile Thr Ala Gln Leu Glu His Ile Asp
145                 150                 155                 160
Gly Gly Leu Asp Gln Leu Ala Asp Gly Arg Val Gly Leu Glu Gln Leu
                165                 170                 175
Val Val Val Ala Gly Ala Asp Val Glu Ala Asp Gly Arg Arg
            180                 185                 190
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<210> 785
<211> 408
<212> DNA
<213> Homo sapiens

<400> 785
accttggact acttcactat cgaccctcgg ctaggcgacg acgatgactt cgatcacctg
60
cttcaggccg cccacgctcg tggtctgtca gtactgctcg acggggtggt caaccacgtc
120
tcgcgtcgca accgcatcgt gcaggatgcg cagagtgctg ggccagattc agacgccggc
180
cgtatggttc gctggtgtga ggggcgcctc gacgttttcg agggtcatag tgacctggtc
240
gcactcaacc acgacaaccc cgcagtgcgg gaacatgtca cccggatcat gaactattgg
300
tgcggtcgcg gtgttgacgg ctggcggctg gacgccgcta ttccgtcaat cctgagttct
360
gggctgcggt gctgcctccg gtgcgagaga agcgccctga cgtgagga
408

<210> 786
<211> 134
<212> PRT
<213> Homo sapiens

<400> 786
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Thr Leu Asp Tyr Phe Thr Ile Asp Pro Arg Leu Gly Asp Asp Asp Asp
 1               5                  10                  15
Phe Asp His Leu Leu Gln Ala Ala His Ala Arg Gly Leu Ser Val Leu
            20                  25                  30
Leu Asp Gly Val Val Asn His Val Ser Arg Arg Asn Arg Ile Val Gln
        35                  40                  45
Asp Ala Gln Ser Ala Gly Pro Asp Ser Asp Ala Gly Arg Met Val Arg
    50                  55                  60
Trp Cys Glu Gly Arg Leu Asp Val Phe Glu Gly His Ser Asp Leu Val
```

65 70 75 80
Ala Leu Asn His Asp Asn Pro Ala Val Arg Glu His Val Thr Arg Ile
85 90 95
Met Asn Tyr Trp Cys Gly Arg Gly Val Asp Gly Trp Arg Leu Asp Ala
100 105 110
Ala Ile Pro Ser Ile Leu Ser Ser Gly Leu Arg Cys Cys Leu Arg Cys
115 120 125
Glu Arg Ser Ala Leu Thr
130

<210> 787
<211> 310
<212> DNA
<213> Homo sapiens

<400> 787
acgcgtgaag gggaatgaaa gggtttttcc tggatcaaaa tgatgcttgt ggcagacaca
60
gttggaacca cagacgatgc cacgcttgtg tcagcagtgc gacactggcc cacgtggcgt
120
ccttggtctc tcctcattgc tgccgtcact gtgtgctggg catgccctgc agttacccca
180
aagctttatg tcacaacatt gaggctggcg gagaaagacc ggccccttca ccccacctta
240
gacttcctgg aagggccgcc cgggtccaca acctggcccg ttaactccct gggcagctgc
300
tgggggagaa
310

<210> 788
<211> 90
<212> PRT
<213> Homo sapiens

<400> 788
Met Met Leu Val Ala Asp Thr Val Gly Thr Thr Asp Asp Ala Thr Leu
1 5 10 15
Val Ser Ala Val Arg His Trp Pro Thr Trp Arg Pro Trp Ser Leu Leu
20 25 30
Ile Ala Ala Val Thr Val Cys Trp Ala Cys Pro Ala Val Thr Pro Lys
35 40 45
Leu Tyr Val Thr Thr Leu Arg Leu Ala Glu Lys Asp Arg Pro Leu His
50 55 60
Pro Thr Leu Asp Phe Leu Glu Gly Pro Pro Gly Ser Thr Thr Trp Pro
65 70 75 80
Val Asn Ser Leu Gly Ser Cys Trp Gly Arg
85 90

<210> 789
<211> 369
<212> DNA
<213> Homo sapiens

<400> 789

acgcgtgaag ttgcagcagc aagcaatctg cctcgcttct ggtgcccacc gaaaccaagg
60
tctgccagac agcagcgctg ggacctctcc cctccccagc aggatgggcc ggctctggaa
120
gcacgaggtg ttccaaagtg caaacaagct gctgttaaat aattattccc aaacgccaaa
180
gcccttgctg gtttgcttgc ttgctttttt ctttttttgc ctcgcacaga tatcgctagg
240
gcagagtatt gacatttcgt tttcttttg ttatgggtga taaagcacgg tgtttcttgt
300
gagtgtatgc ctgtatttcc ctgcagagct gattgccagt ccattttctt ctatcccatc
360
cccattttc
369

<210> 790
<211> 114
<212> PRT
<213> Homo sapiens

<400> 790
Met Asp Trp Gln Ser Ala Leu Gln Gly Asn Thr Gly Ile His Ser Gln
1 5 10 15
Glu Thr Pro Cys Phe Ile Thr His Asn Lys Lys Lys Thr Lys Cys Gln
20 25 30
Tyr Ser Ala Leu Ala Ile Ser Val Arg Gly Lys Lys Arg Lys Lys Gln
35 40 45
Ala Ser Lys Pro Ala Arg Ala Leu Ala Phe Gly Asn Asn Tyr Leu Thr
50 55 60
Ala Ala Cys Leu His Phe Gly Thr Pro Arg Ala Ser Arg Ala Gly Pro
65 70 75 80
Ser Cys Trp Gly Gly Glu Arg Ser Gln Arg Cys Cys Leu Ala Asp Leu
85 90 95
Gly Phe Gly Gly His Gln Lys Arg Gly Arg Leu Leu Ala Ala Ala Thr
100 105 110
Ser Arg

<210> 791
<211> 420
<212> DNA
<213> Homo sapiens

<400> 791
nctctgacca aaaggaaggt atatgaaaac acaacactag gcttcattgt tgaagttgaa
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ggtcttccag ttcctggtgt gaaatggtat cgaaataaat ctttactaga gccagatgaa
120
agaatcaaaa tggaaagagt gggtaatgtg tgttcactgg aaatttctaa cattcaaaaa
180
ggagaagggg gagagtacat gtgtcatgct gtaaacatca taggggaagc aaagagcttt
240
gcaaatgtag acataatgcc ccaggaagaa agagtggtgg cactaccacc tccagtaaca
300

catcagcatg tcatggagtt tgatttggaa cacaccacat catcaagaac accttctcct
360
caagaaattg tcctggaagt tgaattaagt gaaaaagacg ttaaagaatt tgagaagcag
420

<210> 792
<211> 138
<212> PRT
<213> Homo sapiens

<400> 792
Thr Lys Arg Lys Val Tyr Glu Asn Thr Thr Leu Gly Phe Ile Val Glu
1 5 10 15
Val Glu Gly Leu Pro Val Pro Gly Val Lys Trp Tyr Arg Asn Lys Ser
20 25 30
Leu Leu Glu Pro Asp Glu Arg Ile Lys Met Glu Arg Val Gly Asn Val
35 40 45
Cys Ser Leu Glu Ile Ser Asn Ile Gln Lys Gly Glu Gly Gly Glu Tyr
50 55 60
Met Cys His Ala Val Asn Ile Ile Gly Glu Ala Lys Ser Phe Ala Asn
65 70 75 80
Val Asp Ile Met Pro Gln Glu Glu Arg Val Val Ala Leu Pro Pro Pro
85 90 95
Val Thr His Gln His Val Met Glu Phe Asp Leu Glu His Thr Thr Ser
100 105 110
Ser Arg Thr Pro Ser Pro Gln Glu Ile Val Leu Glu Val Glu Leu Ser
115 120 125
Glu Lys Asp Val Lys Glu Phe Glu Lys Gln
130 135

<210> 793
<211> 479
<212> DNA
<213> Homo sapiens

<400> 793
nacgcgtgcc ggttctcgga aattcattat gggaatgtgc gcgttgtgga gatgctcaga
60
ccgcgaacag tactgcggga acccaaacga tcatttttaa ccccagacgt ccctgaacca
120
aagccaaagt ctacaggtca ctggggcaga ggccgcccga aaccagcttc ccctcccggc
180
ctaggcgcgc caggtccccg cccagccggg gcgatccttt ggtcggacag tgaggttggg
240
agcccaccgc acccaagtcc gccgcatcca cccggcgcag gcgacccccg acgggcagcc
300
gctcaccttc tcctggcccc ggcttcagga aaactgcctg gaggtggccg gggttcccta
360
gcggaggctg ggcggcgggc ttcgcgcctg cctcagtctc cccatccgtg gcccggggga
420
tggagcccgc tgcgcgcaga ggctgcggca ggtcccagcc aggtgccctg gaacgtgga
479

<210> 794

<211> 159
<212> PRT
<213> Homo sapiens

<400> 794
Xaa Ala Cys Arg Phe Ser Glu Ile His Tyr Gly Asn Val Arg Val Val
1 5 10 15
Glu Met Leu Arg Pro Arg Thr Val Leu Arg Glu Pro Lys Arg Ser Phe
20 25 30
Leu Thr Pro Asp Val Pro Glu Pro Lys Pro Lys Ser Thr Gly His Trp
35 40 45
Gly Arg Gly Arg Pro Lys Pro Ala Ser Pro Pro Gly Leu Gly Ala Pro
50 55 60
Gly Pro Arg Pro Ala Gly Ala Ile Leu Trp Ser Asp Ser Glu Val Gly
65 70 75 80
Ser Pro Pro His Pro Ser Pro Pro His Pro Pro Gly Ala Gly Asp Pro
85 90 95
Arg Arg Ala Ala Ala His Leu Leu Leu Ala Pro Ala Ser Gly Lys Leu
100 105 110
Pro Gly Gly Gly Arg Gly Ser Leu Ala Glu Ala Gly Arg Arg Ala Ser
115 120 125
Arg Leu Pro Gln Ser Pro His Pro Trp Pro Gly Gly Trp Ser Pro Leu
130 135 140
Arg Ala Glu Ala Ala Ala Gly Pro Ser Gln Val Pro Trp Asn Val
145 150 155

<210> 795
<211> 1418
<212> DNA
<213> Homo sapiens

<400> 795
gccggcggcg gggaggccgg ggcctgcagg cccccggtac gacaagatcc ggactccggc
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ccggactacg aggcgctgcc ggctggagcc actgtcacca cgcacatggt ggcaggcgcc
120
gtggcaggga tcctggagca ctgcgtgatg taccccatcg actgcgtcaa gacccggatg
180
cagagtctac agcctgaccc agctgcccgc tatcgcaatg tgttggaggc cctctggagg
240
attataagaa cggagggcct atggaggccc atgaggggggc tgaacgtcac agcaacaggc
300
gcagggcctg cccacgccct ttattttgcc tgctacgaaa agttaaaaaa gacattgagt
360
gatgtaatcc accctggggg caatagccat attgccaatg gtgcggccgg gtgtgtggca
420
acattacttc atgatgcagc catgaaccct gcggaaggct gatctgctga cttggggctc
480
tgaatctgga tactctccat caccggttgg ctgctgtcac catttccttc ctcgttgatg
540
gcactactag tggtcaagca gaggatgcag atgtacaact caccatacca ccgggtgaca
600
gactgtgtac gggcagtgtg gcaaaatgaa ggggccgggg ccttttaccg cagctacacc
660

acccagctga ccatgaacgt tcctttccaa gccattcact tcatgaccta tgaattcctg
720
caggagcact ttaaccccca gagacggtac aacccaagct cccacgtcct ctctggagct
780
tgcgcaggag ctgtagctgc cgcagccaca accccactgg acgtttgcaa aacactgctc
840
aacacccagg agtccttggc tttgaactca cacattacag gacatatcac aggcatggct
900
agtgccttca ggacggtata tcaagtaggt ggggtgaccg cctatttccg aggggtgcag
960
gccagagtaa tttaccagat cccctccaca gccatcgcat ggtctgtgta tgagttcttc
1020
aaatacctaa tcactaaaag gcaagaagag tggagggctg gcaagtgaag tagcactgaa
1080
cgaagccagg ggttcagatg acactgctgc atcctggtca cattctctgt ctcctggaat
1140
gctcccacct caagtggagt tagaaggaag gtagaggggc tctcccccag gattttggtg
1200
ttttgactaa caccagttcc tgccaacctc tgttgccacc acctttcctt ccaggcccta
1260
agcacgtgca gcaaagcaca ccacagcacc tttgataacc tctctccatc ctgggcctga
1320
tgacctgctc tagactgtta tagagggata agcagctcat tcccctggtt cctaataaaa
1380
agcctttaaa ttaaaaaaaa aaaaaaaaaa aaaaaaaa
1418

<210> 796
<211> 176
<212> PRT
<213> Homo sapiens

<400> 796
Met Ala Leu Leu Val Val Lys Gln Arg Met Gln Met Tyr Asn Ser Pro
1 5 10 15
Tyr His Arg Val Thr Asp Cys Val Arg Ala Val Trp Gln Asn Glu Gly
20 25 30
Ala Gly Ala Phe Tyr Arg Ser Tyr Thr Thr Gln Leu Thr Met Asn Val
35 40 45
Pro Phe Gln Ala Ile His Phe Met Thr Tyr Glu Phe Leu Gln Glu His
50 55 60
Phe Asn Pro Gln Arg Arg Tyr Asn Pro Ser Ser His Val Leu Ser Gly
65 70 75 80
Ala Cys Ala Gly Ala Val Ala Ala Ala Ala Thr Thr Pro Leu Asp Val
85 90 95
Cys Lys Thr Leu Leu Asn Thr Gln Glu Ser Leu Ala Leu Asn Ser His
100 105 110
Ile Thr Gly His Ile Thr Gly Met Ala Ser Ala Phe Arg Thr Val Tyr
115 120 125
Gln Val Gly Gly Val Thr Ala Tyr Phe Arg Gly Val Gln Ala Arg Val
130 135 140
Ile Tyr Gln Ile Pro Ser Thr Ala Ile Ala Trp Ser Val Tyr Glu Phe
145 150 155 160
Phe Lys Tyr Leu Ile Thr Lys Arg Gln Glu Glu Trp Arg Ala Gly Lys

165 170 175

<210> 797
<211> 585
<212> DNA
<213> Homo sapiens

<400> 797
aaatttaccg gcggcaaaac ccacgtcacc gactacacca acgcctcgcg caccatgctc
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ttcaacatcc acacgctgga gtgggatgcg aagatgctgg agattctcga cgtgccgcgc
120
gagatgctgc cggaagttaa gtcgtcttca gaaatctacg gccgcaccaa aagcggtatc
180
gctatcggcg gcatcgcggg cgaccaacag gctgctctgt tcggccagat gtgcgtggaa
240
gccgggcagg ccaagaacac ttatggcacc ggctgcttcc tgctgatgaa caccggcgac
300
aaagccgtca aatccaaaca cggcatgctc accaccatcg cctgcggtcc acgcggcgaa
360
gtggcttatg cgctggaagg cgcggtgttc aacggtggtt cccccgtgca gtggctgcgt
420
gatgagctga agatcatcgc ggacgccacc gacaccgaat acttcgccgg caaggtcaag
480
gacagcaacg gcgtctacct ggtgccggcc tttaccggcc tgggcgctcc gtactgggac
540
ccgtatgccc gtggcgcttt gtttggcctg actcgtggcg tacgc
585

<210> 798
<211> 195
<212> PRT
<213> Homo sapiens

<400> 798
Lys Phe Thr Gly Gly Lys Thr His Val Thr Asp Tyr Thr Asn Ala Ser
1 5 10 15
Arg Thr Met Leu Phe Asn Ile His Thr Leu Glu Trp Asp Ala Lys Met
20 25 30
Leu Glu Ile Leu Asp Val Pro Arg Glu Met Leu Pro Glu Val Lys Ser
35 40 45
Ser Ser Glu Ile Tyr Gly Arg Thr Lys Ser Gly Ile Ala Ile Gly Gly
50 55 60
Ile Ala Gly Asp Gln Gln Ala Ala Leu Phe Gly Gln Met Cys Val Glu
65 70 75 80
Ala Gly Gln Ala Lys Asn Thr Tyr Gly Thr Gly Cys Phe Leu Leu Met
85 90 95
Asn Thr Gly Asp Lys Ala Val Lys Ser Lys His Gly Met Leu Thr Thr
100 105 110
Ile Ala Cys Gly Pro Arg Gly Glu Val Ala Tyr Ala Leu Glu Gly Ala
115 120 125
Val Phe Asn Gly Gly Ser Pro Val Gln Trp Leu Arg Asp Glu Leu Lys
130 135 140
Ile Ile Ala Asp Ala Thr Asp Thr Glu Tyr Phe Ala Gly Lys Val Lys

145 150 155 160
Asp Ser Asn Gly Val Tyr Leu Val Pro Ala Phe Thr Gly Leu Gly Ala
165 170 175
Pro Tyr Trp Asp Pro Tyr Ala Arg Gly Ala Leu Phe Gly Leu Thr Arg
180 185 190
Gly Val Arg
195

<210> 799
<211> 2152
<212> DNA
<213> Homo sapiens

<400> 799
nnttttttttt tttttttgat ggtgcatgta gttttattta tgtgttttca tctggaaaac
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caagtgtccc agcagcatga ctgaacatca ctcacttccc ctacttgatc tacaaggcca
120
acgccgagag cccagaccag gattccaaac acactgcacg agaatattgt ggatccgctg
180
tcaggtaagt gtccgtcact gacccagacg ctgttacgtg gcacatgact gtacagtgcc
240
acgtaacagc actgtacttt tctcccataa acagttacct gccatgtatc tacatgattc
300
agaacatttt gaacagttaa ttctgacact tgaataatcc catcaaaaac cgtaaaatca
360
ctttgatgtt gtaacgacaa catagcatca ctttacgaca gaatcatctg gaaaaacaga
420
acaacgaata catacatctt aaaaaatgct ggggtgggcc aggcacagct cacgcctgta
480
atcccagcac tttgggaggc tgaggcgggt ggatcacgta atcccagcac tttgaggggc
540
agaggtggac agatcatgag gtcaagagat caagaccatc ctggtcaaaa tggtgaaacc
600
ccgtctctac taaaaataca aaaattagct gagcttagtg gcacacacct gtagtcccag
660
ctacttggga ggctgaggca ggagaatcgc ttgaacccag gagacacagg ctgcagtgac
720
tcgagatcac gccactgcac tccagcctgg cgacagagcg agactccatc tcaaaaaaaa
780
aaaccaacaa aaaaactggg gtgaaaatct aacggataat tcagcattgc cgcatagaaa
840
cctccgcaaa accggccaaa caaacgcgga caggcggccc tggcgtcagc gcacgacagt
900
cacgtgggga ggggcagtgg ccaggtcggc cttggacggg tacaccacct tcaggctccc
960
ttccagatcc accacccgga cctgctccac caccagaagg gagggcccgt cctttccagc
1020
actgggattc gttgtgggat ctggaagttg tccagagact gcatcggctt cagtatctga
1080
gagtgatcct tcctctttat tttctaaagt gtactttttc atttctgcca ttttcagaat
1140
gagggcatcc atgacatcct tgcaaatctg cagactggtg gcacttgtta cttccaaaaa
1200

caaatcagaa gtcgttttct taacctttgt cttctcactg ttggttattg gtgggaagga
1260
aatcacatca ccgtctgcat ccacaagaca cgggtaattt tcatttccat ccagcaagtg
1320
aaggtatctg tgcaggcccg acacactctg ccgcttcttc tgcttcctct gctcctcggc
1380
ctccagctgc agctgccgca ccagctcctt ggccttggct tctttccgcc ccaaggggac
1440
aatcttgagg tcctgtgggg gccgggcgca gtacagcagg ggccctttga cggcacggag
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ctcgtgggtg gcaagggtgg cagccgtcct cttctcacag agatcttcgt ggagcttggt
1560
ctgcgaggtg aggaagcgct tgagtgcatt ccctggctgc aggtccatgc ctcgcaccac
1620
ggcccccaca atgtagggcc gcacatcccg gacctcgggg ctcactctga ctgtcagagg
1680
tacggggttt tcagagacgt gcaggaccct gagcagcagc cggccggcat ctcccacgtc
1740
ctgctcctcc ccatcaccac cttcccgcct ctgcttcctc tccctcctct tcctccggct
1800
ctcttccttc tccgagccct cggcacggcc cttgcccttc ccgccaccac ggcctccgac
1860
gcgcaggtac tccaggatgg atctggtctg gcagccgctg accatcttct ccaggcgctt
1920
gtccctcagc ttgttcccac ggaaattgat ctccttgagc ttggggcagt ccgcaagctc
1980
tgcagggatc tcgctcagct ggttgttcga gaggtccaac gtcttgagcg aggccaggtg
2040
ggcgatgtcg gggctgagtt ctcggaggca gttgtcagca gccgccagtt cactgagcag
2100
gggcagcgcg ccggggcgaa agagctcggc gggaaaggag tctaggcaat tg
2152

<210> 800
<211> 95
<212> PRT
<213> Homo sapiens

<400> 800
Cys Cys Asn Asp Asn Ile Ala Ser Leu Tyr Asp Arg Ile Ile Trp Lys
1 5 10 15
Asn Arg Thr Thr Asn Thr Tyr Ile Leu Lys Asn Ala Gly Val Gly Gln
20 25 30
Ala Gln Leu Thr Pro Val Ile Pro Ala Leu Trp Glu Ala Glu Ala Gly
35 40 45
Gly Ser Arg Asn Pro Ser Thr Leu Arg Gly Arg Gly Gly Gln Ile Met
50 55 60
Arg Ser Arg Asp Gln Asp His Pro Gly Gln Asn Gly Glu Thr Pro Ser
65 70 75 80
Leu Leu Lys Ile Gln Lys Leu Ala Glu Leu Ser Gly Thr His Leu
85 90 95

<210> 801
<211> 424

<212> DNA
<213> Homo sapiens

<400> 801
nntcatgaat cgttataaac acaatggtta gtgtatatca tatctatagg agatactatg
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tatcaaatta atcagctgtc ttttttcttat gaaacaaaag aagtgttaaa gaatatttct
120
gtaacatttc ctaccaataa aataacagcc ataattggac cgaatggatg tggtaagtct
180
accctactta gccatctata tcgacttcat tcaacaaaaa acaaaatcac attaaacgga
240
aaacctttag agtcttataa aggtcgcgaa tttgctcaat tggtagcagt cttaacacaa
300
tctagagacg ctatgattga tgatttttctc gtaaaagata tcgttctcat gggacgggat
360
ccgtacaaac aacactttgg cacctatagt tctgaagatg ttaaaattgc agagcattat
420
atgn
424

<210> 802
<211> 122
<212> PRT
<213> Homo sapiens

<400> 802
Met Tyr Gln Ile Asn Gln Leu Ser Phe Ser Tyr Glu Thr Lys Glu Val
 1   5   10   15
Leu Lys Asn Ile Ser Val Thr Phe Pro Thr Asn Lys Ile Thr Ala Ile
            20   25   30
Ile Gly Pro Asn Gly Cys Gly Lys Ser Thr Leu Leu Ser His Leu Tyr
        35   40   45
Arg Leu His Ser Thr Lys Asn Lys Ile Thr Leu Asn Gly Lys Pro Leu
    50   55   60
Glu Ser Tyr Lys Gly Arg Glu Phe Ala Gln Leu Val Ala Val Leu Thr
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Gln Ser Arg Asp Ala Met Ile Asp Asp Phe Leu Val Lys Asp Ile Val
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<211> 6863
<212> DNA
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<211> 1400
<212> PRT
<213> Homo sapiens

<400> 804
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Lys Pro Pro Val Cys Ala Val Cys Lys Val Thr Ile Asp Gly Thr Gly
35 40 45
Val Ser Cys Arg Val Cys Lys Val Ala Thr His Arg Lys Cys Glu Ala
50 55 60
Lys Val Thr Ser Ala Cys Gln Ala Leu Pro Pro Val Glu Leu Arg Arg
65 70 75 80
Asn Thr Ala Pro Val Arg Arg Ile Glu His Leu Gly Ser Thr Lys Ser
85 90 95
Leu Asn His Ser Lys Gln Arg Ser Thr Leu Pro Arg Ser Phe Ser Leu
100 105 110
Asp Pro Leu Met Glu Arg Arg Trp Asp Leu Asp Leu Thr Tyr Val Thr
115 120 125
Glu Arg Ile Leu Ala Ala Ala Phe Pro Ala Arg Pro Asp Glu Gln Arg
130 135 140
His Arg Gly His Leu Arg Glu Leu Ala His Val Leu Gln Ser Lys His
145 150 155 160
Arg Asp Lys Tyr Leu Leu Phe Asn Leu Ser Glu Lys Arg His Asp Leu
165 170 175
Thr Arg Leu Asn Pro Lys Val Gln Asp Phe Gly Trp Pro Glu Leu His
180 185 190
Ala Pro Pro Leu Asp Lys Leu Cys Ser Ile Cys Lys Ala Met Glu Thr
195 200 205
Trp Leu Ser Ala Asp Pro Gln His Val Val Val Leu Tyr Cys Lys Gly
210 215 220
Asn Lys Gly Lys Leu Gly Val Ile Val Ser Ala Tyr Met His Tyr Ser
225 230 235 240
Lys Ile Ser Ala Gly Ala Asp Gln Ala Leu Ala Thr Leu Thr Met Arg
245 250 255
Lys Phe Cys Glu Asp Lys Val Ala Thr Glu Leu Gln Pro Ser Gln Arg
260 265 270
Arg Tyr Ile Ser Tyr Phe Ser Gly Leu Leu Ser Gly Ser Ile Arg Met
275 280 285
Asn Ser Ser Pro Leu Phe Leu His Tyr Val Leu Ile Pro Met Leu Pro

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Ala Phe Glu Pro Gly Thr Gly Phe Gln Pro Phe Leu Lys Ile Tyr Gln
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Ser Met Gln Leu Val Tyr Thr Ser Gly Val Tyr His Ile Ala Gly Pro
                325                 330                 335
Gly Pro Gln Gln Leu Cys Ile Ser Leu Glu Pro Ala Leu Leu Leu Lys
            340                 345                 350
Gly Asp Val Met Val Thr Cys Tyr His Lys Gly Gly Arg Gly Thr Asp
        355                 360                 365
Arg Thr Leu Val Phe Arg Val Gln Phe His Thr Cys Thr Ile His Gly
    370                 375                 380
Pro Gln Leu Thr Phe Pro Lys Asp Gln Leu Asp Glu Ala Trp Thr Asp
385                 390                 395                 400
Glu Arg Phe Pro Phe Gln Ala Ser Val Glu Phe Val Phe Ser Ser Ser
                405                 410                 415
Pro Glu Lys Ile Lys Gly Ser Thr Pro Arg Asn Asp Pro Ser Val Ser
            420                 425                 430
Val Asp Tyr Asn Thr Thr Glu Pro Ala Val Arg Trp Asp Ser Tyr Glu
        435                 440                 445
Asn Phe Asn Gln His His Glu Asp Ser Val Asp Gly Ser Leu Thr His
    450                 455                 460
Thr Arg Gly Pro Leu Asp Gly Ser Pro Tyr Ala Gln Val Gln Arg Pro
465                 470                 475                 480
Pro Arg Gln Thr Pro Pro Ala Pro Ser Pro Glu Pro Pro Pro Pro Pro
                485                 490                 495
Met Leu Ser Val Ser Ser Asp Ser Gly His Ser Ser Thr Leu Thr Thr
            500                 505                 510
Glu Pro Ala Ala Glu Ser Pro Gly Arg Pro Pro Pro Thr Ala Ala Glu
        515                 520                 525
Arg Gln Glu Leu Asp Arg Leu Leu Gly Gly Cys Gly Val Ala Ser Gly
    530                 535                 540
Gly Arg Gly Ala Gly Arg Glu Thr Ala Ile Leu Asp Asp Glu Glu Gln
545                 550                 555                 560
Pro Thr Val Gly Gly Gly Pro His Leu Gly Val Tyr Pro Gly His Arg
                565                 570                 575
Pro Gly Leu Ser Arg His Cys Ser Cys Arg Gln Gly Tyr Arg Glu Pro
            580                 585                 590
Cys Gly Val Pro Asn Gly Gly Tyr Tyr Arg Pro Glu Gly Thr Leu Glu
        595                 600                 605
Arg Arg Arg Leu Ala Tyr Gly Gly Tyr Glu Gly Ser Pro Gln Gly Tyr
    610                 615                 620
Ala Glu Ala Ser Met Glu Lys Arg Arg Leu Cys Arg Ser Leu Ser Glu
625                 630                 635                 640
Gly Leu Tyr Pro Tyr Pro Pro Glu Met Gly Lys Pro Ala Thr Gly Asp
                645                 650                 655
Phe Gly Tyr Arg Ala Pro Gly Tyr Arg Glu Val Val Ile Leu Glu Asp
            660                 665                 670
Pro Gly Leu Pro Ala Leu Tyr Pro Cys Pro Ala Cys Glu Glu Lys Leu
        675                 680                 685
Ala Leu Pro Thr Ala Ala Leu Tyr Gly Leu Arg Leu Glu Arg Glu Ala
    690                 695                 700
Gly Glu Gly Trp Ala Ser Glu Ala Gly Lys Pro Leu Leu His Pro Val
705                 710                 715                 720
Arg Pro Gly His Pro Leu Pro Leu Leu Leu Pro Ala Cys Gly His His
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                725                 730                 735
His Ala Pro Met Pro Asp Tyr Ser Cys Leu Lys Pro Pro Lys Ala Gly
            740                 745                 750
Glu Glu Gly His Glu Gly Cys Ser Tyr Thr Met Cys Pro Glu Gly Arg
        755                 760                 765
Tyr Gly His Pro Gly Tyr Pro Ala Leu Val Thr Tyr Ser Tyr Gly Gly
    770                 775                 780
Ala Val Pro Ser Tyr Cys Pro Ala Tyr Gly Arg Val Pro His Ser Cys
785                 790                 795                 800
Gly Ser Pro Gly Glu Gly Arg Gly Tyr Pro Ser Pro Gly Ala His Ser
                805                 810                 815
Pro Arg Ala Gly Ser Ile Ser Pro Gly Ser Pro Pro Tyr Pro Gln Ser
            820                 825                 830
Arg Lys Leu Ser Tyr Glu Ile Pro Thr Glu Glu Gly Gly Asp Arg Tyr
        835                 840                 845
Pro Leu Pro Gly His Leu Ala Ser Ala Gly Pro Leu Ala Ser Ala Glu
    850                 855                 860
Ser Leu Glu Pro Val Ser Trp Arg Glu Gly Pro Ser Gly His Ser Thr
865                 870                 875                 880
Leu Pro Arg Ser Pro Arg Asp Ala Pro Cys Ser Ala Ser Ser Glu Leu
                885                 890                 895
Ser Gly Pro Ser Thr Pro Leu His Thr Ser Ser Pro Val Gln Gly Lys
            900                 905                 910
Glu Ser Thr Arg Arg Gln Asp Thr Arg Ser Pro Thr Ser Ala Pro Thr
        915                 920                 925
Gln Arg Leu Ser Pro Gly Glu Ala Leu Pro Pro Val Ser Gln Ala Gly
    930                 935                 940
Thr Gly Lys Ala Pro Glu Leu Pro Ser Gly Ser Gly Pro Glu Pro Leu
945                 950                 955                 960
Ala Pro Ser Pro Val Ser Pro Thr Phe Pro Pro Ser Ser Pro Ser Asp
                965                 970                 975
Trp Pro Gln Glu Arg Ser Pro Gly Gly His Ser Asp Gly Ala Ser Pro
            980                 985                 990
Arg Ser Pro Val Pro Thr Thr Leu Pro Gly Leu Arg His Ala Pro Trp
        995                 1000                1005
Gln Gly Pro Arg Gly Pro Pro Asp Ser Pro Asp Gly Ser Pro Leu Thr
    1010                1015                1020
Pro Val Pro Ser Gln Met Pro Trp Leu Val Ala Ser Pro Glu Pro Pro
1025                1030                1035                1040
Gln Ser Ser Pro Thr Pro Ala Phe Pro Leu Ala Ala Ser Tyr Asp Thr
                1045                1050                1055
Asn Gly Leu Ser Gln Pro Pro Leu Pro Glu Lys Arg His Leu Pro Gly
            1060                1065                1070
Pro Gly Gln Gln Pro Gly Pro Trp Gly Pro Glu Gln Ala Ser Ser Pro
        1075                1080                1085
Ala Arg Gly Ile Ser His His Val Thr Phe Ala Pro Leu Leu Ser Asp
    1090                1095                1100
Asn Val Pro Gln Thr Pro Glu Pro Pro Thr Gln Glu Ser Gln Ser Asn
1105                1110                1115                1120
Val Lys Phe Val Gln Asp Thr Ser Lys Phe Trp Tyr Lys Pro His Leu
                1125                1130                1135
Ser Arg Asp Gln Ala Ile Ala Leu Leu Lys Asp Lys Asp Pro Gly Ala
            1140                1145                1150
Phe Leu Ile Arg Asp Ser His Ser Phe Gln Gly Ala Tyr Gly Leu Ala
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Leu Lys Val Ala Thr Pro Pro Pro Ser Ala Gln Pro Trp Lys Gly Asp
    1170                1175                1180
Pro Val Glu Gln Leu Val Arg His Phe Leu Ile Glu Thr Gly Pro Lys
1185                1190                1195                1200
Gly Val Lys Ile Lys Gly Cys Pro Ser Glu Pro Tyr Phe Gly Ser Leu
                1205                1210                1215
Ser Ala Leu Val Ser Gln His Ser Ile Ser Pro Ile Ser Leu Pro Cys
            1220                1225                1230
Cys Leu Arg Ile Pro Ser Lys Asp Pro Leu Glu Glu Thr Pro Glu Ala
        1235                1240                1245
Pro Val Pro Thr Asn Met Ser Thr Ala Ala Asp Leu Leu Arg Gln Gly
    1250                1255                1260
Ala Ala Cys Ser Val Leu Tyr Leu Thr Ser Val Glu Thr Glu Ser Leu
1265                1270                1275                1280
Thr Gly Pro Gln Ala Val Ala Arg Ala Ser Ser Ala Ala Leu Ser Cys
                1285                1290                1295
Ser Pro Arg Pro Thr Pro Ala Val Val His Phe Lys Val Ser Ala Gln
            1300                1305                1310
Gly Ile Thr Leu Thr Asp Asn Gln Arg Lys Leu Phe Phe Arg Arg His
        1315                1320                1325
Tyr Pro Val Asn Ser Ile Thr Phe Ser Ser Thr Asp Pro Gln Asp Arg
    1330                1335                1340
Arg Trp Thr Asn Pro Asp Gly Thr Thr Ser Lys Ile Phe Gly Phe Val
1345                1350                1355                1360
Ala Lys Lys Pro Gly Ser Pro Trp Glu Asn Val Cys His Leu Phe Ala
                1365                1370                1375
Glu Leu Asp Pro Asp Gln Pro Ala Gly Ala Ile Val Thr Phe Ile Thr
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Lys Val Leu Leu Gly Gln Arg Lys
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<211> 550
<212> DNA
<213> Homo sapiens

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<210> 806
<211> 118
<212> PRT
<213> Homo sapiens

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Met Ala Leu Phe Pro Ser Ser Gly His Gln Phe Arg Ser Arg Gly Pro
35 40 45
Met Leu Gly Arg Ala Thr Pro Met Asp Leu Ala Arg Thr Leu Ser His
50 55 60
Arg Phe His Thr Gln Arg Glu Asp Ser Pro Thr Gln Thr Leu Lys Arg
65 70 75 80
Glu His Leu Gly Glu Gly Ser Val Glu Thr Arg Thr Gln Lys Asp Thr
85 90 95
Arg Glu Lys Glu Ala Val His Trp Gly Gly Phe Arg Gly Thr Cys Ala
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Cys His Val Ser Glu Gly
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<210> 807
<211> 287
<212> DNA
<213> Homo sapiens

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<210> 808
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<212> PRT
<213> Homo sapiens

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        35                  40                  45
Arg Tyr Thr Ser Ala Ser Asp Tyr Ile Cys Ala Leu Ile Arg Gln Asp
    50                  55                  60
Gln Glu Arg Ser Asp Gly Leu Arg Gln Leu Gln Thr Leu Ile Thr Glu
65                  70                  75                  80
Gly Phe Asp Ser Gly Ile Ser Ala Ser Ser Leu Asp Asp
                85                  90
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<210> 809
<211> 405
<212> DNA
<213> Homo sapiens

<400> 809
nngggggggg gggggggggg ggtttttttc cccccaaaga aaaaaaaagg gggggggggg
60
gggccccccc ccccccccccc cctttttttc ccccgggggg tttattccca gggccaacag
120
gacgcgtggt cgcgtcaaat ggagagacga tcggtgccgc ccttgcccca cgatcctgat
180
ggccccgaga ttcctgacga tgtcaccacc ctcgcccaac aggtaatggg tctgccacgt
240
cacctgggta tccactcagc tggaatggtg ctgacgcgag aaccagtagg acgcatctgc
300
cccattgagc cggctcgaat gtttggtcgc acggggctgc agtgggacaa anaaaactgt
360
gcctggatgg ggttggggaa gtttgatctg cttgggttgg ggatg
405

<210> 810
<211> 135
<212> PRT
<213> Homo sapiens

<400> 810
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Xaa Gly Gly Gly Gly Gly Gly Val Phe Phe Pro Pro Lys Lys Lys Lys
 1               5                  10                  15
Gly Gly Gly Gly Gly Pro Pro Pro Pro Pro Pro Leu Phe Phe Pro Arg
            20                  25                  30
Gly Val Tyr Ser Gln Gly Gln Gln Asp Ala Trp Ser Arg Gln Met Glu
        35                  40                  45
Arg Arg Ser Val Pro Pro Leu Pro His Asp Pro Asp Gly Pro Glu Ile
    50                  55                  60
Pro Asp Asp Val Thr Thr Leu Ala Gln Gln Val Met Gly Leu Pro Arg
65                  70                  75                  80
His Leu Gly Ile His Ser Ala Gly Met Val Leu Thr Arg Glu Pro Val
                85                  90                  95
Gly Arg Ile Cys Pro Ile Glu Pro Ala Arg Met Phe Gly Arg Thr Gly
            100                 105                 110
Leu Gln Trp Asp Lys Xaa Asn Cys Ala Trp Met Gly Leu Gly Lys Phe
        115                 120                 125
Asp Leu Leu Gly Leu Gly Met
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130 135

<210> 811
<211> 642
<212> DNA
<213> Homo sapiens

<400> 811
acgcgtgaag gggcagtgat aggcgcgcac catttgagcc cccagtgtga tgaatgtaag
60
cagtgccaat gactgccaat ggcaaagaag agctccaacc aaacaccagg tgcttcatgg
120
tggtgacaca ttaacaacac ccgggaagca gtactgccaa cacctagata tgagaaaaag
180
aaaacaggca cttaaagcga ggctaaccca ctttcaggaa tgataaaggg cagaggaccc
240
tgtcacctct acccctgcta ctaaaggcgt ggcccacaga gcagcagcac cagcagcaca
300
taaaatgggg ttaaatatga caggaaaaac aaggtgacag ggaaatgggg tgaagatcaa
360
gttcgtggta ngtctttctt tcctagaggc tttgggcctg agctcttgga gaaagctctc
420
caacacctca gggtgtgcct gttcccctgc cctgtgggga tgctctttgt acgggtggct
480
gactggctcc cactttcctc cgtattgttg tcttgtctct tccctcacaa ccatcaaggc
540
tctttccctt aattctataa gacagtacct ctggcttaga aattatatgc cctcctttaa
600
aaaaacgaaa tgctagagga catagaactt gaggaaaaat tt
642

<210> 812
<211> 106
<212> PRT
<213> Homo sapiens

<400> 812
Met Val Val Arg Glu Glu Thr Arg Gln Gln Tyr Gly Gly Lys Trp Glu
1 5 10 15
Pro Val Ser His Pro Tyr Lys Glu His Pro His Arg Ala Gly Glu Gln
20 25 30
Ala His Pro Glu Val Leu Glu Ser Phe Leu Gln Glu Leu Arg Pro Lys
35 40 45
Ala Ser Arg Lys Glu Arg Xaa Thr Thr Asn Leu Ile Phe Thr Pro Phe
50 55 60
Pro Cys His Leu Val Phe Pro Val Ile Phe Asn Pro Ile Leu Cys Ala
65 70 75 80
Ala Gly Ala Ala Ala Leu Trp Ala Thr Pro Leu Val Ala Gly Val Glu
85 90 95
Val Thr Gly Ser Ser Ala Leu Tyr His Ser
100 105

<210> 813
<211> 558

<212> DNA
<213> Homo sapiens

<400> 813
cccgggcgat agtcgcgtgg ggtcatggcg gatgaggggt taagagcgcg tttactgcgg
60
cgcccgactc cgatcagccg ttcggaaagg cgacgccgaa gatcatgaca ttctcggccg
120
gttcgctgac cagcaccggg ccgcccggct gggccgggaa accgtggaac aagggaagcg
180
ggggcggcgc gcggggtgac gccttcggcc ccctcgcctt cggtcagcgt gcggcgcaat
240
tcggggtcga ggatgatccg cggcccttcg atcttgacca cgatctccag ttgcccgcca
300
ttgtcttcgc cgccgacatc cagcgtgccg ccgcgcacca gcgcctcgct ggcgatcagg
360
gcgaggttca gcatcacctt cagcgcggac ttgggcagcg tctccgtttc cacccaccag
420
ttgaattgcg tgcgcttatt gtcggcaacc agcccctcgt tcgcggtttt cgcttcgcgc
480
gcgtcgacct gttcgccgaa cccgccggcg gcgcagaagg cgaggcggaa gaatttgagc
540
ttgttggcgg atacgcgt
558

<210> 814
<211> 151
<212> PRT
<213> Homo sapiens

<400> 814
Met Thr Phe Ser Ala Gly Ser Leu Thr Ser Thr Gly Pro Pro Gly Trp
 1   5   10   15
Ala Gly Lys Pro Trp Asn Lys Gly Ser Gly Gly Gly Ala Arg Gly Asp
            20   25   30
Ala Phe Gly Pro Leu Ala Phe Gly Gln Arg Ala Ala Gln Phe Gly Val
        35   40   45
Glu Asp Asp Pro Arg Pro Phe Asp Leu Asp His Asp Leu Gln Leu Pro
    50   55   60
Ala Ile Val Phe Ala Ala Asp Ile Gln Arg Ala Ala Ala His Gln Arg
65   70   75   80
Leu Ala Gly Asp Gln Gly Glu Val Gln His His Leu Gln Arg Gly Leu
                85   90   95
Gly Gln Arg Leu Arg Phe His Pro Pro Val Glu Leu Arg Ala Leu Ile
            100   105   110
Val Gly Asn Gln Pro Leu Val Arg Gly Phe Arg Phe Ala Arg Val Asp
        115   120   125
Leu Phe Ala Glu Pro Ala Gly Gly Ala Glu Gly Glu Ala Glu Glu Phe
    130   135   140
Glu Leu Val Gly Gly Tyr Ala
145   150

<210> 815
<211> 315

<212> DNA
<213> Homo sapiens

<400> 815
acgcgttgag actgtcacaa ggctaggcta acttcatata gctatgccat cagatctgcc
60
caaagtggac gatgagaaag ctcacgacgc gcctcacacg gatgggtcgg agcctggaca
120
agctagcgca ggagaaagcc gagacctcac gtccgaagcg gattcagcaa gtgcacaacc
180
ttctacccac gctgaggttt ccagtgaagt tactgctacg tccagtatag atgagcaggt
240
agacctcatt gctgcaccgt taagcgaaga gtccaatgtc agcaagctcg ggccgtcccc
300
tgaggccgat acatc
315

<210> 816
<211> 90
<212> PRT
<213> Homo sapiens

<400> 816
Met Pro Ser Asp Leu Pro Lys Val Asp Asp Glu Lys Ala His Asp Ala
 1   5   10   15
Pro His Thr Asp Gly Ser Glu Pro Gly Gln Ala Ser Ala Gly Glu Ser
            20   25   30
Arg Asp Leu Thr Ser Glu Ala Asp Ser Ala Ser Ala Gln Pro Ser Thr
        35   40   45
His Ala Glu Val Ser Ser Glu Val Thr Ala Thr Ser Ser Ile Asp Glu
    50   55   60
Gln Val Asp Leu Ile Ala Ala Pro Leu Ser Glu Glu Ser Asn Val Ser
65   70   75   80
Lys Leu Gly Pro Ser Pro Glu Ala Asp Thr
                85   90

<210> 817
<211> 321
<212> DNA
<213> Homo sapiens

<400> 817
gaattcaaag agaaatatct gcctagacct tatgtgatta atctaatgga cgaactgacc
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ctgaaaggaa tcacacaata ttatgctttt gttgaagagg ggcagaaggt tcattgcctg
120
aatacacttt tctcaaagct tcaaattaat caatccatta tattctgcaa ctctgttaat
180
agtgttgagc tgctggctaa aaaaataact gaactcggtt attcatgctt ctacattcat
240
gctaagatgt tgcaagacca cagaaatcga gtattccatg attgtcgtaa tggtgcttgc
300
agaaaccttg tgtgcacaga t
321

<210> 818
<211> 107
<212> PRT
<213> Homo sapiens

<400> 818
Glu Phe Lys Glu Lys Tyr Leu Pro Arg Pro Tyr Val Ile Asn Leu Met
1 5 10 15
Asp Glu Leu Thr Leu Lys Gly Ile Thr Gln Tyr Tyr Ala Phe Val Glu
20 25 30
Glu Gly Gln Lys Val His Cys Leu Asn Thr Leu Phe Ser Lys Leu Gln
35 40 45
Ile Asn Gln Ser Ile Ile Phe Cys Asn Ser Val Asn Ser Val Glu Leu
50 55 60
Leu Ala Lys Lys Ile Thr Glu Leu Gly Tyr Ser Cys Phe Tyr Ile His
65 70 75 80
Ala Lys Met Leu Gln Asp His Arg Asn Arg Val Phe His Asp Cys Arg
85 90 95
Asn Gly Ala Cys Arg Asn Leu Val Cys Thr Asp
100 105

<210> 819
<211> 3422
<212> DNA
<213> Homo sapiens

<400> 819
atgaacagta agaaactgtc ttctactgac tgtttcaaaa ccgaggcctt cacatccccg
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gaggccctgc agcctggggg gactgccctg gcgcctaaga agaggagccg gaaaggccgg
120
gcaggggccc atggactctc caaaggcccg ctggagaagc ggccctatct tggcccggct
180
ctgcccctga ctccccgaga cagggccagt ggcacacaag gggccagtga ggacaactct
240
ggtggaggag gcaagaagcc aaagatggag gagctgggcc tggcctccca ccccccggag
300
ggcaggccct gccagcccca gacaagggca cagaaacagc caggccacac caactacagc
360
agctattcca agcggaagcg cctcactcgg ggccgggcca agaacaccac ctcttcaccc
420
tgtaaggggc gtgccaagcg acgacgacag cagcaggtgc tgcccctgga tcccgcagag
480
cctgaaatcc gcctcaagta catttcctct tgcaagcggc tgaggtcaga cagccggacc
540
cccgccttct cacccttcgt gcgggtggag aagcgagacg cgttcaccac catatgcact
600
gttgtcaact cccctggaga tgcgcccaag ccccacagga agccttcctc ctctgcctcc
660
tcttcctcat cctcgtcctc gttctccttg gatgcagccg gggcctccct ggccacactc
720
cctggaggct ccatcctgca gccgcggccc tccttgcccc tctcctccac gatgcacttg
780

gggcctgtgg tttccaaggc cctgagtacc tcttgccttg tttgctgcct ctgccaaaac
840
ccggccaact tcaaggacct tggggacctc tgtgggccct actaccctga acactgcctc
900
cccaaaaaga agccaaaact caaggagaag gtgcggccag aaggcacctg tgaggaggcc
960
tcgctgccgc ttgagagaac actcaaaggt cccgagtgtg cagctgccgc cactgccggg
1020
aagcccccca ggcctgacgg cccagctgac ccggccaagc agggcccact gcgcaccagt
1080
gcccggggcc tgtcccggag gctgcagagc tgctactgct gtgatggccg ggaggatggg
1140
ggcgaggagg cagccccagc cgacaagggt cgcaaacatg agtgcagcaa ggaggctccg
1200
gcagagcccg gcggggaggc ccaggagcac tgggtgcatg aggcctgtgc cgtgtggacc
1260
ggcggcgtct acctggtggc cgggaagctc tttgggctgc aggaggccat gaaggtggcc
1320
gtggacatga tgtgttccag ctgccaagaa gccggggcca ccatcgggtg ctgccacaaa
1380
ggatgcctcc acacctacca ctacccgtgt gccagcgatg caggttgcat attcatcgaa
1440
gagaactttt ctttgaaatg tcccaaacat aagaggctgc cgtagtaatc caccccaacg
1500
gccggaggag ccgccggagc ccgcctgccc gcccgccgcc gaaggagagg agccgcctgc
1560
gcagcccccg ggcctttgag ctgctcccag cgctggtcca gagccgatcc ttgatccggg
1620
tcccggatcg tggatccggc cgcctagggc tcagacttgc ggccccgggt tgggaggaaa
1680
acccgttccg gagccgcctg ctcccggaac cggacggcac agggcgttct tgcccacccc
1740
aggggccagg cttgcggagg gggagcccgc ggagcggcca gactccccgg ggcgctcagc
1800
ctccggcgag ggtgggagac ggctttgtcc tggggacact ttccctctgg aatctcaaga
1860
cgacgtggca cacattccac gtgggtgctg ccgccacccc agtcggtcgt ggcgtgcagc
1920
tgggagccct gggcttgggg gtgggggtcg aaacagtact ggaagaggcg gagggcggct
1980
cctagctccg tggactaggc gggggagaaa ggaagccttt ctgagagcgg gctaggccgg
2040
cactggagag gccggagcct ttggaacaaa ccgtgcggaa cgcgtccagg ggccttcccg
2100
cccagccttt gccagatctc tcgtgcggtt cgggcaaagc cggggtagac ctgggctatg
2160
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2220
gtttgtcccc tttccagtcc tccaccccac ccctggagcc cagcctggga gcgcaaaacc
2280
caagaagcgg ccagaacgca cctccggctc cggcggacgc gcgaccgttg tgcaccacca
2340
gggaccgccg cgcctactct gcacgggagc agggacagcg ctagatttcg tgtacaaaac
2400

ctgtgtaccc ctctatatat atgttacata gaatgtatat atgttgggaa catgctcgct
2460
tctcccgtgt gtcgccgccg tgcgtcgtgc gcccgcaaca gagccccaac cgggcctttg
2520
ccgggtaagg ggctaccgcg acgccacttg tccacgcagc caccaccggc ccgggccagt
2580
ccctgccagt ccgtccgcct gtccgtccgt gtcctcagct ctgtccacgc ttcgataggc
2640
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2700
ggtaaacgtg tgtattatat ctggcctcgt tatatagtgt atatatatgt atacatatac
2760
atatatataa tatatatgaa gactgtaaat gttaagacga ctagtgttct tattagtata
2820
ttgcttcaca ctgaagattg tgtgtatcga gctgtttcta aaagatgttt attttcctta
2880
agagtaaaaa acagtcattg cattcagaaa aaaaaaaaaa aagtcaataa agatacaacg
2940
attgttttgg aaaatctgca gcccgtggat tccgaccaga ttcagctggg agccgggcca
3000
ggctttaggt tggggaatgg gaatgaaggg aggggctggg gggggggca tgaatggagt
3060
cagggagtcg gcctttcaca gaacaggaaa cctcccccgc ccctgtgccc cctctccagt
3120
gtggcggcag gtcgggaggg aggaggcttc tttgctgtga aatgaccagg ggccgggatg
3180
ggggaggtga gacgtgccag acttcttgca gggagaccca agctgtagct cctgtcacac
3240
aacaggtcct ggaagtcagt ccatcctccc gtgccaccca gggaccttgt gtccggaggg
3300
ggaggggaag cctttgccta ggtgctgggg gagggcccaa gcactctcac tagtcagcac
3360
atccatcagc tgaagacaca aaacccagat tataaataat ttcattttta attctctgta
3420
ca
3422

<210> 820
<211> 494
<212> PRT
<213> Homo sapiens

<400> 820
Met Asn Ser Lys Lys Leu Ser Ser Thr Asp Cys Phe Lys Thr Glu Ala
1 5 10 15
Phe Thr Ser Pro Glu Ala Leu Gln Pro Gly Gly Thr Ala Leu Ala Pro
20 25 30
Lys Lys Arg Ser Arg Lys Gly Arg Ala Gly Ala His Gly Leu Ser Lys
35 40 45
Gly Pro Leu Glu Lys Arg Pro Tyr Leu Gly Pro Ala Leu Pro Leu Thr
50 55 60
Pro Arg Asp Arg Ala Ser Gly Thr Gln Gly Ala Ser Glu Asp Asn Ser
65 70 75 80
Gly Gly Gly Gly Lys Lys Pro Lys Met Glu Glu Leu Gly Leu Ala Ser

```
                85                  90                  95
His Pro Pro Glu Gly Arg Pro Cys Gln Pro Gln Thr Arg Ala Gln Lys
            100                 105                 110
Gln Pro Gly His Thr Asn Tyr Ser Ser Tyr Ser Lys Arg Lys Arg Leu
        115                 120                 125
Thr Arg Gly Arg Ala Lys Asn Thr Thr Ser Ser Pro Cys Lys Gly Arg
    130                 135                 140
Ala Lys Arg Arg Arg Gln Gln Gln Val Leu Pro Leu Asp Pro Ala Glu
145                 150                 155                 160
Pro Glu Ile Arg Leu Lys Tyr Ile Ser Ser Cys Lys Arg Leu Arg Ser
                165                 170                 175
Asp Ser Arg Thr Pro Ala Phe Ser Pro Phe Val Arg Val Glu Lys Arg
            180                 185                 190
Asp Ala Phe Thr Thr Ile Cys Thr Val Val Asn Ser Pro Gly Asp Ala
        195                 200                 205
Pro Lys Pro His Arg Lys Pro Ser Ser Ser Ala Ser Ser Ser Ser Ser
    210                 215                 220
Ser Ser Ser Phe Ser Leu Asp Ala Ala Gly Ala Ser Leu Ala Thr Leu
225                 230                 235                 240
Pro Gly Gly Ser Ile Leu Gln Pro Arg Pro Ser Leu Pro Leu Ser Ser
                245                 250                 255
Thr Met His Leu Gly Pro Val Val Ser Lys Ala Leu Ser Thr Ser Cys
            260                 265                 270
Leu Val Cys Cys Leu Cys Gln Asn Pro Ala Asn Phe Lys Asp Leu Gly
        275                 280                 285
Asp Leu Cys Gly Pro Tyr Tyr Pro Glu His Cys Leu Pro Lys Lys Lys
    290                 295                 300
Pro Lys Leu Lys Glu Lys Val Arg Pro Glu Gly Thr Cys Glu Glu Ala
305                 310                 315                 320
Ser Leu Pro Leu Glu Arg Thr Leu Lys Gly Pro Glu Cys Ala Ala Ala
                325                 330                 335
Ala Thr Ala Gly Lys Pro Pro Arg Pro Asp Gly Pro Ala Asp Pro Ala
            340                 345                 350
Lys Gln Gly Pro Leu Arg Thr Ser Ala Arg Gly Leu Ser Arg Arg Leu
        355                 360                 365
Gln Ser Cys Tyr Cys Cys Asp Gly Arg Glu Asp Gly Gly Glu Glu Ala
    370                 375                 380
Ala Pro Ala Asp Lys Gly Arg Lys His Glu Cys Ser Lys Glu Ala Pro
385                 390                 395                 400
Ala Glu Pro Gly Gly Glu Ala Gln Glu His Trp Val His Glu Ala Cys
                405                 410                 415
Ala Val Trp Thr Gly Gly Val Tyr Leu Val Ala Gly Lys Leu Phe Gly
            420                 425                 430
Leu Gln Glu Ala Met Lys Val Ala Val Asp Met Met Cys Ser Ser Cys
        435                 440                 445
Gln Glu Ala Gly Ala Thr Ile Gly Cys Cys His Lys Gly Cys Leu His
    450                 455                 460
Thr Tyr His Tyr Pro Cys Ala Ser Asp Ala Gly Cys Ile Phe Ile Glu
465                 470                 475                 480
Glu Asn Phe Ser Leu Lys Cys Pro Lys His Lys Arg Leu Pro
                485                 490
```

<210> 821
<211> 420

<212> DNA
<213> Homo sapiens

<400> 821
acgcgtcccg tcacctgcgg tatggaccaa gtgagttgtg tgctcgacaa tgggttcgcc
60
gccatcatgg atgtgccggg tttcaactat cgcgcccatc gttacaccga agcctatcgg
120
cgtttgccgc aaaatgtggt gctaggttcg gaaacgacct cgacggtgag cagccgtggt
180
gtctacaagt ttcctgttgt gctgaagtcc gatgccatct atcccgacca tcagtcgtca
240
ggctacgaca cagagtattg ttcgtggtcg aacacccccg atgtcgattt cgccctcgcc
300
gaagactatc cctggacgat ggggcagttt gtctggacgg gcttcgacta cctcggtgaa
360
ccttcgcctt acgacaccga tgcctggccc tctcacgcct ccctcttcgg cattgtcgac
420

<210> 822
<211> 133
<212> PRT
<213> Homo sapiens

<400> 822
Met Asp Gln Val Ser Cys Val Leu Asp Asn Gly Phe Ala Ala Ile Met
 1   5   10   15
Asp Val Pro Gly Phe Asn Tyr Arg Ala His Arg Tyr Thr Glu Ala Tyr
            20   25   30
Arg Arg Leu Pro Gln Asn Val Val Leu Gly Ser Glu Thr Thr Ser Thr
        35   40   45
Val Ser Ser Arg Gly Val Tyr Lys Phe Pro Val Val Leu Lys Ser Asp
    50   55   60
Ala Ile Tyr Pro Asp His Gln Ser Ser Gly Tyr Asp Thr Glu Tyr Cys
65   70   75   80
Ser Trp Ser Asn Thr Pro Asp Val Asp Phe Ala Leu Ala Glu Asp Tyr
                85   90   95
Pro Trp Thr Met Gly Gln Phe Val Trp Thr Gly Phe Asp Tyr Leu Gly
            100   105   110
Glu Pro Ser Pro Tyr Asp Thr Asp Ala Trp Pro Ser His Ala Ser Leu
        115   120   125
Phe Gly Ile Val Asp
    130

<210> 823
<211> 550
<212> DNA
<213> Homo sapiens

<400> 823
tctagattct tgggcagccg agcccctctt gaattcctca gcctaccatc atgatcaaca
60
cctcccatgt tccgtccatg aatgaccgca ctgacagcac tggagagatt taatgggtca
120

ccaattgagg cagtgaaggc actcatggca ctcagagctg gaatggggct gatctgagtt
180
gtactgttga ctgcagtggt gatgacaacc tgcattcctt tgctggctgc atcgacaact
240
gctttgtaaa tggcatctac ggaagcatca cctgggccac ccacaacgag gccatccttc
300
acctgttgac caagagatgg gtcaatcctc ggttgcaact cacaaggtgt atcttgaaaa
360
ggtggaagtg tagtgtttgg attctcagga agtgctgtga gcccaggctg agtgcttatt
420
cttttgttta ggagagctgc atcttcctgc attctcacct gaaagttctg aaacagacaa
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540
ttctggtacc
550

<210> 824
<211> 161
<212> PRT
<213> Homo sapiens

<400> 824
Met Ala Cys Leu Phe Gln Asn Phe Gln Val Arg Met Gln Glu Asp Ala
1 5 10 15
Ala Leu Leu Asn Lys Arg Ile Ser Thr Gln Pro Gly Leu Thr Ala Leu
20 25 30
Pro Glu Asn Pro Asn Thr Thr Leu Pro Pro Phe Gln Asp Thr Pro Cys
35 40 45
Glu Leu Gln Pro Arg Ile Asp Pro Ser Leu Gly Gln Gln Val Lys Asp
50 55 60
Gly Leu Val Val Gly Gly Pro Gly Asp Ala Ser Val Asp Ala Ile Tyr
65 70 75 80
Lys Ala Val Val Asp Ala Ala Ser Lys Gly Met Gln Val Val Ile Thr
85 90 95
Thr Ala Val Asn Ser Thr Thr Gln Ile Ser Pro Ile Pro Ala Leu Ser
100 105 110
Ala Met Ser Ala Phe Thr Ala Ser Ile Gly Asp Pro Leu Asn Leu Ser
115 120 125
Ser Ala Val Ser Ala Val Ile His Gly Arg Asn Met Gly Gly Val Asp
130 135 140
His Asp Gly Arg Leu Arg Asn Ser Arg Gly Ala Arg Leu Pro Lys Asn
145 150 155 160
Leu

<210> 825
<211> 327
<212> DNA
<213> Homo sapiens

<400> 825
gcgtttgcga ccggccgtaa cccgcagaat gcggcggtgt gttgcactga gggtattttg
60

cagttgctgg atgagcgcga gatgcgcggc gtgctcggcc acgagctgat gcacgtgtac
120
aaccgcgata tcctcacctc ttcggtggcg gcgggtatcg cctccatcat cggtacgatt
180
gcgcagattc tttcgtttgg cgcgatgttc ggtggatcca accgcgatgg tgaacgttcc
240
aacccccctcg ccatgttcgt ggttgctatg ctggctccca ttgctactca ggtcatccag
300
atggctatta gccgcacccg tgaattc
327

<210> 826
<211> 109
<212> PRT
<213> Homo sapiens

<400> 826
Ala Phe Ala Thr Gly Arg Asn Pro Gln Asn Ala Ala Val Cys Cys Thr
1 5 10 15
Glu Gly Ile Leu Gln Leu Leu Asp Glu Arg Glu Met Arg Gly Val Leu
20 25 30
Gly His Glu Leu Met His Val Tyr Asn Arg Asp Ile Leu Thr Ser Ser
35 40 45
Val Ala Ala Gly Ile Ala Ser Ile Ile Gly Thr Ile Ala Gln Ile Leu
50 55 60
Ser Phe Gly Ala Met Phe Gly Gly Ser Asn Arg Asp Gly Glu Arg Ser
65 70 75 80
Asn Pro Leu Ala Met Phe Val Val Ala Met Leu Ala Pro Ile Ala Thr
85 90 95
Gln Val Ile Gln Met Ala Ile Ser Arg Thr Arg Glu Phe
100 105

<210> 827
<211> 534
<212> DNA
<213> Homo sapiens

<400> 827
nacgcgtacg tcaatatgca tcgtccagtc gttatcgcaa cgccgaaatc gatgctgcgc
60
aacaagatgg cgacctcgga tcccgaagag ttcaccaccg gtaggtggcg tcctgttcta
120
cccgacccat cgatcaccga cccgacggcc gttacgagga ttatcttgtg ctctggcaag
180
gcgcggtggg agctggtcaa gcaacgtaag gccgccagtc ttgacggaca gctcgccatc
240
atcccgatgg agcgtctcta cccgctacca gtcgacgagt tggctgaggt ttttgcgcct
300
tacaccaacg tcacggatgt ccgctgggtc caagaagagc cagagaacca gggcgcctgg
360
tactacatgc tgacccacct gccccaggcc atgtcggaga agctgccagg attctttgat
420
gggttagtcg gcatcacccg cccaccgtcc tcagctccgt cggtgggaca gcacagcgtc
480

cacatccgtg aagagcagga gttactcgag aaggctatag cctgagcgac ctga
534

<210> 828
<211> 174
<212> PRT
<213> Homo sapiens

<400> 828
Xaa Ala Tyr Val Asn Met His Arg Pro Val Val Ile Ala Thr Pro Lys
1 5 10 15
Ser Met Leu Arg Asn Lys Met Ala Thr Ser Asp Pro Glu Glu Phe Thr
20 25 30
Thr Gly Arg Trp Arg Pro Val Leu Pro Asp Pro Ser Ile Thr Asp Pro
35 40 45
Thr Ala Val Thr Arg Ile Ile Leu Cys Ser Gly Lys Ala Arg Trp Glu
50 55 60
Leu Val Lys Gln Arg Lys Ala Ala Ser Leu Asp Gly Gln Leu Ala Ile
65 70 75 80
Ile Pro Met Glu Arg Leu Tyr Pro Leu Pro Val Asp Glu Leu Ala Glu
85 90 95
Val Phe Ala Pro Tyr Thr Asn Val Thr Asp Val Arg Trp Val Gln Glu
100 105 110
Glu Pro Glu Asn Gln Gly Ala Trp Tyr Tyr Met Leu Thr His Leu Pro
115 120 125
Gln Ala Met Ser Glu Lys Leu Pro Gly Phe Phe Asp Gly Leu Val Gly
130 135 140
Ile Thr Arg Pro Pro Ser Ser Ala Pro Ser Val Gly Gln His Ser Val
145 150 155 160
His Ile Arg Glu Glu Gln Glu Leu Leu Glu Lys Ala Ile Ala
165 170

<210> 829
<211> 492
<212> DNA
<213> Homo sapiens

<400> 829
nagtggccgg gtggccggcg ggtgccagcc gccatggagg ccgtgccccg catgcccatg
60
atctggctgg acctgaagga ggccggtgac tttcacttcc agccagctgt gaagaagttt
120
gtcctgaaga attatggaga gaacccagaa gcctacaatg aagaactgaa gaagctggag
180
ttgctcagac agaatgctgt ccgtgtccca cgagactttg agggctgtag tgtcctccgc
240
aagtacctcg gccagcttca ttacctgcag agtcgggtcc ccatgggctc gggccaggag
300
gccgctgtcc ctgtcacatg gacagagatc ttctcaggca agtctgtggc ccatgaggac
360
atcaagtacg agcaggcctg tattttctcc aacnttggag cgctgcactc catgctgggg
420
gccatggaca agcgggtgtc tgaggagggc atgaaggtct cctgtaccca tttccagtgc
480

gcagccggcg cc
492

<210> 830
<211> 164
<212> PRT
<213> Homo sapiens

<400> 830
Xaa Trp Pro Gly Gly Arg Arg Val Pro Ala Ala Met Glu Ala Val Pro
1 5 10 15
Arg Met Pro Met Ile Trp Leu Asp Leu Lys Glu Ala Gly Asp Phe His
20 25 30
Phe Gln Pro Ala Val Lys Lys Phe Val Leu Lys Asn Tyr Gly Glu Asn
35 40 45
Pro Glu Ala Tyr Asn Glu Glu Leu Lys Lys Leu Glu Leu Leu Arg Gln
50 55 60
Asn Ala Val Arg Val Pro Arg Asp Phe Glu Gly Cys Ser Val Leu Arg
65 70 75 80
Lys Tyr Leu Gly Gln Leu His Tyr Leu Gln Ser Arg Val Pro Met Gly
85 90 95
Ser Gly Gln Glu Ala Ala Val Pro Val Thr Trp Thr Glu Ile Phe Ser
100 105 110
Gly Lys Ser Val Ala His Glu Asp Ile Lys Tyr Glu Gln Ala Cys Ile
115 120 125
Phe Ser Asn Xaa Gly Ala Leu His Ser Met Leu Gly Ala Met Asp Lys
130 135 140
Arg Val Ser Glu Glu Gly Met Lys Val Ser Cys Thr His Phe Gln Cys
145 150 155 160
Ala Ala Gly Ala

<210> 831
<211> 303
<212> DNA
<213> Homo sapiens

<400> 831
gcgttgctgc ggcgtggcga gaccatgacg gcggagaatc agcgtgccaa tgtgcgcatc
60
gccgcaaacc acatcaagga ggttgcggtc gatcacgagg tcgttgtagc ccatggtaat
120
ggcccccagg taggtctgtt ggctctgcaa tcgacagcct acgaggaagt cggtatctat
180
ccgctggatg tcctgggcgc agagtcacag gccatgatcg gctacatgat cgagcaggaa
240
ctcggcaatg tgatgcctca ggatcagcag atcgtcacca tgatcacgat gacagtcgtc
300
gac
303

<210> 832
<211> 101
<212> PRT

<213> Homo sapiens

<400> 832
Ala Leu Leu Arg Arg Gly Glu Thr Met Thr Ala Glu Asn Gln Arg Ala
1 5 10 15
Asn Val Arg Ile Ala Ala Asn His Ile Lys Glu Val Ala Val Asp His
20 25 30
Glu Val Val Val Ala His Gly Asn Gly Pro Gln Val Gly Leu Leu Ala
35 40 45
Leu Gln Ser Thr Ala Tyr Glu Glu Val Gly Ile Tyr Pro Leu Asp Val
50 55 60
Leu Gly Ala Glu Ser Gln Ala Met Ile Gly Tyr Met Ile Glu Gln Glu
65 70 75 80
Leu Gly Asn Val Met Pro Gln Asp Gln Gln Ile Val Thr Met Ile Thr
85 90 95
Met Thr Val Val Asp
100

<210> 833
<211> 466
<212> DNA
<213> Homo sapiens

<400> 833
nngatccgcg cgatcgacga ggcgggtgcg tgatgttgac agcgaaaatg cgcagccggc
60
catttgacga gggctgaaaa cgtcttctac cggtctgctg tgccgcctgg tgtcagcaaa
120
cgacgccatg atcgtccagt gggtatcgat ttgttctgcg gcgctggggg attcagttgc
180
ggattccacc aggccgggtg gcatgttgcg gcggcggttg agcacgacgt gtcggcgtct
240
ctgacctatg tcatgaatct cgctcggccc ggcgtcaaga ttcacatcga ccccgagcac
300
ccggagctgg gcccaagacc accgcgaacc aagaagaaga gcggcggcgc agtgccgttc
360
gatgcgcatg tcggaactgg gtggatcgcc agcgagcccg ccgacgatcc cggctgcgaa
420
cacttctacg tgtacgacgt caagaacctc agcggcgagc ggatcc
466

<210> 834
<211> 142
<212> PRT
<213> Homo sapiens

<400> 834
Gln Arg Lys Cys Ala Ala Gly His Leu Thr Arg Ala Glu Asn Val Phe
1 5 10 15
Tyr Arg Ser Ala Val Pro Pro Gly Val Ser Lys Arg Arg His Asp Arg
20 25 30
Pro Val Gly Ile Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser Cys Gly
35 40 45
Phe His Gln Ala Gly Trp His Val Ala Ala Ala Val Glu His Asp Val

```
    50                  55                  60
Ser Ala Ser Leu Thr Tyr Val Met Asn Leu Ala Arg Pro Gly Val Lys
65                  70                  75                  80
Ile His Ile Asp Pro Glu His Pro Glu Leu Gly Pro Arg Pro Pro Arg
                85                  90                  95
Thr Lys Lys Lys Ser Gly Gly Ala Val Pro Phe Asp Ala His Val Gly
            100                 105                 110
Thr Gly Trp Ile Ala Ser Glu Pro Ala Asp Asp Pro Gly Cys Glu His
        115                 120                 125
Phe Tyr Val Tyr Asp Val Lys Asn Leu Ser Gly Glu Arg Ile
    130                 135                 140
```

<210> 835
<211> 482
<212> DNA
<213> Homo sapiens

<400> 835
acgcgtgaag ggattttgat cacccagaac aaccacctgt ctttttagat caagaagcag
60
aagctcagag caaagaacat cacaccacgt ccctcagtga ttgaagcagt gattgagtca
120
cagaataaat ctggaactca ggtcttctga tctttgctcc agatgttaga gacaaaacta
180
aaagtaaaat accaagtgaa atcaaagcat cacgattgag cccagaacat gaaaaagaac
240
ttcctggccc acttgagaaa ctgttaaacc ggacatacct ttggggactt cttcccttct
300
ctggaataag attgatgttt ccatgctgtg aaagacgatg atgttccttc tcccagattc
360
ctgctgtctt caaaaggcct agcaaaaacc actgctgctg ggtgcagttg agaaagggaa
420
tgaagaacaa tcccatggcc atgcaggcac tcctcccctc cacctctctg cccttcacgc
480
gt
482

<210> 836
<211> 120
<212> PRT
<213> Homo sapiens

<400> 836
```
Met Ala Met Gly Leu Phe Phe Ile Pro Phe Leu Asn Cys Thr Gln Gln
 1               5                  10                  15
Gln Trp Phe Leu Leu Gly Leu Leu Lys Thr Ala Gly Ile Trp Glu Lys
            20                  25                  30
Glu His His Arg Leu Ser Gln His Gly Asn Ile Asn Leu Ile Pro Glu
        35                  40                  45
Lys Gly Arg Ser Pro Gln Arg Tyr Val Arg Phe Asn Ser Phe Ser Ser
    50                  55                  60
Gly Pro Gly Ser Ser Phe Ser Cys Ser Gly Leu Asn Arg Asp Ala Leu
65                  70                  75                  80
Ile Ser Leu Gly Ile Leu Leu Leu Val Leu Ser Leu Thr Ser Gly Ala
```

```
                85                  90                  95
Lys Ile Arg Arg Pro Glu Phe Gln Ile Tyr Ser Val Thr Gln Ser Leu
            100                 105                 110
Leu Gln Ser Leu Arg Asp Val Val
        115                 120
```

<210> 837
<211> 509
<212> DNA
<213> Homo sapiens

<400> 837
acgcgtggac ccccgttctg cccgcctttg cagtcatcgc cctccctgaa gtcaccgctg
60
cagaaatacg caggcactga cctgggggta cagccaggca agggagagac gaggggctca
120
ctctgcacca gccaaggcct gtgtcctggc atggctcccc caggaagcga ggatggcggt
180
gcctggcggt cgagcccctc ttatcctggg gaatgctggg gggcgttcct gagcagacct
240
gcctgctgcc cctgctggct ggcactgccc ctcccccggg gaaaggttgg gtggtccccc
300
caggggaact caaagcaggg gagcccctgg aggccccaag tccctggaat atcttggcgc
360
tcagatggcc cccctcgaac accctcacac ggggggggccg cgcggtggga ggtgacccag
420
cagccactct tacttggcga agacttttct cccaatgcga gcgcgggtgg tatcagcctg
480
agccttcagg ttggtgaggc tggggtacc
509

<210> 838
<211> 119
<212> PRT
<213> Homo sapiens

<400> 838
```
Met Ala Pro Pro Gly Ser Glu Asp Gly Gly Ala Trp Arg Ser Ser Pro
 1               5                  10                  15
Ser Tyr Pro Gly Glu Cys Trp Gly Ala Phe Leu Ser Arg Pro Ala Cys
            20                  25                  30
Cys Pro Cys Trp Leu Ala Leu Pro Leu Pro Arg Gly Lys Val Gly Trp
        35                  40                  45
Ser Pro Gln Gly Asn Ser Lys Gln Gly Ser Pro Trp Arg Pro Gln Val
    50                  55                  60
Pro Gly Ile Ser Trp Arg Ser Asp Gly Pro Pro Arg Thr Pro Ser His
65                  70                  75                  80
Gly Gly Ala Ala Arg Trp Glu Val Thr Gln Gln Pro Leu Leu Leu Gly
                85                  90                  95
Glu Asp Phe Ser Pro Asn Ala Ser Ala Gly Gly Ile Ser Leu Ser Leu
            100                 105                 110
Gln Val Gly Glu Ala Gly Val
        115
```

<210> 839
<211> 347
<212> DNA
<213> Homo sapiens

<400> 839
acgcgtctcg tgttcgtgcg gcacggcagg acggcgttca atgtggaggg tcggctccag
60
ggccgtctcg acatgccgtt ggatgaggtg gggcgccgtc aggcactcac agtggctcaa
120
gtcatcgccg agatggaacc tgacgcgatc atggcctctc cgctacaacg tgcgcgcgac
180
acagctcagg caatcggtgc ttgtgctgga ttgggcgtac agctggatga tcgactcatc
240
gagatcgatg tcggacgttg gtcgggacaa cgggctgcgg acctgcgtcg caacgatcct
300
gagtacgcag caagtgtggt cagccctatc gattaccggg tcggagn
347

<210> 840
<211> 115
<212> PRT
<213> Homo sapiens

<400> 840
Thr Arg Leu Val Phe Val Arg His Gly Arg Thr Ala Phe Asn Val Glu
1 5 10 15
Gly Arg Leu Gln Gly Arg Leu Asp Met Pro Leu Asp Glu Val Gly Arg
20 25 30
Arg Gln Ala Leu Thr Val Ala Gln Val Ile Ala Glu Met Glu Pro Asp
35 40 45
Ala Ile Met Ala Ser Pro Leu Gln Arg Ala Arg Asp Thr Ala Gln Ala
50 55 60
Ile Gly Ala Cys Ala Gly Leu Gly Val Gln Leu Asp Asp Arg Leu Ile
65 70 75 80
Glu Ile Asp Val Gly Arg Trp Ser Gly Gln Arg Ala Ala Asp Leu Arg
85 90 95
Arg Asn Asp Pro Glu Tyr Ala Ala Ser Val Val Ser Pro Ile Asp Tyr
100 105 110
Arg Val Gly
115

<210> 841
<211> 351
<212> DNA
<213> Homo sapiens

<400> 841
tccggaactc accccgacgc cgtcattatg gacgtcatga tgccgcgtct agatggcttg
60
gaagccaccc ggatgctgcg cagcaatggc aacgacgtcc cgatcctcgt cctcaccgcc
120
cgcgatgctg tcgacgatcg cgttgacggc ctcgacgctg gcgccgatga ctacatggtc
180

aagcccttcg ccctcgacga actcctcgct cgcctacgcg ccctcactcg tcgttcccgt
240
cccgagccag agcaaaacga ggcccctgaa caactctcct tcgctgacct cacccttgat
300
ccaggcaccc gcgagatcac ccgcgggaac cgtcgcatca gtttgacgcg t
351

<210> 842
<211> 117
<212> PRT
<213> Homo sapiens

<400> 842
Ser Gly Thr His Pro Asp Ala Val Ile Met Asp Val Met Met Pro Arg
 1   5   10   15
Leu Asp Gly Leu Glu Ala Thr Arg Met Leu Arg Ser Asn Gly Asn Asp
            20   25   30
Val Pro Ile Leu Val Leu Thr Ala Arg Asp Ala Val Asp Asp Arg Val
        35   40   45
Asp Gly Leu Asp Ala Gly Ala Asp Asp Tyr Met Val Lys Pro Phe Ala
    50   55   60
Leu Asp Glu Leu Leu Ala Arg Leu Arg Ala Leu Thr Arg Arg Ser Arg
65   70   75   80
Pro Glu Pro Glu Gln Asn Glu Ala Pro Glu Gln Leu Ser Phe Ala Asp
                85   90   95
Leu Thr Leu Asp Pro Gly Thr Arg Glu Ile Thr Arg Gly Asn Arg Arg
            100   105   110
Ile Ser Leu Thr Arg
        115

<210> 843
<211> 393
<212> DNA
<213> Homo sapiens

<400> 843
ctagcccagg ctctcgtcca cgaggggctg cgcgctgtgg cctctggggc aaacccggtc
60
ggcctcaagc gcggtatcga gaaggctgtc gacgccgttg tggaggagct ccgctctatc
120
tcgcgcgcca tcgacaccac ctcggacatg gccagcgttg ccaccatctc cagccgtgac
180
gagaccatcg gcgccctcat cgctgaggcc ttcgacaagg ttggtaagga cggggttatc
240
accgtcgacg agtcgcagac cttcggcact gagcttgact tcaccgaggg catgcagttc
300
gacaagggtt acctgtcgcc ctacatggtc accgaccagg ttcgcatgga ggctgtgatc
360
gaggatcctt acatcctcat tcactcccgc aag
393

<210> 844
<211> 131
<212> PRT

<213> Homo sapiens

<400> 844
Leu Ala Gln Ala Leu Val His Glu Gly Leu Arg Ala Val Ala Ser Gly
1 5 10 15
Ala Asn Pro Val Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Ala
20 25 30
Val Val Glu Glu Leu Arg Ser Ile Ser Arg Ala Ile Asp Thr Thr Ser
35 40 45
Asp Met Ala Ser Val Ala Thr Ile Ser Ser Arg Asp Glu Thr Ile Gly
50 55 60
Ala Leu Ile Ala Glu Ala Phe Asp Lys Val Gly Lys Asp Gly Val Ile
65 70 75 80
Thr Val Asp Glu Ser Gln Thr Phe Gly Thr Glu Leu Asp Phe Thr Glu
85 90 95
Gly Met Gln Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Met Val Thr Asp
100 105 110
Gln Val Arg Met Glu Ala Val Ile Glu Asp Pro Tyr Ile Leu Ile His
115 120 125
Ser Arg Lys
130

<210> 845
<211> 505
<212> DNA
<213> Homo sapiens

<400> 845
gccacctgcc caaggctgga tgacgggcct agggcacatc taaggaacaa ggacaggaca
60
gaagcaaagc cacagctgct ggggcagggt gggggccggt atgtctggcc agcagcatca
120
cccctgcccc cggcggggct ccaggaccgg gagactcatc agccggaagc tcttggagga
180
ggcggctgcc gtgaagacag gcacccttgc tcctgagagg ggcacccaga gaaccaagac
240
tcagcagagg gaacacaggg ctacgcccag gccccaggcc tgatatccag agtctaaatc
300
ccacctcagc ccaggggga gccttgagag gagctatgtc cctcatggac cccagtttcc
360
tctgcatacg ggctccgagc cctgcactgc ctccagggta gttcccaagg tcttttccca
420
ttacctccta cgtgagcact cagtaaacca atacacatac acaagggtga cattaattcc
480
agccacagaa tcccaggcca cgcgt
505

<210> 846
<211> 130
<212> PRT
<213> Homo sapiens

<400> 846
Met Gly Lys Asp Leu Gly Asn Tyr Pro Gly Gly Ser Ala Gly Leu Gly

```
 1               5                  10                  15
Ala Arg Met Gln Arg Lys Leu Gly Ser Met Arg Asp Ile Ala Pro Leu
            20                  25                  30
Lys Ala Pro Pro Trp Ala Glu Val Gly Phe Arg Leu Trp Ile Ser Gly
        35                  40                  45
Leu Gly Pro Gly Arg Ser Pro Val Phe Pro Leu Leu Ser Leu Gly Ser
    50                  55                  60
Leu Gly Ala Pro Leu Arg Ser Lys Gly Ala Cys Leu His Gly Ser Arg
65                  70                  75                  80
Leu Leu Gln Glu Leu Pro Ala Asp Glu Ser Pro Gly Pro Gly Ala Pro
                85                  90                  95
Pro Gly Ala Gly Val Met Leu Leu Ala Arg His Thr Gly Pro His Pro
            100                 105                 110
Ala Pro Ala Ala Val Ala Leu Leu Leu Ser Cys Pro Cys Ser Leu Asp
        115                 120                 125
Val Pro
    130
```

<210> 847
<211> 448
<212> DNA
<213> Homo sapiens

<400> 847
aagcttttaa aggagcaaga aaacatgaaa gagctagtag tcaaccttct ccgcatgact
60
caaatcaaaa ttgatgaaaa ggaacaaaag tccaaggatt tcctgaaagc tcagcaaaaa
120
tacaccaaca ttgttaaaga aatgaaagca aaggatcttg aaatcaggat acacaagaag
180
aaaaaatgtg aaatttatcg gagactgaga gagcttgcta aactgtatga caccattcga
240
aatgaaagaa acaaatttgt taacttactc cacaaagctc atcagaaagt aaatgaaata
300
aaagaaaggc ataaaatgtc attaaatgaa cttgaaattc tgagaaatag tgccgttagt
360
caagaaagaa agctacaaaa ttccatgctg aaacacgcca acaatgttac catcagagag
420
agcatgcaaa acgatgtgcg caaaattt
448

<210> 848
<211> 149
<212> PRT
<213> Homo sapiens

<400> 848

```
Lys Leu Leu Lys Glu Gln Glu Asn Met Lys Glu Leu Val Val Asn Leu
 1               5                  10                  15
Leu Arg Met Thr Gln Ile Lys Ile Asp Glu Lys Glu Gln Lys Ser Lys
            20                  25                  30
Asp Phe Leu Lys Ala Gln Gln Lys Tyr Thr Asn Ile Val Lys Glu Met
        35                  40                  45
Lys Ala Lys Asp Leu Glu Ile Arg Ile His Lys Lys Lys Lys Cys Glu
```

```
    50                  55                  60
Ile Tyr Arg Arg Leu Arg Glu Leu Ala Lys Leu Tyr Asp Thr Ile Arg
65                  70                  75                  80
Asn Glu Arg Asn Lys Phe Val Asn Leu Leu His Lys Ala His Gln Lys
                85                  90                  95
Val Asn Glu Ile Lys Glu Arg His Lys Met Ser Leu Asn Glu Leu Glu
            100                 105                 110
Ile Leu Arg Asn Ser Ala Val Ser Gln Glu Arg Lys Leu Gln Asn Ser
        115                 120                 125
Met Leu Lys His Ala Asn Asn Val Thr Ile Arg Glu Ser Met Gln Asn
    130                 135                 140
Asp Val Arg Lys Ile
145
```

<210> 849
<211> 463
<212> DNA
<213> Homo sapiens

<400> 849
nnacgcgtga ttgttggggc caaggaatgc catgtggaga gtgcaggtga agtgataagt
60
cttttggaga tggggaatgc agccagacat acaggtacca ctcaaatgaa tgagcactcc
120
agcagatcac atgcaatttt tacaatcagc atttgtcaag ttcataaaaa tatggaggca
180
gctgaagatg gatcatggta ttcccctcgg catattgtct caaagttcca ctttgtggat
240
ttggcaggat cagaaagagt aaccaaaacg gggaatactg gtgaacggtt caaagaatcc
300
attcaaatca atagtggatt gctggcttta ggaaatgtaa taagcgctct tggggaccca
360
cgcaggaaga gttcacatat tccatatagg gatgctaaaa ttacccggct tctgaaagat
420
tctctgggag gcagtgctaa gactgtcatg atcacatgtg tca
463

<210> 850
<211> 154
<212> PRT
<213> Homo sapiens

<400> 850
```
Xaa Arg Val Ile Val Gly Ala Lys Glu Cys His Val Glu Ser Ala Gly
 1               5                  10                  15
Glu Val Ile Ser Leu Leu Glu Met Gly Asn Ala Ala Arg His Thr Gly
            20                  25                  30
Thr Thr Gln Met Asn Glu His Ser Ser Arg Ser His Ala Ile Phe Thr
        35                  40                  45
Ile Ser Ile Cys Gln Val His Lys Asn Met Glu Ala Ala Glu Asp Gly
    50                  55                  60
Ser Trp Tyr Ser Pro Arg His Ile Val Ser Lys Phe His Phe Val Asp
65                  70                  75                  80
Leu Ala Gly Ser Glu Arg Val Thr Lys Thr Gly Asn Thr Gly Glu Arg
```

```
                85                  90                  95
Phe Lys Glu Ser Ile Gln Ile Asn Ser Gly Leu Leu Ala Leu Gly Asn
            100                 105                 110
Val Ile Ser Ala Leu Gly Asp Pro Arg Arg Lys Ser Ser His Ile Pro
        115                 120                 125
Tyr Arg Asp Ala Lys Ile Thr Arg Leu Leu Lys Asp Ser Leu Gly Gly
    130                 135                 140
Ser Ala Lys Thr Val Met Ile Thr Cys Val
145                 150
```

<210> 851
<211> 372
<212> DNA
<213> Homo sapiens

<400> 851
aaatttcctg tttctgatcg acgaaataaa gtttagcgtg atgagtgagc tgcttatgca
60
gttcctccat tcgcttataa acagttttat ttctcatttc gaaaactctc gatgcagaat
120
aaaggctaga gtctggggac caagtcccca gctccgttta cgcgacttcc ttgaccttgt
180
ttgttatgct gataaggtta ttcagcttga cgatttgttc gtggtctttc aaccgttttg
240
cagctggtcg acgatattcc tggtaggaac tacgatagaa gaccagcatc ggaagaactt
300
tgtagatgct gaacaaacac ccaccgatca cttcagcctc gaagtaaggg ttatactgtc
360
taacccacgc gt
372

<210> 852
<211> 110
<212> PRT
<213> Homo sapiens

<400> 852
```
Met Ser Glu Leu Leu Met Gln Phe Leu His Ser Leu Ile Asn Ser Phe
 1               5                  10                  15
Ile Ser His Phe Glu Asn Ser Arg Cys Arg Ile Lys Ala Arg Val Trp
            20                  25                  30
Gly Pro Ser Pro Gln Leu Arg Leu Arg Asp Phe Leu Asp Leu Val Cys
        35                  40                  45
Tyr Ala Asp Lys Val Ile Gln Leu Asp Asp Leu Phe Val Val Phe Gln
    50                  55                  60
Pro Phe Cys Ser Trp Ser Thr Ile Phe Leu Val Gly Thr Thr Ile Glu
65                  70                  75                  80
Asp Gln His Arg Lys Asn Phe Val Asp Ala Glu Gln Thr Pro Thr Asp
                85                  90                  95
His Phe Ser Leu Glu Val Arg Val Ile Leu Ser Asn Pro Arg
            100                 105                 110
```

<210> 853
<211> 423

<212> DNA
<213> Homo sapiens

<400> 853
acgcgttcag aaacttatgg tgaaatggcc gaactagaaa acctagtcga cgaatattac
60
caagctatgg gcatggatgt gcgtcgagaa acctggctgc gcgagcagat actcaagaaa
120
gtccaagaaa cgcatttgtt agaagagctt gcaggcatag aatcaggtga tgatggcgca
180
gtggtggaag agagcgtatt agaaggcctc gatacctatt tatgtgagat aaaagaagca
240
cagattcgtc atggattgca tcgtcttgga gaattaccag aagacgataa attggccgat
300
accttggtcg ccttattgcg tttaccccgt ggcagtgaca ttaccagcaa gggaattttg
360
catgccttaa tggcagattt agagttagaa caagacgatt ttgacccaat gcaaagcacg
420
cgt
423

<210> 854
<211> 141
<212> PRT
<213> Homo sapiens

<400> 854
Thr Arg Ser Glu Thr Tyr Gly Glu Met Ala Glu Leu Glu Asn Leu Val
 1   5   10   15
Asp Glu Tyr Tyr Gln Ala Met Gly Met Asp Val Arg Arg Glu Thr Trp
            20   25   30
Leu Arg Glu Gln Ile Leu Lys Lys Val Gln Glu Thr His Leu Leu Glu
        35   40   45
Glu Leu Ala Gly Ile Glu Ser Gly Asp Asp Gly Ala Val Val Glu Glu
    50   55   60
Ser Val Leu Glu Gly Leu Asp Thr Tyr Leu Cys Glu Ile Lys Glu Ala
65   70   75   80
Gln Ile Arg His Gly Leu His Arg Leu Gly Glu Leu Pro Glu Asp Asp
                85   90   95
Lys Leu Ala Asp Thr Leu Val Ala Leu Leu Arg Leu Pro Arg Gly Ser
            100   105   110
Asp Ile Thr Ser Lys Gly Ile Leu His Ala Leu Met Ala Asp Leu Glu
        115   120   125
Leu Glu Gln Asp Asp Phe Asp Pro Met Gln Ser Thr Arg
    130   135   140

<210> 855
<211> 338
<212> DNA
<213> Homo sapiens

<400> 855
acgcgtgaag ggggagctca aagtagatgg acctctgact agatggagct ctgagtaaga
60

tgaatgtctg tgcggatgtt gctcacagca agatagtgct tggagcgatt ggcacttcga
120
acaagatgga gcatggagca gatggagctc tgagcaagat ggagcgtgga gtagatagag
180
cttggagcaa gaaggagctc caagcaagat ggagcttgca gcaggtgctt ctcagtgtaa
240
gatggagctc agagaagatg atgctcagag taagattgag ctcggtgatt ggcactccaa
300
acattgctct gagcccattg gagnctctga gcagaaag
338

<210> 856
<211> 93
<212> PRT
<213> Homo sapiens

<400> 856
Met Asn Val Cys Ala Asp Val Ala His Ser Lys Ile Val Leu Gly Ala
1 5 10 15
Ile Gly Thr Ser Asn Lys Met Glu His Gly Ala Asp Gly Ala Leu Ser
20 25 30
Lys Met Glu Arg Gly Val Asp Arg Ala Trp Ser Lys Lys Glu Leu Gln
35 40 45
Ala Arg Trp Ser Leu Gln Gln Val Leu Leu Ser Val Arg Trp Ser Ser
50 55 60
Glu Lys Met Met Leu Arg Val Arg Leu Ser Ser Val Ile Gly Thr Pro
65 70 75 80
Asn Ile Ala Leu Ser Pro Leu Glu Xaa Leu Ser Arg Lys
85 90

<210> 857
<211> 435
<212> DNA
<213> Homo sapiens

<400> 857
ccggacagtg ggccaccagt gtttgccccc agcaatcatg tcagtgaagc ccaacctcgg
60
gagacacccc ggcccctcat gcctcctacc aagcctttcc tagcacctga gaccaccagc
120
cctggtgaca gggtggagac ccctgtgggg gagagagccc caacccctgt ctcagcaagc
180
tctgaggtct cccctgagag ccaagaggac tcagagaccc cagcagagga ggacagtggc
240
tctgagcagc ctcccaacag cgtcctgcct gacaaactga aggtgagctg ggagaacccc
300
agcccccagg aggcccctgc tgcagagagt gcagaaccgt cccaggcacc ctgttctgag
360
acttctgagg ctgcccccag ggagggtggg aagcccccta cacccccacc caagatctta
420
tcagagaaac tgaaa
435

<210> 858

<211> 145
<212> PRT
<213> Homo sapiens

<400> 858
Pro Asp Ser Gly Pro Pro Val Phe Ala Pro Ser Asn His Val Ser Glu
1 5 10 15
Ala Gln Pro Arg Glu Thr Pro Arg Pro Leu Met Pro Pro Thr Lys Pro
20 25 30
Phe Leu Ala Pro Glu Thr Thr Ser Pro Gly Asp Arg Val Glu Thr Pro
35 40 45
Val Gly Glu Arg Ala Pro Thr Pro Val Ser Ala Ser Ser Glu Val Ser
50 55 60
Pro Glu Ser Gln Glu Asp Ser Glu Thr Pro Ala Glu Glu Asp Ser Gly
65 70 75 80
Ser Glu Gln Pro Pro Asn Ser Val Leu Pro Asp Lys Leu Lys Val Ser
85 90 95
Trp Glu Asn Pro Ser Pro Gln Glu Ala Pro Ala Ala Glu Ser Ala Glu
100 105 110
Pro Ser Gln Ala Pro Cys Ser Glu Thr Ser Glu Ala Ala Pro Arg Glu
115 120 125
Gly Gly Lys Pro Pro Thr Pro Pro Pro Lys Ile Leu Ser Glu Lys Leu
130 135 140
Lys
145

<210> 859
<211> 561
<212> DNA
<213> Homo sapiens

<400> 859
nacgcgtggt gtggtaatcc ggtttctggt ggcgacggct gccacccctc gtggcaagac
60
atgccgttgc gtgccgatat gccatacgaa gcttggccta gtgcgaaaag ctcgctggaa
120
ccctcgaaga ggcagggtcg gcaggttacc gtggtcggtg tacgcatcgt ttcgacgatg
180
aaccccattc tgggagcaga tatgacgacg taccagtacc tcattgtcgg tggcgggatg
240
gccgctgatt ctgccgcccg cggtatccgc gacatcgaca agaaagggtc gatcgccatc
300
ctcagcgctg acgtcgacgc cccgtatcct cggccagcgc tgagcaagaa gctgtggact
360
gaccctgagt tcacctggga ccaggtcgac cttgctactg tcgctgacac cggcgcggaa
420
ttgcggctcg gcactgaggt gctcagcatt gaccgtgacg gcaagaccgt cctgaccgct
480
tccggccagg tattcggcta ccagaagttg ctgctcgtta ccggccttac cccgtcgcgc
540
attgacgacg acggcgatgc c
561

<210> 860

<211> 187
<212> PRT
<213> Homo sapiens

<400> 860
Xaa Ala Trp Cys Gly Asn Pro Val Ser Gly Gly Asp Gly Cys His Pro
1 5 10 15
Ser Trp Gln Asp Met Pro Leu Arg Ala Asp Met Pro Tyr Glu Ala Trp
20 25 30
Pro Ser Ala Lys Ser Ser Leu Glu Pro Ser Lys Arg Gln Gly Arg Gln
35 40 45
Val Thr Val Val Gly Val Arg Ile Val Ser Thr Met Asn Pro Ile Leu
50 55 60
Gly Ala Asp Met Thr Thr Tyr Gln Tyr Leu Ile Val Gly Gly Gly Met
65 70 75 80
Ala Ala Asp Ser Ala Ala Arg Gly Ile Arg Asp Ile Asp Lys Lys Gly
85 90 95
Ser Ile Ala Ile Leu Ser Ala Asp Val Asp Ala Pro Tyr Pro Arg Pro
100 105 110
Ala Leu Ser Lys Lys Leu Trp Thr Asp Pro Glu Phe Thr Trp Asp Gln
115 120 125
Val Asp Leu Ala Thr Val Ala Asp Thr Gly Ala Glu Leu Arg Leu Gly
130 135 140
Thr Glu Val Leu Ser Ile Asp Arg Asp Gly Lys Thr Val Leu Thr Ala
145 150 155 160
Ser Gly Gln Val Phe Gly Tyr Gln Lys Leu Leu Leu Val Thr Gly Leu
165 170 175
Thr Pro Ser Arg Ile Asp Asp Asp Gly Asp Ala
180 185

<210> 861
<211> 352
<212> DNA
<213> Homo sapiens

<400> 861
ccatgggttt ctatgctctg aggtttcatc tgtggggaac agtattgact tacttacaaa
60
gagataatgg tcatacccta tggtcactca ccatagtctg gcggtacatg gacttctcag
120
ccccagtaag atctgtatcc acaggacact taaagtcacc ttacagaggg ctatcccagt
180
gcctgaggcc tattagaggc gtctcttttc agccatcagt gttagaggcc atctgcatgg
240
gatcccagag cctgcctcgg gaatggcaga agctggctgg tgcttggcgt gggctttgcc
300
tgtttcactg ctttcaggga ggcctgccac aggggagaaa ctgggggggg ga
352

<210> 862
<211> 116
<212> PRT
<213> Homo sapiens

<400> 862
Met Gly Phe Tyr Ala Leu Arg Phe His Leu Trp Gly Thr Val Leu Thr
1 5 10 15
Tyr Leu Gln Arg Asp Asn Gly His Thr Leu Trp Ser Leu Thr Ile Val
20 25 30
Trp Arg Tyr Met Asp Phe Ser Ala Pro Val Arg Ser Val Ser Thr Gly
35 40 45
His Leu Lys Ser Pro Tyr Arg Gly Leu Ser Gln Cys Leu Arg Pro Ile
50 55 60
Arg Gly Val Ser Phe Gln Pro Ser Val Leu Glu Ala Ile Cys Met Gly
65 70 75 80
Ser Gln Ser Leu Pro Arg Glu Trp Gln Lys Leu Ala Gly Ala Trp Arg
85 90 95
Gly Leu Cys Leu Phe His Cys Phe Gln Gly Gly Leu Pro Gln Gly Arg
100 105 110
Asn Trp Gly Gly
115

<210> 863
<211> 327
<212> DNA
<213> Homo sapiens

<400> 863
tccggatcga cccggacgaa ttccacggtc cagccattga cttccaaatg ctctttgaca
60
tacgccgtga catgttcaat gtccaactta cgcatgtcca cccgctcacc ggtctcattg
120
agtttgagct gcgagtagac gttgcggtag ttctcgttga ccgactgctc atacgagatg
180
tgcagaagca tcggtttgcg gccatcctcg gacggcattg gcttgttgta catggccgct
240
tggcggaaca tgttcagggt aaagcccgac ttgaagttgt gcgacagggc agaaacacac
300
agcatttctg accggcgatg acccatn
327

<210> 864
<211> 108
<212> PRT
<213> Homo sapiens

<400> 864
Met Gly His Arg Arg Ser Glu Met Leu Cys Val Ser Ala Leu Ser His
1 5 10 15
Asn Phe Lys Ser Gly Phe Thr Leu Asn Met Phe Arg Gln Ala Ala Met
20 25 30
Tyr Asn Lys Pro Met Pro Ser Glu Asp Gly Arg Lys Pro Met Leu Leu
35 40 45
His Ile Ser Tyr Glu Gln Ser Val Asn Glu Asn Tyr Arg Asn Val Tyr
50 55 60
Ser Gln Leu Lys Leu Asn Glu Thr Gly Glu Arg Val Asp Met Arg Lys
65 70 75 80
Leu Asp Ile Glu His Val Thr Ala Tyr Val Lys Glu His Leu Glu Val

85 90 95
Asn Gly Trp Thr Val Glu Phe Val Arg Val Asp Pro
100 105

<210> 865
<211> 729
<212> DNA
<213> Homo sapiens

<400> 865
acgcgtcatc ctcattcaag aggcccagga ggagcaccac cctccgcata ttgcgcgtgc
60
agctctcgtt ctggtctctg agcatgccca cggcgctctg cacacagctt ctcagcagcc
120
tggtggtgtc caggatcgac acatcactgc ctccgagttc agaggtttcc tttcccacct
180
tctcagaact ttctgtttcc atggcctcct ctgccacctc tgccacctcc cctgatgtgc
240
tggcctccgt ctccatcgcc tcctcatggc cgtcttccgc ccggtgttcc aagcccagct
300
caggcaagtc tccgggcgcg aacagctggc tgatggtgac atgctgcagc ctggtcacat
360
cagaaaccat gagggtggat ctccggaggt catcgatgtg gacagactgc cacagccctc
420
cgtggaagcc cacataggct gttcctcttc ccacccggga cagttttgtg atgaaataga
480
cgaagatacg gtcctcattt tctcgtattt tgttgatttc atttataaca gaatacttag
540
ctgaggcaat gagctgggcg ctacggattc catcttcaaa atctgtctga aaaatgagga
600
ttttacattt ggctgtattc gttaaacagt ttcggacttc tttgaggaat gagtactcgg
660
tgtcaaactg ctgcagccac aggagtgtgg gtttcggagc cctgcctgtg acctctgatt
720
ctaaaattt
729

<210> 866
<211> 83
<212> PRT
<213> Homo sapiens

<400> 866
Ala Cys Pro Arg Arg Ser Ala His Ser Phe Ser Ala Ala Trp Trp Cys
1 5 10 15
Pro Gly Ser Thr His His Cys Leu Arg Val Gln Arg Phe Pro Phe Pro
20 25 30
Pro Ser Gln Asn Phe Leu Phe Pro Trp Pro Pro Leu Pro Pro Leu Pro
35 40 45
Pro Pro Leu Met Cys Trp Pro Pro Ser Pro Ser Pro Pro His Gly Arg
50 55 60
Leu Pro Pro Gly Val Pro Ser Pro Ala Gln Ala Ser Leu Arg Ala Arg
65 70 75 80
Thr Ala Gly

<210> 867
<211> 640
<212> DNA
<213> Homo sapiens

<400> 867
nntccggaac atcaagatcc aggcgcagaa gaccgtcaga agctgcactg gccacctcct
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tcaggtggac tctcgttggt ggccggcgtc gctggccccc tcgcacccgg tcccgtgtca
120
catgctccag ggcgcagctc ttgtccacct ttacctcatc gaaagccttg tttttgcctc
180
ggttaatccc ttcattgagg gctttgatcc aggattcctt ctcctccccg gtgggtgcct
240
ggaatttgat gtcgctgacc ttgttccctg gggatcgcag caggataaag cggtgttttc
300
gcttgaggag ggcacgaagg tcctggcact tctcatagct gcccagctcc acagtctcca
360
cacacttctg atcatcctca ttctcataga ccagcagctg ggcctggcag aggagcagat
420
atcggtcttt ccagaaaccc aggaggcccc cactgctctt cttgatccag ccagccttgt
480
ccaccatctg tgctccccga ggcttctcac cggcttcctt cacaccctcc tcctccatgg
540
cgagtccgcc gaggtcccgc cgctccgcca ctcgcttcca gcgccgcgcg ggctctgcca
600
ccgcgtctac gcccggccag gcggcgactc tccgcgttct
640

<210> 868
<211> 52
<212> PRT
<213> Homo sapiens

<400> 868
Gly Gly His Glu Gly Pro Gly Thr Ser His Ser Cys Pro Ala Pro Gln
1 5 10 15
Ser Pro His Thr Ser Asp His Pro His Ser His Arg Pro Ala Ala Gly
20 25 30
Pro Gly Arg Gly Ala Asp Ile Gly Leu Ser Arg Asn Pro Gly Gly Pro
35 40 45
His Cys Ser Ser
50

<210> 869
<211> 321
<212> DNA
<213> Homo sapiens

<400> 869
ngggtgatgc tgctcgcggc attgagcatc tttgtgctca gcgcgctgtt tatcgacaac
60

ttcctgtcgc cgctgaatat gcgcgggctg ggcctggcga tttcgacggt gggcatcgct
120
gcgtgcacca tgctgttctg cctggcgtcg gggcatttcg acttgtcggt gggctcggtg
180
atcgcctgtg ccggtgtggt cgcggggatt gtgattcgtg acaccgatag cgtggcactc
240
ggcgtgtccg ctgcgttggc catgggcctg gtagtggggc tgatcaacgg catcgtgatc
300
gccaagctgc gcatcaacgc g
321

<210> 870
<211> 107
<212> PRT
<213> Homo sapiens

<400> 870
Xaa Val Met Leu Leu Ala Ala Leu Ser Ile Phe Val Leu Ser Ala Leu
 1   5   10   15
Phe Ile Asp Asn Phe Leu Ser Pro Leu Asn Met Arg Gly Leu Gly Leu
            20   25   30
Ala Ile Ser Thr Val Gly Ile Ala Ala Cys Thr Met Leu Phe Cys Leu
        35   40   45
Ala Ser Gly His Phe Asp Leu Ser Val Gly Ser Val Ile Ala Cys Ala
    50   55   60
Gly Val Val Ala Gly Ile Val Ile Arg Asp Thr Asp Ser Val Ala Leu
65   70   75   80
Gly Val Ser Ala Ala Leu Ala Met Gly Leu Val Val Gly Leu Ile Asn
                85   90   95
Gly Ile Val Ile Ala Lys Leu Arg Ile Asn Ala
            100   105

<210> 871
<211> 320
<212> DNA
<213> Homo sapiens

<400> 871
agatcttcag agtcctcgtc ttttaaatgg gggtaacagc agcaagtcct cagaggtgtc
60
ctgagcctca aaacacatcc tggtttgtaa cgtccgcagc ctcagcaggg gctaggcaca
120
gaacaagcat tcaggacctg gaaggtacca gcgacacctg gtcctccctt cccaggcaca
180
aggcagcccc tctccattca agctctgccc cagcccagca aagagagggg tcctcagcca
240
ctgcccccac cactaccaca atcatactca cctctcctgg tccatacgtg acaaaggacc
300
tgccacggcc agggagacaa
320

<210> 872
<211> 98
<212> PRT

<213> Homo sapiens

<400> 872
Met Gly Val Thr Ala Ala Ser Pro Gln Arg Cys Pro Glu Pro Gln Asn
1 5 10 15
Thr Ser Trp Phe Val Thr Ser Ala Ala Ser Ala Gly Ala Arg His Arg
20 25 30
Thr Ser Ile Gln Asp Leu Glu Gly Thr Ser Asp Thr Trp Ser Ser Leu
35 40 45
Pro Arg His Lys Ala Ala Pro Leu His Ser Ser Ser Ala Pro Ala Gln
50 55 60
Gln Arg Glu Gly Ser Ser Ala Thr Ala Pro Thr Thr Thr Thr Ile Ile
65 70 75 80
Leu Thr Ser Pro Gly Pro Tyr Val Thr Lys Asp Leu Pro Arg Pro Gly
85 90 95
Arg Gln

<210> 873
<211> 363
<212> DNA
<213> Homo sapiens

<400> 873
nttgtttagc atcgtttttt acgggtgtat cagcgcgttt agcagcgttt ttagcggatg
60
catcagcatg ttttgcgtca cgttttacaa ctgtgctacc gtgtttagca tcatttttga
120
cggaggtatc aatacgttta gcatcgtttt taacagatgt atcaacacgg ggttcatccg
180
ctttagcaga atccccagct ctagtagcca ctttagatac ttcagatttt atatgagtcg
240
cagttgtttc agcgtgagcc atgctgaatg tagaaccaag ggccaatgta attgctaaag
300
acaaagataa tttatttagt ttcatgttcg gagagaagtg tgcgaattcg gcgatacagt
360
cag
363

<210> 874
<211> 108
<212> PRT
<213> Homo sapiens

<400> 874
Met Lys Leu Asn Lys Leu Ser Leu Ser Leu Ala Ile Thr Leu Ala Leu
1 5 10 15
Gly Ser Thr Phe Ser Met Ala His Ala Glu Thr Thr Ala Thr His Ile
20 25 30
Lys Ser Glu Val Ser Lys Val Ala Thr Arg Ala Gly Asp Ser Ala Lys
35 40 45
Ala Asp Glu Pro Arg Val Asp Thr Ser Val Lys Asn Asp Ala Lys Arg
50 55 60
Ile Asp Thr Ser Val Lys Asn Asp Ala Lys His Gly Ser Thr Val Val

65 70 75 80
Lys Arg Asp Ala Lys His Ala Asp Ala Ser Ala Lys Asn Ala Ala Lys
85 90 95
Arg Ala Asp Thr Pro Val Lys Asn Asp Ala Lys Gln
100 105

<210> 875
<211> 355
<212> DNA
<213> Homo sapiens

<400> 875
acgcgtgaag gggaccctaa ctcgtctggg ctgtaggatg cgggcgaggc ttccacaaac
60
tcactgtctg ggggagaaga aaagcagaaa acaactcgaa tcgctaccat tcaggacgaa
120
cccgccaagc accagctcaa gcgcaggtcc ccgggaaaaa gcgcgggctt ctctctccca
180
gcgctcagaa tccctgagcc ggaggccccg cgggattcag accgccagat ccccagggag
240
tgacaaatcg ccgcagaaac ttgggggaca actcggccct ggcaccgcgc ggcttccagg
300
cgcgggcagg cgcgcgccaa ctttccccgc gtgccacccc gcggctcccc cggcn
355

<210> 876
<211> 106
<212> PRT
<213> Homo sapiens

<400> 876
Met Arg Ala Arg Leu Pro Gln Thr His Cys Leu Gly Glu Lys Lys Ser
1 5 10 15
Arg Lys Gln Leu Glu Ser Leu Pro Phe Arg Thr Asn Pro Pro Ser Thr
20 25 30
Ser Ser Ser Ala Gly Pro Arg Glu Lys Ala Arg Ala Ser Leu Ser Gln
35 40 45
Arg Ser Glu Ser Leu Ser Arg Arg Pro Arg Gly Ile Gln Thr Ala Arg
50 55 60
Ser Pro Gly Ser Asp Lys Ser Pro Gln Lys Leu Gly Gly Gln Leu Gly
65 70 75 80
Pro Gly Thr Ala Arg Leu Pro Gly Ala Gly Arg Arg Ala Pro Thr Phe
85 90 95
Pro Ala Cys His Pro Ala Ala Pro Pro Ala
100 105

<210> 877
<211> 487
<212> DNA
<213> Homo sapiens

<400> 877
acgcgtactt tgggtaatga actgacgacc gctgagatcg actgccttta tctgtgttac
60

caatccacct atgctaaacg tggtcagcaa ggttatctca cacgagaatt ctttggtttg
120
ttggccaata ccatgggaga tcaaatcctt ttagtacagg cgtacagaga aggcgaagcg
180
atcgccgcgt cgtggtgttt ctttgatgat cattcactat atgggcgtta ttggggctgt
240
atggaagaag tggattgcct gcattttgaa gcttgttatt accaaggaat cgagttttgt
300
ctcgaaaaag ggttacagca tttcgatccg ggtacacaag gggaacacaa gattgcgcgc
360
ggctttgaac ctgtttttag ccacagcgtg cattacattg ctcatcaagg ttttcgtgaa
420
gcgattggga atttctgtga ggaagaagcg caagctgtgc gcgagtatca tcaagatacc
480
cacgcgt
487

<210> 878
<211> 162
<212> PRT
<213> Homo sapiens

<400> 878
Thr Arg Thr Leu Gly Asn Glu Leu Thr Thr Ala Glu Ile Asp Cys Leu
1 5 10 15
Tyr Leu Cys Tyr Gln Ser Thr Tyr Ala Lys Arg Gly Gln Gln Gly Tyr
20 25 30
Leu Thr Arg Glu Phe Phe Gly Leu Leu Ala Asn Thr Met Gly Asp Gln
35 40 45
Ile Leu Leu Val Gln Ala Tyr Arg Glu Gly Glu Ala Ile Ala Ala Ser
50 55 60
Trp Cys Phe Phe Asp Asp His Ser Leu Tyr Gly Arg Tyr Trp Gly Cys
65 70 75 80
Met Glu Glu Val Asp Cys Leu His Phe Glu Ala Cys Tyr Tyr Gln Gly
85 90 95
Ile Glu Phe Cys Leu Glu Lys Gly Leu Gln His Phe Asp Pro Gly Thr
100 105 110
Gln Gly Glu His Lys Ile Ala Arg Gly Phe Glu Pro Val Phe Ser His
115 120 125
Ser Val His Tyr Ile Ala His Gln Gly Phe Arg Glu Ala Ile Gly Asn
130 135 140
Phe Cys Glu Glu Glu Ala Gln Ala Val Arg Glu Tyr His Gln Asp Thr
145 150 155 160
His Ala

<210> 879
<211> 993
<212> DNA
<213> Homo sapiens

<400> 879
nncttagcat ttaagccaac gaggcagcta atgtcctctg aacagcaaag gaaattcagc
60

agccagtcca gtagggctct gacccctcct tcctacagta ctgctaaaaa ttcattggga
120
tcaagatcca gtgaatcctt tgggaagtac acatcgccag taatgagtga gcatggggac
180
gagcacaggc agctcctctc tcacccaatg caaggccctg gactccgtgc agctacctca
240
tccaaccact ctgtggacga gcaactgaag aatactgaca cgcacctcat cgacctggta
300
accaatgaga ttatcaccca aggacctcca gtggactgga atgacattgc tggtctcgac
360
ctggtgaagg ctgtcattaa agaggaggtt ttatggccag tgttgaggtc agacgcgttc
420
agtggactga cggccttacc tcggagcatc cttttatttg gacctcgggg gacaggcaaa
480
acattattgg gcagatgcat cgctagtcag ctgggggcca catttttcaa aattgccggt
540
tctggactag tcgccaaggg gttaggagaa gcagagaaaa ttatccatgc ctcttttctt
600
gtggccaggt gtcgccagcc ctcggtgatt tttgttagtg acattgacat gcttctctcc
660
tctcaagtga atgaggaaca tagtccagtc agtcggatga gaaccgaatt tctgatgcaa
720
ctggacactg tactaacttc ggctgaggac caaatcgtag taatttgtgc caccagtaaa
780
ccagaagaaa tagatgaatc ccttcggagg tacttcatga aacgactttt aatcccactt
840
cctgacagca cagcgaggca ccagataata gtacaactgc tctcacagca caattactgt
900
ctcaatgaca aggagtttgc actgctcgtc cagcgcacag aaggcttttc tggactagat
960
gtggctcatt tgtgtcagga agcagtggtg ggc
993

<210> 880
<211> 331
<212> PRT
<213> Homo sapiens

<400> 880
Xaa Leu Ala Phe Lys Pro Thr Arg Gln Leu Met Ser Ser Glu Gln Gln
 1   5   10   15
Arg Lys Phe Ser Ser Gln Ser Ser Arg Ala Leu Thr Pro Pro Ser Tyr
            20   25   30
Ser Thr Ala Lys Asn Ser Leu Gly Ser Arg Ser Ser Glu Ser Phe Gly
        35   40   45
Lys Tyr Thr Ser Pro Val Met Ser Glu His Gly Asp Glu His Arg Gln
    50   55   60
Leu Leu Ser His Pro Met Gln Gly Pro Gly Leu Arg Ala Ala Thr Ser
65   70   75   80
Ser Asn His Ser Val Asp Glu Gln Leu Lys Asn Thr Asp Thr His Leu
                85   90   95
Ile Asp Leu Val Thr Asn Glu Ile Ile Thr Gln Gly Pro Pro Val Asp
            100   105   110
Trp Asn Asp Ile Ala Gly Leu Asp Leu Val Lys Ala Val Ile Lys Glu

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        115                 120                 125
Glu Val Leu Trp Pro Val Leu Arg Ser Asp Ala Phe Ser Gly Leu Thr
    130                 135                 140
Ala Leu Pro Arg Ser Ile Leu Leu Phe Gly Pro Arg Gly Thr Gly Lys
145                 150                 155                 160
Thr Leu Leu Gly Arg Cys Ile Ala Ser Gln Leu Gly Ala Thr Phe Phe
                165                 170                 175
Lys Ile Ala Gly Ser Gly Leu Val Ala Lys Gly Leu Gly Glu Ala Glu
            180                 185                 190
Lys Ile Ile His Ala Ser Phe Leu Val Ala Arg Cys Arg Gln Pro Ser
        195                 200                 205
Val Ile Phe Val Ser Asp Ile Asp Met Leu Leu Ser Ser Gln Val Asn
    210                 215                 220
Glu Glu His Ser Pro Val Ser Arg Met Arg Thr Glu Phe Leu Met Gln
225                 230                 235                 240
Leu Asp Thr Val Leu Thr Ser Ala Glu Asp Gln Ile Val Val Ile Cys
                245                 250                 255
Ala Thr Ser Lys Pro Glu Glu Ile Asp Glu Ser Leu Arg Arg Tyr Phe
            260                 265                 270
Met Lys Arg Leu Leu Ile Pro Leu Pro Asp Ser Thr Ala Arg His Gln
        275                 280                 285
Ile Ile Val Gln Leu Leu Ser Gln His Asn Tyr Cys Leu Asn Asp Lys
    290                 295                 300
Glu Phe Ala Leu Leu Val Gln Arg Thr Glu Gly Phe Ser Gly Leu Asp
305                 310                 315                 320
Val Ala His Leu Cys Gln Glu Ala Val Val Gly
                325                 330
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<210> 881
<211> 313
<212> DNA
<213> Homo sapiens

<400> 881
cgcgtgagcg tcgacaatgc tccaggaacc ggtgtgtatg aggccgggga ttctaccggt
60
cgtggtttgc agggcatgcg tgagcgcgcc cgtatccatg gcggcaccgc gcgctggggc
120
gactcgcagt attatgaagg cggtttcaac gtcacggtgg agattccaac atgagcggcc
180
aaaggatgaa catggacacg acgcgcccca atcacggtcg gggcttgccg acgatcagcc
240
ggctgggtgc gcaccggttt tgccatggtg ctggattcgc aggacgacat cacggtggcc
300
tggcaagccg acn
313

<210> 882
<211> 57
<212> PRT
<213> Homo sapiens

<400> 882
Arg Val Ser Val Asp Asn Ala Pro Gly Thr Gly Val Tyr Glu Ala Gly

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 1               5                  10                  15
Asp Ser Thr Gly Arg Gly Leu Gln Gly Met Arg Glu Arg Ala Arg Ile
            20                  25                  30
His Gly Gly Thr Ala Arg Trp Gly Asp Ser Gln Tyr Tyr Glu Gly Gly
        35                  40                  45
Phe Asn Val Thr Val Glu Ile Pro Thr
    50                  55
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<210> 883
<211> 576
<212> DNA
<213> Homo sapiens

<400> 883
naattaagat ctggggtccc agtgtcattg gtgaaggcct tgggattcga ggcagctgag
60
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ggaaaacact cccatctttt tcaagcctac cttttagcag aagaggcaga tacacaagcc
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ctaaagatgt aacatcaggc tgagtggagg aaggctgaga agaaaaataa agcaggctca
240
ggaggagaga gtgatgtcag gatgcccttg tgcttactcc agcctccttg tgaaaaccca
300
gctctcctgt ctcccagtga agacttggat ggcagccatc agggaaggct gggtcccagc
360
tgggagtatg ggtgtgagct ctatagacca tccctctctg caatcaataa acacttgcct
420
gtgaaagagg cccaagccac catccgcatg gacaccagtg caagtggccc cacccgcctg
480
gtcctcagtg actgtgccac cagccatggg agcctgcgca tccaactgct gcataagctc
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576

<210> 884
<211> 105
<212> PRT
<213> Homo sapiens

<400> 884
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Met Pro Leu Cys Leu Leu Gln Pro Pro Cys Glu Asn Pro Ala Leu Leu
 1               5                  10                  15
Ser Pro Ser Glu Asp Leu Asp Gly Ser His Gln Gly Arg Leu Gly Pro
            20                  25                  30
Ser Trp Glu Tyr Gly Cys Glu Leu Tyr Arg Pro Ser Leu Ser Ala Ile
        35                  40                  45
Asn Lys His Leu Pro Val Lys Glu Ala Gln Ala Thr Ile Arg Met Asp
    50                  55                  60
Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys Ala Thr
65                  70                  75                  80
Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser Phe Leu
                85                  90                  95
Val Asn Ala Leu Ala Lys Gln Val Met
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100 105

<210> 885
<211> 370
<212> DNA
<213> Homo sapiens

<400> 885
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ggtgaggcga tgctgacgaa cgacacaccg gtgacttggg atggcgggaa agtacggggc
120
aggcgggtgt cgcgcctcgg tgcgatcgag ttgtcgtcga ccccggtccg cccagatccg
180
gtacgggctc gccacgtggc gctggaagca gtgaggtctg ggggacttga cgtagcgagc
240
ctgacgaaga acggtgaatc tttgcgacgc cgtcttgccc tggcccatcg ggtgtttggt
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370

<210> 886
<211> 123
<212> PRT
<213> Homo sapiens

<400> 886
Thr Ser Gly Ala Leu Ile Arg Ala Ala Val Pro Leu Ser Glu Ser Ala
1 5 10 15
Ala Leu Glu Ser Gly Glu Ala Met Leu Thr Asn Asp Thr Pro Val Thr
20 25 30
Trp Asp Gly Gly Lys Val Arg Gly Arg Arg Val Ser Arg Leu Gly Ala
35 40 45
Ile Glu Leu Ser Ser Thr Pro Val Arg Pro Asp Pro Val Arg Ala Arg
50 55 60
His Val Ala Leu Glu Ala Val Arg Ser Gly Gly Leu Asp Val Ala Ser
65 70 75 80
Leu Thr Lys Asn Gly Glu Ser Leu Arg Arg Arg Leu Ala Leu Ala His
85 90 95
Arg Val Phe Gly Asp Pro Trp Pro Asp Val Ser Asp Glu Ala Leu Leu
100 105 110
Ala Cys Ala Glu Glu Trp Leu Asp Leu Asp Ala
115 120

<210> 887
<211> 447
<212> DNA
<213> Homo sapiens

<400> 887
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attatctccg gctgcctgaa ccagcttggt aaacgctatc cgcatctgac cggcgaaggc
120
caactgatgc caaaccgtgc taatgctgat accacggctt cccaaccggc gttctccggt
180
aaagcggacg tgaccaccat tgcctccggc gcgttgctgg ccgtgctgct ttacatggtg
240
ggtaggttgg ttcacaagtt gattggcctg cctgctccgg ttggcatgtt gtttgtggcg
300
gtgctggtca aactgtgcaa cggcgcttct ccccgcctgc tcgaaggctc gcaggtggtt
360
tacaaattct tccagacctc cgtcacctat ccgattctgt tcgccgttgg cgtggcgatt
420
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447

<210> 888
<211> 149
<212> PRT
<213> Homo sapiens

<400> 888
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Leu Thr Ala Ile Ile Ile Ser Gly Cys Leu Asn Gln Leu Gly Lys Arg
            20   25   30
Tyr Pro His Leu Thr Gly Glu Gly Gln Leu Met Pro Asn Arg Ala Asn
        35   40   45
Ala Asp Thr Thr Ala Ser Gln Pro Ala Phe Ser Gly Lys Ala Asp Val
    50   55   60
Thr Thr Ile Ala Ser Gly Ala Leu Leu Ala Val Leu Leu Tyr Met Val
65   70   75   80
Gly Arg Leu Val His Lys Leu Ile Gly Leu Pro Ala Pro Val Gly Met
                85   90   95
Leu Phe Val Ala Val Leu Val Lys Leu Cys Asn Gly Ala Ser Pro Arg
            100   105   110
Leu Leu Glu Gly Ser Gln Val Val Tyr Lys Phe Phe Gln Thr Ser Val
        115   120   125
Thr Tyr Pro Ile Leu Phe Ala Val Gly Val Ala Ile Thr Pro Trp Gln
    130   135   140
Glu Leu Val Asn Ala
145

<210> 889
<211> 450
<212> DNA
<213> Homo sapiens

<400> 889
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60
atctcccctc agtaaaattc aggatgccca gtgaagtttg aatgtcagat aaacaatttg
120
ttagtataag gatgtaccta gcattgaaat gatgccttgt aatttactaa atctgcaact
180

atgcagcctt atttcatggc gggcagtggc ggtgatccca ggtttcaggg gcggggaagg
240
gtgctgggga gatcctgagg tcaggaaccc gtacacctct gcttctgccc tctcttccct
300
gtgccggcca caaggcaatg actcctgtgt gggtgcagag gcagaaatgg gtctggaagg
360
ggattcccag tgtctggcaa gttctggtaa attctgcatt ggaggttctc tctgtagtaa
420
ggggagttgg cctggccgcc cttcacgcgt
450

<210> 890
<211> 100
<212> PRT
<213> Homo sapiens

<400> 890
Met Met Pro Cys Asn Leu Leu Asn Leu Gln Leu Cys Ser Leu Ile Ser
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Trp Arg Ala Val Ala Val Ile Pro Gly Phe Arg Gly Gly Glu Gly Cys
            20   25   30
Trp Gly Asp Pro Glu Val Arg Asn Pro Tyr Thr Ser Ala Ser Ala Leu
        35   40   45
Ser Ser Leu Cys Arg Pro Gln Gly Asn Asp Ser Cys Val Gly Ala Glu
    50   55   60
Ala Glu Met Gly Leu Glu Gly Asp Ser Gln Cys Leu Ala Ser Ser Gly
65   70   75   80
Lys Phe Cys Ile Gly Gly Ser Leu Cys Ser Lys Gly Ser Trp Pro Gly
                85   90   95
Arg Pro Ser Arg
            100

<210> 891
<211> 318
<212> DNA
<213> Homo sapiens

<400> 891
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ctggatccct tccacactga caacaccagt gagcacagtg acctggccac agatggccag
120
actaacggcc cggctgatag cgggactggc acccactctg agcagggaaa ctccgacata
180
tctagccccg tcagctctag tgacgctgct aacaccaccg acagcactgc tggcaatacc
240
ggtgaaggta ctgccgcgaa tatgcctggt gacatggctc attcttcgac ggctacccac
300
ccctatgcaa gcaccggt
318

<210> 892
<211> 106
<212> PRT

<213> Homo sapiens

<400> 892
Xaa Thr Val Pro Val Leu Asp Pro Arg Glu Asp Phe Ala Asp Cys Met
1 5 10 15
His Ile Asp Val Leu Asp Pro Phe His Thr Asp Asn Thr Ser Glu His
20 25 30
Ser Asp Leu Ala Thr Asp Gly Gln Thr Asn Gly Pro Ala Asp Ser Gly
35 40 45
Thr Gly Thr His Ser Glu Gln Gly Asn Ser Asp Ile Ser Ser Pro Val
50 55 60
Ser Ser Ser Asp Ala Ala Asn Thr Thr Asp Ser Thr Ala Gly Asn Thr
65 70 75 80
Gly Glu Gly Thr Ala Ala Asn Met Pro Gly Asp Met Ala His Ser Ser
85 90 95
Thr Ala Thr His Pro Tyr Ala Ser Thr Gly
100 105

<210> 893
<211> 510
<212> DNA
<213> Homo sapiens

<400> 893
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aagtcacaga aaaagcctgt ggaaaacagg atgaaggagg acaaaagcag catcagggaa
120
gcaatcagca aagccaagag tacagcaaat ataaagacag aacaggaagg tgaggcatct
180
gagaagagct tgcatctgag cccacagcat atcacacacc agactatgcc tataggacag
240
agaggcagtg agcaaggcaa acgtgtggag aacattaatg gaacctccta ccctagtcta
300
cagcagaaaa ccaatgctgt taagaaatta cataaatgtg atgaatgtgg gaaatccttc
360
aaatataatt cccgccttgt tcaacataaa attatgcaca ctggggaaaa gcgctatgaa
420
tgtgatgact gtggagggac tttccggagc agctcgagcc ttcgggtcca caaacggatc
480
cacactgggt acggagagaa gacaacgcgt
510

<210> 894
<211> 170
<212> PRT
<213> Homo sapiens

<400> 894
Xaa Asp Pro Ile Pro Glu Ser Lys Val Gly Asp Thr Cys Val Trp Asp
1 5 10 15
Ser Lys Val Glu Lys Ser Gln Lys Lys Pro Val Glu Asn Arg Met Lys
20 25 30
Glu Asp Lys Ser Ser Ile Arg Glu Ala Ile Ser Lys Ala Lys Ser Thr

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        35                  40                  45
Ala Asn Ile Lys Thr Glu Gln Glu Gly Glu Ala Ser Glu Lys Ser Leu
    50                  55                  60
His Leu Ser Pro Gln His Ile Thr His Gln Thr Met Pro Ile Gly Gln
65                  70                  75                  80
Arg Gly Ser Glu Gln Gly Lys Arg Val Glu Asn Ile Asn Gly Thr Ser
                85                  90                  95
Tyr Pro Ser Leu Gln Gln Lys Thr Asn Ala Val Lys Lys Leu His Lys
            100                 105                 110
Cys Asp Glu Cys Gly Lys Ser Phe Lys Tyr Asn Ser Arg Leu Val Gln
        115                 120                 125
His Lys Ile Met His Thr Gly Glu Lys Arg Tyr Glu Cys Asp Asp Cys
    130                 135                 140
Gly Gly Thr Phe Arg Ser Ser Ser Ser Leu Arg Val His Lys Arg Ile
145                 150                 155                 160
His Thr Gly Tyr Gly Glu Lys Thr Thr Arg
                165                 170
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<210> 895
<211> 1119
<212> DNA
<213> Homo sapiens

<400> 895
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120
ccgcaccgga atcgggcttt tcctggggct gccttcctaa atgcggtgtc ctccttgtcg
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240
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300
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360
cgggaggcac atttcccgcc cgcggtgccg tgcggaattg tcgacggtga cccgaaagcg
420
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480
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540
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600
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660
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720
acgcttaccg ccttggtagc cgatccccgt cacgaggtag ctgccgtcct gacgcgtccg
780
gatgcagcag taggacggca ccgtactcca cgtccatgcc cggtcgccaa ggctgccgag
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gaactcggta tccccgccat taaggcgacc agcgtgaagt ccggcgaggg tcacgatgcc
900

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960
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tggcgcggcg ctgctcccat acaacgggcc atcatggcgg gggatgagga gacgggcgct
1080
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1119

<210> 896
<211> 147
<212> PRT
<213> Homo sapiens

<400> 896
Val Arg Leu Leu Phe Ala Gly Thr Pro Asp Val Ala Val Pro Thr Leu
1 5 10 15
Thr Ala Leu Val Ala Asp Pro Arg His Glu Val Ala Ala Val Leu Thr
20 25 30
Arg Pro Asp Ala Ala Val Gly Arg His Arg Thr Pro Arg Pro Cys Pro
35 40 45
Val Ala Lys Ala Ala Glu Glu Leu Gly Ile Pro Ala Ile Lys Ala Thr
50 55 60
Ser Val Lys Ser Gly Glu Gly His Asp Ala Val Thr Ser Leu Asp Val
65 70 75 80
Asp Val Ala Val Val Val Ala Tyr Gly Gly Leu Ile Pro Ala Asp Leu
85 90 95
Leu Ala Val Pro Arg His Gly Trp Ile Asn Leu His Phe Ser Leu Leu
100 105 110
Pro Arg Trp Arg Gly Ala Ala Pro Ile Gln Arg Ala Ile Met Ala Gly
115 120 125
Asp Glu Glu Thr Gly Ala Cys Val Phe Gln Leu Val Glu Ser Leu Asp
130 135 140
Ala Gly Pro
145

<210> 897
<211> 384
<212> DNA
<213> Homo sapiens

<400> 897
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gacgactacc tcgtccagct gtcgaaggaa gggctcgaga cccgtctcgc gcagctgtat
120
ccggtcgaag cccgacgcga cgcgcagcgc gacacctact acaagcgcct cgaattcgag
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240
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ctggtcgcgt atgcgctcgg cattaccgat ctcgaagtac tgcgctacga cctgctgttc
360

gagcgcttcc tgaacccgga acgc
384

<210> 898
<211> 128
<212> PRT
<213> Homo sapiens

<400> 898
Glu Leu Glu Ala Gly Lys Pro Glu Val Pro Leu Phe Pro Thr Pro Asp
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Gly Met Ser Leu Asp Asp Tyr Leu Val Gln Leu Ser Lys Glu Gly Leu
20 25 30
Glu Thr Arg Leu Ala Gln Leu Tyr Pro Val Glu Ala Arg Arg Asp Ala
35 40 45
Gln Arg Asp Thr Tyr Tyr Lys Arg Leu Glu Phe Glu Cys Gly Thr Ile
50 55 60
Thr Lys Met Gly Phe Pro Gly Tyr Phe Leu Ile Val Ala Asp Phe Ile
65 70 75 80
Asn Trp Ala Lys Asn Asn Gly Val Pro Val Gly Pro Gly Arg Gly Ser
85 90 95
Gly Ala Gly Ser Leu Val Ala Tyr Ala Leu Gly Ile Thr Asp Leu Glu
100 105 110
Val Leu Arg Tyr Asp Leu Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg
115 120 125

<210> 899
<211> 6171
<212> DNA
<213> Homo sapiens

<400> 899
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120
aatctcctga cggatcagtg catacctgtc ctggtagggc acctgcacct gcgaatcttg
180
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300
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660

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720
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4680
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4920
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5160
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5280
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5400
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5520

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5640
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5760
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5820
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5940
tggatgtcat ccagacagtg ggctcatatc ttacggtttt gtgcaatcat tgtcgtattg
6000
tagtcttaag actcattata gtgtattttt gatatttttg aaatgtgtta aatttttaa
6060
ttcagtaata tgagccagag catgttgcag caaatctatt gtttgtaaaa ataacaataa
6120
caataataaa taaaataaag tggaatcttt ttcatggctt tgttttaaaa a
6171

<210> 900
<211> 734
<212> PRT
<213> Homo sapiens

<400> 900
Phe Ser Lys Ala Leu Asn Leu Arg Tyr Leu Asn Ala Ser Ala Asn Ser
1 5 10 15
Leu Glu Ser Leu Pro Ser Ala Cys Thr Gly Glu Glu Ser Leu Ser Met
20 25 30
Leu Gln Leu Leu Tyr Leu Thr Asn Asn Leu Leu Thr Asp Gln Cys Ile
35 40 45
Pro Val Leu Val Gly His Leu His Leu Arg Ile Leu His Leu Ala Asn
50 55 60
Asn Gln Leu Gln Thr Phe Pro Ala Ser Lys Leu Asn Lys Leu Glu Gln
65 70 75 80
Leu Glu Glu Leu Asn Leu Ser Gly Asn Lys Leu Lys Thr Ile Pro Thr
85 90 95
Thr Ile Ala Asn Cys Lys Arg Leu His Thr Leu Val Ala His Ser Asn
100 105 110
Asn Ile Ser Ile Phe Pro Glu Ile Leu Gln Leu Pro Gln Ile Gln Phe
115 120 125
Val Asp Leu Ser Cys Asn Asp Leu Thr Glu Ile Leu Ile Pro Glu Ala
130 135 140
Leu Pro Ala Thr Leu Gln Asp Leu Asp Leu Thr Gly Asn Thr Asn Leu
145 150 155 160
Val Leu Glu His Lys Thr Leu Asp Ile Phe Ser His Ile Thr Thr Leu
165 170 175
Lys Ile Asp Gln Lys Pro Leu Pro Thr Thr Asp Ser Thr Val Thr Ser
180 185 190
Thr Phe Trp Ser His Gly Leu Ala Glu Met Ala Gly Gln Arg Asn Lys

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        195                 200                 205
Leu Cys Val Ser Ala Leu Ala Met Asp Ser Phe Ala Glu Gly Val Gly
    210                 215                 220
Ala Val Tyr Gly Met Phe Asp Gly Asp Arg Asn Glu Glu Leu Pro Arg
225                 230                 235                 240
Leu Leu Gln Cys Thr Met Ala Asp Val Leu Leu Glu Glu Val Gln Gln
                245                 250                 255
Ser Thr Asn Asp Thr Val Phe Met Ala Asn Thr Phe Leu Val Ser His
            260                 265                 270
Arg Lys Leu Gly Met Ala Gly Gln Lys Leu Gly Ser Ser Ala Leu Leu
        275                 280                 285
Cys Tyr Ile Arg Pro Asp Thr Ala Asp Pro Ala Ser Ser Phe Ser Leu
    290                 295                 300
Thr Val Ala Asn Val Gly Thr Cys Gln Ala Val Leu Cys Arg Gly Gly
305                 310                 315                 320
Lys Pro Val Pro Leu Ser Lys Val Phe Ser Leu Glu Gln Asp Pro Glu
                325                 330                 335
Glu Ala Gln Arg Val Lys Asp Gln Lys Ala Ile Ile Thr Glu Asp Asn
            340                 345                 350
Lys Val Asn Gly Val Thr Cys Cys Thr Arg Met Leu Gly Cys Thr Tyr
        355                 360                 365
Leu Tyr Pro Trp Ile Leu Pro Lys Pro His Ile Ser Ser Thr Pro Leu
    370                 375                 380
Thr Ile Gln Asp Glu Leu Leu Ile Leu Gly Asn Lys Ala Leu Trp Glu
385                 390                 395                 400
His Leu Ser Tyr Thr Glu Ala Val Asn Ala Val Arg His Val Gln Asp
                405                 410                 415
Pro Leu Ala Ala Ala Lys Lys Leu Cys Thr Leu Ala Gln Ser Tyr Gly
            420                 425                 430
Cys Gln Asp Ser Val Gly Ala Met Val Val Tyr Leu Asn Ile Gly Glu
        435                 440                 445
Glu Gly Cys Thr Cys Glu Met Asn Gly Leu Thr Leu Pro Gly Pro Val
    450                 455                 460
Gly Phe Ala Ser Thr Thr Thr Ile Lys Asp Ala Pro Lys Pro Ala Thr
465                 470                 475                 480
Pro Ser Ser Ser Ser Gly Ile Ala Ser Glu Phe Ser Ser Glu Met Ser
                485                 490                 495
Thr Ser Glu Val Ser Ser Glu Val Gly Ser Thr Ala Ser Asp Glu His
            500                 505                 510
Asn Ala Gly Gly Leu Asp Thr Ala Leu Leu Pro Arg Pro Glu Arg Arg
        515                 520                 525
Cys Ser Leu His Pro Thr Pro Thr Ser Gly Leu Phe Gln Arg Gln Pro
    530                 535                 540
Ser Ser Ala Thr Phe Ser Ser Asn Gln Ser Asp Asn Gly Leu Asp Ser
545                 550                 555                 560
Asp Asp Asp Gln Pro Val Glu Gly Val Ile Thr Asn Gly Ser Lys Val
                565                 570                 575
Glu Val Glu Val Asp Ile His Cys Cys Arg Gly Arg Asp Leu Glu Asn
            580                 585                 590
Ser Pro Pro Leu Ile Glu Ser Ser Pro Thr Leu Cys Ser Glu Glu His
        595                 600                 605
Ala Arg Gly Ser Cys Phe Gly Ile Arg Arg Gln Asn Ser Val Asn Ser
    610                 615                 620
Gly Met Leu Leu Pro Met Ser Lys Asp Arg Met Glu Leu Gln Lys Ser
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625 630 635 640
Pro Ser Thr Ser Cys Leu Tyr Gly Lys Lys Leu Ser Asn Gly Ser Ile
645 650 655
Val Pro Leu Glu Asp Ser Leu Asn Leu Ile Glu Val Ala Thr Glu Val
660 665 670
Pro Lys Arg Lys Thr Gly Tyr Phe Ala Ala Pro Thr Gln Met Glu Pro
675 680 685
Glu Asp Gln Phe Val Val Pro His Asp Leu Glu Glu Glu Val Lys Glu
690 695 700
Gln Met Lys Gln His Gln Asp Ser Arg Leu Glu Pro Glu Pro His Glu
705 710 715 720
Glu Asp Arg Thr Glu Pro Pro Glu Glu Phe Asp Thr Ala Leu
725 730

<210> 901
<211> 309
<212> DNA
<213> Homo sapiens

<400> 901
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atttcctttt tctcttaatg caacaaggtc atcccaagat caggcttcct tcagtttctg
120
tggtaagtag tgatggacac ttatggagtt ttcagagact tatgcattgg gtaacaaggc
180
actgcaagag accccagata gcacagcatc atctcacatt tacaccacat cacatcaaca
240
tcgatgctag gaggtctaaa gctgatgcca ccttcagagc tgcaagtatc caaaagactc
300
cactcatga
309

<210> 902
<211> 102
<212> PRT
<213> Homo sapiens

<400> 902
Met Ile His Leu Pro Arg Pro Pro Lys Val Leu Gly Leu His Thr Asp
1 5 10 15
Gly Lys Leu His Phe Leu Phe Leu Leu Met Gln Gln Gly His Pro Lys
20 25 30
Ile Arg Leu Pro Ser Val Ser Val Val Ser Ser Asp Gly His Leu Trp
35 40 45
Ser Phe Gln Arg Leu Met His Trp Val Thr Arg His Cys Lys Arg Pro
50 55 60
Gln Ile Ala Gln His His Leu Thr Phe Thr Pro His His Ile Asn Ile
65 70 75 80
Asp Ala Arg Arg Ser Lys Ala Asp Ala Thr Phe Arg Ala Ala Ser Ile
85 90 95
Gln Lys Thr Pro Leu Met
100

<210> 903
<211> 349
<212> DNA
<213> Homo sapiens

<400> 903
agatcttagt gaaaactgga agcaggaaga ataagttagt catggaagcc actttggctc
60
taagggcttt gatggcctca tgggttgaca ggaacagaag acaaagacta gggcccaccc
120
aaggtgtgaa gtctaatagg aaacctttc tccataaggc tacaatgggt ctaccaaaaa
180
taaaaccatg ccaccccagg gactgcagcc caattttata tcaccatgag gtccaaaaaa
240
ttccaagctg tgaatttagt ttcaaatggc cttggtctcc agtatcccta gccatgtggc
300
aaaaacaaac aattctcttt ggaggataca tctttatctt aagacttgn
349

<210> 904
<211> 102
<212> PRT
<213> Homo sapiens

<400> 904
Met Glu Ala Thr Leu Ala Leu Arg Ala Leu Met Ala Ser Trp Val Asp
1 5 10 15
Arg Asn Arg Arg Gln Arg Leu Gly Pro Thr Gln Gly Val Lys Ser Asn
20 25 30
Arg Lys Pro Phe Leu His Lys Ala Thr Met Gly Leu Pro Lys Ile Lys
35 40 45
Pro Cys His Pro Arg Asp Cys Ser Pro Ile Leu Tyr His His Glu Val
50 55 60
Gln Lys Ile Pro Ser Cys Glu Phe Ser Phe Lys Trp Pro Trp Ser Pro
65 70 75 80
Val Ser Leu Ala Met Trp Gln Lys Gln Thr Ile Leu Phe Gly Gly Tyr
85 90 95
Ile Phe Ile Leu Arg Leu
100

<210> 905
<211> 377
<212> DNA
<213> Homo sapiens

<400> 905
nntccggaac cggtggtgtg gaccgagcac gattctcacc tagctcaccc ggatcagcgt
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ctcaacgaag acatcattat cgcgggtgac cgggcagacg cggtgattag cgtatcccag
120
gggctctgcg acaggctggc tggacatggc gtgacctcaa cggtggttcc caacatcgtt
180
gacgtcgagc tgtttgaccg tcctgatcga cgacatgagg ggacgatcgt cgtcagcgtc
240

gccacccctca acccgggaaa gggcatgatt gagttagctc aggctgttga gcgtcttccc
300
gaggttcagt tgagaatcat cggagatgga ccgcagcggc accaactgga ggccattgcc
360
gctgataatc cacgcgt
377

<210> 906
<211> 125
<212> PRT
<213> Homo sapiens

<400> 906
Xaa Pro Glu Pro Val Val Trp Thr Glu His Asp Ser His Leu Ala His
1 5 10 15
Pro Asp Gln Arg Leu Asn Glu Asp Ile Ile Ile Ala Gly Asp Arg Ala
20 25 30
Asp Ala Val Ile Ser Val Ser Gln Gly Leu Cys Asp Arg Leu Ala Gly
35 40 45
His Gly Val Thr Ser Thr Val Val Pro Asn Ile Val Asp Val Glu Leu
50 55 60
Phe Asp Arg Pro Asp Arg Arg His Glu Gly Thr Ile Val Val Ser Val
65 70 75 80
Ala Thr Leu Asn Pro Gly Lys Gly Met Ile Glu Leu Ala Gln Ala Val
85 90 95
Glu Arg Leu Pro Glu Val Gln Leu Arg Ile Ile Gly Asp Gly Pro Gln
100 105 110
Arg His Gln Leu Glu Ala Ile Ala Ala Asp Asn Pro Arg
115 120 125

<210> 907
<211> 332
<212> DNA
<213> Homo sapiens

<400> 907
acgcgtagga tgatgaagtc cgtcactgga tcgttcttgg gtggcaaccg ggaagtcggt
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gaccagttct tcaacggcga ggttcaactg aaccttgtgc cgcagggtac attcgccgag
120
cgcattcgtg ccggcgctgc tggtattgca gcattcttca cgcctactgg ctatggtaca
180
gccgtgcaga agggtgagct tgttcttaag tatgaaaaga aggacggtaa ggctgtgcca
240
gtcatgacgt ccaagccgcg tgaagtgcgc tcgtttgacg gccgtgacta tataatagaa
300
gaggttatta aggatgaata ggatatggtg aa
332

<210> 908
<211> 106
<212> PRT
<213> Homo sapiens

<400> 908
Thr Arg Arg Met Met Lys Ser Val Thr Gly Ser Phe Leu Gly Gly Asn
1 5 10 15
Arg Glu Val Gly Asp Gln Phe Phe Asn Gly Glu Val Gln Leu Asn Leu
20 25 30
Val Pro Gln Gly Thr Phe Ala Glu Arg Ile Arg Ala Gly Ala Ala Gly
35 40 45
Ile Ala Ala Phe Phe Thr Pro Thr Gly Tyr Gly Thr Ala Val Gln Lys
50 55 60
Gly Glu Leu Val Leu Lys Tyr Glu Lys Lys Asp Gly Lys Ala Val Pro
65 70 75 80
Val Met Thr Ser Lys Pro Arg Glu Val Arg Ser Phe Asp Gly Arg Asp
85 90 95
Tyr Ile Ile Glu Glu Val Ile Lys Asp Glu
100 105

<210> 909
<211> 318
<212> DNA
<213> Homo sapiens

<400> 909
acgcgtcggg catggcagct gtacagatct atcgcgtcag cagggcctac gcacacatga
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tgccgcaggg gcaccgacgc tgtcgccatc aaaagagccg cctcgcgccc gcagcgcctc
120
ccagggacgg cgactcacgt ggctcgacac gcgcgcgcga gtcgcgtggg tgtgtcacgc
180
ccctttttt cccaccccaa caccgaaccg gcgggccatg gctgaggatt cgcaccccat
240
tcgctccggc ttgcgcatgc tcaagcgctc ctggagctcg aatgagaatg taccgccgcc
300
acaaagctcg ccgccggc
318

<210> 910
<211> 102
<212> PRT
<213> Homo sapiens

<400> 910
Met Ala Ala Val Gln Ile Tyr Arg Val Ser Arg Ala Tyr Ala His Met
1 5 10 15
Met Pro Gln Gly His Arg Arg Cys Arg His Gln Lys Ser Arg Leu Ala
20 25 30
Pro Ala Ala Pro Pro Arg Asp Gly Asp Ser Arg Gly Ser Thr Arg Ala
35 40 45
Arg Glu Ser Arg Gly Cys Val Thr Pro Leu Phe Phe Pro Pro Gln His
50 55 60
Arg Thr Gly Gly Pro Trp Leu Arg Ile Arg Thr Pro Phe Ala Pro Ala
65 70 75 80
Cys Ala Cys Ser Ser Ala Pro Gly Ala Arg Met Arg Met Tyr Arg Arg
85 90 95
His Lys Ala Arg Arg Arg

100

<210> 911
<211> 506
<212> DNA
<213> Homo sapiens

<400> 911
acgcgtgtgc agcactctcc acaagctggc cccaatcact tttgcatcaa attggtacag
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caaccttatg aggctggcct tgggggaacc ctgttttagg gatgagctga acttaccggg
120
aggctgcatg cgaggttggt gtgaaatgca tatctggctt tgtagctggt cggctcacct
180
ctggggttgg cacaggggcg ggggttctgc catggctaga atgcgctaag gggtggaaac
240
gaagcctgct gggcccggga accacagagc agcctggcct ttgaaggaga ccctgtggca
300
ccccctgccc acccccaagt ccagccattt cacttccctg gagatggtgc aaagcaagaa
360
aaaaaaaaaa atccagtgtt ctcaggtcag ccttccacca gccaggattc atcgtctgat
420
ctgtttgggg agagagcatg gagtggtgga gatgggttgg gccccagtgt tttctgatta
480
actcgcagtt cacctgaaac attttg
506

<210> 912
<211> 129
<212> PRT
<213> Homo sapiens

<400> 912
Met Phe Gln Val Asn Cys Glu Leu Ile Arg Lys His Trp Gly Pro Thr
1 5 10 15
His Leu His His Ser Met Leu Ser Pro Gln Thr Asp Gln Thr Met Asn
20 25 30
Pro Gly Trp Trp Lys Ala Asp Leu Arg Thr Leu Asp Phe Phe Phe Phe
35 40 45
Leu Ala Leu His His Leu Gln Gly Ser Glu Met Ala Gly Leu Gly Gly
50 55 60
Gly Gln Gly Val Pro Gln Gly Leu Leu Gln Arg Pro Gly Cys Ser Val
65 70 75 80
Val Pro Gly Pro Ser Arg Leu Arg Phe His Pro Leu Ala His Ser Ser
85 90 95
His Gly Arg Thr Pro Ala Pro Val Pro Thr Pro Glu Val Ser Arg Pro
100 105 110
Ala Thr Lys Pro Asp Met His Phe Thr Pro Thr Ser His Ala Ala Ser
115 120 125
Arg

<210> 913
<211> 339

<212> DNA
<213> Homo sapiens

<400> 913
cgcttcatgg cgtggttcag gcgtacggtt ccggctactg gtgactaccg tggcacgaaa
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tttttcgttc gcgagaacgg taaaaccctc gcaacctcga tgttcatggt ttgtgtcgcc
120
ctgggcgcca cggacctgct tttcgccctc gactcgattc cggcgtccta tggtttcacc
180
aacgaggggt accttatcct taccgctaac gtctttgctc tcatgggctt gcgtcagttg
240
tatttcctta ttggaagcct gttggaacgt ctggtgtact tgtcgctggg actggtcgtg
300
attttgggct ttatcgccct caagctcatt ggccacgcg
339

<210> 914
<211> 113
<212> PRT
<213> Homo sapiens

<400> 914
Arg Phe Met Ala Trp Phe Arg Arg Thr Val Pro Ala Thr Gly Asp Tyr
1 5 10 15
Arg Gly Thr Lys Phe Phe Val Arg Glu Asn Gly Lys Thr Leu Ala Thr
20 25 30
Ser Met Phe Met Val Cys Val Ala Leu Gly Ala Thr Asp Leu Leu Phe
35 40 45
Ala Leu Asp Ser Ile Pro Ala Ser Tyr Gly Phe Thr Asn Glu Gly Tyr
50 55 60
Leu Ile Leu Thr Ala Asn Val Phe Ala Leu Met Gly Leu Arg Gln Leu
65 70 75 80
Tyr Phe Leu Ile Gly Ser Leu Leu Glu Arg Leu Val Tyr Leu Ser Leu
85 90 95
Gly Leu Val Val Ile Leu Gly Phe Ile Ala Leu Lys Leu Ile Gly His
100 105 110
Ala

<210> 915
<211> 663
<212> DNA
<213> Homo sapiens

<400> 915
nnggtacctg tcaatcagta tgtaaacctc actttatgtc gtggttatcc acttcctgat
60
gacagtgaag atcctgttgt ggacattgtt gctgctaccc ctgtcatcaa tggacagtca
120
ttaaccaagg gagagacttg catgaatcct caggatttta agccaggagc aatggttctg
180
gagcagaatg gaaaatcggg acacactttg actggtgatg gtctcaatgg accatcagat
240

gcaagtgagc agagagtatc catggcatcg tcaggcagct cccagcctga actagtgact
300
atccctttga ttaagggccc taaagggttt gggtttgcaa ttgctgacag ccctactgga
360
cagaaggtga aaatgatact ggatagtcag tggtgtcaag gccttcagaa aggagatata
420
attaaggaaa tataccatca aaatgtgcag aatttaacac atctccaagt ggtagaggtg
480
ctaaagcagt ttccagtagg tgctgatgta ccattgctta tcttaagagg aggtcccccc
540
tcaccaacca aaagtgccaa aatgaaaaca gataaaaagg aaaatgcagg aagtttggag
600
gccataaatg agcctattcc tcagcctatg ccttttccac cgagcattat caggtcagga
660
tcc
663

<210> 916
<211> 221
<212> PRT
<213> Homo sapiens

<400> 916
Xaa Val Pro Val Asn Gln Tyr Val Asn Leu Thr Leu Cys Arg Gly Tyr
1 5 10 15
Pro Leu Pro Asp Asp Ser Glu Asp Pro Val Val Asp Ile Val Ala Ala
20 25 30
Thr Pro Val Ile Asn Gly Gln Ser Leu Thr Lys Gly Glu Thr Cys Met
35 40 45
Asn Pro Gln Asp Phe Lys Pro Gly Ala Met Val Leu Glu Gln Asn Gly
50 55 60
Lys Ser Gly His Thr Leu Thr Gly Asp Gly Leu Asn Gly Pro Ser Asp
65 70 75 80
Ala Ser Glu Gln Arg Val Ser Met Ala Ser Ser Gly Ser Ser Gln Pro
85 90 95
Glu Leu Val Thr Ile Pro Leu Ile Lys Gly Pro Lys Gly Phe Gly Phe
100 105 110
Ala Ile Ala Asp Ser Pro Thr Gly Gln Lys Val Lys Met Ile Leu Asp
115 120 125
Ser Gln Trp Cys Gln Gly Leu Gln Lys Gly Asp Ile Ile Lys Glu Ile
130 135 140
Tyr His Gln Asn Val Gln Asn Leu Thr His Leu Gln Val Val Glu Val
145 150 155 160
Leu Lys Gln Phe Pro Val Gly Ala Asp Val Pro Leu Leu Ile Leu Arg
165 170 175
Gly Gly Pro Pro Ser Pro Thr Lys Ser Ala Lys Met Lys Thr Asp Lys
180 185 190
Lys Glu Asn Ala Gly Ser Leu Glu Ala Ile Asn Glu Pro Ile Pro Gln
195 200 205
Pro Met Pro Phe Pro Pro Ser Ile Ile Arg Ser Gly Ser
210 215 220

<210> 917
<211> 615

<212> DNA
<213> Homo sapiens

<400> 917
atcgtggacc agaagttccc tgagtgtggc ttctacggcc tttacgacaa gatcctgctt
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ttcaaacatg accccacgtc ggccaacctc ctgcagctgg tgcgctcgtc cggagacatc
120
caggagggcg acctggtgga ggtggtgctg tcggcctcgg ccaccttcga ggacttccag
180
atccgcccgc acgccctcac ggtgcactcc tatcgggcgc ctgccttctg tgatcactgc
240
ggggagatgc tcttcggcct agtgcgccag ggcctcaagt gcgatggctg cgggctgaac
300
taccacaagc gctgtgcctt cagcatcccc aacaactgta gtggggcccg caaacggcgc
360
ctgtcatcca cgtctctggc cagtggccac tcggtgcgcc tcggcacctc cgagtccctg
420
ccctgcacgg ctgaagagga gccgtagcac caccgaactc ctgcctcgcc gtccccgtca
480
tcctcttcct cctcttctgc ctcatcgtat acgggccgcc ccattgagct ggacaagatg
540
ctgctctcca aggtcaaggt gccgcacacc ttcctcatcc acagctatac acggcccacc
600
gtttgccagg cttgc
615

<210> 918
<211> 148
<212> PRT
<213> Homo sapiens

<400> 918
Ile Val Asp Gln Lys Phe Pro Glu Cys Gly Phe Tyr Gly Leu Tyr Asp
 1   5   10   15
Lys Ile Leu Leu Phe Lys His Asp Pro Thr Ser Ala Asn Leu Leu Gln
            20   25   30
Leu Val Arg Ser Ser Gly Asp Ile Gln Glu Gly Asp Leu Val Glu Val
        35   40   45
Val Leu Ser Ala Ser Ala Thr Phe Glu Asp Phe Gln Ile Arg Pro His
    50   55   60
Ala Leu Thr Val His Ser Tyr Arg Ala Pro Ala Phe Cys Asp His Cys
65   70   75   80
Gly Glu Met Leu Phe Gly Leu Val Arg Gln Gly Leu Lys Cys Asp Gly
                85   90   95
Cys Gly Leu Asn Tyr His Lys Arg Cys Ala Phe Ser Ile Pro Asn Asn
            100   105   110
Cys Ser Gly Ala Arg Lys Arg Arg Leu Ser Ser Thr Ser Leu Ala Ser
        115   120   125
Gly His Ser Val Arg Leu Gly Thr Ser Glu Ser Leu Pro Cys Thr Ala
    130   135   140
Glu Glu Glu Pro
145

<210> 919
<211> 294
<212> DNA
<213> Homo sapiens

<400> 919
accggtatgc gtccgctggc tgtgctcggc gacaacatca ccaccgacca tctatcgccg
60
acaaatgcga tcctgctcga tagcgcagcg ggtgagtacc tcgccaagat gggcccgccg
120
gaagaagact tcatttcgaa cgcgacccat cgtggcgatc acctgaccgc acagcgcgcc
180
accttcgcca acccgacctt gctcaacgag atggccgtag tcgatggtga agtgaagaaa
240
ggctcgcttg cccgcgtgga accggaaggc catgtgatgc gcatgtggga agcc
294

<210> 920
<211> 98
<212> PRT
<213> Homo sapiens

<400> 920
Thr Gly Met Arg Pro Leu Ala Val Leu Gly Asp Asn Ile Thr Thr Asp
1 5 10 15
His Leu Ser Pro Thr Asn Ala Ile Leu Leu Asp Ser Ala Ala Gly Glu
20 25 30
Tyr Leu Ala Lys Met Gly Pro Pro Glu Glu Asp Phe Ile Ser Asn Ala
35 40 45
Thr His Arg Gly Asp His Leu Thr Ala Gln Arg Ala Thr Phe Ala Asn
50 55 60
Pro Thr Leu Leu Asn Glu Met Ala Val Val Asp Gly Glu Val Lys Lys
65 70 75 80
Gly Ser Leu Ala Arg Val Glu Pro Glu Gly His Val Met Arg Met Trp
85 90 95
Glu Ala

<210> 921
<211> 378
<212> DNA
<213> Homo sapiens

<400> 921
acgcgtttgc gcatcgcttt gaccggtctg acgatggctg agtacttccg cgatgttcag
60
aaccaggacg tgctgttgtt catcgacaac atcttccggt tctcccaggc tggttctgag
120
gtttcaaccc tgctaggtcg tatgccctcg gcggtgggct accagcccaa cttggccgac
180
gagatgggcc aattgcagga gcgaatcacc tcgacccgtg gtcactccat cacctcgatg
240
caggccgtct acgtccccgc tgacgattac accgacccgg ctccggcgac gaccttcgcc
300

cacctggatg ccaccacgga gctttctcgt gagattgcct ctcgtggcct gtacccggcc
360
gtggatccgc tggcgtcg
378

<210> 922
<211> 126
<212> PRT
<213> Homo sapiens

<400> 922
Thr Arg Leu Arg Ile Ala Leu Thr Gly Leu Thr Met Ala Glu Tyr Phe
1 5 10 15
Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe
20 25 30
Arg Phe Ser Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met
35 40 45
Pro Ser Ala Val Gly Tyr Gln Pro Asn Leu Ala Asp Glu Met Gly Gln
50 55 60
Leu Gln Glu Arg Ile Thr Ser Thr Arg Gly His Ser Ile Thr Ser Met
65 70 75 80
Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala
85 90 95
Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Ser Arg Glu Ile
100 105 110
Ala Ser Arg Gly Leu Tyr Pro Ala Val Asp Pro Leu Ala Ser
115 120 125

<210> 923
<211> 571
<212> DNA
<213> Homo sapiens

<400> 923
accggtatcg aactgccgca agacacgggc aagcatgtcg ccgacgaaca actgcaacgc
60
ctggacaccg cgctggagca cgtgcgcgga gaaatccgca ttaccctgga gcatgcacgc
120
caacgcaaga atgtcgaaga agaagacatc ttcgccgccc accttgcgct attggaagac
180
cccacgctgc tggacgccgc cactggtgcc atcgaacacg gcagcgccgc cacccacgcc
240
tggcgcgatg caatccaggc gcaatgcgcc gtgttgctgg ccctgggcaa accgctgttt
300
gccgagcgcg ccaacgacct gcgcgatctg caacagcgag tactgcgtgc gctgttgggg
360
gaagcctggc acttcgaatt gccggccggg ccgattttca ggnnggccat taacttaccc
420
ccttccgcct tgttgcaact gagtgcccaa aacgccgtgg gtatttgcat ggccgaaggc
480
ggcgctacgt ctcacgtcgc gattttggcc cgaggcaaag gcttgccgtg cgtggtcgcg
540
ctgggcgccg aagtgctcga cgtgccccaa g
571

<210> 924
<211> 190
<212> PRT
<213> Homo sapiens

<400> 924
Thr Gly Ile Glu Leu Pro Gln Asp Thr Gly Lys His Val Ala Asp Glu
1 5 10 15
Gln Leu Gln Arg Leu Asp Thr Ala Leu Glu His Val Arg Gly Glu Ile
20 25 30
Arg Ile Thr Leu Glu His Ala Arg Gln Arg Lys Asn Val Glu Glu Glu
35 40 45
Asp Ile Phe Ala Ala His Leu Ala Leu Leu Glu Asp Pro Thr Leu Leu
50 55 60
Asp Ala Ala Thr Gly Ala Ile Glu His Gly Ser Ala Ala Thr His Ala
65 70 75 80
Trp Arg Asp Ala Ile Gln Ala Gln Cys Ala Val Leu Leu Ala Leu Gly
85 90 95
Lys Pro Leu Phe Ala Glu Arg Ala Asn Asp Leu Arg Asp Leu Gln Gln
100 105 110
Arg Val Leu Arg Ala Leu Leu Gly Glu Ala Trp His Phe Glu Leu Pro
115 120 125
Ala Gly Pro Ile Phe Arg Xaa Ala Ile Asn Leu Pro Pro Ser Ala Leu
130 135 140
Leu Gln Leu Ser Ala Gln Asn Ala Val Gly Ile Cys Met Ala Glu Gly
145 150 155 160
Gly Ala Thr Ser His Val Ala Ile Leu Ala Arg Gly Lys Gly Leu Pro
165 170 175
Cys Val Val Ala Leu Gly Ala Glu Val Leu Asp Val Pro Gln
180 185 190

<210> 925
<211> 620
<212> DNA
<213> Homo sapiens

<400> 925
acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
60
ncatggtgtg tgcacgtgtg cnactgtgta tgcatggtaa tgtgcacgtg tgcactgtgt
120
gtggtgtgta tgcatggtgt gtgcacgtgt gcactgtgtg tgtgtgtatg catgtgtgtg
180
cacgtgtgcc tgtgtgtatg catggtaatg tgcgtgtgca ctgtgtggtg tgtatgcatg
240
tgtgtgcacg tgtgcactgt gtatgcatag tgtgtgcacg tgtgcactgt gtgtggatgc
300
atggtaatgt gcacgtgtgc actgtgtgtg gtgtgtatga tggtgtgtgc acgtgtgcac
360
ggtgtgtggt gtgtatgcat gtgtgtgcac gtgtgcactg tgtggcaggg gtgtttggtg
420
tgtgtgcatg tatgcatggt gtgtgcatac gtgtgcagca gcacctggtc ccatctccag
480

tgcccagcag catcacacgc actttggtgc tttataaatg catggtcagt gaggctgcca
540
gcaccaagct gtccctttac cataacacct ggaatagtca cctgtgataa gctatcacat
600
aggaaacatt tttaaaattt
620

<210> 926
<211> 89
<212> PRT
<213> Homo sapiens

<400> 926
Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
1 5 10 15
Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
20 25 30
Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val Cys
35 40 45
Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Val Cys Leu
50 55 60
Cys Val Cys Met Val Met Cys Val Cys Thr Val Trp Cys Val Cys Met
65 70 75 80
Cys Val His Val Cys Thr Val Tyr Ala
85

<210> 927
<211> 360
<212> DNA
<213> Homo sapiens

<400> 927
gtgcacactc tggaagccac aggatggagc tcctagagat agtgaggcat gaccagaggg
60
aagaggcatt tggggtcctg ttcagatcat tccaacagca aaccgggcat ggagacccca
120
tctcaggtct gtgcttctct gggggccacc cagccatcct gcccaccagc tcagaggcag
180
ggacaaagcc ctcccaagag gcagcaggca gcaagggtca gccagcgcag tggggacagg
240
caggtacaac ctggaaaccc caaaggaccc cagatggcaa tgtgacacgg cccatccacc
300
aagcacctgt aatgccggct tcccacagag gcgagccaga tcctggcact attctttaag
360

<210> 928
<211> 111
<212> PRT
<213> Homo sapiens

<400> 928
Met Glu Leu Leu Glu Ile Val Arg His Asp Gln Arg Glu Glu Ala Phe
1 5 10 15
Gly Val Leu Phe Arg Ser Phe Gln Gln Gln Thr Gly His Gly Asp Pro

```
            20                  25                  30
Ile Ser Gly Leu Cys Phe Ser Gly Gly His Pro Ala Ile Leu Pro Thr
        35                  40                  45
Ser Ser Glu Ala Gly Thr Lys Pro Ser Gln Glu Ala Ala Gly Ser Lys
    50                  55                  60
Gly Gln Pro Ala Gln Trp Gly Gln Ala Gly Thr Thr Trp Lys Pro Gln
65                  70                  75                  80
Arg Thr Pro Asp Gly Asn Val Thr Arg Pro Ile His Gln Ala Pro Val
                85                  90                  95
Met Pro Ala Ser His Arg Gly Glu Pro Asp Pro Gly Thr Ile Leu
            100                 105                 110
```

<210> 929
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 929
nnctccccag ggccgagtct tccggagtca gcagagagcc tggatggatc acaggaggat
60
aagcctcggg gctcatgtgc ggagcccact tttactgata cgggaatggt ggctcacata
120
aacaacagcc ggctcaaggc caagggcgtg ggccagcacg acaacgccca gaactttggt
180
aaccagagct ttgaggagct gcgagcagcc tgtctaagaa aggggagct cttcgaggac
240
cccttattcc ctgctgaacc cagctcactg ggcttcaagg acctgggccc caactccaaa
300
aatgtgcaga acatctcctg gcagcggccc aaggatatca taaacaaccc tctattcatc
360
atggatggga tttctccaac agacatctgc caggggatcc tcggggactg ctggctgctg
420
gctgccatcg gctcccttac cacctgcccc aaactgctat accgcgtggt gcccagagga
480
cagagcttca agaaaaacta tgctggcatc ttccattttc agatttggca gtttggacag
540
tgggtgaacg tggtggtaga tgaccggctg cccacaaaga atgacaagct ggtgtttgtg
600
cactcaaccg aacgcagtga gttctggagt gccctgctgg agaaggcgta tgccaagctg
660
agtgggtcct atgaagcatt gtcaggggge agtaccatgg agggccttga ggacttcaca
720
ggaggcgtgg cccagagctt ccaactccag aggccccctc agaacctgct caggctcctt
780
aggaaggccg tggagcgatc ctccctcatg ggttgctcca ttgaagtcac cagtgatagt
840
gaactggaat ccatgactga caagatgctg gtgagagggc acgcttactc tgtgactggc
900
cttcaggatg tccactacag aggcaaaatg gaaacactga ttcgggtccg gaatccctgg
960
ggccggattg agtggaatgg agcttggagt gacagtgcca gggagtggga agaggtggcc
1020
tcagacatcc agatgcagct gctgcacaag acggaggacg gggagttctg gatgtcctac
1080

caagatttcc tgaacaactt cacgctcctg gagatctgca acctcacgcc tgatacactc
1140
tctggggact acaagagcta ctggcacacc accttctacg agggcagctg gcgcagaggc
1200
agctccgcag ggggctgcag gaaccaccct ggcacgttct ggaccaaccc ccagtttaag
1260
atctctcttc ctgaggggga tgacccagag gatgacgcag agggcaatgt tgtggtctgc
1320
acctgcctgg tggccctaat gcagaagaac tggcggcatg cacggcagca gggagcccag
1380
ctgcagacca ttggctttgt cctctacgcg gtcccaaaag agtttcagaa cattcaggat
1440
gtccacttga agaaggaatt cttcacgaag tatcaggacc acggcttctc agagatcttc
1500
accaactcac gggaggtgag cagccaactc cggctgcctc cgggggaata tatcattatt
1560
ccctccacct ttgagccaca cagagatgct gacttcctgc ttcgggtctt caccgagaag
1620
cacagcgagt catgggaatt ggatgaagtc aactatgctg agcaactcca agaggaaaag
1680
gtctctgagg atgacatgga ccaggacttc ctacatttgt ttaagatagt ggcaggagag
1740
ggcaaggaga taggggtgta tgagctccag aggctgctca acaggatggc catcaaattc
1800
aaaagcttca agaccaaggg ctttggcctg gatgcttgcc gctgcatgat caacctcatg
1860
gataaagatg gctctggcaa gctggggctt ctagagttca agatcctgtg gaaaaaactc
1920
aagaaatgga tggacatctt cagagagtgt gaccaggacc attcaggcac cttgaactcc
1980
tatgagatgc gcctggttat tgagaaagca ggcatcaagc tgaacaacaa ggtaatgcag
2040
gtcctggtgg ccaggtatgc agatgatggc ctgatcatag actttgacag cttcatcagc
2100
tgtttcctga ggctaaagac catgttcaca ttctttctaa ccatggaccc caagaatact
2160
ggccatattt gcttgagcct ggaacagtgg ctgcagatga ccatgtgggg atagaggcgc
2220
tgtaggagcc tggtcatctc taccagcagc agcagcagcg aggttctagc ccaggagggt
2280
ggggtgcttc ttgtagccct cagctctcca gtctctgctg atgaaatggg atccaggtgg
2340

<210> 930
<211> 702
<212> PRT
<213> Homo sapiens

<400> 930
Met Val Ala His Ile Asn Asn Ser Arg Leu Lys Ala Lys Gly Val Gly
 1   5   10   15
Gln His Asp Asn Ala Gln Asn Phe Gly Asn Gln Ser Phe Glu Glu Leu
            20   25   30
Arg Ala Ala Cys Leu Arg Lys Gly Glu Leu Phe Glu Asp Pro Leu Phe

```
        35                  40                  45
Pro Ala Glu Pro Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser
    50                  55                  60
Lys Asn Val Gln Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn
65                  70                  75                  80
Asn Pro Leu Phe Ile Met Asp Gly Ile Ser Pro Thr Asp Ile Cys Gln
                85                  90                  95
Gly Ile Leu Gly Asp Cys Trp Leu Leu Ala Ala Ile Gly Ser Leu Thr
            100                 105                 110
Thr Cys Pro Lys Leu Leu Tyr Arg Val Val Pro Arg Gly Gln Ser Phe
        115                 120                 125
Lys Lys Asn Tyr Ala Gly Ile Phe His Phe Gln Ile Trp Gln Phe Gly
    130                 135                 140
Gln Trp Val Asn Val Val Val Asp Asp Arg Leu Pro Thr Lys Asn Asp
145                 150                 155                 160
Lys Leu Val Phe Val His Ser Thr Glu Arg Ser Glu Phe Trp Ser Ala
                165                 170                 175
Leu Leu Glu Lys Ala Tyr Ala Lys Leu Ser Gly Ser Tyr Glu Ala Leu
            180                 185                 190
Ser Gly Gly Ser Thr Met Glu Gly Leu Glu Asp Phe Thr Gly Gly Val
        195                 200                 205
Ala Gln Ser Phe Gln Leu Gln Arg Pro Pro Gln Asn Leu Leu Arg Leu
    210                 215                 220
Leu Arg Lys Ala Val Glu Arg Ser Ser Leu Met Gly Cys Ser Ile Glu
225                 230                 235                 240
Val Thr Ser Asp Ser Glu Leu Glu Ser Met Thr Asp Lys Met Leu Val
                245                 250                 255
Arg Gly His Ala Tyr Ser Val Thr Gly Leu Gln Asp Val His Tyr Arg
            260                 265                 270
Gly Lys Met Glu Thr Leu Ile Arg Val Arg Asn Pro Trp Gly Arg Ile
        275                 280                 285
Glu Trp Asn Gly Ala Trp Ser Asp Ser Ala Arg Glu Trp Glu Glu Val
    290                 295                 300
Ala Ser Asp Ile Gln Met Gln Leu Leu His Lys Thr Glu Asp Gly Glu
305                 310                 315                 320
Phe Trp Met Ser Tyr Gln Asp Phe Leu Asn Asn Phe Thr Leu Leu Glu
                325                 330                 335
Ile Cys Asn Leu Thr Pro Asp Thr Leu Ser Gly Asp Tyr Lys Ser Tyr
            340                 345                 350
Trp His Thr Thr Phe Tyr Glu Gly Ser Trp Arg Arg Gly Ser Ser Ala
        355                 360                 365
Gly Gly Cys Arg Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe
    370                 375                 380
Lys Ile Ser Leu Pro Glu Gly Asp Asp Pro Glu Asp Asp Ala Glu Gly
385                 390                 395                 400
Asn Val Val Val Cys Thr Cys Leu Val Ala Leu Met Gln Lys Asn Trp
                405                 410                 415
Arg His Ala Arg Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly Phe Val
            420                 425                 430
Leu Tyr Ala Val Pro Lys Glu Phe Gln Asn Ile Gln Asp Val His Leu
        435                 440                 445
Lys Lys Glu Phe Phe Thr Lys Tyr Gln Asp His Gly Phe Ser Glu Ile
    450                 455                 460
Phe Thr Asn Ser Arg Glu Val Ser Ser Gln Leu Arg Leu Pro Pro Gly
```

```
465                 470                 475                 480
Glu Tyr Ile Ile Ile Pro Ser Thr Phe Glu Pro His Arg Asp Ala Asp
                485                 490                 495
Phe Leu Leu Arg Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu
            500                 505                 510
Asp Glu Val Asn Tyr Ala Glu Gln Leu Gln Glu Glu Lys Val Ser Glu
        515                 520                 525
Asp Asp Met Asp Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly
    530                 535                 540
Glu Gly Lys Glu Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg
545                 550                 555                 560
Met Ala Ile Lys Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp
                565                 570                 575
Ala Cys Arg Cys Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys
            580                 585                 590
Leu Gly Leu Leu Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys Lys Trp
        595                 600                 605
Met Asp Ile Phe Arg Glu Cys Asp Gln Asp His Ser Gly Thr Leu Asn
    610                 615                 620
Ser Tyr Glu Met Arg Leu Val Ile Glu Lys Ala Gly Ile Lys Leu Asn
625                 630                 635                 640
Asn Lys Val Met Gln Val Leu Val Ala Arg Tyr Ala Asp Asp Gly Leu
                645                 650                 655
Ile Ile Asp Phe Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu Lys Thr
            660                 665                 670
Met Phe Thr Phe Phe Leu Thr Met Asp Pro Lys Asn Thr Gly His Ile
        675                 680                 685
Cys Leu Ser Leu Glu Gln Trp Leu Gln Met Thr Met Trp Gly
    690                 695                 700
```

<210> 931
<211> 297
<212> DNA
<213> Homo sapiens

<400> 931
tcgcgaaggg agcctgacat gggccagaaa atcaatcccc atggtttccg tctcggtgtg
60
acgaccgatc acaagacccg ctggtacgcc gagaagcagt acgccgagct cgtgggtgag
120
gatgtcaaga tccgagagtg gctccacaag aatctggagc gcgccggtct ttcgtccatc
180
gagatcgagc gtcgctccga gcgcgtgacc attttccttt acgccgctcg cccgggcatc
240
gttatcgggc gcaatggccg ggaggccgag cgcgtgcgtn ntgagctcga aaagctt
297

<210> 932
<211> 93
<212> PRT
<213> Homo sapiens

<400> 932
Met Gly Gln Lys Ile Asn Pro His Gly Phe Arg Leu Gly Val Thr Thr

```
 1               5                  10                  15
Asp His Lys Thr Arg Trp Tyr Ala Glu Lys Gln Tyr Ala Glu Leu Val
            20                  25                  30
Gly Glu Asp Val Lys Ile Arg Glu Trp Leu His Lys Asn Leu Glu Arg
        35                  40                  45
Ala Gly Leu Ser Ser Ile Glu Ile Glu Arg Arg Ser Glu Arg Val Thr
    50                  55                  60
Ile Phe Leu Tyr Ala Ala Arg Pro Gly Ile Val Ile Gly Arg Asn Gly
65                  70                  75                  80
Arg Glu Ala Glu Arg Val Arg Xaa Glu Leu Glu Lys Leu
                85                  90
```

<210> 933
<211> 305
<212> DNA
<213> Homo sapiens

<400> 933
nnacgcgtcg ccaagctgtt gatggccgaa tacaaggggc tcaacgtcat cgtcaaaacc
60
tccgccgatc cggcaagcca agccaatgcc gtgcaggatc tggcgggggc aggcatcgac
120
gcgctggcca tcctgccgac cgacccggat cagctggttt cggcgatcca gcaggtcaag
180
gacgacggca agttcgtggc gctggtcgac cgtgcgcctt ccgtcaacga caacacgatc
240
cgcgatctct acgtggccgg caacaacccg gcgctcggcg aagtggcggg caaattcatg
300
ggcga
305

<210> 934
<211> 101
<212> PRT
<213> Homo sapiens

<400> 934
```
Xaa Arg Val Ala Lys Leu Leu Met Ala Glu Tyr Lys Gly Leu Asn Val
 1               5                  10                  15
Ile Val Lys Thr Ser Ala Asp Pro Ala Ser Gln Ala Asn Ala Val Gln
            20                  25                  30
Asp Leu Ala Gly Ala Gly Ile Asp Ala Leu Ala Ile Leu Pro Thr Asp
        35                  40                  45
Pro Asp Gln Leu Val Ser Ala Ile Gln Gln Val Lys Asp Asp Gly Lys
    50                  55                  60
Phe Val Ala Leu Val Asp Arg Ala Pro Ser Val Asn Asp Asn Thr Ile
65                  70                  75                  80
Arg Asp Leu Tyr Val Ala Gly Asn Asn Pro Ala Leu Gly Glu Val Ala
                85                  90                  95
Gly Lys Phe Met Gly
            100
```

<210> 935
<211> 333

<212> DNA
<213> Homo sapiens

<400> 935
acgcgtgaag ggctgatgag tgctatgaaa aagccagggg cccgaggaca ctggggtgga
60
caggctcccc tggggaagtc ctcttagaac tgagggatca acactggagg agactgcaag
120
gggtacggga taaatgttcc tggtgaagga aacagcaggg gcaaaggccc tgcagcagaa
180
aggagcgagg ccctttggag taacagaaag accatggtga caggagctca gaaagaccac
240
tggtgttaag actataagcc agtggaggcc agattgggga atgggatggg aggggtgctt
300
gaagaccatg gtgaggctct cttggtcttt act
333

<210> 936
<211> 103
<212> PRT
<213> Homo sapiens

<400> 936
Met Val Phe Lys His Pro Ser His Pro Ile Pro Gln Ser Gly Leu His
 1   5   10   15
Trp Leu Ile Val Leu Thr Pro Val Val Phe Leu Ser Ser Cys His His
            20   25   30
Gly Leu Ser Val Thr Pro Lys Gly Leu Ala Pro Phe Cys Cys Arg Ala
        35   40   45
Phe Ala Pro Ala Val Ser Phe Thr Arg Asn Ile Tyr Pro Val Pro Leu
    50   55   60
Ala Val Ser Ser Ser Val Asp Pro Ser Val Leu Arg Gly Leu Pro Gln
65   70   75   80
Gly Ser Leu Ser Thr Pro Val Ser Ser Gly Pro Trp Leu Phe His Ser
                85   90   95
Thr His Gln Pro Phe Thr Arg
            100

<210> 937
<211> 464
<212> DNA
<213> Homo sapiens

<400> 937
nnnttatctg cggagggggt ggccaccctg cccacactca tgctgcaggc ctccaccgac
60
ccggcggacg acgagctcaa ggatctgttg acggccgacc tcatggacca gcacaacctc
120
gaccgtgccc tggcagggtt gcgtgccagt cacgtcatcg acgaagctcg cgccgaggtg
180
cagcggcgtg ccgatctcgc ccgtggccat ctcgccatcc ttcccgcagg cgatgcccgt
240
acggcgttgg agaccctgtg cgacgaggtg ggttcccggg cggcctgaac cccgaccctg
300

ccagnctgcg tcccatctcc tggccgggac cgctccagcg tctgctctct gacagctcat
360
cgttcttccg acaccaagga gtttctcgtg gcccgtcatc tcgatctcat cggcattggt
420
cccggcaacc cggactggat caccctggct gccgtcaagg ccan
464

<210> 938
<211> 95
<212> PRT
<213> Homo sapiens

<400> 938
Xaa Leu Ser Ala Glu Gly Val Ala Thr Leu Pro Thr Leu Met Leu Gln
1 5 10 15
Ala Ser Thr Asp Pro Ala Asp Asp Glu Leu Lys Asp Leu Leu Thr Ala
20 25 30
Asp Leu Met Asp Gln His Asn Leu Asp Arg Ala Leu Ala Gly Leu Arg
35 40 45
Ala Ser His Val Ile Asp Glu Ala Arg Ala Glu Val Gln Arg Arg Ala
50 55 60
Asp Leu Ala Arg Gly His Leu Ala Ile Leu Pro Ala Gly Asp Ala Arg
65 70 75 80
Thr Ala Leu Glu Thr Leu Cys Asp Glu Val Gly Ser Arg Ala Ala
85 90 95

<210> 939
<211> 385
<212> DNA
<213> Homo sapiens

<400> 939
ntgactatcc tcgaccccga tggtcaggag acgactccag gaagtgtcat cgaagggctt
60
ggactgctgc cggtcgaggt ggacttcgcc gccacgaaga cccttgcctt gtcgcacggg
120
acatggcggg ggatcgaggt tggtggctat gaaatccatc acgggcgtct gtcgttcgct
180
gaggacgctg aagccttcct cgacggcgta cacgtcggtc cggtatgggg gacgatgtgg
240
cacggggcat tcgagcacga cgaattccgt cgcacgtggc tggctgacgc ggcccgtcac
300
gctggatcat cctggcgtcc gcactccgac gagctgggtt atcaggctcg acgcgaggcg
360
atgatcgaaa ccctcgccga cgcgt
385

<210> 940
<211> 128
<212> PRT
<213> Homo sapiens

<400> 940
Xaa Thr Ile Leu Asp Pro Asp Gly Gln Glu Thr Thr Pro Gly Ser Val

```
 1               5                  10                  15
Ile Glu Gly Leu Gly Leu Leu Pro Val Glu Val Asp Phe Ala Ala Thr
            20                  25                  30
Lys Thr Leu Ala Leu Ser His Gly Thr Trp Arg Gly Ile Glu Val Gly
        35                  40                  45
Gly Tyr Glu Ile His His Gly Arg Leu Ser Phe Ala Glu Asp Ala Glu
    50                  55                  60
Ala Phe Leu Asp Gly Val His Val Gly Pro Val Trp Gly Thr Met Trp
65                  70                  75                  80
His Gly Ala Phe Glu His Asp Glu Phe Arg Arg Thr Trp Leu Ala Asp
                85                  90                  95
Ala Ala Arg His Ala Gly Ser Ser Trp Arg Pro His Ser Asp Glu Leu
            100                 105                 110
Gly Tyr Gln Ala Arg Arg Glu Ala Met Ile Glu Thr Leu Ala Asp Ala
        115                 120                 125
```

<210> 941
<211> 348
<212> DNA
<213> Homo sapiens

<400> 941
atcttctggt cggcggtgat cacgctggtg accatcggcc tgctgtttgc cggcaacttc
60
gaagccatgc aaaccatggt cgtgctggcc gggctgccgt tctcggtggt gctgattttc
120
ttcatgttcg gtttgcacaa ggcgatgcgc caggacgtgg ccatggagca ggagcaggca
180
caattggctg aacgtggtcg ccgtggtttc agcgagcgcc tgaccgcgct ggacctgcaa
240
ccgagccagg gcaccgtgca acgctttatg gacaaacatg tgacgccggc gttggaacaa
300
gcggcgactg cgttgcgtga tcaagggctg gaagtgcaga ccctgctt
348

<210> 942
<211> 116
<212> PRT
<213> Homo sapiens

<400> 942

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Ile Phe Trp Ser Ala Val Ile Thr Leu Val Thr Ile Gly Leu Leu Phe
 1               5                  10                  15
Ala Gly Asn Phe Glu Ala Met Gln Thr Met Val Val Leu Ala Gly Leu
            20                  25                  30
Pro Phe Ser Val Val Leu Ile Phe Phe Met Phe Gly Leu His Lys Ala
        35                  40                  45
Met Arg Gln Asp Val Ala Met Glu Gln Glu Gln Ala Gln Leu Ala Glu
    50                  55                  60
Arg Gly Arg Arg Gly Phe Ser Glu Arg Leu Thr Ala Leu Asp Leu Gln
65                  70                  75                  80
Pro Ser Gln Gly Thr Val Gln Arg Phe Met Asp Lys His Val Thr Pro
                85                  90                  95
Ala Leu Glu Gln Ala Ala Thr Ala Leu Arg Asp Gln Gly Leu Glu Val
```

100 105 110
Gln Thr Leu Leu
115

<210> 943
<211> 439
<212> DNA
<213> Homo sapiens

<400> 943
ccatggcagg agcagagcag atagagcagg acctcgtctc cttctctttg cattttgtgc
60
ctcctctaat gcatcctggg ctcctgctaa ccctgtggga aacaccgtct cttctctcct
120
ttgccctctt ctgtgatcac atcctcactt ctgagcctat ctgcccatcc agtcaatccc
180
ccttggttct gggatgctat ttccctggcc gcctccctct aggagtgttt agaaccctca
240
ctgtgggcag aagggaggga agatggctga ggtacctgga aagggacgtg tggatccccg
300
ggcatggaag gaaggaggca ggagagctag aaaaagggat gagatctaat gttccctaag
360
gaacctggct tagtgctggc ccttcacata ctgagacatg gaatccttac tactgttctc
420
tgaggaaaga ggctgttcc
439

<210> 944
<211> 118
<212> PRT
<213> Homo sapiens

<400> 944
Met Ala Gly Ala Glu Gln Ile Glu Gln Asp Leu Val Ser Phe Ser Leu
1 5 10 15
His Phe Val Pro Pro Leu Met His Pro Gly Leu Leu Leu Thr Leu Trp
20 25 30
Glu Thr Pro Ser Leu Leu Ser Phe Ala Leu Phe Cys Asp His Ile Leu
35 40 45
Thr Ser Glu Pro Ile Cys Pro Ser Ser Gln Ser Pro Leu Val Leu Gly
50 55 60
Cys Tyr Phe Pro Gly Arg Leu Pro Leu Gly Val Phe Arg Thr Leu Thr
65 70 75 80
Val Gly Arg Arg Glu Gly Arg Trp Leu Arg Tyr Leu Glu Arg Asp Val
85 90 95
Trp Ile Pro Gly His Gly Arg Lys Glu Ala Gly Glu Leu Glu Lys Gly
100 105 110
Met Arg Ser Asn Val Pro
115

<210> 945
<211> 339
<212> DNA
<213> Homo sapiens

<400> 945
ngaattcgtg aagcgttcca tatttttttc cttttaataa tttcaattgc actttatgtc
60
gagatggtga tatatatata tactcacaca catatatatg tgtgtgtgtg tatatatgta
120
tatatatata gcgtgtacaa caaaacatgc actgtttact cagcaccccg tgtttgtctc
180
agcaatagct tttctaaaga actgctacta tttgaaatgg agggggaggg gggtcctgga
240
cagagtattg tgcaagttga aagtctctgg atggggctat gtatatccta ccagccaatt
300
tgggtgcaaa ttggatttga aggcctgcct ctgtccacn
339

<210> 946
<211> 113
<212> PRT
<213> Homo sapiens

<400> 946
Xaa Ile Arg Glu Ala Phe His Ile Phe Phe Leu Leu Ile Ile Ser Ile
 1   5   10   15
Ala Leu Tyr Val Glu Met Val Ile Tyr Ile Tyr Thr His Thr His Ile
            20   25   30
Tyr Val Cys Val Cys Ile Tyr Val Tyr Ile Tyr Ser Val Tyr Asn Lys
        35   40   45
Thr Cys Thr Val Tyr Ser Ala Pro Arg Val Cys Leu Ser Asn Ser Phe
    50   55   60
Ser Lys Glu Leu Leu Leu Phe Glu Met Glu Gly Glu Gly Gly Pro Gly
65   70   75   80
Gln Ser Ile Val Gln Val Glu Ser Leu Trp Met Gly Leu Cys Ile Ser
                85   90   95
Tyr Gln Pro Ile Trp Val Gln Ile Gly Phe Glu Gly Leu Pro Leu Ser
            100   105   110
Thr

<210> 947
<211> 648
<212> DNA
<213> Homo sapiens

<400> 947
tctagatctg ttctcaggga agctgagatg gagatgagtg ggcagcaggt ttatggagtg
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ctcgtggcat cacacctgtg cacgggggtg gggaaggagt ggacaggagt ggacaagtca
120
agtagtgctg ccggctcaag cgatgcctca gcctttctgc tgtgtgcgaa gctttgcaga
180
ggagatgatg cttcaaagtt gtccctgttg gggatgagca gccaggcctt tatacactgg
240
gacagtcagt catggatacg tggatactct ggaaaccctc atccctggag gtctgagccc
300

ctggatacca tgcccttctt aggctggagt tgctgccctt gtccatttac cataaaaatt
360
ggacaagaga ataccaggac acacctgagt ttctcatcgt atgctaaacc tgttcttcca
420
cgtacatccc caatgtgtac agccctactt ttttctgctg atcaagttca attacttctg
480
ctaagatggt gactattctt gcctgctggt ccttggatgc aaggacccca atgttcaggc
540
agcctttggt gccttctagc atacgaatca gagcattatc tttaggtgtg gaataagctg
600
ccccaaaacc tgttgaagcc agccaggcac tgtgctccct tcacgcgt
648

<210> 948
<211> 154
<212> PRT
<213> Homo sapiens

<400> 948
Met Glu Met Ser Gly Gln Gln Val Tyr Gly Val Leu Val Ala Ser His
1 5 10 15
Leu Cys Thr Gly Val Gly Lys Glu Trp Thr Gly Val Asp Lys Ser Ser
20 25 30
Ser Ala Ala Gly Ser Ser Asp Ala Ser Ala Phe Leu Leu Cys Ala Lys
35 40 45
Leu Cys Arg Gly Asp Asp Ala Ser Lys Leu Ser Leu Leu Gly Met Ser
50 55 60
Ser Gln Ala Phe Ile His Trp Asp Ser Gln Ser Trp Ile Arg Gly Tyr
65 70 75 80
Ser Gly Asn Pro His Pro Trp Arg Ser Glu Pro Leu Asp Thr Met Pro
85 90 95
Phe Leu Gly Trp Ser Cys Cys Pro Cys Pro Phe Thr Ile Lys Ile Gly
100 105 110
Gln Glu Asn Thr Arg Thr His Leu Ser Phe Ser Ser Tyr Ala Lys Pro
115 120 125
Val Leu Pro Arg Thr Ser Pro Met Cys Thr Ala Leu Leu Phe Ser Ala
130 135 140
Asp Gln Val Gln Leu Leu Leu Leu Arg Trp
145 150

<210> 949
<211> 661
<212> DNA
<213> Homo sapiens

<400> 949
acgcgtactg gttggctcat tcactgaaaa tatgatgaca tttaaaggaa atgcaagaat
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aagtaatgtg gaattttatc acagtggtca agaaggcttc agggatagca cagatccaag
120
atatgctgta acgtttctta acctaggaca gattcaagaa catggctcat cttatattcg
180
aggctgtgct tttcaccatg gcttctctcc agcaattggt gtatttggga cagatggatt
240

ggacatagat gacaacatca ttcactttac agtgggggaa ggcataagaa tatgggggaa
300
tgccaaccga gtccgaggga atttgattgc actttcggtt tggccaggaa cctatcagaa
360
cagaaaagat ttaagttcaa ctctctggca tgcagcaatt gagataaata gagggaccaa
420
tacagtttta cagaataatg tagtggctgg atttggaaga gcaggatacc gcattgatgg
480
tgaaccttgc ccaggccagt ttaatcctgt ggaaaagtgg tttgacaatg aagcccatgg
540
aggtttatat gggatctata tgaaccaaga tggccttcct ggatgttctc ttatacaagg
600
atttaccatt tggacatgct gggattatgg aatttatttt cagaccacag agagtgtgca
660
c
661

<210> 950
<211> 210
<212> PRT
<213> Homo sapiens

<400> 950
Met Met Thr Phe Lys Gly Asn Ala Arg Ile Ser Asn Val Glu Phe Tyr
 1   5   10   15
His Ser Gly Gln Glu Gly Phe Arg Asp Ser Thr Asp Pro Arg Tyr Ala
            20   25   30
Val Thr Phe Leu Asn Leu Gly Gln Ile Gln Glu His Gly Ser Ser Tyr
        35   40   45
Ile Arg Gly Cys Ala Phe His His Gly Phe Ser Pro Ala Ile Gly Val
    50   55   60
Phe Gly Thr Asp Gly Leu Asp Ile Asp Asp Asn Ile Ile His Phe Thr
65   70   75   80
Val Gly Glu Gly Ile Arg Ile Trp Gly Asn Ala Asn Arg Val Arg Gly
                85   90   95
Asn Leu Ile Ala Leu Ser Val Trp Pro Gly Thr Tyr Gln Asn Arg Lys
            100   105   110
Asp Leu Ser Ser Thr Leu Trp His Ala Ala Ile Glu Ile Asn Arg Gly
        115   120   125
Thr Asn Thr Val Leu Gln Asn Asn Val Val Ala Gly Phe Gly Arg Ala
    130   135   140
Gly Tyr Arg Ile Asp Gly Glu Pro Cys Pro Gly Gln Phe Asn Pro Val
145   150   155   160
Glu Lys Trp Phe Asp Asn Glu Ala His Gly Gly Leu Tyr Gly Ile Tyr
                165   170   175
Met Asn Gln Asp Gly Leu Pro Gly Cys Ser Leu Ile Gln Gly Phe Thr
            180   185   190
Ile Trp Thr Cys Trp Asp Tyr Gly Ile Tyr Phe Gln Thr Thr Glu Ser
        195   200   205
Val His
    210

<210> 951
<211> 2615

<212> DNA
<213> Homo sapiens

<400> 951
nntccagccc ccaccatgcc gtggcccctg ctgctgctgc tggccgtgag tggggcccag
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acaacccggc catgcttccc cgggtgccaa tgcgaggtgg agaccttcgg ccttttcgac
120
agcttcagcc tgactcgggt ggattgtagc ggcctgggcc cccacatcat gccggtgccc
180
atccctctgg acacagccca cttggacctg tcctccaacc ggctggagat ggtgaatgag
240
tcggtgttgg cggggccggg ctacacgacg ttggctggcc tggatctcag ccacaacctg
300
ctcaccagca tctcacccac tgccttctcc cgccttcgct acctggagtc gcttgacctc
360
agccacaatg gcctgacagc cctgccagcc gagagcttca ccagctcacc cctgagcgac
420
gtgaacctta gccacaacca gctccgggag gtctcagtgt ctgccttcac gacgcacagt
480
cagggccggg cactacacgt ggacctctcc cacaacctct caccgcctcg tgccccaccc
540
cacgagggcc ggcctgcctg cgcccaccat tcagagcctg aacctggcct ggaaccggct
600
ccatgccgtg cccaacctcg agacttgccc ctgcgctacc tgagcctgga tgggaaccct
660
ctagctgtca ttggtccggg tgccttcgcg gggctgggag gccttacaca cctgtctctg
720
gccagcctgc agaggctccc tgagctggcg cccagtggct tccgtgagct accgggcctg
780
caggtcctgg acctgtcggg caaccccaag cttaactggg caggagctga ggtgttttca
840
ggcctgagct ccctgcagga gctggacctt tcgggcacca acctggtgcc cctgcctgag
900
gcgctgctcc tccacctccc ggcactgcag agcgtcagcg tgggccagga tgtgcggtgc
960
cggcgcctgg tgcgggaggg cacctacccc cggaggcctg gctccagccc caaggtggcc
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1080
gtgtggccca gggccacata acagactgct gtcctgggct gcctcaggtc ccgagtaact
1140
tatgttcaat gtgccaacac cagtggggag cccgcaggcc tatgtggcag cgtcaccaca
1200
ggagttgtgg gcctaggaga ggctttggac ctgggagcca cacctaggag caaagtctca
1260
ccccctttgtc tacgttgctt ccccaaacca tgagcagagg gacttcgatg ccaaaccaga
1320
ctcgggtccc ctcctgcttc ccttccccac ttatccccca agtgccttcc ctcatgcctg
1380
ggccggcctg acccgcaatg ggcagagggt gggtgggacc ccctgctgca gggcagagtt
1440
caggtccact gggctgagtg tccccttggg cccatggccc agtcactcag gggcgagttt
1500

cttttctaac atagcccttt ctttgccatg aggccatgag gcccgcttca tccttttcta
1560
tttccctaga accttaatgg tagaaggaat tgcaaagaat caagtccacc cttctcatgt
1620
gacagatggg gaaactgagg ccttgagaag gaaaaaggct aatctaagtt cctgcgggca
1680
gtggcatgac tggagcacag cctcctgcct cccagcccgg acccaatgca ctttcttgtc
1740
tcctctaata agccccaccc tccccgcctg ggctcccctt gctgcccttg cctgttcccc
1800
attagcacag gagtagcagc agtaggacag gcaagagcct cacaagtggg actctgggcc
1860
tctgaccagc tgtgcggcat gggctaagtc actctgccct tcggagcctc tggaagctta
1920
gggcacattg gttccagcct agccagtttc tcaccctggg ttggggtccc ccagcatcca
1980
gactggaaac ctacccattt tcccctgagc atcctctaga tgctgcccca aggagttgct
2040
gcagttctgg agcctcatct ggctgggatc tccaaggggc ctcctggatt cagtccccac
2100
tggccctgag cacgacagcc cttcttaccc tcccaggaat gccgtgaaag gagacaaggt
2160
ctgcccgacc catgtctatg ctctaccccc agggtagcat ctcagcttcc gaaccctggg
2220
ctgtttcctt agtcttcatt ttataaaagt tgttgccttt ttaacggagt gtcactttca
2280
accggcctcc cctacccctg ctggccgggg atggagacat gtcatttgta aaagcagaaa
2340
aaggttgcat ttgttcactt ttgtaatatt gtcctgggcc tgtgttgggg tgttggggga
2400
agctgggcat cagtggccac atgggcatca ggggctggcc ccacagagac cccacagggc
2460
agtgagctct gtcttccccc acctgcctag cccatcatct atctaaccgg tccttgattt
2520
aataaacact ataaaatgaa gactaaggaa acagcccagg gttcggaagc tgagatgcta
2580
ccctgggggt agagcataga catgggtcgg gcaga
2615

<210> 952
<211> 357
<212> PRT
<213> Homo sapiens

<400> 952
Xaa Pro Ala Pro Thr Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val
1 5 10 15
Ser Gly Ala Gln Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu
20 25 30
Val Glu Thr Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp
35 40 45
Cys Ser Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp
50 55 60
Thr Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu

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65                  70                  75                  80
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu
                85                  90                  95
Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser Arg Leu
            100                 105                 110
Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu Thr Ala Leu
        115                 120                 125
Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp Val Asn Leu Ser
    130                 135                 140
His Asn Gln Leu Arg Glu Val Ser Val Ser Ala Phe Thr Thr His Ser
145                 150                 155                 160
Gln Gly Arg Ala Leu His Val Asp Leu Ser His Asn Leu Ser Pro Pro
                165                 170                 175
Arg Ala Pro Pro His Glu Gly Arg Pro Ala Cys Ala His His Ser Glu
            180                 185                 190
Pro Glu Pro Gly Leu Glu Pro Ala Pro Cys Arg Ala Gln Pro Arg Asp
        195                 200                 205
Leu Pro Leu Arg Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Val Ile
    210                 215                 220
Gly Pro Gly Ala Phe Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu
225                 230                 235                 240
Ala Ser Leu Gln Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu
                245                 250                 255
Leu Pro Gly Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn
            260                 265                 270
Trp Ala Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu
        275                 280                 285
Asp Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
    290                 295                 300
His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys
305                 310                 315                 320
Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser
                325                 330                 335
Pro Lys Val Ala Leu His Cys Val Asp Thr Arg Glu Ser Ala Ala Arg
            340                 345                 350
Gly Pro Thr Ile Leu
        355
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<210> 953
<211> 347
<212> DNA
<213> Homo sapiens

<400> 953
acgcgtgaag ccatccctgt gcgcaggcca gtctcgcggg ggtcaccacg gagcgtgtgc
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accacacttt ccccatccct tgatccatca ttgggcgttg aggttttccc atgtcttgac
120
tgttgtacct ggcggctctg cggagtaacc gctgcggaca cacagtagga cgggagggag
180
aagccattgc gtttcaccct ttcatggccc ttcctttccc cttccaagtg agctctttga
240
ggtgagtcat ggagggcagt gtccctctgc atcctgtctg gggttgtcaa atatggccaa
300

gtgggctcca tcggggcagc gggtggggtg gggggtgtct gtcagag
347

<210> 954
<211> 103
<212> PRT
<213> Homo sapiens

<400> 954
Met Glu Pro Thr Trp Pro Tyr Leu Thr Thr Pro Asp Arg Met Gln Arg
1 5 10 15
Asp Thr Ala Leu His Asp Ser Pro Gln Arg Ala His Leu Glu Gly Glu
20 25 30
Arg Lys Gly His Glu Arg Val Lys Arg Asn Gly Phe Ser Leu Pro Ser
35 40 45
Tyr Cys Val Ser Ala Ala Val Thr Pro Gln Ser Arg Gln Val Gln Gln
50 55 60
Ser Arg His Gly Lys Thr Ser Thr Pro Asn Asp Gly Ser Arg Asp Gly
65 70 75 80
Glu Ser Val Val His Thr Leu Arg Gly Asp Pro Arg Glu Thr Gly Leu
85 90 95
Arg Thr Gly Met Ala Ser Arg
100

<210> 955
<211> 634
<212> DNA
<213> Homo sapiens

<400> 955
acgcgtgaag ggctctgcag gtgagcggct ctgcaggtga agggttctgc aggtgagcgg
60
ctctgcaggt gaatggttct gcaggtgaag ggctctgcag gtgaacggtt ctgcaggtga
120
agggctctgc aggtgaacgg ttctgcaggt gagcggctct gcaggtgagc ggctctgcat
180
gtgagtgcct ctgtgactgg ctcgcaagca gcatttgtgc acacttgact ggccacaaca
240
gaatgttctt ctctgttgtc agcactgagg aggaagctcc tgcctaagcg accacagcca
300
ggcacccgct ccatggagac attgctctct ccagactcca ttcagactca ggaaacctga
360
gctcctggaa tgcaggctga ggcagctccc acacaaaagc tatctactct ggcagttatc
420
agaggcctcc gttgcacaaa tcacacacct actgtgcctg acgtggctgg gcctccagca
480
ggacccgctc ctgagaacac acgggtgcta gtccaagttc acagcacggc tcaagtcact
540
cccacaaacc tctctataca aacacacaaa gctctgggag gctaccctgc atccaagagt
600
caccatctca cacctggaac aagggttacg gccg
634

<210> 956

<211> 113
<212> PRT
<213> Homo sapiens

<400> 956
Met Glu Ser Gly Glu Ser Asn Val Ser Met Glu Arg Val Pro Gly Cys
1 5 10 15
Gly Arg Leu Gly Arg Ser Phe Leu Leu Ser Ala Asp Asn Arg Glu Glu
20 25 30
His Ser Val Val Ala Ser Gln Val Cys Thr Asn Ala Ala Cys Glu Pro
35 40 45
Val Thr Glu Ala Leu Thr Cys Arg Ala Ala His Leu Gln Ser Arg Ser
50 55 60
Pro Ala Glu Pro Phe Thr Cys Arg Ala Leu His Leu Gln Asn Arg Ser
65 70 75 80
Pro Ala Glu Pro Phe Thr Cys Arg Thr Ile His Leu Gln Ser Arg Ser
85 90 95
Pro Ala Glu Pro Phe Thr Cys Arg Ala Ala His Leu Gln Ser Pro Ser
100 105 110
Arg

<210> 957
<211> 823
<212> DNA
<213> Homo sapiens

<400> 957
acgcgtggcc tgaccaccgt gtcccgccca tctacaggtg cccgagatcg tgagcgtcct
60
gcgctccaag cttcaggagg cccagggaga gcacgtcctg ccggccaccc agcacagcgt
120
gtacctcctg gccacccagc actgcgcagc cgtggtgtcc agcctcctgg gcagcccctt
180
gcccttggac aggtacccag ctcagactcc aggcttaggg gtccctctgg aatgatgctc
240
cccctggaat gatgctcccc gagccctcca cccggctctg caccccgact ttctgcatga
300
gttcccatgg ctgtaggcca cgtgggacag aaagtgacat ggagccaggc cccagtctct
360
caggtaccca cggggacctc tcctctccag gcgttttggg atcctcactg gctccggtgg
420
gccctgcaca gcacccccac agggaagctg ctgtttctgc cttcctctaa ggtcccaaaa
480
ctgcctggct gctctgttgg ccccaggctc cagcacacac tggaggctgc ccctcaccct
540
gtgtcttggt tccggctact ccaagccttg tcctctgcag ggcatccact gctgcctgtg
600
agcagacccc tgggaactgc ctgatctgag ccccctcagg agcccaagga caaccttgtc
660
tgtaccatac atcactatgt cttcccaagc tcacacctcc cagctcccag caaagggcag
720
ggcgtgtcta ccacccacca gcccactggg gtcccccttc ctcgccgagg cctccggagc
780

atgggtctgc tggcccttcc tttctttgcc tcttagtctg gaa
823

<210> 958
<211> 105
<212> PRT
<213> Homo sapiens

<400> 958
Met Ala Val Gly His Val Gly Gln Lys Val Thr Trp Ser Gln Ala Pro
1 5 10 15
Val Ser Gln Val Pro Thr Gly Thr Ser Pro Leu Gln Ala Phe Trp Asp
20 25 30
Pro His Trp Leu Arg Trp Ala Leu His Ser Thr Pro Thr Gly Lys Leu
35 40 45
Leu Phe Leu Pro Ser Ser Lys Val Pro Lys Leu Pro Gly Cys Ser Val
50 55 60
Gly Pro Arg Leu Gln His Thr Leu Glu Ala Ala Pro His Pro Val Ser
65 70 75 80
Trp Phe Arg Leu Leu Gln Ala Leu Ser Ser Ala Gly His Pro Leu Leu
85 90 95
Pro Val Ser Arg Pro Leu Gly Thr Ala
100 105

<210> 959
<211> 586
<212> DNA
<213> Homo sapiens

<400> 959
ngtcatgact gcatggccaa gcatgactcc aacaccatca ttaagtttgc cgacgacaca
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acagtggtag gcctgatcac cgacaacgat gaggcagcct atagggagga ggtcagagac
120
ctggcagtgt ggtgccagga taacaacctc tccctcaacg tgatcaagac cacgaagatg
180
atcgtggact acaggaaaag gagggtcgag cacgccccca ttctcattga tggggctgta
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300
tccaaacaca ccaagacagt agtgaagagg gtgcgacaat gcctattcca cctcggtaga
360
caaaaaagat ttggaatgga tcctcagacc ctcaaaaagt ttgacatcta caccatcgag
420
agcatcatga ctggttgcat caccgcctgg tatggcaact gctcggcctc cgaccgcaag
480
gcactacaga gggtagtgcg tacggcccag tacatcactg gggctaagct tcctgccatc
540
caggacctct ataccaggcg gtgtcagcgg aagaccctga caattg
586

<210> 960
<211> 195
<212> PRT

<213> Homo sapiens

<400> 960
Xaa His Asp Cys Met Ala Lys His Asp Ser Asn Thr Ile Ile Lys Phe
1 5 10 15
Ala Asp Asp Thr Thr Val Val Gly Leu Ile Thr Asp Asn Asp Glu Ala
20 25 30
Ala Tyr Arg Glu Glu Val Arg Asp Leu Ala Val Trp Cys Gln Asp Asn
35 40 45
Asn Leu Ser Leu Asn Val Ile Lys Thr Thr Lys Met Ile Val Asp Tyr
50 55 60
Arg Lys Arg Arg Val Glu His Ala Pro Ile Leu Ile Asp Gly Ala Val
65 70 75 80
Trp Glu Pro Val Glu Ser Phe Lys Phe Leu Gly Val His Ile Thr Ile
85 90 95
Glu Leu Ser Trp Ser Lys His Thr Lys Thr Val Val Lys Arg Val Arg
100 105 110
Gln Cys Leu Phe His Leu Gly Arg Gln Lys Arg Phe Gly Met Asp Pro
115 120 125
Gln Thr Leu Lys Lys Phe Asp Ile Tyr Thr Ile Glu Ser Ile Met Thr
130 135 140
Gly Cys Ile Thr Ala Trp Tyr Gly Asn Cys Ser Ala Ser Asp Arg Lys
145 150 155 160
Ala Leu Gln Arg Val Val Arg Thr Ala Gln Tyr Ile Thr Gly Ala Lys
165 170 175
Leu Pro Ala Ile Gln Asp Leu Tyr Thr Arg Arg Cys Gln Arg Lys Thr
180 185 190
Leu Thr Ile
195

<210> 961
<211> 502
<212> DNA
<213> Homo sapiens

<400> 961
acgcgttgtc gtctctccgt agaccattca gtttggcaaa acttccactg gagtctgtgc
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atgactggat ggtctctttg acagccctgt caaggaatac caacagaata ttgattctcc
120
taaactgtat agtaacctgc taaccagtcg gaaagagcta ccacccaatg gagatactaa
180
atccatggta atggaccatc gagggcaacc tccagagttg gctgctcttc ccactcctga
240
gtctacaccc gtgcttcacc agaagaccct gcaggccatg aagagccact cagaaaaggc
300
ccatggccat ggagcttcaa ggaaagaaac ccctcagttt tttccgtcta gtccgccacc
360
tcattcccca ataagtcatg ggcatatccc cagtgccatt gttcttccaa atgctaccca
420
tgactacaac acgtctttct caaactccaa tgctcacaaa gctgaaaaga agcttcaaaa
480
cattgatcac cccttcacgc gt
502

<210> 962
<211> 106
<212> PRT
<213> Homo sapiens

<400> 962
Met Val Met Asp His Arg Gly Gln Pro Pro Glu Leu Ala Ala Leu Pro
1 5 10 15
Thr Pro Glu Ser Thr Pro Val Leu His Gln Lys Thr Leu Gln Ala Met
20 25 30
Lys Ser His Ser Glu Lys Ala His Gly His Gly Ala Ser Arg Lys Glu
35 40 45
Thr Pro Gln Phe Phe Pro Ser Ser Pro Pro Pro His Ser Pro Ile Ser
50 55 60
His Gly His Ile Pro Ser Ala Ile Val Leu Pro Asn Ala Thr His Asp
65 70 75 80
Tyr Asn Thr Ser Phe Ser Asn Ser Asn Ala His Lys Ala Glu Lys Lys
85 90 95
Leu Gln Asn Ile Asp His Pro Phe Thr Arg
100 105

<210> 963
<211> 1298
<212> DNA
<213> Homo sapiens

<400> 963
nntcgcgagc acactccagc ctctggggag caggccacag aacgcagggt gaaacccaag
60
gcgctctaga ggagatgaat tatggatccg ccctcccgga atcctggctc ggccctcccc
120
acgccaccca gggccagtcg ggtctgctca cagcccgagg aggccgcgtg tccagccgcg
180
ggcaagagac agagcaggtc cctgtgtatc caagtccctg agcccgtgac accggcccca
240
ggccctgtag agagccagca gccaccatgg cgaaggagga agatgaggag aagaaagcca
300
agaaagggaa gaaggggaag aaggcaccgg acccggagaa gcccaaacgg agcctgaagg
360
ggacgtcgcg ggtgttcatg ggcttccgcg accgaacacc caagatctac aagaagggcc
420
agttccgcag cgcctcggcc ttcttctggg gcctccacac cggcccccac aagaccaagc
480
gcacgaggaa ggcccgcacc gtgctcgggt acacgtcaga gcttatgacg cacatgcgca
540
tgggcaagaa gaagcgggcg atgaagggca agaagccgtc cttcatggtg atccgcttcc
600
caggccgccg tggctacggc cgcctgcggc cgcgcgcccg gtcactcagc aaagcgtcca
660
cggccatcaa ctggctcaca aaaaagttcc tcctcaagaa ggccgaggag tcgggcagcg
720
aacaggccac agtggacgcc tggctgcagc gctcgagctc ccgcatgggc tcccgcaaac
780

tccccttccc gtcgggtgcc gagatcctgc ggcctggggg ccggctccgg aggttccccc
840
gcagccgcag catctacgcg tcaggcgagc ccctgggctt cctgcccttc gaggacgagg
900
ccccattcca tcactcgggc tcccgcaagt cgctgtacgg gcttgagggc ttccaggacc
960
tgggcgagta ttatgactat caccgcgacg gcgacgacta ctacgaccgg cagtcactcc
1020
accgctacga ggagcaggaa ccctacctgg cgggcctcgg cccctacagc ccggcctggc
1080
caccctacgg cgaccactac tacgggtacc cgcccgagga tccctacgac tactaccacc
1140
ccgactatta cggtggcccc gttgatccgg ggtacaccta cggctacggc tacgacgatt
1200
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1260
acgagggcga ggcgcaccct tatggctact acctggat
1298

<210> 964
<211> 235
<212> PRT
<213> Homo sapiens

<400> 964
Ser Ala Ser Gln Ala Ala Val Ala Thr Ala Ala Cys Gly Arg Ala Pro
1 5 10 15
Gly His Ser Ala Lys Arg Pro Arg Pro Ser Thr Gly Ser Gln Lys Ser
20 25 30
Ser Ser Ser Arg Arg Pro Arg Ser Arg Ala Ala Asn Arg Pro Gln Trp
35 40 45
Thr Pro Gly Cys Ser Ala Arg Ala Pro Ala Trp Ala Pro Ala Asn Ser
50 55 60
Pro Ser Arg Arg Val Pro Arg Ser Cys Gly Leu Gly Ala Gly Ser Gly
65 70 75 80
Gly Ser Pro Ala Ala Ala Ala Ser Thr Arg Gln Ala Ser Pro Trp Ala
85 90 95
Ser Cys Pro Ser Arg Thr Arg Pro His Ser Ile Thr Arg Ala Pro Ala
100 105 110
Ser Arg Cys Thr Gly Leu Arg Ala Ser Arg Thr Trp Ala Ser Ile Met
115 120 125
Thr Ile Thr Ala Thr Ala Thr Thr Thr Thr Thr Gly Ser His Ser Thr
130 135 140
Ala Thr Arg Ser Arg Asn Pro Thr Trp Arg Ala Ser Ala Pro Thr Ala
145 150 155 160
Arg Pro Gly His Pro Thr Ala Thr Thr Thr Thr Gly Thr Arg Pro Arg
165 170 175
Ile Pro Thr Thr Thr Thr Thr Pro Thr Ile Thr Val Ala Pro Leu Ile
180 185 190
Arg Gly Thr Pro Thr Ala Thr Ala Thr Thr Ile Thr Asn Pro His Met
195 200 205
Arg Pro Arg Arg Gly Thr Arg Leu Leu Thr Ala Thr Thr Met Gly Thr
210 215 220
Arg Ala Arg Arg Thr Leu Met Ala Thr Thr Trp

225 230 235

<210> 965
<211> 336
<212> DNA
<213> Homo sapiens

<400> 965
nnngtgacca ttatgggtgg tgcccgtacc cgtgaagtgg aaggcgttga ttttgttggc
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cgggtcagcg atgccgaaaa ggctgaaatc ctcggccgcg ccgatgtgta tgtcgccccc
120
aataccggcg gtgagagctt tggcattgtc ttggtggaag ccatggcggc aggcgcagcc
180
gttgttgctt cagacttgga ggccttccgc gcagtgtgca acgccgattc cgatgatgtt
240
gccggcgcgc tatatcgcaa tgaggatagt aatgaccttg ctcgtgtact caacgaggtg
300
ctcgaggatc ctgagtatcg tgcccgctta gtgcac
336

<210> 966
<211> 112
<212> PRT
<213> Homo sapiens

<400> 966
Xaa Val Thr Ile Met Gly Gly Ala Arg Thr Arg Glu Val Glu Gly Val
1 5 10 15
Asp Phe Val Gly Arg Val Ser Asp Ala Glu Lys Ala Glu Ile Leu Gly
20 25 30
Arg Ala Asp Val Tyr Val Ala Pro Asn Thr Gly Gly Glu Ser Phe Gly
35 40 45
Ile Val Leu Val Glu Ala Met Ala Ala Gly Ala Ala Val Val Ala Ser
50 55 60
Asp Leu Glu Ala Phe Arg Ala Val Cys Asn Ala Asp Ser Asp Asp Val
65 70 75 80
Ala Gly Ala Leu Tyr Arg Asn Glu Asp Ser Asn Asp Leu Ala Arg Val
85 90 95
Leu Asn Glu Val Leu Glu Asp Pro Glu Tyr Arg Ala Arg Leu Val His
100 105 110

<210> 967
<211> 393
<212> DNA
<213> Homo sapiens

<400> 967
ncaaatggca attcatagcc cgccagatcg gacacggagc tggtggtatc cacggattcg
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ggcgcggagg cgtcgggctc aagctccgct tcggcaccgg tcggcactga ggaatctccg
120
tcggcctccg cttcggccgc agcctgggct gcgccagact ctgcgggagg caccttctcc
180

cgggttcgcc agccaaatgg cgttgcaggc tccagcatcc agtccggtgc cttcggcacc
240
cccgcactgc gcagagaggc cgccagaaac gatggcaccg gcggcgcggg aggtgataca
300
ggcgcttcgg ccggagcgct cacggactcc ggcactacag gtgcagcttg cgcttcctgc
360
ggcggagcaa cagggtcact tcgaggcggg gat
393

<210> 968
<211> 125
<212> PRT
<213> Homo sapiens

<400> 968
Pro Ala Arg Ser Asp Thr Glu Leu Val Val Ser Thr Asp Ser Gly Ala
 1   5   10   15
Glu Ala Ser Gly Ser Ser Ser Ala Ser Ala Pro Val Gly Thr Glu Glu
            20   25   30
Ser Pro Ser Ala Ser Ala Ser Ala Ala Ala Trp Ala Ala Pro Asp Ser
        35   40   45
Ala Gly Gly Thr Phe Ser Arg Val Arg Gln Pro Asn Gly Val Ala Gly
    50   55   60
Ser Ser Ile Gln Ser Gly Ala Phe Gly Thr Pro Ala Leu Arg Arg Glu
65   70   75   80
Ala Ala Arg Asn Asp Gly Thr Gly Gly Ala Gly Gly Asp Thr Gly Ala
                85   90   95
Ser Ala Gly Ala Leu Thr Asp Ser Gly Thr Thr Gly Ala Ala Cys Ala
            100   105   110
Ser Cys Gly Gly Ala Thr Gly Ser Leu Arg Gly Gly Asp
        115   120   125

<210> 969
<211> 880
<212> DNA
<213> Homo sapiens

<400> 969
caattgtcat gcaggacacc aaagatgaac acaggcttca cagtggcaaa ctctgtctga
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ttatccttac atgtattgca gaggatcaat atgaccatgc atttttgcat gatgatcaac
120
atgaattttc gagtaaactt acatagaatg cctatgagac acaggaagaa ggcagcagac
180
aagaatctta ccctgccgtc tttagtatgt gaagtactgg acctgatggt agagtttatt
240
gtaacacaca tgatgaagga gtttcctatg gatctctata tacgctgcat ccaggtagta
300
cacaaactgc tctgctacca gaagaagtgt cgggtacgcc tgcattacac ctggcgggag
360
ctctggtcag ccttgataaa tttgctgaag ttccttatgt caaatgagac tgtacttttg
420
gccaaacaca acatttttac attagccctt atgattgtga acctatttaa tatgtttatc
480

acatatggcg acacatttct gccaaccccc agcagctatg atgaacttta ctatgagatt
540
atccgcatgc accagagctt tgacaacctc tactccatgg tcctgaggct ttctaccaat
600
gcaggccagt ggaaggaagc agctagcaag gtgacccatg cattggttaa tatcagagcc
660
atcatcaacc actttaaccc caaaattgag tcctacgctg ctgtgaatca catatcccaa
720
ctgtcagagg agcaggtgct ggaggtggtg agagccaact atgacacgct cacgctgaag
780
ctgcaggatg gcctggacca gtatgagcgc tactcagagc agcacaagga agctgccttc
840
ttcaaagagc tggttcgatc cattagcacc aacgtccgga
880

<210> 970
<211> 263
<212> PRT
<213> Homo sapiens

<400> 970
Met Thr Met His Phe Cys Met Met Ile Asn Met Asn Phe Arg Val Asn
1 5 10 15
Leu His Arg Met Pro Met Arg His Arg Lys Lys Ala Ala Asp Lys Asn
20 25 30
Leu Thr Leu Pro Ser Leu Val Cys Glu Val Leu Asp Leu Met Val Glu
35 40 45
Phe Ile Val Thr His Met Met Lys Glu Phe Pro Met Asp Leu Tyr Ile
50 55 60
Arg Cys Ile Gln Val Val His Lys Leu Leu Cys Tyr Gln Lys Lys Cys
65 70 75 80
Arg Val Arg Leu His Tyr Thr Trp Arg Glu Leu Trp Ser Ala Leu Ile
85 90 95
Asn Leu Leu Lys Phe Leu Met Ser Asn Glu Thr Val Leu Leu Ala Lys
100 105 110
His Asn Ile Phe Thr Leu Ala Leu Met Ile Val Asn Leu Phe Asn Met
115 120 125
Phe Ile Thr Tyr Gly Asp Thr Phe Leu Pro Thr Pro Ser Ser Tyr Asp
130 135 140
Glu Leu Tyr Tyr Glu Ile Ile Arg Met His Gln Ser Phe Asp Asn Leu
145 150 155 160
Tyr Ser Met Val Leu Arg Leu Ser Thr Asn Ala Gly Gln Trp Lys Glu
165 170 175
Ala Ala Ser Lys Val Thr His Ala Leu Val Asn Ile Arg Ala Ile Ile
180 185 190
Asn His Phe Asn Pro Lys Ile Glu Ser Tyr Ala Ala Val Asn His Ile
195 200 205
Ser Gln Leu Ser Glu Glu Gln Val Leu Glu Val Val Arg Ala Asn Tyr
210 215 220
Asp Thr Leu Thr Leu Lys Leu Gln Asp Gly Leu Asp Gln Tyr Glu Arg
225 230 235 240
Tyr Ser Glu Gln His Lys Glu Ala Ala Phe Phe Lys Glu Leu Val Arg
245 250 255
Ser Ile Ser Thr Asn Val Arg

260

<210> 971
<211> 337
<212> DNA
<213> Homo sapiens

<400> 971
tcgcgaggcc tcactatgga gccttctgag gtgctcaacc ttattaaaga ctccggacta
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cgcggtcgtg gtggtgcagg cttccccact ggggtgaaat ggtcctttgt tccccaaaac
120
aatcccaacc ccaaatacct ggttgttaac ggagacgaat ccgaacccgg cacgtgcaag
180
gacatgccgc tcattatggc aagcccgcac acgcttgtcg aaggtgctct tatctcccgc
240
tacgctttcg gatccgagca ggctttcatc tacctccgtg gagaagttgt tcaggtagcc
300
cggcgccttg aagaaaaaaa aaaaatgcga nnnnnnn
337

<210> 972
<211> 112
<212> PRT
<213> Homo sapiens

<400> 972
Ser Arg Gly Leu Thr Met Glu Pro Ser Glu Val Leu Asn Leu Ile Lys
1 5 10 15
Asp Ser Gly Leu Arg Gly Arg Gly Gly Ala Gly Phe Pro Thr Gly Val
20 25 30
Lys Trp Ser Phe Val Pro Gln Asn Asn Pro Asn Pro Lys Tyr Leu Val
35 40 45
Val Asn Gly Asp Glu Ser Glu Pro Gly Thr Cys Lys Asp Met Pro Leu
50 55 60
Ile Met Ala Ser Pro His Thr Leu Val Glu Gly Ala Leu Ile Ser Arg
65 70 75 80
Tyr Ala Phe Gly Ser Glu Gln Ala Phe Ile Tyr Leu Arg Gly Glu Val
85 90 95
Val Gln Val Ala Arg Arg Leu Glu Glu Lys Lys Lys Met Arg Xaa Xaa
100 105 110

<210> 973
<211> 360
<212> DNA
<213> Homo sapiens

<400> 973
acgcgtgaag gggaaagggg gagtcgtctc cttggttcct aagtgcgccc tctccaggtt
60
ccagcagggc ggcacagcca aggaaatggc atggtcctgc tgcatggttc tcagtggggt
120
ccgggacctt ctgtataggc atcacttagg aaccagtcag accatcagat tctcaggacc
180

cactggatca actgagtcag gaactcaggg ttttcaacac atcctccggg gggattccag
240
tggctgtgta actttgagga ccactggcaa agtggctctg gggtcagaga tccgagttca
300
tattctgggt ctgcctctga ctgactgcaa cggtgggcaa gtcacttgcc gtgcccagcc
360

<210> 974
<211> 91
<212> PRT
<213> Homo sapiens

<400> 974
Met Ala Trp Ser Cys Cys Met Val Leu Ser Gly Val Arg Asp Leu Leu
1 5 10 15
Tyr Arg His His Leu Gly Thr Ser Gln Thr Ile Arg Phe Ser Gly Pro
20 25 30
Thr Gly Ser Thr Glu Ser Gly Thr Gln Gly Phe Gln His Ile Leu Arg
35 40 45
Gly Asp Ser Ser Gly Cys Val Thr Leu Arg Thr Thr Gly Lys Val Ala
50 55 60
Leu Gly Ser Glu Ile Arg Val His Ile Leu Gly Leu Pro Leu Thr Asp
65 70 75 80
Cys Asn Gly Gly Gln Val Thr Cys Arg Ala Gln
85 90

<210> 975
<211> 2604
<212> DNA
<213> Homo sapiens

<400> 975
gcagcctctc tgagctggag cgtctgaagc tgcaagagac tgcttaccac gaactcgtgg
60
ccagacattt cctctccgaa ttcaaacctg acagagctct gcctattgac cgtccgaaca
120
ccttggataa gtggtttctg attttgagag gacagcagag ggctgtatca cacaagacat
180
ttggcattag cctggaagag gtcctggtga acgagtttac ccgccgcaag catcttgaac
240
tgaccagcca cgatgcaggt tgaagaagcc accggtcagg ctgcgggccg tcgtcgggga
300
aacgtggtgc gaagggtgtt tggccgcatc cggcgctttt tcagtcgcag gcggaatgag
360
cccaccttgc cccgggagtt cactcgccgt gggcgtcgag gtgcagtgtc tgtggatagt
420
ctggctgagc tggaagacgg agccctgctg ctgcagaccc tgcagctttc aaaaatttcc
480
tttccaattg gccaacgact tctgggatcc aaaaggaaga tgagtctcaa tccgattgcg
540
aaacaaatcc cccaggttgt tgaggcttgc tgccaattca ttgaaaaaca tggcttaagc
600
gcagtgggga tttttaccct tgaatactcc gtgcagcgag tgcgtcagct ccgtgaagaa
660

tttgatcaag gtctggatgt agtgctggat gacaatcaga atgtgcatga tgtggctgca
720
ctcctcaagg agtttttccg tgacatgaag gattctctgc tgccagatga tctgtacatg
780
tcattcctcc tgacagcaac tttaaagccc caggatcagc tttctgccct gcagttgctg
840
gtctacctga cgccaccctg ccacagtgat accctggagc gtctgctgaa ggccctgcat
900
aaaatcactg agaactgcga ggactcaatt ggcattgatg gacagttggt cccaggcaac
960
cgtatgactt ccactaactt ggccttggtg tttggatctg ctctcctgaa aaaaggaaag
1020
tttggcaaga gagagtccag gaaaacaaag ctggggattg atcactatgt tgcttctgtc
1080
aatgtggtcc gtgccatgat tgataactgg gatgtcctct tccaggtgcc tccccatatt
1140
cagaggcagg ttgctaagcg cgtgtggaag tccagcccgg aagcacttga ttttatcaga
1200
cgcaggaact tgaggaagat ccagagtgca cgcataaaga tggaagagga tgcactactt
1260
tctgatccag tggaaacctc tgctgaagcc cgggctgctg tccttgctca aagcaagcct
1320
tctgatgaag gttcctctga ggagccagct gtgccttccg gcactgcccg ttcccatgac
1380
gatgaggaag gagcgggtaa ccctcccatt ccggagcaag accgcccatt gctccgtgtg
1440
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1500
ctataaggtg ccagacaggg gaaaagggtg ggggtacatc tgggatgtca caggaaacat
1560
taaggagaga gttgaaggta aagatctgaa ggtaagaagg agttccacct gatgctcggg
1620
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1680
gctggtaaaa gcagagatgt ttctgtgtca tgcccaagct ccccggtgct accttgcctt
1740
tctcttttac ccctgatctt ggctttctct ctctctctgc agactttcct ttaattgatg
1800
tgacatttgt ggtaaacacc tttcccaggg aacctcacaa atcttgagat gctttccctt
1860
ccccaaatgg gattgcatga tttccctgac tttcctaccc tcctccagag agctcagttg
1920
gaaaggccct caagaggcat gctagaacgt taggtcagcc tactgacagc tgacaaacaa
1980
ttaatgcgaa atcatgtcac accaacccat agccgtgtcc acgcagcaac tccaccacct
2040
taggatttcc ccctccaaat tattcagacc aatggcttgc caaatggcct ctcccaaaat
2100
tctgtacagt tttgctcagg tcacgccaac agggaaacct caagtgtagg tctaattagt
2160
gtttctggga tccaaagtta gaggaaaatt tagattttat tgcctggatc tgctttaaag
2220
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2280

ccaagtaggt aaagtcactt gattacaaat gttcttaact atcgtctctg taattccttt
2340
atacaggaca gtacaaaatt gtgggacatg ctctggtaac acacagatat gggttgcata
2400
tgatccagaa ttacagctga tattatggat gacaactgct aaggtccata aaatgaagac
2460
tgtattgtat tgagggatag aaattgatca tttaatgggt aacaactgct gagctcaaag
2520
atttgtgatt gttaaaactt ctctggcatt taatcattaa taaacatctg tattgtgaca
2580
gcaaaaaaaa aaaaaaaaaa aaaa
2604

<210> 976
<211> 411
<212> PRT
<213> Homo sapiens

<400> 976
Met Gln Val Glu Glu Ala Thr Gly Gln Ala Ala Gly Arg Arg Arg Gly
1 5 10 15
Asn Val Val Arg Arg Val Phe Gly Arg Ile Arg Arg Phe Phe Ser Arg
20 25 30
Arg Arg Asn Glu Pro Thr Leu Pro Arg Glu Phe Thr Arg Arg Gly Arg
35 40 45
Arg Gly Ala Val Ser Val Asp Ser Leu Ala Glu Leu Glu Asp Gly Ala
50 55 60
Leu Leu Leu Gln Thr Leu Gln Leu Ser Lys Ile Ser Phe Pro Ile Gly
65 70 75 80
Gln Arg Leu Leu Gly Ser Lys Arg Lys Met Ser Leu Asn Pro Ile Ala
85 90 95
Lys Gln Ile Pro Gln Val Val Glu Ala Cys Cys Gln Phe Ile Glu Lys
100 105 110
His Gly Leu Ser Ala Val Gly Ile Phe Thr Leu Glu Tyr Ser Val Gln
115 120 125
Arg Val Arg Gln Leu Arg Glu Glu Phe Asp Gln Gly Leu Asp Val Val
130 135 140
Leu Asp Asp Asn Gln Asn Val His Asp Val Ala Ala Leu Leu Lys Glu
145 150 155 160
Phe Phe Arg Asp Met Lys Asp Ser Leu Leu Pro Asp Asp Leu Tyr Met
165 170 175
Ser Phe Leu Leu Thr Ala Thr Leu Lys Pro Gln Asp Gln Leu Ser Ala
180 185 190
Leu Gln Leu Leu Val Tyr Leu Thr Pro Pro Cys His Ser Asp Thr Leu
195 200 205
Glu Arg Leu Leu Lys Ala Leu His Lys Ile Thr Glu Asn Cys Glu Asp
210 215 220
Ser Ile Gly Ile Asp Gly Gln Leu Val Pro Gly Asn Arg Met Thr Ser
225 230 235 240
Thr Asn Leu Ala Leu Val Phe Gly Ser Ala Leu Leu Lys Lys Gly Lys
245 250 255
Phe Gly Lys Arg Glu Ser Arg Lys Thr Lys Leu Gly Ile Asp His Tyr
260 265 270
Val Ala Ser Val Asn Val Val Arg Ala Met Ile Asp Asn Trp Asp Val

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        275                 280                 285
Leu Phe Gln Val Pro Pro His Ile Gln Arg Gln Val Ala Lys Arg Val
    290                 295                 300
Trp Lys Ser Ser Pro Glu Ala Leu Asp Phe Ile Arg Arg Arg Asn Leu
305                 310                 315                 320
Arg Lys Ile Gln Ser Ala Arg Ile Lys Met Glu Glu Asp Ala Leu Leu
                325                 330                 335
Ser Asp Pro Val Glu Thr Ser Ala Glu Ala Arg Ala Ala Val Leu Ala
            340                 345                 350
Gln Ser Lys Pro Ser Asp Glu Gly Ser Ser Glu Glu Pro Ala Val Pro
        355                 360                 365
Ser Gly Thr Ala Arg Ser His Asp Asp Glu Glu Gly Ala Gly Asn Pro
    370                 375                 380
Pro Ile Pro Glu Gln Asp Arg Pro Leu Leu Arg Val Pro Arg Glu Lys
385                 390                 395                 400
Glu Ala Lys Thr Gly Val Ser Tyr Phe Phe Pro
                405                 410
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<210> 977
<211> 378
<212> DNA
<213> Homo sapiens

<400> 977
cgcgtgaagg gggccatcca gaggagcacg gagacgggcc tggcagtgga gatgcccagc
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cggacactgc gccaggccag ccacgagtcc attgaggaca gcatgaacag ctatggctca
120
gagggcaacc ttaactatgg aggagtttgc ctggcgtcgg acgcccagtt cagtgacttc
180
ctgggaagca tggggccggc acagtttgtg ggccgccaga ccctggccac cacacccatg
240
ggggatgtgg agatcggtct gcaggagcgg aacggtcagt tggaggtgga cattatccag
300
gctcggggac tgacagccaa gccaggctcc aagacactgc cagcggccta catcaaggcc
360
tacctgctag agatggca
378

<210> 978
<211> 126
<212> PRT
<213> Homo sapiens

<400> 978
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Arg Val Lys Gly Ala Ile Gln Arg Ser Thr Glu Thr Gly Leu Ala Val
 1               5                  10                  15
Glu Met Pro Ser Arg Thr Leu Arg Gln Ala Ser His Glu Ser Ile Glu
            20                  25                  30
Asp Ser Met Asn Ser Tyr Gly Ser Glu Gly Asn Leu Asn Tyr Gly Gly
        35                  40                  45
Val Cys Leu Ala Ser Asp Ala Gln Phe Ser Asp Phe Leu Gly Ser Met
    50                  55                  60
Gly Pro Ala Gln Phe Val Gly Arg Gln Thr Leu Ala Thr Thr Pro Met
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65 70 75 80
Gly Asp Val Glu Ile Gly Leu Gln Glu Arg Asn Gly Gln Leu Glu Val
85 90 95
Asp Ile Ile Gln Ala Arg Gly Leu Thr Ala Lys Pro Gly Ser Lys Thr
100 105 110
Leu Pro Ala Ala Tyr Ile Lys Ala Tyr Leu Leu Glu Met Ala
115 120 125

<210> 979
<211> 3500
<212> DNA
<213> Homo sapiens

<400> 979
nntttttttt ttccagggga aaatgcttta ttgagtaaag tatccgagga agtgatgcag
60
ggcaggtaaa cagctggtgc tcagcagcga gaggacgcgt cactctgccg ttctgcaggg
120
tgacgccctc cccgtacctc gctgagagcc acctgcagac acagcaggcc acagcagaat
180
gcacaggtca ctgttgtagg ggaacaaatc gtaatgccca gagaaaacct cagcctccca
240
aagtgctggg attacaggcg tgagccacgg cgcctggcct ccttccttca cttttgaaat
300
taaagcctct ttgcaagtcc tgctctgaga aatggtcact gcacatggta aagaggccct
360
gagccccatg gccatctctc ttggtgaggg gtggcgggcc cgggtgctgt ctgagatgcc
420
agctcaggag ggctccatcc tggctctgct gccccagggc cggcgttccc ggagggctcc
480
aggttcccgg ttctagtcct ggaaaggcag aagggagagg ggaagggaag ggtgggaggg
540
gcctctggga ggtgcagccc caccccatgc cccacacccc gggactcctc gcagacgggg
600
acacgtgtgg gagtgtccgc ggagcttcac atttcagggc cgtctcagcc agtgcctctg
660
aagtggccgc agccttgggg ccaggttccc tcctgagtcc acctgggcca cattgctccc
720
acggtgcaca ctccagcaca agaatggctc agccttgatc ccccaaactg ggcaccgtcc
780
ctgcatgtag gtgtgtgggg gggcctcagc agcagacggg gccatgggcc tctggtgggg
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900
agatatggtc ccagcctccc ccgatgccgt agtcccagcc gtggcccttg ggctcgtgag
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gctgcacgcc ggtgcgatga cacactgtcc cccggctcag gctgtggctg ccctgcactt
1020
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1080
acacgtgctc ccagctggag ccctgcgggt agctgggcgt gatcccttgg cgataccaca
1140
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<212> PRT
<213> Homo sapiens

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            20   25   30
Cys Phe Gln Val Leu Thr Ala Ser Gly Trp Ser Leu Glu Ala Thr Glu
        35   40   45
Glu Arg Asn Ala Trp Leu Arg Ala Ala Glu His Ser Glu Ala Ser Arg
    50   55   60
Glu Asp Ser Arg Pro Ala Arg Ala Pro
65   70

<210> 981
<211> 404
<212> DNA
<213> Homo sapiens

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accgcactcg cggaggcggg tgcgcgaggc ggggcgggta accaccggtt tggtggagac
240
cggccaggat ccgatcgagt actcggcaga caaagacttc aacaacccag acacctccaa
300
ccatccggtg caccggacca agcgtgtgga ggaacagcta gcggcgcaca aggcggcgcg
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404

<210> 982
<211> 134
<212> PRT
<213> Homo sapiens

<400> 982
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Pro Asp Pro His Ala Trp Asp Leu Cys Glu Arg His Ser Ala His Ile
20 25 30
Thr Ala Pro Val Gly Trp Glu Leu Val Arg Val Glu His Val Glu Leu
35 40 45
Asp Asp Glu Asp Val Asp Asp Glu Asn Thr Asp Ile Thr Ala Leu Ala
50 55 60
Glu Ala Gly Ala Arg Gly Gly Ala Gly Asn His Arg Phe Gly Gly Asp
65 70 75 80
Arg Pro Gly Ser Asp Arg Val Leu Gly Arg Gln Arg Leu Gln Gln Pro
85 90 95
Arg His Leu Gln Pro Ser Gly Ala Pro Asp Gln Ala Cys Gly Gly Thr
100 105 110
Ala Ser Gly Ala Gln Gly Gly Ala Pro Leu Pro Pro Ala His Cys Pro
115 120 125
Gly Ser Glu Pro Gly Arg
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<210> 983
<211> 579
<212> DNA
<213> Homo sapiens

<400> 983
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120
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360
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420

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<210> 984
<211> 103
<212> PRT
<213> Homo sapiens

<400> 984
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20 25 30
Ile Thr Leu Asn Ile Thr His Ser Ser Pro Ala Thr Leu Ala Ser Leu
35 40 45
Leu Phe Pro Lys Arg Ala Arg Tyr Pro Ser Phe Ser Gly Pro Leu Tyr
50 55 60
Leu Phe Phe Ser Leu Pro Glu Thr Pro Phe Leu Leu Asn Asn Leu Met
65 70 75 80
Ser Cys Pro Ser Thr Ser Ser Val Leu Lys Cys His Leu Pro Arg Glu
85 90 95
Val Phe Pro Asp Gln His Ile
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<210> 985
<211> 313
<212> DNA
<213> Homo sapiens

<400> 985
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180
tattgattat gcaaaattga ttaaagaatc cgatgcgctg ccagtagatc aacaagtcgc
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300
gttgagcggg ttc
313

<210> 986
<211> 98
<212> PRT
<213> Homo sapiens

<400> 986
Met Asn Gly Leu Ala Val Thr Val His Thr Lys Leu Asp Lys Lys Gln

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Gln Leu Gly Asn Ile Gln Met Ser Tyr Ser Ala Lys Asn Ile Asp Val
            20                  25                  30
Ala Asn Phe Lys Ala His Asp Leu Lys Leu Val Thr Glu Ile Asn His
        35                  40                  45
Leu Asp Asn Gln Ile Phe Ile Asp Tyr Ala Lys Leu Ile Lys Glu Ser
    50                  55                  60
Asp Ala Leu Pro Val Asp Gln Gln Val Ala Phe Phe Leu Asn Asn Met
65                  70                  75                  80
Gln Ser Ile Ile Asp Gly Lys Pro Glu Leu Asn Ile Thr Glu Leu Ser
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Gly Phe
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<210> 987
<211> 4224
<212> DNA
<213> Homo sapiens

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120
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180
gaagcaatct gaccaagatc acatcccttt ttttttttcg gagatggagg gggagtctca
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300
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360
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420
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<210> 988
<211> 873
<212> PRT
<213> Homo sapiens

<400> 988
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Met Leu Leu Arg Gly Leu Thr Gln Ile Gln Ser Arg Ile Leu Gly Pro
35 40 45
Gly Arg Lys Cys Cys Ala Leu Ala Asn Leu Ala Asp Met Leu Thr Val
50 55 60
Phe Ala Leu Thr Glu Asp Asp Pro Gln Glu Val Ser Ala Thr Val Tyr
65 70 75 80
Leu Asp Lys Leu Ala Thr Val Ile Ser Val Trp Asn Ser Asp Thr Gln
85 90 95
Asn Pro Tyr His Gln Gln Ala Leu Ala Glu Lys Val Lys Glu Ala Glu
100 105 110
Arg Asp Val Ser Leu Thr Ser Leu Ala Lys Leu Pro Ser Glu Thr Ile
115 120 125
Phe Val Gly Cys Glu Phe Leu His His Leu Leu Arg Glu Trp Gly Glu
130 135 140
Glu Leu Gln Ala Val Leu Arg Ser Ser Gln Gly Thr Ser Tyr Asp Ser
145 150 155 160
Tyr Arg Leu Cys Asp Ser Leu Thr Ser Phe Ser Gln Asn Ala Thr Leu
165 170 175
Tyr Leu Asn Arg Thr Ser Leu Ser Lys Glu Asp Arg Gln Val Val Ser
180 185 190
Glu Leu Ala Glu Cys Val Arg Asp Phe Leu Arg Lys Thr Ser Thr Val
195 200 205
Leu Lys Asn Arg Ala Leu Glu Asp Ile Thr Ala Ser Ile Ala Met Ala
210 215 220
Val Ile Gln Gln Lys Met Asp Arg His Met Glu Val Cys Tyr Ile Phe
225 230 235 240
Ala Ser Glu Lys Lys Trp Ala Phe Ser Asp Glu Trp Val Ala Cys Leu
245 250 255
Gly Ser Asn Arg Ala Leu Phe Arg Glu Pro Asp Leu Val Leu Arg Leu
260 265 270
Leu Glu Thr Val Ile Asp Val Ser Thr Ala Asp Arg Ala Ile Pro Glu
275 280 285
Ser Gln Ile Arg Gln Val Ile His Leu Ile Leu Glu Cys Tyr Ala Asp
290 295 300
Leu Ser Leu Pro Gly Lys Asn Lys Val Leu Ala Gly Ile Leu Arg Ser
305 310 315 320
Trp Gly Arg Lys Gly Leu Ser Glu Lys Leu Leu Ala Tyr Val Glu Gly
325 330 335
Phe Gln Glu Asp Leu Asn Thr Thr Phe Asn Gln Leu Thr Gln Ser Ala
340 345 350
Ser Glu Gln Gly Leu Ala Lys Ala Val Ala Ser Val Ala Arg Leu Val
355 360 365
Ile Val His Pro Glu Val Thr Val Lys Lys Met Cys Ser Leu Ala Val

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Val Asn Leu Gly Thr His Lys Phe Leu Ala Gln Ile Leu Thr Ala Phe
385                 390                 395                 400
Pro Ala Leu Arg Phe Val Glu Val Gln Gly Pro Asn Ser Ser Ala Thr
                405                 410                 415
Phe Met Val Ser Cys Leu Lys Glu Thr Val Trp Met Lys Phe Ser Thr
            420                 425                 430
Pro Lys Glu Glu Lys Gln Phe Leu Glu Leu Leu Asn Cys Leu Met Ser
        435                 440                 445
Pro Val Lys Pro Gln Gly Ile Pro Val Ala Ala Leu Leu Glu Pro Asp
    450                 455                 460
Glu Val Leu Lys Glu Phe Val Leu Pro Phe Leu Arg Leu Asp Val Glu
465                 470                 475                 480
Glu Val Asp Leu Ser Leu Arg Ile Phe Ile Gln Thr Leu Glu Ala Asn
                485                 490                 495
Ala Cys Arg Glu Glu Tyr Trp Leu Gln Thr Cys Ser Pro Phe Pro Leu
            500                 505                 510
Leu Phe Ser Leu Cys Gln Leu Leu Asp Arg Phe Ser Lys Tyr Trp Gln
        515                 520                 525
Leu Pro Lys Glu Lys Arg Cys Leu Ser Leu Asp Arg Lys Asp Leu Ala
    530                 535                 540
Ile His Ile Leu Glu Leu Leu Cys Glu Ile Val Ser Ala Asn Ala Glu
545                 550                 555                 560
Thr Phe Ser Pro Asp Val Trp Ile Lys Ser Leu Ser Trp Leu His Arg
                565                 570                 575
Lys Leu Glu Gln Leu Asp Trp Thr Val Gly Leu Arg Leu Lys Ser Phe
            580                 585                 590
Phe Glu Gly His Phe Lys Cys Glu Val Pro Ala Thr Leu Phe Glu Ile
        595                 600                 605
Cys Lys Leu Ser Glu Asp Glu Trp Thr Ser Gln Ala His Pro Gly Tyr
    610                 615                 620
Gly Ala Gly Thr Gly Leu Leu Ala Trp Met Glu Cys Cys Cys Val Ser
625                 630                 635                 640
Ser Gly Ile Ser Glu Arg Met Leu Ser Leu Leu Val Val Asp Val Gly
                645                 650                 655
Asn Pro Glu Glu Val Arg Leu Phe Ser Lys Gly Phe Leu Val Ala Leu
            660                 665                 670
Val Gln Val Met Pro Trp Cys Ser Pro Gln Glu Trp Gln Arg Leu His
        675                 680                 685
Gln Leu Thr Arg Arg Leu Leu Glu Lys Gln Leu Leu His Val Pro Tyr
    690                 695                 700
Ser Leu Glu Tyr Ile Gln Phe Val Pro Leu Leu Asn Leu Lys Pro Phe
705                 710                 715                 720
Ala Gln Glu Leu Gln Leu Ser Val Leu Phe Leu Arg Thr Phe Gln Phe
                725                 730                 735
Leu Cys Ser His Ser Cys Arg Asn Trp Leu Pro Leu Glu Gly Trp Asn
            740                 745                 750
His Val Val Lys Leu Leu Cys Gly Ser Leu Thr Arg Leu Leu Asp Ser
        755                 760                 765
Val Arg Ala Ile Gln Ala Ala Gly Pro Trp Val Gln Gly Pro Glu Gln
    770                 775                 780
Asp Leu Thr Gln Glu Ala Leu Phe Val Tyr Thr Gln Val Phe Cys His
785                 790                 795                 800
Ala Leu His Ile Met Ala Met Leu His Pro Glu Val Cys Glu Pro Leu
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805 810 815
Tyr Val Leu Ala Leu Glu Thr Leu Thr Cys Tyr Glu Thr Leu Ser Lys
820 825 830
Thr Asn Pro Ser Val Ser Ser Leu Leu Gln Arg Ala His Glu Gln Cys
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Phe Leu Lys Ser Ile Ala Glu Gly Ile Gly Pro Glu Glu Arg Arg Gln
850 855 860
Thr Leu Leu Gln Lys Met Ser Ser Phe
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<210> 989
<211> 402
<212> DNA
<213> Homo sapiens

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402

<210> 990
<211> 134
<212> PRT
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35 40 45
Leu Leu Asp Glu Pro Thr Asn His Leu Asp Ala Glu Ser Val Asn Trp
50 55 60
Leu Glu Gly His Leu Lys Ser Tyr Pro Gly Ala Val Leu Ala Val Thr
65 70 75 80
His Asp Arg Tyr Phe Leu Asp His Val Ala Glu Trp Ile Cys Glu Val
85 90 95
Asp Arg Gly Gln Leu His Pro Tyr Glu Gly Asn Tyr Ser Thr Tyr Leu
100 105 110
Asp Thr Lys Arg Lys Arg Leu Gln Ile Glu Gly Lys Lys Asp Ala Lys
115 120 125
Arg Ala Lys Ile Leu Glu

130

<210> 991
<211> 359
<212> DNA
<213> Homo sapiens

<400> 991
tctagaatta aagccaaaaa aactcaggct gaagtggcag aagctgtaaa gatgtcgcaa
60
cccgcctatc aggctttaga gtcagggaaa aatttaaaat ctgcatttct tcctttaatt
120
gcccaatttt taggagtaga tggttattgg ttaacgacgg ggaatactga agattctttt
180
agagaaagtg atgtatttag cccgactgta gtgagtgcag aatctactga tcagtatgtt
240
tggattgaag ttgtagaagc taacttttct tgcgggacag gtgaatctat tgaatttcac
300
tttgatgcta ttaatggaaa aattccattc cctgcttcat tctttaaaga aaaacgcgt
359

<210> 992
<211> 119
<212> PRT
<213> Homo sapiens

<400> 992
Ser Arg Ile Lys Ala Lys Lys Thr Gln Ala Glu Val Ala Glu Ala Val
 1   5   10   15
Lys Met Ser Gln Pro Ala Tyr Gln Ala Leu Glu Ser Gly Lys Asn Leu
            20   25   30
Lys Ser Ala Phe Leu Pro Leu Ile Ala Gln Phe Leu Gly Val Asp Gly
        35   40   45
Tyr Trp Leu Thr Thr Gly Asn Thr Glu Asp Ser Phe Arg Glu Ser Asp
    50   55   60
Val Phe Ser Pro Thr Val Val Ser Ala Glu Ser Thr Asp Gln Tyr Val
65   70   75   80
Trp Ile Glu Val Val Glu Ala Asn Phe Ser Cys Gly Thr Gly Glu Ser
                85   90   95
Ile Glu Phe His Phe Asp Ala Ile Asn Gly Lys Ile Pro Phe Pro Ala
            100   105   110
Ser Phe Phe Lys Glu Lys Arg
        115

<210> 993
<211> 450
<212> DNA
<213> Homo sapiens

<400> 993
ngcgcgccgg gcaccacata cgacgacggg acgttattca cctctaacgt gtagccgccg
60
tcgcggtccg gatccgcgat gatggccgcg tggcctgaag caatggggta ggtgcccgtg
120

atgcgtcgct ttggcgcacg aggtttacgc cgtggggagt tcataaggga aataccagca
180
cagggtcgga ccagttgtta cgatcgctgc atgatctact tgtcgcagga ttatatcggt
240
gagctaccca agcaacatat ctcgctggga aagtttgatc ccgacaatat tcctgcggac
300
ccgaacgaac tgtttgccac gtggtttaaa gaagccgttg agaacgaagt cggcgaccct
360
actgcggtca ccgtggccac ggtggacgac aacggtcagc ccgatgcgcg agtcgtcgac
420
cttctgtacc tcaactccga cggcttccac
450

<210> 994
<211> 110
<212> PRT
<213> Homo sapiens

<400> 994
Met Arg Arg Phe Gly Ala Arg Gly Leu Arg Arg Gly Glu Phe Ile Arg
1 5 10 15
Glu Ile Pro Ala Gln Gly Arg Thr Ser Cys Tyr Asp Arg Cys Met Ile
20 25 30
Tyr Leu Ser Gln Asp Tyr Ile Gly Glu Leu Pro Lys Gln His Ile Ser
35 40 45
Leu Gly Lys Phe Asp Pro Asp Asn Ile Pro Ala Asp Pro Asn Glu Leu
50 55 60
Phe Ala Thr Trp Phe Lys Glu Ala Val Glu Asn Glu Val Gly Asp Pro
65 70 75 80
Thr Ala Val Thr Val Ala Thr Val Asp Asp Asn Gly Gln Pro Asp Ala
85 90 95
Arg Val Val Asp Leu Leu Tyr Leu Asn Ser Asp Gly Phe His
100 105 110

<210> 995
<211> 924
<212> DNA
<213> Homo sapiens

<400> 995
cgggagctgg tggaccagga cgtgcagcct gcccgctacc acatcgcctt tgggcccgtg
60
gtggatggcg acgtggtccc cgatgaccct gagatcctca tgcagcaggg agaattcctc
120
aactacgaca tgctcatcgg cgtcaaccag ggagagggcc tcaagttcgt ggaggactct
180
gcagagagcg aggacggtgt gtctgccagc gcctttgact tcactgtctc caactttgtg
240
gacaacctgt atggctaccc ggaaggcaag gatgtgcttc gggagaccat caagtttatg
300
tacacagact gggccgaccg ggacaatggc gaaatgcgcc gcaaaaccct gctggcgctc
360
tttactgacc accaatgggt ggcaccagct gtggccactg ccaagctgca cgccgactac
420

cagtctcccg tctactttta caccttctac caccactgcc aggcggaggg ccggcctgag
480
tgggcagatg cggcgcacgg ggatgaactg ccctatgtct ttggcgtgcc catggtgggt
540
gccaccgacc tcttcccctg taacttctcc aagaatgacg tcatgctcag tgccgtggtc
600
atgacctact ggaccaactt cgccaagact ggggacccca accagccggt gccgcaggat
660
accaagttca tccacaccaa gcccaatcgc ttcgaggagg tggtgtggag caaattcaac
720
agcaaggaga agcagtatct gcacataggc ctgaagccac gcgtgcgtga caactaccgc
780
gccaacaagg tggccttctg gctggagctc gtgccccacc tgcacaacct gcacacggag
840
ctcttcacca ccaccacgcg cctgcctccc tacgccacgc gctggccgcc tcgtcccccc
900
gctggcgccc cgggcacacg ccgg
924

<210> 996
<211> 308
<212> PRT
<213> Homo sapiens

<400> 996
Arg Glu Leu Val Asp Gln Asp Val Gln Pro Ala Arg Tyr His Ile Ala
1 5 10 15
Phe Gly Pro Val Val Asp Gly Asp Val Val Pro Asp Asp Pro Glu Ile
20 25 30
Leu Met Gln Gln Gly Glu Phe Leu Asn Tyr Asp Met Leu Ile Gly Val
35 40 45
Asn Gln Gly Glu Gly Leu Lys Phe Val Glu Asp Ser Ala Glu Ser Glu
50 55 60
Asp Gly Val Ser Ala Ser Ala Phe Asp Phe Thr Val Ser Asn Phe Val
65 70 75 80
Asp Asn Leu Tyr Gly Tyr Pro Glu Gly Lys Asp Val Leu Arg Glu Thr
85 90 95
Ile Lys Phe Met Tyr Thr Asp Trp Ala Asp Arg Asp Asn Gly Glu Met
100 105 110
Arg Arg Lys Thr Leu Leu Ala Leu Phe Thr Asp His Gln Trp Val Ala
115 120 125
Pro Ala Val Ala Thr Ala Lys Leu His Ala Asp Tyr Gln Ser Pro Val
130 135 140
Tyr Phe Tyr Thr Phe Tyr His His Cys Gln Ala Glu Gly Arg Pro Glu
145 150 155 160
Trp Ala Asp Ala Ala His Gly Asp Glu Leu Pro Tyr Val Phe Gly Val
165 170 175
Pro Met Val Gly Ala Thr Asp Leu Phe Pro Cys Asn Phe Ser Lys Asn
180 185 190
Asp Val Met Leu Ser Ala Val Val Met Thr Tyr Trp Thr Asn Phe Ala
195 200 205
Lys Thr Gly Asp Pro Asn Gln Pro Val Pro Gln Asp Thr Lys Phe Ile
210 215 220
His Thr Lys Pro Asn Arg Phe Glu Glu Val Val Trp Ser Lys Phe Asn

225 230 235 240
Ser Lys Glu Lys Gln Tyr Leu His Ile Gly Leu Lys Pro Arg Val Arg
245 250 255
Asp Asn Tyr Arg Ala Asn Lys Val Ala Phe Trp Leu Glu Leu Val Pro
260 265 270
His Leu His Asn Leu His Thr Glu Leu Phe Thr Thr Thr Thr Arg Leu
275 280 285
Pro Pro Tyr Ala Thr Arg Trp Pro Pro Arg Pro Pro Ala Gly Ala Pro
290 295 300
Gly Thr Arg Arg
305

<210> 997
<211> 320
<212> DNA
<213> Homo sapiens

<400> 997
aaatttaata ccatagcctt ctcttggttg atccttctag gcatgagtta tggcattaaa
60
acgggcatcc atcttggtgt cgatatcgta cttaatgccg tgcctaaacg agtatcaaga
120
gccttgtctt tgttcggtgc ctttgccgct attatgtacg gtctcattct acttgattct
180
acctggttag ccttactcgg tatcgatgta cgaggtggtg ccatcgaata ttgggcgaag
240
atgttcaaaa taggtattgg tactgaagag cttcgttacc ctatctttat gcaagatatg
300
tttgatttgc gcccacgcgt
320

<210> 998
<211> 106
<212> PRT
<213> Homo sapiens

<400> 998
Lys Phe Asn Thr Ile Ala Phe Ser Trp Leu Ile Leu Leu Gly Met Ser
1 5 10 15
Tyr Gly Ile Lys Thr Gly Ile His Leu Gly Val Asp Ile Val Leu Asn
20 25 30
Ala Val Pro Lys Arg Val Ser Arg Ala Leu Ser Leu Phe Gly Ala Phe
35 40 45
Ala Ala Ile Met Tyr Gly Leu Ile Leu Leu Asp Ser Thr Trp Leu Ala
50 55 60
Leu Leu Gly Ile Asp Val Arg Gly Gly Ala Ile Glu Tyr Trp Ala Lys
65 70 75 80
Met Phe Lys Ile Gly Ile Gly Thr Glu Glu Leu Arg Tyr Pro Ile Phe
85 90 95
Met Gln Asp Met Phe Asp Leu Arg Pro Arg
100 105

<210> 999
<211> 401

<212> DNA
<213> Homo sapiens

<400> 999
acgcgttcag gcggttaaca atcgcgctaa gaagctgacc aaggaaaatg tcggcatggt
60
acatctgagc aagagcttca tcggtgttta tctctactca gaaggcaagt ttgtgaccag
120
caactatctc aatcgtggct acaaggacat tctgagctat gcagacgatg ctagtctttt
180
gcaaaagcct ccagcagtgg cttcagatga tctggataca ggtctcttga agagggcctt
240
ggatgagtgg gtggctgatg ctaagaacca cattctcaat actgaaaact tctttagcgg
300
gtcaaccggt ctcaacattg acagtttcta cgtctttggt gaccaagaca tctgctggca
360
gttggcagct attctgaagc agagcatgaa tcgggaattg t
401

<210> 1000
<211> 115
<212> PRT
<213> Homo sapiens

<400> 1000
Met Val His Leu Ser Lys Ser Phe Ile Gly Val Tyr Leu Tyr Ser Glu
1 5 10 15
Gly Lys Phe Val Thr Ser Asn Tyr Leu Asn Arg Gly Tyr Lys Asp Ile
20 25 30
Leu Ser Tyr Ala Asp Asp Ala Ser Leu Leu Gln Lys Pro Pro Ala Val
35 40 45
Ala Ser Asp Asp Leu Asp Thr Gly Leu Leu Lys Arg Ala Leu Asp Glu
50 55 60
Trp Val Ala Asp Ala Lys Asn His Ile Leu Asn Thr Glu Asn Phe Phe
65 70 75 80
Ser Gly Ser Thr Gly Leu Asn Ile Asp Ser Phe Tyr Val Phe Gly Asp
85 90 95
Gln Asp Ile Cys Trp Gln Leu Ala Ala Ile Leu Lys Gln Ser Met Asn
100 105 110
Arg Glu Leu
115

<210> 1001
<211> 351
<212> DNA
<213> Homo sapiens

<400> 1001
cgcggtattg caatgcgcct ggtgccgaat gctaaacctg ctcttgattg cccggtactg
60
ttcccttatg cccctaatgc ggtgattgtt ggcttcctgg ccactaccgt tggttcaatt
120
atcggtatga ttgtcttccc gctgtttggt ctggcgatga tccttccggg tctgctaact
180

aacttcttcg ctggtggtgc cgctggagtc tttggcaacg cgatgggagg acgtaaaggg
240
gcaattattg gcggcgtagt gcacgggctg tttatcaccc tgttaccagc gatgctaatc
300
cccttactgg aaaccttcgg cttcaaaggc gtcaccttca gtgattccga t
351

<210> 1002
<211> 117
<212> PRT
<213> Homo sapiens

<400> 1002
Arg Gly Ile Ala Met Arg Leu Val Pro Asn Ala Lys Pro Ala Leu Asp
 1   5   10   15
Cys Pro Val Leu Phe Pro Tyr Ala Pro Asn Ala Val Ile Val Gly Phe
            20   25   30
Leu Ala Thr Thr Val Gly Ser Ile Ile Gly Met Ile Val Phe Pro Leu
        35   40   45
Phe Gly Leu Ala Met Ile Leu Pro Gly Leu Leu Thr Asn Phe Phe Ala
    50   55   60
Gly Gly Ala Ala Gly Val Phe Gly Asn Ala Met Gly Gly Arg Lys Gly
65   70   75   80
Ala Ile Ile Gly Gly Val Val His Gly Leu Phe Ile Thr Leu Leu Pro
                85   90   95
Ala Met Leu Ile Pro Leu Leu Glu Thr Phe Gly Phe Lys Gly Val Thr
            100   105   110
Phe Ser Asp Ser Asp
        115

<210> 1003
<211> 444
<212> DNA
<213> Homo sapiens

<400> 1003
acgcgtcctc ctttagtcga tcgcgaatat gataggcgaa gcgacgtgat ggtgtgacgc
60
acgagcactg ccccatctcc taggcttagg gttatgcaga ctcccatcga cgctacctcc
120
acccccgcat ggggcacact ctccggccta aagtcccgct tcgctgacgg gccacataaa
180
ctgcgccgtt tgttcgacgc cgaccctcac cgcgctgagc gctacacctt tgacgtcgcg
240
gatttgcacg tcgatttatc gaagaacctc cttaccgacg agattcgtga cgctctcctc
300
gaactggctg cgcagatgcg cgtcaccgag cgtcgtgacg cgatgtatgc cggtgagcac
360
atcaacgtca ccgaggaccg cgccgtcctc cataccgcgc tgtgtcgtcc ccgcactgac
420
gagctgcatg ttgacggtca ggat
444

<210> 1004

<211> 117
<212> PRT
<213> Homo sapiens

<400> 1004
Met Gln Thr Pro Ile Asp Ala Thr Ser Thr Pro Ala Trp Gly Thr Leu
1 5 10 15
Ser Gly Leu Lys Ser Arg Phe Ala Asp Gly Pro His Lys Leu Arg Arg
20 25 30
Leu Phe Asp Ala Asp Pro His Arg Ala Glu Arg Tyr Thr Phe Asp Val
35 40 45
Ala Asp Leu His Val Asp Leu Ser Lys Asn Leu Leu Thr Asp Glu Ile
50 55 60
Arg Asp Ala Leu Leu Glu Leu Ala Ala Gln Met Arg Val Thr Glu Arg
65 70 75 80
Arg Asp Ala Met Tyr Ala Gly Glu His Ile Asn Val Thr Glu Asp Arg
85 90 95
Ala Val Leu His Thr Ala Leu Cys Arg Pro Arg Thr Asp Glu Leu His
100 105 110
Val Asp Gly Gln Asp
115

<210> 1005
<211> 299
<212> DNA
<213> Homo sapiens

<400> 1005
ccatggccat tcctctggtg actgcatcca gtccgatgga tttaaacacc cccaatgtgc
60
tggtgactcc caagtttaca cctccagcca gggcttctct cctgggtttg catacccacc
120
tatctatctg ccttagccac tcgtgtctga cgagcacctc acacctccag aggctcctca
180
tttcttccca tgcctgcttc tcccacactc ctccctctca catgagggca acttcatcct
240
cccagttgct caggccccaa acctccatca gttttgactc ttctctcgca cactactcg
299

<210> 1006
<211> 99
<212> PRT
<213> Homo sapiens

<400> 1006
Met Ala Ile Pro Leu Val Thr Ala Ser Ser Pro Met Asp Leu Asn Thr
1 5 10 15
Pro Asn Val Leu Val Thr Pro Lys Phe Thr Pro Pro Ala Arg Ala Ser
20 25 30
Leu Leu Gly Leu His Thr His Leu Ser Ile Cys Leu Ser His Ser Cys
35 40 45
Leu Thr Ser Thr Ser His Leu Gln Arg Leu Leu Ile Ser Ser His Ala
50 55 60
Cys Phe Ser His Thr Pro Pro Ser His Met Arg Ala Thr Ser Ser Ser

65 70 75 80
Gln Leu Leu Arg Pro Gln Thr Ser Ile Ser Phe Asp Ser Ser Leu Ala
85 90 95
His Tyr Ser

<210> 1007
<211> 389
<212> DNA
<213> Homo sapiens

<400> 1007
gccggcgcga agatctaaag agctggaaag gcaaccgcaa gagagcgggg ttcttgcctg
60
atgagcgcgc tttcatggac tccatcttcg gcccggggcc tggtgtgacg gtctctgaaa
120
tcaacgacgc caccgaggca cccagaggtg tgacgttgag tgatggccga cgacagggca
180
acgccggagc aatcggtgac ttcttcgcat cgaaggacta caagccgtcc gcggcgagcc
240
tccgaggtcc ggcgagggat ccgaaatgga tcgacgttca acgctcattc cacgagaacg
300
aagaaggccc gtacagctgg tacacctggc gcgggcaggc ttttgacacg ggcgctggat
360
ggcgtaaata cgtccatgcc gcgacaacg
389

<210> 1008
<211> 105
<212> PRT
<213> Homo sapiens

<400> 1008
Met Asp Ser Ile Phe Gly Pro Gly Pro Gly Val Thr Val Ser Glu Ile
1 5 10 15
Asn Asp Ala Thr Glu Ala Pro Arg Gly Val Thr Leu Ser Asp Gly Arg
20 25 30
Arg Gln Gly Asn Ala Gly Ala Ile Gly Asp Phe Phe Ala Ser Lys Asp
35 40 45
Tyr Lys Pro Ser Ala Ala Ser Leu Arg Gly Pro Ala Arg Asp Pro Lys
50 55 60
Trp Ile Asp Val Gln Arg Ser Phe His Glu Asn Glu Glu Gly Pro Tyr
65 70 75 80
Ser Trp Tyr Thr Trp Arg Gly Gln Ala Phe Asp Thr Gly Ala Gly Trp
85 90 95
Arg Lys Tyr Val His Ala Ala Thr Thr
100 105

<210> 1009
<211> 324
<212> DNA
<213> Homo sapiens

<400> 1009

ngccttcatg gctgntatgc ctggcctcat ccccatccct ggcacccgtg acgatagcca
60
cattccactg gtgtttcccc aggaaagcca accctacctg catctcagca gagcttccac
120
ggagttggaa ccccgctccg agagggtgtg ggctcagggg ccaggggtca cacaaactcc
180
agaaggagga cgtagttggt ttgcaaggct gtcctttgcc ctggttgaat aaccttcggt
240
ctgccccgag aggaacgtgg gcattaggct gcacccgcag gaagccatgt attttctgag
300
aaacttggcc catggtgcag atct
324

<210> 1010
<211> 104
<212> PRT
<213> Homo sapiens

<400> 1010
Met Gly Gln Val Ser Gln Lys Ile His Gly Phe Leu Arg Val Gln Pro
1 5 10 15
Asn Ala His Val Pro Leu Gly Ala Asp Arg Arg Leu Phe Asn Gln Gly
20 25 30
Lys Gly Gln Pro Cys Lys Pro Thr Thr Ser Ser Phe Trp Ser Leu Cys
35 40 45
Asp Pro Trp Pro Leu Ser Pro His Pro Leu Gly Ala Gly Phe Gln Leu
50 55 60
Arg Gly Ser Ser Ala Glu Met Gln Val Gly Leu Ala Phe Leu Gly Lys
65 70 75 80
His Gln Trp Asn Val Ala Ile Val Thr Gly Ala Arg Asp Gly Asp Glu
85 90 95
Ala Arg His Xaa Ser His Glu Gly
100

<210> 1011
<211> 330
<212> DNA
<213> Homo sapiens

<400> 1011
ctgcagaaaa ggaggggttt cccatgccaa ggcagaactg tctgggacag acgctgcccg
60
gatccctgcg gctgcctgca ctctggacca cgagctctga gagcagcagg ttgagggccg
120
gtgggcagca gctcggaggc tccgcgaggt gcaggagacg caggcatggc cggtgagctg
180
actcctgagg aggaggccca gtacaaaaag gctttctccg cggttgacac ggatggaaac
240
ggcaccatca atgcccagga gctgggcgcg gcgctgaagg ccacgggcaa gaacctctcg
300
gaggcccagc taaagaaact catctccgag
330

<210> 1012

<211> 55
<212> PRT
<213> Homo sapiens

<400> 1012
Met Ala Gly Glu Leu Thr Pro Glu Glu Glu Ala Gln Tyr Lys Lys Ala
1 5 10 15
Phe Ser Ala Val Asp Thr Asp Gly Asn Gly Thr Ile Asn Ala Gln Glu
20 25 30
Leu Gly Ala Ala Leu Lys Ala Thr Gly Lys Asn Leu Ser Glu Ala Gln
35 40 45
Leu Lys Lys Leu Ile Ser Glu
50 55

<210> 1013
<211> 432
<212> DNA
<213> Homo sapiens

<400> 1013
nacttgcaca tcgtggtggc gtcgctgcgt gcggcactga caatgtgact ggcgcattcg
60
tggcggcgtc tcctcgtcgc cgggagcggc gaggaaggat taacgatgac cagcgacgtc
120
cccgggattg gctcgaacgc cgccactttg gcgcgttccc aggctcgcag tgacaaggtc
180
gaggctgatt tggcggtcca tcccgacaag tggcgcattc tgggggggga ccgtcctact
240
ggcagcctgc acatcggtca ctacttcggg tcgctggcga atcgggtacg cgtgcagaac
300
aagggcattg agtctttcct tgtcgtcgct gactaccagg ttatctatga ccgcgggggg
360
ggtggtgacc tgcaggccaa tgttatgtcg aatgtcgccg attacctggc aatcggcatt
420
gacccaacgc gt
432

<210> 1014
<211> 109
<212> PRT
<213> Homo sapiens

<400> 1014
Met Thr Ser Asp Val Pro Gly Ile Gly Ser Asn Ala Ala Thr Leu Ala
1 5 10 15
Arg Ser Gln Ala Arg Ser Asp Lys Val Glu Ala Asp Leu Ala Val His
20 25 30
Pro Asp Lys Trp Arg Ile Leu Gly Gly Asp Arg Pro Thr Gly Ser Leu
35 40 45
His Ile Gly His Tyr Phe Gly Ser Leu Ala Asn Arg Val Arg Val Gln
50 55 60
Asn Lys Gly Ile Glu Ser Phe Leu Val Val Ala Asp Tyr Gln Val Ile
65 70 75 80
Tyr Asp Arg Gly Gly Gly Gly Asp Leu Gln Ala Asn Val Met Ser Asn

85 90 95
Val Ala Asp Tyr Leu Ala Ile Gly Ile Asp Pro Thr Arg
100 105

<210> 1015
<211> 467
<212> DNA
<213> Homo sapiens

<400> 1015
nngaattcga tggctgtgaa aggtcgagct cttaagtgtt ttcatatccc ctgtgtggtt
60
gaaaacttcc cgatgaaagc gcgcacggtt gaagagctga aagaattgga aagagtttta
120
cagcaaaaga agattgaagc agagtgtctt aaactacgga aggaaattgt agaggctcag
180
tctggagtta agttgattaa acagcgtcat gaagaggatg atgaagaaga ggaagaggaa
240
gacaagacag taaaatatag caatttgccc aattacctgc ttggtagtct gagtactgat
300
tttggggtag atacctcttt attgtcaagc caattggagc ttcattccag agaagagaaa
360
atcaaccaaa ttatattatt gaaagatatc atttacaagg taaaaactgt tttcaataat
420
gagtttgacg ctgcatataa acaaaaagag tttgaaattg cacgcgt
467

<210> 1016
<211> 155
<212> PRT
<213> Homo sapiens

<400> 1016
Xaa Asn Ser Met Ala Val Lys Gly Arg Ala Leu Lys Cys Phe His Ile
1 5 10 15
Pro Cys Val Val Glu Asn Phe Pro Met Lys Ala Arg Thr Val Glu Glu
20 25 30
Leu Lys Glu Leu Glu Arg Val Leu Gln Gln Lys Lys Ile Glu Ala Glu
35 40 45
Cys Leu Lys Leu Arg Lys Glu Ile Val Glu Ala Gln Ser Gly Val Lys
50 55 60
Leu Ile Lys Gln Arg His Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu
65 70 75 80
Asp Lys Thr Val Lys Tyr Ser Asn Leu Pro Asn Tyr Leu Leu Gly Ser
85 90 95
Leu Ser Thr Asp Phe Gly Val Asp Thr Ser Leu Leu Ser Ser Gln Leu
100 105 110
Glu Leu His Ser Arg Glu Glu Lys Ile Asn Gln Ile Ile Leu Leu Lys
115 120 125
Asp Ile Ile Tyr Lys Val Lys Thr Val Phe Asn Asn Glu Phe Asp Ala
130 135 140
Ala Tyr Lys Gln Lys Glu Phe Glu Ile Ala Arg
145 150 155

<210> 1017
<211> 335
<212> DNA
<213> Homo sapiens

<400> 1017
acgcgtggct ggttgggtat gtggaaccat gtgcgcgcta atgagaagga tgcgaagggg
60
aacattaaag tgggtcgccc cggctacttt gcggaggtca tggatttcta tgcgcattat
120
ctgaagggtg cggttacccg tttccgtccg aattttattg tgcaggataa tacgggccgt
180
tggcgtgttc agtcgtcgtg gccgcagccg aatcgcactg ttacttttgc gggaccccgc
240
ggcattgtcc gctacggtac gacgttggcg gcccgcacgc atgggaatgg tcaggctatt
300
ccgcaggcgg atgcacagtc tcttaaccgc gagaa
335

<210> 1018
<211> 105
<212> PRT
<213> Homo sapiens

<400> 1018
Met Trp Asn His Val Arg Ala Asn Glu Lys Asp Ala Lys Gly Asn Ile
 1   5   10   15
Lys Val Gly Arg Pro Gly Tyr Phe Ala Glu Val Met Asp Phe Tyr Ala
            20   25   30
His Tyr Leu Lys Gly Ala Val Thr Arg Phe Arg Pro Asn Phe Ile Val
        35   40   45
Gln Asp Asn Thr Gly Arg Trp Arg Val Gln Ser Ser Trp Pro Gln Pro
    50   55   60
Asn Arg Thr Val Thr Phe Ala Gly Pro Arg Gly Ile Val Arg Tyr Gly
65   70   75   80
Thr Thr Leu Ala Ala Arg Thr His Gly Asn Gly Gln Ala Ile Pro Gln
                85   90   95
Ala Asp Ala Gln Ser Leu Asn Arg Glu
            100   105

<210> 1019
<211> 454
<212> DNA
<213> Homo sapiens

<400> 1019
acgcgtgaag gggtagtcgt agtagaagtc gtccacaaac acgggccccg gcaggtccag
60
ctctggagcc tcctcctcaa tggcgttgcc catggtgcct ggcttgggtg atgaggcggg
120
tgaagggcgt ggggccaggt ggtgcgggat gaagtcagcc tcgttgaaga gctcgtggct
180
ggaggagccg ctgcctgagc cttcagggcc cagtgtgccc aggggccacc gacagagtgg
240

cagagagcag gtgacttcct ggcactgcgg agcgaggacc cggagaagta cttcctcaat
300
ggtggctgga ccatccagtg gaacggggac taccaggtgg cagggaccac cttcacatac
360
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atccagctgc tgttccagga gagcaaccct gggg
454

<210> 1020
<211> 125
<212> PRT
<213> Homo sapiens

<400> 1020
Met Ala Leu Pro Met Val Pro Gly Leu Gly Asp Glu Ala Gly Glu Gly
1 5 10 15
Arg Gly Ala Arg Trp Cys Gly Met Lys Ser Ala Ser Leu Lys Ser Ser
20 25 30
Trp Leu Glu Glu Pro Leu Pro Glu Pro Ser Gly Pro Ser Val Pro Arg
35 40 45
Gly His Arg Gln Ser Gly Arg Glu Gln Val Thr Ser Trp His Cys Gly
50 55 60
Ala Arg Thr Arg Arg Ser Thr Ser Ser Met Val Ala Gly Pro Ser Ser
65 70 75 80
Gly Thr Gly Thr Thr Arg Trp Gln Gly Pro Pro Ser His Thr His Ala
85 90 95
Gly Ala Thr Gly Arg Thr Ser Arg Pro Arg Val Pro Pro Arg Ser Leu
100 105 110
Ser Gly Ser Ser Cys Cys Ser Arg Arg Ala Thr Leu Gly
115 120 125

<210> 1021
<211> 366
<212> DNA
<213> Homo sapiens

<400> 1021
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gccgagatta tctgacagga ccaaagcata taaagttgac tgaagcagga gcaaacacgc
120
tggttgaggg tcaagtgctg gggcagcagc aacaacaaac caaaaaaaag ccctttgaac
180
tcccttaatg ttgcccaaag gttctggtag agaacaagtc acatgcctaa gaaggtcttt
240
taaagggcac tcttgcagtt tcagcatttg gtccggggaa ttgcacaagg ctctgcttaa
300
atgcagagct ctttctagca tcttcatatt caaggcggaa aaactgagct tggcgaggaa
360
ccctgt
366

<210> 1022

<211> 109
<212> PRT
<213> Homo sapiens

<400> 1022
Met Lys Met Leu Glu Arg Ala Leu His Leu Ser Arg Ala Leu Cys Asn
1 5 10 15
Ser Pro Asp Gln Met Leu Lys Leu Gln Glu Cys Pro Leu Lys Asp Leu
20 25 30
Leu Arg His Val Thr Cys Ser Leu Pro Glu Pro Leu Gly Asn Ile Lys
35 40 45
Gly Val Gln Arg Ala Phe Phe Trp Phe Val Val Ala Ala Ala Pro Ala
50 55 60
Leu Asp Pro Gln Pro Ala Cys Leu Leu Leu Leu Gln Ser Thr Leu Tyr
65 70 75 80
Ala Leu Val Leu Ser Asp Asn Leu Gly Ser Met Ser Ile Phe His Ala
85 90 95
Leu Pro Leu Ser Gly Leu Gln Glu Val Thr Thr Gln Leu
100 105

<210> 1023
<211> 426
<212> DNA
<213> Homo sapiens

<400> 1023
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agcgtgatcg gtccgatggc agcctaccgg gccttgcgcc gccagtacgt gcctgcgaag
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ccgcagatga cattcttcgt gggctcgcgt ggcgtgcacc ggggtgaacc gctgggagat
240
aggcaggtgc atcgagtgtt ctgtcagctg cgcgagcaat tgggttggat cgatcgcggc
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ggccatggcc gaccgcgggt gcatgacctg cgccatagct tcgccgtgag acggatgatc
360
ctgtggcacc agcagggagc gaaccttgac caacgaatgc tggccctgtc cacgtacatg
420
ggccac
426

<210> 1024
<211> 142
<212> PRT
<213> Homo sapiens

<400> 1024
Ala Gly Leu Arg Val Ser Glu Ala Ile Asn Leu Ala Asp Ser Asp Ala
1 5 10 15
Asp Leu Asp Gly Gly Ile Leu Thr Ile Gln Gln Thr Lys Phe Gly Lys
20 25 30
Ser Arg Met Val Pro Leu His Pro Ser Val Ile Gly Pro Met Ala Ala

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        35                  40                  45
Tyr Arg Ala Leu Arg Arg Gln Tyr Val Pro Ala Lys Pro Gln Met Thr
    50                  55                  60
Phe Phe Val Gly Ser Arg Gly Val His Arg Gly Glu Pro Leu Gly Asp
65                  70                  75                  80
Arg Gln Val His Arg Val Phe Cys Gln Leu Arg Glu Gln Leu Gly Trp
                85                  90                  95
Ile Asp Arg Gly Gly His Gly Arg Pro Arg Val His Asp Leu Arg His
            100                 105                 110
Ser Phe Ala Val Arg Arg Met Ile Leu Trp His Gln Gln Gly Ala Asn
        115                 120                 125
Leu Asp Gln Arg Met Leu Ala Leu Ser Thr Tyr Met Gly His
    130                 135                 140
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<210> 1025
<211> 518
<212> DNA
<213> Homo sapiens

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gatagcggcg ctgcgtacgc gatgatggat gagccgtggt gggaagggcg cgtcgcctcg
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gacgtccact gcaccctgcg cgagaaggaa ctgaagctgc ccaccttccg agcccactcc
240
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300
cagctctgcc ctgcagcccg gcacctggcc gtctacctgc tggaccactt catggatcgc
360
tacaacgtca ccacctccaa gcagctctac accgtggccg tctcctgcct cctgcttgca
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518

<210> 1026
<211> 125
<212> PRT
<213> Homo sapiens

<400> 1026
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Cys Thr Leu Arg Glu Lys Glu Leu Lys Leu Pro Thr Phe Arg Ala His
            20                  25                  30
Ser Pro Leu Leu Lys Ser Arg Arg Phe Phe Val Asp Ile Leu Thr Leu
        35                  40                  45
Leu Ser Ser His Cys Gln Leu Cys Pro Ala Ala Arg His Leu Ala Val
    50                  55                  60
Tyr Leu Leu Asp His Phe Met Asp Arg Tyr Asn Val Thr Thr Ser Lys
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65 70 75 80
Gln Leu Tyr Thr Val Ala Val Ser Cys Leu Leu Leu Ala Ser Lys Phe
85 90 95
Glu Asp Arg Glu Asp His Val Pro Lys Leu Glu Gln Ile Asn Ser Thr
100 105 110
Arg Ile Leu Ser Ser Gln Asn Phe Thr Leu Thr Lys Lys
115 120 125

<210> 1027
<211> 465
<212> DNA
<213> Homo sapiens

<400> 1027
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120
gtgctgggca gcctggtgaa caccngtcct gaagcacatc atnnctggct gaaggtcatc
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240
aagatccccc tggacatggt ggctggattc aacacgcccc tggtcaagac catcgtggag
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ttccacatga cgactgaggc ccaagccacc atccgcatgg acaccagtgc aagtggcccc
360
acccgcctgg tcctcagtga ctgtgccacc agccatggga gcctgcgcat ccaactgctg
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465

<210> 1028
<211> 155
<212> PRT
<213> Homo sapiens

<400> 1028
Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys Asp His
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Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Lys Ala Met Arg
20 25 30
Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser Leu Val Asn Thr
35 40 45
Xaa Pro Glu Ala His His Xaa Trp Leu Lys Val Ile Thr Ala Asn Ile
50 55 60
Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp Gln Glu Leu Leu Val
65 70 75 80
Lys Ile Pro Leu Asp Met Val Ala Gly Phe Asn Thr Pro Leu Val Lys
85 90 95
Thr Ile Val Glu Phe His Met Thr Thr Glu Ala Gln Ala Thr Ile Arg
100 105 110
Met Asp Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys
115 120 125
Ala Thr Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser

130 135 140
Phe Lys Leu Asn Ala Ser Ala Lys Gln Val Met
145 150 155

<210> 1029
<211> 479
<212> DNA
<213> Homo sapiens

<400> 1029
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caagcactgg ccacaaatgc ctggcagaac aactgctcat aagtgtgtag ttgttgttat
120
tattactaac caagtgagga aaattatccc tagcaggtcc agatgaccgt gtgcatgaat
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cacagggaga ccctaaagga tttcctcctg taaagctctt tccccaccta tttgctactg
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479

<210> 1030
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1030
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Leu Trp His Glu Arg Phe Cys Phe Leu Leu Lys Gln Phe Gln Ala Val
20 25 30
Ala Asn Arg Trp Gly Lys Ser Phe Thr Gly Gly Asn Pro Leu Gly Ser
35 40 45
Pro Cys Asp Ser Cys Thr Arg Ser Ser Gly Pro Ala Arg Asp Asn Phe
50 55 60
Pro His Leu Val Ser Asn Asn Asn Asn Asn Tyr Thr Leu Met Ser Ser
65 70 75 80
Cys Ser Ala Arg His Leu Trp Pro Val Leu Gly Arg Gln Tyr Leu Phe
85 90 95
Glu Pro Ser His Ser Ser Val Arg Thr Val Ser Leu His Ala
100 105 110

<210> 1031
<211> 322
<212> DNA
<213> Homo sapiens

<400> 1031

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atcgacggcg aaaccgatgt acccgacccg gcatccaggg cgcaagccaa cgatgtgcat
180
gggtggagcg tcgtcgtcga cccgctcgcc tatcaatggc gacaccctaa ctggcaaggc
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cgcccctggc atgaggcggt gatttacgag ctgcacgttg gcgtactggg cgggtacgcc
300
gctgttgaac agcaactgcc gc
322

<210> 1032
<211> 107
<212> PRT
<213> Homo sapiens

<400> 1032
Xaa Ala Phe Tyr Val Ser Val Glu Leu Glu Asp Gly Lys Ser Ile Ala
1 5 10 15
Met Leu Pro Gln Ala Asp Gly Trp Phe Glu Val Glu Val Lys Cys Pro
20 25 30
Ala Gly Thr His Tyr Arg Tyr Asn Ile Asp Gly Glu Thr Asp Val Pro
35 40 45
Asp Pro Ala Ser Arg Ala Gln Ala Asn Asp Val His Gly Trp Ser Val
50 55 60
Val Val Asp Pro Leu Ala Tyr Gln Trp Arg His Pro Asn Trp Gln Gly
65 70 75 80
Arg Pro Trp His Glu Ala Val Ile Tyr Glu Leu His Val Gly Val Leu
85 90 95
Gly Gly Tyr Ala Ala Val Glu Gln Gln Leu Pro
100 105

<210> 1033
<211> 579
<212> DNA
<213> Homo sapiens

<400> 1033
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240
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420

aaagccgatc gaggaatctt tttctgcggc accgggatgg gcatggccat cacggccaac
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aaggtgccag gcattcgcgc ctgcaccgcc cacgactcct tctccgtaga gcggctcatc
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579

<210> 1034
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1034
Met Gly Leu Arg Ile Val Val Ala Ala Asp Pro Ala Ala Val Glu Tyr
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Lys Asp Val Val Lys Ala Asp Leu Glu Ala Asp Ser Arg Val Asp Asp
20 25 30
Val Ile Asp Val Gly Val Gln Ala Gly Asp Asp Thr Leu Tyr Pro Arg
35 40 45
Ile Gly Ile Lys Gly Ala His Val Ile Lys Asp Gly Lys Ala Asp Arg
50 55 60
Gly Ile Phe Phe Cys Gly Thr Gly Met Gly Met Ala Ile Thr Ala Asn
65 70 75 80
Lys Val Pro Gly Ile Arg Ala Cys Thr Ala His Asp Ser Phe Ser Val
85 90 95
Glu Arg Leu Ile Met Ser Asn Asp Ala His Val Leu Cys Leu Gly Gln
100 105 110
Arg

<210> 1035
<211> 363
<212> DNA
<213> Homo sapiens

<400> 1035
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240
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300
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360
atn
363

<210> 1036
<211> 121
<212> PRT

<213> Homo sapiens

<400> 1036

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 1               5                  10                  15
Met Xaa Ile Cys Val Cys Ile Xaa Met Cys Val Cys Val Xaa Glu Cys
            20                  25                  30
Val Cys Val Xaa Glu Ala Val Cys Ile Cys Xaa Cys Leu Cys Ala Cys
        35                  40                  45
Thr Xaa Met Cys Ala Cys Met Glu Cys Ile Cys Val Cys Val Trp Thr
    50                  55                  60
Val Cys Val Ile Met Gln Tyr Val Arg Val Cys Val Trp Ser Val Ser
65                  70                  75                  80
Val Trp His Val Cys Val Tyr Leu Leu Cys Val Ser Val Cys Val Xaa
                85                  90                  95
Thr Cys Ile Cys Ile Glu Ser Val Cys Ala Val Cys Met Cys Val Ser
            100                 105                 110
Ile Glu Arg Val Gly Asp Val Val Xaa
        115                 120
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<210> 1037
<211> 5832
<212> DNA
<213> Homo sapiens

<400> 1037

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840
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5100
cctgacaacg atccggaaac tgctcctcac cactcccgtc atgcctgctg tcggcgtttg
5160
accttccacg tgacagttct tcacaattcc tttcatcatt ttttaaatat tttttttact
5220
gcctatgggc tgtgatgtat atagaagttg tacattaaac ataccctcat tttttttttt
5280
tctttttttt tttttttag tacaaagttt tagtttcttt ttcatgatgt ggtaactacg
5340
aagtgatggt agatttaaat aatttttttat ttttatttta tatatttttt cattagggcc
5400
atatctccaa aaaaagaaag aaaaaataca aaaaacaaaa acaaaaaaaa aagagggtaa
5460
tgtacaagtt tctgtatgta taaagtcatg ctcgatttca ggagagcagc tgatcacaat
5520
ttgcttcatg aatcaaggtg tggaaatggt tatatatgga ttgatttaga aaatggttac
5580
cagtacagtc aaaaaagaga aaatgaaaaa aatacaacta aaaggaagaa acacaacttc
5640
aaagattttt cagtgatgag aatccacatt tgtatttcaa gataatgtag tttaaaaaaa
5700

aaaaaaagaa aaaaacttga tgtaaattcc tccttttcct ctggcttaat gaatatcatt
5760
tattcagtat aaaatcttta tatgttccac atgttaagaa taaatgtaca ttaaatcttg
5820
ttaagcactg tg
5832

<210> 1038
<211> 1485
<212> PRT
<213> Homo sapiens

<400> 1038
Pro Ser Pro Gly Gly Gln Met His Ala Gly Ile Ser Ser Phe Gln Gln
1 5 10 15
Ser Asn Ser Ser Gly Thr Tyr Gly Pro Gln Met Ser Gln Tyr Gly Pro
20 25 30
Gln Gly Asn Tyr Ser Arg Pro Pro Ala Tyr Ser Gly Val Pro Ser Ala
35 40 45
Ser Tyr Ser Gly Pro Gly Pro Gly Met Gly Ile Ser Ala Asn Asn Gln
50 55 60
Met His Gly Gln Gly Pro Ser Gln Pro Cys Gly Ala Val Pro Leu Gly
65 70 75 80
Arg Met Pro Ser Ala Gly Met Gln Asn Arg Pro Phe Pro Gly Asn Met
85 90 95
Ser Ser Met Thr Pro Ser Ser Pro Gly Met Ser Gln Gln Gly Gly Pro
100 105 110
Gly Met Gly Pro Pro Met Pro Thr Val Asn Arg Lys Ala Gln Glu Ala
115 120 125
Ala Ala Ala Val Met Gln Ala Ala Ala Asn Ser Ala Gln Ser Arg Gln
130 135 140
Gly Ser Phe Pro Gly Met Asn Gln Ser Gly Leu Met Ala Ser Ser Ser
145 150 155 160
Pro Tyr Ser Gln Pro Met Asn Asn Ser Ser Ser Leu Met Asn Thr Gln
165 170 175
Ala Pro Pro Tyr Ser Met Ala Pro Ala Met Val Asn Ser Ser Ala Ala
180 185 190
Ser Val Gly Leu Ala Asp Met Met Ser Pro Gly Glu Ser Lys Leu Pro
195 200 205
Leu Pro Leu Lys Ala Asp Gly Lys Glu Glu Gly Thr Pro Gln Pro Glu
210 215 220
Ser Lys Ser Lys Asp Ser Tyr Ser Ser Gln Gly Ile Ser Gln Pro Pro
225 230 235 240
Thr Pro Gly Asn Leu Pro Val Pro Ser Pro Met Ser Pro Ser Ser Ala
245 250 255
Ser Ile Ser Ser Phe His Gly Asp Glu Ser Asp Ser Ile Ser Ser Pro
260 265 270
Gly Trp Pro Lys Thr Pro Ser Ser Pro Lys Ser Ser Ser Ser Thr Thr
275 280 285
Thr Gly Glu Lys Ile Thr Lys Val Tyr Glu Leu Gly Asn Glu Pro Glu
290 295 300
Arg Lys Leu Trp Val Asp Arg Tyr Leu Thr Phe Met Glu Glu Arg Gly
305 310 315 320
Ser Pro Val Ser Ser Leu Pro Ala Val Gly Lys Lys Pro Leu Asp Leu

```
                325                 330                 335
Phe Arg Leu Tyr Val Cys Val Lys Glu Ile Gly Gly Leu Ala Gln Val
            340                 345                 350
Asn Lys Asn Lys Lys Trp Arg Glu Leu Ala Thr Asn Leu Asn Val Gly
        355                 360                 365
Thr Ser Ser Ser Ala Ala Ser Ser Leu Lys Lys Gln Tyr Ile Gln Tyr
    370                 375                 380
Leu Phe Ala Phe Glu Cys Lys Ile Glu Arg Gly Glu Glu Pro Pro Pro
385                 390                 395                 400
Glu Val Phe Ser Thr Gly Asp Thr Lys Lys Gln Pro Lys Leu Gln Pro
                405                 410                 415
Pro Ser Pro Ala Asn Ser Gly Ser Leu Gln Gly Pro Gln Thr Pro Gln
            420                 425                 430
Ser Thr Gly Ser Asn Ser Met Ala Glu Val Pro Gly Asp Leu Lys Pro
        435                 440                 445
Pro Thr Pro Ala Ser Thr Pro His Gly Gln Met Thr Pro Met Gln Gly
    450                 455                 460
Gly Arg Ser Ser Thr Ile Ser Val His Asp Pro Phe Ser Asp Val Ser
465                 470                 475                 480
Asp Ser Ser Phe Pro Lys Arg Asn Ser Met Thr Pro Asn Ala Pro Tyr
                485                 490                 495
Gln Gln Gly Met Ser Met Pro Asp Val Met Gly Arg Met Pro Tyr Glu
            500                 505                 510
Pro Asn Lys Asp Pro Phe Gly Gly Met Arg Lys Val Pro Gly Ser Ser
        515                 520                 525
Glu Pro Phe Met Thr Gln Gly Gln Met Pro Asn Ser Ser Met Gln Asp
    530                 535                 540
Met Tyr Asn Gln Ser Pro Ser Gly Ala Met Ser Asn Leu Gly Met Gly
545                 550                 555                 560
Gln Arg Gln Gln Phe Pro Tyr Gly Ala Ser Tyr Asp Arg Arg His Glu
                565                 570                 575
Pro Tyr Gly Gln Gln Tyr Pro Gly Gln Gly Pro Pro Ser Gly Gln Pro
            580                 585                 590
Pro Tyr Gly Gly His Gln Pro Gly Leu Tyr Pro Gln Gln Pro Asn Tyr
        595                 600                 605
Lys Arg His Met Asp Gly Met Tyr Gly Pro Pro Ala Lys Arg His Glu
    610                 615                 620
Gly Asp Met Tyr Asn Met Gln Tyr Ser Ser Gln Gln Gln Glu Met Tyr
625                 630                 635                 640
Asn Gln Tyr Gly Gly Ser Tyr Ser Gly Pro Asp Arg Arg Pro Ile Gln
                645                 650                 655
Gly Gln Tyr Pro Tyr Pro Tyr Ser Arg Glu Arg Met Gln Gly Pro Gly
            660                 665                 670
Gln Ile Gln Thr His Gly Ile Pro Leu Gln Met Met Gly Gly Pro Leu
        675                 680                 685
Gln Ser Ser Ser Ser Glu Gly Pro Gln Gln Asn Met Trp Ala Ala Arg
    690                 695                 700
Asn Asp Met Pro Tyr Pro Tyr Gln Asn Arg Gln Gly Pro Gly Gly Pro
705                 710                 715                 720
Thr Gln Ala Pro Pro Tyr Pro Gly Met Asn Arg Thr Asp Asp Met Met
                725                 730                 735
Val Pro Asp Gln Arg Ile Asn His Glu Ser Gln Trp Pro Ser His Val
            740                 745                 750
Ser Gln Arg Gln Pro Tyr Met Ser Ser Ser Ala Ser Met Gln Pro Ile
```

```
        755                 760                 765
Thr Arg Pro Pro Gln Pro Ser Tyr Gln Thr Pro Pro Ser Leu Pro Asn
    770                 775                 780
His Ile Ser Arg Ala Pro Ser Pro Ala Ser Phe Gln Arg Ser Leu Glu
785                 790                 795                 800
Asn Arg Met Ser Pro Ser Lys Ser Pro Phe Leu Pro Ser Met Lys Met
                805                 810                 815
Gln Lys Val Met Pro Thr Val Pro Thr Ser Gln Val Thr Gly Pro Pro
            820                 825                 830
Pro Gln Pro Pro Pro Ile Arg Arg Glu Ile Thr Phe Pro Pro Gly Ser
        835                 840                 845
Val Glu Ala Ser Gln Pro Val Leu Lys Gln Arg Arg Lys Ile Thr Ser
    850                 855                 860
Lys Asp Ile Val Thr Pro Glu Ala Trp Arg Val Met Met Ser Leu Lys
865                 870                 875                 880
Ser Gly Leu Leu Ala Glu Ser Thr Trp Ala Leu Asp Thr Ile Asn Ile
                885                 890                 895
Leu Leu Tyr Asp Asp Ser Thr Val Ala Thr Phe Asn Leu Ser Gln Leu
            900                 905                 910
Ser Gly Phe Leu Glu Leu Leu Val Glu Tyr Phe Arg Lys Cys Leu Ile
        915                 920                 925
Asp Ile Phe Gly Ile Leu Met Glu Tyr Glu Val Gly Asp Pro Ser Gln
    930                 935                 940
Lys Ala Leu Asp His Asn Ala Ala Arg Lys Asp Asp Ser Gln Ser Leu
945                 950                 955                 960
Ala Asp Asp Ser Gly Lys Glu Glu Glu Asp Ala Glu Cys Ile Asp Asp
                965                 970                 975
Asp Glu Glu Asp Glu Glu Asp Glu Glu Glu Asp Ser Glu Lys Thr Glu
            980                 985                 990
Ser Asp Glu Lys Ser Ser Ile Ala Leu Thr Ala Pro Asp Ala Ala Ala
        995                 1000                1005
Asp Pro Lys Glu Lys Pro Lys Gln Ala Ser Lys Phe Asp Lys Leu Pro
    1010                1015                1020
Ile Lys Ile Val Lys Lys Asn Asn Leu Phe Val Val Asp Arg Ser Asp
1025                1030                1035                1040
Lys Leu Gly Arg Val Gln Glu Phe Asn Ser Gly Leu Leu His Trp Gln
                1045                1050                1055
Leu Gly Gly Gly Asp Thr Thr Glu His Ile Gln Thr His Phe Glu Ser
            1060                1065                1070
Lys Met Glu Ile Pro Pro Arg Arg Arg Pro Pro Pro Pro Leu Ser Ser
        1075                1080                1085
Ala Gly Lys Lys Lys Glu Leu Ala Gly Lys Gly Asp Ser Glu Glu Gln
    1090                1095                1100
Gln Glu Lys Ser Ile Ile Ala Thr Ile Asp Asp Val Leu Ser Ala Arg
1105                1110                1115                1120
Pro Gly Ala Leu Pro Glu Asp Ala Asn Pro Gly Pro Gln Thr Glu Ser
                1125                1130                1135
Ser Lys Phe Pro Phe Gly Ile Gln Gln Ala Lys Ser His Arg Asn Ile
            1140                1145                1150
Lys Leu Leu Glu Asp Glu Pro Arg Ser Arg Asp Glu Thr Pro Leu Cys
        1155                1160                1165
Thr Ile Ala His Trp Gln Asp Ser Leu Ala Lys Arg Cys Il  Cys Val
    1170                1175                1180
Ser Asn Ile Val Arg Ser Leu Ser Phe Val Pro Gly Asn Asp Ala Glu
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1185 1190 1195 1200
Met Ser Lys His Pro Gly Leu Val Leu Ile Leu Gly Lys Leu Ile Leu
1205 1210 1215
Leu His His Glu His Pro Glu Arg Lys Arg Ala Pro Gln Thr Tyr Glu
1220 1225 1230
Lys Glu Glu Asp Glu Asp Lys Gly Val Ala Cys Ser Lys Asp Glu Trp
1235 1240 1245
Trp Trp Asp Cys Leu Glu Val Leu Arg Asp Asn Thr Leu Val Thr Leu
1250 1255 1260
Ala Asn Ile Ser Gly Gln Leu Asp Leu Ser Ala Tyr Thr Glu Ser Ile
1265 1270 1275 1280
Cys Leu Pro Ile Leu Asp Gly Leu Leu His Trp Met Val Cys Pro Ser
1285 1290 1295
Ala Glu Ala Gln Asp Pro Phe Pro Thr Val Gly Pro Asn Ser Val Pro
1300 1305 1310
Ser Pro Gln Arg Leu Val Leu Glu Thr Leu Cys Lys Leu Ser Ile Gln
1315 1320 1325
Asp Asn Asn Val Asp Leu Ile Leu Ala Thr Pro Pro Phe Ser Arg Gln
1330 1335 1340
Glu Lys Phe Tyr Ala Thr Leu Val Arg Tyr Val Gly Asp Arg Lys Asn
1345 1350 1355 1360
Pro Val Cys Arg Glu Met Ser Met Ala Leu Leu Ser Asn Leu Ala Gln
1365 1370 1375
Gly Asp Ala Leu Ala Ala Arg Ala Ile Ala Val Gln Lys Gly Ser Ile
1380 1385 1390
Gly Asn Leu Ile Ser Phe Leu Glu Asp Gly Val Thr Met Ala Gln Tyr
1395 1400 1405
Gln Gln Ser Gln His Asn Leu Met His Met Gln Pro Pro Pro Leu Glu
1410 1415 1420
Pro Pro Ser Val Asp Met Met Cys Arg Ala Ala Lys Ala Leu Leu Ala
1425 1430 1435 1440
Met Ala Arg Val Asp Glu Asn Arg Ser Glu Phe Leu Leu His Glu Gly
1445 1450 1455
Arg Leu Leu Asp Ile Ser Ile Ser Ala Val Leu Asn Ser Leu Val Ala
1460 1465 1470
Ser Val Ile Cys Asp Val Leu Phe Gln Ile Gly Gln Leu
1475 1480 1485

<210> 1039
<211> 379
<212> DNA
<213> Homo sapiens

<400> 1039
gcaggagcca gggatgctgc tgaacatccc gcagtgcacg agacaggcct ccaccacacg
60
gaattacctt ggcctgaggt gttacgagag cacagagaga aaccaggtac agacgcgggg
120
cagaggggag agagggagag agtgtgagag ctaaggtttc gggagaagac tttgtggaaa
180
aagtctttgg ctgggtcctg caacatagcc aggattcagt gacaggtgag gaccactcca
240
gattttgtat gtattgaagg ccctgaatac ttttttgaaa gagaatgaca tgagtacacc
300

tggtcagcca cacgtgagag gggttggagg agggaagtac cagaggcagg gagaccaggt
360
agaaagacct cgccatagt
379

<210> 1040
<211> 125
<212> PRT
<213> Homo sapiens

<400> 1040
Met Ala Arg Ser Phe Tyr Leu Val Ser Leu Pro Leu Val Leu Pro Ser
 1   5   10   15
Ser Asn Pro Ser His Val Trp Leu Thr Arg Cys Thr His Val Ile Leu
            20   25   30
Phe Gln Lys Ser Ile Gln Gly Leu Gln Tyr Ile Gln Asn Leu Glu Trp
        35   40   45
Ser Ser Pro Val Thr Glu Ser Trp Leu Cys Cys Arg Thr Gln Pro Lys
    50   55   60
Thr Phe Ser Thr Lys Ser Ser Pro Glu Thr Leu Ala Leu Thr Leu Ser
65   70   75   80
Pro Ser Leu Pro Ser Ala Pro Arg Leu Tyr Leu Val Ser Leu Cys Ala
                85   90   95
Leu Val Thr Pro Gln Ala Lys Val Ile Pro Cys Gly Gly Gly Leu Ser
            100   105   110
Arg Ala Leu Arg Asp Val Gln Gln His Pro Trp Leu Leu
        115   120   125

<210> 1041
<211> 388
<212> DNA
<213> Homo sapiens

<400> 1041
ttagtggccg tggaggccat cggctacatc gcgagtattg acaaggccga tatgtcaatc
60
gaaacggcgt acctgccgcg gctgttggtt tccctggccc tgaccatccc ggtgctcgcc
120
ttgtcgatga tcccggccct gcacttcccg cattggccgt tgtgggcgtt ggcgcttacc
180
accccggtgg tgttctgggg tgcctggccg ctgcaccacg ccgcgtggac caacctgcgg
240
cacggcgcgg ccatcatgga caccctggtg tcgctcggcg tcctcacttc gtacctctgg
300
tcggtatgga tgctgaccac aggcggcgag cacctctacc tggaggtagc cgtccaccgt
360
cacgacgctg atcctggccg gcaaattt
388

<210> 1042
<211> 129
<212> PRT
<213> Homo sapiens

<400> 1042
Leu Val Ala Val Glu Ala Ile Gly Tyr Ile Ala Ser Ile Asp Lys Ala
1 5 10 15
Asp Met Ser Ile Glu Thr Ala Tyr Leu Pro Arg Leu Leu Val Ser Leu
20 25 30
Ala Leu Thr Ile Pro Val Leu Ala Leu Ser Met Ile Pro Ala Leu His
35 40 45
Phe Pro His Trp Pro Leu Trp Ala Leu Ala Leu Thr Thr Pro Val Val
50 55 60
Phe Trp Gly Ala Trp Pro Leu His His Ala Ala Trp Thr Asn Leu Arg
65 70 75 80
His Gly Ala Ala Ile Met Asp Thr Leu Val Ser Leu Gly Val Leu Thr
85 90 95
Ser Tyr Leu Trp Ser Val Trp Met Leu Thr Thr Gly Gly Glu His Leu
100 105 110
Tyr Leu Glu Val Ala Val His Arg His Asp Ala Asp Pro Gly Arg Gln
115 120 125
Ile

<210> 1043
<211> 555
<212> DNA
<213> Homo sapiens

<400> 1043
accggtgaaa ccctgatcgg ccaatcgttt tccaccgttc ccggcggcaa gggcgcaaac
60
caggcggtcg cttcggcgcg tcttggggcc gaagtcgcga tggtcggttg cgtgggtacc
120
gatgcctacg gcgcgcaatt acgcgacgca ttgttggtgg aaggcatcga ttgccaggcc
180
gtcagcaccg tcgacggttc cagcggtgtg gcgctgatcg tggtggatga cagcagccag
240
aatgcgatcg ttatcgtcgc cggtagcaat ggcgagctga ctccggccaa gttacagacc
300
tttgacagcg tgctgcaggc tgccgacgtg attgtctgcc agcttgagac gccgatggac
360
actgtcggcc atgcgcctaa gcgcggtcgc gaactgggca agacggtgat cctcaatccg
420
gcgccggcca gcggcccgct gcctgaggat tggtacgccg ccatcgatta cctgattccc
480
aacgaaagcg aagcctcggc cttgagtggc gtggtggtgg attcactgga cagcgccaag
540
gtcgctgcta cgcgt
555

<210> 1044
<211> 185
<212> PRT
<213> Homo sapiens

<400> 1044
Thr Gly Glu Thr Leu Ile Gly Gln Ser Phe Ser Thr Val Pro Gly Gly

```
 1               5                  10                  15
Lys Gly Ala Asn Gln Ala Val Ala Ser Ala Arg Leu Gly Ala Glu Val
            20                  25                  30
Ala Met Val Gly Cys Val Gly Thr Asp Ala Tyr Gly Ala Gln Leu Arg
        35                  40                  45
Asp Ala Leu Leu Val Glu Gly Ile Asp Cys Gln Ala Val Ser Thr Val
    50                  55                  60
Asp Gly Ser Ser Gly Val Ala Leu Ile Val Val Asp Asp Ser Ser Gln
65                  70                  75                  80
Asn Ala Ile Val Ile Val Ala Gly Ser Asn Gly Glu Leu Thr Pro Ala
                85                  90                  95
Lys Leu Gln Thr Phe Asp Ser Val Leu Gln Ala Ala Asp Val Ile Val
            100                 105                 110
Cys Gln Leu Glu Thr Pro Met Asp Thr Val Gly His Ala Pro Lys Arg
        115                 120                 125
Gly Arg Glu Leu Gly Lys Thr Val Ile Leu Asn Pro Ala Pro Ala Ser
    130                 135                 140
Gly Pro Leu Pro Glu Asp Trp Tyr Ala Ala Ile Asp Tyr Leu Ile Pro
145                 150                 155                 160
Asn Glu Ser Glu Ala Ser Ala Leu Ser Gly Val Val Val Asp Ser Leu
                165                 170                 175
Asp Ser Ala Lys Val Ala Ala Thr Arg
            180                 185
```

<210> 1045
<211> 371
<212> DNA
<213> Homo sapiens

<400> 1045
ctattgccat actaccgccg cggcaaccta caggacatga tcaacgccaa cctcttcaat
60
cactccaaat tccccgagac gcaccttatg aatctatttc tcggcgtctg caaggccctg
120
cgcgccatgc acgattacca cgcaccgccg gcagagcgca tgccaattgg gcaccgaagg
180
cagaccacca cccaggtgca aagcaacagt ggtagagcgg tcgctcatcg acgaaacgta
240
cggaagaaga cgaagagacg gagcaggaaa gacctgttat ggaatcacag aaccacatcg
300
ggcagggcgg cgagcacaaa accatatgcg catcgcgaca ttaaaccagg tacgtgctgc
360
aagctcctcg g
371

<210> 1046
<211> 123
<212> PRT
<213> Homo sapiens

<400> 1046
```
Leu Leu Pro Tyr Tyr Arg Arg Gly Asn Leu Gln Asp Met Ile Asn Ala
 1               5                  10                  15
Asn Leu Phe Asn His Ser Lys Phe Pro Glu Thr His Leu Met Asn Leu
```

```
            20                  25                  30
Phe Leu Gly Val Cys Lys Ala Leu Arg Ala Met His Asp Tyr His Ala
        35                  40                  45
Pro Pro Ala Glu Arg Met Pro Ile Gly His Arg Arg Gln Thr Thr Thr
    50                  55                  60
Gln Val Gln Ser Asn Ser Gly Arg Ala Val Ala His Arg Arg Asn Val
65                  70                  75                  80
Arg Lys Lys Thr Lys Arg Arg Ser Arg Lys Asp Leu Leu Trp Asn His
                85                  90                  95
Arg Thr Thr Ser Gly Arg Ala Ala Ser Thr Lys Pro Tyr Ala His Arg
            100                 105                 110
Asp Ile Lys Pro Gly Thr Cys Cys Lys Leu Leu
        115                 120
```

<210> 1047
<211> 754
<212> DNA
<213> Homo sapiens

<400> 1047
natgcccaga aggacctgga cgaggcgttg ccagccctgg atgcggctct ggccagccta
60
cgcaacctca acaagaacga agtgacccag gtacgtgcca tgcagcggcc acccccgggt
120
gtgaaactgg tcatagaagc tgtgtgcatt atgaaaggca tcaagcccaa gaaggtgcct
180
ggagaaaagc caggcaccaa ggtggatgac tactgggagc ctggcaaggg gctgctgcag
240
gacccgggcc acttccttga gagcctcttc aagtttgaca aggacaacat tggagatgtg
300
gtgatcaaag ccatccagcc gtacatcgat aatgaagagt tccagccagc caccattgcc
360
aaggtgtcca agggttgccc cttcatttgg ccgtgggggg gggcaatgcc caagtacccc
420
tttgtggcca aggccgtgga gcccaagcgg caagccctgc tggaggccca ggatgacctg
480
ggggtgacac agaggatcct ggatgaggca aaacagcgcc ttcgtgaggt ggaggacggc
540
atcgccacaa tgcaggctaa gtaccgggaa tgcattacca agaaggagga gctggagctg
600
aagtgtgagc agtgtgagca gcggctgggc cacgctggca aggtgcgcac cctcctcctg
660
caaggcctgc aagcgggccc ggcccagaca ggggccagaa aggaccaggg cgccggtggg
720
tcctggggtg gctgtccaac cccctccctg gcaa
754

<210> 1048
<211> 251
<212> PRT
<213> Homo sapiens

<400> 1048
Xaa Ala Gln Lys Asp Leu Asp Glu Ala Leu Pro Ala Leu Asp Ala Ala

```
 1               5                  10                  15
Leu Ala Ser Leu Arg Asn Leu Asn Lys Asn Glu Val Thr Gln Val Arg
            20                  25                  30
Ala Met Gln Arg Pro Pro Pro Gly Val Lys Leu Val Ile Glu Ala Val
        35                  40                  45
Cys Ile Met Lys Gly Ile Lys Pro Lys Lys Val Pro Gly Glu Lys Pro
    50                  55                  60
Gly Thr Lys Val Asp Asp Tyr Trp Glu Pro Gly Lys Gly Leu Leu Gln
65                  70                  75                  80
Asp Pro Gly His Phe Leu Glu Ser Leu Phe Lys Phe Asp Lys Asp Asn
                85                  90                  95
Ile Gly Asp Val Val Ile Lys Ala Ile Gln Pro Tyr Ile Asp Asn Glu
            100                 105                 110
Glu Phe Gln Pro Ala Thr Ile Ala Lys Val Ser Lys Gly Cys Pro Phe
        115                 120                 125
Ile Trp Pro Trp Gly Gly Ala Met Pro Lys Tyr Pro Phe Val Ala Lys
    130                 135                 140
Ala Val Glu Pro Lys Arg Gln Ala Leu Leu Glu Ala Gln Asp Asp Leu
145                 150                 155                 160
Gly Val Thr Gln Arg Ile Leu Asp Glu Ala Lys Gln Arg Leu Arg Glu
                165                 170                 175
Val Glu Asp Gly Ile Ala Thr Met Gln Ala Lys Tyr Arg Glu Cys Ile
            180                 185                 190
Thr Lys Lys Glu Glu Leu Glu Leu Lys Cys Glu Gln Cys Glu Gln Arg
        195                 200                 205
Leu Gly His Ala Gly Lys Val Arg Thr Leu Leu Leu Gln Gly Leu Gln
    210                 215                 220
Ala Gly Pro Ala Gln Thr Gly Ala Arg Lys Asp Gln Gly Ala Gly Gly
225                 230                 235                 240
Ser Trp Gly Gly Cys Pro Thr Pro Ser Leu Ala
                245                 250
```

<210> 1049
<211> 558
<212> DNA
<213> Homo sapiens

<400> 1049
cgcagcaata gctgcacttg accagactgg gctttgcaat aagcgcattc cccgggctga
60
atgctgcaga tccttacagg ctgactgcag ggtgtttcag attctcctgg agtcacacgt
120
gccagcttga tttcaagaaa caactagaat aacagttttc tgataagaag tctatagcac
180
tttatggctt acataatcca gagatagatg ggctgggcat gattcccatt ttctgttggg
240
gaaaccgact cacagagaag ttaagggaca agtataaagt gatgaaactg tgtactgaac
300
ctcatgtctc ccagactccc gggtccccgg gctttttctc ggggcggccc cattcacatt
360
gcaattcatg gccggggcaa atgctcaccc acagagatat taagcactcc aacactccat
420
ccaccaggtt gcagccaaag gattcagaag acaatgatca ttccatcagc atgcactatg
480

cagctaaaga aaggttttgg catgctctgc tttattgttt cacagaagat aagaaaataa
540
actgcaaagt aacttaag
558

<210> 1050
<211> 112
<212> PRT
<213> Homo sapiens

<400> 1050
Met Ile Pro Ile Phe Cys Trp Gly Asn Arg Leu Thr Glu Lys Leu Arg
1 5 10 15
Asp Lys Tyr Lys Val Met Lys Leu Cys Thr Glu Pro His Val Ser Gln
20 25 30
Thr Pro Gly Ser Pro Gly Phe Phe Ser Gly Arg Pro His Ser His Cys
35 40 45
Asn Ser Trp Pro Gly Gln Met Leu Thr His Arg Asp Ile Lys His Ser
50 55 60
Asn Thr Pro Ser Thr Arg Leu Gln Pro Lys Asp Ser Glu Asp Asn Asp
65 70 75 80
His Ser Ile Ser Met His Tyr Ala Ala Lys Glu Arg Phe Trp His Ala
85 90 95
Leu Leu Tyr Cys Phe Thr Glu Asp Lys Lys Ile Asn Cys Lys Val Thr
100 105 110

<210> 1051
<211> 317
<212> DNA
<213> Homo sapiens

<400> 1051
gcgttgagtc gggatgtcgc attcatgccc ggcgaacctt tttttgccga accggagcgt
60
aatccgggta atcttcgtct caatttcagt cacatcgcac cggagcgtct ggacgaaggt
120
ctcaagcgcc tggctgctgt catccgtcac gcacaggctg cacaagcggc ttaaggggag
180
ggccatgtac aaggtttatg gcgattacca gtcgggcaat tgctacaaga tcaagctgat
240
gctgcacctg ctggggcagg aatatcgctg gcacccgggg gacatcctca aggtgacacc
300
gagaccccgg aattttt
317

<210> 1052
<211> 57
<212> PRT
<213> Homo sapiens

<400> 1052
Ala Leu Ser Arg Asp Val Ala Phe Met Pro Gly Glu Pro Phe Phe Ala
1 5 10 15
Glu Pro Glu Arg Asn Pro Gly Asn Leu Arg Leu Asn Phe Ser His Ile

```
            20                  25                  30
Ala Pro Glu Arg Leu Asp Glu Gly Leu Lys Arg Leu Ala Ala Val Ile
        35                  40                  45
Arg His Ala Gln Ala Ala Gln Ala Ala
    50                  55
```

<210> 1053
<211> 318
<212> DNA
<213> Homo sapiens

<400> 1053
caattggcta cgcgatccga acgggcgcat gggtctctat gactggcaag ccgtcgctcg
60
cggggagtgg gccctcgact atgcctacgc gatgtcggtg aacctgacca ccgagaaccg
120
gcgtgcctgg gaacgcgacc tgctcgagcg ttatctgtgg cgcctcgccg aagagggtgt
180
cgccaacccg ccctcgttcg agcaagcgtg gctacgctac cggcaacagc cgttccacgt
240
cgggatcttc tcactcttga ccatcggcgc cggacgcttt caaccggcca tgcaaccggc
300
ggactcnnnn ccccncnc
318

<210> 1054
<211> 96
<212> PRT
<213> Homo sapiens

<400> 1054
```
Met Gly Leu Tyr Asp Trp Gln Ala Val Ala Arg Gly Glu Trp Ala Leu
 1               5                  10                  15
Asp Tyr Ala Tyr Ala Met Ser Val Asn Leu Thr Thr Glu Asn Arg Arg
            20                  25                  30
Ala Trp Glu Arg Asp Leu Leu Glu Arg Tyr Leu Trp Arg Leu Ala Glu
        35                  40                  45
Glu Gly Val Ala Asn Pro Pro Ser Phe Glu Gln Ala Trp Leu Arg Tyr
    50                  55                  60
Arg Gln Gln Pro Phe His Val Gly Ile Phe Ser Leu Leu Thr Ile Gly
65                  70                  75                  80
Ala Gly Arg Phe Gln Pro Ala Met Gln Pro Ala Asp Ser Xaa Pro Xaa
                85                  90                  95
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<210> 1055
<211> 391
<212> DNA
<213> Homo sapiens

<400> 1055
tacaatgtat catcaaccag aaatacaatg agaaccacct gccagtctcc caaatactat
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120

aagaatcatc tctctgctca ggcaccggga gcaaggggca tctgtcgctc tgcagaacgg
180
aggggaccag gcctgatgaa caccatcctg ggcccagaaa cctgggaggg taaagagaac
240
tgccaggggt gaagtccaag gatgggaaaa aggcctccgg ggcagagtcc tgaaatgtca
300
gaagtacacc aaagaggaaa cagcatcacg ttattgctga ggcagggcct cattctgttg
360
ccaaggctgc agtgcagtgg tgacaccatg g
391

<210> 1056
<211> 83
<212> PRT
<213> Homo sapiens

<400> 1056
Met Val Ser Pro Leu His Cys Ser Leu Gly Asn Arg Met Arg Pro Cys
 1   5   10   15
Leu Ser Asn Asn Val Met Leu Phe Pro Leu Trp Cys Thr Ser Asp Ile
            20   25   30
Ser Gly Leu Cys Pro Gly Gly Leu Phe Pro Ile Leu Gly Leu His Pro
        35   40   45
Trp Gln Phe Ser Leu Pro Ser Gln Val Ser Gly Pro Arg Met Val Phe
    50   55   60
Ile Arg Pro Gly Pro Leu Arg Ser Ala Glu Arg Gln Met Pro Leu Ala
65   70   75   80
Pro Gly Ala

<210> 1057
<211> 341
<212> DNA
<213> Homo sapiens

<400> 1057
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120
tatcaggcgc tgttcgatgc ggtaccgtcc aaggcgaacg gcatctgcct gtgcacgggt
180
tcgctcggcg tgcgcgcgga gaacgatctg cctgaaatgg ccgaacgttt cggcccgcgt
240
atcgcctttg cgcatctgcg cgcgaccaag cgcgacgccg atggcctgtc gtttcatgaa
300
tccgaccatc tcgacggcga tgtcgacatg gtcgcgtgct c
341

<210> 1058
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1058
Glu Phe Pro Ala Arg Val Thr Pro Val Ala Glu Gln Leu Gly Val Ser
1 5 10 15
Leu Thr Leu His Pro Asp Asp Pro Pro Arg Pro Leu Phe Gly Leu Pro
20 25 30
Arg Ile Ala Ser Ser Ala Glu Asp Tyr Gln Ala Leu Phe Asp Ala Val
35 40 45
Pro Ser Lys Ala Asn Gly Ile Cys Leu Cys Thr Gly Ser Leu Gly Val
50 55 60
Arg Ala Glu Asn Asp Leu Pro Glu Met Ala Glu Arg Phe Gly Pro Arg
65 70 75 80
Ile Ala Phe Ala His Leu Arg Ala Thr Lys Arg Asp Ala Asp Gly Leu
85 90 95
Ser Phe His Glu Ser Asp His Leu Asp Gly Asp Val Asp Met Val Ala
100 105 110
Cys

<210> 1059
<211> 372
<212> DNA
<213> Homo sapiens

<400> 1059
nagctgaccg gctggcagat caacatcatg acgccggaag aaagcgtgaa ccgccgggaa
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120
gccgacatcc tgatcgacga aggtttcacc ggtatcgagg aaatcgccta cgtccccatg
180
caggaactgc tggagatcga ggcgttcgac gaagacacca tcaacgagtt gcgcgcccgt
240
gcccgcaatg cgctgctgac cgaggccatc gcccaggaag agcgccttga gaccgcgcag
300
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360
gtgcgtacgc gt
372

<210> 1060
<211> 124
<212> PRT
<213> Homo sapiens

<400> 1060
Xaa Leu Thr Gly Trp Gln Ile Asn Ile Met Thr Pro Glu Glu Ser Val
1 5 10 15
Asn Arg Arg Glu Val Glu Arg Ser Gly Leu Arg Thr Thr Phe Met Asn
20 25 30
Lys Leu Asp Val Asp Glu Glu Val Ala Asp Ile Leu Ile Asp Glu Gly
35 40 45
Phe Thr Gly Ile Glu Glu Ile Ala Tyr Val Pro Met Gln Glu Leu Leu
50 55 60
Glu Ile Glu Ala Phe Asp Glu Asp Thr Ile Asn Glu Leu Arg Ala Arg

65 70 75 80
Ala Arg Asn Ala Leu Leu Thr Glu Ala Ile Ala Gln Glu Glu Arg Leu
85 90 95
Glu Thr Ala Gln Asp Leu Leu Glu Leu Glu Gly Val Thr Pro Glu Leu
100 105 110
Ala Ala Lys Leu Ala Glu Arg Gln Val Arg Thr Arg
115 120

<210> 1061
<211> 456
<212> DNA
<213> Homo sapiens

<400> 1061
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cccttcgagg aaacccttttt gcaggccaag caagggctgc aagtgtttgg gagctgagag
120
gagaaggagg attctggagc attgtatttg gcagccggag cgggcagtgg gcgggggggtt
180
gggacacgaa gggctcttcg gacccctgtg cctcttctgc cccaagggcg agaagacggg
240
cttcgcagcg accctcgggg gtccatggag ccgcctgcct tcgccccctc gctcttccca
300
ggtctgaacc tggatgggga gaagaaattg aagtgctttg gagacggggg ggcttaaaac
360
actagggagc ctcatcgccc agccttgggc ccactttcct ttcgatcgtg aggattccgc
420
accccgaagc cgtcttctcg gggctccggg gcgcgc
456

<210> 1062
<211> 125
<212> PRT
<213> Homo sapiens

<400> 1062
Met Arg Leu Pro Ser Val Leu Ser Pro Pro Val Ser Lys Ala Leu Gln
1 5 10 15
Phe Leu Leu Pro Ile Gln Val Gln Thr Trp Glu Glu Arg Gly Gly Glu
20 25 30
Gly Arg Arg Leu His Gly Pro Pro Arg Val Ala Ala Lys Pro Val Phe
35 40 45
Ser Pro Leu Gly Gln Lys Arg His Arg Gly Pro Lys Ser Pro Ser Cys
50 55 60
Pro Asn Pro Pro Pro Thr Ala Arg Ser Gly Cys Gln Ile Gln Cys Ser
65 70 75 80
Arg Ile Leu Leu Leu Leu Ser Ala Pro Lys His Leu Gln Pro Leu Leu
85 90 95
Gly Leu Gln Lys Gly Phe Leu Glu Gly Ala Lys Gly Thr Phe Tyr Leu
100 105 110
Ser Tyr Leu Pro Ala Gln Pro Gly Ala Met Glu Ser Arg
115 120 125

<210> 1063
<211> 3760
<212> DNA
<213> Homo sapiens

<400> 1063
ntagtagaga cagggtttca ccatgttggc caggctggtc ttgaactcct gagcttgtga
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tccacccgcc tcagcctccc aaagtgctgg gattacaggc gtgacgactg cacccagcct
120
taaggtctta taactagtaa atatctgcat taaagaacga gttgaatgaa aattctgata
180
aattcctact taaagtgtat ccaaagaaaa cggaaaaagt ctaggagtta gtgatattag
240
attcagaaga atgagctttg taattcttaa aaattagtct cagaatagaa aggattttaa
300
aagtaattga gtaaagtcat aggaaatgtg accatataaa ggaatggctc taaatgtatt
360
aatccagaag gaagcaacag gttaaacagt aagaggtaag aaacaaaaaa taaggaacga
420
gagagagaga gtgacaggga gagagagaca gagcggggaa ggagagaatg agaaggaaaa
480
tcaggaaaac gaggagaaac agaattaagg aggtgatact ggaatagtat cagaccattc
540
tgaatcaatt taagaattgc catgtctaat tcttatatgg aagatttgaa atacaaggat
600
attgaaagga ataacaaatt ataatgaatg catagaaatc cttatgtaat ccaaggtcat
660
taatttgaag gaagacatca agaaaatgtg atctagaaat aaaggttgag attgctccat
720
ttacaaaatt attatgctct ataatcttcc catatgcaaa tatttcatat tccctctttt
780
gtcccatgga catatttcac agcaacaacg aatcaagtgc tgacctaaat ggggtatctg
840
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900
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1020
gttgcatcac agatgaaaaa gtaaggccga agaagaccag agaagagttg gttgaatgtg
1080
tagatataag atccatctgt gacattgtag aatgaaattt caccggcttc atagtccaag
1140
aaaatcccaa tgcagtgagg actttccagt tggagaagag gcactgatgg ggaggcaagg
1200
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1320
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1380
cagggccatg tgtcaaatcg ctcagggttg ttggggacat ccctccatgg ttctccatcc
1440

tgcacactgc gcaggtcggc ggtcaagagc agactcgggt gcgccgtggc gggatccagc
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1680
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1860
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1920
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1980
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2040
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2160
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2220
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2280
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2460
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2520
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2580
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2700
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2760
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2820
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2880
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3060

acattttctt gatgtcttcc ttcaaattaa tgaccttgga ttacataagg atttctatgc
3120
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3180
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3360
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3480
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3540
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3600
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3660
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3760

<210> 1064
<211> 483
<212> PRT
<213> Homo sapiens

<400> 1064
Met Gln Gly His Val Ser Asn Arg Ser Gly Leu Leu Gly Thr Ser Leu
1 5 10 15
His Gly Ser Pro Ser Cys Thr Leu Arg Arg Ser Ala Val Lys Ser Arg
20 25 30
Leu Gly Cys Ala Val Ala Gly Ser Ser Phe Thr Ser Thr Trp Asn Phe
35 40 45
Leu Lys Ser Ser Leu Leu Pro Gly Met Gln His Ala Val Phe Ser Ser
50 55 60
Met Gly Met Phe Ser Ala Ser Ser Leu Val Thr Ala Leu Leu Leu Leu
65 70 75 80
Arg Thr Pro Leu Thr Pro Ser Ser Arg Pro Arg Ala Gly Arg Trp His
85 90 95
Leu Ser Cys Ser Ser Ser Ala Ser Ser Phe Arg Ala Leu Leu Cys Trp
100 105 110
Thr Ser Arg Leu Leu Leu Ser Arg Ser Leu Cys Ser Val Ala Arg Ser
115 120 125
Ser Ala Ser Ser Arg Leu Ser Tyr Gln Val Lys Leu Gln Met Ala Leu
130 135 140
Glu Leu Met Arg Lys Glu Leu Glu Asp Ala Leu Thr Gln Glu Ala Asn
145 150 155 160
Val Gly Lys Lys Thr Val Ile Trp Lys Glu Lys Val Glu Met Gln Arg
165 170 175
Gln Arg Phe Arg Leu Glu Phe Glu Lys His Arg Gly Phe Leu Ala Gln

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            180                 185                 190
Glu Glu Gln Arg Gln Leu Arg Arg Leu Glu Ala Glu Glu Arg Ala Thr
        195                 200                 205
Leu Gln Arg Leu Arg Glu Ser Lys Ser Arg Leu Val Gln Gln Ser Lys
    210                 215                 220
Ala Leu Lys Glu Leu Ala Asp Glu Leu Gln Glu Arg Cys Gln Arg Pro
225                 230                 235                 240
Ala Leu Gly Leu Leu Glu Gly Val Arg Gly Val Leu Ser Arg Ser Lys
                245                 250                 255
Ala Val Thr Arg Leu Glu Ala Glu Asn Ile Pro Met Glu Leu Lys Thr
            260                 265                 270
Ala Cys Cys Ile Pro Gly Arg Arg Glu Leu Leu Arg Lys Phe Gln Val
        275                 280                 285
Asp Val Lys Leu Asp Pro Ala Thr Ala His Pro Ser Leu Leu Leu Thr
    290                 295                 300
Ala Asp Leu Arg Ser Val Gln Asp Gly Glu Pro Trp Arg Asp Val Pro
305                 310                 315                 320
Asn Asn Pro Glu Arg Phe Asp Thr Trp Pro Cys Ile Leu Gly Leu Gln
                325                 330                 335
Ser Phe Ser Ser Gly Arg His Tyr Trp Glu Val Leu Val Gly Glu Gly
            340                 345                 350
Ala Glu Trp Gly Leu Gly Val Cys Gln Asp Thr Leu Pro Arg Lys Gly
        355                 360                 365
Glu Thr Met Pro Ser Pro Glu Asn Gly Val Trp Ala Leu Trp Leu Leu
    370                 375                 380
Lys Gly Asn Glu Tyr Met Val Leu Ala Ser Pro Ser Val Pro Leu Leu
385                 390                 395                 400
Gln Leu Glu Ser Pro Arg Cys Ile Gly Ile Phe Leu Asp Tyr Glu Ala
                405                 410                 415
Gly Glu Ile Ser Phe Tyr Asn Val Thr Asp Gly Ser Tyr Ile Tyr Thr
            420                 425                 430
Phe Asn Gln Leu Phe Ser Gly Leu Leu Arg Pro Tyr Phe Phe Ile Cys
        435                 440                 445
Asp Ala Thr Pro Leu Ile Leu Pro Pro Thr Thr Ile Ala Gly Ser Gly
    450                 455                 460
Asn Trp Ala Ser Arg Asp His Leu Asp Pro Ala Ser Asp Val Arg Asp
465                 470                 475                 480
Asp His Leu
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<210> 1065
<211> 892
<212> DNA
<213> Homo sapiens

<400> 1065
nacgcgtggt gtcatgggga ggtgggctgc agtgatgaga aaaggccggg ggctgtgcaa
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taccatgctt cacaaaggga gaagatcaaa gtgaccctcc cccatggctt tggaaccttc
120
ttgtccagtc tggaaggggg gaagaagaga tgaggggaag gctgtccagg ggggtgccag
180
gccctagaga cccagcagag aagggactct ggccactgaa ggggccctcc cattgtggct
240

ctggttccct agagcagctc cagcttcttg gcctcccccg tctgatgctt agctcatccc
300
atcccctgga gtgctgtgga gcttagatga aacagcccag tgctcactct tcaatgagcc
360
cacccagagc agcatcaaga tgcagttggc ggggtactgg aactggcttg gcaagggctg
420
cgcaggcaac aggtcccagc aagagtcagc tagcctagct cagccctgca cacctggaga
480
cctgggggtg ctccagacac ctcggccctt taggtccctt taattgaatg tgtgtggatc
540
agtgaaggtt gaggaatcat ttctctatgg cccaagacgt ttctctctgc agttgtcatg
600
ttagtacctg ccagcttttc ctctcttaca taaatttcat gccagagcct ggaaatgtgt
660
gcccctttgta ggaggggcat cacaggctgg ctcacctcag cagtgccagg cagagcccgt
720
ccctctcatt gcaggaggcg catgaagcgt gtctgggacc gagctgtgga gttcctggcc
780
tccaacgaat cccggatcca gacggagtcc caccgcgttg caggagagga catgctggtg
840
ttgagatgga ctaagccctc ttccttctct gactcagagc gataagcccg gg
892

<210> 1066
<211> 76
<212> PRT
<213> Homo sapiens

<400> 1066
Met Cys Ala Leu Cys Arg Arg Gly Ile Thr Gly Trp Leu Thr Ser Ala
 1   5   10   15
Val Pro Gly Arg Ala Arg Pro Ser His Cys Arg Arg Arg Met Lys Arg
            20   25   30
Val Trp Asp Arg Ala Val Glu Phe Leu Ala Ser Asn Glu Ser Arg Ile
        35   40   45
Gln Thr Glu Ser His Arg Val Ala Gly Glu Asp Met Leu Val Leu Arg
    50   55   60
Trp Thr Lys Pro Ser Ser Phe Ser Asp Ser Glu Arg
65   70   75

<210> 1067
<211> 418
<212> DNA
<213> Homo sapiens

<400> 1067
gaattcgagg tcaccgcgaa tgtgttccgc gaaggccacg acgccgtcgg ggctagtgtc
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gttctcaccg atcccgaggg caaccgtcac ctcactgaca tgcaccaggt cgagccctgg
120
ggactagaca tctggaaagc ccgagtctcc gctgacatcg aaggcgactg gactatgcac
180
gttgaaggct ggtcagacac ctggggcacg tggcatcaca atgccaatgc caagctcgcc
240

gctgccatcg acgtcgaact ggtgtgcgcc gaaggccatg ccctcataaa cgaggcggtc
300
cggcacgccg agcaatccgg ggatactgac gcgatcacgg ctctgcgcga gaccgatgcc
360
aacctaaccc ttgaccgtgc ccccgactcg ctacaacagg tcatcaacac ctacgcgt
418

<210> 1068
<211> 139
<212> PRT
<213> Homo sapiens

<400> 1068
Glu Phe Glu Val Thr Ala Asn Val Phe Arg Glu Gly His Asp Ala Val
1 5 10 15
Gly Ala Ser Val Val Leu Thr Asp Pro Glu Gly Asn Arg His Leu Thr
20 25 30
Asp Met His Gln Val Glu Pro Trp Gly Leu Asp Ile Trp Lys Ala Arg
35 40 45
Val Ser Ala Asp Ile Glu Gly Asp Trp Thr Met His Val Glu Gly Trp
50 55 60
Ser Asp Thr Trp Gly Thr Trp His His Asn Ala Asn Ala Lys Leu Ala
65 70 75 80
Ala Ala Ile Asp Val Glu Leu Val Cys Ala Glu Gly His Ala Leu Ile
85 90 95
Asn Glu Ala Val Arg His Ala Glu Gln Ser Gly Asp Thr Asp Ala Ile
100 105 110
Thr Ala Leu Arg Glu Thr Asp Ala Asn Leu Thr Leu Asp Arg Ala Pro
115 120 125
Asp Ser Leu Gln Gln Val Ile Asn Thr Tyr Ala
130 135

<210> 1069
<211> 371
<212> DNA
<213> Homo sapiens

<400> 1069
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cagttcatat gccgtcactc ccagggacca ccagtcaaca gcaaaggaat agcctgctcc
120
ttttctggag ctgaacatct caggtgccat gtaaggcttg gtgccagcca tggtggagac
180
ctgcgttatc acctgcaaca gaacgtccac ttcaaggaag aaacagtgaa gctcttcatc
240
tgtgagctgg tcatggccct ggactacctg cagaaccagc gcatcattca cagggatatg
300
aagcctgaca atattttact tgacgaacat gggcacgtgc acatcacaga tttcaacatt
360
gctgcgatgc t
371

<210> 1070

<211> 123
<212> PRT
<213> Homo sapiens

<400> 1070
Xaa Tyr Asn Phe Leu Ala Gly Ser Thr Gly Ala Asn Met Ile Arg Ser
1 5 10 15
Pro Ala Ser Gln Gln Phe Ile Cys Arg His Ser Gln Gly Pro Pro Val
20 25 30
Asn Ser Lys Gly Ile Ala Cys Ser Phe Ser Gly Ala Glu His Leu Arg
35 40 45
Cys His Val Arg Leu Gly Ala Ser His Gly Gly Asp Leu Arg Tyr His
50 55 60
Leu Gln Gln Asn Val His Phe Lys Glu Glu Thr Val Lys Leu Phe Ile
65 70 75 80
Cys Glu Leu Val Met Ala Leu Asp Tyr Leu Gln Asn Gln Arg Ile Ile
85 90 95
His Arg Asp Met Lys Pro Asp Asn Ile Leu Leu Asp Glu His Gly His
100 105 110
Val His Ile Thr Asp Phe Asn Ile Ala Ala Met
115 120

<210> 1071
<211> 998
<212> DNA
<213> Homo sapiens

<400> 1071
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ggagtttcgt caaggaagac ggacaaatcg tcattgatga gaatggcaac agggtttgat
120
cccacccgaa gtacgtggcc ttggagtgcc attcgcactc cacttggcca ccgtttgcat
180
tcgacctaac cagcaattgc atctcgtttg acctgctcgc gttgtcaaca tcatagcaac
240
gagcggccaa tagcagagtt ctggtcatcc tgttccgccc ttcctcctat ttgaagcctc
300
agtttcagca aagagctgtt tatgagtttt ccgtcaaacg gcgcttgtat aggcataggg
360
ggtataccta tgatgcgtgt attcacagtt aaaaaggttt ctctcatggg ccatacagct
420
tcaaacaaag acgatcttct caaacgcgtg aaacgcatcg cggggcaaat ccaggccgtt
480
gagcgtgcac tggagtcgga tgccgattgc gcgaaaacat tgcatctcgt agctgccaca
540
cgtggagcta tcaacggctt gatggacgaa attattgagg atcacgccag aaaacatgtg
600
gcgagcccaa cgcttagcga ttaataacgc aacaagggtg tcgaagagct tcttgaagcc
660
attcgccgct actccaagtg aagaatccag gtacatgtcc atgagtagca gccccaatat
720
cgagattagc cacatacatg accatgtgtt ccttgggtca gcacgcgaag aaaatgccaa
780

gcgtaccctt tgggttgtgg cgcttacggt ggtgatgatg gttggcgaaa tcgtcgccgg
840
ctatctcact ggctcaatgg ctttacttgc cgacgggttt tcacaaggca accccatgca
900
ggcgctttgg gcatcgctgc agctgcctac ggttacgcaa aacgccacgc ttccagcagt
960
cgttatagct tcggtacggg caaggttgga gacctagg
998

<210> 1072
<211> 72
<212> PRT
<213> Homo sapiens

<400> 1072
Met Gly His Thr Ala Ser Asn Lys Asp Asp Leu Leu Lys Arg Val Lys
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Arg Ile Ala Gly Gln Ile Gln Ala Val Glu Arg Ala Leu Glu Ser Asp
            20   25   30
Ala Asp Cys Ala Lys Thr Leu His Leu Val Ala Ala Thr Arg Gly Ala
        35   40   45
Ile Asn Gly Leu Met Asp Glu Ile Ile Glu Asp His Ala Arg Lys His
    50   55   60
Val Ala Ser Pro Thr Leu Ser Asp
65   70

<210> 1073
<211> 468
<212> DNA
<213> Homo sapiens

<400> 1073
tgtacaacac tcccatcctc tactctctgc atataccctg tatgtacttc atgttatagc
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tacaatggac aattttctat tcttcaagta cactcttccc atgtcccaac tgggatgctt
120
ttcccccact gataaaatct tgcttctctt caaactccta ggcaaatttc tcctacttca
180
gaaagtcttg tttctccata tccttcgtaa ccaccacctg gtgcacatgc tgaaggcaga
240
attcattgtc tcctctcctt cactctcgaa tagctttgcc cagaccctca ggtactcctt
300
catcctctgt ataatatttg gttttcacct ctttatgaac tcttttgtat tctcattact
360
ggctctggaa cccagaacat accacgggtt caaggtatgt tttaatgaat tgaatggaat
420
aaattttgtt gtgcttatgc agatacagat gccactaaac actgatca
468

<210> 1074
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1074
Met Asp Asn Phe Leu Phe Phe Lys Tyr Thr Leu Pro Met Ser Gln Leu
1 5 10 15
Gly Cys Phe Ser Pro Thr Asp Lys Ile Leu Leu Leu Phe Lys Leu Leu
20 25 30
Gly Lys Phe Leu Leu Leu Gln Lys Val Leu Phe Leu His Ile Leu Arg
35 40 45
Asn His His Leu Val His Met Leu Lys Ala Glu Phe Ile Val Ser Ser
50 55 60
Pro Ser Leu Ser Asn Ser Phe Ala Gln Thr Leu Arg Tyr Ser Phe Ile
65 70 75 80
Leu Cys Ile Ile Phe Gly Phe His Leu Phe Met Asn Ser Phe Val Phe
85 90 95
Ser Leu Leu Ala Leu Glu Pro Arg Thr Tyr His Gly Phe Lys Val Cys
100 105 110
Phe Asn Glu Leu Asn Gly Ile Asn Phe Val Val Leu Met Gln Ile Gln
115 120 125
Met Pro Leu Asn Thr Asp
130

<210> 1075
<211> 1633
<212> DNA
<213> Homo sapiens

<400> 1075
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cagcagcaag aacaaacagc ttcgcaacga cttcaagctg gtggagaaca ttctggccaa
120
gcgcctgctg atcctgcccc aggaggagga ctatggcttt gacatcgagg agaagaacaa
180
ggctgtggtg gtgaagtccg tccagagggg cttgctggct gaggtggctg gcctgcaggt
240
ggggaggaag atctactcca tcaatgagga cctggtgttc ctgcggccgt tttcagaggt
300
ggagtccatc ctcaaccagt ccttctgctc ccgccgccct ctgcgcctcc tggtggccac
360
gaaggccaaa gagatcatca aaatccccga ccagccggac acactgtgct tccagattcg
420
tggagctgcc ccaccgtacg tctatgctgt ggggagaggc tctgaggcca tggctgcagg
480
gctctgtgct ggtcagtgca ttctgaaggt caatggcagc aacgtgatga acgatggtgc
540
ccctgaggtc ctggagcact tccaggcatt ccggagtcgg cgcgaagagg ccctgggcct
600
gtaccagtgg atctaccaca cccatgagga tgcccaggaa gcacgagcca gtcaggaggc
660
ctccactgag gaccccagtg gcgagcaggc ccaggaggaa gaccaggctg attcagcctt
720
cccactgctg tccctgggtc cccggctgag cctgtgtgag ggcagcccca tggtcaccct
780
gactgtggac aacgtgcacc tggaacacgg cgtggtgtat gagtatgtga gcacggcagg
840

cgtcaggtgc catgtgctgg agaagatcgt ggagccccgc ggctgcttcg gcctcaccgc
900
caagatcctc gaggcctttg ctgccaatga cagcgtcttc gtggagaact gcaggcggct
960
catggccctg agcagcgcca tcgtgaccat gccccacttt gagttccgca acatctgtga
1020
caccaagctg gagagcattg gccagaggat tgcctgctac caggagtttg cagcccaact
1080
gaagagcagg gtcagcccac ccttcaaaca agccccctg gagccccacc cgctgtgtgg
1140
cctacttctg ccccaccaat tgccacatca acctcatgga agtgtcctac cccaagacca
1200
ccccctcagt gggcaggtcc ttcagcatcc gctttggacg caaaccctcc ctcatcggcc
1260
ttgacccgga gcaaggccac ctgaacccca tgtcgtacac ccagcactgc atcaccacca
1320
tggctgctcc ctcctggaag tgcttgcctg ctgcagaggg tgatccccaa ggccagggtc
1380
tccatgatgg cagcttcggg ccagccagtg ggacccttgg tcaggaagac cggggcctca
1440
gcttcctact caagcaggag gaccgtgaga tccaggatgc ctacctgcag ctcttcacca
1500
agctggatgt ggccctgaag gagatgaagc aatatgtcac ccagatcaac aggctgctgt
1560
ccaccatcac agagcccacc tcgggtgggt cctgcgacgc atccttggct gaggaggcct
1620
cctccctgcc cct
1633

<210> 1076
<211> 87
<212> PRT
<213> Homo sapiens

<400> 1076
His Gln Ala Gly Glu His Trp Pro Glu Asp Cys Leu Leu Pro Gly Val
 1   5   10   15
Cys Ser Pro Thr Glu Glu Gln Gly Gln Pro Thr Leu Gln Thr Ser Pro
            20   25   30
Pro Gly Ala Pro Pro Ala Val Trp Pro Thr Ser Ala Pro Pro Ile Ala
        35   40   45
Thr Ser Thr Ser Trp Lys Cys Pro Thr Pro Arg Pro Pro Pro Gln Trp
    50   55   60
Ala Gly Pro Ser Ala Ser Ala Leu Asp Ala Asn Pro Pro Ser Ser Ala
65   70   75   80
Leu Thr Arg Ser Lys Ala Thr
                85

<210> 1077
<211> 419
<212> DNA
<213> Homo sapiens

<400> 1077

nnacgcgtaa cgcgcctcgc gacgcgcctc cacagcatgt cgaccaagtg gacgtgcaat
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gcaaacgagg caacatgttt gcgcctcgcc ggagcaccct cacccagcga tgctttgttt
120
cacccagagt ttacatatcc aatttttgga gaggctgagg caatttacgg ctacaacggc
180
ttgcacatga atcttgcctt tgcgagcggc agcctggtgc cgtcgctcga aatcacttac
240
cgcgctaaga atacgacgac gtccgctaaa gtagatgacg tggagcaggc tctgcgcgga
300
gtgctcccgc cagatgtcgt tactcctgca gaacttgatg ctatcgttgc acgcgacgcc
360
agggcggtcc gggcgcattt acgccgccgg gcaccaagat tgcgacgtac actcgcgcg
419

<210> 1078
<211> 139
<212> PRT
<213> Homo sapiens

<400> 1078
Xaa Arg Val Thr Arg Leu Ala Thr Arg Leu His Ser Met Ser Thr Lys
1 5 10 15
Trp Thr Cys Asn Ala Asn Glu Ala Thr Cys Leu Arg Leu Ala Gly Ala
20 25 30
Pro Ser Pro Ser Asp Ala Leu Phe His Pro Glu Phe Thr Tyr Pro Ile
35 40 45
Phe Gly Glu Ala Glu Ala Ile Tyr Gly Tyr Asn Gly Leu His Met Asn
50 55 60
Leu Ala Phe Ala Ser Gly Ser Leu Val Pro Ser Leu Glu Ile Thr Tyr
65 70 75 80
Arg Ala Lys Asn Thr Thr Thr Ser Ala Lys Val Asp Asp Val Glu Gln
85 90 95
Ala Leu Arg Gly Val Leu Pro Pro Asp Val Val Thr Pro Ala Glu Leu
100 105 110
Asp Ala Ile Val Ala Arg Asp Ala Arg Ala Val Arg Ala His Leu Arg
115 120 125
Arg Arg Ala Pro Arg Leu Arg Arg Thr Leu Ala
130 135

<210> 1079
<211> 584
<212> DNA
<213> Homo sapiens

<400> 1079
acgcgtgaag ggtctgcagc ctgtacaact cagacatgct tcacgtggtc tcagccagtc
60
agccttggga aatgtacccc catgctgtgg catctacaat cggcctcctg ttcttactct
120
gctcaaactg cttcccaagc cagcagggag gggaaccatg ctgcctgctg acctgggtag
180
ttctatttag gtcttgtgac acaacagtgg gcaaggtgat gccctctgtg accaaaagta
240

tttaccccaa gttccccag gccctccctt tcgtctgcaa agacacacat ctgtttcact
300
gtgtcttctg caaagacaca catctgtttc actggggttt tctgcaaaga cacccatttg
360
tttccccttt taagggtttt ccccctccatc ttgtctattt ttaaaaaaat aaaccgggtt
420
cccaggatag ccttcccccc cagatcaaga gcccatgtga aatgaggggg ccgacttgac
480
cacagcacct tgttcctttc tgtaatctag acacttctgc acaatagagg gcccacccct
540
caagggcaca ggccatggtt tgtcctcagg ctccctccac gcgt
584

<210> 1080
<211> 122
<212> PRT
<213> Homo sapiens

<400> 1080
Met Leu His Val Val Ser Ala Ser Gln Pro Trp Glu Met Tyr Pro His
1 5 10 15
Ala Val Ala Ser Thr Ile Gly Leu Leu Phe Leu Leu Cys Ser Asn Cys
20 25 30
Phe Pro Ser Gln Gln Gly Gly Glu Pro Cys Cys Leu Leu Thr Trp Val
35 40 45
Val Leu Phe Arg Ser Cys Asp Thr Thr Val Gly Lys Val Met Pro Ser
50 55 60
Val Thr Lys Ser Ile Tyr Pro Lys Phe Pro Gln Ala Leu Pro Phe Val
65 70 75 80
Cys Lys Asp Thr His Leu Phe His Cys Val Phe Cys Lys Asp Thr His
85 90 95
Leu Phe His Trp Gly Phe Leu Gln Arg His Pro Phe Val Ser Pro Phe
100 105 110
Lys Gly Phe Pro Leu His Leu Val Tyr Phe
115 120

<210> 1081
<211> 3077
<212> DNA
<213> Homo sapiens

<400> 1081
naaccagtag tagaagtcta ttcttgttcc tattgtacaa attcgccaat attcaacagc
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gttcttaaac tgaacaagca tatcaaagag aatcataaaa acattccctt ggccctgaat
120
tatatccaca atgggaagaa atccagggcc ttaagccccc tatctcctgt ggccatagag
180
cagacatctc ttaagatgat gcaggcagta ggaggtgcac ctgcacgtcc cactggagaa
240
tatatctgta atcaatgtgg tgctaagtac acatccctag acagctttca gactcaccca
300
aaaactcatc tcgacactgt gcttccaaaa ttgacctgtc ctcagtgcaa caaggaattc
360

cccaaccaag aatccttgct gaagcatgtt accattcact ttatgatcac ttcaacgtat
420
tacatctgtg agagttgtga caagcaattc acatcagtgg atgaccttca gaaacacctg
480
ctggacatgc acacctttgt cttctttcgc tgcaccctct gccaggaagt ttttgactca
540
aaagtctcca ttcagctcca cttggctgtg aagcacagta acgaaaagaa agtctatagg
600
tgcacatctt gcaactggga cttccgcaac gaaactgact tgcagctcca tgtgaaacac
660
aaccacctgg aaaaccaagg gaaagtgcat aagtgcattt tctgcggtga gtcctttggc
720
accgaggtgg agctgcaatg ccacatcacc actcacagta agaagtacaa ctgcaagttc
780
tgtagcaaag ccttccatgc gatcattttg ttagaaaaac acttgcgaga aaaacactgt
840
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900agctgcagac tttgctgacc aacagccagg agtcccacaa cagtcacgat 960
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1020
gcctacacta tggaaacttt gctgcagaat caccagctcc gagaccacaa catcagacct
1080
ggagaaagtg ccatcgtgaa aaagaaagct gagctcatta aagggaatta caagtgcagc
1140
gtgtgctctc gaaccttctt ctccgaaaat ggcctccggg aacatatgca gacccaccta
1200
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1260
cttactgaac acaaagtcac gcatagtaag agtcttgata ctggaaactg ccggatttgc
1320
aagatgcctc tccagagtga agaggagttt ttagagcatt gccaaatgca ccctgacttg
1380
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1440
gaactcaaaa tccatgggac gttccacatg caaaagacag ggaatgggtc tgcagttcag
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1560
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1620
gccggctgcg tgaatctcag taagagcgcc agcccaggca ttaacgtccc tcccggcacg
1680
aatagaccag gcttgggcca gaatgagaat ctgagtgcca ttggggaaag gcaaggtggg
1740
gggactgaaa cacgctgctc tagctgcaac gttaagtttg agtctgaaag tgaactccag
1800
aaccacatcc aaaccatcca ccgagagctc gtgccagaca gcaacagcac acagttgaaa
1860
acgccccaag tatcaccaat gcccagaatc agtccctccc agtcggatga gaagaagacc
1920
tatcaatgca tcaagtgtca gatggttttc tacaatgaat gggatattca ggttcatgtt
1980
gcaaatcaca tgattgatga aggactgaac catgaatgca aactctgcag ccagaccttt
2040

gactctcctg ccaaactcca gtgccacctg atagagcaca gcttcgaagg gatgggaggc
2100
accttcaagt gtccagtctg ctttacagta tttgttcaag caaacaagtt gcagcagcat
2160
attttctctg cccatggaca agaagacaag atctatgact gtacacaatg tccacagaag
2220
tttttcttcc aaacagagct gcagaatcat acaatgaccc aacacagcag ttagtgcaag
2280
tacagtctct caaggagaat tgattttgtg gcacaaaaag ggaacatgtt ttactctttg
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cacgaaactt tcattgttaa tgtatattat tcagaaacat tgtattgtac cataaaactt
2400
gtattatcaa actgttggat gttcatgtgt ttgaactttt gcgcaccgga tagacccctt
2460
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2520
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2580
gcttaagata aagtattttt aaggaagaaa gattaaaaac aactgttata catgagacta
2640
tggttggact tccttttctt tacacttaag cctagaattt ctctttaggt atatcagcgc
2700
ttaaatccaa gactattttt tattgctgaa gattcttgca aaccatgaag agatgttctc
2760
acagaacaga accccacagc tggataaggc ccgtatatat atatttgtaa gccttgcaat
2820
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2880
tttccctgga tacatttgaa gctttgagtg ttcaaggttt tccttaatga tttcacgcag
2940
ccaaattctt gaatcagttg aactaacctg tatgttactg ttattaatgt ttactctgca
3000
gtctgaacct ggagattact ggaattgttt tccaagagga aataaattca gtttaccatt
3060
aggaaaaaaa aaaaaaa
3077

<210> 1082
<211> 757
<212> PRT
<213> Homo sapiens

<400> 1082
Xaa Pro Val Val Glu Val Tyr Ser Cys Ser Tyr Cys Thr Asn Ser Pro
1 5 10 15
Ile Phe Asn Ser Val Leu Lys Leu Asn Lys His Ile Lys Glu Asn His
20 25 30
Lys Asn Ile Pro Leu Ala Leu Asn Tyr Ile His Asn Gly Lys Lys Ser
35 40 45
Arg Ala Leu Ser Pro Leu Ser Pro Val Ala Ile Glu Gln Thr Ser Leu
50 55 60
Lys Met Met Gln Ala Val Gly Gly Ala Pro Ala Arg Pro Thr Gly Glu
65 70 75 80
Tyr Ile Cys Asn Gln Cys Gly Ala Lys Tyr Thr Ser Leu Asp Ser Phe

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                85                  90                  95
Gln Thr His Leu Lys Thr His Leu Asp Thr Val Leu Pro Lys Leu Thr
            100                 105                 110
Cys Pro Gln Cys Asn Lys Glu Phe Pro Asn Gln Glu Ser Leu Leu Lys
        115                 120                 125
His Val Thr Ile His Phe Met Ile Thr Ser Thr Tyr Tyr Ile Cys Glu
    130                 135                 140
Ser Cys Asp Lys Gln Phe Thr Ser Val Asp Asp Leu Gln Lys His Leu
145                 150                 155                 160
Leu Asp Met His Thr Phe Val Phe Phe Arg Cys Thr Leu Cys Gln Glu
                165                 170                 175
Val Phe Asp Ser Lys Val Ser Ile Gln Leu His Leu Ala Val Lys His
            180                 185                 190
Ser Asn Glu Lys Lys Val Tyr Arg Cys Thr Ser Cys Asn Trp Asp Phe
        195                 200                 205
Arg Asn Glu Thr Asp Leu Gln Leu His Val Lys His Asn His Leu Glu
    210                 215                 220
Asn Gln Gly Lys Val His Lys Cys Ile Phe Cys Gly Glu Ser Phe Gly
225                 230                 235                 240
Thr Glu Val Glu Leu Gln Cys His Ile Thr Thr His Ser Lys Lys Tyr
                245                 250                 255
Asn Cys Lys Phe Cys Ser Lys Ala Phe His Ala Ile Ile Leu Leu Glu
            260                 265                 270
Lys His Leu Arg Glu Lys His Cys Val Phe Glu Thr Lys Thr Pro Asn
        275                 280                 285
Cys Gly Thr Asn Gly Ala Ser Glu Gln Val Gln Lys Glu Glu Val Glu
    290                 295                 300
Leu Gln Thr Leu Leu Thr Asn Ser Gln Glu Ser His Asn Ser His Asp
305                 310                 315                 320
Gly Ser Glu Glu Asp Val Asp Thr Ser Glu Pro Met Tyr Gly Cys Asp
                325                 330                 335
Ile Cys Gly Ala Ala Tyr Thr Met Glu Thr Leu Leu Gln Asn His Gln
            340                 345                 350
Leu Arg Asp His Asn Ile Arg Pro Gly Glu Ser Ala Ile Val Lys Lys
        355                 360                 365
Lys Ala Glu Leu Ile Lys Gly Asn Tyr Lys Cys Ser Val Cys Ser Arg
    370                 375                 380
Thr Phe Phe Ser Glu Asn Gly Leu Arg Glu His Met Gln Thr His Leu
385                 390                 395                 400
Gly Pro Val Lys His Tyr Met Cys Pro Ile Cys Gly Glu Arg Phe Pro
                405                 410                 415
Ser Leu Leu Thr Leu Thr Glu His Lys Val Thr His Ser Lys Ser Leu
            420                 425                 430
Asp Thr Gly Asn Cys Arg Ile Cys Lys Met Pro Leu Gln Ser Glu Glu
        435                 440                 445
Glu Phe Leu Glu His Cys Gln Met His Pro Asp Leu Arg Asn Ser Leu
    450                 455                 460
Thr Gly Phe Arg Cys Val Val Cys Met Gln Thr Val Thr Ser Thr Leu
465                 470                 475                 480
Glu Leu Lys Ile His Gly Thr Phe His Met Gln Lys Thr Gly Asn Gly
                485                 490                 495
Ser Ala Val Gln Thr Thr Gly Arg Gly Gln His Val Gln Lys Leu Tyr
            500                 505                 510
Lys Cys Ala Ser Cys Leu Lys Glu Phe Arg Ser Lys Gln Asp Leu Val
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     515                 520                 525
Lys Leu Asp Ile Asn Gly Leu Pro Tyr Gly Leu Cys Ala Gly Cys Val
    530                 535                 540
Asn Leu Ser Lys Ser Ala Ser Pro Gly Ile Asn Val Pro Pro Gly Thr
545                 550                 555                 560
Asn Arg Pro Gly Leu Gly Gln Asn Glu Asn Leu Ser Ala Ile Gly Glu
                565                 570                 575
Arg Gln Gly Gly Gly Thr Glu Thr Arg Cys Ser Ser Cys Asn Val Lys
            580                 585                 590
Phe Glu Ser Glu Ser Glu Leu Gln Asn His Ile Gln Thr Ile His Arg
        595                 600                 605
Glu Leu Val Pro Asp Ser Asn Ser Thr Gln Leu Lys Thr Pro Gln Val
    610                 615                 620
Ser Pro Met Pro Arg Ile Ser Pro Ser Gln Ser Asp Glu Lys Lys Thr
625                 630                 635                 640
Tyr Gln Cys Ile Lys Cys Gln Met Val Phe Tyr Asn Glu Trp Asp Ile
                645                 650                 655
Gln Val His Val Ala Asn His Met Ile Asp Glu Gly Leu Asn His Glu
            660                 665                 670
Cys Lys Leu Cys Ser Gln Thr Phe Asp Ser Pro Ala Lys Leu Gln Cys
        675                 680                 685
His Leu Ile Glu His Ser Phe Glu Gly Met Gly Gly Thr Phe Lys Cys
    690                 695                 700
Pro Val Cys Phe Thr Val Phe Val Gln Ala Asn Lys Leu Gln Gln His
705                 710                 715                 720
Ile Phe Ser Ala His Gly Gln Glu Asp Lys Ile Tyr Asp Cys Thr Gln
                725                 730                 735
Cys Pro Gln Lys Phe Phe Phe Gln Thr Glu Leu Gln Asn His Thr Met
            740                 745                 750
Thr Gln His Ser Ser
        755
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<210> 1083
<211> 516
<212> DNA
<213> Homo sapiens

<400> 1083
naccggtgag gcatctctgc agggtgtccg gctagctaag cagagcggct ggaaggctcc
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agatccgaat aacctgcccg ctcccgctga gcccgtggaa gaggagaaga agtgaccgat
120
ccactgaccc cggttctgtc ggccaattgg gatgaagagc gcagttggaa gctgcttaac
180
tacgagcgac agggcggata cacggccctt cgtaaggctt tgacgatgcc gcctgacgac
240
gttgtctcgc tggttaagga cgctaacctg cgtggccgtg gtggcgccgg gttccccacc
300
ggcatgaagt ggtccttcgt gcctaaggac aatcccaacc cgacctacct cgttgtcaac
360
ggcgacgagt ctgagccggg cacgtgcaag gacatgccgc tcatgatggc ctccccgcac
420
accctcgtcg agggcgtcat cattgcctcc tacgccatca aggccaagat ggccttcatc
480

tacatccgcg gtgaggtgct gcacgtcgtc cgacgc
516

<210> 1084
<211> 142
<212> PRT
<213> Homo sapiens

<400> 1084
Ala Arg Gly Arg Gly Glu Glu Val Thr Asp Pro Leu Thr Pro Val Leu
1 5 10 15
Ser Ala Asn Trp Asp Glu Glu Arg Ser Trp Lys Leu Leu Asn Tyr Glu
20 25 30
Arg Gln Gly Gly Tyr Thr Gly Leu Arg Lys Ala Leu Thr Met Pro Pro
35 40 45
Asp Asp Val Val Ser Leu Val Lys Asp Ala Asn Leu Arg Gly Arg Gly
50 55 60
Gly Ala Gly Phe Pro Thr Gly Met Lys Trp Ser Phe Val Pro Lys Asp
65 70 75 80
Asn Pro Asn Pro Thr Tyr Leu Val Val Asn Gly Asp Glu Ser Glu Pro
85 90 95
Gly Thr Cys Lys Asp Met Pro Leu Met Met Ala Ser Pro His Thr Leu
100 105 110
Val Glu Gly Val Ile Ile Ala Ser Tyr Ala Ile Lys Ala Lys Met Ala
115 120 125
Phe Ile Tyr Ile Arg Gly Glu Val Leu His Val Val Arg Arg
130 135 140

<210> 1085
<211> 374
<212> DNA
<213> Homo sapiens

<400> 1085
acgcgtagcg tttatacata gttttcacgt agccatacct ccatgtgggt catacgttca
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aaatcgtaga gtgtctctga gctgcctagg gggctgtttg cgatcttgcg gacagtgtct
120
atatccacaa ggttcagctc cgccaggaga ctgtcgccga tcattttcag gaagttttct
180
ttgctgcgtt cgtagtcttg gtgcaggtcg aagctgtagt cgcttttgta gatgtcccgg
240
tagaagaact cgggcagggt gcctttcatg gcttccagga tgacgggttt gctcatcccg
300
tgcccgctca gaacacccgg gtacaccagg gaagagcgga tcatgtcgtc ctcaaggtag
360
ggggcggcga attc
374

<210> 1086
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1086
Met Ile Arg Ser Ser Leu Val Tyr Pro Gly Val Leu Ser Gly His Gly
1 5 10 15
Met Ser Lys Pro Val Ile Leu Glu Ala Met Lys Gly Thr Leu Pro Glu
20 25 30
Phe Phe Tyr Arg Asp Ile Tyr Lys Ser Asp Tyr Ser Phe Asp Leu His
35 40 45
Gln Asp Tyr Glu Arg Ser Lys Glu Asn Phe Leu Lys Met Ile Gly Asp
50 55 60
Ser Leu Leu Ala Glu Leu Asn Leu Val Asp Ile Asp Thr Val Arg Lys
65 70 75 80
Ile Ala Asn Ser Pro Leu Gly Ser Ser Glu Thr Leu Tyr Asp Phe Glu
85 90 95
Arg Met Thr His Met Glu Val Trp Leu Arg Glu Asn Tyr Val
100 105 110

<210> 1087
<211> 423
<212> DNA
<213> Homo sapiens

<400> 1087
atgacgatcg tggccccacc accgccgacc gcgggcgccg ccattagctt ccttgtcgac
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ggcatccacc cgcacgacct cggccaggtc ctcgacgacc acggcgtgag catccgggtg
120
nggcaccact gtgcctggcc catccaccgg agtctagggg tgcaatccac cgcccgtgca
180
tcgttctact tctacaacac tttcccggaa gtggatgcgt tagcgtcggc ggtgcgggcc
240
gcccgggaat ttttcggagt gcattaggat tggtctgaac gtgaaccttg aatccatgta
300
ccaggaagtc atcctggacc actacaagaa tcccacgcac gcagggttga aggctccctt
360
tgatgccgaa gtgcaccatg tgaacccttc ctgcggtgac ganaccgtct ccgggtgaag
420
ctt
423

<210> 1088
<211> 88
<212> PRT
<213> Homo sapiens

<400> 1088
Met Thr Ile Val Ala Pro Pro Pro Thr Ala Gly Ala Ala Ile Ser
1 5 10 15
Phe Leu Val Asp Gly Ile His Pro His Asp Leu Gly Gln Val Leu Asp
20 25 30
Asp His Gly Val Ser Ile Arg Val Xaa His His Cys Ala Trp Pro Ile
35 40 45
His Arg Ser Leu Gly Val Gln Ser Thr Ala Arg Ala Ser Phe Tyr Phe
50 55 60
Tyr Asn Thr Phe Pro Glu Val Asp Ala Leu Ala Ser Ala Val Arg Ala

65 70 75 80
Ala Arg Glu Phe Phe Gly Val His
85

<210> 1089
<211> 750
<212> DNA
<213> Homo sapiens

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agagtggtaa gaatggggct cggggaagaa gccttacccc ttttcttctt taatttggcg
180
aaaggacttt tgggccaagg tcaccctagc cttctcttgg gggcctcaat tttccttcat
240
tctgtaaaaa atgggggggt aattcagaag taccctcctt attgtcaggg ttttggggaa
300
gggagtaaaa agaaattggc ttgggaaaat acttaataca gggcctgggc atgtaacaaa
360
tattcacaaa atgctagcag ttatcaccac agtgggagcc acagggagct ctgaggataa
420
gcagggatgt cgagggatgg gacagaactt gattgaaggc agacagacct ccaaattctt
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gactcagaca gaatgatcac tgatccagcg agacgtcagg atcgagagga gtgtagcaag
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aacacagaag ggcatgtgcg gagacacacg tgatcacgct agtgatgcag aggcagaccc
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<210> 1090
<211> 103
<212> PRT
<213> Homo sapiens

<400> 1090
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Cys Glu Asp Lys Thr Lys Gly Gly Arg Val Gly Gln Arg Gln Tyr Ile
20 25 30
Arg Val Val Arg Met Gly Leu Gly Glu Glu Ala Leu Pro Leu Phe Phe
35 40 45
Phe Asn Leu Ala Lys Gly Leu Leu Gly Gln Gly His Pro Ser Leu Leu
50 55 60
Leu Gly Ala Ser Ile Phe Leu His Ser Val Lys Asn Gly Gly Val Ile
65 70 75 80
Gln Lys Tyr Pro Pro Tyr Cys Gln Gly Phe Gly Glu Gly Ser Lys Lys

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Lys Leu Ala Trp Glu Asn Thr
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<210> 1091
<211> 438
<212> DNA
<213> Homo sapiens

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120
catggctttg ccgaggcgag tcagcacttt tttggacgac ctttaaaaga acttaatatc
180
gacgagtttg ccttgttagt aggaatggtg aaagggcctt ctatttataa tcctgaacga
240
caccctaaac gtgctttatc acgcagaaat acggtattag caattttaaa aagccaagat
300
cgtttaaccg agtcggatta taatatttta cggaaacaac ccattcgctt ggcagataaa
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420
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438

<210> 1092
<211> 146
<212> PRT
<213> Homo sapiens

<400> 1092
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Tyr Ser Lys Ser Ala Ile Ile Thr Ala Tyr Met Asn Glu Val Tyr Leu
20 25 30
Ala Gln Val Gly Asn Glu Gly Leu His Gly Phe Ala Glu Ala Ser Gln
35 40 45
His Phe Phe Gly Arg Pro Leu Lys Glu Leu Asn Ile Asp Glu Phe Ala
50 55 60
Leu Leu Val Gly Met Val Lys Gly Pro Ser Ile Tyr Asn Pro Glu Arg
65 70 75 80
His Pro Lys Arg Ala Leu Ser Arg Arg Asn Thr Val Leu Ala Ile Leu
85 90 95
Lys Ser Gln Asp Arg Leu Thr Glu Ser Asp Tyr Asn Ile Leu Arg Lys
100 105 110
Gln Pro Ile Arg Leu Ala Asp Lys His Gln Glu Arg Ser Val Tyr Gly
115 120 125
Asp Tyr Leu Asp Leu Val Ser Met Gln Leu Ser Arg Asp Phe Asp Arg
130 135 140
Cys Met
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<210> 1093
<211> 351
<212> DNA
<213> Homo sapiens

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180
gagattggcc gtctgcgtga acaaattccg caaaccaact ccgaaaccaa gatcaagaag
240
ctgtccaagc gtctgaagtt gatggaagcc ttccagggtt ccggcaactt gccagagtgg
300
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351

<210> 1094
<211> 117
<212> PRT
<213> Homo sapiens

<400> 1094
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Thr Leu Glu Lys Gly Gln Leu Leu Asn Asp Glu Gln Tyr Phe Glu Ala
20 25 30
Leu Glu Glu Phe Gly Asp Asp Phe Asp Ala Arg Met Gly Ala Glu Ala
35 40 45
Val Arg Glu Leu Leu His Ala Ile Asp Leu Glu His Glu Ile Gly Arg
50 55 60
Leu Arg Glu Gln Ile Pro Gln Thr Asn Ser Glu Thr Lys Ile Lys Lys
65 70 75 80
Leu Ser Lys Arg Leu Lys Leu Met Glu Ala Phe Gln Gly Ser Gly Asn
85 90 95
Leu Pro Glu Trp Met Val Leu Thr Val Leu Pro Val Leu Pro Pro Asp
100 105 110
Leu Arg Pro Leu Val
115

<210> 1095
<211> 619
<212> DNA
<213> Homo sapiens

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180

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gagcggacgc tgttccagtt ggatgaggcc atcgaggccc tggatgctgc cattgagtat
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aagaatgagg ccatcacatg ccgccagcgg gtgcttcggg cctcagcctc gttgctgtcc
360
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420
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<210> 1096
<211> 195
<212> PRT
<213> Homo sapiens

<400> 1096
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20 25 30
Gln Leu Arg Gln Gly Ser Ala Gln Ser Gln Arg Gln Ile Arg Gly Glu
35 40 45
Ile Asp Ser Leu Arg Gln Glu Lys Asp Ser Leu Leu Lys Gln Arg Leu
50 55 60
Glu Ile Asp Gly Lys Leu Arg Gln Gly Ser Leu Leu Ser Pro Glu Glu
65 70 75 80
Glu Arg Thr Leu Phe Gln Leu Asp Glu Ala Ile Glu Ala Leu Asp Ala
85 90 95
Ala Ile Glu Tyr Lys Asn Glu Ala Ile Thr Cys Arg Gln Arg Val Leu
100 105 110
Arg Ala Ser Ala Ser Leu Leu Ser Gln Cys Glu Met Asn Leu Met Ala
115 120 125
Lys Leu Ser Tyr Leu Ser Ser Ser Glu Thr Arg Ala Leu Leu Cys Lys
130 135 140
Tyr Phe Asp Lys Val Gly Gln Gln Pro Met Ala Pro Pro Ala Pro Pro
145 150 155 160
His Gly Thr Cys Gly Glu Val Ser His Gly Ser Cys Ser Ser Gly Tyr
165 170 175
Pro Val Ser Ser Gln Thr Gly Gly Gln Asn Gln Asp Gln Leu Ile Cys
180 185 190
Arg Ala Ala
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<210> 1097
<211> 5108
<212> DNA
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<210> 1098
<211> 1336
<212> PRT
<213> Homo sapiens

<400> 1098
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Lys His Gly Leu Glu Lys Pro Ile Ser Phe Val Lys Asn Thr Gln Ser
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Ser Ser Glu Glu Ala Arg Lys Leu Met Val Arg Leu Thr Arg His Thr
35 40 45
Gly Arg Lys Gln Pro Pro Val Ser Glu Ser His Trp Arg Thr Leu Leu
50 55 60
Gln Asp Met Leu Thr Met Gln Gln Asn Val Tyr Thr Cys Leu Asp Ser
65 70 75 80
Asp Ala Cys Tyr Glu Ile Phe Thr Glu Ser Leu Leu Cys Ser Ser Arg
85 90 95
Leu Glu Asn Ile His Leu Ala Gly Gln Met Met His Cys Ser Ala Cys
100 105 110
Ser Glu Asn Pro Pro Ala Gly Ile Ala His Lys Gly Lys Pro His Tyr
115 120 125
Arg Val Ser Tyr Glu Lys Ser Ile Asp Leu Val Leu Ala Ala Ser Arg
130 135 140
Glu Tyr Phe Asn Ser Ser Thr Asn Leu Thr Asp Ser Cys Met Asp Leu
145 150 155 160
Ala Arg Cys Cys Leu Gln Leu Ile Thr Asp Arg Pro Pro Ala Ile Gln
165 170 175
Glu Glu Leu Asp Leu Ile Gln Ala Val Gly Cys Leu Glu Glu Phe Gly
180 185 190
Val Lys Ile Leu Pro Leu Gln Val Arg Leu Cys Pro Asp Arg Ile Ser
195 200 205
Leu Ile Lys Glu Cys Ile Ser Gln Ser Pro Thr Cys Tyr Lys Gln Ser
210 215 220
Thr Lys Leu Leu Gly Leu Ala Glu Leu Leu Arg Val Ala Gly Glu Asn
225 230 235 240
Pro Glu Glu Arg Arg Gly Gln Val Leu Ile Leu Leu Val Glu Gln Ala
245 250 255
Leu Arg Phe His Asp Tyr Lys Ala Ala Ser Met His Cys Gln Glu Leu
260 265 270
Met Ala Thr Gly Tyr Pro Lys Ser Trp Asp Val Cys Ser Gln Leu Gly

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Gln Ser Glu Gly Tyr Gln Asp Leu Ala Thr Arg Gln Glu Leu Met Ala
    290                 295                 300
Phe Ala Leu Thr His Cys Pro Pro Ser Ser Ile Glu Leu Leu Leu Ala
305                 310                 315                 320
Ala Ser Ser Ser Leu Gln Thr Glu Ile Leu Tyr Gln Arg Val Asn Phe
                325                 330                 335
Gln Ile His His Glu Gly Gly Glu Asn Ile Ser Ala Ser Pro Leu Thr
            340                 345                 350
Ser Lys Ala Val Gln Glu Asp Glu Val Gly Val Pro Gly Ser Asn Ser
        355                 360                 365
Ala Asp Leu Leu Arg Trp Thr Thr Ala Thr Thr Met Lys Val Leu Ser
    370                 375                 380
Asn Thr Thr Thr Thr Thr Lys Ala Val Leu Gln Ala Val Ser Asp Gly
385                 390                 395                 400
Gln Trp Trp Lys Lys Ser Leu Thr Tyr Leu Arg Pro Leu Gln Gly Gln
                405                 410                 415
Lys Cys Gly Gly Ala Tyr Gln Ile Gly Thr Thr Ala Asn Glu Asp Leu
            420                 425                 430
Glu Lys Gln Gly Cys His Pro Phe Tyr Glu Ser Val Ile Ser Asn Pro
        435                 440                 445
Phe Val Ala Glu Ser Glu Gly Thr Tyr Asp Thr Tyr Gln His Val Pro
    450                 455                 460
Val Glu Ser Phe Ala Glu Val Leu Leu Arg Thr Gly Lys Leu Ala Glu
465                 470                 475                 480
Ala Lys Asn Lys Gly Glu Val Phe Pro Thr Thr Glu Val Leu Leu Gln
                485                 490                 495
Leu Ala Ser Glu Ala Leu Pro Asn Asp Met Thr Leu Ala Leu Ala Tyr
            500                 505                 510
Leu Leu Ala Leu Pro Gln Val Leu Asp Ala Asn Arg Cys Phe Glu Lys
        515                 520                 525
Gln Ser Pro Ser Ala Leu Ser Leu Gln Leu Ala Ala Tyr Tyr Tyr Ser
    530                 535                 540
Leu Gln Ile Tyr Ala Arg Leu Ala Pro Cys Phe Arg Asp Lys Cys His
545                 550                 555                 560
Pro Leu Tyr Arg Ala Asp Pro Lys Glu Leu Ile Lys Met Val Thr Arg
                565                 570                 575
His Val Thr Arg His Glu His Glu Ala Trp Pro Glu Asp Leu Ile Ser
            580                 585                 590
Leu Thr Lys Gln Leu His Cys Tyr Asn Glu Arg Leu Leu Asp Phe Thr
        595                 600                 605
Gln Ala Gln Ile Leu Gln Gly Leu Arg Lys Gly Val Asp Val Gln Arg
    610                 615                 620
Phe Thr Ala Asp Asp Gln Tyr Lys Arg Glu Thr Ile Leu Gly Leu Ala
625                 630                 635                 640
Glu Thr Leu Glu Glu Ser Val Tyr Ser Ile Ala Ile Ser Leu Ala Gln
                645                 650                 655
Arg Tyr Ser Val Ser Arg Trp Glu Val Phe Met Thr His Leu Glu Phe
            660                 665                 670
Pro Phe Thr Asp Ser Gly Leu Ser Thr Leu Glu Ile Glu Asn Arg Ala
        675                 680                 685
Gln Asp Leu His Leu Phe Glu Thr Leu Lys Thr Asp Pro Glu Ala Phe
    690                 695                 700
His Gln His Met Val Lys Tyr Ile Tyr Pro Thr Ile Gly Gly Phe Asp
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705                 710                 715                 720
His Glu Arg Leu Gln Tyr Tyr Phe Thr Leu Leu Glu Asn Cys Gly Cys
                725                 730                 735
Ala Asp Leu Gly Asn Cys Ala Ile Lys Pro Glu Thr His Ile Arg Leu
            740                 745                 750
Leu Lys Lys Phe Lys Val Val Ala Ser Gly Leu Asn Tyr Lys Lys Leu
        755                 760                 765
Thr Asp Glu Asn Met Ser Pro Leu Glu Ala Leu Glu Pro Val Leu Ser
    770                 775                 780
Ser Gln Asn Ile Leu Ser Ile Ser Lys Leu Val Pro Lys Ile Pro Glu
785                 790                 795                 800
Lys Asp Gly Gln Met Leu Ser Pro Ser Ser Leu Tyr Thr Ile Trp Leu
                805                 810                 815
Gln Lys Leu Phe Trp Thr Gly Asp Pro His Leu Ile Lys Gln Val Pro
            820                 825                 830
Gly Ser Ser Pro Glu Trp Leu His Ala Tyr Asp Val Cys Met Lys Tyr
        835                 840                 845
Phe Asp Arg Leu His Pro Gly Asp Leu Ile Thr Val Val Asp Ala Val
    850                 855                 860
Thr Phe Ser Pro Lys Ala Val Thr Lys Leu Ser Val Glu Ala Arg Lys
865                 870                 875                 880
Glu Met Thr Arg Lys Ala Ile Lys Thr Val Lys His Phe Ile Glu Lys
                885                 890                 895
Pro Arg Lys Arg Asn Ser Glu Asp Glu Ala Gln Glu Ala Lys Asp Ser
            900                 905                 910
Lys Val Thr Tyr Ala Asp Thr Leu Asn His Leu Glu Lys Ser Leu Ala
        915                 920                 925
His Leu Glu Thr Leu Ser His Ser Phe Ile Leu Ser Leu Lys Asn Ser
    930                 935                 940
Glu Gln Glu Thr Leu Gln Lys Tyr Ser His Leu Tyr Asp Leu Ser Arg
945                 950                 955                 960
Ser Glu Lys Glu Lys Leu His Asp Glu Ala Val Ala Ile Cys Leu Asp
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Gly Gln Pro Leu Ala Met Ile Gln Gln Leu Leu Glu Val Ala Val Gly
            980                 985                 990
Pro Leu Asp Ile Ser Pro Lys Asp Ile Val Gln Ser Ala Ile Met Lys
        995                 1000                1005
Ile Ile Ser Ala Leu Ser Gly Gly Ser Ala Asp Leu Gly Gly Pro Arg
    1010                1015                1020
Asp Pro Leu Lys Val Leu Glu Gly Val Val Ala Ala Val His Thr Ser
1025                1030                1035                1040
Val Asp Lys Gly Glu Glu Leu Val Ser Pro Glu Asp Leu Leu Glu Trp
                1045                1050                1055
Leu Arg Pro Phe Cys Ala Asp Asp Ala Trp Pro Val Arg Pro Arg Ile
            1060                1065                1070
His Val Leu Gln Ile Leu Gly Gln Ser Phe His Leu Thr Glu Glu Asp
        1075                1080                1085
Ser Lys Leu Leu Val Phe Phe Arg Thr Glu Ala Ile Leu Lys Ala Ser
    1090                1095                1100
Trp Pro Gln Arg Gln Val Asp Ile Ala Asp Ile Glu Asn Glu Glu Asn
1105                1110                1115                1120
Arg Tyr Cys Leu Phe Met Glu Leu Leu Glu Ser Ser His His Glu Ala
                1125                1130                1135
Glu Phe Gln His Leu Val Leu Leu Leu Gln Ala Trp Pro Pro Met Lys
```

```
            1140                1145                1150
Ser Glu Tyr Val Ile Thr Asn Asn Pro Trp Val Arg Leu Ala Thr Val
        1155                1160                1165
Met Leu Thr Arg Cys Thr Met Glu Asn Lys Glu Gly Leu Gly Asn Glu
    1170                1175                1180
Val Leu Lys Met Cys Arg Ser Leu Tyr Asn Thr Lys Gln Met Leu Pro
1185                1190                1195                1200
Ala Glu Gly Val Lys Glu Leu Cys Leu Leu Leu Leu Asn Gln Ser Leu
                1205                1210                1215
Leu Leu Pro Ser Leu Lys Leu Leu Leu Glu Ser Arg Asp Glu His Leu
            1220                1225                1230
His Glu Met Ala Leu Glu Gln Ile Thr Ala Val Thr Thr Val Asn Asp
        1235                1240                1245
Ser Asn Cys Asp Gln Glu Leu Leu Ser Leu Leu Leu Asp Ala Lys Leu
    1250                1255                1260
Leu Val Lys Cys Val Ser Thr Pro Phe Tyr Pro Arg Ile Val Asp His
1265                1270                1275                1280
Leu Leu Ala Ser Leu Gln Gln Gly Arg Trp Asp Ala Glu Glu Leu Gly
                1285                1290                1295
Arg His Leu Arg Glu Ala Gly His Glu Ala Glu Ala Gly Ser Leu Leu
            1300                1305                1310
Leu Ala Val Arg Gly Thr His Gln Ala Phe Arg Thr Phe Ser Thr Ala
        1315                1320                1325
Leu Arg Ala Ala Gln His Trp Val
    1330                1335
```

<210> 1099
<211> 309
<212> DNA
<213> Homo sapiens

<400> 1099
acgcgtgctc tctcccgctt ggcaatcagc atggcctttt cgagctcggc ggtgcgcaat
60
tgaaccattt cttccagttg cgatttttca gaaagcagcg tcgattgacc ttcggtcagc
120
ttgcgcacat agcgcttggt gcggctggca aggatatagg cgagtatcaa tgcacctgcg
180
agggcgagga tcgaggcaat ggtcagccag aagcgcaact tgtccatggc tatgttgcgg
240
gcgattagcc gacgatcttc ttcacccagg aaactgttga tggttttcct gacgtcatcc
300
atctggcca
309

<210> 1100
<211> 100
<212> PRT
<213> Homo sapiens

<400> 1100
```
Met Asp Asp Val Arg Lys Thr Ile Asn Ser Phe Leu Gly Glu Glu Asp
 1               5                  10                  15
Arg Arg Leu Ile Ala Arg Asn Ile Ala Met Asp Lys Leu Arg Phe Trp
```

```
            20                  25                  30
Leu Thr Ile Ala Ser Ile Leu Ala Leu Ala Gly Ala Leu Ile Leu Ala
        35                  40                  45
Tyr Ile Leu Ala Ser Arg Thr Lys Arg Tyr Val Arg Lys Leu Thr Glu
    50                  55                  60
Gly Gln Ser Thr Leu Leu Ser Glu Lys Ser Gln Leu Glu Glu Met Val
65                  70                  75                  80
Gln Leu Arg Thr Ala Glu Leu Glu Lys Ala Met Leu Ile Ala Lys Arg
                85                  90                  95
Glu Arg Ala Arg
            100
```

<210> 1101
<211> 540
<212> DNA
<213> Homo sapiens

<400> 1101
gtcgacgtta ccaactacgt catgttggag tctggtcagc cgcttcatgc ctatgatgcc
60
gacaacgtca gcgggacgat tgtggtccgt aaggcccacg agggtgagca tctattgacc
120
ctcgacgaca ccgatcgcac cctcgatcct gacgatctag tcatcgccga cgactcggga
180
gccattggcc tggctggcgt catgggtggt gcggccaccg aagtgactgc tgagacgacg
240
tcaatcatcc tcgagggcgc tcacttcgac ccgatgacgg gcgctcgtgc ttaccgacgc
300
cacaagctcg gttcggaggc ctcccgccgc tttgagcggg gcgttgatcc gatttgcgcc
360
cataccgcag ccgttcgcgc agcggaattg ctcgcccagt acggcggtgc caccgtcggt
420
gagcccaccg tcgttggtga ggtccccgag atgccacgtc aaacgatcaa cgctgattta
480
cctaaccgga ttctcggcac gaaggtgcca actgaagagg tcatcgagat cttgacgcgt
540

<210> 1102
<211> 180
<212> PRT
<213> Homo sapiens

<400> 1102
```
Val Asp Val Thr Asn Tyr Val Met Leu Glu Ser Gly Gln Pro Leu His
 1               5                  10                  15
Ala Tyr Asp Ala Asp Asn Val Ser Gly Thr Ile Val Val Arg Lys Ala
            20                  25                  30
His Glu Gly Glu His Leu Leu Thr Leu Asp Asp Thr Asp Arg Thr Leu
        35                  40                  45
Asp Pro Asp Asp Leu Val Ile Ala Asp Asp Ser Gly Ala Ile Gly Leu
    50                  55                  60
Ala Gly Val Met Gly Gly Ala Ala Thr Glu Val Thr Ala Glu Thr Thr
65                  70                  75                  80
Ser Ile Ile Leu Glu Gly Ala His Phe Asp Pro Met Thr Gly Ala Arg
```

```
                85                  90                  95
Ala Tyr Arg Arg His Lys Leu Gly Ser Glu Ala Ser Arg Arg Phe Glu
            100                 105                 110
Arg Gly Val Asp Pro Ile Cys Ala His Thr Ala Ala Val Arg Ala Ala
        115                 120                 125
Glu Leu Leu Ala Gln Tyr Gly Gly Ala Thr Val Gly Glu Pro Thr Val
    130                 135                 140
Val Gly Glu Val Pro Glu Met Pro Arg Gln Thr Ile Asn Ala Asp Leu
145                 150                 155                 160
Pro Asn Arg Ile Leu Gly Thr Lys Val Pro Thr Glu Glu Val Ile Glu
                165                 170                 175
Ile Leu Thr Arg
            180
```

<210> 1103
<211> 537
<212> DNA
<213> Homo sapiens

<400> 1103
cctttcctcc aaccaggcgc tgcggcgccg gcacttgccc gacgttataa aacaattcaa
60
cgtcaggttt accatcgctg tactcaacca aatggtagcc gtatccacct tccccaccga
120
tcgcgaccca ggtgatcttt ccctcggcat agattgacgt ggcattctcg tcggagtgaa
180
tcaagcagcg cttaggcagc tgctgggccg gcggcttcgc ctagctcgcc ggagcacacg
240
aacccttccc gaagataacc gccaaggcct ggcacacctt ctgctgcacc cattccggct
300
tgacgccgac cgccaccgca ctggtgaaca tagccgcaat aaggagaatt gcgatgtatt
360
ccggcgcggc ggcaccccga tcgtcccttg tccgcatggg tctcccctcc actacctacc
420
caatacaggg gagagcataa aaagaaaccc atagccgcac ctgagcccat ggccccaaac
480
cggggcccaa gccgggccca aaccatggga tcaaccggat gtccgtacat cacgcgt
537

<210> 1104
<211> 112
<212> PRT
<213> Homo sapiens

<400> 1104
```
Met Tyr Gly His Pro Val Asp Pro Met Val Trp Ala Arg Leu Gly Pro
 1               5                  10                  15
Arg Phe Gly Ala Met Gly Ser Gly Ala Ala Met Gly Phe Phe Leu Cys
            20                  25                  30
Ser Pro Leu Tyr Trp Val Gly Ser Gly Gly Glu Thr His Ala Asp Lys
        35                  40                  45
Gly Arg Ser Gly Cys Arg Arg Ala Gly Ile His Arg Asn Ser Pro Tyr
    50                  55                  60
Cys Gly Tyr Val His Gln Cys Gly Gly Gly Arg Arg Gln Ala Gly Met
```

65 70 75 80
Gly Ala Ala Glu Gly Val Pro Gly Leu Gly Gly Tyr Leu Arg Glu Gly
85 90 95
Phe Val Cys Ser Gly Glu Leu Gly Glu Ala Ala Gly Pro Ala Ala Ala
100 105 110

<210> 1105
<211> 448
<212> DNA
<213> Homo sapiens

<400> 1105
agggacctgg ggcagcacgt gcacgtgggt gggaggctcc ttgctaccga cagccagcca
60
tggggtgggc ccttccgagg ctgcctccag gacctgcgac tcgatggctg ccacctcccc
120
ttctttcctc tgccactgga taactcaagc cagcccagcg agctcggcgg caggcagtcc
180
tggaacctca ctgcgggctg cgtctccgag gacatgtgca gtcctgaccc ctgtttcaat
240
ggtgggactt gcctcgtcac ctggaatgac ttccactgta cctgccctgc caatttcacg
300
gggcctacat gtgcccagca gctgtggtgt cccggccagc cctgtctccc acctgccacg
360
tgtgaggagg tccctgatgg ctttgtgtgt gtggcggagg ccacgttccg cgagggtccc
420
cccgccgcgt tcagcgggca caacgcgt
448

<210> 1106
<211> 149
<212> PRT
<213> Homo sapiens

<400> 1106
Arg Asp Leu Gly Gln His Val His Val Gly Gly Arg Leu Leu Ala Thr
1 5 10 15
Asp Ser Gln Pro Trp Gly Gly Pro Phe Arg Gly Cys Leu Gln Asp Leu
20 25 30
Arg Leu Asp Gly Cys His Leu Pro Phe Phe Pro Leu Pro Leu Asp Asn
35 40 45
Ser Ser Gln Pro Ser Glu Leu Gly Gly Arg Gln Ser Trp Asn Leu Thr
50 55 60
Ala Gly Cys Val Ser Glu Asp Met Cys Ser Pro Asp Pro Cys Phe Asn
65 70 75 80
Gly Gly Thr Cys Leu Val Thr Trp Asn Asp Phe His Cys Thr Cys Pro
85 90 95
Ala Asn Phe Thr Gly Pro Thr Cys Ala Gln Gln Leu Trp Cys Pro Gly
100 105 110
Gln Pro Cys Leu Pro Pro Ala Thr Cys Glu Glu Val Pro Asp Gly Phe
115 120 125
Val Cys Val Ala Glu Ala Thr Phe Arg Glu Gly Pro Pro Ala Ala Phe
130 135 140
Ser Gly His Asn Ala

145

<210> 1107
<211> 618
<212> DNA
<213> Homo sapiens

<400> 1107
acgcgttgat gaagtacctg ccacgcttca gcaatgacgg ctcggtgaac ggcttctata
60
tctttgttat cgatgagacc gaacgcaaac tcaccgaaga ggccctgcgc cacctcaacg
120
agaacctcga agagcgcgtc gcccagcgca cacaggcgct ggctgaagcc aaccaacgcc
180
tggcaaaaca aaatgttcaa acgcaagcgc gccgaagacg cgctgcgtca cgcgcagaaa
240
atggaagccg ggggccagct caccggcggc atcgcccatg atttcaacaa catgctgacc
300
gggattatcg gcagcctgga cttgatgcag cgctacatcn aggccgggcg cagcgacgaa
360
atcggccgnc ttactgacgc cgccgtatcg tccgcccatc gcgcggccgc cctcacccat
420
cggctgctgg cgttctcgcg ccgccagtcg ctggcccccc gcccgctgga ccccaaccag
480
ctggtagcgt ccctggagga tctgttccag cgaaccaaag gcgcgcatat cacgctcaaa
540
gtgcaactgg gccgcgatat ctggcccgtg aataccgatg ccagccagtt ggaaaacgcc
600
ctgctcaacc tggcgatc
618

<210> 1108
<211> 182
<212> PRT
<213> Homo sapiens

<400> 1108
Met Arg Pro Asn Ala Asn Ser Pro Lys Arg Pro Cys Ala Thr Ser Thr
1 5 10 15
Arg Thr Ser Lys Ser Ala Ser Pro Ser Ala His Arg Arg Trp Leu Lys
20 25 30
Pro Thr Asn Ala Trp Gln Asn Lys Met Phe Lys Arg Lys Arg Ala Glu
35 40 45
Asp Ala Leu Arg His Ala Gln Lys Met Glu Ala Gly Gly Gln Leu Thr
50 55 60
Gly Gly Ile Ala His Asp Phe Asn Asn Met Leu Thr Gly Ile Ile Gly
65 70 75 80
Ser Leu Asp Leu Met Gln Arg Tyr Ile Xaa Ala Gly Arg Ser Asp Glu
85 90 95
Ile Gly Arg Leu Thr Asp Ala Ala Val Ser Ser Ala His Arg Ala Ala
100 105 110
Ala Leu Thr His Arg Leu Leu Ala Phe Ser Arg Arg Gln Ser Leu Ala
115 120 125
Pro Arg Pro Leu Asp Pro Asn Gln Leu Val Ala Ser Leu Glu Asp Leu

```
    130                 135                 140
Phe Gln Arg Thr Lys Gly Ala His Ile Thr Leu Lys Val Gln Leu Gly
145                 150                 155                 160
Arg Asp Ile Trp Pro Val Asn Thr Asp Ala Ser Gln Leu Glu Asn Ala
                165                 170                 175
Leu Leu Asn Leu Ala Ile
            180
```

<210> 1109
<211> 325
<212> DNA
<213> Homo sapiens

<400> 1109
accggtgagc atcagggagg caccatgcag acgactctcc catccagtct caagccgtcc
60
agcctcaaga tcgtcgcacc gctgggggggc atcctcgtgc ccctggatca ggtgcccgat
120
cccgttttcg cccagaagat ggtgggagac gggatctccc tggaccccat ctcaaacgaa
180
ttgctggcgc cggtcgccgg caccgtgacc cagctccaca acgcccacca cgcgctcacg
240
atcacgaccc cggaaggcat cgaggttctg gtccatatcg gactggatac cgtgatgctg
300
cgcggcgaca gctatccccc ccccn
325

<210> 1110
<211> 108
<212> PRT
<213> Homo sapiens

<400> 1110
```
Thr Gly Glu His Gln Gly Gly Thr Met Gln Thr Thr Leu Pro Ser Ser
 1               5                  10                  15
Leu Lys Pro Ser Ser Leu Lys Ile Val Ala Pro Leu Gly Gly Ile Leu
            20                  25                  30
Val Pro Leu Asp Gln Val Pro Asp Pro Val Phe Ala Gln Lys Met Val
        35                  40                  45
Gly Asp Gly Ile Ser Leu Asp Pro Ile Ser Asn Glu Leu Leu Ala Pro
    50                  55                  60
Val Ala Gly Thr Val Thr Gln Leu His Asn Ala His His Ala Leu Thr
65                  70                  75                  80
Ile Thr Thr Pro Glu Gly Ile Glu Val Leu Val His Ile Gly Leu Asp
                85                  90                  95
Thr Val Met Leu Arg Gly Asp Ser Tyr Pro Pro Pro
            100                 105
```

<210> 1111
<211> 385
<212> DNA
<213> Homo sapiens

<400> 1111

nnacgcgtcg ccccggtgcg cctggcagtg ggagaagagc atgaccttac cgagctcgcg
60
actgaactcg tcaacgccgc ctatagccgg gttgacatgg tggaacgccg tggcgaattc
120
gcagtacgtg gcggcatcgt cgacgtcttc ccaccggtgc tagaacaccc ggtccgtatc
180
gatttttttg gtgacgagat cgaggaaatg acctccttcg cggtagccga ccagcgatcc
240
accgacgaga ctcaccaaga actgatctgc gctccttgcc gtgagctcat cctcaccgac
300
gaggtacgtt cccgagccaa ggctttgctg accgaccatc ccgaattagc tgacatgttg
360
gagcggatcg gcaacggtca agctt
385

<210> 1112
<211> 128
<212> PRT
<213> Homo sapiens

<400> 1112
Xaa Arg Val Ala Pro Val Arg Leu Ala Val Gly Glu Glu His Asp Leu
1 5 10 15
Thr Glu Leu Ala Thr Glu Leu Val Asn Ala Ala Tyr Ser Arg Val Asp
20 25 30
Met Val Glu Arg Arg Gly Glu Phe Ala Val Arg Gly Gly Ile Val Asp
35 40 45
Val Phe Pro Pro Val Leu Glu His Pro Val Arg Ile Asp Phe Phe Gly
50 55 60
Asp Glu Ile Glu Glu Met Thr Ser Phe Ala Val Ala Asp Gln Arg Ser
65 70 75 80
Thr Asp Glu Thr His Gln Glu Leu Ile Cys Ala Pro Cys Arg Glu Leu
85 90 95
Ile Leu Thr Asp Glu Val Arg Ser Arg Ala Lys Ala Leu Leu Thr Asp
100 105 110
His Pro Glu Leu Ala Asp Met Leu Glu Arg Ile Gly Asn Gly Gln Ala
115 120 125

<210> 1113
<211> 400
<212> DNA
<213> Homo sapiens

<400> 1113
nnncgaccga tgagcgatcg cgaacccgtc aacctgggat acccctacgt cgagtctttc
60
cactcggact tctcggggac cggcggagtc gatcagaccg accgttctac caatatcgac
120
gagcacacca tcgaggagat gcatcagatc gcctcgcgtt accccgactc ccgttcggcg
180
ttgctgccga tcctgcacct ggttcagtcg gtggacggac gcatctcgcc ggtcggtatt
240
gagactgcgg ctgaagtgct cggcattacc accgcccagg tatccggggt ggcgaccttc
300

tacaccatgt ataagaagca ccctgcgggc cagcatcaca tcggtgtctg caccacggcg
360
ctgtgcgccg tcatgggtgg cgaggaggtg cttgcccgtn
400

<210> 1114
<211> 133
<212> PRT
<213> Homo sapiens

<400> 1114
Xaa Arg Pro Met Ser Asp Arg Glu Pro Val Asn Leu Gly Tyr Pro Tyr
1 5 10 15
Val Glu Ser Phe His Ser Asp Phe Ser Gly Thr Gly Gly Val Asp Gln
20 25 30
Thr Asp Arg Ser Thr Asn Ile Asp Glu His Thr Ile Glu Glu Met His
35 40 45
Gln Ile Ala Ser Arg Tyr Pro Asp Ser Arg Ser Ala Leu Leu Pro Ile
50 55 60
Leu His Leu Val Gln Ser Val Asp Gly Arg Ile Ser Pro Val Gly Ile
65 70 75 80
Glu Thr Ala Ala Glu Val Leu Gly Ile Thr Thr Ala Gln Val Ser Gly
85 90 95
Val Ala Thr Phe Tyr Thr Met Tyr Lys Lys His Pro Ala Gly Gln His
100 105 110
His Ile Gly Val Cys Thr Thr Ala Leu Cys Ala Val Met Gly Gly Glu
115 120 125
Glu Val Leu Ala Arg
130

<210> 1115
<211> 402
<212> DNA
<213> Homo sapiens

<400> 1115
tctccgactg cacagattag agaaaggact gcgatgacca ttcgcaccac tcatgttggt
60
tccctgcccc gcacccccga gctgatcgag gcgaatcgtg cgcgccgtga gggttcgctc
120
ggcgaggctg acttcacgtc gctgctgcag gatcaggttg acggcgttgt gaagcgtcag
180
gctgagattg gcctggatat cgtcaatgac ggcgagtacg gtcacgcgat gcttgacacg
240
gttgattacg gcgcgtggtg gacgtattcc atctctcgtt tcggcgggct gtcctttgag
300
gacgtgcagc gttttgatgt gcgtcccccg jctggccgtg acggtcgcct gtctttctcg
360
tcgttcgctg agcgccgcga ctggcagcgt ttccggacgc gt
402

<210> 1116
<211> 134
<212> PRT

<213> Homo sapiens

<400> 1116
Ser Pro Thr Ala Gln Ile Arg Glu Arg Thr Ala Met Thr Ile Arg Thr
1 5 10 15
Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Ile Glu Ala Asn
20 25 30
Arg Ala Arg Arg Glu Gly Ser Leu Gly Glu Ala Asp Phe Thr Ser Leu
35 40 45
Leu Gln Asp Gln Val Asp Gly Val Val Lys Arg Gln Ala Glu Ile Gly
50 55 60
Leu Asp Ile Val Asn Asp Gly Glu Tyr Gly His Ala Met Leu Asp Thr
65 70 75 80
Val Asp Tyr Gly Ala Trp Trp Thr Tyr Ser Ile Ser Arg Phe Gly Gly
85 90 95
Leu Ser Phe Glu Asp Val Gln Arg Phe Asp Val Arg Pro Pro Ala Gly
100 105 110
Arg Asp Gly Arg Leu Ser Phe Ser Ser Phe Ala Glu Arg Arg Asp Trp
115 120 125
Gln Arg Phe Arg Thr Arg
130

<210> 1117
<211> 307
<212> DNA
<213> Homo sapiens

<400> 1117
ggcgccggtc ttgccctggc tggaagtggc atgcagacct tggtgcggaa cccgctggct
60
gacccctacc tgctaggtgt atcggctggc gcaagtgtgg gagcaaccgc agtcatcgct
120
ttggggatgt tcacttcgtg gggaactcac cgactcactc ttggtgccct tgtaggggcc
180
ttggcggcag ctgcattggt ctatctcatt tccatggcgc aaggaggcat gacgccgctt
240
cggttggtgc tgtcgggcgt ggtgttgtcc tcggcgttct cgcgttggcg agtttcctcg
300
tctttcg
307

<210> 1118
<211> 102
<212> PRT
<213> Homo sapiens

<400> 1118
Gly Ala Gly Leu Ala Leu Ala Gly Ser Gly Met Gln Thr Leu Val Arg
1 5 10 15
Asn Pro Leu Ala Asp Pro Tyr Leu Leu Gly Val Ser Ala Gly Ala Ser
20 25 30
Val Gly Ala Thr Ala Val Ile Ala Leu Gly Met Phe Thr Ser Trp Gly
35 40 45
Thr His Arg Leu Thr Leu Gly Ala Leu Val Gly Ala Leu Ala Ala Ala

```
    50                  55                  60
Ala Leu Val Tyr Leu Ile Ser Met Ala Gln Gly Gly Met Thr Pro Leu
65                  70                  75                  80
Arg Leu Val Leu Ser Gly Val Val Leu Ser Ser Ala Phe Ser Arg Trp
                85                  90                  95
Arg Val Ser Ser Ser Phe
            100
```

<210> 1119
<211> 353
<212> DNA
<213> Homo sapiens

<400> 1119
cgcgtccttg agatgcttga gcaggtcggt attgaggatc cagccagggt gatggattcc
60
tatccgcatc aactgtccgg tggccagcgt caacgggttc tgcttgccat ggcgttggtg
120
aactcgccgg atctgctcat ttgtgacgag ccgacgaccg ccttggacgt cacggtgcag
180
tctcaggtac tggcgactat cgatgaggtg cttgactcgg ttggtgccgc atgcctattt
240
attacccacg atttggcggt tgtctcgcac atctgccggg agcttatcgt gatgacgtcg
300
ggcaaggtcg ttgaagccgg atcagcgcgt gatgtgttat ctcaccctga tca
353

<210> 1120
<211> 117
<212> PRT
<213> Homo sapiens

<400> 1120
```
Arg Val Leu Glu Met Leu Glu Gln Val Gly Ile Glu Asp Pro Ala Arg
 1               5                  10                  15
Val Met Asp Ser Tyr Pro His Gln Leu Ser Gly Gly Gln Arg Gln Arg
            20                  25                  30
Val Leu Leu Ala Met Ala Leu Val Asn Ser Pro Asp Leu Leu Ile Cys
        35                  40                  45
Asp Glu Pro Thr Thr Ala Leu Asp Val Thr Val Gln Ser Gln Val Leu
    50                  55                  60
Ala Thr Ile Asp Glu Val Leu Asp Ser Val Gly Ala Ala Cys Leu Phe
65                  70                  75                  80
Ile Thr His Asp Leu Ala Val Val Ser His Ile Cys Arg Glu Leu Ile
                85                  90                  95
Val Met Thr Ser Gly Lys Val Val Glu Ala Gly Ser Ala Arg Asp Val
            100                 105                 110
Leu Ser His Pro Asp
        115
```

<210> 1121
<211> 406
<212> DNA
<213> Homo sapiens

<400> 1121
tgatcaccca tgctccactc gaccgcgcgc tcgacgatgc gacggctgag acgatgctcg
60
cccagggcac ggtgttcatc ccgaccttga cgatgatgaa aggcgtcgcc gcgaatctca
120
ccgcagcggg cgttcccggt gtgagctatg cacacgccca cgagagcacg cgcgcgatgc
180
atgccgcggg cgttccggtc ctggccggca ccgacgccta catcgggtcc ttcacacggg
240
catcgccgcc atacggcgag agcatgcacg acgaagacgc ctacatcggg ctcctcgaac
300
gggcaatgcc gccatacggc gagagcatgc acgacgaact cgctctgctc gtggacgccg
360
gcctgtcaac agccgaagcg ctgcgcgctg ccacctcgac gggcgc
406

<210> 1122
<211> 117
<212> PRT
<213> Homo sapiens

<400> 1122
Met Leu Ala Gln Gly Thr Val Phe Ile Pro Thr Leu Thr Met Met Lys
1 5 10 15
Gly Val Ala Ala Asn Leu Thr Ala Ala Gly Val Pro Gly Val Ser Tyr
20 25 30
Ala His Ala His Glu Ser Thr Arg Ala Met His Ala Ala Gly Val Pro
35 40 45
Val Leu Ala Gly Thr Asp Ala Tyr Ile Gly Ser Phe Thr Arg Ala Ser
50 55 60
Pro Pro Tyr Gly Glu Ser Met His Asp Glu Asp Ala Tyr Ile Gly Leu
65 70 75 80
Leu Glu Arg Ala Met Pro Pro Tyr Gly Glu Ser Met His Asp Glu Leu
85 90 95
Ala Leu Leu Val Asp Ala Gly Leu Ser Thr Ala Glu Ala Leu Arg Ala
100 105 110
Ala Thr Ser Thr Gly
115

<210> 1123
<211> 337
<212> DNA
<213> Homo sapiens

<400> 1123
gccggcgatg cgttcattaa ggcctaagat gcgccgacgc ctccccgctt tcctcgccct
60
cgcctccacc gcccttgccg cagcggggat ggtggggtgc tcgtccgagg gggcatcgcc
120
aagcgaatgc tcccctgttg atattgccgc agtgcgcgag gccctgccgc attcgctcgc
180
taaggcgaag ctcgacccgc actccaccaa cgaggatgaa cactcctttt ccatgctcta
240

ccgcgcgcaa gataaggagc aggtcagctt gctggggacg aagtatgagg ccgacggtgc
300
acccgtctgc cccgatgacc ccaatgaggc agcgcgc
337

<210> 1124
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1124
Met Arg Ser Leu Arg Pro Lys Met Arg Arg Arg Leu Pro Ala Phe Leu
 1   5   10   15
Ala Leu Ala Ser Thr Ala Leu Ala Ala Ala Gly Met Val Gly Cys Ser
            20   25   30
Ser Glu Gly Ala Ser Pro Ser Glu Cys Ser Pro Val Asp Ile Ala Ala
        35   40   45
Val Arg Glu Ala Leu Pro His Ser Leu Ala Lys Ala Lys Leu Asp Pro
    50   55   60
His Ser Thr Asn Glu Asp Glu His Ser Phe Ser Met Leu Tyr Arg Ala
65   70   75   80
Gln Asp Lys Glu Gln Val Ser Leu Leu Gly Thr Lys Tyr Glu Ala Asp
                85   90   95
Gly Ala Pro Val Cys Pro Asp Asp Pro Asn Glu Ala Ala Arg
            100   105   110

<210> 1125
<211> 555
<212> DNA
<213> Homo sapiens

<400> 1125
nncttgaatc gaatcggcat tgcgtctaaa catgacgttg agacactctc tgctaagctc
60
gaagagctga cggcattgct agaacgtgtc gcgcgtaaac actaaggaga catcgggatg
120
gctgttaaaa agactactca gaaagaaggc agctcgtgga tcggggaagt tgaaaaatat
180
tcccgtaaaa tctggcttgc tggtttaggc gtgtactcga aggttagcag tgacggcggc
240
aaatacttcg agacgttggt caaggacggc gagaaggccg agaagttgac caagagccca
300
gtcggtaaaa aagtagaggc ggcaaaagcg agcgccggtt ctgcgaaatc gagcatttcg
360
gatacctggg gcaagttgga agagactttc gacaagcgtc tcaacagtgc tatttcgcga
420
ttgggcgtgc ccagcaaagc ggaactgaag acgctgcaca gcaaggtcga taccctgacc
480
aagcaaatcg aaaaactcac cggtgccaaa gtggccccgg ctaaaacggc agccgctaaa
540
cctgctgcca agctt
555

<210> 1126

<211> 146
<212> PRT
<213> Homo sapiens

<400> 1126
Met Ala Val Lys Lys Thr Thr Gln Lys Glu Gly Ser Ser Trp Ile Gly
1 5 10 15
Glu Val Glu Lys Tyr Ser Arg Lys Ile Trp Leu Ala Gly Leu Gly Val
20 25 30
Tyr Ser Lys Val Ser Ser Asp Gly Gly Lys Tyr Phe Glu Thr Leu Val
35 40 45
Lys Asp Gly Glu Lys Ala Glu Lys Leu Thr Lys Ser Pro Val Gly Lys
50 55 60
Lys Val Glu Ala Ala Lys Ala Ser Ala Gly Ser Ala Lys Ser Ser Ile
65 70 75 80
Ser Asp Thr Trp Gly Lys Leu Glu Glu Thr Phe Asp Lys Arg Leu Asn
85 90 95
Ser Ala Ile Ser Arg Leu Gly Val Pro Ser Lys Ala Glu Leu Lys Thr
100 105 110
Leu His Ser Lys Val Asp Thr Leu Thr Lys Gln Ile Glu Lys Leu Thr
115 120 125
Gly Ala Lys Val Ala Pro Ala Lys Thr Ala Ala Ala Lys Pro Ala Ala
130 135 140
Lys Leu
145

<210> 1127
<211> 352
<212> DNA
<213> Homo sapiens

<400> 1127
cccgaccgcg tactcgtggt cggtgccgga gtgatgggtg cagcacacgc acacgcgctc
60
cgcgggtccc tccaggcagt cgtgtgcggc gtggtcgacc tgcaggagcg agcagcgcaa
120
tcactcgctt cggaagtggg cgtacccggg ttcaccgacc tggtgaaggc gatcgagtcg
180
accgctccgg acgccgcggt catcgccacg ccggactcgg ctcaccgcca accggctgag
240
accgccatcg acgccggcct tgccgtcctg gtcgagaaac cgctcgccac gaccgtcgat
300
gacgccgaag cgatcgtgct ccgcgctgaa cgggccggcg tccgtctcat ga
352

<210> 1128
<211> 117
<212> PRT
<213> Homo sapiens

<400> 1128
Pro Asp Arg Val Leu Val Val Gly Ala Gly Val Met Gly Ala Ala His
1 5 10 15
Ala His Ala Leu Arg Gly Ser Leu Gln Ala Val Val Cys Gly Val Val

```
            20                  25                  30
Asp Leu Gln Glu Arg Ala Ala Gln Ser Leu Ala Ser Glu Val Gly Val
        35                  40                  45
Pro Gly Phe Thr Asp Leu Val Lys Ala Ile Glu Ser Thr Ala Pro Asp
    50                  55                  60
Ala Ala Val Ile Ala Thr Pro Asp Ser Ala His Arg Gln Pro Ala Glu
65                  70                  75                  80
Thr Ala Ile Asp Ala Gly Leu Ala Val Leu Val Glu Lys Pro Leu Ala
                85                  90                  95
Thr Thr Val Asp Asp Ala Glu Ala Ile Val Leu Arg Ala Glu Arg Ala
            100                 105                 110
Gly Val Arg Leu Met
        115
```

<210> 1129
<211> 336
<212> DNA
<213> Homo sapiens

<400> 1129
ntggcagccc tggaggagcc gatggtggac ctggacggcg agctgccttt cgtgcggccc
60
ctgccccaca ttgccgtgct ccaggacgag ctgccgcaac tcttccagga tgacgacgtc
120
ggggccgatg aggaagaggc agagttgcgg ggcgaacaca cgctcacaga gaagtttgtc
180
tgcctggatg actcctttgg ccatgactgc agcttgacct gtgatgactg caggaacgga
240
gggacctgcc tcctgggcct ggatggctgg gattgccccg agggctggac tgggctcatc
300
tgcaatgaga cttggtcctc gggctgcatg gatatt
336

<210> 1130
<211> 112
<212> PRT
<213> Homo sapiens

<400> 1130

```
Xaa Ala Ala Leu Glu Glu Pro Met Val Asp Leu Asp Gly Glu Leu Pro
 1               5                  10                  15
Phe Val Arg Pro Leu Pro His Ile Ala Val Leu Gln Asp Glu Leu Pro
            20                  25                  30
Gln Leu Phe Gln Asp Asp Asp Val Gly Ala Asp Glu Glu Glu Ala Glu
        35                  40                  45
Leu Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp
    50                  55                  60
Ser Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly
65                  70                  75                  80
Gly Thr Cys Leu Leu Gly Leu Asp Gly Trp Asp Cys Pro Glu Gly Trp
                85                  90                  95
Thr Gly Leu Ile Cys Asn Glu Thr Trp Ser Ser Gly Cys Met Asp Ile
            100                 105                 110
```

<210> 1131
<211> 672
<212> DNA
<213> Homo sapiens

<400> 1131
gcgttggtgg tgctcatggc ccgggaaaat ccgctggatc aatacctctt tgagcacccc
60
gaattattgt tctcgtcctc ggtggaatcg actgtgttgc acccggataa cccgtatgtg
120
ctcggcccgc acgtggccgc ggccgcccag gaggcatacc tctcccctgc ggacgaagag
180
ttttacgggt cggcctttgc cgggatatgc aaaacgctga caggccagaa cgtactgcga
240
cgtcgcggaa atcggctgtt ctggactcgt ccggaacggg ctgtcgacgc catcgacctg
300
cgatcggcgg caggcaaagg gattgacatt atcgacgtgt ccaccgggag ggtcatcggg
360
gtagtcgacg aagccgccgc agaccgtacc gtgcatccag gcgcggtgta cctgcatcag
420
ggggatcagt ggctggtcga cgaatacaac ccggtcgagc accacgccct ggtgcaccag
480
gacctgccgg gatattggac tcaaccgcag tcagcgtcga cggtgagaat ccttcgggag
540
gagagacgtc gcgcttgtgg tcccggatat gtggcgtgcg ggcaggtgga actgacagag
600
caagttgttg ggtatctgcg tcgcgacgaa ttcaccaatg atgtgtggta ctcgctggcc
660
ctcgagatgc cc
672

<210> 1132
<211> 224
<212> PRT
<213> Homo sapiens

<400> 1132
Ala Leu Val Val Leu Met Ala Arg Glu Asn Pro Leu Asp Gln Tyr Leu
1 5 10 15
Phe Glu His Pro Glu Leu Leu Phe Ser Ser Ser Val Glu Ser Thr Val
20 25 30
Leu His Pro Asp Asn Pro Tyr Val Leu Gly Pro His Val Ala Ala Ala
35 40 45
Ala Gln Glu Ala Tyr Leu Ser Pro Ala Asp Glu Glu Phe Tyr Gly Ser
50 55 60
Ala Phe Ala Gly Ile Cys Lys Thr Leu Thr Gly Gln Asn Val Leu Arg
65 70 75 80
Arg Arg Gly Asn Arg Leu Phe Trp Thr Arg Pro Glu Arg Ala Val Asp
85 90 95
Ala Ile Asp Leu Arg Ser Ala Ala Gly Lys Gly Ile Asp Ile Ile Asp
100 105 110
Val Ser Thr Gly Arg Val Ile Gly Val Val Asp Glu Ala Ala Ala Asp
115 120 125
Arg Thr Val His Pro Gly Ala Val Tyr Leu His Gln Gly Asp Gln Trp

```
    130                 135                 140
Leu Val Asp Glu Tyr Asn Pro Val Glu His His Ala Leu Val His Gln
145                 150                 155                 160
Asp Leu Pro Gly Tyr Trp Thr Gln Pro Gln Ser Ala Ser Thr Val Arg
                165                 170                 175
Ile Leu Arg Glu Glu Arg Arg Arg Ala Cys Gly Pro Gly Tyr Val Ala
            180                 185                 190
Cys Gly Gln Val Glu Leu Thr Glu Gln Val Val Gly Tyr Leu Arg Arg
        195                 200                 205
Asp Glu Phe Thr Asn Asp Val Trp Tyr Ser Leu Ala Leu Glu Met Pro
    210                 215                 220
```

<210> 1133
<211> 796
<212> DNA
<213> Homo sapiens

<400> 1133
acgcgtgaag gggggtccag cgggtgtggc actcgatgac aagacagttt gagagcggct
60
tgtctccggg gacctggcgt aggtctcctc tgccttaacc cttggctttt gcacttcctc
120
tgtctgtcct ccatacaagc ttcttgcccc tagggaggac gggcttctta acaggggggag
180
ccggttcctg tcctaacccc actggcatct tacactctgg gagatagctt ccccctgaga
240
ggcgagtgag ccacgtaagg ggaggtgggc gatggcttcc cttctgtctt gggttggggg
300
agtcaggtac agtatttttt cttttaaagc atcattgatc acataataag gtttgtcata
360
gtccttaatc acagacctgt gaaatttgga gaattcacgg cacctaggat gggagtgagc
420
ttctgattgt gagctgattt gggagctaac ctcaaggaaa ctcctcttgc aagccccctg
480
ctgggtgtcg gggccttcgc cagggacctc ccggggactc tggacgctct ttgtctgccc
540
ttccttttcc ctcacctcgc tcccccgtga gaaagtgggg ctcatgcagc tcagctcagt
600
gacagagggt ttattagggg tagctctggg acccatcttt tggtgatttc ttctctctct
660
ttctctaatg gaataattgt ttctgtctac acttctttat tttctcctct ctacagctgc
720
cttctaaaaa tgtgcttttc tgttcctgca gaactgaagc ttgcatggcc tttgttgtga
780
ctttcccttc acgcgt
796

<210> 1134
<211> 147
<212> PRT
<213> Homo sapiens

<400> 1134
Met Gly Pro Arg Ala Thr Pro Asn Lys Pro Ser Val Thr Glu Leu Ser

```
 1               5                  10                  15
Cys Met Ser Pro Thr Phe Ser Arg Gly Ser Glu Val Arg Glu Lys Glu
            20                  25                  30
Gly Gln Thr Lys Ser Val Gln Ser Pro Arg Glu Val Pro Gly Glu Gly
        35                  40                  45
Pro Asp Thr Gln Gln Gly Ala Cys Lys Arg Ser Phe Leu Glu Val Ser
    50                  55                  60
Ser Gln Ile Ser Ser Gln Ser Glu Ala His Ser His Pro Arg Cys Arg
65                  70                  75                  80
Glu Phe Ser Lys Phe His Arg Ser Val Ile Lys Asp Tyr Asp Lys Pro
                85                  90                  95
Tyr Tyr Val Ile Asn Asp Ala Leu Lys Glu Lys Ile Leu Tyr Leu Thr
            100                 105                 110
Pro Pro Thr Gln Asp Arg Arg Glu Ala Ile Ala His Leu Pro Leu Arg
        115                 120                 125
Gly Ser Leu Ala Ser Gln Gly Glu Ala Ile Ser Gln Ser Val Arg Cys
    130                 135                 140
Gln Trp Gly
145
```

<210> 1135
<211> 376
<212> DNA
<213> Homo sapiens

<400> 1135
gatcaggcca cacaggacaa cttcgagaag ggctccatct tcccaccctt caccagcatc
60
agaaagatct ctgcgcacat cgctgcagcc gtggctgcaa aagcctacga gctcggtctg
120
gcgacccgtc tgcctccccc cagcgacctg gtgaaatatg cagagaactg catgtacact
180
cccgtctacc gcaactaccg gtagtgctgc ggggatcaat tttgcagtaa taaaaaatct
240
actatcaacg cggatggtac tctgttgttt atagtccctg ctgctaacca cccttgttgc
300
tggtgctgct ggagaggcat tgtacctgtc catgcatata tgatatatat atgttgtaac
360
gttgtgaaag caaact
376

<210> 1136
<211> 67
<212> PRT
<213> Homo sapiens

<400> 1136
```
Asp Gln Ala Thr Gln Asp Asn Phe Glu Lys Gly Ser Ile Phe Pro Pro
 1               5                  10                  15
Phe Thr Ser Ile Arg Lys Ile Ser Ala His Ile Ala Ala Ala Val Ala
            20                  25                  30
Ala Lys Ala Tyr Glu Leu Gly Leu Ala Thr Arg Leu Pro Pro Pro Ser
        35                  40                  45
Asp Leu Val Lys Tyr Ala Glu Asn Cys Met Tyr Thr Pro Val Tyr Arg
```

50 55 60
Asn Tyr Arg
65

<210> 1137
<211> 357
<212> DNA
<213> Homo sapiens

<400> 1137
acgcgtcgct ggaacccgaa gatgaagcgc ttcatcttca ccgagcgcaa cggtatctac
60
atcattgacc tgcaccagtc gctgacctac attgataagg cgtacgcctt cgtcaaggag
120
actgtcgcca agggcggcca gattcttttc gtcggcacga agaagcaggc ccaggagtcc
180
atcgttgagc aggccactcg cgttggcatg ccctatgtca accagcgttg gcttggggga
240
atgctcacta atttccagac catctcgaag cgcattgccc ggctcaagga gctcgaggcc
300
atggactttg acaaggtttc cggctccggt ctcaccaaga aggagctgct tatgctc
357

<210> 1138
<211> 119
<212> PRT
<213> Homo sapiens

<400> 1138
Thr Arg Arg Trp Asn Pro Lys Met Lys Arg Phe Ile Phe Thr Glu Arg
1 5 10 15
Asn Gly Ile Tyr Ile Ile Asp Leu His Gln Ser Leu Thr Tyr Ile Asp
20 25 30
Lys Ala Tyr Ala Phe Val Lys Glu Thr Val Ala Lys Gly Gly Gln Ile
35 40 45
Leu Phe Val Gly Thr Lys Lys Gln Ala Gln Glu Ser Ile Val Glu Gln
50 55 60
Ala Thr Arg Val Gly Met Pro Tyr Val Asn Gln Arg Trp Leu Gly Gly
65 70 75 80
Met Leu Thr Asn Phe Gln Thr Ile Ser Lys Arg Ile Ala Arg Leu Lys
85 90 95
Glu Leu Glu Ala Met Asp Phe Asp Lys Val Ser Gly Ser Gly Leu Thr
100 105 110
Lys Lys Glu Leu Leu Met Leu
115

<210> 1139
<211> 456
<212> DNA
<213> Homo sapiens

<400> 1139
gtgcacaggt cgtctgaggc catgccgcgg acgatcgatc cgagtatggc ggcaccttca
60

ccaatcccgt aggacccgtc tcgtccagca tcgaccaagg cgctgttgag gcgttcggct
120
tcggtaatga actcgatgcg ctcaatatcc acgggggtag cgaaatcgta gatcttggcc
180
agactgaggc cttggaggag cgcggccgtc gggggacgt ggcctgcggc cgggcgttcc
240
ttgctctcaa ggacttcgtc gtcgcggctg acaaggaata cgtttgtgtg gtcgcctgca
300
atgcatgctc gagcgtggtg accatcgagg tgaaggacgg tttcggcata gaggtcatcg
360
tccacatcgg ccacagtgag ttcgacgact cctgagtcga ctagatgacg cgccttctct
420
gccgcgtctt cgctgacgtc ggccaggacc gctagc
456

<210> 1140
<211> 122
<212> PRT
<213> Homo sapiens

<400> 1140
Met Trp Thr Met Thr Ser Met Pro Lys Pro Ser Phe Thr Ser Met Val
1 5 10 15
Thr Thr Leu Glu His Ala Leu Gln Ala Thr Thr Gln Thr Tyr Ser Leu
20 25 30
Ser Ala Ala Thr Thr Lys Ser Leu Arg Ala Arg Asn Ala Arg Pro Gln
35 40 45
Ala Thr Ser Pro Arg Arg Pro Arg Ser Ser Lys Ala Ser Val Trp Pro
50 55 60
Arg Ser Thr Ile Ser Leu Pro Pro Trp Ile Leu Ser Ala Ser Ser Ser
65 70 75 80
Leu Pro Lys Pro Asn Ala Ser Thr Ala Pro Trp Ser Met Leu Asp Glu
85 90 95
Thr Gly Pro Thr Gly Leu Val Lys Val Pro Pro Tyr Ser Asp Arg Ser
100 105 110
Ser Ala Ala Trp Pro Gln Thr Thr Cys Ala
115 120

<210> 1141
<211> 354
<212> DNA
<213> Homo sapiens

<400> 1141
ggcgccatgc tcggcgggct ggtgctgggt gtggccgaag cctttggcgc cgatatcttc
60
ggcgaccagt acaaggacgt ggtggcgttt ggcctgttgg ttctggtgct gttgttccgt
120
ccgaccggca ttctgggccg tccggaggtt gagaaagtat gagcagatat cttaaatcgg
180
cgtttttcag cgccctgttg gtgtgggccg tggcctttcc ggtactcggc ctcaagctga
240
gcattgtcgg gatcaaccac gaagtgcatg gcaccggtcc cgtgaccttg accatcatcg
300

ccctgtgctc ggtgccgatg ttcctgcgcg tgctgtttac ccagcaagtc ggtg
354

<210> 1142
<211> 53
<212> PRT
<213> Homo sapiens

<400> 1142
Gly Ala Met Leu Gly Gly Leu Val Leu Gly Val Ala Glu Ala Phe Gly
1 5 10 15
Ala Asp Ile Phe Gly Asp Gln Tyr Lys Asp Val Val Ala Phe Gly Leu
20 25 30
Leu Val Leu Val Leu Leu Phe Arg Pro Thr Gly Ile Leu Gly Arg Pro
35 40 45
Glu Val Glu Lys Val
50

<210> 1143
<211> 353
<212> DNA
<213> Homo sapiens

<400> 1143
acgcgttgca catcccccag gaccatcaac cgcggcattg ccgcatagac ctggagatcc
60
catgcaacgt gaaatgaagt tcgaatcgat caaggcaaag gccaaggcga tgctcatcgg
120
cgcagccgac gacacagcaa gcgcaggcgc gaccaaccga gggtggctca acagcgccgc
180
attcgaaatc ctggcccacg tggccgtcaa tgcccaacac tacgcgctct ccgagagacc
240
ggcgctggag gagttcgcca agagcttcca gccgcgcaac aaccaggact acgtggccgc
300
gatcgccaag aaggccgcga accacaccat gcatcccggc aggcagtcga ttt
353

<210> 1144
<211> 102
<212> PRT
<213> Homo sapiens

<400> 1144
Met His Gly Val Val Arg Gly Leu Leu Gly Asp Arg Gly His Val Val
1 5 10 15
Leu Val Val Ala Arg Leu Glu Ala Leu Gly Glu Leu Leu Gln Arg Arg
20 25 30
Ser Leu Gly Glu Arg Val Val Leu Gly Ile Asp Gly His Val Gly Gln
35 40 45
Asp Phe Glu Cys Gly Ala Val Glu Pro Pro Ser Val Gly Arg Ala Cys
50 55 60
Ala Cys Cys Val Val Gly Cys Ala Asp Glu His Arg Leu Gly Leu Cys
65 70 75 80
Leu Asp Arg Phe Glu Leu His Phe Thr Leu His Gly Ile Ser Arg Ser

85 90 95
Met Arg Gln Cys Arg Gly
100

<210> 1145
<211> 360
<212> DNA
<213> Homo sapiens

<400> 1145
gtcttcggcg ggctcggcct gttctattgc gtcatgaccc cggtgtactg gttctcggcc
60
catgaagtgg ccggcacctg ggtactcggg ctgtcggcgg cgatggctct gatggtgttt
120
ttctacgtcc aggtcatcgc caagaagatc aatcctcgac cctccgacga gaaggacgcc
180
gaggtgatcg acggggctgg tccggtcggt ttcttcccgc cacagagtat ctggccgttc
240
tggtgcgcgc tcgttgtcgc catcatgtgc ctcggcccga tcttcggctg gtggatctct
300
ctgctcgggc tgggcattgt tatctgggcc gcctcgggtt gggcttttga gtactaccgc
360

<210> 1146
<211> 120
<212> PRT
<213> Homo sapiens

<400> 1146
Val Phe Gly Gly Leu Gly Leu Phe Tyr Cys Val Met Thr Pro Val Tyr
1 5 10 15
Trp Phe Ser Ala His Glu Val Ala Gly Thr Trp Val Leu Gly Leu Ser
20 25 30
Ala Ala Met Ala Leu Met Val Phe Phe Tyr Val Gln Val Ile Ala Lys
35 40 45
Lys Ile Asn Pro Arg Pro Ser Asp Glu Lys Asp Ala Glu Val Ile Asp
50 55 60
Gly Ala Gly Pro Val Gly Phe Phe Pro Pro Gln Ser Ile Trp Pro Phe
65 70 75 80
Trp Cys Ala Leu Val Val Ala Ile Met Cys Leu Gly Pro Ile Phe Gly
85 90 95
Trp Trp Ile Ser Leu Leu Gly Leu Gly Ile Val Ile Trp Ala Ala Ser
100 105 110
Gly Trp Ala Phe Glu Tyr Tyr Arg
115 120

<210> 1147
<211> 409
<212> DNA
<213> Homo sapiens

<400> 1147
tgtacattgg ctatgcagtc tggcctcctg aaggttatga tagtagccaa aaatatagaa
60

gccaaaaagg catccacctt cttcatcaat ccagaattga tcatgctcat gcctgtgggt
120
ggatcactat gtgctctcca aattgggagg ggaagtctac tctcctctct cctctctctc
180
ccaccttccc ctctctcttc tctcctttct attcccaggg cagtggaaca tgatgaggtt
240
cttttccctt catggatatc ctctttctgc cctccacata aaggggcatt gatggatctt
300
caagaatggg atgcctttcc ctagaaaggc taaatattca tgaggctgaa tgtgaggatc
360
cagagtacac tgaaatataa ctggtcatca gtacacatag aatctgatn
409

<210> 1148
<211> 103
<212> PRT
<213> Homo sapiens

<400> 1148
Met Gln Ser Gly Leu Leu Lys Val Met Ile Val Ala Lys Asn Ile Glu
1 5 10 15
Ala Lys Lys Ala Ser Thr Phe Phe Ile Asn Pro Glu Leu Ile Met Leu
20 25 30
Met Pro Val Gly Gly Ser Leu Cys Ala Leu Gln Ile Gly Arg Gly Ser
35 40 45
Leu Leu Ser Ser Leu Leu Ser Leu Pro Pro Ser Pro Leu Ser Ser Leu
50 55 60
Leu Ser Ile Pro Arg Ala Val Glu His Asp Glu Val Leu Phe Pro Ser
65 70 75 80
Trp Ile Ser Ser Phe Cys Pro Pro His Lys Gly Ala Leu Met Asp Leu
85 90 95
Gln Glu Trp Asp Ala Phe Pro
100

<210> 1149
<211> 309
<212> DNA
<213> Homo sapiens

<400> 1149
gtcgacttct gcatggaaaa acgcgatctg gtgattgagc acgttgcgga gatgtacggc
60
cgtgaggcgg tatcgcagat cattaccttc ggtaccatgg cggcgaaagc ggttattcgt
120
gacgtgggcc gtgtactggg tcacccgtat ggcttcgtcg atcgcatctc caagctggtg
180
ccgcccgatc cgggcatgac gctggaaaaa gcctttgccg ccgaaccgca gttgccggaa
240
atctacgagg ccgatgagga agtcaaagcg ctgatcgaca tggcgcgcaa gctgggaagg
300
gtgacgcgg
309

<210> 1150

<211> 103
<212> PRT
<213> Homo sapiens

<400> 1150
Val Asp Phe Cys Met Glu Lys Arg Asp Leu Val Ile Glu His Val Ala
1 5 10 15
Glu Met Tyr Gly Arg Glu Ala Val Ser Gln Ile Ile Thr Phe Gly Thr
20 25 30
Met Ala Ala Lys Ala Val Ile Arg Asp Val Gly Arg Val Leu Gly His
35 40 45
Pro Tyr Gly Phe Val Asp Arg Ile Ser Lys Leu Val Pro Pro Asp Pro
50 55 60
Gly Met Thr Leu Glu Lys Ala Phe Ala Ala Glu Pro Gln Leu Pro Glu
65 70 75 80
Ile Tyr Glu Ala Asp Glu Glu Val Lys Ala Leu Ile Asp Met Ala Arg
85 90 95
Lys Leu Gly Arg Val Thr Arg
100

<210> 1151
<211> 360
<212> DNA
<213> Homo sapiens

<400> 1151
gcgcgcattt tttgcaaccc aagcgacgtc attatggccg agtcgccggc ttatgtcggg
60
gcgctcaata ccttcgcctc gtaccaaact gaggtcattc acgtcgacat ggacgacagc
120
gggttggttc cggaatccct gcgtgagaaa gtgactgcag cgcgtcaaga cggcaagtcg
180
gtgaagttcc tttacacggt tcctaactac tcgaacccgt cgggaatctc gcaatccacc
240
gagcgtcgcc gggagatcct agcggtggct gacgagctgg atctgttggt ggttgaggac
300
aacccgtacg ggttactcaa cctcgatggt gatccactgc cgacgttgaa gtcgatggat
360

<210> 1152
<211> 120
<212> PRT
<213> Homo sapiens

<400> 1152
Ala Arg Ile Phe Cys Asn Pro Ser Asp Val Ile Met Ala Glu Ser Pro
1 5 10 15
Ala Tyr Val Gly Ala Leu Asn Thr Phe Ala Ser Tyr Gln Thr Glu Val
20 25 30
Ile His Val Asp Met Asp Asp Ser Gly Leu Val Pro Glu Ser Leu Arg
35 40 45
Glu Lys Val Thr Ala Ala Arg Gln Asp Gly Lys Ser Val Lys Phe Leu
50 55 60
Tyr Thr Val Pro Asn Tyr Ser Asn Pro Ser Gly Ile Ser Gln Ser Thr

```
65                  70                  75                  80
Glu Arg Arg Arg Glu Ile Leu Ala Val Ala Asp Glu Leu Asp Leu Leu
                85                  90                  95
Val Val Glu Asp Asn Pro Tyr Gly Leu Leu Asn Leu Asp Gly Asp Pro
            100                 105                 110
Leu Pro Thr Leu Lys Ser Met Asp
        115                 120
```

<210> 1153
<211> 416
<212> DNA
<213> Homo sapiens

<400> 1153
gcgtggattc gtcctggcgg cgtcgctacc gacctgcccg agaccgggct cgaccagttg
60
cgtgacctca tcaagcggat ggaaaagtac ctccccgaga tcggtcagtt ctgcaatgag
120
aatccgatct ttaaggcccg cactcagggc attggttacg ctgatctgtc tacctgtatg
180
gccctgggag ttactggtcc tgctctgcgc gctaccggcc tgccgtggga cctgcgcaag
240
acccagccct attgcgatta cgacacgtat gacttcgacg tcgccacctg ggatacctgt
300
gactgttacg ggcgtttccg catccgcctg gaagagatgg accagtcggt gcgcattctc
360
aagcaatgcc tcaaacgcct cgaggacacc cagggtgacc gtaatatggt cgagga
416

<210> 1154
<211> 138
<212> PRT
<213> Homo sapiens

<400> 1154
```
Ala Trp Ile Arg Pro Gly Gly Val Ala Thr Asp Leu Pro Glu Thr Gly
 1               5                  10                  15
Leu Asp Gln Leu Arg Asp Leu Ile Lys Arg Met Glu Lys Tyr Leu Pro
            20                  25                  30
Glu Ile Gly Gln Phe Cys Asn Glu Asn Pro Ile Phe Lys Ala Arg Thr
        35                  40                  45
Gln Gly Ile Gly Tyr Ala Asp Leu Ser Thr Cys Met Ala Leu Gly Val
    50                  55                  60
Thr Gly Pro Ala Leu Arg Ala Thr Gly Leu Pro Trp Asp Leu Arg Lys
65                  70                  75                  80
Thr Gln Pro Tyr Cys Asp Tyr Asp Thr Tyr Asp Phe Asp Val Ala Thr
                85                  90                  95
Trp Asp Thr Cys Asp Cys Tyr Gly Arg Phe Arg Ile Arg Leu Glu Glu
            100                 105                 110
Met Asp Gln Ser Val Arg Ile Leu Lys Gln Cys Leu Lys Arg Leu Glu
        115                 120                 125
Asp Thr Gln Gly Asp Arg Asn Met Val Glu
    130                 135
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<210> 1155
<211> 339
<212> DNA
<213> Homo sapiens

<400> 1155
cttaagttat tttggtcttt gcctctctcc tcaggttgtg aagattacag aaatctggga
60
tggcttatgg gacgcttctc agccctaagt aggaaaacag cagtgaaaat ggcaaccaaa
120
acatcacgca ggactggggg ttttggggaa acagctcact ttagagcagt gcagtgtaga
180
gctttccgtc ttctaccagg gtccaccttt aacactgttt atctgaaaat tttccccctg
240
gcttactcgc ttgcagctgc ccactttgca gaaagatggc gctctgatct ctacgctccc
300
tgttccttca gggactccat agtatttttt ttcacgcgt
339

<210> 1156
<211> 91
<212> PRT
<213> Homo sapiens

<400> 1156
Met Gly Arg Phe Ser Ala Leu Ser Arg Lys Thr Ala Val Lys Met Ala
 1   5   10   15
Thr Lys Thr Ser Arg Arg Thr Gly Gly Phe Gly Glu Thr Ala His Phe
            20   25   30
Arg Ala Val Gln Cys Arg Ala Phe Arg Leu Leu Pro Gly Ser Thr Phe
        35   40   45
Asn Thr Val Tyr Leu Lys Ile Phe Pro Leu Ala Tyr Ser Leu Ala Ala
    50   55   60
Ala His Phe Ala Glu Arg Trp Arg Ser Asp Leu Tyr Ala Pro Cys Ser
65   70   75   80
Phe Arg Asp Ser Ile Val Phe Phe Phe Thr Arg
                85   90

<210> 1157
<211> 426
<212> DNA
<213> Homo sapiens

<400> 1157
nnacagcctc tctccgaccc ggcggcggtt gcacacgtcc ccgtctgagg agtattcgtg
60
ctggcaaaac tcgtgacccg acacctgagg gcctatcggt tgcacgttgc cgtcatcatc
120
gttatgcagg tttgcgccca aatcgcggcc ctgaccttgc caaccatcaa cgcagacatc
180
atcaacaagg gcgtcgtgac agcggatacc ggatatgtca ccacccactc cctcttcatg
240
ctggcggtcg ctttagggca ggccatctgc caggtcattg cggtttatct cgccgctcag
300

gtggcgatgg gaatgggccg tgacgttcgc gacgccatct tcacccgcac ccttgacttc
360
tcggcccggg agatcaacaa attcggagca ccatcactca ttacccggac taccaacgac
420
gtccag
426

<210> 1158
<211> 123
<212> PRT
<213> Homo sapiens

<400> 1158
Val Leu Ala Lys Leu Val Thr Arg His Leu Arg Ala Tyr Arg Leu His
1 5 10 15
Val Ala Val Ile Ile Val Met Gln Val Cys Ala Gln Ile Ala Ala Leu
20 25 30
Thr Leu Pro Thr Ile Asn Ala Asp Ile Ile Asn Lys Gly Val Val Thr
35 40 45
Ala Asp Thr Gly Tyr Val Thr Thr His Ser Leu Phe Met Leu Ala Val
50 55 60
Ala Leu Gly Gln Ala Ile Cys Gln Val Ile Ala Val Tyr Leu Ala Ala
65 70 75 80
Gln Val Ala Met Gly Met Gly Arg Asp Val Arg Asp Ala Ile Phe Thr
85 90 95
Arg Thr Leu Asp Phe Ser Ala Arg Glu Ile Asn Lys Phe Gly Ala Pro
100 105 110
Ser Leu Ile Thr Arg Thr Thr Asn Asp Val Gln
115 120

<210> 1159
<211> 434
<212> DNA
<213> Homo sapiens

<400> 1159
tctctccgac cgcgcctggg gcccggtggg gtcctgcggg gacgcgggcg aggacggcgc
60
ggacgaggca ggagcaggcc gggctctcgc catgggtcac tgtcgcctct gccacgggaa
120
gttttcctcg agaagcctgc gcagcatctc cgagagggcg cctggagcga gcatggagag
180
gccatccgca gaggagcgcg tgctcgtacg ggacttccag cgcctgcttg gtgtggctgt
240
ccgccaggac cccaccttgt ctccgtttgt ctgcaagagc tgccacgccc agttctacca
300
gtgccacagc cttctcaagt ccttcctgca gagggtcaac gcctccccgg ctggtcgccg
360
gaagccttgt gcaaaggtcg gtgcccagcc cccaacaggg gcagaggagg gagcgtgtct
420
ggtggatctg atca
434

<210> 1160

<211> 114
<212> PRT
<213> Homo sapiens

<400> 1160
Met Gly His Cys Arg Leu Cys His Gly Lys Phe Ser Ser Arg Ser Leu
1 5 10 15
Arg Ser Ile Ser Glu Arg Ala Pro Gly Ala Ser Met Glu Arg Pro Ser
20 25 30
Ala Glu Glu Arg Val Leu Val Arg Asp Phe Gln Arg Leu Leu Gly Val
35 40 45
Ala Val Arg Gln Asp Pro Thr Leu Ser Pro Phe Val Cys Lys Ser Cys
50 55 60
His Ala Gln Phe Tyr Gln Cys His Ser Leu Leu Lys Ser Phe Leu Gln
65 70 75 80
Arg Val Asn Ala Ser Pro Ala Gly Arg Arg Lys Pro Cys Ala Lys Val
85 90 95
Gly Ala Gln Pro Pro Thr Gly Ala Glu Glu Gly Ala Cys Leu Val Asp
100 105 110
Leu Ile

<210> 1161
<211> 355
<212> DNA
<213> Homo sapiens

<400> 1161
ctgcacacac accaggccac gcccacgagg acggccagtc agcatgcagc caatacaccc
60
acagagggat ggggagcagc cctcagtgcc agctccaaca ggcccactgc aggtcctgtc
120
actgcaccca aggagctgcc ttccatttca cctgacattt ccactaaggg cccagcgttt
180
atcattccag aagagcagca ggcagaacct tcacctccca agagctgcaa gtgcgctgtg
240
gcaggaaaag aagatctggc gtctgaagtc agctcctgct ctccaggaaa agagggacga
300
tgacatagga cttgagcaaa atgagagccc cgtgatggga gagaacacct gatca
355

<210> 1162
<211> 102
<212> PRT
<213> Homo sapiens

<400> 1162
Met Gln Pro Ile His Pro Gln Arg Asp Gly Glu Gln Pro Ser Val Pro
1 5 10 15
Ala Pro Thr Gly Pro Leu Gln Val Leu Ser Leu His Pro Arg Ser Cys
20 25 30
Leu Pro Phe His Leu Thr Phe Pro Leu Arg Ala Gln Arg Leu Ser Phe
35 40 45
Gln Lys Ser Ser Arg Gln Asn Leu His Leu Pro Arg Ala Ala Ser Ala

```
    50                  55                  60
Leu Trp Gln Glu Lys Lys Ile Trp Arg Leu Lys Ser Ala Pro Ala Leu
65                  70                  75                  80
Gln Glu Lys Arg Asp Asp Asp Ile Gly Leu Glu Gln Asn Glu Ser Pro
                85                  90                  95
Val Met Gly Glu Asn Thr
            100
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<210> 1163
<211> 466
<212> DNA
<213> Homo sapiens

<400> 1163
ngcgcgccag gaagcgggag gtcagctgta cacccagggt aatagaactt ctaccctcag
60
aggagtcaaa gagaaggcag aactatggca ggaaagctcc ggaagtccca catccctgga
120
gtgagcatct ggcagctggt ggaggagatc cctgaaggct gcagcacgcc ggactttgag
180
cagaagcccg tcacctcggc tctgccagag gggaaaaatg ctgtctttcg ggctgtggtc
240
tgtggggagc ccaggcccga ggtgcgttgg cagaactcca aaggtgacct cagtgattcc
300
agcaagtaca agatctcctc cagccctggc agcaaggagc acgtgctgca gatcaacaag
360
ctgacaggcg aggacacgga tctgtaccac tgcacagcag taaatgcgta cggagaggcc
420
gcttgctcag tgagactcac cgtcatcgaa gttggctttc ggaaga
466

<210> 1164
<211> 127
<212> PRT
<213> Homo sapiens

<400> 1164
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Met Ala Gly Lys Leu Arg Lys Ser His Ile Pro Gly Val Ser Ile Trp
 1               5                  10                  15
Gln Leu Val Glu Glu Ile Pro Glu Gly Cys Ser Thr Pro Asp Phe Glu
            20                  25                  30
Gln Lys Pro Val Thr Ser Ala Leu Pro Glu Gly Lys Asn Ala Val Phe
        35                  40                  45
Arg Ala Val Val Cys Gly Glu Pro Arg Pro Glu Val Arg Trp Gln Asn
    50                  55                  60
Ser Lys Gly Asp Leu Ser Asp Ser Ser Lys Tyr Lys Ile Ser Ser Ser
65                  70                  75                  80
Pro Gly Ser Lys Glu His Val Leu Gln Ile Asn Lys Leu Thr Gly Glu
                85                  90                  95
Asp Thr Asp Leu Tyr His Cys Thr Ala Val Asn Ala Tyr Gly Glu Ala
            100                 105                 110
Ala Cys Ser Val Arg Leu Thr Val Ile Glu Val Gly Phe Arg Lys
        115                 120                 125
```

<210> 1165
<211> 414
<212> DNA
<213> Homo sapiens

<400> 1165
tgggtggttc cggacacana aaatcacgtg ttgaaccgaa tttcaggcat ggtgaaaggc
60
tgctttagta aagtccttgt tgagccgcgt ctgctcaagc tcaacttgac nattatgtgt
120
ctgcacattc tgctgatgtc cacgttcgtg gccctgcccg gtcagttggc tgcagcagga
180
ttccccgccg ctgaacactg gaaagtgtat ctggtgacga tgctcatctc cttcgtctcc
240
gttgtccctt tcattatcta tgcagaagtg aaacgccgca tgaagcgcgt attcctgacg
300
tgtgttgcgc tgctgttgat tgccgaaatc gtactatggg gctccggtcc acacttctgg
360
gaactggtca tcggcgtaca gcttttcttc ctcgccttta atctcatgga agcc
414

<210> 1166
<211> 138
<212> PRT
<213> Homo sapiens

<400> 1166
Trp Val Val Pro Asp Thr Xaa Asn His Val Leu Asn Arg Ile Ser Gly
1 5 10 15
Met Val Lys Gly Cys Phe Ser Lys Val Leu Val Glu Pro Arg Leu Leu
20 25 30
Lys Leu Asn Leu Thr Ile Met Cys Leu His Ile Leu Leu Met Ser Thr
35 40 45
Phe Val Ala Leu Pro Gly Gln Leu Ala Ala Ala Gly Phe Pro Ala Ala
50 55 60
Glu His Trp Lys Val Tyr Leu Val Thr Met Leu Ile Ser Phe Val Ser
65 70 75 80
Val Val Pro Phe Ile Ile Tyr Ala Glu Val Lys Arg Arg Met Lys Arg
85 90 95
Val Phe Leu Thr Cys Val Ala Leu Leu Leu Ile Ala Glu Ile Val Leu
100 105 110
Trp Gly Ser Gly Pro His Phe Trp Glu Leu Val Ile Gly Val Gln Leu
115 120 125
Phe Phe Leu Ala Phe Asn Leu Met Glu Ala
130 135

<210> 1167
<211> 464
<212> DNA
<213> Homo sapiens

<400> 1167
gtcgaccccg tgggcaagag tcgcggcccc tgacgataac ttcaccccgc cggccttgag
60

ctgttgggac cggctggcta aggcctgggc accggtagcg gcctggtgga taccctcatg
120
tagccgggtg acctgcctga ccatcttcgg caaaccagtg cgcagttgtg tggtgaactc
180
attgacccct cgagacagtc gtgaggaacc gtcagcaagt tcgtcgatgc cgtcgtcgat
240
gctcttgcca gagttcggat ccttgatcgc catcgccttg acggccaccc ccgacccagc
300
ccgcacgccc agggcgtacc catcggtcat cgcgtcgcgg acgatgggta ccaggtcgtg
360
gcattcctgc gcggtgtggc ttcgcacgca tcgacgcagg aagtcagcct cgccccggga
420
cagggcttcc ttactaagtt ccgcggtttt ctttcccgac gcgt
464

<210> 1168
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1168
Met Thr Asp Gly Tyr Ala Leu Gly Val Arg Ala Gly Ser Gly Val Ala
1 5 10 15
Val Lys Ala Met Ala Ile Lys Asp Pro Asn Ser Gly Lys Ser Ile Asp
20 25 30
Asp Gly Ile Asp Glu Leu Ala Asp Gly Ser Ser Arg Leu Ser Arg Gly
35 40 45
Val Asn Glu Phe Thr Thr Gln Leu Arg Thr Gly Leu Pro Lys Met Val
50 55 60
Arg Gln Val Thr Arg Leu His Glu Gly Ile His Gln Ala Ala Thr Gly
65 70 75 80
Ala Gln Ala Leu Ala Ser Arg Ser Gln Gln Leu Lys Ala Gly Gly Val
85 90 95
Lys Leu Ser Ser Gly Ala Ala Thr Leu Ala His Gly Val Asp
100 105 110

<210> 1169
<211> 486
<212> DNA
<213> Homo sapiens

<400> 1169
nacgcgtgaa gggagcagaa cggacaccag ttactagtgg ctctggtcgg ggacagcctc
60
ctagagcctt tctggccaat gggaacagga atagcccggg gctttctagc tgctatggac
120
tctgcctgga tggtccgaag ttggtctcta ggaacgagcc ctttggaagt gctggcagag
180
agggaaagta tttacaggtt gctgcctcag accacccctg agaatgtgag taagaacttc
240
agccagtaca gtatcgaccc tgtcactcgg tatcccaata tcaacgtcaa cttcctccgg
300
ccaagccagg tgcgccattt atatgatact ggcgaaacaa aagatattca cctggaaatg
360

gagagcctgg tgaattcccg aaccaccccc aaattgactc gcaatgagtc tgtagctcgt
420
tcaagcaaac tgctgggttg gtgccagagg cagacagatg gctatgcagg ggtaaacgtg
480
acagat
486

<210> 1170
<211> 159
<212> PRT
<213> Homo sapiens

<400> 1170
Arg Glu Gln Asn Gly His Gln Leu Leu Val Ala Leu Val Gly Asp Ser
1 5 10 15
Leu Leu Glu Pro Phe Trp Pro Met Gly Thr Gly Ile Ala Arg Gly Phe
20 25 30
Leu Ala Ala Met Asp Ser Ala Trp Met Val Arg Ser Trp Ser Leu Gly
35 40 45
Thr Ser Pro Leu Glu Val Leu Ala Glu Arg Glu Ser Ile Tyr Arg Leu
50 55 60
Leu Pro Gln Thr Thr Pro Glu Asn Val Ser Lys Asn Phe Ser Gln Tyr
65 70 75 80
Ser Ile Asp Pro Val Thr Arg Tyr Pro Asn Ile Asn Val Asn Phe Leu
85 90 95
Arg Pro Ser Gln Val Arg His Leu Tyr Asp Thr Gly Glu Thr Lys Asp
100 105 110
Ile His Leu Glu Met Glu Ser Leu Val Asn Ser Arg Thr Thr Pro Lys
115 120 125
Leu Thr Arg Asn Glu Ser Val Ala Arg Ser Ser Lys Leu Leu Gly Trp
130 135 140
Cys Gln Arg Gln Thr Asp Gly Tyr Ala Gly Val Asn Val Thr Asp
145 150 155

<210> 1171
<211> 429
<212> DNA
<213> Homo sapiens

<400> 1171
acgcgttcaa caaagcacag aaccggagat gcagtgggag ccgagagcag gaagcgcgga
60
ggcagcgcca ggtgctggcg ctgcccgagg ccccgtgcca agtggggccc atagcagccg
120
actcgctaga ccctcccaaa acgcacacca cgcgcgacca ggaccgagag gcccgcacgg
180
ccctgctagg ccacaaacac tccactgtct ccagggtaaa agacaaacac agcctcgctt
240
gtccctccaa gagtacaacc tctgtctgat gaaaaacaaa cgacccagag aggaggcagc
300
tgccgggaca ctgcaggctg ggcccgccgc gcccttggag ggcaggtcaa aatcccggaa
360
caggcacagt gttcaggctg attgactgtc ccaggccagg gcggcctcaa ctgccagagc
420

acctcctac
429

<210> 1172
<211> 118
<212> PRT
<213> Homo sapiens

<400> 1172
Met Gln Trp Glu Pro Arg Ala Gly Ser Ala Glu Ala Ala Pro Gly Ala
1 5 10 15
Gly Ala Ala Arg Gly Pro Val Pro Ser Gly Ala His Ser Ser Arg Leu
20 25 30
Ala Arg Pro Ser Gln Asn Ala His His Ala Arg Pro Gly Pro Arg Gly
35 40 45
Pro His Gly Pro Ala Arg Pro Gln Thr Leu His Cys Leu Gln Gly Lys
50 55 60
Arg Gln Thr Gln Pro Arg Leu Ser Leu Gln Glu Tyr Asn Leu Cys Leu
65 70 75 80
Met Lys Asn Lys Arg Pro Arg Glu Glu Ala Ala Ala Gly Thr Leu Gln
85 90 95
Ala Gly Pro Ala Ala Pro Leu Glu Gly Arg Ser Lys Ser Arg Asn Arg
100 105 110
His Ser Val Gln Ala Asp
115

<210> 1173
<211> 435
<212> DNA
<213> Homo sapiens

<400> 1173
cgcgtcaatg acgacggcga gcattctgcc gagcaggtga tgcgagccac ccgcggtgct
60
ggacttgggg ccgaggccaa gcgtcgcatc atcttgggta cctatgcctt gtcggctggg
120
tactatgacg cctactacgg ctcggctcag aaagtccgta ccctcatcca acgcgacttc
180
gagaaagcat ggcagatgtg cgatgtgctc gtgtcaccgg ccacgccaac gactgccttc
240
cggctgggtg agcgtactgc tgacccgatg gcgatgtacc gctccgatct atgcacggtc
300
ccggccaata tggccggaag tcccgcagga tctttcccga tcggtctatc agagaccgac
360
ggcatgcccg tcggcatgca ggtgatggcg ccaatcatgg cggacgatcg aatctaccga
420
gttggggccg ctcta
435

<210> 1174
<211> 145
<212> PRT
<213> Homo sapiens

<400> 1174
Arg Val Asn Asp Asp Gly Glu His Ser Ala Glu Gln Val Met Arg Ala
1 5 10 15
Thr Arg Gly Ala Gly Leu Gly Ala Glu Ala Lys Arg Arg Ile Ile Leu
20 25 30
Gly Thr Tyr Ala Leu Ser Ala Gly Tyr Tyr Asp Ala Tyr Tyr Gly Ser
35 40 45
Ala Gln Lys Val Arg Thr Leu Ile Gln Arg Asp Phe Glu Lys Ala Trp
50 55 60
Gln Met Cys Asp Val Leu Val Ser Pro Ala Thr Pro Thr Thr Ala Phe
65 70 75 80
Arg Leu Gly Glu Arg Thr Ala Asp Pro Met Ala Met Tyr Arg Ser Asp
85 90 95
Leu Cys Thr Val Pro Ala Asn Met Ala Gly Ser Pro Ala Gly Ser Phe
100 105 110
Pro Ile Gly Leu Ser Glu Thr Asp Gly Met Pro Val Gly Met Gln Val
115 120 125
Met Ala Pro Ile Met Ala Asp Asp Arg Ile Tyr Arg Val Gly Ala Ala
130 135 140
Leu
145

<210> 1175
<211> 729
<212> DNA
<213> Homo sapiens

<400> 1175
gatcgcactg caatccaccc acatctactt gatatgaaaa ttggtcaagg caaatatgag
60
caggggttct ttccaaagtt acagtccgat gtcttggcaa caggaccaac cagtaacaat
120
cgctgggtaa gtcggagtgc cactgcacag cgcaggaaag gacgccttcg ccagcattct
180
gagcatgttg ggctggacaa cgacttgagg gagaaatata tgcaagaggc acgaagttta
240
ggaaaaaacc tgaggcaacc caaactgtca gacctctctc ctgcagttat tgcacagacc
300
aactgtaaat tcgtagaagg cttattaaaa gaatgtagaa ataagacaaa gcgcatgttg
360
gtggagaaga tgggacatga agcggtggaa cttggccatg gagaagcaaa catcaccggc
420
ctggaggaga acaccttgat cgccagcctt tgtgacctgc tggagaggat atggagccat
480
ggcttgcagg tcaagcaggg gaagtcggtt ttgtggtcac atttaattcc ttttcaggac
540
agagaagaga accaagagcc ccttgcagaa tcaccagttg ccctcggacc agaaagaaaa
600
aaatctgact caggagttat gttgccaacg ctcagggtct ctcttattca ggacatgagg
660
catattcaaa acatgagtga gatcaagact gatgttggac gagctcgggc gtggataaga
720
ctgtctcta
729

<210> 1176
<211> 243
<212> PRT
<213> Homo sapiens

<400> 1176
Asp Arg Thr Ala Ile His Pro His Leu Leu Asp Met Lys Ile Gly Gln
1 5 10 15
Gly Lys Tyr Glu Gln Gly Phe Phe Pro Lys Leu Gln Ser Asp Val Leu
20 25 30
Ala Thr Gly Pro Thr Ser Asn Asn Arg Trp Val Ser Arg Ser Ala Thr
35 40 45
Ala Gln Arg Arg Lys Gly Arg Leu Arg Gln His Ser Glu His Val Gly
50 55 60
Leu Asp Asn Asp Leu Arg Glu Lys Tyr Met Gln Glu Ala Arg Ser Leu
65 70 75 80
Gly Lys Asn Leu Arg Gln Pro Lys Leu Ser Asp Leu Ser Pro Ala Val
85 90 95
Ile Ala Gln Thr Asn Cys Lys Phe Val Glu Gly Leu Leu Lys Glu Cys
100 105 110
Arg Asn Lys Thr Lys Arg Met Leu Val Glu Lys Met Gly His Glu Ala
115 120 125
Val Glu Leu Gly His Gly Glu Ala Asn Ile Thr Gly Leu Glu Glu Asn
130 135 140
Thr Leu Ile Ala Ser Leu Cys Asp Leu Leu Glu Arg Ile Trp Ser His
145 150 155 160
Gly Leu Gln Val Lys Gln Gly Lys Ser Val Leu Trp Ser His Leu Ile
165 170 175
Pro Phe Gln Asp Arg Glu Glu Asn Gln Glu Pro Leu Ala Glu Ser Pro
180 185 190
Val Ala Leu Gly Pro Glu Arg Lys Lys Ser Asp Ser Gly Val Met Leu
195 200 205
Pro Thr Leu Arg Val Ser Leu Ile Gln Asp Met Arg His Ile Gln Asn
210 215 220
Met Ser Glu Ile Lys Thr Asp Val Gly Arg Ala Arg Ala Trp Ile Arg
225 230 235 240
Leu Ser Leu

<210> 1177
<211> 581
<212> DNA
<213> Homo sapiens

<400> 1177
acgcgtgatg agttgcgcga gaccagcaac tgcagccgaa cacagttttc ttgtgtaccc
60
cgtcgcacag ctgcgagagg tgggcattgc cgagtgaggc aacgatgtct aaggcggaaa
120
gctcatcctc ggcagacggg aagactttgt cgtcggggat gttgtcaatg agagcgggga
180
cgtcgatctc ggtactgccc atggcgtcat gaaggatcgc gcgatacggg gcgacgaccc
240

cgatgagggc gtcgtcgaat ccagcgatga tcgatacctc tctcggtagc acgtccgtgg
300
ccaacaggtg gtcgacttgg gcgggggcta gccatgtaat tgttccgagc acatggaggg
360
tggctgccag gaggcggatg gccggttctg gggcatcttt ggagatcttc agccggacat
420
cagtgggcag tccggccggg acttggcaga gggcctgggc gggatgggag cgctgggcga
480
cgacgaaacg ccccgacgcc gtaacgccgt gggcttggag atcgcaggtc cacttctctg
540
ggctttcacc ggcagagatc atggtgtgga ccaccattgt g
581

<210> 1178
<211> 192
<212> PRT
<213> Homo sapiens

<400> 1178
Met Val Val His Thr Met Ile Ser Ala Gly Glu Ser Pro Glu Lys Trp
1 5 10 15
Thr Cys Asp Leu Gln Ala His Gly Val Thr Ala Ser Gly Arg Phe Val
20 25 30
Val Ala Gln Arg Ser His Pro Ala Gln Ala Leu Cys Gln Val Pro Ala
35 40 45
Gly Leu Pro Thr Asp Val Arg Leu Lys Ile Ser Lys Asp Ala Pro Glu
50 55 60
Pro Ala Ile Arg Leu Leu Ala Ala Thr Leu His Val Leu Gly Thr Ile
65 70 75 80
Thr Trp Leu Ala Pro Ala Gln Val Asp His Leu Leu Ala Thr Asp Val
85 90 95
Leu Pro Arg Glu Val Ser Ile Ile Ala Gly Phe Asp Asp Ala Leu Ile
100 105 110
Gly Val Val Ala Pro Tyr Arg Ala Ile Leu His Asp Ala Met Gly Ser
115 120 125
Thr Glu Ile Asp Val Pro Ala Leu Ile Asp Asn Ile Pro Asp Asp Lys
130 135 140
Val Phe Pro Ser Ala Glu Asp Glu Leu Ser Ala Leu Asp Ile Val Ala
145 150 155 160
Ser Leu Gly Asn Ala His Leu Ser Gln Leu Cys Asp Gly Val His Lys
165 170 175
Lys Thr Val Phe Gly Cys Ser Cys Trp Ser Arg Ala Thr His His Ala
180 185 190

<210> 1179
<211> 597
<212> DNA
<213> Homo sapiens

<400> 1179
gtgcactttc tggcttctaa ctgtggcccc agccctgact ccttgaggtg ctcctgtgct
60
gattggggct tctggacatg ctgccacaag atgtctggaa actccagggg gcacctgccg
120

agaccctgcc ctgggaacgg ccggaagaat cccaaaacat gagattccgg tgcagctgag
180
ccccgccaat tcattgtctc tttcagtccc ttctgaaggc tgcatttggc aatgtgaccc
240
tcggggtggg gaaggcatca gaggaataca ggctatggga cgccagaggc agcgtcctgg
300
ggacaaagcc cacttcttcc catgcccagg gcttcctcat ggacccagca tggtggacgt
360
ggccctcaga cgtccatggg tggtggggga ggcacgtgct gtttggccct gtctctgctc
420
agagtctcat aggaagatgc atggtccaca caacagtgag tcggcaggga gtccaggctt
480
cccctcccaa ccagtggtgt tgagacgctt ggtttataac ccaagatccc ttgtcccatt
540
ggtgcctcct gaatctccca cctcccgcgg cacctgcatg gcctctacct gacgcgt
597

<210> 1180
<211> 105
<212> PRT
<213> Homo sapiens

<400> 1180
Met Gly Arg Gln Arg Gln Arg Pro Gly Asp Lys Ala His Phe Phe Pro
 1   5   10   15
Cys Pro Gly Leu Pro His Gly Pro Ser Met Val Asp Val Ala Leu Arg
            20   25   30
Arg Pro Trp Val Val Gly Glu Ala Arg Ala Val Trp Pro Cys Leu Cys
        35   40   45
Ser Glu Ser His Arg Lys Met His Gly Pro His Asn Ser Glu Ser Ala
    50   55   60
Gly Ser Pro Gly Phe Pro Ser Gln Pro Val Val Leu Arg Arg Leu Val
65   70   75   80
Tyr Asn Pro Arg Ser Leu Val Pro Leu Val Pro Pro Glu Ser Pro Thr
                85   90   95
Ser Arg Gly Thr Cys Met Ala Ser Thr
            100   105

<210> 1181
<211> 352
<212> DNA
<213> Homo sapiens

<400> 1181
gtcgactacc tcgatgtttc cccgcgtcag atggtctccg tggctactgc catgattccg
60
ttcctcgagc acgacgacgc taaccgtgcc ctgatgggtg cgaacatgca gcgtcaggct
120
gtgccgctgc tgcgttcgga ggctccgttc gtcggtaccg gtatggagca gcgtgctgct
180
tacgacgccg gcgatgtcat tgtcgcttcg gccacaggtg tggtcgagac cgtgtcggca
240
ggcttcatca ccatcatgga cgatgagggc cagcgccaca cctacctgct gcgcaagttc
300

gagcgcacca accagggcac ctgctacaac cagaagccac tgttgacgag gg
352

<210> 1182
<211> 117
<212> PRT
<213> Homo sapiens

<400> 1182
Val Asp Tyr Leu Asp Val Ser Pro Arg Gln Met Val Ser Val Ala Thr
1 5 10 15
Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met
20 25 30
Gly Ala Asn Met Gln Arg Gln Ala Val Pro Leu Leu Arg Ser Glu Ala
35 40 45
Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly
50 55 60
Asp Val Ile Val Ala Ser Ala Thr Gly Val Val Glu Thr Val Ser Ala
65 70 75 80
Gly Phe Ile Thr Ile Met Asp Asp Glu Gly Gln Arg His Thr Tyr Leu
85 90 95
Leu Arg Lys Phe Glu Arg Thr Asn Gln Gly Thr Cys Tyr Asn Gln Lys
100 105 110
Pro Leu Leu Thr Arg
115

<210> 1183
<211> 432
<212> DNA
<213> Homo sapiens

<400> 1183
gatccttctg ggcgctggtc caagcgcgtg gtgaggccgt cctctcctgc agaaccccgg
60
cctcttcgcc cctgcccgct cacctgttct gtcctgctca cctcctccag gaagcctgcc
120
tggccttctc catgctgatg ggcgtggccc ttgtccctgc agccatgcat tgacctccgt
180
ggctcctgga ggccaggcca cgtcctcatc ccctctgggt gagtgagagg cacagcctgg
240
gtgcgtgggg ccgtggcggc tccgaggcgc caccgctgtg tcctctcatg agtgggtgcc
300
gtccaggtct gtcctgggct ggctgcgagg aggaggttgg cctcgcgcgg ccatgtgcgt
360
gacagtggag acatcgccag cctcctgctt gcacagctga cggcagcccc tctctctcca
420
gccatgtccc ca
432

<210> 1184
<211> 141
<212> PRT
<213> Homo sapiens

<400> 1184
Met Ala Gly Glu Arg Gly Ala Ala Val Ser Cys Ala Ser Arg Arg Leu
1 5 10 15
Ala Met Ser Pro Leu Ser Arg Thr Trp Pro Arg Glu Ala Asn Leu Leu
20 25 30
Leu Ala Ala Ser Pro Gly Gln Thr Trp Thr Ala Pro Thr His Glu Arg
35 40 45
Thr Gln Arg Trp Arg Leu Gly Ala Ala Thr Ala Pro Arg Thr Gln Ala
50 55 60
Val Pro Leu Thr His Pro Glu Gly Met Arg Thr Trp Pro Gly Leu Gln
65 70 75 80
Glu Pro Arg Arg Ser Met His Gly Cys Arg Asp Lys Gly His Ala His
85 90 95
Gln His Gly Glu Gly Gln Ala Gly Phe Leu Glu Glu Val Ser Arg Thr
100 105 110
Glu Gln Val Ser Gly Gln Gly Arg Arg Gly Arg Gly Ser Ala Gly Glu
115 120 125
Asp Gly Leu Thr Thr Arg Leu Asp Gln Arg Pro Glu Gly
130 135 140

<210> 1185
<211> 423
<212> DNA
<213> Homo sapiens

<400> 1185
accggtgaat ttggccttaa cagcgatgga actcctggcc catcttatga acctggcatg
60
gaattacgcg gcaaatatgt attgttgggt gaaggtgtac ggggctctct atctaaacaa
120
gtcatcaata aataccaatt atccgagggt catgaaccac aaaagttcgg ccttggctta
180
aaagaaattt gggaaataga cccagaaaaa cacaaagaag gcagagtcag tcataccatg
240
ggctggccat taaatggcaa tgctggcggc ggttctttta tttatcatgc agaaaacaat
300
caagtcttta tcggctttgt ggtgcatctt aattacgcca acccttacct atccccttac
360
caagaatttc aacgctttaa acaccatccg attatcgcgg agctattaac tggcggtaaa
420
cgc
423

<210> 1186
<211> 141
<212> PRT
<213> Homo sapiens

<400> 1186
Thr Gly Glu Phe Gly Leu Asn Ser Asp Gly Thr Pro Gly Pro Ser Tyr
1 5 10 15
Glu Pro Gly Met Glu Leu Arg Gly Lys Tyr Val Leu Leu Gly Glu Gly
20 25 30
Val Arg Gly Ser Leu Ser Lys Gln Val Ile Asn Lys Tyr Gln Leu Ser

```
        35                  40                  45
Glu Gly His Glu Pro Gln Lys Phe Gly Leu Gly Leu Lys Glu Ile Trp
    50                  55                  60
Glu Ile Asp Pro Glu Lys His Lys Glu Gly Arg Val Ser His Thr Met
65                  70                  75                  80
Gly Trp Pro Leu Asn Gly Asn Ala Gly Gly Gly Ser Phe Ile Tyr His
                85                  90                  95
Ala Glu Asn Asn Gln Val Phe Ile Gly Phe Val Val His Leu Asn Tyr
            100                 105                 110
Ala Asn Pro Tyr Leu Ser Pro Tyr Gln Glu Phe Gln Arg Phe Lys His
        115                 120                 125
His Pro Ile Ile Ala Glu Leu Leu Thr Gly Gly Lys Arg
    130                 135                 140
```

<210> 1187
<211> 387
<212> DNA
<213> Homo sapiens

<400> 1187
acgcgtgctg gtgagtttaa attgaatgct gatggtaatt tggtgacgaa ttcaggggct
60
aaggtccagg gctataatgc aatagatggc atagtcggtg ggaacttaga agatatggta
120
gtacccactg ctcgaatttc tcctcaagca acatcaagtg ttgatttaaa agtgaatctt
180
aattccgaag gtgaggatgt gccgccttat attcgagcgg actttgatcc agccaatcca
240
gatacttatg actatactca gacccaaacg gttgcggatg ggagtggtaa taatcattta
300
attagttatt actatgctaa aagtgatgta gcaaatacct atcaggttta tgccacggta
360
gatgggaagt cgactgatga taccggt
387

<210> 1188
<211> 129
<212> PRT
<213> Homo sapiens

<400> 1188
```
Thr Arg Ala Gly Glu Phe Lys Leu Asn Ala Asp Gly Asn Leu Val Thr
 1               5                  10                  15
Asn Ser Gly Ala Lys Val Gln Gly Tyr Asn Ala Ile Asp Gly Ile Val
            20                  25                  30
Gly Gly Asn Leu Glu Asp Met Val Val Pro Thr Ala Arg Ile Ser Pro
        35                  40                  45
Gln Ala Thr Ser Ser Val Asp Leu Lys Val Asn Leu Asn Ser Glu Gly
    50                  55                  60
Glu Asp Val Pro Pro Tyr Ile Arg Ala Asp Phe Asp Pro Ala Asn Pro
65                  70                  75                  80
Asp Thr Tyr Asp Tyr Thr Gln Thr Gln Thr Val Ala Asp Gly Ser Gly
                85                  90                  95
Asn Asn His Leu Ile Ser Tyr Tyr Tyr Ala Lys Ser Asp Val Ala Asn
```

```
            100                 105                 110
Thr Tyr Gln Val Tyr Ala Thr Val Asp Gly Lys Ser Thr Asp Asp Thr
        115                 120                 125
Gly


<210> 1189
<211> 330
<212> DNA
<213> Homo sapiens

<400> 1189
tcgatcgccg accgcccggg ccttgccccc ggcatgatcg gtggcctgtt ggccagcacc
60
ctgggtgctg gtttcattgg cggcatcgtt gcaggttttc tggccggtta cagcgccaag
120
gccattgccc gctgggcacg gctgcccagc agcctggatg cgctcaaacc gattctgatc
180
atttcgctgc tggccagcct gttcactggg ttggtgatga tctacgtggt cggccagccg
240
gtggcggcca tgctcggagg cctgacacac tttctcgaca gcatgggtac caccaacgcc
300
attctcctgg gcntgttgct cggcggctag
330

<210> 1190
<211> 109
<212> PRT
<213> Homo sapiens

<400> 1190
Ser Ile Ala Asp Arg Pro Gly Leu Ala Pro Gly Met Ile Gly Gly Leu
 1               5                  10                  15
Leu Ala Ser Thr Leu Gly Ala Gly Phe Ile Gly Gly Ile Val Ala Gly
            20                  25                  30
Phe Leu Ala Gly Tyr Ser Ala Lys Ala Ile Ala Arg Trp Ala Arg Leu
        35                  40                  45
Pro Ser Ser Leu Asp Ala Leu Lys Pro Ile Leu Ile Ile Ser Leu Leu
    50                  55                  60
Ala Ser Leu Phe Thr Gly Leu Val Met Ile Tyr Val Val Gly Gln Pro
65                  70                  75                  80
Val Ala Ala Met Leu Gly Gly Leu Thr His Phe Leu Asp Ser Met Gly
                85                  90                  95
Thr Thr Asn Ala Ile Leu Leu Gly Xaa Leu Leu Gly Gly
            100                 105

<210> 1191
<211> 351
<212> DNA
<213> Homo sapiens

<400> 1191
cggccgacga tgtgcggtga gcaagagatt tggagagcca tgatgacgtc agcagacaaa
60
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gcagggacta acggacagac catgcagaca ccgccggtgg tgtcgccgca ggactgggag
120
gcagcccgtc agcaactgct cgtgaaggaa aaggcgcata cccgtgcccg cgacgcactc
180
gccgccgaac ggaggcgcat gccgtggatg gaagtgacaa aaacctacgc attcgaggcg
240
ccctcgggca aggccagtct gctcgatctg ttccagggcc ggaagcagct gatcctgtac
300
cgggccttct tcgagccggg cgtgttcggc tggcccgacc atgcctgccg c
351

<210> 1192
<211> 114
<212> PRT
<213> Homo sapiens

<400> 1192
Met Cys Gly Glu Gln Glu Ile Trp Arg Ala Met Met Thr Ser Ala Asp
1 5 10 15
Lys Ala Gly Thr Asn Gly Gln Thr Met Gln Thr Pro Pro Val Val Ser
20 25 30
Pro Gln Asp Trp Glu Ala Ala Arg Gln Gln Leu Leu Val Lys Glu Lys
35 40 45
Ala His Thr Arg Ala Arg Asp Ala Leu Ala Ala Glu Arg Arg Arg Met
50 55 60
Pro Trp Met Glu Val Thr Lys Thr Tyr Ala Phe Glu Ala Pro Ser Gly
65 70 75 80
Lys Ala Ser Leu Leu Asp Leu Phe Gln Gly Arg Lys Gln Leu Ile Leu
85 90 95
Tyr Arg Ala Phe Phe Glu Pro Gly Val Phe Gly Trp Pro Asp His Ala
100 105 110
Cys Arg

<210> 1193
<211> 722
<212> DNA
<213> Homo sapiens

<400> 1193
ggatcccagc ctccagatcc catcttgtag ctcttctttc tctacactna ggttgctccc
60
cgacttagga cgcccagttt gtactcagtg tttgctcttt tatggcagag cctctgcact
120
cccagcctcc tggccccttc tgtacatgat tttccttgtg gccactccat gcatttttct
180
tggctcagga cttagtgggc ctccatggga cttggtacct ctacttgttc ccttctggaa
240
tctgtaactt tgtgttcccc accattcttt cctttatgaa ccgatggtgc aacagcatga
300
ctacctgaaa ttcttagtca ctcccagctg ctttagtgga gggaaaatgc ccacagcaca
360
ggaaatagtc ctgcccttcg agagaggcca ggggatggga gcgtgtccag agaagggcga
420

tgggttgatg aagggtggcc acagcgcccg ggaggaaggg gccagaacgc tctctgttct
480
gttccatgag gaggattatg ttggtgtgtg tagtcccctg gttcagagtt gtccagaaat
540
agctcagtgt aaggaacaat tttccaaaga tcaaaagagc tgtctcaaga tagcagtgcg
600
ttcccagccc ctacaggtgt atacagcaca aagggaggga ccccctagtg tggctgtcac
660
agagggaagt ggacgtcctg tggtttgacc ccaccagatg gctttagaga tctgggcccg
720
ag
722

<210> 1194
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1194
Met Val Gln Gln His Asp Tyr Leu Lys Phe Leu Val Thr Pro Ser Cys
1 5 10 15
Phe Ser Gly Gly Lys Met Pro Thr Ala Gln Glu Ile Val Leu Pro Phe
20 25 30
Glu Arg Gly Gln Gly Met Gly Ala Cys Pro Glu Lys Gly Asp Gly Leu
35 40 45
Met Lys Gly Gly His Ser Ala Arg Glu Glu Gly Ala Arg Thr Leu Ser
50 55 60
Val Leu Phe His Glu Glu Asp Tyr Val Gly Val Cys Ser Pro Leu Val
65 70 75 80
Gln Ser Cys Pro Glu Ile Ala Gln Cys Lys Glu Gln Phe Ser Lys Asp
85 90 95
Gln Lys Ser Cys Leu Lys Ile Ala Val Arg Ser Gln Pro Leu Gln Val
100 105 110
Tyr Thr Ala Gln Arg Glu Gly Pro Pro Ser Val Ala Val Thr Glu Gly
115 120 125
Ser Gly Arg Pro Val Val
130

<210> 1195
<211> 391
<212> DNA
<213> Homo sapiens

<400> 1195
tctagagcat gatattccgc gggcgcggcc gggtggactt tggttcgaga gtggaactaa
60
gtgagtaatg ggggcggcgc ggccagacgc gctcccagcc tcctggcgag agtgctgccc
120
ggtttcccgg gggcacggga gtgtgtctag gaggggaggc caggatcctt cctcgagtcc
180
tgtcctgaac aaaagaaaac gaggtgggtg gtgcttgaac ggccctgttt actctgcaga
240
tagccgaact ggtaggactc cggcgcgccc tatttatctt gattggctct gcctgaaggc
300

aagcgttaat cccgtccaac ctgtatcact gcgaagagct cgttcgggag cgctttttgg
360
aaatgcagat tcttagcccc cacccagatc t
391

<210> 1196
<211> 102
<212> PRT
<213> Homo sapiens

<400> 1196
Met Gly Ala Ala Arg Pro Asp Ala Leu Pro Ala Ser Trp Arg Glu Cys
1 5 10 15
Cys Pro Val Ser Arg Gly His Gly Ser Val Ser Arg Arg Gly Gly Gln
20 25 30
Asp Pro Ser Ser Ser Pro Val Leu Asn Lys Arg Lys Arg Gly Gly Trp
35 40 45
Cys Leu Asn Gly Pro Val Tyr Ser Ala Asp Ser Arg Thr Gly Arg Thr
50 55 60
Pro Ala Arg Pro Ile Tyr Leu Asp Trp Leu Cys Leu Lys Ala Ser Val
65 70 75 80
Asn Pro Val Gln Pro Val Ser Leu Arg Arg Ala Arg Ser Gly Ala Leu
85 90 95
Phe Gly Asn Ala Asp Ser
100

<210> 1197
<211> 386
<212> DNA
<213> Homo sapiens

<400> 1197
acgcgtgatg atcatgaaaa tggtacagag cgtctagcag aagtcgcctc tgtgatgggc
60
tggcagcaag atgaaatcat cgttaacgta caaggggatg aacccttttct gcctgttgca
120
cttattcatg ccacggttaa agcgttagcc gatgatgctg aatctgaaat ggccacgatt
180
gcctgtgcga ttgataacgt agcagagctg tttaacccaa atgtagttaa agtcgtttgt
240
gatgaaaaac agcgcgcctt gtatttcagt cgtgcgccta tgccatggga ccgtaatggt
300
tttatggaaa aaacagacga tcaagcgtta ccagcggatt ttcctgcgtt gcgtcatatt
360
ggtccgtatg tttaccgcac gacatn
386

<210> 1198
<211> 128
<212> PRT
<213> Homo sapiens

<400> 1198
Thr Arg Asp Asp His Glu Asn Gly Thr Glu Arg Leu Ala Glu Val Ala

```
 1               5                  10                  15
Ser Val Met Gly Trp Gln Gln Asp Glu Ile Ile Val Asn Val Gln Gly
            20                  25                  30
Asp Glu Pro Phe Leu Pro Val Ala Leu Ile His Ala Thr Val Lys Ala
        35                  40                  45
Leu Ala Asp Asp Ala Glu Ser Glu Met Ala Thr Ile Ala Cys Ala Ile
    50                  55                  60
Asp Asn Val Ala Glu Leu Phe Asn Pro Asn Val Val Lys Val Val Cys
65                  70                  75                  80
Asp Glu Lys Gln Arg Ala Leu Tyr Phe Ser Arg Ala Pro Met Pro Trp
                85                  90                  95
Asp Arg Asn Gly Phe Met Glu Lys Thr Asp Asp Gln Ala Leu Pro Ala
            100                 105                 110
Asp Phe Pro Ala Leu Arg His Ile Gly Pro Tyr Val Tyr Arg Thr Thr
        115                 120                 125
```

<210> 1199
<211> 318
<212> DNA
<213> Homo sapiens

<400> 1199
acgcgttcag cgtcatgtac agccccgggc cggtcaattt gatgggcctc aatgccgggc
60
ttacgggcaa attgcgtcgc tccagcggtt tctacatcgg cgtggggtgc gcgatgctgc
120
tgatggtcgg gctggttggg ctcaccggcg aagcgatcat ctcccaggcg gcgctgccgt
180
atatttcttt gattggcggg gtgtacacgc tgtacctcgc ctaccaggtg ttcaccgcac
240
gtaccgaagt ggatgacgcc ccaagcgcgc ctgccaagac cttgaccttc tggaatggcc
300
tggtgatcca gttgctcc
318

<210> 1200
<211> 101
<212> PRT
<213> Homo sapiens

<400> 1200

```
Met Tyr Ser Pro Gly Pro Val Asn Leu Met Gly Leu Asn Ala Gly Leu
 1               5                  10                  15
Thr Gly Lys Leu Arg Arg Ser Ser Gly Phe Tyr Ile Gly Val Gly Cys
            20                  25                  30
Ala Met Leu Leu Met Val Gly Leu Val Gly Leu Thr Gly Glu Ala Ile
        35                  40                  45
Ile Ser Gln Ala Ala Leu Pro Tyr Ile Ser Leu Ile Gly Gly Val Tyr
    50                  55                  60
Thr Leu Tyr Leu Ala Tyr Gln Val Phe Thr Ala Arg Thr Glu Val Asp
65                  70                  75                  80
Asp Ala Pro Ser Ala Pro Ala Lys Thr Leu Thr Phe Trp Asn Gly Leu
                85                  90                  95
Val Ile Gln Leu Leu
```

100

<210> 1201
<211> 360
<212> DNA
<213> Homo sapiens

<400> 1201
gtcgacgcac aactccagct ggtcgctccc aacagcccga acatcccccc ttatcgcgat
60
atgatcctca ccgtgctgcg catggccaag gatgaccgca accgttggaa tgcaaaaatc
120
acgctgcagg cgatccgcga gctggataac gccttccgcg tgctggaaca gttcaagggc
180
cgccgcaagg tcacggtgtt tggctcggcg cgcacgccgg tcgaaagccc gctgtacgcc
240
ttggcaaggg aagtcggcac gctgctggcg caatccgacc tgatggtgat caccggcggt
300
ggcggcggca tcatggccgc tgcccacgag ggcgcaaggt ctggaacaca gcctgggggt
360

<210> 1202
<211> 120
<212> PRT
<213> Homo sapiens

<400> 1202
Val Asp Ala Gln Leu Gln Leu Val Ala Pro Asn Ser Pro Asn Ile Pro
1 5 10 15
Leu Tyr Arg Asp Met Ile Leu Thr Val Leu Arg Met Ala Lys Asp Asp
20 25 30
Arg Asn Arg Trp Asn Ala Lys Ile Thr Leu Gln Ala Ile Arg Glu Leu
35 40 45
Asp Asn Ala Phe Arg Val Leu Glu Gln Phe Lys Gly Arg Arg Lys Val
50 55 60
Thr Val Phe Gly Ser Ala Arg Thr Pro Val Glu Ser Pro Leu Tyr Ala
65 70 75 80
Leu Ala Arg Glu Val Gly Thr Leu Leu Ala Gln Ser Asp Leu Met Val
85 90 95
Ile Thr Gly Gly Gly Gly Gly Ile Met Ala Ala Ala His Glu Gly Ala
100 105 110
Arg Ser Gly Thr Gln Pro Gly Gly
115 120

<210> 1203
<211> 477
<212> DNA
<213> Homo sapiens

<400> 1203
ccggatatgg cagctcgact tcattcgacc agagttcttg gaacatttgg ctatcatgca
60
cctgagtatg caatgactgg acaacttagc tctaagagtg acgtttacag ttttggagtt
120

ggtcttctgg agctcctgac tggaagaaag cctgtggatc ttccattacc aagaggacag
180
caaagtcttg tgacatgggc aactccacgg ctttgtgaag ataaagttag gcaatgcgtt
240
gattcaagac ttggagtaga atatcctcct aaatccgttg caaagtttgc agctgttgct
300
gcactgtgtg tgcaatatga agctgacttt cgacccaaca tgagcatcgt ggtgaaggcg
360
cttcagcccc tgctgaatgc acgtgcatcc aacaaccctg gatgaatgaa tgaatgactg
420
ccgttgcttt tccctgacga gagtatctga atcagacaat catgtagcat tgaattc
477

<210> 1204
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1204
Pro Asp Met Ala Ala Arg Leu His Ser Thr Arg Val Leu Gly Thr Phe
1 5 10 15
Gly Tyr His Ala Pro Glu Tyr Ala Met Thr Gly Gln Leu Ser Ser Lys
20 25 30
Ser Asp Val Tyr Ser Phe Gly Val Gly Leu Leu Glu Leu Leu Thr Gly
35 40 45
Arg Lys Pro Val Asp Leu Pro Leu Pro Arg Gly Gln Gln Ser Leu Val
50 55 60
Thr Trp Ala Thr Pro Arg Leu Cys Glu Asp Lys Val Arg Gln Cys Val
65 70 75 80
Asp Ser Arg Leu Gly Val Glu Tyr Pro Pro Lys Ser Val Ala Lys Phe
85 90 95
Ala Ala Val Ala Ala Leu Cys Val Gln Tyr Glu Ala Asp Phe Arg Pro
100 105 110
Asn Met Ser Ile Val Val Lys Ala Leu Gln Pro Leu Leu Asn Ala Arg
115 120 125
Ala Ser Asn Asn Pro Gly
130

<210> 1205
<211> 407
<212> DNA
<213> Homo sapiens

<400> 1205
acgcgttgcc attgaagact ggcaattaca cgatttacac atcattgatg ctgcagttga
60
tgtgcacagg gaaacactag ctaccgtgca gcaggaaatg atgggagaaa tcagccatgg
120
taacaagaac caagccatcc tggacacaga cggccggggt tgtgcgaacg gaacgttagt
180
ctatcaatgt gttgcggaac gattcaaggg atgctggccc cccccatcac ttgcccaatc
240
aagatgtgga gggaatctgt ctgcgcagaa cctggatctc gtggttgtac gacgttgtcc
300

ccttctcgct cggacgccgc tcatgctccg ccacgtcgct gagcgagtga caaggtatcc
360
tgggaccatg cgtatggttt caactgaagc gctggcgaat cgtaaan
407

<210> 1206
<211> 103
<212> PRT
<213> Homo sapiens

<400> 1206
Met Met Gly Glu Ile Ser His Gly Asn Lys Asn Gln Ala Ile Leu Asp
1 5 10 15
Thr Asp Gly Arg Gly Cys Ala Asn Gly Thr Leu Val Tyr Gln Cys Val
20 25 30
Ala Glu Arg Phe Lys Gly Cys Trp Pro Pro Pro Ser Leu Ala Gln Ser
35 40 45
Arg Cys Gly Gly Asn Leu Ser Ala Gln Asn Leu Asp Leu Val Val Val
50 55 60
Arg Arg Cys Pro Leu Leu Ala Arg Thr Pro Leu Met Leu Arg His Val
65 70 75 80
Ala Glu Arg Val Thr Arg Tyr Pro Gly Thr Met Arg Met Val Ser Thr
85 90 95
Glu Ala Leu Ala Asn Arg Lys
100

<210> 1207
<211> 292
<212> DNA
<213> Homo sapiens

<400> 1207
gctagcatgt cacttttttc ttcagtagat ggcactggag agacattgca ggatgaagag
60
gcttgccttc attcctatgt gctttcccgt ccttgcttct ccagccatgt gtgggacaac
120
caggggtgct caccacctag tgagtttcag ggacactcca catgtcccag caagtcttat
180
cagcatctta gctggcttct caacaagact cagtggcacc cctgtggatg tctcccatca
240
agtttcatta gtgccccagg gggagactcc cagaaagttt cagcagcacc ac
292

<210> 1208
<211> 95
<212> PRT
<213> Homo sapiens

<400> 1208
Met Ser Leu Phe Ser Ser Val Asp Gly Thr Gly Glu Thr Leu Gln Asp
1 5 10 15
Glu Glu Ala Cys Leu His Ser Tyr Val Leu Ser Arg Pro Cys Phe Ser
20 25 30
Ser His Val Trp Asp Asn Gln Gly Cys Ser Pro Pro Ser Glu Phe Gln

```
        35                  40                  45
Gly His Ser Thr Cys Pro Ser Lys Ser Tyr Gln His Leu Ser Trp Leu
    50                  55                  60
Leu Asn Lys Thr Gln Trp His Pro Cys Gly Cys Leu Pro Ser Ser Phe
65                  70                  75                  80
Ile Ser Ala Pro Gly Gly Asp Ser Gln Lys Val Ser Ala Ala Pro
                85                  90                  95
```

<210> 1209
<211> 431
<212> DNA
<213> Homo sapiens

<400> 1209
ttggttccta taatggcggt agcttacatt tttgctggta tcattatttt gttaatgcat
60
gccagtgaag ttattccggc aatatcaact attgtcgagt atgcctttac gccagcttct
120
gcgcagggtg gttttgctgg tgcaacggta tggatggcga ttcgttttgg tgttgcccgt
180
ggtgtatttt caaatgaggc aggtttaggt tcggcgccga tcgctcatgc cagtgcacaa
240
actaatgaac cggttcgcca agggttggtg gcgatgttag gtactttcct tgatacactt
300
attatttgta caggtttagt gattgttatt tctggtgctt ggacagaagg attgtcgggt
360
gctgcgttaa catctgctgc atttaatctg gcgttacctg gttgggggggg atacttagtc
420
gctatcagct g
431

<210> 1210
<211> 143
<212> PRT
<213> Homo sapiens

<400> 1210
```
Leu Val Pro Ile Met Ala Val Ala Tyr Ile Phe Ala Gly Ile Ile Ile
 1               5                  10                  15
Leu Leu Met His Ala Ser Glu Val Ile Pro Ala Ile Ser Thr Ile Val
            20                  25                  30
Glu Tyr Ala Phe Thr Pro Ala Ser Ala Gln Gly Gly Phe Ala Gly Ala
        35                  40                  45
Thr Val Trp Met Ala Ile Arg Phe Gly Val Ala Arg Gly Val Phe Ser
    50                  55                  60
Asn Glu Ala Gly Leu Gly Ser Ala Pro Ile Ala His Ala Ser Ala Gln
65                  70                  75                  80
Thr Asn Glu Pro Val Arg Gln Gly Leu Val Ala Met Leu Gly Thr Phe
                85                  90                  95
Leu Asp Thr Leu Ile Ile Cys Thr Gly Leu Val Ile Val Ile Ser Gly
            100                 105                 110
Ala Trp Thr Glu Gly Leu Ser Gly Ala Ala Leu Thr Ser Ala Ala Phe
        115                 120                 125
Asn Leu Ala Leu Pro Gly Trp Gly Gly Tyr Leu Val Ala Ile Ser
```

130 135 140

<210> 1211
<211> 480
<212> DNA
<213> Homo sapiens

<400> 1211
gaggagggac gagaggctgg tgagatggag tccagcaccc tgcaggagag ccccagggcc
60
agagccgaag ctgtgcttct ccatgagatg gatgaagatg atctggccaa tgccctgatc
120
tggcctgaga ttcaacagga gctgaaaatc attgaatctg aggaggagct ctcatcgttg
180
ccacctcctg ctctgaagac cagcccaatt cagcctattc tcgagtcgag tctggggccc
240
tttattccct cagagcctcc tgggagcttg ccttgtggct ccttccctgc tccagtctcc
300
acccctctgg aggtgtggac tagggatcca gccaatcaga gcacacaggg ggcttccaca
360
gcagccagca gagagaagcc ggaacctgag cagggcctgc acccagacct cgccagcctg
420
gctcctctgg aaatagttcc ttttgagaag gcatctccag aggctggagt gtgctcgcga
480

<210> 1212
<211> 160
<212> PRT
<213> Homo sapiens

<400> 1212
Glu Glu Gly Arg Glu Ala Gly Glu Met Glu Ser Ser Thr Leu Gln Glu
1 5 10 15
Ser Pro Arg Ala Arg Ala Glu Ala Val Leu Leu His Glu Met Asp Glu
20 25 30
Asp Asp Leu Ala Asn Ala Leu Ile Trp Pro Glu Ile Gln Gln Glu Leu
35 40 45
Lys Ile Ile Glu Ser Glu Glu Glu Leu Ser Ser Leu Pro Pro Pro Ala
50 55 60
Leu Lys Thr Ser Pro Ile Gln Pro Ile Leu Glu Ser Ser Leu Gly Pro
65 70 75 80
Phe Ile Pro Ser Glu Pro Pro Gly Ser Leu Pro Cys Gly Ser Phe Pro
85 90 95
Ala Pro Val Ser Thr Pro Leu Glu Val Trp Thr Arg Asp Pro Ala Asn
100 105 110
Gln Ser Thr Gln Gly Ala Ser Thr Ala Ala Ser Arg Glu Lys Pro Glu
115 120 125
Pro Glu Gln Gly Leu His Pro Asp Leu Ala Ser Leu Ala Pro Leu Glu
130 135 140
Ile Val Pro Phe Glu Lys Ala Ser Pro Glu Ala Gly Val Cys Ser Arg
145 150 155 160

<210> 1213
<211> 1141

<212> DNA
<213> Homo sapiens

<400> 1213
nntcatgatg gcggcctggt gtgtgggtat gtccacgatg ggcgcgtcac gcgtgtcgcc
60
cgtgatgctc aggggcgggt taccgggata gaggggccat cagggcgttg gagttacggc
120
tacaacgagg ctgggtcact catcagcgcg acggggcccc gcacacaaca taactggact
180
cacgacgcct atggccggct caccagccac gccacatccg gaaccgacac caccttcgcc
240
tgggaccagg aaggccacct ggcgcagacg tgtacgcgtg cacacgggca tgccactgcc
300
acccagtatc gctatgacgc agcgggacgg cgcgtcagtg cgaccagctc agacggccag
360
gaggagcgtt actcctggga tggacggggt tggctgtctg acatcaccac cgacgccacg
420
accgtatcga ctcacgtcga tgcattgggg cgcgccagtc gtatcaccac taagggccag
480
caggtacgag tggactggga cctcgtgacc ggagccccca cctcgattga tggtcgtcct
540
gtgcttcccc tgcccggagg acgcatcctc ggcgccacac ccatcggcga taccaaccta
600
tggcgtgagg tcatgcccac cgaccctgac aacccttacc agcccgccac ggccactatt
660
gagggtgtcc ccgagacgat caggatggcc gggaacacgc tagtggttga tggtcaccct
720
tggtgggggc gcgcctctac gacccaacta ccaccacctt cttgtctcct gacccgttaa
780
ccccgcccgc cggcgcgcta tgggccaaca acccctacga ctacgccaac aacaaccccc
840
tcaccctcac cgatcctctc gggacccacc ccgtcaccga cgaccaactg gcactcctca
900
cccaccccat cggcacactc gcacactacg tcgccaactc cgtcagcaca ctcgtgcatc
960
acatcaccga tccgatcagc cactggtggg ccacccacaa agaccggatc ctctcccggg
1020
acttcctgat cggtgccggc ctcgtcatcg gcggtatcgc gtagcggcca cgggcgtagg
1080
aggacccctc ctagccgcgg ccatttccgg gggactcatc tcaggcggct tttccgctag
1140
c
1141

<210> 1214
<211> 259
<212> PRT
<213> Homo sapiens

<400> 1214
Xaa His Asp Gly Gly Leu Val Cys Gly Tyr Val His Asp Gly Arg Val
 1   5   10   15
Thr Arg Val Ala Arg Asp Ala Gln Gly Arg Val Thr Gly Ile Glu Gly

```
            20                  25                  30
Pro Ser Gly Arg Trp Ser Tyr Gly Tyr Asn Glu Ala Gly Ser Leu Ile
        35                  40                  45
Ser Ala Thr Gly Pro Arg Thr Gln His Asn Trp Thr His Asp Ala Tyr
    50                  55                  60
Gly Arg Leu Thr Ser His Ala Thr Ser Gly Thr Asp Thr Thr Phe Ala
65                  70                  75                  80
Trp Asp Gln Glu Gly His Leu Ala Gln Thr Cys Thr Arg Ala His Gly
                85                  90                  95
His Ala Thr Ala Thr Gln Tyr Arg Tyr Asp Ala Ala Gly Arg Arg Val
            100                 105                 110
Ser Ala Thr Ser Ser Asp Gly Gln Glu Glu Arg Tyr Ser Trp Asp Gly
        115                 120                 125
Arg Gly Trp Leu Ser Asp Ile Thr Thr Asp Ala Thr Thr Val Ser Thr
    130                 135                 140
His Val Asp Ala Leu Gly Arg Ala Ser Arg Ile Thr Thr Lys Gly Gln
145                 150                 155                 160
Gln Val Arg Val Asp Trp Asp Leu Val Thr Gly Ala Pro Thr Ser Ile
                165                 170                 175
Asp Gly Arg Pro Val Leu Pro Leu Pro Gly Gly Arg Ile Leu Gly Ala
            180                 185                 190
Thr Pro Ile Gly Asp Thr Asn Leu Trp Arg Glu Val Met Pro Thr Asp
        195                 200                 205
Pro Asp Asn Pro Tyr Gln Pro Ala Thr Ala Thr Ile Glu Gly Val Pro
    210                 215                 220
Glu Thr Ile Arg Met Ala Gly Asn Thr Leu Val Val Asp Gly His Pro
225                 230                 235                 240
Trp Trp Gly Arg Ala Ser Thr Thr Gln Leu Pro Pro Pro Ser Cys Leu
                245                 250                 255
Leu Thr Arg
```

<210> 1215
<211> 317
<212> DNA
<213> Homo sapiens

<400> 1215
acgcgttcgc tgcagatcga gtcgccggtg agctcgatct acctgtggat gtactacgtg
60
ggcgtgccga catccggcat cgggggggat cccaacctgc ttacctttta ttggaaccgc
120
ccccggggtc aacccggcca tcaccgggag aacgccgctc ctcggagggg gtgttctcgc
180
agtcgccggc gtgggtgcgt ggaagaagta ccgcggcacg accttcggcg ggctgctccc
240
gtcgctgtcc ctcggcctcg tgctcgcgtt catcgtgctg aacaaggtcg gctcgccgca
300
gtacatcgcc tggatcn
317

<210> 1216
<211> 102
<212> PRT

<213> Homo sapiens

<400> 1216
Met Tyr Cys Gly Glu Pro Thr Leu Phe Ser Thr Met Asn Ala Ser Thr
1 5 10 15
Arg Pro Arg Asp Ser Asp Gly Ser Ser Pro Pro Lys Val Val Pro Arg
20 25 30
Tyr Phe Phe His Ala Pro Thr Pro Ala Thr Ala Arg Thr Pro Pro Pro
35 40 45
Arg Ser Gly Val Leu Pro Val Met Ala Gly Leu Thr Pro Gly Ala Val
50 55 60
Pro Ile Lys Gly Lys Gln Val Gly Ile Pro Pro Asp Ala Gly Cys Arg
65 70 75 80
His Ala His Val Val His Pro Gln Val Asp Arg Ala His Arg Arg Leu
85 90 95
Asp Leu Gln Arg Thr Arg
100

<210> 1217
<211> 548
<212> DNA
<213> Homo sapiens

<400> 1217
nacgcgtggg ttgacgcgct attaaacgat aagagcaaaa aaacatttcc tcatttatta
60
cgttgtcggg tgaatgatgt ttctggtgat agtcagtgga tagagatgcg aggcagtgtg
120
acaggttggg acagccgtca tcgagctcag atggtgagag ggacattcga gcgtattaac
180
catcttattg acgctgaaaa tgaattaatt gcggcccgtg aagatgctca gcgacgagag
240
cttattttat cggctttgct aaataatatt ccagaccctg tttggtctaa agatgaaagc
300
ggtcgttatt tggactgtaa ccatgcgttt tgtctgttta atggtttaga gcagagtgat
360
gttcaggggc aaaaagacag tgaattaaac ttagataata atggtcaata ttatcaagat
420
atgggcggtg aggtattagc gcgaggggag atttttcatg aacattgttg gggtacgcct
480
gcagatggaa gtgacaaccg cttgtttgaa gtatatcgag tccctatcaa agagcctacc
540
gtgaattc
548

<210> 1218
<211> 182
<212> PRT
<213> Homo sapiens

<400> 1218
Xaa Ala Trp Val Asp Ala Leu Leu Asn Asp Lys Ser Lys Lys Thr Phe
1 5 10 15
Pro His Leu Leu Arg Cys Arg Val Asn Asp Val Ser Gly Asp Ser Gln

```
            20                  25                  30
Trp Ile Glu Met Arg Gly Ser Val Thr Gly Trp Asp Ser Arg His Arg
        35                  40                  45
Ala Gln Met Val Arg Gly Thr Phe Glu Arg Ile Asn His Leu Ile Asp
    50                  55                  60
Ala Glu Asn Glu Leu Ile Ala Ala Arg Glu Asp Ala Gln Arg Arg Glu
65                  70                  75                  80
Leu Ile Leu Ser Ala Leu Leu Asn Asn Ile Pro Asp Pro Val Trp Ser
                85                  90                  95
Lys Asp Glu Ser Gly Arg Tyr Leu Asp Cys Asn His Ala Phe Cys Leu
            100                 105                 110
Phe Asn Gly Leu Glu Gln Ser Asp Val Gln Gly Gln Lys Asp Ser Glu
        115                 120                 125
Leu Asn Leu Asp Asn Asn Gly Gln Tyr Tyr Gln Asp Met Gly Gly Glu
    130                 135                 140
Val Leu Ala Arg Gly Glu Ile Phe His Glu His Cys Trp Gly Thr Pro
145                 150                 155                 160
Ala Asp Gly Ser Asp Asn Arg Leu Phe Glu Val Tyr Arg Val Pro Ile
                165                 170                 175
Lys Glu Pro Thr Val Asn
            180
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<210> 1219
<211> 308
<212> DNA
<213> Homo sapiens

<400> 1219
acgcgtgaag ggaggaatac agatggagaa atgggtccac caaaaaatga tgagggtacc
60
tccagagaaa attaccaaga ccattctgtt agtattttcc agctccacag gcctttggaa
120
gttcccagac caccctccct cttttcaaac taaaacaggg atggctctta accaccaccc
180
aaaggcaagg ggggtcttaa aacccaaacc aagtggggca ggggccagcc tcttcaggag
240
ggcccaaccc tgcagcctct gcccatttgg gaaagaccgt gagttggaat tatgggtcgg
300
tgggggggc
308

<210> 1220
<211> 95
<212> PRT
<213> Homo sapiens

<400> 1220

```
Met Glu Lys Trp Val His Gln Lys Met Met Arg Val Pro Pro Glu Lys
 1               5                  10                  15
Ile Thr Lys Thr Ile Leu Leu Val Phe Ser Ser Ser Thr Gly Leu Trp
            20                  25                  30
Lys Phe Pro Asp His Pro Pro Ser Phe Gln Thr Lys Thr Gly Met Ala
        35                  40                  45
Leu Asn His His Pro Lys Ala Arg Gly Val Leu Lys Pro Lys Pro Ser
```

```
    50                  55                  60
Gly Ala Gly Ala Ser Leu Phe Arg Arg Ala Gln Pro Cys Ser Leu Cys
65                  70                  75                  80
Pro Phe Gly Lys Asp Arg Glu Leu Glu Leu Trp Val Gly Gly Gly
                85                  90                  95
```

<210> 1221
<211> 569
<212> DNA
<213> Homo sapiens

<400> 1221
gcgcgccagg ggcaggtagc ctgtggcagg tgaggctgcg tgtggggtgt gctcccagag
60
gcccgtccag gaaagctgca cctcagagaa gcagtttcct tccttacctg ggaagtttct
120
tctgtaacac gttaagcccc acaggtaagg cctgatcccc cctggacggc tcccctctcc
180
agtgttccca gtctggaggt antcttttct aagccatcct ctcagaatgt gatgggtacc
240
aggatgcaca cccggtggcc ctgtggtgtg aggcctcagc aaacacggtc agaagatgaa
300
cacacagaga cccgcccgtc ggaaggagag gagggagcgg atacggaggc ccacgtgcca
360
gaagggtccc ttgcagtggt gtggttatgt gcctgcaatc ccagagtgtc ctcgaaggac
420
ctcagatcta acgagctcag ccggcagctg cacgtgggac cagccctctg agcttcactt
480
gttttcctct gtgccatcag aaaccaatac gaagataaaa tgggaaaaaa aaaaatccca
540
ttcacggcac agcctgccga gaaacgcgt
569

<210> 1222
<211> 91
<212> PRT
<213> Homo sapiens

<400> 1222
```
Met Asn Thr Gln Arg Pro Ala Arg Arg Lys Glu Arg Arg Glu Arg Ile
 1               5                  10                  15
Arg Arg Pro Thr Cys Gln Lys Gly Pro Leu Gln Trp Cys Gly Tyr Val
            20                  25                  30
Pro Ala Ile Pro Glu Cys Pro Arg Arg Thr Ser Asp Leu Thr Ser Ser
        35                  40                  45
Ala Gly Ser Cys Thr Trp Asp Gln Pro Ser Glu Leu His Leu Phe Ser
    50                  55                  60
Ser Val Pro Ser Glu Thr Asn Thr Lys Ile Lys Trp Glu Lys Lys Lys
65                  70                  75                  80
Ser His Ser Arg His Ser Leu Pro Arg Asn Ala
                85                  90
```

<210> 1223
<211> 450

<212> DNA
<213> Homo sapiens

<400> 1223
aagcttgctc aggctagtgc cgacgctgct gctctcaaac tcgtcgatgc ccaccggttg
60
ttgtgcgctc accgagaggg gccatacggg gtagacgagt ggtctcagcg catggttact
120
gtactttcag atgtgttgcc tggtgttggc caaggccggt gggttctcgg cgaaactgca
180
atagtaacgc ataacctcgc acaattggga gtcaataacg gtgattgcgg ggtcatcgtt
240
gaaacaaggc ccgtccccac gatagctcta ccgggacccg gtggagtccc cagacggttg
300
ccctgttccc tcatcccatc gctgcaaccc ttacaggcga tgacgattca caaagcgcag
360
ggcagccaat tcacggacgt aacggtggtc ctgccaccac ccgactcgcc cctcctctct
420
cgtgagttgc tctataccgc catcacgcgt
450

<210> 1224
<211> 150
<212> PRT
<213> Homo sapiens

<400> 1224
Lys Leu Ala Gln Ala Ser Ala Asp Ala Ala Ala Leu Lys Leu Val Asp
 1   5   10   15
Ala His Arg Leu Leu Cys Ala His Arg Glu Gly Pro Tyr Gly Val Asp
            20   25   30
Glu Trp Ser Gln Arg Met Val Thr Val Leu Ser Asp Val Leu Pro Gly
        35   40   45
Val Gly Gln Gly Arg Trp Val Leu Gly Glu Thr Ala Ile Val Thr His
    50   55   60
Asn Leu Ala Gln Leu Gly Val Asn Asn Gly Asp Cys Gly Val Ile Val
65   70   75   80
Glu Thr Arg Pro Val Pro Thr Ile Ala Leu Pro Gly Pro Gly Gly Val
                85   90   95
Pro Arg Arg Leu Pro Cys Ser Leu Ile Pro Ser Leu Gln Pro Leu Gln
            100   105   110
Ala Met Thr Ile His Lys Ala Gln Gly Ser Gln Phe Thr Asp Val Thr
        115   120   125
Val Val Leu Pro Pro Pro Asp Ser Pro Leu Leu Ser Arg Glu Leu Leu
    130   135   140
Tyr Thr Ala Ile Thr Arg
145   150

<210> 1225
<211> 436
<212> DNA
<213> Homo sapiens

<400> 1225

ncccatcccc cacccgggat ggtgaacact gggatggcca cttgggagct caaagtgttg
60
tcagtgggag gacaaggtcc tcaattcctg gcacattggc ccagagaagt catgaaaacc
120
caaagccccc cgaaagtaag aagtagaaaa aaacccgacc ccgaccagat gaagggacct
180
gggaagtttt tggaaaagag actgctgaag tgtctccttg caggcatcac cgtgagctgg
240
ggctttgcac acagcatctt catggctttc cacaatgatc ccagaactga tccagagaaa
300
cccagggatc aggggttgac ccgaccctgt catcatccca ttctacaaat gaggacactg
360
aggcctggtg aaaagggagg ggtggatgga accaggtggc ctggctctaa gacccagagg
420
ctggagtgtg ctcatg
436

<210> 1226
<211> 139
<212> PRT
<213> Homo sapiens

<400> 1226
Met Val Asn Thr Gly Met Ala Thr Trp Glu Leu Lys Val Leu Ser Val
1 5 10 15
Gly Gly Gln Gly Pro Gln Phe Leu Ala His Trp Pro Arg Glu Val Met
20 25 30
Lys Thr Gln Ser Pro Pro Lys Val Arg Ser Arg Lys Lys Pro Asp Pro
35 40 45
Asp Gln Met Lys Gly Pro Gly Lys Phe Leu Glu Lys Arg Leu Leu Lys
50 55 60
Cys Leu Leu Ala Gly Ile Thr Val Ser Trp Gly Phe Ala His Ser Ile
65 70 75 80
Phe Met Ala Phe His Asn Asp Pro Arg Thr Asp Pro Glu Lys Pro Arg
85 90 95
Asp Gln Gly Leu Thr Arg Pro Cys His His Pro Ile Leu Gln Met Arg
100 105 110
Thr Leu Arg Pro Gly Glu Lys Gly Gly Val Asp Gly Thr Arg Trp Pro
115 120 125
Gly Ser Lys Thr Gln Arg Leu Glu Cys Ala His
130 135

<210> 1227
<211> 756
<212> DNA
<213> Homo sapiens

<400> 1227
gttgagttcc acgtgaaaca aaatgcactt tacaatagaa tgacgattcg tatcaaagat
60
aatggtattg gaataccgat taacaaggta gataaaatct ttgatagatt ctaccgtgtc
120
gacaaagcac gtacacgtaa gatgggcggt acaggactag gtctagctat ttccaaagag
180

attgtcgaag cacataatgg ccgtatttgg gcaaatagtg tcgaaggaca aggtacatct
240
atcttcatta ccctaccatg tgaaattatt gaagatggtg attgggatga atagtaaaga
300
atacatcaaa acgattatcc tgatactact tgtattaatg agtatcgtct taacctacat
360
ggtatggaac ttctcacctg atctatcaaa tgctgatagt acgtcatcag ataataagaa
420
agataattct aaacctattg gaaaaccaat gagtgcgaaa acggataaaa ccatcacacc
480
atttcaaatc gttcaatcta atggcgaaaa aacaaaaggt atgccagcaa caggtcatgc
540
agtatctcaa attttaagcc cattaaaaga taaaaatgtt gattcagtac aacatttaaa
600
acgaaatcat aacttaatta ttcctgaatt aagtgataac tttatcgttc ttgatttcac
660
atatgattta ccgttatcaa tttacttaag ccaagtatta aacatagatg ctaagacacc
720
taatcatttt aactttaatc gactactgat tgatca
756

<210> 1228
<211> 97
<212> PRT
<213> Homo sapiens

<400> 1228
Val Glu Phe His Val Lys Gln Asn Ala Leu Tyr Asn Arg Met Thr Ile
1 5 10 15
Arg Ile Lys Asp Asn Gly Ile Gly Ile Pro Ile Asn Lys Val Asp Lys
20 25 30
Ile Phe Asp Arg Phe Tyr Arg Val Asp Lys Ala Arg Thr Arg Lys Met
35 40 45
Gly Gly Thr Gly Leu Gly Leu Ala Ile Ser Lys Glu Ile Val Glu Ala
50 55 60
His Asn Gly Arg Ile Trp Ala Asn Ser Val Glu Gly Gln Gly Thr Ser
65 70 75 80
Ile Phe Ile Thr Leu Pro Cys Glu Ile Ile Glu Asp Gly Asp Trp Asp
85 90 95
Glu

<210> 1229
<211> 377
<212> DNA
<213> Homo sapiens

<400> 1229
nacgcgtcgt gaacgcggcg tcaacagctt ttcggatata cctctgagga gcccaagatg
60
cttgtcgccc ccatggcaaa ccaggggggtc gaggccactg gagcgatggg aaccgacacc
120
ccgctggccg tgctatctaa ctgtccgcgg atgctctggg actatttcag tcagcttttc
180

gctcaggtaa ccaatccgcc cttggacgct atccgcgagg agcttgtcac ctccctgacg
240
ggcaccatcg gcccggaggc gaacttgctt gagcctggcc cggaatcatg tcggcaagtg
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gtcgtcaact acccgatcat cgattccgac cagcttgcca agatcattca catcgacgct
360
gacggggagc atccgga
377

<210> 1230
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1230
Thr Arg Arg Gln Gln Leu Phe Gly Tyr Thr Ser Glu Glu Pro Lys Met
1 5 10 15
Leu Val Ala Pro Met Ala Asn Gln Gly Val Glu Ala Thr Gly Ala Met
20 25 30
Gly Thr Asp Thr Pro Leu Ala Val Leu Ser Asn Cys Pro Arg Met Leu
35 40 45
Trp Asp Tyr Phe Ser Gln Leu Phe Ala Gln Val Thr Asn Pro Pro Leu
50 55 60
Asp Ala Ile Arg Glu Glu Leu Val Thr Ser Leu Thr Gly Thr Ile Gly
65 70 75 80
Pro Glu Ala Asn Leu Leu Glu Pro Gly Pro Glu Ser Cys Arg Gln Val
85 90 95
Val Val Asn Tyr Pro Ile Ile Asp Ser Asp Gln Leu Ala Lys Ile Ile
100 105 110
His Ile Asp Ala Asp Gly Glu His Pro
115 120

<210> 1231
<211> 351
<212> DNA
<213> Homo sapiens

<400> 1231
aaatttcatt taaaatcaat tgattgctta ataaggcag ttcatctgct gcgccaggag
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cggaagtaag gagtttttat ggcggtttta atcaccggag acgccggtta tatcggttct
120
cacactgttc tggctttgtt agaacatggc gaagatgttg tagtgttaga taatttatca
180
aactcttccg atgagtctct gcgtcgcgtt gagaaactcg cgggtagaag tgctcagttc
240
taccaaggcg atatcttgga tgctgagtgt ctgcatcgca tcttcgaggc tcacgacatc
300
tcggctgtga tccattttgc tgggctaaag ggtgtcggag agtcgacgcg t
351

<210> 1232
<211> 91
<212> PRT

<213> Homo sapiens

<400> 1232

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Met Ala Val Leu Ile Thr Gly Asp Ala Gly Tyr Ile Gly Ser His Thr
 1               5                  10                  15
Val Leu Ala Leu Leu Glu His Gly Glu Asp Val Val Val Leu Asp Asn
            20                  25                  30
Leu Ser Asn Ser Ser Asp Glu Ser Leu Arg Arg Val Glu Lys Leu Ala
        35                  40                  45
Gly Arg Ser Ala Gln Phe Tyr Gln Gly Asp Ile Leu Asp Ala Glu Cys
    50                  55                  60
Leu His Arg Ile Phe Glu Ala His Asp Ile Ser Ala Val Ile His Phe
65                  70                  75                  80
Ala Gly Leu Lys Gly Val Gly Glu Ser Thr Arg
                85                  90
```

<210> 1233
<211> 4982
<212> DNA
<213> Homo sapiens

<400> 1233

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nnggcttaag cagtggtaac aacgcagagt acgcggggtg atggcctccc tgaaattaaa
60
catttctatt agtggcttcc cgttaatctc atccttctta gatcaaacct cgttatatct
120
cctgcctatc tcttttgcat tccaaagttc agttttatta aatcccaggg tctaagattt
180
tttctttgag aatttatctc cagtgtttct atggaaatta aaaaagaaaa ttaggataat
240
tcaatgtcga aatgttgcat gcatcttttg agaaatttat attttgtagg ttgaaggact
300
tgctttttgg gcagcgtatt tttggaggtg gaatgtagtt attttaataa ccatgtccta
360
attatttata gcttcctgcc tgacacagct cacttcaaga agtgcacaat gtcagaacgt
420
ggaattaagt gggcttgtga atattgtacg tatgaaaact ggccatctgc aatcaagtgt
480
accatgtgtc gtgcccaaag acctagtgga acaattatta cagaagatcc atttaaaagt
540
ggttcaagtg atgttggtag agattgggat ccttccagca ccgaaggagg aagtagtcct
600
ttgatatgtc cagactctag tgcaagacca agggtgaaat cttcgtatag catggaaaat
660
gcaaataagt ggtcatgcca catgtgtaca tatttgaact ggccaagagc aatcagatgt
720
acccagtgct tatcccaacg taggaccagg agtcctacag aatctcctca gtcctcagga
780
tctggctcaa gaccagttgc tttttctgtt gatccttgtg aggaatacaa tgatagaaat
840
aaactgaaca ctaggacaca gcactggact tgctctgttt gcacatatga aaactgggcc
900
aaggctaaaa gatgtgttgt ttgtgatcat cccagaccta ataacattga agcaatagaa
960
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ttggcagaga ctgaagaggc ttcttcaata ataaatgagc aagacagagc tcgatggagg
1020
ggaagttgca gtagtggtaa tagccaaagg agatcacctc ctgctacgaa gcgggactct
1080
gaagtgaaaa tggattttca gaggattgaa ttggctggtg ctgtgggaag caaggaggaa
1140
cttgaagtag actttaaaaa actaaagcaa attaaaaaca ggatgaaaaa gactgattgg
1200
ctcttcctca atgcttgtgt gggggttgta gaaggtgatt tagctgccat agaagcatac
1260
aagtcatcag gaggagacat tgcacgtcag ctcaccgcag atgaagtacg cttgctgaat
1320
cgtccttctg cctttgatgt tggctatact cttgtacact tggctatacg ttttcagagg
1380
caggatatgc tagcaatatt gcttacagag gtgtctcaac aagcagcaaa gtgtattcca
1440
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<210> 1234
<211> 708
<212> PRT
<213> Homo sapiens

<400> 1234

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			20					25					30		
Ser	Gly	Thr	Ile	Ile	Thr	Glu	Asp	Pro	Phe	Lys	Ser	Gly	Ser	Ser	Asp
		35					40					45			
Val	Gly	Arg	Asp	Trp	Asp	Pro	Ser	Ser	Thr	Glu	Gly	Gly	Ser	Ser	Pro
	50					55					60				
Leu	Ile	Cys	Pro	Asp	Ser	Ser	Ala	Arg	Pro	Arg	Val	Lys	Ser	Ser	Tyr
65					70					75					80
Ser	Met	Glu	Asn	Ala	Asn	Lys	Trp	Ser	Cys	His	Met	Cys	Thr	Tyr	Leu
				85					90					95	
Asn	Trp	Pro	Arg	Ala	Ile	Arg	Cys	Thr	Gln	Cys	Leu	Ser	Gln	Arg	Arg
			100					105					110		
Thr	Arg	Ser	Pro	Thr	Glu	Ser	Pro	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Arg
		115					120					125			
Pro	Val	Ala	Phe	Ser	Val	Asp	Pro	Cys	Glu	Glu	Tyr	Asn	Asp	Arg	Asn
	130					135					140				
Lys	Leu	Asn	Thr	Arg	Thr	Gln	His	Trp	Thr	Cys	Ser	Val	Cys	Thr	Tyr

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145                 150                 155                 160
Glu Asn Trp Ala Lys Ala Lys Arg Cys Val Val Cys Asp His Pro Arg
                165                 170                 175
Pro Asn Asn Ile Glu Ala Ile Glu Leu Ala Glu Thr Glu Glu Ala Ser
            180                 185                 190
Ser Ile Ile Asn Glu Gln Asp Arg Ala Arg Trp Arg Gly Ser Cys Ser
        195                 200                 205
Ser Gly Asn Ser Gln Arg Arg Ser Pro Pro Ala Thr Lys Arg Asp Ser
    210                 215                 220
Glu Val Lys Met Asp Phe Gln Arg Ile Glu Leu Ala Gly Ala Val Gly
225                 230                 235                 240
Ser Lys Glu Glu Leu Glu Val Asp Phe Lys Lys Leu Lys Gln Ile Lys
                245                 250                 255
Asn Arg Met Lys Lys Thr Asp Trp Leu Phe Leu Asn Ala Cys Val Gly
            260                 265                 270
Val Val Glu Gly Asp Leu Ala Ala Ile Glu Ala Tyr Lys Ser Ser Gly
        275                 280                 285
Gly Asp Ile Ala Arg Gln Leu Thr Ala Asp Glu Val Arg Leu Leu Asn
    290                 295                 300
Arg Pro Ser Ala Phe Asp Val Gly Tyr Thr Leu Val His Leu Ala Ile
305                 310                 315                 320
Arg Phe Gln Arg Gln Asp Met Leu Ala Ile Leu Leu Thr Glu Val Ser
                325                 330                 335
Gln Gln Ala Ala Lys Cys Ile Pro Ala Met Val Cys Pro Glu Leu Thr
            340                 345                 350
Glu Gln Ile Arg Arg Glu Ile Ala Ala Ser Leu His Gln Arg Lys Gly
        355                 360                 365
Asp Phe Ala Cys Tyr Phe Leu Thr Asp Leu Val Thr Phe Thr Leu Pro
    370                 375                 380
Ala Asp Ile Glu Asp Leu Pro Pro Thr Val Gln Glu Lys Leu Phe Asp
385                 390                 395                 400
Glu Val Leu Asp Arg Asp Val Gln Lys Glu Leu Glu Glu Glu Ser Pro
                405                 410                 415
Ile Ile Asn Trp Ser Leu Glu Leu Ala Thr Arg Leu Asp Ser Arg Leu
            420                 425                 430
Tyr Ala Leu Trp Asn Arg Thr Ala Gly Asp Cys Leu Leu Asp Ser Val
        435                 440                 445
Leu Gln Ala Thr Trp Gly Ile Tyr Asp Lys Asp Ser Val Leu Arg Lys
    450                 455                 460
Ala Leu His Asp Ser Leu His Asp Cys Ser His Trp Phe Tyr Thr Arg
465                 470                 475                 480
Trp Lys Asp Trp Glu Ser Trp Tyr Ser Gln Ser Phe Gly Leu His Phe
                485                 490                 495
Ser Leu Arg Glu Glu Gln Trp Gln Glu Asp Trp Ala Phe Ile Leu Ser
            500                 505                 510
Leu Ala Ser Gln Pro Gly Ala Ser Leu Glu Gln Thr His Ile Phe Val
        515                 520                 525
Leu Ala His Ile Leu Arg Arg Pro Ile Ile Val Tyr Gly Val Lys Tyr
    530                 535                 540
Tyr Lys Ser Phe Arg Gly Glu Thr Leu Gly Tyr Thr Arg Phe Gln Gly
545                 550                 555                 560
Val Tyr Leu Pro Leu Leu Trp Glu Gln Ser Phe Cys Trp Lys Ser Pro
                565                 570                 575
Ile Ala Leu Gly Tyr Thr Arg Gly His Phe Ser Ala Leu Val Ala Met
```

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            580                 585                 590
Glu Asn Asp Gly Tyr Gly Asn Arg Gly Ala Gly Ala Asn Leu Asn Thr
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Asp Asp Asp Val Thr Ile Thr Phe Leu Pro Leu Val Asp Ser Glu Arg
    610                 615                 620
Lys Leu Leu His Val His Phe Leu Ser Ala Gln Glu Leu Gly Asn Glu
625                 630                 635                 640
Glu Gln Gln Glu Lys Leu Leu Arg Glu Trp Leu Asp Cys Cys Val Thr
                645                 650                 655
Glu Gly Gly Val Leu Val Ala Met Gln Lys Ser Ser Arg Arg Arg Asn
            660                 665                 670
His Pro Leu Val Thr Gln Met Val Glu Lys Trp Leu Asp Arg Tyr Arg
        675                 680                 685
Gln Ile Arg Pro Cys Thr Ser Leu Ser Asp Gly Glu Glu Asp Glu Asp
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Asp Glu Asp Glu
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<210> 1235
<211> 383
<212> DNA
<213> Homo sapiens

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120
gacctcctcg ctgagctacc gcccttcctc ggaggcggcg agatgatcga ggtcgtgcgc
180
atggagggat cgacctacgc cgagcctcca catcgttttg aggcaggcac cccgccgatc
240
gcacagctgg ctgccctcgg ggtggccgcc gactacctag atggcatcgg gatgcaggcc
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ggagtgcagc cggagagagg ctg
383

<210> 1236
<211> 127
<212> PRT
<213> Homo sapiens

<400> 1236
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 1               5                  10                  15
Ala Asp Leu Val Ala Phe Thr Gly His Lys Met Cys Gly Pro Thr Gly
            20                  25                  30
Ile Gly Ile Leu Trp Gly Arg Tyr Asp Leu Leu Ala Glu Leu Pro Pro
        35                  40                  45
Phe Leu Gly Gly Gly Glu Met Ile Glu Val Val Arg Met Glu Gly Ser
    50                  55                  60
Thr Tyr Ala Glu Pro Pro His Arg Phe Glu Ala Gly Thr Pro Pro Ile
```

65 70 75 80
Ala Gln Leu Ala Ala Leu Gly Val Ala Ala Asp Tyr Leu Asp Gly Ile
85 90 95
Gly Met Gln Ala Ile Ala Glu His Glu His Glu Leu Ala Ala Arg Met
100 105 110
Leu Glu Asp Tyr Gln Thr Val Lys Gly Val Gln Pro Glu Arg Gly
115 120 125

<210> 1237
<211> 1608
<212> DNA
<213> Homo sapiens

<400> 1237
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acaccagcac attctgactc aacatggcta tacggttgtc atcgctgaag aaaggctcaa
120
tgctggccta gggccggggc tactagaaca aggtgatctg ggctcttggg atctgctcat
180
ttgcctgtct tctaagaaag cagaaggaac accctgtata tccaaggaag tcatgtgcca
240
gttaggttta catcaaaagg caaacagatt accagaaata cagcagccac tttgcagaaa
300
ggaaggatta tgtcaaatag ttagaagatt cccagaactg caacttccag tgagtccctc
360
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420
agtgaagcca cgtgtgtgga aaccagggga ctggagtcgt gaacagctga atgaaacgac
480
agtccttgct ccacatgaaa caatctttcg agccaaagat ctatctgtga ttcttaaagc
540
gtatgtgttg gtgacgtcct taaccccttt gcgtgcattc attcattcga ctggcacagt
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720
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<210> 1238
<211> 458
<212> PRT
<213> Homo sapiens

<400> 1238
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Phe Pro Glu Leu Gln Leu Pro Val Ser Pro Ser Val Cys Leu Asp Gln
35 40 45
Gly Met Gln Leu Lys Pro Ser Thr Ser Ser His Leu Leu Lys Thr Val
50 55 60
Lys Pro Arg Val Trp Lys Pro Gly Asp Trp Ser Arg Glu Gln Leu Asn
65 70 75 80
Glu Thr Thr Val Leu Ala Pro His Glu Thr Ile Phe Arg Ala Lys Asp
85 90 95
Leu Ser Val Ile Leu Lys Ala Tyr Val Leu Val Thr Ser Leu Thr Pro
100 105 110
Leu Arg Ala Phe Ile His Ser Thr Gly Thr Val Trp Asn Pro Pro Lys
115 120 125
Lys Lys Arg Phe Thr Val Lys Leu Gln Thr Phe Phe Glu Thr Phe Leu
130 135 140
Arg Ala Ser Ser Pro Gln Gln Ala Phe Asp Ile Met Lys Glu Ala Ile
145 150 155 160
Gly Lys Leu Leu Leu Ala Ala Glu Val Phe Ser Glu Thr Ser Thr Leu
165 170 175
Gly Pro Lys Thr Phe His Arg Cys Arg Phe Cys Phe Gln Leu Leu Thr
180 185 190
Phe Asp Ile Gly Tyr Gly Ser Phe Met Tyr Pro Val Val Leu Gln Val
195 200 205
His Glu His Leu Asn Phe Gln Asp Tyr Asp Asn Met Asp Phe Glu Asp
210 215 220
Gln Asn Thr Glu Glu Phe Leu Leu Asn Asp Thr Phe Asn Phe Leu Phe
225 230 235 240
Pro Asn Glu Ser Ser Leu Ser Ile Phe Ser Glu Ile Phe Gln Arg Leu
245 250 255
Tyr Arg Ser Asp Val Phe Lys Gly Glu Asn Tyr Gln Lys Glu Leu Asn

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            260                 265                 270
Gln Cys Leu Ser Leu Glu Glu Ile Asn Ser Ile Met Thr Phe Ile Lys
        275                 280                 285
Glu Leu Gly Ser Leu Gly Gln Phe Gln Leu Leu Phe Pro Ser Thr Thr
    290                 295                 300
Pro Gly Ile Gln Ser Leu Met His Glu Phe Tyr Asp Val Ala Asn Pro
305                 310                 315                 320
Val Gly Asn Pro Gly Ser Val Leu Thr Gln Tyr Trp Ser Leu Leu Asn
                325                 330                 335
Val Phe Glu Gln Phe Gln Phe Met Asn Lys Lys Thr Gln Pro His Pro
            340                 345                 350
Leu Glu Trp Asn Ser Phe Thr Glu Asp Lys Asn Ile Glu Lys Pro Gln
        355                 360                 365
Val Pro Phe Asp Ala Ile Glu Asn Lys Lys Ala Ala Val Pro Gln Ile
    370                 375                 380
Lys Asn Glu Asn Lys Glu Ile His Cys Ser Asp Asp Glu Asn Thr Pro
385                 390                 395                 400
Cys His Ile Lys Gln Ile Phe Thr His Pro His Leu Glu Leu Asn Pro
                405                 410                 415
Asp Phe His Pro Lys Ile Lys Asp Tyr Tyr Cys Glu Val Pro Phe Asp
            420                 425                 430
Val Val Thr Val Thr Ile Gly Val Glu Thr Pro Lys Cys Leu Cys Lys
        435                 440                 445
Val His Leu Tyr Glu Gln Ala Gly Pro Ser
    450                 455
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<210> 1239
<211> 447
<212> DNA
<213> Homo sapiens

<400> 1239
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atgcagaagg atttggagaa tattacatcc aaagagataa gaacagagtt ggaaatgcaa
120
atggtgtgca acttgcggga attcaaggaa tttatagaca atgaaatgat agtgatcctt
180
ggtcaaatgg atagccctac acagatattt gagcatgtgt tcctgggctc agaatggaat
240
gcctccaact tagaggactt acagaaccga ggggtacggt atatcttgaa tgtcactcga
300
gagatagata acttttccc aggagtcttt gagtatcata acattcgggt atatgatgaa
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420
aaacatggat ctaaatgcct tgtgcac
447

<210> 1240
<211> 149
<212> PRT
<213> Homo sapiens

<400> 1240
Ile Pro Thr Glu Arg Glu Arg Thr Glu Arg Leu Ile Lys Thr Lys Leu
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Arg Glu Ile Met Met Gln Lys Asp Leu Glu Asn Ile Thr Ser Lys Glu
20 25 30
Ile Arg Thr Glu Leu Glu Met Gln Met Val Cys Asn Leu Arg Glu Phe
35 40 45
Lys Glu Phe Ile Asp Asn Glu Met Ile Val Ile Leu Gly Gln Met Asp
50 55 60
Ser Pro Thr Gln Ile Phe Glu His Val Phe Leu Gly Ser Glu Trp Asn
65 70 75 80
Ala Ser Asn Leu Glu Asp Leu Gln Asn Arg Gly Val Arg Tyr Ile Leu
85 90 95
Asn Val Thr Arg Glu Ile Asp Asn Phe Phe Pro Gly Val Phe Glu Tyr
100 105 110
His Asn Ile Arg Val Tyr Asp Glu Glu Ala Thr Asp Leu Leu Ala Tyr
115 120 125
Trp Asn Asp Thr Tyr Lys Phe Ile Ser Lys Ala Lys Lys His Gly Ser
130 135 140
Lys Cys Leu Val His
145

<210> 1241
<211> 489
<212> DNA
<213> Homo sapiens

<400> 1241
acgcgtgtgc agcgtatcca gcaccgtcct cagaataata gctgtgaaaa ggaggaaggg
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aactaggcag acagaccgac agataggggg aaaccgggat gtttaatgtg tccgaacaag
120
taggaagatc aatgaggcgc gagtgtgtgt gtgtacgtgt gcgcgtgtgt gtgtgagaga
180
gagagaaaga aagaagaaag gtcccgattg caacgtgtca gatcttgcaa ccttcccccc
240
acccaacaca acaaccctca gacacaaaaa caccattgct gactgatacc ccaggtcttc
300
agggttaaag gaaccgtgtg ttggcagcgc aattgtgcag acgctgtaag gccaaaacga
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ggatttgtgt tgtgaggtcg gtggtgcgtt cttttctttc tcttctcgcc tgttttcccg
420
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480
attcatgct
489

<210> 1242
<211> 127
<212> PRT
<213> Homo sapiens

<400> 1242
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Leu Ala Thr Gln Ala Leu Arg Glu Asn Arg Arg Glu Glu Lys Glu Lys
            20                  25                  30
Asn Ala Pro Pro Thr Ser Gln His Lys Ser Ser Phe Trp Pro Tyr Ser
        35                  40                  45
Val Cys Thr Ile Ala Leu Pro Thr His Gly Ser Phe Asn Pro Glu Asp
    50                  55                  60
Leu Gly Tyr Gln Ser Ala Met Val Phe Leu Cys Leu Arg Val Val Val
65                  70                  75                  80
Leu Gly Gly Gly Lys Val Ala Arg Ser Asp Thr Leu Gln Ser Gly Pro
                85                  90                  95
Phe Phe Phe Leu Ser Leu Ser Leu Thr His Thr Arg Ala His Val His
            100                 105                 110
Thr His Thr Arg Ala Ser Leu Ile Phe Leu Leu Val Arg Thr His
        115                 120                 125
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<210> 1243
<211> 390
<212> DNA
<213> Homo sapiens

<400> 1243
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120
gtcctagaga ggcgcgacga gggtttggtg cgtgccgtaa aagtcacgtt tggcgccgaa
180
ccgtctgaca cggaattgta cgggtgggtt agccgtcatg gcaacgcact tatagagcga
240
ttggagtcta ccgctgctgt ccctaccacc cgcagtcccc gagccaagcg actgaacccc
300
aagagggcgt tacgagatgc agcgcgagct gcccaagcac accgtgccag cacgnccgca
360
caggccgcga ttaaggccga tcaggaagct
390

<210> 1244
<211> 130
<212> PRT
<213> Homo sapiens

<400> 1244
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 1               5                  10                  15
Ser Ala Tyr Trp Glu Met Ile Tyr Leu Pro Gly Met Phe Thr Val Tyr
            20                  25                  30
Phe Asp Gly Gln Phe Trp Val Gly Val Leu Glu Arg Arg Asp Glu Gly
        35                  40                  45
Leu Val Arg Ala Val Lys Val Thr Phe Gly Ala Glu Pro Ser Asp Thr
    50                  55                  60
Glu Leu Tyr Gly Trp Val Ser Arg His Gly Asn Ala Leu Ile Glu Arg
65                  70                  75                  80
Leu Glu Ser Thr Ala Ala Val Pro Thr Thr Arg Ser Pro Arg Ala Lys
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85 90 95
Arg Leu Asn Pro Lys Arg Ala Leu Arg Asp Ala Ala Arg Ala Ala Gln
100 105 110
Ala His Arg Ala Ser Thr Xaa Ala Gln Ala Ala Ile Lys Ala Asp Gln
115 120 125
Glu Ala
130

<210> 1245
<211> 339
<212> DNA
<213> Homo sapiens

<400> 1245
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ccacaatcta tgcccgtgac ttttctgagc tccaggagtt ttttagcact gccagacttc
120
tctggagagg aggaggtttc tgccactttt caatttcgaa cttggaataa ggcagggctt
180
ctgctgttca gtgaacttca gctgatttca gggggtatcc tcctctttct gagtgatgga
240
aaacttaagt cgaatctcta ccagccaaga aaattaccca gtgacatcac agcaggtgtc
300
gaattaaatg atgggcagtg gcattctgtc tctttatct
339

<210> 1246
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1246
Ala Lys Gln Gln Lys Pro Gln Ile Ile Ala Met Gly Asn Val Ser Phe
1 5 10 15
Ser Cys Ser Gln Pro Gln Ser Met Pro Val Thr Phe Leu Ser Ser Arg
20 25 30
Ser Phe Leu Ala Leu Pro Asp Phe Ser Gly Glu Glu Glu Val Ser Ala
35 40 45
Thr Phe Gln Phe Arg Thr Trp Asn Lys Ala Gly Leu Leu Leu Phe Ser
50 55 60
Glu Leu Gln Leu Ile Ser Gly Gly Ile Leu Leu Phe Leu Ser Asp Gly
65 70 75 80
Lys Leu Lys Ser Asn Leu Tyr Gln Pro Arg Lys Leu Pro Ser Asp Ile
85 90 95
Thr Ala Gly Val Glu Leu Asn Asp Gly Gln Trp His Ser Val Ser Leu
100 105 110
Ser

<210> 1247
<211> 366
<212> DNA
<213> Homo sapiens

<400> 1247
ttgacctcca acccgggcac gcgcatcctg ccccagatcc cgatggatgg gcatgacctc
60
aacccggtgt ggcgggacgt cggcctgatc gtgcacccgc cgatgctcta catgggctac
120
gtcggtttct ccgtggcctt tgcgtttgcc atcgccgcct tgctcggcgg gcgcctcgat
180
gcggcctggg cgcgctggtc gcggccatgg accattgtgg cctgggcgtt cctcggtatc
240
ggtatcaccc tcggttcgtg gtgggcctac tacgaactcg gctggngcgg ctggtggttc
300
tgggaccccg gggaaaaccc cttcttcatg ccctggctgg ggggcacccc gctgattcac
360
tcgctg
366

<210> 1248
<211> 122
<212> PRT
<213> Homo sapiens

<400> 1248
Leu Thr Ser Asn Pro Gly Thr Arg Ile Leu Pro Gln Ile Pro Met Asp
1 5 10 15
Gly His Asp Leu Asn Pro Val Trp Arg Asp Val Gly Leu Ile Val His
20 25 30
Pro Pro Met Leu Tyr Met Gly Tyr Val Gly Phe Ser Val Ala Phe Ala
35 40 45
Phe Ala Ile Ala Ala Leu Leu Gly Gly Arg Leu Asp Ala Ala Trp Ala
50 55 60
Arg Trp Ser Arg Pro Trp Thr Ile Val Ala Trp Ala Phe Leu Gly Ile
65 70 75 80
Gly Ile Thr Leu Gly Ser Trp Trp Ala Tyr Tyr Glu Leu Gly Trp Xaa
85 90 95
Gly Trp Trp Phe Trp Asp Pro Gly Glu Asn Pro Phe Phe Met Pro Trp
100 105 110
Leu Gly Gly Thr Pro Leu Ile His Ser Leu
115 120

<210> 1249
<211> 374
<212> DNA
<213> Homo sapiens

<400> 1249
acgcgtgtcc tcaacaccct ggcgccca g ctgattgccg tggaaccggt gccggcaatg
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ggcgcgcagt tgagcaagct gctgccggat gtgcacctgg tcaatggcac tgccgaggcc
120
attccactgg aaagcgccgt ggcggatgcg gtggtgtgcg cacaagcctt ccattgttt
180
tccagcgagg cggccctggc ggaaatccat cgggtactca aaccggatgg gcgcctgggg
240

ctggtgtgga atgtgcgcga cgagtcggtg gattgggtcg ccgccattac tcaaatcatc
300
acgccttatg aaggcgacac gccgcgcttt cataccggcc gttggcgcga agccttcact
360
ggcgagtatt tttg
374

<210> 1250
<211> 124
<212> PRT
<213> Homo sapiens

<400> 1250
Thr Arg Val Leu Asn Thr Leu Ala Pro Thr Leu Ile Ala Val Glu Pro
1 5 10 15
Val Pro Ala Met Gly Ala Gln Leu Ser Lys Leu Leu Pro Asp Val His
20 25 30
Leu Val Asn Gly Thr Ala Glu Ala Ile Pro Leu Glu Ser Ala Val Ala
35 40 45
Asp Ala Val Val Cys Ala Gln Ala Phe His Trp Phe Ser Ser Glu Ala
50 55 60
Ala Leu Ala Glu Ile His Arg Val Leu Lys Pro Asp Gly Arg Leu Gly
65 70 75 80
Leu Val Trp Asn Val Arg Asp Glu Ser Val Asp Trp Val Ala Ala Ile
85 90 95
Thr Gln Ile Ile Thr Pro Tyr Glu Gly Asp Thr Pro Arg Phe His Thr
100 105 110
Gly Arg Trp Arg Glu Ala Phe Thr Gly Glu Tyr Phe
115 120

<210> 1251
<211> 742
<212> DNA
<213> Homo sapiens

<400> 1251
accggtctct tcctcggaaa ggcagggccg aggggcttgc ggggcagcca tggaggcgac
60
gcggaggcgg cagcacgtgg gagcgacggg cggcccaggc gcgcagttgg gcgcctcctt
120
ccctgcaggc caggcatggc tctgtgagcg ctgatgaggc tgcccgcacg gctcccttcc
180
acctcgacct ctggttctac ttcacactgc agaactgggt tctggacttt gggcgtccca
240
ttgccatgct ggtattccct ctcgagtggt ttccactcaa caagcccagt gttggggact
300
acttccacat ggcctacaac gtcatcacgc cctttctctt gctcaagctc atcgagcggt
360
ccccccgcac cctgctacgc tccatcacgt acgtgagcat catcatcttc atcatgggtg
420
ccagcatcca cctggtgggt gactctgtca accaccgcct gctcttcagt ggctaccagc
480
accacctgtc tgtccgtgag aaccccatca tcaagaatct caagccggag acgctgatcg
540

actcctttga gctgctctac tattatgatg agtacctggg tcactgcatg tggtacatcc
600
ccttcttcct catcctcttc atgtacttca gcggctgctn ttactgcctc taaagctgag
660
agcttgattc cagggcctgc cctgctcctg gtggcaccca gtggcctgta ctactggtac
720
ctggtcaccg agggccagat ct
742

<210> 1252
<211> 80
<212> PRT
<213> Homo sapiens

<400> 1252
Met Arg Leu Pro Ala Arg Leu Pro Ser Thr Ser Thr Ser Gly Ser Thr
 1   5   10   15
Ser His Cys Arg Thr Gly Phe Trp Thr Leu Gly Val Pro Leu Pro Cys
            20   25   30
Trp Tyr Ser Leu Ser Ser Gly Phe His Ser Thr Ser Pro Val Leu Gly
        35   40   45
Thr Thr Ser Thr Trp Pro Thr Thr Ser Ser Arg Pro Phe Ser Cys Ser
    50   55   60
Ser Ser Ser Ser Gly Pro Pro Ala Pro Cys Tyr Ala Pro Ser Arg Thr
65   70   75   80

<210> 1253
<211> 675
<212> DNA
<213> Homo sapiens

<400> 1253
gggccccctc ccaggcgctt tctgggagct tttagaactg cgctctgaag tttccagaga
60
gcgaggagct tttgcggcag gcagagacaa tggaagaaaa tgaaagccag aaatgtgagc
120
cgtgccttcc ttactcagca gacagaagac agatgcagga acaaggcaaa ggcaatctgc
180
atgtaacatc accagaagat gcagaatgcc gcagaaccaa ggaacgcctt tctaatggaa
240
acagtcgtgg ttcagtttcc aagtcttccc gcaatatccc aaggagacac accctagggg
300
ggccccgaag ttccaaggaa atactgggaa tgcaaacatc tgagatggat cggaagagag
360
gaaaaagcgt tcctagaaca tctgaagcag aagtaccccc accacgcctc tgcaatcatg
420
ggtcaccaag agaggctgag agaccagaca aggatcccca aactgtctca cagtcctcaa
480
ccacccagtg tgggtgaccc ggtcgagcat ttatcagaga cgtccgctga ttctttggaa
540
gccatgtctg agggggatgc tccaacccct ttttccagag gcagccggac tcgtgcgagc
600
cttcctgtgg tgaggtcaac caaccagacg aaagaaagat ctctgggggt tctctatctc
660

cagtatggag atgaa
675

<210> 1254
<211> 86
<212> PRT
<213> Homo sapiens

<400> 1254
Met Gly His Gln Glu Arg Leu Arg Asp Gln Thr Arg Ile Pro Lys Leu
1 5 10 15
Ser His Ser Pro Gln Pro Pro Ser Val Gly Asp Pro Val Glu His Leu
20 25 30
Ser Glu Thr Ser Ala Asp Ser Leu Glu Ala Met Ser Glu Gly Asp Ala
35 40 45
Pro Thr Pro Phe Ser Arg Gly Ser Arg Thr Arg Ala Ser Leu Pro Val
50 55 60
Val Arg Ser Thr Asn Gln Thr Lys Glu Arg Ser Leu Gly Val Leu Tyr
65 70 75 80
Leu Gln Tyr Gly Asp Glu
85

<210> 1255
<211> 401
<212> DNA
<213> Homo sapiens

<400> 1255
ncgccgatta ccaaggctat ggatgtgtgg gccttgggcg taacgctata ctgtctgctg
60
ttcggtcgag tgccatttga tgcagagacg gagtacttgc tgctggaaag tatcctgcat
120
gacgattatg ccgtcccgac gcacatgggt agcgaccgcg tgttggtagg cccgcgacca
180
gcacgttggc cctcgtcgca agagacgccc aacgtgccgc tgtccggcga ggcgcatgca
240
gtacgccatc tgctcgatgc ccttctcgac aaggatccag cgacgcgcct cactctcgat
300
cgtgttataa cacacccatg gctcgtggca gagtcatggt aatagtagca attgtatata
360
ccctcatcac caagatggcc aaagcggtac aaggcccgcg g
401

<210> 1256
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1256
Xaa Pro Ile Thr Lys Ala Met Asp Val Trp Ala Leu Gly Val Thr Leu
1 5 10 15
Tyr Cys Leu Leu Phe Gly Arg Val Pro Phe Asp Ala Glu Thr Glu Tyr
20 25 30
Leu Leu Leu Glu Ser Ile Leu His Asp Asp Tyr Ala Val Pro Thr His

```
        35                  40                  45
Met Gly Ser Asp Arg Val Leu Val Gly Pro Arg Pro Ala Arg Trp Pro
    50                  55                  60
Ser Ser Gln Glu Thr Pro Asn Val Pro Leu Ser Gly Glu Ala His Ala
65                  70                  75                  80
Val Arg His Leu Leu Asp Ala Leu Leu Asp Lys Asp Pro Ala Thr Arg
                85                  90                  95
Leu Thr Leu Asp Arg Val Ile Thr His Pro Trp Leu Val Ala Glu Ser
            100                 105                 110
Trp
```

<210> 1257
<211> 294
<212> DNA
<213> Homo sapiens

<400> 1257
cgcgtacagc tgattgaagg tgatgtcgcc aacgccgacc tggtggcgca agccgccatc
60
ggcgccacgg cggtggtgca tttggcagcg gtggcttcgg tgcaagcctc ggtggatgac
120
ccggtcagca cgcgccagag caattttgtc ggcaccttga atgtctgcga agccatgcgc
180
aaggccggtg tgaagcgtgt ggtatttgct tccagcgttg cggtgtatgg caacaatggc
240
gagggcgctt cgattgacga agagaccatc aaggccccgc tgacgcctta cgcg
294

<210> 1258
<211> 98
<212> PRT
<213> Homo sapiens

<400> 1258
```
Arg Val Gln Leu Ile Glu Gly Asp Val Ala Asn Ala Asp Leu Val Ala
 1               5                  10                  15
Gln Ala Ala Ile Gly Ala Thr Ala Val Val His Leu Ala Ala Val Ala
            20                  25                  30
Ser Val Gln Ala Ser Val Asp Asp Pro Val Ser Thr Arg Gln Ser Asn
        35                  40                  45
Phe Val Gly Thr Leu Asn Val Cys Glu Ala Met Arg Lys Ala Gly Val
    50                  55                  60
Lys Arg Val Val Phe Ala Ser Ser Val Ala Val Tyr Gly Asn Asn Gly
65                  70                  75                  80
Glu Gly Ala Ser Ile Asp Glu Glu Thr Ile Lys Ala Pro Leu Thr Pro
                85                  90                  95
Tyr Ala
```

<210> 1259
<211> 417
<212> DNA
<213> Homo sapiens

<400> 1259
nnacactcta gcctctgact caaggaagct gcccagggtc ttgcccttcg gtttgggggg
60
atcccgtctc ccttcgtctg gagcagacat agtgagaacg tgagaagctg caggcgtggc
120
ctcaccgtgg tgtgttccaa gatgtccagg gccaaggatg ccgtgtcctc cggggtggcc
180
agcgtggtgg acgtggctaa gggagtggtc cagggaggcc tggacaccac tcggtctgca
240
cttacgggca ccaaggaggc ggtgtccagc ggggtcacag gggccatgga catggctaag
300
ggggccgtcc aaggggtct ggacacctcg aaggctgtcc tcaccggcac caaggacacg
360
gtgtccactg ggctcacggg ggcagtgaat gtggccaaag ggcccgtaca ggccggc
417

<210> 1260
<211> 133
<212> PRT
<213> Homo sapiens

<400> 1260
Leu Lys Glu Ala Ala Gln Gly Leu Ala Leu Arg Phe Gly Gly Ile Pro
1 5 10 15
Ser Pro Phe Val Trp Ser Arg His Ser Glu Asn Val Arg Ser Cys Arg
20 25 30
Arg Gly Leu Thr Val Val Cys Ser Lys Met Ser Arg Ala Lys Asp Ala
35 40 45
Val Ser Ser Gly Val Ala Ser Val Val Asp Val Ala Lys Gly Val Val
50 55 60
Gln Gly Gly Leu Asp Thr Thr Arg Ser Ala Leu Thr Gly Thr Lys Glu
65 70 75 80
Ala Val Ser Ser Gly Val Thr Gly Ala Met Asp Met Ala Lys Gly Ala
85 90 95
Val Gln Gly Gly Leu Asp Thr Ser Lys Ala Val Leu Thr Gly Thr Lys
100 105 110
Asp Thr Val Ser Thr Gly Leu Thr Gly Ala Val Asn Val Ala Lys Gly
115 120 125
Pro Val Gln Ala Gly
130

<210> 1261
<211> 330
<212> DNA
<213> Homo sapiens

<400> 1261
ngtgcacgtg ccgttcggca tcaggagatg aacatggatt tgaacgctga agtcgatcag
60
ctggtccgcc aatcccagac ctggatcccc ttgatcatgg agtacggcag ccgcctgctg
120tgaccctggc ggtcggctgg tggatcgaca acaaggtcag cgcccgcctg 180
ggcaaactgg taggcctgcg caacgccgac ctggcactgc aaggctttat cagcaccttg
240

tcgaacatcg ggctgaaagt gctgctgttc gtcagtgtgg cgtcgatgat cggcattgag
300
accacctcgt tcgtcgcgga catcggtgct
330

<210> 1262
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1262
Xaa Ala Arg Ala Val Arg His Gln Glu Met Asn Met Asp Leu Asn Ala
1 5 10 15
Glu Val Asp Gln Leu Val Arg Gln Ser Gln Thr Trp Ile Pro Leu Ile
20 25 30
Met Glu Tyr Gly Ser Arg Leu Leu Leu Ala Leu Leu Thr Leu Ala Val
35 40 45
Gly Trp Trp Ile Asp Asn Lys Val Ser Ala Arg Leu Gly Lys Leu Val
50 55 60
Gly Leu Arg Asn Ala Asp Leu Ala Leu Gln Gly Phe Ile Ser Thr Leu
65 70 75 80
Ser Asn Ile Gly Leu Lys Val Leu Leu Phe Val Ser Val Ala Ser Met
85 90 95
Ile Gly Ile Glu Thr Thr Ser Phe Val Ala Asp Ile Gly Ala
100 105 110

<210> 1263
<211> 351
<212> DNA
<213> Homo sapiens

<400> 1263
acgcgtggac gatggacttc gtcggtctgc ggtacgacga agggctcaac attgccggtg
60
gcatcgatga tgagtttgct cgcctgggca acacctagca gcaatggcat cgatagtccc
120
tgcccagcct gctccatttc gacgacgatg gtcgccgggt tcagtttctt ctcgctccac
180
gtcaacagac cgtcaccgtg gttgacgatc tcgccggtgg aggcgtcctt gacgacgatc
240
tggccacgcg ccagggaata catctcccca tccacccaaa agaacgcccc caagctgggc
300
atcttggcca gcccgatgat cgagagggtt tcaacaagcg actcgggatc c
351

<210> 1264
<211> 100
<212> PRT
<213> Homo sapiens

<400> 1264
Met Pro Ser Leu Gly Ala Phe Phe Trp Val Asp Gly Glu Met Tyr Ser
1 5 10 15
Leu Ala Arg Gly Gln Ile Val Val Lys Asp Ala Ser Thr Gly Glu Ile

```
            20                  25                  30
Val Asn His Gly Asp Gly Leu Leu Thr Trp Ser Glu Lys Lys Leu Asn
        35                  40                  45
Pro Ala Thr Ile Val Val Glu Met Glu Gln Ala Gly Gln Gly Leu Ser
    50                  55                  60
Met Pro Leu Leu Leu Gly Val Ala Gln Ala Ser Lys Leu Ile Ile Asp
65                  70                  75                  80
Ala Thr Gly Asn Val Glu Pro Phe Val Val Pro Gln Thr Asp Glu Val
                85                  90                  95
His Arg Pro Arg
            100
```

<210> 1265
<211> 318
<212> DNA
<213> Homo sapiens

<400> 1265
accggtgtat gcaactgaaa tgctgtccga tatgcctgcg ctccagctcg tgaatcgaaa
60
gttggataac gctcgcttgg tggaatcgtc gctacggaag cttatcaagg atacggatgc
120
tgctgcaccg ccaaaattat ggacgccccc cgaccccact cgctctgacg ataccattgc
180
acagccgaaa gtgcaaccag cccaagcagt gggagatgac tcgatcatgt cggtcgatga
240
gcctgatgca accgtccatg acatgccact caccacgaca ctcgacaacg tgggtcgctc
300
agatccatcg cgacgcgt
318

<210> 1266
<211> 99
<212> PRT
<213> Homo sapiens

<400> 1266
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Met Leu Ser Asp Met Pro Ala Leu Gln Leu Val Asn Arg Lys Leu Asp
 1               5                  10                  15
Asn Ala Arg Leu Val Glu Ser Ser Leu Arg Lys Leu Ile Lys Asp Thr
            20                  25                  30
Asp Ala Ala Ala Pro Pro Lys Leu Trp Thr Pro Pro Asp Pro Thr Arg
        35                  40                  45
Ser Asp Asp Thr Ile Ala Gln Pro Lys Val Gln Pro Ala Gln Ala Val
    50                  55                  60
Gly Asp Asp Ser Ile Met Ser Val Asp Glu Pro Asp Ala Thr Val His
65                  70                  75                  80
Asp Met Pro Leu Thr Thr Thr Leu Asp Asn Val Gly Arg Ser Asp Pro
                85                  90                  95
Ser Arg Arg
```

<210> 1267
<211> 343

<212> DNA
<213> Homo sapiens

<400> 1267
nggacacttg tgggaaatgc cccacagcct gtgtttttat tccccttgtg aacacttgtg
60
ggaactgtcc cacggcccgt gtttctgtgc gcctgcagac actcgtggga aatgccccac
120
aacctgtgtt tttgttcccc ttgtgaacac tcgtgggaaa tgccccacaa cctgtgtttt
180
tattcccctt gtgaacactc gtgggaaatg tcccatggcc cgtgtttccg tgcacctgcg
240
gatactcatc aaacaccagg ctgtcattgg ggacagggtg agctctggct gttggtgcag
300
catggtagga agagcaccaa gtcctggact ctgttgattt ata
343

<210> 1268
<211> 106
<212> PRT
<213> Homo sapiens

<400> 1268
Met Pro His Ser Leu Cys Phe Tyr Ser Pro Cys Glu His Leu Trp Glu
 1   5   10   15
Leu Ser His Gly Pro Cys Phe Cys Ala Pro Ala Asp Thr Arg Gly Lys
            20   25   30
Cys Pro Thr Thr Cys Val Phe Val Pro Leu Val Asn Thr Arg Gly Lys
        35   40   45
Cys Pro Thr Thr Cys Val Phe Ile Pro Leu Val Asn Thr Arg Gly Lys
    50   55   60
Cys Pro Met Ala Arg Val Ser Val His Leu Arg Ile Leu Ile Lys His
65   70   75   80
Gln Ala Val Ile Gly Asp Arg Val Ser Ser Gly Cys Trp Cys Ser Met
                85   90   95
Val Gly Arg Ala Pro Ser Pro Gly Leu Cys
            100   105

<210> 1269
<211> 391
<212> DNA
<213> Homo sapiens

<400> 1269
tcgcgatccg gagcgatcgg tgctgcagat ggctggcgac gccctgcggg gcgcattgcg
60
ggacgccgac ctggagccgg ccgccctaga cgggctgatc gtccaggtgg ggtccccccg
120
cggcgcggac tacgacaccg tgtccgaaac ctttggtctt tcgccacaat tctgcagcca
180
gacctggggc gcacggccgg ttcaccgcaa cggtgatcct ggcagcggcc atggcggtgt
240
ccagcggcct cgcgcggcgg gtggcttgcc tcatgggcat gaagaattcg gacctcgggc
300

ggttgggtga ggcggacaat ccctttcatc atgagcaatt ccgggagaat ggcgggccgc
360
acggggaaga gggttggatc ggcatggcct c
391

<210> 1270
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1270
Met Met Lys Gly Ile Val Arg Leu Thr Gln Pro Pro Glu Val Arg Ile
1 5 10 15
Leu His Ala His Glu Ala Ser His Pro Pro Arg Glu Ala Ala Gly His
20 25 30
Arg His Gly Arg Cys Gln Asp His Arg Cys Gly Glu Pro Ala Val Arg
35 40 45
Pro Arg Ser Gly Cys Arg Ile Val Ala Lys Asp Gln Arg Phe Arg Thr
50 55 60
Arg Cys Arg Ser Pro Arg Arg Gly Gly Thr Pro Pro Gly Arg Ser Ala
65 70 75 80
Arg Leu Gly Arg Pro Ala Pro Gly Arg Arg Pro Ala Met Arg Pro Ala
85 90 95
Gly Arg Arg Gln Pro Ser Ala Ala Pro Ile Ala Pro Asp Arg
100 105 110

<210> 1271
<211> 661
<212> DNA
<213> Homo sapiens

<400> 1271
acgcgtcgtt actggccacc tgcgagcgca ccagggtagg cagcactcgg tctccgtcga
60
accagaaagc gtcatcgggg tggtgaacga gaacgggcga tgttgtggtg ggacggataa
120
cccccggttg cgtcaccata tggcccacta aagagttcac cagggttgat ttaccagccc
180
cggtcgaccc tcctaccacc gccagaagcg gcgcatcaat agtctctaag cgcggcaaaa
240
tatagtcgtt aagctggtta gcgatgcgtc gtgccagccc ggcctgagta atagcctccg
300
gcaaatccaa ggggaactgg gcctgacgca ggttgtgccg cagatcggtc aacgacagca
360
gtatctgctc agtgttcatg gtgatccttc ctggtcactc gtcaggcctg tggcggcgcc
420
cactgcaact cgttgttgac cggctggttg cgacgtcgct tgaggaatgc gggcagtctc
480
ggcttcgaca atttggcacc tcgggcgacg gtgatagccg ccgggcgcag cacgttcata
540
cggttgatga gctcgatctg aagcggacca ggatcatcgt ccaacccacg cacaatggcg
600
tcacgaagat aagcaagatc tgtcccaacg cgcaggaact ctaacgtgtg ccaccaccgg
660

t
661

<210> 1272
<211> 126
<212> PRT
<213> Homo sapiens

<400> 1272
Met Asn Thr Glu Gln Ile Leu Leu Ser Leu Thr Asp Leu Arg His Asn
1 5 10 15
Leu Arg Gln Ala Gln Phe Pro Leu Asp Leu Pro Glu Ala Ile Thr Gln
20 25 30
Ala Gly Leu Ala Arg Arg Ile Ala Asn Gln Leu Asn Asp Tyr Ile Leu
35 40 45
Pro Arg Leu Glu Thr Ile Asp Ala Pro Leu Leu Ala Val Val Gly Gly
50 55 60
Ser Thr Gly Ala Gly Lys Ser Thr Leu Val Asn Ser Leu Val Gly His
65 70 75 80
Met Val Thr Gln Pro Gly Val Ile Arg Pro Thr Thr Thr Ser Pro Val
85 90 95
Leu Val His His Pro Asp Asp Ala Phe Trp Phe Asp Gly Asp Arg Val
100 105 110
Leu Pro Thr Leu Val Arg Ser Gln Val Ala Ser Asn Asp Ala
115 120 125

<210> 1273
<211> 489
<212> DNA
<213> Homo sapiens

<400> 1273
gccggcgaga ccggtgccgg aaagaccatg gtggtcaccg gtattggttt gctgctcggc
60
gacaaggctg acactggatt ggtccggcat ggctgcgatc gtgccgtcgt cgaagccgtt
120
ctcgacacgc ctgatgccgg tcgcgtcagc gagcttggcg gaacagtcga ggatggtgag
180
gttatctgcg ctcgacacat cacgagtcgt cgctctcgag cgctgcttgg aggagctcaa
240
gttaccgcta gtcagctggc ccacatcgtt ggggatcagg tgaccatcca tggccaatct
300
gaacaagtga ggttggtcga cgcagcgcgg cagctcgacg tcgttgaccg ggctgccgga
360
gatgagctgg caggctacct aagtcgacat gcacagctgt ggtcggagtt tcgtgctgca
420
tcccagcgtc ttcagcgcct caacgaggat cgcgctgggg ccgagatgga acgcgaggtg
480
cttacgcgt
489

<210> 1274
<211> 163
<212> PRT

<213> Homo sapiens

<400> 1274
Ala Gly Glu Thr Gly Ala Gly Lys Thr Met Val Val Thr Gly Ile Gly
1 5 10 15
Leu Leu Leu Gly Asp Lys Ala Asp Thr Gly Leu Val Arg His Gly Cys
20 25 30
Asp Arg Ala Val Val Glu Ala Val Leu Asp Thr Pro Asp Ala Gly Arg
35 40 45
Val Ser Glu Leu Gly Gly Thr Val Glu Asp Gly Glu Val Ile Cys Ala
50 55 60
Arg His Ile Thr Ser Arg Arg Ser Arg Ala Leu Leu Gly Gly Ala Gln
65 70 75 80
Val Thr Ala Ser Gln Leu Ala His Ile Val Gly Asp Gln Val Thr Ile
85 90 95
His Gly Gln Ser Glu Gln Val Arg Leu Val Asp Ala Ala Arg Gln Leu
100 105 110
Asp Val Val Asp Arg Ala Ala Gly Asp Glu Leu Ala Gly Tyr Leu Ser
115 120 125
Arg His Ala Gln Leu Trp Ser Glu Phe Arg Ala Ala Ser Gln Arg Leu
130 135 140
Gln Arg Leu Asn Glu Asp Arg Ala Gly Ala Glu Met Glu Arg Glu Val
145 150 155 160
Leu Thr Arg

<210> 1275
<211> 384
<212> DNA
<213> Homo sapiens

<400> 1275
nngctagcaa gtgcaagtac gagcaaaagt tatcagcaac agcgggaggc tgaacttctc
60
gtcgcacggc tagaggggga aatgcacgca cacagcgacc cgaccccgtc gccacaacca
120
cccgaggatg cagggttgat tgatgttgcc ctgaaagagg cgaagaaagc ctttgatgaa
180
ggcaaggtcg atctaatgga taaactcaat caggagatac ttcgcctggc aaacgaattc
240
ggtgcgctcg ggcttgaatc tattgagctt ggctccgacg cgaagatggc agtacgcaaa
300
ggcaatcaga aatcagcgtt cagcaggctg actcccggtg aacgtctcag gctgcgcatt
360
gctacagcca tcgcgttgtt acgc
384

<210> 1276
<211> 128
<212> PRT
<213> Homo sapiens

<400> 1276
Xaa Leu Ala Ser Ala Ser Thr Ser Lys Ser Tyr Gln Gln Gln Arg Glu

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 1               5                  10                  15
Ala Glu Leu Leu Val Ala Arg Leu Glu Gly Glu Met His Ala His Ser
            20                  25                  30
Asp Pro Thr Pro Ser Pro Gln Pro Pro Glu Asp Ala Gly Leu Ile Asp
        35                  40                  45
Val Ala Leu Lys Glu Ala Lys Lys Ala Phe Asp Glu Gly Lys Val Asp
    50                  55                  60
Leu Met Asp Lys Leu Asn Gln Glu Ile Leu Arg Leu Ala Asn Glu Phe
65                  70                  75                  80
Gly Ala Leu Gly Leu Glu Ser Ile Glu Leu Gly Ser Asp Ala Lys Met
                85                  90                  95
Ala Val Arg Lys Gly Asn Gln Lys Ser Ala Phe Ser Arg Leu Thr Pro
            100                 105                 110
Gly Glu Arg Leu Arg Leu Arg Ile Ala Thr Ala Ile Ala Leu Leu Arg
        115                 120                 125
```

<210> 1277
<211> 392
<212> DNA
<213> Homo sapiens

<400> 1277
cagtttcagc cccgctgtgt gtccccaatt cctgtctctc ctaccagccg gattcagaac
60
ccagtggctt tcctcagctc tgttctgcct tctctccctg ccatcccacc cacaaatgcc
120
atggggctgc ctagaagtgc accatccatg ccatcccagg gattagcgaa gaaaaataca
180
aagtctcctc aaccagtgaa tgatgataac attcgtgaaa ctaagaacgc agtgattcga
240
gacttgggga aaaaaataac tttcagtgat gtcagaccaa accagcagga gtacaaaatt
300
tcaagctttg agcagaggct gatgaatgaa atagagtttc gcttggaacg tactcctgtt
360
gatgaatcac atgatgaaat tcaacatgat gg
392

<210> 1278
<211> 130
<212> PRT
<213> Homo sapiens

<400> 1278
```
Gln Phe Gln Pro Arg Cys Val Ser Pro Ile Pro Val Ser Pro Thr Ser
 1               5                  10                  15
Arg Ile Gln Asn Pro Val Ala Phe Leu Ser Ser Val Leu Pro Ser Leu
            20                  25                  30
Pro Ala Ile Pro Pro Thr Asn Ala Met Gly Leu Pro Arg Ser Ala Pro
        35                  40                  45
Ser Met Pro Ser Gln Gly Leu Ala Lys Lys Asn Thr Lys Ser Pro Gln
    50                  55                  60
Pro Val Asn Asp Asp Asn Ile Arg Glu Thr Lys Asn Ala Val Ile Arg
65                  70                  75                  80
Asp Leu Gly Lys Lys Ile Thr Phe Ser Asp Val Arg Pro Asn Gln Gln
```

```
                85                  90                  95
Glu Tyr Lys Ile Ser Ser Phe Glu Gln Arg Leu Met Asn Glu Ile Glu
            100                 105                 110
Phe Arg Leu Glu Arg Thr Pro Val Asp Glu Ser His Asp Glu Ile Gln
        115                 120                 125
His Asp
    130
```

<210> 1279
<211> 297
<212> DNA
<213> Homo sapiens

<400> 1279
atggagtcgc agactctccg ccacatgatc gaggacgact gcgccgacaa cggcatccca
60
ctccccaacg tcaactccag gatcctctct aaggtcatcg agtactgcaa cagtcacgtc
120
cacgccgccg ccaaacccgc tgactccgct gcctccgagg gcggcgagga cctcaagagc
180
tgggacgcga agttcgtcaa ggtggaccag gctacgctct tcgacctcat cctggctgcc
240
aactatctga acatcaaggg attgctggac ctgacctgcc agacgggtgc tgacatg
297

<210> 1280
<211> 99
<212> PRT
<213> Homo sapiens

<400> 1280
```
Met Glu Ser Gln Thr Leu Arg His Met Ile Glu Asp Asp Cys Ala Asp
 1               5                  10                  15
Asn Gly Ile Pro Leu Pro Asn Val Asn Ser Arg Ile Leu Ser Lys Val
            20                  25                  30
Ile Glu Tyr Cys Asn Ser His Val His Ala Ala Ala Lys Pro Ala Asp
        35                  40                  45
Ser Ala Ala Ser Glu Gly Gly Glu Asp Leu Lys Ser Trp Asp Ala Lys
    50                  55                  60
Phe Val Lys Val Asp Gln Ala Thr Leu Phe Asp Leu Ile Leu Ala Ala
65                  70                  75                  80
Asn Tyr Leu Asn Ile Lys Gly Leu Leu Asp Leu Thr Cys Gln Thr Gly
                85                  90                  95
Ala Asp Met
```

<210> 1281
<211> 515
<212> DNA
<213> Homo sapiens

<400> 1281
acgcgtgaag ggggctttgg aggggatggc ttctggactg cacgatgggt gaacacagtt
60

ttttaaactc ttttccacat ctgtataggt ttgaaaatta tcaacaactc atggggaggg
120
tggcgtgcca ggtcatggct gcctggagcc cttctgagga gggccggctc aaccgaggac
180
gccctcccca ctaccaagta ggcactgcgg gcaggagtcg ccacccccac cccaaggaag
240
ttcagaacag gcaacaggag gagcctgact ccaacagagt tggtgtcatc cggcgcatcg
300
ctaaggacgt cacaacacat caactctggg agcccaaggg ggtgtgtggt ccactcaagg
360
ggaagatgat ccagaagctc tgctccctcc ctttgctttt gaagaacaca ggagtgacac
420
gtggggaatc taccggctta atttcttctt agtaacaggc atagtaggat caaaaaattt
480
ttgcttctaa tttttaaaaa cattcaatgt gtaca
515

<210> 1282
<211> 135
<212> PRT
<213> Homo sapiens

<400> 1282
Met Gly Glu His Ser Phe Leu Asn Ser Phe Pro His Leu Tyr Arg Phe
1 5 10 15
Glu Asn Tyr Gln Gln Leu Met Gly Arg Val Ala Cys Gln Val Met Ala
20 25 30
Ala Trp Ser Pro Ser Glu Glu Gly Arg Leu Asn Arg Gly Arg Pro Pro
35 40 45
His Tyr Gln Val Gly Thr Ala Gly Arg Ser Arg His Pro His Pro Lys
50 55 60
Glu Val Gln Asn Arg Gln Gln Glu Glu Pro Asp Ser Asn Arg Val Gly
65 70 75 80
Val Ile Arg Arg Ile Ala Lys Asp Val Thr Thr His Gln Leu Trp Glu
85 90 95
Pro Lys Gly Val Cys Gly Pro Leu Lys Gly Lys Met Ile Gln Lys Leu
100 105 110
Cys Ser Leu Pro Leu Leu Leu Lys Asn Thr Gly Val Thr Arg Gly Glu
115 120 125
Ser Thr Gly Leu Ile Ser Ser
130 135

<210> 1283
<211> 296
<212> DNA
<213> Homo sapiens

<400> 1283
gaattcctca caatgaactg cagtgtctgg aggaccagtt gggtagcctt actccgggtc
60
tccactgcag aacttataca tatatgcttt gtgcacacaa agaaaaacag cagcccaaaa
120
gaatcccggc tggggctctt aggagggagg aaagttccca caggtaactc actggttaat
180

tttaaagagc tcaggaaagg aaggaaggat ggctttttct cttgtgagtc aagacaaggt
240
cctgatgata accctcccag atcagaacgt aactttcaac ccacgagtgc tgctcn
296

<210> 1284
<211> 94
<212> PRT
<213> Homo sapiens

<400> 1284
Met Asn Cys Ser Val Trp Arg Thr Ser Trp Val Ala Leu Leu Arg Val
1 5 10 15
Ser Thr Ala Glu Leu Ile His Ile Cys Phe Val His Thr Lys Lys Asn
20 25 30
Ser Ser Pro Lys Glu Ser Arg Leu Gly Leu Leu Gly Gly Arg Lys Val
35 40 45
Pro Thr Gly Asn Ser Leu Val Asn Phe Lys Glu Leu Arg Lys Gly Arg
50 55 60
Lys Asp Gly Phe Phe Ser Cys Glu Ser Arg Gln Gly Pro Asp Asp Asn
65 70 75 80
Pro Pro Arg Ser Glu Arg Asn Phe Gln Pro Thr Ser Ala Ala
85 90

<210> 1285
<211> 526
<212> DNA
<213> Homo sapiens

<400> 1285
gggccccttc ttacctgccc cttccccgtg ccaccaaccc gtagacaggg agggcaagca
60
gtgaaaggtc catctagagg aggtaaaaga cagggctgag ggaaaacgcc ttgtacagtc
120
aggatggcag atgtactctg tcagggaaga cagccccaca gaaaaggctc ggcttggcca
180
agaagcaaca aaagggattc tacacctcag accagggagg gggaatgtgt acaaagattg
240
gatttactaa attcagagcc acagactttc aggtacttcg gtgaagatca gtgctctttc
300
aaacccacac ttcagaggca ggctttaaaa cgcctgactt ctgtcagggc cacaggctgg
360
gctgcccaaa gctcctacgg ggctgggggа tccgagagag gacttcccac tagtccaaga
420
tgtggtgact agtttcaagc cagagattga ggagcagacc tgatgccctt tcgggccccc
480
gctaagaacc tgattcgagg aaaaggaagt gaagacagta acgcgt
526

<210> 1286
<211> 102
<212> PRT
<213> Homo sapiens

<400> 1286
Met Ala Asp Val Leu Cys Gln Gly Arg Gln Pro His Arg Lys Gly Ser
1 5 10 15
Ala Trp Pro Arg Ser Asn Lys Arg Asp Ser Thr Pro Gln Thr Arg Glu
20 25 30
Gly Glu Cys Val Gln Arg Leu Asp Leu Leu Asn Ser Glu Pro Gln Thr
35 40 45
Phe Arg Tyr Phe Gly Glu Asp Gln Cys Ser Phe Lys Pro Thr Leu Gln
50 55 60
Arg Gln Ala Leu Lys Arg Leu Thr Ser Val Arg Ala Thr Gly Trp Ala
65 70 75 80
Ala Gln Ser Ser Tyr Gly Ala Gly Gly Ser Glu Arg Gly Leu Pro Thr
85 90 95
Ser Pro Arg Cys Gly Asp
100

<210> 1287
<211> 333
<212> DNA
<213> Homo sapiens

<400> 1287
acgcgtgaag gggagaggca gctccaggtg gagggaagtg catgaggaag cagagaggca
60
ggcgacaggc agcgtggctg gggctgggca ggccttccag tttgattgca gcccagaggt
120
caggtgagaa gaaggtacaa caagcaagga aggccccagg aagccactgg gggtgtttga
180
gccattgaat attctggatt ttaggacatt tctgtggctg actccactgc catcagagtt
240
catccacccc aactccagcc tgagagtgct ggggcactgg gcactccgga attcttcaaa
300
gctctgatgc aacatgtccc cagggtgtct gac
333

<210> 1288
<211> 105
<212> PRT
<213> Homo sapiens

<400> 1288
Met Leu His Gln Ser Phe Glu Glu Phe Arg Ser Ala Gln Cys Pro Ser
1 5 10 15
Thr Leu Arg Leu Glu Leu Gly Trp Met Asn Ser Asp Gly Ser Gly Val
20 25 30
Ser His Arg Asn Val Leu Lys Ser Arg Ile Phe Asn Gly Ser Asn Thr
35 40 45
Pro Ser Gly Phe Leu Gly Pro Ser Leu Leu Val Val Pro Ser Ser His
50 55 60
Leu Thr Ser Gly Leu Gln Ser Asn Trp Lys Ala Cys Pro Ala Pro Ala
65 70 75 80
Thr Leu Pro Val Ala Cys Leu Ser Ala Ser Ser Cys Thr Ser Leu His
85 90 95
Leu Glu Leu Pro Leu Pro Phe Thr Arg

100 105

<210> 1289
<211> 336
<212> DNA
<213> Homo sapiens

<400> 1289
acgcgtgtct gtgtacaggt ggaaggggat gggtatgaga tggtgcagcg tgtgcatggg
60
cacggcgtat ggtgtgtgag tgcactcgtg tgccggagag ctgtaagctg ctggctgagt
120
cctgcacggt ggaggaggca aggtggcccc tgcctgtggg cacagagccc accttccggt
180
ccagcccgag gccccttcc cagagccccc tcccaagggg ccataccacc tgcatcccca
240
agatggcgtg gggcgtccct ggtgcaggag caggggacag tcagggaggc gtgtggcgga
300
cagtagcagc cccccagccc ccctcccccc accggt
336

<210> 1290
<211> 89
<212> PRT
<213> Homo sapiens

<400> 1290
Met Val Cys Glu Cys Thr Arg Val Pro Glu Ser Cys Lys Leu Leu Ala
1 5 10 15
Glu Ser Cys Thr Val Glu Glu Ala Arg Trp Pro Leu Pro Val Gly Thr
20 25 30
Glu Pro Thr Phe Arg Ser Ser Pro Arg Pro Leu Ser Gln Ser Pro Leu
35 40 45
Pro Arg Gly His Thr Thr Cys Ile Pro Lys Met Ala Trp Gly Val Pro
50 55 60
Gly Ala Gly Ala Gly Asp Ser Gln Gly Gly Val Trp Arg Thr Val Ala
65 70 75 80
Ala Pro Gln Pro Pro Ser Pro His Arg
85

<210> 1291
<211> 379
<212> DNA
<213> Homo sapiens

<400> 1291
tggccatcca cctctgtcag ctgttccggc aacccattca gatcattgtg gtagtaacga
60
atcttctgca acggcccggc accgtccacg cgagccagag gttgatagcc ttcatcctca
120
taaacgtaca ggcttgtctg gctgtgttta tgctcctgca ataaccgcaa accatcccag
180
gtaaaccggg tttcccccaa cggataccca tcactgccat gctcggtttt ttctatccga
240

cgccccagcg ggtcatacac catcctgacc acgctaccat cgtcattacg cacttcaacc
300
agccggcttt cagcgtcata cgcaaaccgc tgcacgccac gcttggcact gcgcttctcg
360
accatccgcc caaacgcgt
379

<210> 1292
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1292
Met Val Glu Lys Arg Ser Ala Lys Arg Gly Val Gln Arg Phe Ala Tyr
1 5 10 15
Asp Ala Glu Ser Arg Leu Val Glu Val Arg Asn Asp Asp Gly Ser Val
20 25 30
Val Arg Met Val Tyr Asp Pro Leu Gly Arg Arg Ile Glu Lys Thr Glu
35 40 45
His Gly Ser Asp Gly Tyr Pro Leu Gly Glu Thr Arg Phe Thr Trp Asp
50 55 60
Gly Leu Arg Leu Leu Gln Glu His Lys His Ser Gln Thr Ser Leu Tyr
65 70 75 80
Val Tyr Glu Asp Glu Gly Tyr Gln Pro Leu Ala Arg Val Asp Gly Ala
85 90 95
Gly Pro Leu Gln Lys Ile Arg Tyr Tyr His Asn Asp Leu Asn Gly Leu
100 105 110
Pro Glu Gln Leu Thr Glu Val Asp Gly
115 120

<210> 1293
<211> 340
<212> DNA
<213> Homo sapiens

<400> 1293
nngccggccg cccgagagct gttcgaggcg tgccgcaacg gggacgtgga acgagtcaag
60
aggctggtga cgcctgagaa ggtgaacagc cgcgacacgg cgggcaggaa atccaccccg
120
ctgcacttcg ccgcaggttt tgggcggaaa gacgtagttg aatatttgct tcagaatggt
180
gcaaatgtcc aagcacgtga tgatgggggc cttattcctc ttcataatgc atgctctttt
240
ggtcatgctg aagtagtcaa tctccttttg cgacatggtg cagaccccaa tgcttgagat
300
aattggaatt atactcctag agggtggagt gtgctcgcga
340

<210> 1294
<211> 98
<212> PRT
<213> Homo sapiens

<400> 1294
Xaa Pro Ala Ala Arg Glu Leu Phe Glu Ala Cys Arg Asn Gly Asp Val
1 5 10 15
Glu Arg Val Lys Arg Leu Val Thr Pro Glu Lys Val Asn Ser Arg Asp
20 25 30
Thr Ala Gly Arg Lys Ser Thr Pro Leu His Phe Ala Ala Gly Phe Gly
35 40 45
Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn Gly Ala Asn Val Gln
50 55 60
Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala Cys Ser Phe
65 70 75 80
Gly His Ala Glu Val Val Asn Leu Leu Leu Arg His Gly Ala Asp Pro
85 90 95
Asn Ala

<210> 1295
<211> 351
<212> DNA
<213> Homo sapiens

<400> 1295
ggatcccgga gacctcgtcg gcgaacgtca cctcgtccag ggccgaggcg cggaacaccg
60
acgtgtcgat gccctcgccc tcgatgcagt cggtcagcgg tacgacggcg ccgcgggagg
120
cgaaggtgcc gatctggctg cgctcggcgt agaccagcga cggcggttcg cccgacgcca
180
cggaggagag gaactgctgg atgtcgaggt caccctcgat cagcttgacc ttggcgtcgc
240
cgagctcctc cttcgcccgg tcgagccgca ccgtcgcgat ctcgtcgccg gcaccgaagc
300
ccatcacctc gacctcgccg gagagcttcg ccccgctgtc gaaagacgcg t
351

<210> 1296
<211> 75
<212> PRT
<213> Homo sapiens

<400> 1296
Gly Ser Arg Arg Pro Arg Arg Arg Thr Ser Pro Arg Pro Gly Pro Arg
1 5 10 15
Arg Gly Thr Pro Thr Cys Arg Cys Pro Arg Pro Arg Cys Ser Arg Ser
20 25 30
Ala Val Arg Arg Arg Arg Gly Arg Arg Arg Cys Arg Ser Gly Cys Ala
35 40 45
Arg Arg Arg Pro Ala Thr Ala Val Arg Pro Thr Pro Arg Arg Arg Gly
50 55 60
Thr Ala Gly Cys Arg Gly His Pro Arg Ser Ala
65 70 75

<210> 1297
<211> 356

<212> DNA
<213> Homo sapiens

<400> 1297
gtgcacccgg attcccattg ccaccgactt cgagtaaact ccagtcccga ggacacgaga
60
gacacccagg cctcaggccc catgggcacg ctccacgcca cggctcctac cagagggaca
120
gatacactct acaaatctcg gggcccacca caccaagaag acacggagga gccaacaaaa
180
gaaggaccat acgaaatgca cccccaaagc aaccaaccaa tccaagaaaa aatacgtctc
240
agggttctgt gggccctctt gcatgggctg ccctgccccc ctgttctggc ctggctcaag
300
caccttaccc cagcctgctc gaaagagccc tggctaccag agcagagcac tggcct
356

<210> 1298
<211> 91
<212> PRT
<213> Homo sapiens

<400> 1298
Met Gly Thr Leu His Ala Thr Ala Pro Thr Arg Gly Thr Asp Thr Leu
1 5 10 15
Tyr Lys Ser Arg Gly Pro Pro His Gln Glu Asp Thr Glu Glu Pro Thr
20 25 30
Lys Glu Gly Pro Tyr Glu Met His Pro Gln Ser Asn Gln Pro Ile Gln
35 40 45
Glu Lys Ile Arg Leu Arg Val Leu Trp Ala Leu Leu His Gly Leu Pro
50 55 60
Cys Pro Pro Val Leu Ala Trp Leu Lys His Leu Thr Pro Ala Cys Ser
65 70 75 80
Lys Glu Pro Trp Leu Pro Glu Gln Ser Thr Gly
85 90

<210> 1299
<211> 307
<212> DNA
<213> Homo sapiens

<400> 1299
ggatccactt ctaagatgtc tcactcacgt ggtgatggca gcaggcctca gactctggtg
60
gttgttggca ggatgtctca gttccttgcc atgtgggtct ctacacaggg cagcttcctg
120
tgtctttgcc atatggcaac tgagaatgat cttggctacc ttctccagcc cgggagtcgg
180
gagttttctg gggtggggtc acgggtcttg cccggagttc gccctggcaa aggcctgtgc
240
cagtgatcct ggagcggagc gaagtgtttc cgtgactctg cagccgcagt tcttagggct
300
tccttag
307

<210> 1300
<211> 90
<212> PRT
<213> Homo sapiens

<400> 1300
Met Ala Ala Gly Leu Arg Leu Trp Trp Leu Leu Ala Gly Cys Leu Ser
1 5 10 15
Ser Leu Pro Cys Gly Ser Leu His Arg Ala Ala Ser Cys Val Phe Ala
20 25 30
Ile Trp Gln Leu Arg Met Ile Leu Ala Thr Phe Ser Ser Pro Gly Val
35 40 45
Gly Ser Phe Leu Gly Trp Gly His Gly Ser Cys Pro Glu Phe Ala Leu
50 55 60
Ala Lys Ala Cys Ala Ser Asp Pro Gly Ala Glu Arg Ser Val Ser Val
65 70 75 80
Thr Leu Gln Pro Gln Phe Leu Gly Leu Pro
85 90

<210> 1301
<211> 408
<212> DNA
<213> Homo sapiens

<400> 1301
ctgagcaagt taaaagaagt tcttgaattt tataacttta ttttgacaaa ctattataaa
60
gttgagccta tttcctttga tgcagtatac gctgaaggtt tggaaatggc tgagttcttg
120
cgccctatgg tgtcagatac gattacactt ttgcatgacc ttagaaggtc tggcgcaaac
180
atcatgtttg aaggcgcgca agggtctttg ttggatgttg atcatggtac ttacccgtat
240
gtgacttcat ctaatacgac tgcgggcgga gcgccagcgg gaacaggttt tggtcctttg
300
tacttagatt atgtattagg tatcactaag gcttatacga ctcgcgttgg ttctggacct
360
ttccctactg agttgtttga cgaagatggt gagcgtcttg gtacgcgt
408

<210> 1302
<211> 136
<212> PRT
<213> Homo sapiens

<400> 1302
Leu Ser Lys Leu Lys Glu Val Leu Glu Phe Tyr Asn Phe Ile Leu Thr
1 5 10 15
Asn Tyr Tyr Lys Val Glu Pro Ile Ser Phe Asp Ala Val Tyr Ala Glu
20 25 30
Gly Leu Glu Met Ala Glu Phe Leu Arg Pro Met Val Ser Asp Thr Ile
35 40 45
Thr Leu Leu His Asp Leu Arg Arg Ser Gly Ala Asn Ile Met Phe Glu

```
    50                  55                  60
Gly Ala Gln Gly Ser Leu Leu Asp Val Asp His Gly Thr Tyr Pro Tyr
65                  70                  75                  80
Val Thr Ser Ser Asn Thr Thr Ala Gly Gly Ala Pro Ala Gly Thr Gly
                85                  90                  95
Phe Gly Pro Leu Tyr Leu Asp Tyr Val Leu Gly Ile Thr Lys Ala Tyr
            100                 105                 110
Thr Thr Arg Val Gly Ser Gly Pro Phe Pro Thr Glu Leu Phe Asp Glu
        115                 120                 125
Asp Gly Glu Arg Leu Gly Thr Arg
    130                 135
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<210> 1303
<211> 1037
<212> DNA
<213> Homo sapiens

<400> 1303
gccgggggggg ggatgctatc taacatcttc atgttcaacc cagagaagaa acatcccgcc
60
gtttgccctg gggccctctc atcccacatc atttttttcaa cccttcccca nccttttcnga
120
aatagggcca acccccttaaa aancaaatnt tcanataaac ccttttcccct ccacccttttt
180
cccatcccat ccttttttccc tcacaaacac aaacaaaang cctctttcct ttgccatttc
240
cactcctttt ggaagaaaca ggccctgttc cctccctgct caccacttca cccagctcag
300
ctggcacaaa aatactgcca ccacaccttc accctgccta gcccaacctg gcagggcctc
360
ggagtagcct gccagctaaa atacgggttg cccagataac tgtgaatgtc agataagaat
420
cttctgggac aagtatgtcc catgccatat ttgggacata cttacactaa taaatttctg
480
tttatctgaa actcaaattt gcctgggcgt cctgtacttt tcttaactaa atttggtgcc
540
tctacacaca aggtccctgg ggtgggggggg cacaggagca agccccttcc caggctgggt
600
ccctgccggc atctcccaca ggccaggact ggccacccag atggagcccg tgccaggcag
660
ccggcgacag acggacaaag gctgctcagg agacactgca caccttcctc tttcttgtct
720
gggggctcaa gaatccagac gcccacctcc ccgagcgagc accaagacag gaagccaacc
780
tgcaatgccc agcccactgc gaccacaggg ctctgccggg gtcctgccgg aacccagggt
840
tccggtccag aagccaggga taaatgccgc ttctcctata gggacggtca gagtagagag
900
ggggaggcct acagtctcac ctgcagggag aggaagtcct cggggcgggc acgtgggggg
960
cctgacagct ccgagcacac ccggccacag tgaccacgga ctgcacacgc agaagcagtc
1020
tggatcccac gcgtggc
1037

<210> 1304
<211> 132
<212> PRT
<213> Homo sapiens

<400> 1304
Met Glu Pro Val Pro Gly Ser Arg Arg Gln Thr Asp Lys Gly Cys Ser
1 5 10 15
Gly Asp Thr Ala His Leu Pro Leu Ser Cys Leu Gly Ala Gln Glu Ser
20 25 30
Arg Arg Pro Pro Pro Arg Ala Ser Thr Lys Thr Gly Ser Gln Pro Ala
35 40 45
Met Pro Ser Pro Leu Arg Pro Gln Gly Ser Ala Gly Val Leu Pro Glu
50 55 60
Pro Arg Val Pro Val Gln Lys Pro Gly Ile Asn Ala Ala Ser Pro Ile
65 70 75 80
Gly Thr Val Arg Val Glu Arg Gly Arg Pro Thr Val Ser Pro Ala Gly
85 90 95
Arg Gly Ser Pro Arg Gly Gly His Val Gly Gly Leu Thr Ala Pro Ser
100 105 110
Thr Pro Gly His Ser Asp His Gly Leu His Thr Gln Lys Gln Ser Gly
115 120 125
Ser His Ala Trp
130

<210> 1305
<211> 775
<212> DNA
<213> Homo sapiens

<400> 1305
nacgcgttct gcgaggccat gcgggtctat gccccgcggc cgttgacctc gcccacactc
60
ccggcccccgc tgcgggtgga gagacgtcgg gccctctacg ggtcctggta cgagtttttc
120
ccgcgctctc agggtgctta tgtcgatgcg gacggtcact gggtttcagg tactttcgac
180
acctcctggg agcgcctgga cgccgccgct gcgatgggat ttgacgttgt ttacctgccc
240
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cccaaaaagt atcaggacat ctacccgatc aacttcgaca atgaccctga cggtatctac
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caggaatgct tgcggctgct ggagttatgg atctcccacg gcgtgacgat tttccgcgtc
660

gataatccac ataccaagcc tctgaatttc tgggcctggc tcatggaaca ggttcatcgt
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775

<210> 1306
<211> 258
<212> PRT
<213> Homo sapiens

<400> 1306
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Tyr Gly Ser Trp Tyr Glu Phe Phe Pro Arg Ser Gln Gly Ala Tyr Val
35 40 45
Asp Ala Asp Gly His Trp Val Ser Gly Thr Phe Asp Thr Ser Trp Glu
50 55 60
Arg Leu Asp Ala Ala Ala Ala Met Gly Phe Asp Val Val Tyr Leu Pro
65 70 75 80
Ala Ile His Pro Met Gly Gln Ala Phe Arg Lys Gly Lys Asp Asn Thr
85 90 95
Leu Thr Pro Gly Pro Asp Asp Pro Gly Ser Pro Trp Ala Ile Gly Ser
100 105 110
Ser Asp Gly Gly His Asp Thr Ile His Pro Asp Leu Gly Thr Phe Asp
115 120 125
Asp Leu Asp Arg Phe Val Ala His Ala His Asp Leu Gly Met Glu Val
130 135 140
Ala Leu Asp Phe Ala Leu Gln Ala Ser Pro Asp His Pro Trp Val His
145 150 155 160
Gln His Pro Glu Trp Phe Thr Thr Arg Val Asp Gly Thr Ile Ala Tyr
165 170 175
Ala Glu Asn Ser Pro Lys Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe
180 185 190
Asp Asn Asp Pro Asp Gly Ile Tyr Gln Glu Cys Leu Arg Leu Leu Glu
195 200 205
Leu Trp Ile Ser His Gly Val Thr Ile Phe Arg Val Asp Asn Pro His
210 215 220
Thr Lys Pro Leu Asn Phe Trp Ala Trp Leu Met Glu Gln Val His Arg
225 230 235 240
Arg His Pro Glu Val Ile Phe Leu Ala Glu Ala Phe Thr Arg Pro Glu
245 250 255
Met Ile

<210> 1307
<211> 624
<212> DNA
<213> Homo sapiens

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atgctgggca catgcggtca gggccctgtg cctgagccgt ggaactccac agccattcca
120
catgttcagt cccacaccct gaggccaagg caccccgagt ccctgaggga gcaaggccct
180
gccacccgag gctgccgctg cagaggcaaa cagccccgag caaggcccgg caaccccagg
240
ctgtggctgc atggggcaaa cacagcctgg cctgaggctg ccggccagtc ggggtggcca
300
taggctaacg agaagccagg gcctccctcc ccactgggct ttccacaaaa acctgactaa
360
tgtccaggga cagccaaagg ccttgaggtc agctgggtgg aacacctttc ccctaccatc
420
ccgagatatt gtcttcttgg atggagtttt caaagccctc catgtggagg tctcgggatg
480
agaggcctcg gctgagctct gtgcagagga gcaggaagct gcagaatggg cacccgcctc
540
cctcccagca cctccagtcg ctgccacgcc ccaagctcct gagctgctct gcccaagacc
600
tcccccaacc ttggtctgac gcgt
624

<210> 1308
<211> 100
<212> PRT
<213> Homo sapiens

<400> 1308
Met Ala Thr Pro Thr Gly Arg Gln Pro Gln Ala Arg Leu Cys Leu Pro
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His Ala Ala Thr Ala Trp Gly Cys Arg Ala Leu Leu Gly Ala Val Cys
20 25 30
Leu Cys Ser Gly Ser Leu Gly Trp Gln Gly Leu Ala Pro Ser Gly Thr
35 40 45
Arg Gly Ala Leu Ala Ser Gly Cys Gly Thr Glu His Val Glu Trp Leu
50 55 60
Trp Ser Ser Thr Ala Gln Ala Gln Gly Pro Asp Arg Met Cys Pro Ala
65 70 75 80
Ser Leu Thr Ser Pro Glu Val Gly Cys Arg Glu Pro Gly Ala Trp His
85 90 95
Ser Pro Pro Ala
100

<210> 1309
<211> 563
<212> DNA
<213> Homo sapiens

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120
ttctggctgg cgggcaatgt gttgattgac cggggcaacg cgcacaaggc gcgccgctca
180

atgctcacca ccacccacac cttgcagcat aaagacacat cgatctgggt atttgccgaa
240
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300
attgccgcag gtgtgccgat cgtgcaggtg tgtgtcagca cgtatgtgaa gcacatgaag
360
ctcaatcgtt gggacagtgg cgatatttta attcgctcgt tgccgccaat tcctacgacc
420
ggactgacgt tggatgacat gccacggttg atggagacct gccgtcaaca aatgcgcgag
480
tgcattgagg caatggaccg cgagctggaa atcgtccctt gtaggaacga attggctcgc
540
gaagggcgtt aacgactacg cgt
563

<210> 1310
<211> 183
<212> PRT
<213> Homo sapiens

<400> 1310
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Thr Gly Val Pro Tyr Arg Thr Val Cys Ile Gly Lys Lys Ser Leu Lys
            20   25   30
Trp Val Pro Leu Phe Gly Gln Leu Phe Trp Leu Ala Gly Asn Val Leu
        35   40   45
Ile Asp Arg Gly Asn Ala His Lys Ala Arg Arg Ser Met Leu Thr Thr
    50   55   60
Thr His Thr Leu Gln His Lys Asp Thr Ser Ile Trp Val Phe Ala Glu
65   70   75   80
Gly Thr Arg Asn Phe Gly Glu Thr Leu Leu Pro Phe Lys Lys Gly Ala
                85   90   95
Phe Gln Met Ala Ile Ala Ala Gly Val Pro Ile Val Gln Val Cys Val
            100   105   110
Ser Thr Tyr Val Lys His Met Lys Leu Asn Arg Trp Asp Ser Gly Asp
        115   120   125
Ile Leu Ile Arg Ser Leu Pro Pro Ile Pro Thr Thr Gly Leu Thr Leu
    130   135   140
Asp Asp Met Pro Arg Leu Met Glu Thr Cys Arg Gln Gln Met Arg Glu
145   150   155   160
Cys Ile Glu Ala Met Asp Arg Glu Leu Glu Ile Val Pro Cys Arg Asn
                165   170   175
Glu Leu Ala Arg Glu Gly Arg
            180

<210> 1311
<211> 674
<212> DNA
<213> Homo sapiens

<400> 1311
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60

tccagggccg acccggcaca caccgtcggg ctgacggatg atctgagctg ggtcaagcgc
120
atctcccggc cgccgaaagc cggaatacca cgaggcgctg gatcggcgat tctgttcaca
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gggctgaccc ccgatcagga tcgactgacc aacgagtggg cgcaggcgca cgggttgggg
240
gaattttatg tcatggcccc ccgaatcctc ggtgatgtcc cgctgccaac gatcaccatc
300
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gagagagccg ccaacagtga tctggtgacc agcctcaaac gcatcggatt gggcaggcgt
420
tgggtggacc aggtcatcct tgtggaggtg gctaccacaa tgctggccgc cctgatatgc
480
ggggtgatct cctcggttgt cgcggtgtgg ctcacaggca ggatcctgtc gggagccttg
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gacctgcttg gggccgcgtg gtgggtcttc ggtgcgttgg ccgccgggat gttcggtgga
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tccttgctgg gggccgccat ccatcgccgt taccacttcg acatgagagc tacctgatcc
660
acgaccccgt gaca
674

<210> 1312
<211> 196
<212> PRT
<213> Homo sapiens

<400> 1312
Met Asp Gly Gly Pro Gln Gln Gly Ser Thr Glu His Pro Gly Gly Gln
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20 25 30
Gln Asp Pro Ala Cys Glu Pro His Arg Asp Asn Arg Gly Asp His Pro
35 40 45
Ala Tyr Gln Gly Gly Gln His Cys Gly Ser His Leu His Lys Asp Asp
50 55 60
Leu Val His Pro Thr Pro Ala Gln Ser Asp Ala Phe Glu Ala Gly His
65 70 75 80
Gln Ile Thr Val Gly Gly Ser Leu Leu Leu Arg Gln Gln Ala Arg His
85 90 95
Asp Gly Arg Gln His Asp Glu Gly Asp Gly Arg Asp Asp Gly Asp Arg
100 105 110
Trp Gln Arg Asp Ile Thr Glu Asp Ser Gly Gly His Asp Ile Lys Phe
115 120 125
Pro Gln Pro Val Arg Leu Arg Pro Leu Val Gly Gln Ser Ile Leu Ile
130 135 140
Gly Gly Gln Pro Cys Glu Gln Asn Arg Arg Ser Ser Ala Ser Trp Tyr
145 150 155 160
Ser Gly Phe Arg Arg Pro Gly Asp Ala Leu Asp Pro Ala Gln Ile Ile
165 170 175
Arg Gln Pro Asp Gly Val Cys Arg Val Gly Pro Gly Gly Ile Ile Gly
180 185 190
Gln Val Pro Ala

195

<210> 1313
<211> 367
<212> DNA
<213> Homo sapiens

<400> 1313
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gtggtggcag ctagcgtagg acagtcacga gatttaggag ataaaataga aggtggcggc
120
aaggaaggga gaggacagag cctggtgtga ctcctgggtt tctggtgtgt atagctggtg
180
gacagtggtg tctttgccaa gaggggagcc ctggaagagg agaggtttgc agggcaggtg
240
ctgagtccgg ttttggacac gctgaatttg aggtatctgt cagatatgag acccaaaagg
300
tgagggcggg gaagtggatg tgcaggccct gagctctggg aggggtctgg gtatgctgtg
360
gtcatga
367

<210> 1314
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1314
Met Thr Thr Ala Tyr Pro Asp Pro Ser Gln Ser Ser Gly Pro Ala His
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Pro Leu Pro Arg Pro His Leu Leu Gly Leu Ile Ser Asp Arg Tyr Leu
            20   25   30
Lys Phe Ser Val Ser Lys Thr Gly Leu Ser Thr Cys Pro Ala Asn Leu
        35   40   45
Ser Ser Ser Arg Ala Pro Leu Leu Ala Lys Thr Pro Leu Ser Thr Ser
    50   55   60
Tyr Thr His Gln Lys Pro Arg Ser His Thr Arg Leu Cys Pro Leu Pro
65   70   75   80
Ser Leu Pro Pro Pro Ser Ile Leu Ser Pro Lys Ser Arg Asp Cys Pro
                85   90   95
Thr Leu Ala Ala Thr Thr Ala Ala Ala Pro Ala Ala Pro Pro Ala Pro
            100   105   110
Ala Thr Trp Arg Gly Cys Met Asp Ile
        115   120

<210> 1315
<211> 5245
<212> DNA
<213> Homo sapiens

<400> 1315
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gacatggatg atgcatctaa gcttcttcag gattatgata ttcgaactgg caacaccagg
120
gaagctttga gtccttgtcc aagtactgta agtaccaagt ctcagccagg cagcagtgct
180
tcttctagtt ctggagttaa aatgaccagc tttgctgaac aaaaattcag gaaactgaat
240
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300
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360
ggacgggaca ctacccagct gttggcctct gaaatggtgc atcttaggat gaaactagaa
420
gaaaagaggc gtgctataga agcccagaaa aagaaaatgg aagctgcttt taccaaacag
480
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540
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600
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660
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720
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780
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840
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1080
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1140
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1200
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1260
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1620
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1680

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5245

<210> 1316
<211> 856
<212> PRT
<213> Homo sapiens

<400> 1316
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20 25 30
Gly Asn Thr Arg Glu Ala Leu Ser Pro Cys Pro Ser Thr Val Ser Thr
35 40 45
Lys Ser Gln Pro Gly Ser Ser Ala Ser Ser Ser Ser Gly Val Lys Met
50 55 60
Thr Ser Phe Ala Glu Gln Lys Phe Arg Lys Leu Asn His Thr Asp Gly
65 70 75 80
Lys Ser Ser Gly Ser Ser Ser Gln Lys Thr Thr Pro Glu Gly Ser Glu
85 90 95
Leu Asn Ile Pro His Val Val Ala Trp Ala Gln Ile Pro Glu Glu Thr
100 105 110
Gly Leu Pro Gln Gly Arg Asp Thr Thr Gln Leu Leu Ala Ser Glu Met
115 120 125
Val His Leu Arg Met Lys Leu Glu Glu Lys Arg Arg Ala Ile Glu Ala
130 135 140
Gln Lys Lys Lys Met Glu Ala Ala Phe Thr Lys Gln Arg Gln Lys Met
145 150 155 160
Gly Arg Thr Ala Phe Leu Thr Val Val Lys Lys Lys Gly Asp Gly Ile
165 170 175
Ser Pro Leu Arg Glu Glu Ala Ala Gly Ala Glu Asp Glu Lys Val Tyr
180 185 190
Thr Asp Arg Ala Lys Glu Lys Glu Ser Gln Lys Thr Asp Gly Gln Arg
195 200 205
Ser Lys Ser Leu Ala Asp Ile Lys Glu Ser Met Glu Asn Pro Gln Ala
210 215 220
Lys Trp Leu Lys Ser Pro Thr Thr Pro Ile Asp Pro Glu Lys Gln Trp
225 230 235 240
Asn Leu Ala Ser Pro Ser Glu Glu Thr Leu Asn Glu Gly Glu Ile Leu
245 250 255
Glu Tyr Thr Lys Ser Ile Glu Lys Leu Asn Ser Ser Leu His Phe Leu
260 265 270
Gln Gln Glu Met Gln Arg Leu Ser Leu Gln Gln Glu Met Leu Met Gln

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        275                 280                 285
Met Arg Glu Gln Gln Ser Trp Val Ile Ser Pro Pro Gln Pro Ser Pro
    290                 295                 300
Gln Lys Gln Ile Arg Asp Phe Lys Pro Ser Lys Gln Ala Gly Leu Ser
305                 310                 315                 320
Ser Ala Ile Ala Pro Phe Ser Ser Asp Ser Pro Arg Pro Thr His Pro
                325                 330                 335
Ser Pro Gln Ser Ser Asn Arg Lys Ser Ala Ser Phe Ser Val Lys Ser
            340                 345                 350
Gln Arg Thr Pro Arg Pro Asn Glu Leu Lys Ile Thr Pro Leu Asn Arg
        355                 360                 365
Thr Leu Thr Pro Pro Arg Ser Val Asp Ser Leu Pro Arg Leu Arg Arg
    370                 375                 380
Phe Ser Pro Ser Gln Val Pro Ile Gln Thr Arg Ser Phe Val Cys Phe
385                 390                 395                 400
Gly Asp Asp Gly Glu Pro Gln Leu Lys Glu Ser Lys Pro Lys Glu Glu
                405                 410                 415
Val Lys Lys Glu Glu Leu Glu Ser Lys Gly Thr Leu Glu Gln Arg Gly
            420                 425                 430
His Asn Pro Glu Glu Lys Glu Ile Lys Pro Phe Glu Ser Thr Val Ser
        435                 440                 445
Glu Val Leu Ser Leu Pro Val Thr Glu Thr Val Cys Leu Thr Pro Asn
    450                 455                 460
Glu Asp Gln Leu Asn Gln Pro Thr Glu Pro Pro Pro Lys Pro Val Phe
465                 470                 475                 480
Pro Pro Thr Ala Pro Lys Asn Val Asn Leu Ile Glu Val Ser Leu Ser
                485                 490                 495
Asp Leu Lys Pro Pro Glu Lys Ala Asp Val Pro Val Glu Lys Tyr Asp
            500                 505                 510
Gly Glu Ser Asp Lys Glu Gln Phe Asp Asp Asp Gln Lys Val Cys Cys
        515                 520                 525
Gly Phe Phe Phe Lys Asp Asp Gln Lys Ala Glu Asn Asp Met Ala Met
    530                 535                 540
Lys Arg Ala Ala Leu Leu Glu Lys Arg Leu Arg Arg Glu Lys Glu Thr
545                 550                 555                 560
Gln Leu Arg Lys Gln Gln Leu Glu Ala Glu Met Glu His Lys Lys Glu
                565                 570                 575
Glu Thr Arg Arg Lys Thr Glu Glu Glu Arg Gln Lys Lys Glu Asp Glu
            580                 585                 590
Arg Ala Arg Arg Glu Phe Ile Arg Gln Glu Tyr Met Arg Arg Lys Gln
        595                 600                 605
Leu Lys Leu Met Glu Asp Met Asp Thr Val Ile Lys Pro Arg Pro Gln
    610                 615                 620
Val Val Lys Gln Lys Lys Gln Arg Pro Lys Ser Ile His Arg Asp His
625                 630                 635                 640
Ile Glu Ser Pro Lys Thr Pro Ile Lys Gly Pro Pro Val Ser Ser Leu
                645                 650                 655
Ser Leu Ala Ser Leu Asn Thr Gly Asp Asn Glu Ser Val His Ser Gly
            660                 665                 670
Lys Arg Thr Pro Arg Ser Glu Ser Val Glu Gly Phe Leu Ser Pro Ser
        675                 680                 685
Arg Cys Gly Ser Arg Asn Gly Glu Lys Asp Trp Glu Asn Ala Ser Thr
    690                 695                 700
Thr Ser Ser Val Ala Ser Gly Thr Glu Tyr Thr Gly Pro Lys Leu Tyr
```

```
705                 710                 715                 720
Lys Glu Pro Ser Ala Lys Ser Asn Lys His Ile Ile Gln Asn Ala Leu
                725                 730                 735
Ala His Cys Cys Leu Ala Gly Lys Val Asn Glu Gly Gln Lys Lys Lys
            740                 745                 750
Ile Leu Glu Glu Met Glu Lys Ser Asp Ala Asn Asn Phe Leu Ile Leu
        755                 760                 765
Phe Arg Asp Ser Gly Cys Gln Phe Arg Ser Leu Tyr Thr Tyr Cys Pro
    770                 775                 780
Glu Thr Glu Glu Ile Asn Lys Leu Thr Gly Ile Gly Pro Lys Ser Ile
785                 790                 795                 800
Thr Lys Lys Met Ile Glu Gly Leu Tyr Lys Tyr Asn Ser Asp Arg Lys
                805                 810                 815
Gln Phe Ser His Ile Pro Ala Lys Thr Leu Ser Ala Ser Val Asp Ala
            820                 825                 830
Ile Thr Ile His Ser His Leu Trp Gln Thr Lys Arg Pro Val Thr Pro
        835                 840                 845
Lys Lys Leu Leu Pro Thr Lys Ala
    850                 855
```

<210> 1317
<211> 1123
<212> DNA
<213> Homo sapiens

<400> 1317

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ncggccgagg gcattcacct caacatggca gcaggcagcg gtgtccccgg cagtggactg
60
ggcgaggagg tgccctgtgc catgatggag ggtgtggcag cctacaccca gacagagccc
120
gagggtagcc agcctagcac catggacgcc accgcagtag caggcatcga gaccaagaaa
180
gagaaggagg acctgtgctt gctaaagaag gaggagaagg aggagccagt agccccggag
240
ctggcaacaa cggtgcctga gagcgcagag cctgaggcag aggcggacgg ggaggagctg
300
gacggcagcg acatgtcagc catcatctat gaaatcccca aggagcctga gaagaggcgg
360
cggagcaagc ggtcgcgggt gatggatgct gacggcctgc tcgagatgtt ccactgccca
420
tacgagggct gcagccaagt ctacgtggcc ctcagcagct tccagaacca cgtcaatctt
480
gtgcatcgga aaggaaagac caaagtgtgc cctcatcctg gctgtggcaa gaagttctat
540
ttatccaacc acctgcggcg gcacatgatc atccattcag gtgtccgtga attcacctgc
600
gagacctgcg gcaagtcctt caagaggaag aaccacctgg aggtacatcg gcgcacccac
660
accggcgaga ccccccctgca gtgcgtgatc tgtggctacc agtgccggca gcgcgcgtcg
720
ctcaactggc acatgaagaa gcacactgcg gaggtgcagt acaacttcac gtgcgatgcc
780
tgcgggaagc gcttcgagaa gctggacagc gtcaagttcc acacgctcaa aagccacccg
840
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gatcacaagc ccacctgacc cacctgacca ctgaccgccc ctatttattc gtccgctcgg
900
acaccacagc ccgggcttgc cggggcctgg acagctgcga gggccggccg gaccgcgggc
960
cggaaggagc gcccccgccc cgccccagag ctggcgcccc tgggcaggtt ccccacccca
1020
ccccaccgca tccttctcgg agctggtgcc tggggctgca ttgctggaac tgtgtcaaga
1080
gagcagagtg agattaaaga gcgagaaagg aaaaaaaaaa aaa
1123

<210> 1318
<211> 285
<212> PRT
<213> Homo sapiens

<400> 1318
Xaa Ala Glu Gly Ile His Leu Asn Met Ala Ala Gly Ser Gly Val Pro
1 5 10 15
Gly Ser Gly Leu Gly Glu Glu Val Pro Cys Ala Met Met Glu Gly Val
20 25 30
Ala Ala Tyr Thr Gln Thr Glu Pro Glu Gly Ser Gln Pro Ser Thr Met
35 40 45
Asp Ala Thr Ala Val Ala Gly Ile Glu Thr Lys Lys Glu Lys Glu Asp
50 55 60
Leu Cys Leu Leu Lys Lys Glu Glu Lys Glu Glu Pro Val Ala Pro Glu
65 70 75 80
Leu Ala Thr Thr Val Pro Glu Ser Ala Glu Pro Glu Ala Glu Ala Asp
85 90 95
Gly Glu Glu Leu Asp Gly Ser Asp Met Ser Ala Ile Ile Tyr Glu Ile
100 105 110
Pro Lys Glu Pro Glu Lys Arg Arg Arg Ser Lys Arg Ser Arg Val Met
115 120 125
Asp Ala Asp Gly Leu Leu Glu Met Phe His Cys Pro Tyr Glu Gly Cys
130 135 140
Ser Gln Val Tyr Val Ala Leu Ser Ser Phe Gln Asn His Val Asn Leu
145 150 155 160
Val His Arg Lys Gly Lys Thr Lys Val Cys Pro His Pro Gly Cys Gly
165 170 175
Lys Lys Phe Tyr Leu Ser Asn His Leu Arg Arg His Met Ile Ile His
180 185 190
Ser Gly Val Arg Glu Phe Thr Cys Glu Thr Cys Gly Lys Ser Phe Lys
195 200 205
Arg Lys Asn His Leu Glu Val His Arg Arg Thr His Thr Gly Glu Thr
210 215 220
Pro Leu Gln Cys Val Ile Cys Gly Tyr Gln Cys Arg Gln Arg Ala Ser
225 230 235 240
Leu Asn Trp His Met Lys Lys His Thr Ala Glu Val Gln Tyr Asn Phe
245 250 255
Thr Cys Asp Ala Cys Gly Lys Arg Phe Glu Lys Leu Asp Ser Val Lys
260 265 270
Phe His Thr Leu Lys Ser His Pro Asp His Lys Pro Thr
275 280 285

<210> 1319
<211> 538
<212> DNA
<213> Homo sapiens

<400> 1319
cgggagcgga gcccagctct tggctggtga tgagggcctg gaagcagatg gcctctcagt
60
cctccatttg ggaggactcc caaaatagtg caggctcgag ggggtgggga atggctcctg
120
ctgaatgtgt gaatgggtcc ctgggtgctt tccttcctct gggagctccg tgggagagtg
180
gagtcgatgc caagtcagag agcagttggg gaggaaccca gaagccctgg gatggtgtct
240
gcatgggaat gtgtagggag gcagccacaa tgggcctggg ccttcctttc tctccttcct
300
gtccccctcc cccatccccc tctctcctcc cttccttctg gaaacccagt actgggggaa
360
acacacacag gtgggatgca ggtatccggg aagctcatag aagctgccac gctgctggag
420
tttgcctcat acaggagcgt gggcatgccc cgcgtggagt tgtgctgtgt gtgtgcatat
480
gtatggttgt gtgtgcatgg gggtggggga ttctgacctg gggtcactcc caaagctt
538

<210> 1320
<211> 169
<212> PRT
<213> Homo sapiens

<400> 1320
Met Arg Ala Trp Lys Gln Met Ala Ser Gln Ser Ser Ile Trp Glu Asp
 1   5   10   15
Ser Gln Asn Ser Ala Gly Ser Arg Gly Trp Gly Met Ala Pro Ala Glu
            20   25   30
Cys Val Asn Gly Ser Leu Gly Ala Phe Leu Pro Leu Gly Ala Pro Trp
        35   40   45
Glu Ser Gly Val Asp Ala Lys Ser Glu Ser Ser Trp Gly Gly Thr Gln
    50   55   60
Lys Pro Trp Asp Gly Val Cys Met Gly Met Cys Arg Glu Ala Ala Thr
65   70   75   80
Met Gly Leu Gly Leu Pro Phe Ser Pro Ser Cys Pro Pro Pro Pro Ser
                85   90   95
Pro Ser Leu Leu Pro Ser Phe Trp Lys Pro Ser Thr Gly Gly Asn Thr
            100   105   110
His Arg Trp Asp Ala Gly Ile Arg Glu Ala His Arg Ser Cys His Ala
        115   120   125
Ala Gly Val Cys Leu Ile Gln Glu Arg Gly His Ala Pro Arg Gly Val
    130   135   140
Val Leu Cys Val Cys Ile Cys Met Val Val Cys Ala Trp Gly Trp Gly
145   150   155   160
Ile Leu Thr Trp Gly His Ser Gln Ser
                165

<210> 1321
<211> 1292
<212> DNA
<213> Homo sapiens

<400> 1321
nacgcgtacc gtcgctgatc tcccccgtgg tcgtgaccaa cgcggccggg ttcaccatct
60
cggaacgcag caatgatccg gcgtcagtgc tctcagtcac cgcaggatga cccggtgcaa
120
cgcccggatc gctcacggta cgcaacgacg aagcagggat cgctcagacc cgggcacgtc
180
atcgtcaaga agatttacaa caacaatgtc cttctcggcg tcaacggttc ggggaccgaa
240
atggtcgtca atgctcgcgg tatcgcctac ggacgacacc gcggggagat cgtcgatgcc
300
tcgtcggccc agcgatatgt cgcagagggt gcctatcgca cgaccgccat cgcatcactg
360
ctaacgaacg ccactcacac cgaggtgcga gtggcacagg caatcgtcga attggcgcgc
420
gaagagctgg gcactcccca tgcccgacgg atgatgctgc ccatcctcga tcacctcgtc
480
gcagctgtgc accgagctaa gcaggggggcc gtcatcgatt ttcccctgga atgggaagtc
540
cgtcagctct atcccgatga ggcggaactg ggccgacgcg ctgtcgaaat cgtcgacggt
600
gctctcgaaa tccatttgca acccgaggaa tgggtggcat tctccctgca cttcatcaat
660
cagcggtggg acagtagaga cgtttcgcgg accatgtcga tgactcagac gatctgcgac
720
gttttcaccg agctggagga cctgtggcac gttgagatcg accgttcgtc catgagcgca
780
tcccgcttcg tcacccacct tcgctatctg ttcgctcggg cctcggacaa caagcagctc
840
tctcacgttg acctggacat tgtgggactc atgtcagatc gctacccaga agccacattg
900
gcagctagcc aagtggccga gcacatatcg aaagcaatcg gcaacgacct gacggaagcc
960
gaaatcaact acatcgcctt acacaccacc cggctctaca acgaggtgat ggggatggat
1020
gactgacgat cgcgcacctg ttaaggctca tcggtagtgg gcaatacaca aaatggcgat
1080
gaccttcctg ccggaaagcc agcaccaaag tcacccagat caaaattcag atgcgtgcct
1140
aattcccacc ccgacatcca agaggtcagg gggggttgt tgggggtggt gggtgggggt
1200
ggggggggttt gcatgctcag gggtgggggc tttgttgaag ccatcatgaa gttgcaaacc
1260
caggactgtt ccactagtaa agcccctgcc tt
1292

<210> 1322
<211> 317
<212> PRT

<213> Homo sapiens

<400> 1322

```
Met Ile Arg Arg Gln Cys Ser Gln Ser Pro Gln Asp Asp Pro Val Gln
 1               5                  10                  15
Arg Pro Asp Arg Ser Arg Tyr Ala Thr Thr Lys Gln Gly Ser Leu Arg
            20                  25                  30
Pro Gly His Val Ile Val Lys Lys Ile Tyr Asn Asn Asn Val Leu Leu
        35                  40                  45
Gly Val Asn Gly Ser Gly Thr Glu Met Val Val Asn Ala Arg Gly Ile
    50                  55                  60
Ala Tyr Gly Arg His Arg Gly Glu Ile Val Asp Ala Ser Ser Ala Gln
65                  70                  75                  80
Arg Tyr Val Ala Glu Gly Ala Tyr Arg Thr Thr Ala Ile Ala Ser Leu
                85                  90                  95
Leu Thr Asn Ala Thr His Thr Glu Val Arg Val Ala Gln Ala Ile Val
            100                 105                 110
Glu Leu Ala Arg Glu Glu Leu Gly Thr Pro His Ala Arg Arg Met Met
        115                 120                 125
Leu Pro Ile Leu Asp His Leu Val Ala Ala Val His Arg Ala Lys Gln
    130                 135                 140
Gly Ala Val Ile Asp Phe Pro Leu Glu Trp Glu Val Arg Gln Leu Tyr
145                 150                 155                 160
Pro Asp Glu Ala Glu Leu Gly Arg Arg Ala Val Glu Ile Val Asp Gly
                165                 170                 175
Ala Leu Glu Ile His Leu Gln Pro Glu Glu Trp Val Ala Phe Ser Leu
            180                 185                 190
His Phe Ile Asn Gln Arg Trp Asp Ser Arg Asp Val Ser Arg Thr Met
        195                 200                 205
Ser Met Thr Gln Thr Ile Cys Asp Val Phe Thr Glu Leu Glu Asp Leu
    210                 215                 220
Trp His Val Glu Ile Asp Arg Ser Ser Met Ser Ala Ser Arg Phe Val
225                 230                 235                 240
Thr His Leu Arg Tyr Leu Phe Ala Arg Ala Ser Asp Asn Lys Gln Leu
                245                 250                 255
Ser His Val Asp Leu Asp Ile Val Gly Leu Met Ser Asp Arg Tyr Pro
            260                 265                 270
Glu Ala Thr Leu Ala Ala Ser Gln Val Ala Glu His Ile Ser Lys Ala
        275                 280                 285
Ile Gly Asn Asp Leu Thr Glu Ala Glu Ile Asn Tyr Ile Ala Leu His
    290                 295                 300
Thr Thr Arg Leu Tyr Asn Glu Val Met Gly Met Asp Asp
305                 310                 315
```

<210> 1323
<211> 306
<212> DNA
<213> Homo sapiens

<400> 1323

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cgcgtgatgg gaatgcgtca ctatgatgtt cagttgattg gtggtatcac tctgcacgaa
60
ggcaaaattg ctgagatgcg tacaggtgaa ggtaaaaccc tgatgggtac tttagcgtgt
120
```

tacctcaatg cattgagtgg tcagggtgtg catgtcatca ccgtcaatga ctatcttgca
180
caacgtgatg ctgaactcaa ccgcccatta tttgagtttt tgggtttaag catcggtgtg
240
atttattcga tgcaaatgcc tgctgagaaa gcacaagctt atttagcaga cattacttac
300
ggtacc
306

<210> 1324
<211> 102
<212> PRT
<213> Homo sapiens

<400> 1324
Arg Val Met Gly Met Arg His Tyr Asp Val Gln Leu Ile Gly Gly Ile
1 5 10 15
Thr Leu His Glu Gly Lys Ile Ala Glu Met Arg Thr Gly Glu Gly Lys
20 25 30
Thr Leu Met Gly Thr Leu Ala Cys Tyr Leu Asn Ala Leu Ser Gly Gln
35 40 45
Gly Val His Val Ile Thr Val Asn Asp Tyr Leu Ala Gln Arg Asp Ala
50 55 60
Glu Leu Asn Arg Pro Leu Phe Glu Phe Leu Gly Leu Ser Ile Gly Val
65 70 75 80
Ile Tyr Ser Met Gln Met Pro Ala Glu Lys Ala Gln Ala Tyr Leu Ala
85 90 95
Asp Ile Thr Tyr Gly Thr
100

<210> 1325
<211> 391
<212> DNA
<213> Homo sapiens

<400> 1325
gtgcacatgg gcccactggc gaatccgacg cgcggcctac ggcgcgcaat actggcggcc
60
attgtcgccg catgttccgt ctccgctcat gccggaagct ggccagagaa accgatcacg
120
atggtcgtgc cgtttcccgc cggaggcggc accgatctcg tggcgcgctc gatccagccg
180
cttttgcagc gcgaactcgg acaaccggtg gtgatcgaca accgcagcgg cgcaggcggc
240
acgctcggct ccagcttcgt ggcgcgggcc gttgccgacg gctacacggc tggcgtggtc
300
accacgagca cccacgcggt aagcgtcgcg ctctatcccc ggctggccta caacccgaca
360
gcggactttg catacgccgg cttcatcggc n
391

<210> 1326
<211> 130
<212> PRT

<213> Homo sapiens

<400> 1326
Val His Met Gly Pro Leu Ala Asn Pro Thr Arg Gly Leu Arg Arg Ala
1 5 10 15
Ile Leu Ala Ala Ile Val Ala Ala Cys Ser Val Ser Ala His Ala Gly
20 25 30
Ser Trp Pro Glu Lys Pro Ile Thr Met Val Val Pro Phe Pro Ala Gly
35 40 45
Gly Gly Thr Asp Leu Val Ala Arg Ser Ile Gln Pro Leu Leu Gln Arg
50 55 60
Glu Leu Gly Gln Pro Val Val Ile Asp Asn Arg Ser Gly Ala Gly Gly
65 70 75 80
Thr Leu Gly Ser Ser Phe Val Ala Arg Ala Val Ala Asp Gly Tyr Thr
85 90 95
Ala Gly Val Val Thr Thr Ser Thr His Ala Val Ser Val Ala Leu Tyr
100 105 110
Pro Arg Leu Ala Tyr Asn Pro Thr Ala Asp Phe Ala Tyr Ala Gly Phe
115 120 125
Ile Gly
130

<210> 1327
<211> 324
<212> DNA
<213> Homo sapiens

<400> 1327
nnacgcgtga tttcggaact gcagcagttc gagcagtcgc atggacagag cgacgggagc
60
tactggctat ggttcgagct gctgtggcga gactatttcc gctttctgca tcttcggcat
120
ggcgctcggc tgtaccgcgc acgcggcctc gcaaatgagg tacggcacgc ggagcgccca
180
gatgtgcagg gcttcgagcg ctggcgtcgt gcatcgaccg gcgagccgct cgtcgatgcc
240
gcgatgcgcg agctggagac caccggctac ctcagcaaca ggctcagaca ggtggtcgcg
300
agctacctcg tgcacgagct ggga
324

<210> 1328
<211> 108
<212> PRT
<213> Homo sapiens

<400> 1328
Xaa Arg Val Ile Ser Glu Leu Gln Gln Phe Glu Gln Ser His Gly Gln
1 5 10 15
Ser Asp Gly Ser Tyr Trp Leu Trp Phe Glu Leu Leu Trp Arg Asp Tyr
20 25 30
Phe Arg Phe Leu His Leu Arg His Gly Ala Arg Leu Tyr Arg Ala Arg
35 40 45
Gly Leu Ala Asn Glu Val Arg His Ala Glu Arg Pro Asp Val Gln Gly

```
    50                  55                  60
Phe Glu Arg Trp Arg Arg Ala Ser Thr Gly Glu Pro Leu Val Asp Ala
65                  70                  75                  80
Ala Met Arg Glu Leu Glu Thr Thr Gly Tyr Leu Ser Asn Arg Leu Arg
                85                  90                  95
Gln Val Val Ala Ser Tyr Leu Val His Glu Leu Gly
            100                 105
```

<210> 1329
<211> 438
<212> DNA
<213> Homo sapiens

<400> 1329
ngtgcacgct tagcattaga tttagcttcc agtggcaaaa ctacgtcgtt gatttcaagc
60
ggcgatatcg gcatttacgc gatggcgacc ctggtgtttg aactgctgga tagacaactc
120
cagggccttg aagaccatcc tgaatggtta gatgttgaaa tcgatgtggt acctggcatc
180
tctgcaatgc aagctggtgc aagtcgtatt ggtgcgatgt taggtcatga cttttgtacg
240
gtgagtttgt ctgatttatt aacccccttgg gaaactatta ataaacgtat tcatagtgca
300
ggtgaggggg attttgttat ctctttttat aaccctgttt ctaagaaacg tgattggcag
360
cttaaccacg cgcgtgatgt attattgaaa taccgtccag catcaacgcc agttttatta
420
ggtcgtcagt tgacgcgt
438

<210> 1330
<211> 146
<212> PRT
<213> Homo sapiens

<400> 1330
```
Xaa Ala Arg Leu Ala Leu Asp Leu Ala Ser Ser Gly Lys Thr Thr Ser
 1               5                  10                  15
Leu Ile Ser Ser Gly Asp Ile Gly Ile Tyr Ala Met Ala Thr Leu Val
            20                  25                  30
Phe Glu Leu Leu Asp Arg Gln Leu Gln Gly Leu Glu Asp His Pro Glu
        35                  40                  45
Trp Leu Asp Val Glu Ile Asp Val Val Pro Gly Ile Ser Ala Met Gln
    50                  55                  60
Ala Gly Ala Ser Arg Ile Gly Ala Met Leu Gly His Asp Phe Cys Thr
65                  70                  75                  80
Val Ser Leu Ser Asp Leu Leu Thr Pro Trp Glu Thr Ile Asn Lys Arg
                85                  90                  95
Ile His Ser Ala Gly Glu Gly Asp Phe Val Ile Ser Phe Tyr Asn Pro
            100                 105                 110
Val Ser Lys Lys Arg Asp Trp Gln Leu Asn His Ala Arg Asp Val Leu
        115                 120                 125
Leu Lys Tyr Arg Pro Ala Ser Thr Pro Val Leu Leu Gly Arg Gln Leu
```

```
    130                 135                 140
Thr Arg
145

<210> 1331
<211> 453
<212> DNA
<213> Homo sapiens

<400> 1331
gcgtaccgct ccgcggaact ggtgatgatg accgaggcac cgggatgcgg aatcccctgg
60
catcttctgg ccggcatcgg acgcatcgaa tccggtcacg ccaacggcgg caagacgacc
120
tcggtgggta cgaacgtcac cccgatcctc ggccccatcc tcgacggacg gctggcaggc
180
aacgaagtca ttcgggacac cgacaagggc aatcgacggc gacccactca cgaccgcgcc
240
gtcgggccga tgcagttcat tccggccacc tgggccggat atgccagcga cggcaacggg
300
gacggaatca aggaccccaa caacgtcttc gatgcggcac tctcggcagc gaagtacctc
360
tgcagcggcg gactcaacct gcgcgatgtc gcccaggaga ccaaagctgt tctgcgatac
420
aacaactcgg ccgcttacgc agcaaacgtg atc
453

<210> 1332
<211> 151
<212> PRT
<213> Homo sapiens

<400> 1332
Ala Tyr Arg Ser Ala Glu Leu Val Met Met Thr Glu Ala Pro Gly Cys
 1               5                  10                  15
Gly Ile Pro Trp His Leu Leu Ala Gly Ile Gly Arg Ile Glu Ser Gly
            20                  25                  30
His Ala Asn Gly Gly Lys Thr Thr Ser Val Gly Thr Asn Val Thr Pro
        35                  40                  45
Ile Leu Gly Pro Ile Leu Asp Gly Arg Leu Ala Gly Asn Glu Val Ile
    50                  55                  60
Arg Asp Thr Asp Lys Gly Asn Arg Arg Arg Pro Thr His Asp Arg Ala
65                  70                  75                  80
Val Gly Pro Met Gln Phe Ile Pro Ala Thr Trp Ala Gly Tyr Ala Ser
                85                  90                  95
Asp Gly Asn Gly Asp Gly Ile Lys Asp Pro Asn Asn Val Phe Asp Ala
            100                 105                 110
Ala Leu Ser Ala Ala Lys Tyr Leu Cys Ser Gly Gly Leu Asn Leu Arg
        115                 120                 125
Asp Val Ala Gln Glu Thr Lys Ala Val Leu Arg Tyr Asn Asn Ser Ala
    130                 135                 140
Ala Tyr Ala Ala Asn Val Ile
145                 150
```

<210> 1333
<211> 540
<212> DNA
<213> Homo sapiens

<400> 1333
acgcgtcgcc cacactgttg ccgccgaggc ggctcgagcc gggtgtgagg aaggatccgc
60
ggcacagctc gtcggtcaag atgggtctag tgctgctcgt atggcggcgg aggcatccgc
120
gcgaagggct aaagcggatg gactaagcca gcttgtcatc gatgtcaatg gagacgccgt
180
cagcgtcgcg acggaaatca cccggcctac tcgtctatta gcccttattg gactaaccga
240
agtacacggt cgggcgagcg aaatgtgtat tttgctggct cgctgaggcc gttgcagcga
300
tacaatgatg aggtgtctaa gtattttccg gtccacccgg agaacccgca gcagcgttct
360
ctcaatcaga tcgtcgacat cctgcaccat ggcggtctta tcgcctaccc gacagacacg
420
ggttatgcct tcggtgcccg gntagggaat aaggatgccg tggaccggat tcgcaaactt
480
cgccagttat ttgacaagca tcacttcacc ctggtcatga gccagtttgc gcaggttggc
540

<210> 1334
<211> 70
<212> PRT
<213> Homo sapiens

<400> 1334
Val His Pro Glu Asn Pro Gln Gln Arg Ser Leu Asn Gln Ile Val Asp
 1   5   10   15
Ile Leu His His Gly Gly Leu Ile Ala Tyr Pro Thr Asp Thr Gly Tyr
            20   25   30
Ala Phe Gly Ala Arg Xaa Gly Asn Lys Asp Ala Val Asp Arg Ile Arg
        35   40   45
Lys Leu Arg Gln Leu Phe Asp Lys His His Phe Thr Leu Val Met Ser
    50   55   60
Gln Phe Ala Gln Val Gly
65   70

<210> 1335
<211> 748
<212> DNA
<213> Homo sapiens

<400> 1335
nctctcatac ttttttttccc tattcctatc ccccctctct ccgaccgcgt gaagcgttct
60
gtgaatgcca agaagaagcg tcgtgaggtc ctcgatcagg cctccggtta ccgtggtcag
120
cgctcgcgcc tgtaccgcaa ggccaaggag cagaccctcc attcggccac ttattcgttc
180

cgtgaccgtc gtgctaagaa gggtgacttc cgctcgctgt ggatccagcg catcaatgct
240
gcttcccgtg cccagggcat gacctacaac cgtttcatca acggtctgaa gaacgctggc
300
gtcgaggtcg accgcaagat gctcgctgag cttgccgtct ccgacattaa cgccttcaac
360
agcctggtcg aggtcgctaa ggctagccag ccgcagaacg ctgctgcctg agatggccat
420
gactggcggg ccgaacgacg actatttggg atgggatcgc atctcgaagg ggtcattgcg
480
ttcggcccgt cgtctttcat ctcggcgcgg acgcgatgag tccgggctgt tcttggtaga
540
aggtgcgcag gcagttcgtg aagccctagc atggccgggt aaagtcaatt tgttggcaac
600
ctcggaccca gctcgcgatg ctgagcatgt cgaggtggct acatgtcgtg gcgttcgggt
660
cgtggtgctc actgacgagg atgtcaatgc gctttctgat accgtcacca gtcaggggat
720
cttcgcggta tgtcggcagg ttacgcgt
748

<210> 1336
<211> 136
<212> PRT
<213> Homo sapiens

<400> 1336
Xaa Leu Ile Leu Phe Phe Pro Ile Pro Ile Pro Pro Leu Ser Asp Arg
 1   5   10   15
Val Lys Arg Ser Val Asn Ala Lys Lys Lys Arg Arg Glu Val Leu Asp
            20   25   30
Gln Ala Ser Gly Tyr Arg Gly Gln Arg Ser Arg Leu Tyr Arg Lys Ala
        35   40   45
Lys Glu Gln Thr Leu His Ser Ala Thr Tyr Ser Phe Arg Asp Arg Arg
    50   55   60
Ala Lys Lys Gly Asp Phe Arg Ser Leu Trp Ile Gln Arg Ile Asn Ala
65   70   75   80
Ala Ser Arg Ala Gln Gly Met Thr Tyr Asn Arg Phe Ile Asn Gly Leu
                85   90   95
Lys Asn Ala Gly Val Glu Val Asp Arg Lys Met Leu Ala Glu Leu Ala
            100   105   110
Val Ser Asp Ile Asn Ala Phe Asn Ser Leu Val Glu Val Ala Lys Ala
        115   120   125
Ser Gln Pro Gln Asn Ala Ala Ala
    130   135

<210> 1337
<211> 364
<212> DNA
<213> Homo sapiens

<400> 1337
acgcgtgagg ccaggccact gggcaccgcc gttagccagg gcagcctcct tcagtggtca
60

aggcagactc agctcatggg cgagcatgtc agtgaagggc acagcaaggc tcacgagtgg
120
gcctcttgcc tcatggtcag tgtgggtcag tgctttcgct gtatgagact acagggtttc
180
tctgcctcac catgggggac gattgggtct gggtcacttc ctgctgtggg acctgtcctg
240
ggcactgcag gatgtggggc agggctccta cgtgccagct accagatgcc agcagcaccc
300
ccagaagtga caaccacaac catctccagg tgttgccagt gtcccctggg ggtcagagtg
360
gccc
364

<210> 1338
<211> 96
<212> PRT
<213> Homo sapiens

<400> 1338
Met Gly Glu His Val Ser Glu Gly His Ser Lys Ala His Glu Trp Ala
 1   5   10   15
Ser Cys Leu Met Val Ser Val Gly Gln Cys Phe Arg Cys Met Arg Leu
            20   25   30
Gln Gly Phe Ser Ala Ser Pro Trp Gly Thr Ile Gly Ser Gly Ser Leu
        35   40   45
Pro Ala Val Gly Pro Val Leu Gly Thr Ala Gly Cys Gly Ala Gly Leu
    50   55   60
Leu Arg Ala Ser Tyr Gln Met Pro Ala Ala Pro Pro Glu Val Thr Thr
65   70   75   80
Thr Thr Ile Ser Arg Cys Cys Gln Cys Pro Leu Gly Val Arg Val Ala
                85   90   95

<210> 1339
<211> 653
<212> DNA
<213> Homo sapiens

<400> 1339
cgcgttgtct tcaacatcga cgaaaagcag tgcattgacc tggcgcaccg tggtactgag
60
tgggtcgtca ggtacgccga caagtacctc ggcgacgttg agttcggcta cgagtactct
120
ccggagatgt ttagccagac ccgcacggac ttcgctatcg acgtctgtca ctccgtgatg
180
gacgtgtggc agccggggcc aggccgtgag attatcctta atctgccggc taccgtcgag
240
atgagtactc cgaacaccta cgccgaccaa atcgagtact tctgccgcaa tatccgtgat
300
cgtgagcacg tgtgcgtctc tttgcacccg cacaatgatc gtggcacggc gatcgcggcc
360
gccgagttcg cgcagatggc gggcgccgat cgcgtcgagg gctgtttctt tggccccggc
420
gagcgcccgg gcaccgtcga cctggtcacc ctgggcatga acctcgtcag ccagggagtt
480

gacgccggta tcgacttctc cgacatgccc aagatccgcc gcaccgtcga gtactgcacc
540
tgtctgccag taccggcccg ccagccctac tccggcgatc tggtcttcac cgccttctcc
600
ggttcccacc aggacgccat caagaagggt ctggaagacc tggcccggcg cgc
653

<210> 1340
<211> 217
<212> PRT
<213> Homo sapiens

<400> 1340
Arg Val Val Phe Asn Ile Asp Glu Lys Gln Cys Ile Asp Leu Ala His
1 5 10 15
Arg Gly Thr Glu Trp Val Val Arg Tyr Ala Asp Lys Tyr Leu Gly Asp
20 25 30
Val Glu Phe Gly Tyr Glu Tyr Ser Pro Glu Met Phe Ser Gln Thr Arg
35 40 45
Thr Asp Phe Ala Ile Asp Val Cys His Ser Val Met Asp Val Trp Gln
50 55 60
Pro Gly Pro Gly Arg Glu Ile Ile Leu Asn Leu Pro Ala Thr Val Glu
65 70 75 80
Met Ser Thr Pro Asn Thr Tyr Ala Asp Gln Ile Glu Tyr Phe Cys Arg
85 90 95
Asn Ile Arg Asp Arg Glu His Val Cys Val Ser Leu His Pro His Asn
100 105 110
Asp Arg Gly Thr Ala Ile Ala Ala Ala Glu Phe Ala Gln Met Ala Gly
115 120 125
Ala Asp Arg Val Glu Gly Cys Phe Phe Gly Pro Gly Glu Arg Pro Gly
130 135 140
Thr Val Asp Leu Val Thr Leu Gly Met Asn Leu Val Ser Gln Gly Val
145 150 155 160
Asp Ala Gly Ile Asp Phe Ser Asp Met Pro Lys Ile Arg Arg Thr Val
165 170 175
Glu Tyr Cys Thr Cys Leu Pro Val Pro Ala Arg Gln Pro Tyr Ser Gly
180 185 190
Asp Leu Val Phe Thr Ala Phe Ser Gly Ser His Gln Asp Ala Ile Lys
195 200 205
Lys Gly Leu Glu Asp Leu Ala Arg Arg
210 215

<210> 1341
<211> 666
<212> DNA
<213> Homo sapiens

<400> 1341
accggttgct gatttccttg ttggagtctt caccactatg agcagtgact ccattgtttt
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gcaaagtttc ttgccttgct ttgatcatat tttcacaact ggattcccaa cagaagtgtg
120
gcaatctgta atagaaaagt tggcaaagaa aggattatgg cattcatttc tgcttctgtc
180

agcaaaaaaa gaccgattac caagaaatat tcatgtccca gagttatcac tgaaaagtct
240
ctttgagaaa tacgttttca ttggacttta tgagaagatg gaacaagtgc ccaagttagt
300
ccagtggctc atctccattg gtgcaagtgt tgagactata ggaccgtatc cccttcatgc
360
cctcatgcga ctctgtatcc aagccagaga aaaccatctt ttccggtggt taatggatca
420
caagcccgag tggaaaggcc gcattaacca gaaggatggg gatggctgca ctgtcctgca
480
cgtcgtcgct gcccactccc caggatacct cgttaagcga caaacagagg atgtgcagat
540
gctcctgcgc tttggggcag atcccacttt gctggatcga cagtctcggt ctgttgtgga
600
tgtcctgaag aggaataaga acttcaaagc catcgagaaa atcaacagtc acttagaaaa
660
gctagc
666

<210> 1342
<211> 209
<212> PRT
<213> Homo sapiens

<400> 1342

Met	Ser	Ser	Asp	Ser	Ile	Val	Leu	Gln	Ser	Phe	Leu	Pro	Cys	Phe	Asp
1				5				10					15		
His	Ile	Phe	Thr	Thr	Gly	Phe	Pro	Thr	Glu	Val	Trp	Gln	Ser	Val	Ile
			20					25					30		
Glu	Lys	Leu	Ala	Lys	Lys	Gly	Leu	Trp	His	Ser	Phe	Leu	Leu	Leu	Ser
		35					40					45			
Ala	Lys	Lys	Asp	Arg	Leu	Pro	Arg	Asn	Ile	His	Val	Pro	Glu	Leu	Ser
	50					55					60				
Leu	Lys	Ser	Leu	Phe	Glu	Lys	Tyr	Val	Phe	Ile	Gly	Leu	Tyr	Glu	Lys
65					70					75					80
Met	Glu	Gln	Val	Pro	Lys	Leu	Val	Gln	Trp	Leu	Ile	Ser	Ile	Gly	Ala
				85					90					95	
Ser	Val	Glu	Thr	Ile	Gly	Pro	Tyr	Pro	Leu	His	Ala	Leu	Met	Arg	Leu
			100					105					110		
Cys	Ile	Gln	Ala	Arg	Glu	Asn	His	Leu	Phe	Arg	Trp	Leu	Met	Asp	His
		115					120					125			
Lys	Pro	Glu	Trp	Lys	Gly	Arg	Ile	Asn	Gln	Lys	Asp	Gly	Asp	Gly	Cys
	130					135					140				
Thr	Val	Leu	His	Val	Val	Ala	Ala	His	Ser	Pro	Gly	Tyr	Leu	Val	Lys
145					150					155					160
Arg	Gln	Thr	Glu	Asp	Val	Gln	Met	Leu	Leu	Arg	Phe	Gly	Ala	Asp	Pro
				165					170					175	
Thr	Leu	Leu	Asp	Arg	Gln	Ser	Arg	Ser	Val	Val	Asp	Val	Leu	Lys	Arg
			180					185					190		
Asn	Lys	Asn	Phe	Lys	Ala	Ile	Glu	Lys	Ile	Asn	Ser	His	Leu	Glu	Lys
		195					200					205			
Leu															

<210> 1343
<211> 270
<212> DNA
<213> Homo sapiens

<400> 1343
ccggaaatgt gccgagttct cctgacgcac gaagtgatgt gtagtcgatg ctgcgaaaag
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aaaagctgtg gaaaccgaaa tgagactcca tcggacccag tcataattga cagattcttt
120
ttaaaatttt tcctcaagtg caatcagaat tgtttgaaaa cagcaggaaa cccaagggac
180
atgagacggt ttcaggttgt gttgtcaaca acggtgaatg tggatggaca cgtcctggct
240
gtttctgaca acatgtttgt tcataacaac
270

<210> 1344
<211> 90
<212> PRT
<213> Homo sapiens

<400> 1344
Pro Glu Met Cys Arg Val Leu Leu Thr His Glu Val Met Cys Ser Arg
1 5 10 15
Cys Cys Glu Lys Lys Ser Cys Gly Asn Arg Asn Glu Thr Pro Ser Asp
20 25 30
Pro Val Ile Ile Asp Arg Phe Phe Leu Lys Phe Phe Leu Lys Cys Asn
35 40 45
Gln Asn Cys Leu Lys Thr Ala Gly Asn Pro Arg Asp Met Arg Arg Phe
50 55 60
Gln Val Val Leu Ser Thr Thr Val Asn Val Asp Gly His Val Leu Ala
65 70 75 80
Val Ser Asp Asn Met Phe Val His Asn Asn
85 90

<210> 1345
<211> 402
<212> DNA
<213> Homo sapiens

<400> 1345
acgcgtttga aacccaccga tgacttgtcg gtgatcctgg gtacccgcgt cagcaacttc
60
agcggcaccg acaacaccga cttctacgac ccgaccaagg ccgacaaccg tctcacctac
120
cgccagacgg gcgtcgtcac gccctatgcc ggcatcgtct acgacctgaa tgacatctgg
180
tcggtgtaca ccagctacac caagatctac aagccgcaga acagcaagga cgccgaccgc
240
aagttgctcg atccgattga aggtgacacc tacgaagccg ggctcaaggc agcgtttttc
300
gacggccgcc tgaacgccag ttttgccgca ttccgcatcg aacaggacaa cgtcgcacag
360

tacgtttccg ggtttgagac cgactcgtgt atcgcccatt gc
402

<210> 1346
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1346
Thr Arg Leu Lys Pro Thr Asp Asp Leu Ser Val Ile Leu Gly Thr Arg
1 5 10 15
Val Ser Asn Phe Ser Gly Thr Asp Asn Thr Asp Phe Tyr Asp Pro Thr
20 25 30
Lys Ala Asp Asn Arg Leu Thr Tyr Arg Gln Thr Gly Val Val Thr Pro
35 40 45
Tyr Ala Gly Ile Val Tyr Asp Leu Asn Asp Ile Trp Ser Val Tyr Thr
50 55 60
Ser Tyr Thr Lys Ile Tyr Lys Pro Gln Asn Ser Lys Asp Ala Asp Arg
65 70 75 80
Lys Leu Leu Asp Pro Ile Glu Gly Asp Thr Tyr Glu Ala Gly Leu Lys
85 90 95
Ala Ala Phe Phe Asp Gly Arg Leu Asn Ala Ser Phe Ala Ala Phe Arg
100 105 110
Ile Glu Gln Asp Asn Val Ala Gln Tyr Val Ser Gly Phe Glu Thr Asp
115 120 125
Ser Cys Ile Ala His Cys
130

<210> 1347
<211> 415
<212> DNA
<213> Homo sapiens

<400> 1347
naccaccttc tgggcaggct ctcattcttt cattccaaga agcatttatt aaagactggc
60
tagggcgagg gaacccagct aggggctggg gataaaaaat aagaaataac tgaaggacct
120
tgctcttaag gaactccatc ttactgggtg gagccaaacg agaaaagaga gctcgggagg
180
gcaccaaagc ggtcttgccg aaattgcctg aggcagggga aggggcacgc tttctgaaaa
240
acccccccaa accgattcca ggaagcccaa agggcggccc ctctgcccgc agcactgcct
300
tcacgtttac ttccatcccg gcctcctcct tcccctaagg cttggcatgc aacatccctg
360
cttctcaccc acctttttatt taagactcct attatctgca cacaatggaa gttag
415

<210> 1348
<211> 105
<212> PRT
<213> Homo sapiens

<400> 1348
Met Glu Val Asn Val Lys Ala Val Leu Arg Ala Glu Gly Pro Pro Phe
1 5 10 15
Gly Leu Pro Gly Ile Gly Leu Gly Gly Phe Phe Arg Lys Arg Ala Pro
20 25 30
Ser Pro Ala Ser Gly Asn Phe Gly Lys Thr Ala Leu Val Pro Ser Arg
35 40 45
Ala Leu Phe Ser Arg Leu Ala Pro Pro Ser Lys Met Glu Phe Leu Lys
50 55 60
Ser Lys Val Leu Gln Leu Phe Leu Ile Phe Tyr Pro Gln Pro Leu Ala
65 70 75 80
Gly Phe Pro Arg Pro Ser Gln Ser Leu Ile Asn Ala Ser Trp Asn Glu
85 90 95
Arg Met Arg Ala Cys Pro Glu Gly Gly
100 105

<210> 1349
<211> 924
<212> DNA
<213> Homo sapiens

<400> 1349
gccgggatcg tcacaccaca gcaggtcgcg ttaccccatg acgtcttccg tgagcttggc
60
gctcagacgg tcatgcgttc gatcgccgaa aagcttggcc ttccggtcat cgttaagccg
120
gcacgtgggg gctcaagcct cggcgtcaca aaagtcgatg gcgtcgacga tcttcctcag
180
gccgtcgcga acgcctatgc ctatgacgac atggttgtag tcgaggaatt cattgtgggc
240
aacgaactcg caataggcat gatcacgacg tctgaaggca cgcgtgtgct gccagccgtc
300
gagattcgcc ctgtcggtgg tgtttatgat tattcagcga tgtacaccgg tggtgagaca
360
cgactaacag ctcctgcaga cattagcgat acggcggccc aaaccgcgac ggcgatggcc
420
cgagtcgtgc aaaaggagct cgatttctcc gggatatctc gtgtcgatgc gatcgtggac
480
gagtccggtc gcccagtttt cttggaggcc ggtgctgctc ccgggatgac agctacttcg
540
ctcgtacccg tggctatgaa agctgccggt ctagaccttg gcgaggtgtg ctctcgacta
600
gtcgatgacg tcgctcgcaa ccatggctga cagtgtgcac acgaggggct cgcgccacgc
660
cgtgcgcgtc aagcaggcat ctgtcgtctt gctcggcgtc gtccttgcca gtgtgatggt
720
cttcctcgga ctgtggcaga tgaacgtttt tgagtcccaa cgtgacgact cgacgcaggc
780
gcgtatcaac gagccagtga tcacctggaa tgaggcgcct aagaaggcca gtgtcatggc
840
tcagtacgga cgccgggtga cggtgacggg cacgttccaa ccgtcgacca caaccttgat
900
aggcacatcg tggccagtac gcgt
924

<210> 1350
<211> 209
<212> PRT
<213> Homo sapiens

<400> 1350
Ala Gly Ile Val Thr Pro Gln Gln Val Ala Leu Pro His Asp Val Phe
1 5 10 15
Arg Glu Leu Gly Ala Gln Thr Val Met Arg Ser Ile Ala Glu Lys Leu
20 25 30
Gly Leu Pro Val Ile Val Lys Pro Ala Arg Gly Gly Ser Ser Leu Gly
35 40 45
Val Thr Lys Val Asp Gly Val Asp Asp Leu Pro Gln Ala Val Ala Asn
50 55 60
Ala Tyr Ala Tyr Asp Asp Met Val Val Val Glu Glu Phe Ile Val Gly
65 70 75 80
Asn Glu Leu Ala Ile Gly Met Ile Thr Thr Ser Glu Gly Thr Arg Val
85 90 95
Leu Pro Ala Val Glu Ile Arg Pro Val Gly Gly Val Tyr Asp Tyr Ser
100 105 110
Ala Met Tyr Thr Gly Gly Glu Thr Arg Leu Thr Ala Pro Ala Asp Ile
115 120 125
Ser Asp Thr Ala Ala Gln Thr Ala Thr Ala Met Ala Arg Val Val Gln
130 135 140
Lys Glu Leu Asp Phe Ser Gly Ile Ser Arg Val Asp Ala Ile Val Asp
145 150 155 160
Glu Ser Gly Arg Pro Val Phe Leu Glu Ala Gly Ala Ala Pro Gly Met
165 170 175
Thr Ala Thr Ser Leu Val Pro Val Ala Met Lys Ala Ala Gly Leu Asp
180 185 190
Leu Gly Glu Val Cys Ser Arg Leu Val Asp Asp Val Ala Arg Asn His
195 200 205
Gly

<210> 1351
<211> 398
<212> DNA
<213> Homo sapiens

<400> 1351
nngtgcacgg agggcgtgct ggtctacgcc ctgtatctgc tgtctcgatg cacgatgggc
60
gacgagacgc aaaacgcatt gcttctcagt attctgctgc accccggtct gctcatcgtc
120
gaccacattc acttccagta caacgggttc ctaattcgcg ggccccttta tcgtttgggg
180
gcccgcacgg acgcatcggc cctctttctc tgaaccgccc tgtttgcctc gctgctccag
240
ttcaagcaca tttacgtata cgtcgcgccg gcgtactttg tgtacctgct gcgtgcgtac
300
atgctcccga gcatgccgac gtccgcatcg acggggagcg cggcgatcga tcgcaccatc
360

aagcttggcg cagcgacgct ggtgccttcc tgctgagc
398

<210> 1352
<211> 70
<212> PRT
<213> Homo sapiens

<400> 1352
Xaa Cys Thr Glu Gly Val Leu Val Tyr Ala Leu Tyr Leu Leu Ser Arg
1 5 10 15
Cys Thr Met Gly Asp Glu Thr Gln Asn Ala Leu Leu Leu Ser Ile Leu
20 25 30
Leu His Pro Gly Leu Leu Ile Val Asp His Ile His Phe Gln Tyr Asn
35 40 45
Gly Phe Leu Ile Arg Gly Pro Leu Tyr Arg Leu Gly Ala Arg Thr Asp
50 55 60
Ala Ser Ala Leu Phe Leu
65 70

<210> 1353
<211> 480
<212> DNA
<213> Homo sapiens

<400> 1353
ngggccccaa tccctagcct agggcctgga ggtcccctga gtttgctcag ccaactcatt
60
accctcacac ccaccccacc cccagtcaca cggatcgtgc ggggcattgg acagcctcgg
120
ggcaacatgc tcctggtggg tatcgggggc agcggacgcc agagtctggc ccgcctggct
180
tcatccatct gcgactacac caccttccag atcgaggtca ccaaacatta tcggaagcag
240
gagttccgag atgatatcaa gcgtctgtat cgccaggctg gggtggagct caagaccacg
300
tccttcattt ttgtggacac ccaaatagct gatgagtcct tcctagagga catcaacaac
360
atcctcagct caggcgaggt gccccatctt ttcaggcctg atgaatttga agagatccag
420
tcgcatatca tagaccaggc ccgggtggag caggtgcctg agtcatcgga cagcctcttc
480

<210> 1354
<211> 160
<212> PRT
<213> Homo sapiens

<400> 1354
Xaa Ala Pro Ile Pro Ser Leu Gly Pro Gly Gly Pro Leu Ser Leu Leu
1 5 10 15
Ser Gln Leu Ile Thr Leu Thr Pro Thr Pro Pro Pro Val Thr Arg Ile
20 25 30
Val Arg Gly Ile Gly Gln Pro Arg Gly Asn Met Leu Leu Val Gly Ile

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        35                  40                  45
Gly Gly Ser Gly Arg Gln Ser Leu Ala Arg Leu Ala Ser Ser Ile Cys
    50                  55                  60
Asp Tyr Thr Thr Phe Gln Ile Glu Val Thr Lys His Tyr Arg Lys Gln
65                  70                  75                  80
Glu Phe Arg Asp Asp Ile Lys Arg Leu Tyr Arg Gln Ala Gly Val Glu
                85                  90                  95
Leu Lys Thr Thr Ser Phe Ile Phe Val Asp Thr Gln Ile Ala Asp Glu
            100                 105                 110
Ser Phe Leu Glu Asp Ile Asn Asn Ile Leu Ser Ser Gly Glu Val Pro
        115                 120                 125
His Leu Phe Arg Pro Asp Glu Phe Glu Glu Ile Gln Ser His Ile Ile
    130                 135                 140
Asp Gln Ala Arg Val Glu Gln Val Pro Glu Ser Ser Asp Ser Leu Phe
145                 150                 155                 160
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<210> 1355
<211> 1063
<212> DNA
<213> Homo sapiens

<400> 1355
ngagaacgca ggtctccatc ctgacctgca ggcaaggggg actctactga cccctgaggt
60
gccctgtcct aggccccacc cggtcagtgc acacctgctc cccagtcccg cctccacaaa
120
ggccctgtga gaccctgtcc tccaccgcct ctttccttgt gtccattccc tgagcctggg
180
gaagttgcgt cagagccaca ggtcggngag acgctgagtc tgggcgagcg cttgctgccg
240
gacagctgga gaaacagcag cgggggccg tgtccatgtg gcaagccaag ccatcgaggg
300
gatcacaggc cccttcaggg aagggactga gcacctgcca cctgcctcca ggatgggcct
360
gatcccccct cctgtgtacc ccacaggctg cagtgcacct gccagcacaa cacctgcggg
420
ggcacctgcg accgctgctg ccccggcttc aatcagcagc cgtggaagcc tgcgactgcc
480
aacagtgcca acgagtgcca gtcctgtaac tgctacggcc atgccaccga ctgttactac
540
gaccctgagg tggaccggcg ccgcgccagc cagagcctgg atggcaccta tcagggtggg
600
ggtgtctgta tcgactgcca gcaccacacc gccggcgtca actgtgagcg ctgcctgccc
660
ggcttctacc gctctcccaa ccaccctctc gactcgcccc acgtctgccg ccgctgcaac
720
tgcgagtccg acttcacgga tggcacctgc gaggacctga cgggtcgatg ctactgccgg
780
cccaacttct ctggggagcg gtgtgacgtg tgtgccgagg gcttcacggg cttcccaagc
840
tgctacccga cgccctcgtc ctccaatgac accagggagc aggtgctgcc agccggccag
900
attgtgaatt gtgactgcag cgcggcaggg acccagggca acgcctgccg gaaggaccca
960

agggtgggcc gctgttttgc caaccccaac ttccaaggca cccattgtga gctctgcgcg
1020
ccagggttct acggccccgg ctgccctggg tcccttcacg cgt
1063

<210> 1356
<211> 244
<212> PRT
<213> Homo sapiens

<400> 1356
Ala Pro Ala Thr Cys Leu Gln Asp Gly Pro Asp Pro Pro Ser Cys Val
1 5 10 15
Pro His Arg Leu Gln Cys Thr Cys Gln His Asn Thr Cys Gly Gly Thr
20 25 30
Cys Asp Arg Cys Cys Pro Gly Phe Asn Gln Gln Pro Trp Lys Pro Ala
35 40 45
Thr Ala Asn Ser Ala Asn Glu Cys Gln Ser Cys Asn Cys Tyr Gly His
50 55 60
Ala Thr Asp Cys Tyr Tyr Asp Pro Glu Val Asp Arg Arg Arg Ala Ser
65 70 75 80
Gln Ser Leu Asp Gly Thr Tyr Gln Gly Gly Gly Val Cys Ile Asp Cys
85 90 95
Gln His His Thr Ala Gly Val Asn Cys Glu Arg Cys Leu Pro Gly Phe
100 105 110
Tyr Arg Ser Pro Asn His Pro Leu Asp Ser Pro His Val Cys Arg Arg
115 120 125
Cys Asn Cys Glu Ser Asp Phe Thr Asp Gly Thr Cys Glu Asp Leu Thr
130 135 140
Gly Arg Cys Tyr Cys Arg Pro Asn Phe Ser Gly Glu Arg Cys Asp Val
145 150 155 160
Cys Ala Glu Gly Phe Thr Gly Phe Pro Ser Cys Tyr Pro Thr Pro Ser
165 170 175
Ser Ser Asn Asp Thr Arg Glu Gln Val Leu Pro Ala Gly Gln Ile Val
180 185 190
Asn Cys Asp Cys Ser Ala Ala Gly Thr Gln Gly Asn Ala Cys Arg Lys
195 200 205
Asp Pro Arg Val Gly Arg Cys Phe Ala Asn Pro Asn Phe Gln Gly Thr
210 215 220
His Cys Glu Leu Cys Ala Pro Gly Phe Tyr Gly Pro Gly Cys Pro Gly
225 230 235 240
Ser Leu His Ala

<210> 1357
<211> 663
<212> DNA
<213> Homo sapiens

<400> 1357
ntccccccc ccccgggggg gggggggggg ggaaacaaca ccagaaaagt agacagatac
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ccaagttggt ccagctggtc catatacggc cccaggtgcg gattcggtac cgaagttgaa
120

ttcaacaccc ccgttttgcc tgtgggggg gtacgccctg taatcctgca aaggcccggt
180
tggtgtccgg gggttttcgt cggtctcccc aaccatcatc tagacggcgt ggcgatgtgg
240
tgcgagctgc ttgcggcggt gttctgtgcc cgagcttgcc tcgcctggct gcaagaatcc
300
ctggctcatc gagcttcagc gtcagtcaag tcgcaattgc ggcgcgacat cctgcaagcc
360
aggttgtcgc gtcccactga cgcaacaatg ccgtcgagaa ccctcatcag cctgatgaca
420
acaggtctgg acgccctcga cggctactac tcgaagtacc ttccccagct tgtgctggcc
480
gtcatcgtgc cagcagtgct agccaccgct atcggcctaa acgacctcac cagcctcgtc
540
atcgtcgtcg tgacgatccc gctcatcccc gttttcatgg ccctcattgg ctggcggacc
600
gaggcggccg tagcaaaacg gttcaaggta gccacccgac tggccaacca cttcgctgat
660
ctg
663

<210> 1358
<211> 221
<212> PRT
<213> Homo sapiens

<400> 1358
Xaa Pro Pro Pro Pro Gly Gly Gly Gly Gly Gly Asn Asn Thr Arg Lys
 1   5   10   15
Val Asp Arg Tyr Pro Ser Trp Ser Ser Trp Ser Ile Tyr Gly Pro Arg
            20   25   30
Cys Gly Phe Gly Thr Glu Val Glu Phe Asn Thr Pro Val Leu Pro Val
        35   40   45
Gly Gly Val Arg Pro Val Ile Leu Gln Arg Pro Gly Trp Cys Pro Gly
    50   55   60
Val Phe Val Gly Leu Pro Asn His His Leu Asp Gly Val Ala Met Trp
65   70   75   80
Cys Glu Leu Leu Ala Ala Val Phe Cys Ala Arg Ala Cys Leu Ala Trp
                85   90   95
Leu Gln Glu Ser Leu Ala His Arg Ala Ser Ala Ser Val Lys Ser Gln
            100   105   110
Leu Arg Arg Asp Ile Leu Gln Ala Arg Leu Ser Arg Pro Thr Asp Ala
        115   120   125
Thr Met Pro Ser Arg Thr Leu Ile Ser Leu Met Thr Thr Gly Leu Asp
    130   135   140
Ala Leu Asp Gly Tyr Tyr Ser Lys Tyr Leu Pro Gln Leu Val Leu Ala
145   150   155   160
Val Ile Val Pro Ala Val Leu Ala Thr Ala Ile Gly Leu Asn Asp Leu
                165   170   175
Thr Ser Leu Val Ile Val Val Val Thr Ile Pro Leu Ile Pro Val Phe
            180   185   190
Met Ala Leu Ile Gly Trp Arg Thr Glu Ala Ala Val Ala Lys Arg Phe
        195   200   205
Lys Val Ala Thr Arg Leu Ala Asn His Phe Ala Asp Leu

210 215 220

<210> 1359
<211> 423
<212> DNA
<213> Homo sapiens

<400> 1359
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<212> PRT
<213> Homo sapiens

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35 40 45
Val Gly Tyr Trp Leu Ala Asp Tyr Thr Ser Leu Ser Ile Lys Gln Ile
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Asp Lys Gln Pro Phe Val Ser Arg Thr Pro Cys Asp Ile Leu Glu Ser
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<212> PRT
<213> Homo sapiens

<400> 1362
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35 40 45
Gln Ala Ser His Thr Cys Gly Ser Pro Pro Glu Asp Phe Cys Pro His
50 55 60
Val Gly Ala Ala Gly Ala Gly Ala His Cys Gln Arg Cys Asp Ala Ala
65 70 75 80
Asp Pro Gln Arg His His Asn Ala Ser Tyr Leu Thr Asp Phe His Ser
85 90 95
Gln Asp Glu Ser Thr Trp Trp Gln Ser Pro Ser Met Ala Phe Gly Val
100 105 110
Gln Tyr Pro Thr Ser Val Asn Ile Thr Leu Arg Leu Gly Lys Ala Tyr
115 120 125
Glu Ile Thr Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser
130 135 140
Phe Ala Ile Tyr Lys Arg Ser Arg Ala Asp Gly Pro Trp Glu Pro Tyr
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Gln Phe Tyr Ser Ala Ser Cys Gln Lys Thr Tyr Gly Arg Pro Glu Gly
165 170 175
Gln Tyr Leu Arg Pro Gly Glu Asp Glu Arg Val Ala Phe Cys Thr Ser
180 185 190
Glu Phe Ser Asp Ile Ser Pro Leu Ser Gly Gly Asn Val Ala Phe Ser
195 200 205
Thr Leu Glu Gly Arg Pro Ser Ala Tyr Asn Phe Glu Glu Ser Pro Gly
210 215 220
Leu Gln Glu Trp Val Thr Ser Thr Glu Leu Leu Ile Ser Leu Asp Arg
225 230 235 240
Leu Asn Thr Phe Gly Asp Asp Ile Phe Lys Asp Pro Lys Val Leu Gln
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Ser Tyr Tyr Tyr Ala Val Ser Asp Phe Ser Val Gly Gly Arg Cys Lys

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Leu Pro Phe Phe Gln Asp Arg Pro Trp Ala Arg Gly Thr Ala Glu Ala
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Ala His Glu Cys Leu Pro Cys Asn Cys Ser Gly Arg Ser Glu Glu Cys
                325                 330                 335
Thr Phe Asp Arg Glu Leu Phe Arg Ser Thr Gly His Gly Gly Arg Cys
            340                 345                 350
His His Cys Arg Asp His Thr Ala Gly Pro His Cys Glu Arg Cys Gln
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Glu Asn Phe Tyr His Trp Asp Pro Arg Met Pro Cys Gln Pro Cys Asp
    370                 375                 380
Cys Gln Ser Ala Gly Ser Leu His Leu Gln Cys Asp Asp Thr Gly Thr
385                 390                 395                 400
Cys Ala Cys Lys Pro Thr Val Thr Gly Trp Lys Cys Asp Arg Cys Leu
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Pro Gly Phe His Ser Leu Ser Glu Gly Gly Cys Arg Pro Cys Thr Cys
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        435                 440                 445
Pro Cys Lys Glu Asn Val Glu Gly Asn Leu Cys Asp Arg Cys Arg Pro
    450                 455                 460
Gly Thr Phe Asn Leu Gln Pro His Asn Pro Ala Gly Cys Ser Ser Cys
465                 470                 475                 480
Phe Cys Tyr Gly His Ser Lys Val Cys Ala Ser Thr Ala Gln Phe Gln
                485                 490                 495
Val His His Ile Leu Ser Asp Phe His Gln Gly Ala Glu Gly Trp Trp
            500                 505                 510
Ala Arg Ser Val Gly Gly Ser Glu His Ser Pro Gln Trp Ser Pro Asn
        515                 520                 525
Gly Val Leu Leu Ser Pro Glu Asp Glu Glu Glu Leu Thr Ala Pro Gly
    530                 535                 540
Lys Phe Leu Gly Asp Gln Arg Phe Ser Tyr Gly Gln Pro Leu Ile Leu
545                 550                 555                 560
Thr Phe Arg Val Pro Pro Gly Asp Ser Pro Leu Pro Val Gln Leu Arg
                565                 570                 575
Leu Glu Gly Thr Gly Leu Ala Leu Ser Leu Arg His Ser Ser Leu Ser
            580                 585                 590
Gly Pro Gln Asp Ala Arg Ala Ser Gln Gly Gly Arg Ala Gln Val Pro
        595                 600                 605
Leu Gln Glu Thr Ser Glu Asp Val Ala Pro Pro Leu Pro Pro Phe His
    610                 615                 620
Phe Gln Arg Leu Leu Ala Asn Leu Thr Ser Leu Arg Leu Arg Val Ser
625                 630                 635                 640
Pro Gly Pro Ser Pro Ala Gly Pro Val Phe Leu Thr Glu Val Arg Leu
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Thr Ser Ala Arg Pro Gly Leu Ser Pro Pro Ala Ser Trp Val Glu Ile
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Cys Ser Cys Pro Thr Gly Tyr Thr Gly Gln Phe Cys Glu Ser Cys Ala
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Pro Gly Tyr Lys Arg Glu Met Pro Gln Gly Gly Pro Tyr Ala Ser Cys
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Leu Pro Gly Phe Tyr Gly Asn Pro Phe Ala Gly Gln Ala Asp Asp Cys
            740                 745                 750
Gln Pro Cys Pro Cys Pro Gly Gln Ser Ala Cys Thr Thr Ile Pro Glu
        755                 760                 765
Ser Gly Glu Val Val Cys Thr His Cys Pro Pro Gly Gln Arg Gly Arg
    770                 775                 780
Arg Cys Glu Val Cys Asp Asp Gly Phe Phe Gly Asp Pro Leu Gly Leu
785                 790                 795                 800
Phe Gly His Pro Gln Pro Cys His Gln Cys Gln Cys Ser Gly Asn Val
                805                 810                 815
Asp Pro Asn Ala Val Gly Asn Cys Asp Pro Leu Ser Gly His Cys Leu
            820                 825                 830
Arg Cys Leu His Asn Thr Thr Gly Asp His Cys Glu His Cys Gln Glu
        835                 840                 845
Gly Phe Tyr Gly Ser Ala Leu Ala Pro Arg Pro Ala Asp Lys Cys Met
    850                 855                 860
Pro Cys Ser Cys His Pro Gln Gly Ser Val Ser Glu Gln Met Pro Cys
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Gly Cys Arg Ser Cys Lys Cys His Pro Leu Gly Ser Gln Glu Asp Gln
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Cys His Pro Lys Thr Gly Gln Cys Thr Cys Arg Pro Gly Val Thr Gly
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Gln Ala Cys Asp Arg Cys Gln Leu Gly Phe Phe Gly Ser Ser Ile Lys
945                 950                 955                 960
Gly Cys Arg Ala Cys Arg Cys Ser Pro Leu Gly Ala Ala Ser Ala Gln
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Cys His Tyr Asn Gly Thr Cys Val Cys Arg Pro Gly Phe Glu Gly Tyr
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Lys Cys Asp Arg Cys His Tyr Asn Phe Phe Leu Thr Ala Asp Gly Thr
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His Cys Gln Gln Cys Pro Ser Cys Tyr Ala Leu Val Lys Glu Glu Thr
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Ser Asp Cys Gly Ser Pro Trp Gly Pro Leu Asp Ile Leu Leu Gly Glu
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Ala Pro Arg Gly Asp Val Tyr Gln Gly His His Leu Leu Pro Gly Ala
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Arg Glu Ala Phe Leu Glu Gln Met Met Gly Leu Glu Gly Ala Val Lys
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Ala Ala Arg Glu Gln Leu Gln Arg Leu Asn Lys Gly Ala Arg Cys Ala
    1090                1095                1100
Gln Ala Gly Ser Gln Lys Thr Cys Thr Gln Leu Ala Asp Leu Glu Ala
1105                1110                1115                1120
Val Leu Glu Ser Ser Glu Glu Glu Ile Leu His Ala Ala Ala Ile Leu
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Thr Ala Thr Lys Ile Ala Ala Thr Ala Trp Arg Ala Leu Leu Ala Ser
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Ala Glu Asp Leu Gly Leu Lys Ala Lys Ala Leu Glu Lys Thr Val Ala
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1345                1350                1355                1360
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Ser Leu Glu Lys Asp Ile Glu Thr Leu Ser Glu Leu Leu Ala Arg Leu
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Gly Ser Leu Asp Thr His Gln Ala Pro Ala Gln Ala Leu Asn Glu Thr
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Gln Trp Ala Leu Glu Arg Leu Arg Leu Gln Leu Gly Ser Pro Gly Ser
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Leu Gln Arg Lys Leu Ser Leu Leu Glu Gln Glu Ser Gln Gln Gln Glu
            1540                1545                1550
Leu Gln Ile Gln Gly Phe Glu Ser Asp Leu Ala Glu Ile Arg Ala Asp
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<211> 392
<212> DNA
<213> Homo sapiens

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<211> 104
<212> PRT
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Phe Met Val Ala Pro Pro Met Arg His Leu His Leu Pro Ser His Pro
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Leu Lys Gln Pro His Leu Cys Arg Phe Arg Arg Phe Leu Leu Arg Leu
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<210> 1365
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<212> DNA
<213> Homo sapiens

<400> 1365

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<211> 150
<212> PRT
<213> Homo sapiens

<400> 1366
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35 40 45
Lys Ser Val Ala Val Asn Lys Gly Arg Leu Lys Arg Leu Gly Ile Thr
50 55 60
His Ile Leu Asn Ala Ala His Gly Thr Gly Val Tyr Thr Gly Pro Glu
65 70 75 80
Phe Tyr Thr Gly Leu Glu Ile Gln Tyr Leu Gly Val Glu Val Asp Asp
85 90 95
Phe Pro Glu Val Asp Ile Ser Gln His Phe Arg Lys Ala Ser Glu Phe
100 105 110
Leu Asp Glu Ala Leu Leu Thr Tyr Arg Gly Lys Val Leu Val Ser Ser
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Ile Phe His Asn Met Ala
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<212> DNA
<213> Homo sapiens

<400> 1367
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120

tcgtcgtcgc attgctgctg gtcatcgtcg cactgcccgt cagcgcactc gtcggccaga
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gcttcttcga ccgcgaaggc gccttcgtcg gcctcgccaa cttcgctcgc tacctcgaca
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<210> 1368
<211> 82
<212> PRT
<213> Homo sapiens

<400> 1368
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20 25 30
Ala Ser Ser Thr Ala Lys Ala Pro Ser Ser Ala Ser Pro Thr Ser Leu
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Ala Thr Ser Thr Thr Pro Pro Trp Ser Ser Pro Pro Ser Thr Ala Ser
50 55 60
Gly Trp Pro Arg Ser Ala Pro Ser Ser Ala Pro Pro Ser Pro Thr Ser
65 70 75 80
Thr Arg

<210> 1369
<211> 356
<212> DNA
<213> Homo sapiens

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cccctggacc cctacagcca ggagcagcgg gagcagctgc aggtcctacg ccaggctgcc
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240
tgtgcccgag agttccgcaa actgggcttt tctaacagca acccagcaca ggacctggag
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<210> 1370
<211> 104
<212> PRT
<213> Homo sapiens

<400> 1370
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            20                  25                  30
Gln Glu Gln Arg Glu Gln Leu Gln Val Leu Arg Gln Ala Ala Phe Glu
        35                  40                  45
Val Glu Gly Glu Ser Ser Gly Ala Gly Leu Ser Ala Asp Arg Arg Arg
    50                  55                  60
Ser Leu Cys Ala Arg Glu Phe Arg Lys Leu Gly Phe Ser Asn Ser Asn
65                  70                  75                  80
Pro Ala Gln Asp Leu Glu Arg Val Pro Pro Gly Leu Leu Ala Leu Asp
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Asn Met Leu Tyr Phe Ser Arg Asn
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<210> 1371
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<212> DNA
<213> Homo sapiens

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420
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480
tgcatggaaa tttgggattt ctagttagag gctttataaa ggtagaatca tgcagacaca
540
tatacctgga aatattcgga acattctatt agcagaaatg caatgtagga agcttattgg
600
ttctagaaga atgtgtcatt gtcagtaatt ggaattactg acagatct
648

<210> 1372
<211> 101
<212> PRT
<213> Homo sapiens

<400> 1372
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 1               5                  10                  15
Cys Pro Leu Arg Ser Leu Leu Ser Ser Phe Pro Leu Leu Leu Ser Leu
            20                  25                  30
Phe Leu Phe Val Glu Arg Ala Val Arg Leu Thr Gln Gln Leu Leu Glu
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        35                  40                  45
Cys Leu Gly His Leu Arg Ala Trp Lys Val His Ala Leu Thr Arg Val
    50                  55                  60
Met Thr Thr Ile Ser Pro Lys Leu Ser Ser Cys His Pro Ile Gly Ser
65                  70                  75                  80
Ile Asp Gln Lys Gly Lys Ser Ser Val Leu Lys Leu Ile Asn Gln Leu
                85                  90                  95
Lys Leu Tyr Leu Gln
            100
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<210> 1373
<211> 369
<212> DNA
<213> Homo sapiens

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120
acatgggttt catgggtcga catgggttcc gtgtcctgct tgccgggcct gagctgtttg
180
tcaggtgtac aaccgagaac cttgcagacc agaatccaag actccgcagc atgtgtgtgc
240
cggggcggga cacgagctgt tggaggagaa agccatcagt gtatttagag gcaaagggct
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ctctccgca
369

<210> 1374
<211> 98
<212> PRT
<213> Homo sapiens

<400> 1374
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Met Gly Phe Met Gly Arg His Gly Phe Arg Val Leu Leu Ala Gly Pro
            20                  25                  30
Glu Leu Phe Val Arg Cys Thr Thr Glu Asn Leu Ala Asp Gln Asn Pro
        35                  40                  45
Arg Leu Arg Ser Met Cys Val Pro Gly Arg Asp Thr Ser Cys Trp Arg
    50                  55                  60
Arg Lys Pro Ser Val Tyr Leu Glu Ala Lys Gly Phe Leu Asn Arg Gly
65                  70                  75                  80
Cys Ala Gly Leu Leu Lys Val Leu Thr Gln Ala Ser Glu Val Asn Pro
                85                  90                  95
Leu Arg
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<210> 1375
<211> 282

<212> DNA
<213> Homo sapiens

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120
ctggtggccc agtcgttcat gagcgtggag aacccggccg ccacaaagga gtcccagtga
180
cattgggacg atccggaaat tcgcaatgca cacggtgcag gacaccaatc tgaagagaac
240
ggcccccagc atgagcggcc gcggcttggc cctcatgcta gc
282

<210> 1376
<211> 59
<212> PRT
<213> Homo sapiens

<400> 1376
Xaa Ala Phe Asp Arg Ala Thr Arg Gly His Val Ile Asp Tyr Ile Asp
 1   5   10   15
Phe His Leu His Gly Trp His Trp Pro Ala Phe Asn Ile Ala Asp Met
            20   25   30
Ala Ile Val Gly Gly Ala Ile Ala Leu Val Ala Gln Ser Phe Met Ser
        35   40   45
Val Glu Asn Pro Ala Ala Thr Lys Glu Ser Gln
    50   55

<210> 1377
<211> 6306
<212> DNA
<213> Homo sapiens

<400> 1377
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420
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540

ccgtctctac ttaagaagct cttactggca ccagccaaca ctcagctaag ttataatgaa
600
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720
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<210> 1378
<211> 798
<212> PRT
<213> Homo sapiens

<400> 1378
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35 40 45
Asp Ser Phe Leu Gly Gly Leu Lys Trp Cys Ser Asp Gln Ser Glu Ile
50 55 60
Ile Ser Asn Gln Tyr Asn Asn Glu Pro Ser Asn Ile Phe Glu Lys Ile
65 70 75 80
Asp Glu Glu Asn Glu Ala Asn Leu Leu Ala Val Leu Thr Glu Thr Leu
85 90 95
Asp Ser Leu Pro Val Asp Glu Asp Gly Leu Pro Ser Phe Asp Ala Leu
100 105 110
Thr Asp Gly Asp Val Thr Thr Asp Asn Glu Ala Ser Pro Ser Ser Met

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        115                 120                 125
Pro Asp Gly Thr Pro Pro Pro Gln Glu Ala Glu Glu Pro Ser Leu Leu
    130                 135                 140
Lys Lys Leu Leu Leu Ala Pro Ala Asn Thr Gln Leu Ser Tyr Asn Glu
145                 150                 155                 160
Cys Ser Gly Leu Ser Thr Gln Asn His Ala Asn His Asn His Arg Ile
                165                 170                 175
Arg Thr Asn Pro Ala Ile Val Lys Thr Glu Asn Ser Trp Ser Asn Lys
            180                 185                 190
Ala Lys Ser Ile Cys Gln Gln Gln Lys Pro Gln Arg Arg Pro Cys Ser
        195                 200                 205
Glu Leu Leu Lys Tyr Leu Thr Thr Asn Asp Asp Pro Pro His Thr Lys
    210                 215                 220
Pro Thr Glu Asn Arg Asn Ser Ser Arg Asp Lys Cys Thr Ser Lys Lys
225                 230                 235                 240
Lys Ser His Thr Gln Ser Gln Ser Gln His Leu Gln Ala Lys Pro Thr
                245                 250                 255
Thr Leu Ser Leu Pro Leu Thr Pro Glu Ser Pro Asn Asp Pro Lys Gly
            260                 265                 270
Ser Pro Phe Glu Asn Lys Thr Ile Glu Arg Thr Leu Ser Val Glu Leu
        275                 280                 285
Ser Gly Thr Ala Gly Leu Thr Pro Pro Thr Thr Pro Pro His Lys Ala
    290                 295                 300
Asn Gln Asp Asn Pro Phe Arg Ala Ser Pro Lys Leu Lys Ser Ser Cys
305                 310                 315                 320
Lys Thr Val Val Pro Pro Pro Ser Lys Lys Pro Arg Tyr Ser Glu Ser
                325                 330                 335
Ser Gly Thr Gln Gly Asn Asn Ser Thr Lys Lys Gly Pro Glu Gln Ser
            340                 345                 350
Glu Leu Tyr Ala Gln Leu Ser Lys Ser Ser Val Leu Thr Gly Gly His
        355                 360                 365
Glu Glu Arg Lys Thr Lys Arg Pro Ser Leu Arg Leu Phe Gly Asp His
    370                 375                 380
Asp Tyr Cys Gln Ser Ile Asn Ser Lys Thr Glu Ile Leu Ile Asn Ile
385                 390                 395                 400
Ser Gln Glu Leu Gln Asp Ser Arg Gln Leu Glu Asn Lys Asp Val Ser
                405                 410                 415
Ser Asp Trp Gln Gly Gln Ile Cys Ser Ser Thr Asp Ser Asp Gln Cys
            420                 425                 430
Tyr Leu Arg Glu Thr Leu Glu Ala Ser Lys Gln Val Ser Pro Cys Ser
        435                 440                 445
Thr Arg Lys Gln Leu Gln Asp Gln Glu Ile Arg Ala Glu Leu Asn Lys
    450                 455                 460
His Phe Gly His Pro Ser Gln Ala Val Phe Asp Asp Glu Ala Asp Lys
465                 470                 475                 480
Thr Gly Glu Leu Arg Asp Ser Asp Phe Ser Asn Glu Gln Phe Ser Lys
                485                 490                 495
Leu Pro Met Phe Ile Asn Ser Gly Leu Ala Met Asp Gly Leu Phe Asp
            500                 505                 510
Asp Ser Glu Asp Glu Ser Asp Lys Leu Ser Tyr Pro Trp Asp Gly Thr
        515                 520                 525
Gln Ser Tyr Ser Leu Phe Asn Val Ser Pro Ser Cys Ser Ser Phe Asn
    530                 535                 540
Ser Pro Cys Arg Asp Ser Val Ser Pro Pro Lys Ser Leu Phe Ser Gln
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Ser Arg Ser Ser Ser Arg Ser Cys Tyr Tyr Tyr Glu Ser Ser His Tyr
        595                 600                 605
Arg His Arg Thr His Arg Asn Ser Pro Leu Tyr Val Arg Ser Arg Ser
    610                 615                 620
Arg Ser Pro Tyr Ser Arg Arg Pro Arg Tyr Asp Ser Tyr Glu Glu Tyr
625                 630                 635                 640
Gln His Glu Arg Leu Lys Arg Glu Glu Tyr Arg Arg Glu Tyr Glu Lys
                645                 650                 655
Arg Glu Ser Glu Arg Ala Lys Gln Arg Glu Arg Gln Arg Gln Lys Ala
            660                 665                 670
Ile Glu Glu Arg Arg Val Ile Tyr Val Gly Lys Ile Arg Pro Asp Thr
        675                 680                 685
Thr Arg Thr Glu Leu Arg Asp Arg Phe Glu Val Phe Gly Glu Ile Glu
    690                 695                 700
Glu Cys Thr Val Asn Leu Arg Asp Asp Gly Asp Ser Tyr Gly Phe Ile
705                 710                 715                 720
Thr Tyr Arg Tyr Thr Cys Asp Ala Phe Ala Ala Leu Glu Asn Gly Tyr
                725                 730                 735
Thr Leu Arg Arg Ser Asn Glu Thr Asp Phe Glu Leu Tyr Phe Cys Gly
            740                 745                 750
Arg Lys Gln Phe Phe Lys Ser Asn Tyr Ala Asp Leu Asp Ser Asn Ser
        755                 760                 765
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Phe Asp Ser Leu Leu Lys Glu Ala Gln Arg Ser Leu Arg Arg
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<210> 1379
<211> 590
<212> DNA
<213> Homo sapiens

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gaggacgtga gggcaatctg gtgtccctgc cgtgtggccg cgtcacccat ctctgccctc
300
ggtgtccctg ccctgtggcc gcgtcaccca tctctgccct cggagtccct gccgtgtggc
360
cgcgtcnacc catctctgcc ctcggagtcc ctgccgtgtg gccgtgtcna cccacctctg
420
ccctcggtgt ccctgccgtg tggccgagtc nacccacctc tgccctcggt gtccctgccg
480

tgtggccgcg tcnacccacc tctgccctcg gtgtccccgc cgtgtggccg cgtcnaccca
540
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590

<210> 1380
<211> 141
<212> PRT
<213> Homo sapiens

<400> 1380
Asn Arg Val Gln Phe Leu Leu Lys Pro Gly Gly Arg Lys Pro Leu Asn
1 5 10 15
Lys Gly Leu Trp Gly Leu Val Pro Trp Glu Asp Val Arg Ala Ile Trp
20 25 30
Cys Pro Cys Arg Val Ala Ala Ser Pro Ile Ser Ala Leu Gly Val Pro
35 40 45
Ala Leu Trp Pro Arg His Pro Ser Leu Pro Ser Glu Ser Leu Pro Cys
50 55 60
Gly Arg Val Xaa Pro Ser Leu Pro Ser Glu Ser Leu Pro Cys Gly Arg
65 70 75 80
Val Xaa Pro Pro Leu Pro Ser Val Ser Leu Pro Cys Gly Arg Val Xaa
85 90 95
Pro Pro Leu Pro Ser Val Ser Leu Pro Cys Gly Arg Val Xaa Pro Pro
100 105 110
Leu Pro Ser Val Ser Pro Pro Cys Gly Arg Val Xaa Pro Ser Leu Pro
115 120 125
Ser Val Ser Pro Pro Cys Gly Arg Val Thr His Leu Cys
130 135 140

<210> 1381
<211> 433
<212> DNA
<213> Homo sapiens

<400> 1381
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cagatcatgc tggccccctt gacgaagcat gcactttctg gcctaggccg gatacgatgt
120
gtgaggccac ggagagtcca ggccggagca cactgaccgc cttggctaag cattcatttc
180
cgtgtcctgg ctgccatcag agaggaggca ggtcccacag atctgctctt gtttctgctg
240
gtctgaagtg gggtttcagt ttctgtgtgg aacaattcat taggggtttg atctcaaagc
300
ccaggcattg gccctgtacc tgttcctcac ggaagccgaa ctcctgctta tgggccccag
360
cctacaggca gccaaatggg ctagccccag ccaaggggct gtttggcgac ctctgaacca
420
cagctctcca tgg
433

<210> 1382

<211> 123
<212> PRT
<213> Homo sapiens

<400> 1382
Met Met Cys Glu Ser Ala Asp His Ala Gly Pro Leu Asp Glu Ala Cys
1 5 10 15
Thr Phe Trp Pro Arg Pro Asp Thr Met Cys Glu Ala Thr Glu Ser Pro
20 25 30
Gly Arg Ser Thr Leu Thr Ala Leu Ala Lys His Ser Phe Pro Cys Pro
35 40 45
Gly Cys His Gln Arg Gly Gly Arg Ser His Arg Ser Ala Leu Val Ser
50 55 60
Ala Gly Leu Lys Trp Gly Phe Ser Phe Cys Val Glu Gln Phe Ile Arg
65 70 75 80
Gly Leu Ile Ser Lys Pro Arg His Trp Pro Cys Thr Cys Ser Ser Arg
85 90 95
Lys Pro Asn Ser Cys Leu Trp Ala Pro Ala Tyr Arg Gln Pro Asn Gly
100 105 110
Leu Ala Pro Ala Lys Gly Leu Phe Gly Asp Leu
115 120

<210> 1383
<211> 906
<212> DNA
<213> Homo sapiens

<400> 1383
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caccacagca cacctgcctc tggcttgcag gccaagatgg cccctatgtc aaccagggtt
120
tctgcagctg gtcctgggag acccacggcc tcctctctcc tgcccctgac caatacacca
180
caaacgcctc acatgagctc acccacaccc ccaagagcca tggtgctcac aaagcaaaga
240
ccaagccaga ctcaatcctg tggccccagg gtcagccgca gagcagacaa ctagaacctc
300
acaagaagct gaacacaggc tgggtcacct ataaacaggg aggccatcct gaagggagga
360
agcacccaac cagaggtgaa ctcaccttgg accattcgac aatgcagtcc aggcagaagt
420
aatgggcaca gttctnccgg cgtccccacg gcctggtctc tgaatgcgtt gagacagatt
480
gggcagctct ctgcatcatc atcagaattg aaagagccag cggcttccag tttcccctga
540
gtacccgcta cctccagcaa tgtctccccg tcgtcttcag aatcctcgga accagatctg
600
tcttccaggt cttcctcctc agacgccccc tcgtcttctc cgtctgtgcc atctccatgc
660
tcgctgtcac tgtcgtcccc agagtcccca ctgctgccca cgctgctttc ttcaaagtca
720
cctgccgggt ccgcagggcc gacctgtggg tgtccatccg gccctgggct ccgggccaca
780

agctcatcca ggctgtcgtc atccattgct gcacattgag ctcagctccg gaaacctcgt
840
gtcccgcagg cgctcgcgag cgctcgccgc cgctgcacga ccgagagtcg ctcctaggcc
900
cggccg
906

<210> 1384
<211> 97
<212> PRT
<213> Homo sapiens

<400> 1384
Xaa Pro Val Phe Ser Val Ser Thr Glu Arg Thr Thr Cys Gln Gly Ser
1 5 10 15
Lys Val Thr Thr His His Ser Thr Pro Ala Ser Gly Leu Gln Ala Lys
20 25 30
Met Ala Pro Met Ser Thr Arg Val Ser Ala Ala Gly Pro Gly Arg Pro
35 40 45
Thr Ala Ser Ser Leu Leu Pro Leu Thr Asn Thr Pro Gln Thr Pro His
50 55 60
Met Ser Ser Pro Thr Pro Pro Arg Ala Met Val Leu Thr Lys Gln Arg
65 70 75 80
Pro Ser Gln Thr Gln Ser Cys Gly Pro Arg Val Ser Arg Arg Ala Asp
85 90 95
Asn

<210> 1385
<211> 210
<212> DNA
<213> Homo sapiens

<400> 1385
acgcgtgcac tgggtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
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ncatggtgtg tgcacgtgtg cnactgtgta tgcatggtaa tgtgcacgtg tgcactgtgt
120
gtggcgtgta tgcatggtgt gtgcacgtgt gcactgtgtg tggggtgtat gncatggtgg
180
gtgcacatat gcactggggg gtgtgtatgc
210

<210> 1386
<211> 70
<212> PRT
<213> Homo sapiens

<400> 1386
Thr Arg Ala Leu Gly Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
1 5 10 15
Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
20 25 30
Val Met Cys Thr Cys Ala Leu Cys Val Ala Cys Met His Gly Val Cys

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        35                  40                  45
  ır Cys Ala Leu Cys Val Gly Cys Met Xaa Trp Trp Val His Ile Cys
     50                  55                  60
 Thr Gly Gly Cys Val Cys
 65                  70
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<210> 1387
<211> 521
<212> DNA
<213> Homo sapiens

<400> 1387
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gtccaagccg aaggtgtttc cggttgcggc aaacactccc caggaggcca gcacacagaa
120
gccggtgagg acgaaggcgt agttgccgcc gatggcagct ccgacagcac cgccggcgat
180
ggcggcaagg agtccgaaga cgaagactcc gatagaggtg gtgaacatcg gtgttccttt
240
gtgagggcgg ggtatcccgc gatctgtcat ccgcacgcag cgacgggtgc ggcattttct
300
ggacatccct aggcgttgac ccaggggtgg ggtggttcag acgtgtgccg gcgcacgtct
360
gaaccacccg gtatcagcag gtgccagggg cggattcccc agcacctgac tcatatgcgt
420
cgatgagatc gatgttggcc ttggagtggg aactcgggtc gaaggtgtac ccgatgaact
480
cgtgggctaa gcgacgggcg agttcgcgac cgatgacgcg t
521

<210> 1388
<211> 103
<212> PRT
<213> Homo sapiens

<400> 1388
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Gly Arg Asn Ser Thr Ser Glu Gly Asp Val Arg Ala His Glu Gly Thr
 1               5                  10                  15
Lys Gly Gln Val Val Gln Ala Glu Gly Val Ser Gly Cys Gly Lys His
            20                  25                  30
Ser Pro Gly Gly Gln His Thr Glu Ala Gly Glu Asp Glu Gly Val Val
        35                  40                  45
Ala Ala Asp Gly Ser Ser Asp Ser Thr Ala Gly Asp Gly Gly Lys Glu
    50                  55                  60
Ser Glu Asp Glu Asp Ser Asp Arg Gly Gly Glu His Arg Cys Ser Phe
65                  70                  75                  80
Val Arg Ala Gly Tyr Pro Ala Ile Cys His Pro His Ala Ala Thr Gly
                85                  90                  95
Ala Ala Phe Ser Gly His Pro
            100
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<210> 1389
<211> 4013

<212> DNA
<213> Homo sapiens

<400> 1389
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cgcacagcca catcaccacc ccccacaacc tcccagacca tcatttccac cattcccagc
120
actgccatgc acacccgctc cacagctgcc cccatcccca tcctgcctga gagaggagtt
180
tccctcttcc cctatggggc agacgccggg gacctggagt tcgtcaggag gaccgtggac
240
ttcacctccc cactcttcaa gccggcgact ggcttccccc ttggctcctc tctccgtgat
300
tccctctact tcacagacaa tggccagatc atcttcccag agtcagacta ccagattttc
360
tcctacccca acccactccc aacaggcttc acaggccggg accctgtggc cctggtggct
420
ccgttctggg acgatgctga cttctccact ggtcggggga ccacatttta tcaggaatac
480
gagacgttct atggtgaaca cagcctgcta gtccagcagg ccgagtcttg gattagaaag
540
atcacaaaca acgggggcta caaggccagg tgggccctaa aggtcacgtg ggtcaatgcc
600
cacgcctatc ctgcccagtg gaccctcggg agcaacacct accaagccat cctctccacg
660
gacgggagca ggtcctatgc cctgtttctc taccagagcg gtgggatgca gtgggacgtg
720
gcccagcgct caggcaaccc ggtgctcatg ggcttctcta gtggagatgg ctatttcgaa
780
aacagcccac tgatgtccca gccagtgtgg gagaggtatc gccctgatag attcctgaat
840
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900
taccgtctcg agtgcctgca gtggctgaag agccagcctc ggtggcccag ctggggctgg
960
aaccaggtct cctgcccttg ttcctggcag cagggacgac gggacttacg attccaaccc
1020
gtcagcatag gtcgctgggg cctcggcagt aggcagctgt gcagcttcac ctcttggcga
1080
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1140
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1260
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1320
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1380
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1440
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gagcctcacg acgcaatccg tgtcctgctg gataaccaga ctgtgacatt tcagcctgac
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1620
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1800
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1860
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1980
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2100
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2160
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2280
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2820
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3120

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3600
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3660
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3780
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3840
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3900
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3960
agtgtggagg ttaagtgctg ggcagcagtg gagcattagg ggcagctgga tcc
4013

<210> 1390
<211> 1156
<212> PRT
<213> Homo sapiens

<400> 1390
Pro Leu Lys Met Glu Thr Ser Gly Met Thr Thr Pro Ser Leu Lys Thr
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Asp Gly Gly Arg Arg Thr Ala Thr Ser Pro Pro Pro Thr Thr Ser Gln
20 25 30
Thr Ile Ile Ser Thr Ile Pro Ser Thr Ala Met His Thr Arg Ser Thr
35 40 45
Ala Ala Pro Ile Pro Ile Leu Pro Glu Arg Gly Val Ser Leu Phe Pro
50 55 60
Tyr Gly Ala Asp Ala Gly Asp Leu Glu Phe Val Arg Arg Thr Val Asp
65 70 75 80
Phe Thr Ser Pro Leu Phe Lys Pro Ala Thr Gly Phe Pro Leu Gly Ser
85 90 95
Ser Leu Arg Asp Ser Leu Tyr Phe Thr Asp Asn Gly Gln Ile Ile Phe
100 105 110
Pro Glu Ser Asp Tyr Gln Ile Phe Ser Tyr Pro Asn Pro Leu Pro Thr
115 120 125
Gly Phe Thr Gly Arg Asp Pro Val Ala Leu Val Ala Pro Phe Trp Asp

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    130                 135                 140
Asp Ala Asp Phe Ser Thr Gly Arg Gly Thr Thr Phe Tyr Gln Glu Tyr
145                 150                 155                 160
Glu Thr Phe Tyr Gly Glu His Ser Leu Leu Val Gln Gln Ala Glu Ser
                165                 170                 175
Trp Ile Arg Lys Ile Thr Asn Asn Gly Gly Tyr Lys Ala Arg Trp Ala
            180                 185                 190
Leu Lys Val Thr Trp Val Asn Ala His Ala Tyr Pro Ala Gln Trp Thr
        195                 200                 205
Leu Gly Ser Asn Thr Tyr Gln Ala Ile Leu Ser Thr Asp Gly Ser Arg
    210                 215                 220
Ser Tyr Ala Leu Phe Leu Tyr Gln Ser Gly Gly Met Gln Trp Asp Val
225                 230                 235                 240
Ala Gln Arg Ser Gly Asn Pro Val Leu Met Gly Phe Ser Ser Gly Asp
                245                 250                 255
Gly Tyr Phe Glu Asn Ser Pro Leu Met Ser Gln Pro Val Trp Glu Arg
            260                 265                 270
Tyr Arg Pro Asp Arg Phe Leu Asn Ser Asn Ser Gly Leu Gln Gly Leu
        275                 280                 285
Gln Phe Tyr Arg Leu His Arg Glu Glu Arg Pro Asn Tyr Arg Leu Glu
    290                 295                 300
Cys Leu Gln Trp Leu Lys Ser Gln Pro Arg Trp Pro Ser Trp Gly Trp
305                 310                 315                 320
Asn Gln Val Ser Cys Pro Cys Ser Trp Gln Gln Gly Arg Arg Asp Leu
                325                 330                 335
Arg Phe Gln Pro Val Ser Ile Gly Arg Trp Gly Leu Gly Ser Arg Gln
            340                 345                 350
Leu Cys Ser Phe Thr Ser Trp Arg Gly Gly Val Cys Cys Ser Tyr Gly
        355                 360                 365
Pro Trp Gly Glu Phe Arg Glu Gly Trp His Val Gln Arg Pro Trp Gln
    370                 375                 380
Leu Ala Gln Glu Leu Glu Pro Gln Ser Trp Cys Cys Arg Trp Asn Asp
385                 390                 395                 400
Lys Pro Tyr Leu Cys Ala Leu Tyr Gln Gln Arg Arg Pro His Val Gly
                405                 410                 415
Cys Ala Thr Tyr Arg Pro Pro Gln Pro Ala Trp Met Phe Gly Asp Pro
            420                 425                 430
His Ile Thr Thr Leu Asp Gly Val Ser Tyr Thr Phe Asn Gly Leu Gly
        435                 440                 445
Asp Phe Leu Leu Val Gly Ala Gln Asp Gly Asn Ser Ser Phe Leu Leu
    450                 455                 460
Gln Gly Arg Thr Ala Gln Thr Gly Ser Ala Gln Ala Thr Asn Phe Ile
465                 470                 475                 480
Ala Phe Ala Ala Gln Tyr Arg Ser Ser Ser Leu Gly Pro Val Thr Val
                485                 490                 495
Gln Trp Leu Leu Glu Pro His Asp Ala Ile Arg Val Leu Leu Asp Asn
            500                 505                 510
Gln Thr Val Thr Phe Gln Pro Asp His Glu Asp Gly Gly Gly Gln Glu
        515                 520                 525
Thr Phe Asn Ala Thr Gly Val Leu Leu Ser Arg Asn Gly Ser Glu Val
    530                 535                 540
Ser Ala Ser Phe Asp Gly Trp Ala Thr Val Ser Val Ile Ala Leu Ser
545                 550                 555                 560
Asn Ile Leu His Ala Ser Ala Ser Leu Pro Pro Glu Tyr Gln Asn Arg
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                565                 570                 575
Thr Glu Gly Leu Leu Gly Val Trp Asn Asn Asn Pro Glu Asp Asp Phe
            580                 585                 590
Arg Met Pro Asn Gly Ser Thr Ile Pro Pro Gly Ser Pro Glu Glu Met
        595                 600                 605
Leu Phe His Phe Gly Met Thr Trp Gln Ile Asn Gly Thr Gly Leu Leu
    610                 615                 620
Gly Lys Arg Asn Asp Gln Leu Pro Ser Asn Phe Thr Pro Val Phe Tyr
625                 630                 635                 640
Ser Gln Leu Gln Lys Asn Ser Ser Trp Ala Glu His Leu Ile Ser Asn
                645                 650                 655
Cys Asp Gly Asp Ser Ser Cys Ile Tyr Asp Thr Leu Ala Leu Arg Asn
            660                 665                 670
Ala Ser Ile Gly Leu His Thr Arg Glu Val Ser Lys Asn Tyr Glu Gln
        675                 680                 685
Ala Asn Ala Thr Leu Asn Gln Tyr Pro Pro Ser Ile Asn Gly Gly Arg
    690                 695                 700
Val Ile Glu Ala Tyr Lys Gly Gln Thr Thr Leu Ile Gln Tyr Thr Ser
705                 710                 715                 720
Asn Ala Glu Asp Ala Asn Phe Thr Leu Arg Asp Ser Cys Thr Asp Leu
                725                 730                 735
Glu Leu Phe Glu Asn Gly Thr Leu Leu Trp Thr Pro Lys Ser Leu Glu
            740                 745                 750
Pro Phe Thr Leu Glu Ile Leu Ala Arg Ser Ala Lys Ile Gly Leu Ala
        755                 760                 765
Ser Ala Leu Gln Pro Arg Thr Val Val Cys His Cys Asn Ala Glu Ser
    770                 775                 780
Gln Cys Leu Tyr Asn Gln Thr Ser Arg Val Gly Asn Ser Ser Leu Glu
785                 790                 795                 800
Val Ala Gly Cys Lys Cys Asp Gly Gly Thr Phe Gly Arg Tyr Cys Glu
                805                 810                 815
Gly Ser Glu Asp Ala Cys Glu Glu Pro Cys Phe Pro Ser Val His Cys
            820                 825                 830
Val Pro Gly Lys Gly Cys Glu Ala Cys Pro Pro Asn Leu Thr Gly Asp
        835                 840                 845
Gly Arg His Cys Ala Ala Leu Gly Ser Ser Phe Leu Cys Gln Asn Gln
    850                 855                 860
Ser Cys Pro Val Asn Tyr Cys Tyr Asn Gln Gly His Cys Tyr Ile Ser
865                 870                 875                 880
Gln Thr Leu Gly Cys Gln Pro Met Cys Thr Cys Pro Pro Ala Phe Thr
                885                 890                 895
Asp Ser Arg Cys Phe Leu Ala Gly Asn Asn Phe Ser Pro Thr Val Asn
            900                 905                 910
Leu Glu Leu Pro Leu Arg Val Ile Gln Leu Leu Leu Ser Glu Glu Glu
        915                 920                 925
Asn Ala Ser Met Ala Glu Val Asn Ala Ser Val Ala Tyr Arg Leu Gly
    930                 935                 940
Thr Leu Asp Met Arg Ala Phe Leu Arg Asn Ser Gln Val Glu Arg Ile
945                 950                 955                 960
Asp Ser Ala Ala Pro Ala Ser Gly Ser Pro Ile Gln His Trp Met Val
                965                 970                 975
Ile Ser Glu Phe Gln Tyr Arg Pro Arg Gly Pro Val Ile Asp Phe Leu
            980                 985                 990
Asn Asn Gln Leu Leu Ala Ala Val Val Glu Ala Phe Leu Tyr His Val
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995 1000 1005
Pro Arg Arg Ser Glu Glu Pro Arg Asn Asp Val Val Phe Gln Pro Ile
1010 1015 1020
Ser Gly Glu Asp Val Arg Asp Val Thr Ala Leu Asn Val Ser Thr Leu
1025 1030 1035 1040
Lys Ala Tyr Phe Arg Cys Asp Gly Tyr Lys Gly Tyr Asp Leu Val Tyr
1045 1050 1055
Ser Pro Gln Ser Gly Phe Thr Cys Val Ser Pro Cys Ser Arg Gly Tyr
1060 1065 1070
Cys Asp His Gly Gly Gln Cys Gln His Leu Pro Ser Gly Pro Arg Cys
1075 1080 1085
Ser Cys Val Ser Phe Ser Ile Tyr Thr Ala Trp Gly Glu His Cys Glu
1090 1095 1100
His Leu Ser Met Lys Leu Asp Ala Phe Phe Gly Ile Phe Phe Gly Ala
1105 1110 1115 1120
Leu Gly Gly Leu Leu Leu Leu Gly Val Gly Thr Phe Val Val Leu Arg
1125 1130 1135
Phe Trp Gly Cys Ser Gly Ala Arg Phe Ser Tyr Phe Leu Asn Ser Ala
1140 1145 1150
Glu Ala Leu Pro
1155

<210> 1391
<211> 481
<212> DNA
<213> Homo sapiens

<400> 1391
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ggcattgtgt tccagcagtg gaacgccttc ccgcacctca ccgtgctgga aaacgtgatg
120
ctggcgccgc gcaaggtgct cggtaaaagc aagcagaagg ccgaggagct ggcggtccgg
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caactgaccc acgtgggcct gagcgacaag ctcaagacct ttcccgcana gctttccggc
240
ggccagcaac agcgcatggc gattgcccgg gccctggcca tgtcgccgga ctacatgctg
300
ttcgacgaag ccacctcggc ccttgatccg cagttggtgg gcgaggtgct ggacaccatg
360
cgcatgctcg ccgaagacgg catgaccatg gtcctggtga cccatgaaat ccgctttgcc
420
cgcgatgtgt ccgatcgcgt ggcgttcttt cgcaacggcc tggtgcacga gatcggcgcg
480
c
481

<210> 1392
<211> 160
<212> PRT
<213> Homo sapiens

<400> 1392
Val Asp Gly Ile Glu Val His Asp Lys Ala Thr Asp Leu Asn Arg Leu

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Arg Gln Lys Ile Gly Ile Val Phe Gln Gln Trp Asn Ala Phe Pro His
            20                  25                  30
Leu Thr Val Leu Glu Asn Val Met Leu Ala Pro Arg Lys Val Leu Gly
        35                  40                  45
Lys Ser Lys Gln Lys Ala Glu Glu Leu Ala Val Arg Gln Leu Thr His
    50                  55                  60
Val Gly Leu Ser Asp Lys Leu Lys Thr Phe Pro Ala Xaa Leu Ser Gly
65                  70                  75                  80
Gly Gln Gln Gln Arg Met Ala Ile Ala Arg Ala Leu Ala Met Ser Pro
                85                  90                  95
Asp Tyr Met Leu Phe Asp Glu Ala Thr Ser Ala Leu Asp Pro Gln Leu
            100                 105                 110
Val Gly Glu Val Leu Asp Thr Met Arg Met Leu Ala Glu Asp Gly Met
        115                 120                 125
Thr Met Val Leu Val Thr His Glu Ile Arg Phe Ala Arg Asp Val Ser
    130                 135                 140
Asp Arg Val Ala Phe Phe Arg Asn Gly Leu Val His Glu Ile Gly Ala
145                 150                 155                 160
```

<210> 1393
<211> 309
<212> DNA
<213> Homo sapiens

<400> 1393
cggccgccat cggcgcgggc cttgtgggat atggccatta ctgaggtgct ggccggctac
60
tacgaacccg acgaacacgg acaccgcaag cccgagtcgt tgtacggcgc ggtcaagatg
120
tgggcccttc tgcgccgtca gggcatcagg tggcccgctg cancggtgga gcgcctcatg
180
cgggacaacc ggtggcgtgg ggtgacccgc cgtaagaagg ttncgcacca ccatcgctga
240
cccggctgcc gggcgagccc cggatctggt ggaccgccag ttccgcgtcg aggcgcccaa
300
caagttgct
309

<210> 1394
<211> 79
<212> PRT
<213> Homo sapiens

<400> 1394

```
Arg Pro Pro Ser Ala Arg Ala Leu Trp Asp Met Ala Ile Thr Glu Val
 1               5                  10                  15
Leu Ala Gly Tyr Tyr Glu Pro Asp Glu His Gly His Arg Lys Pro Glu
            20                  25                  30
Ser Leu Tyr Gly Ala Val Lys Met Trp Ala Leu Leu Arg Arg Gln Gly
        35                  40                  45
Ile Arg Trp Pro Ala Ala Xaa Val Glu Arg Leu Met Arg Asp Asn Arg
    50                  55                  60
Trp Arg Gly Val Thr Arg Arg Lys Lys Val Xaa His His His Arg
```

65 70 75

<210> 1395
<211> 347
<212> DNA
<213> Homo sapiens

<400> 1395
accggtgggg ttcgtggtgg cctggttact ttttggcgcg agcggtgtgg tgtgggccgt
60
tatgacggta gtcgtgggcg aaacggtgct tgtcgttgtg cgccgtcaac gtcgaagagc
120
ccagattctt aaaggcggtc gcgatgttgc ccgggcgaca agggccttgg ctggacgggt
180
gtcggtgggg gagatcccct cagttgcact agagcacgtg gccgatgacg tggaggtatt
240
ggctcaggct aggcgggctc atgcagtggg cggaagcgtt tccgacgccc tcattgccac
300
ctcccggcaa ccagggatgg ctggtctggt gccactagcc cacgcgt
347

<210> 1396
<211> 95
<212> PRT
<213> Homo sapiens

<400> 1396
Met Thr Val Val Val Gly Glu Thr Val Leu Val Val Val Arg Arg Gln
1 5 10 15
Arg Arg Arg Ala Gln Ile Leu Lys Gly Gly Arg Asp Val Ala Arg Ala
20 25 30
Thr Arg Ala Leu Ala Gly Arg Val Ser Val Gly Glu Ile Pro Ser Val
35 40 45
Ala Leu Glu His Val Ala Asp Asp Val Glu Val Leu Ala Gln Ala Arg
50 55 60
Arg Ala His Ala Val Gly Gly Ser Val Ser Asp Ala Leu Ile Ala Thr
65 70 75 80
Ser Arg Gln Pro Gly Met Ala Gly Leu Val Pro Leu Ala His Ala
85 90 95

<210> 1397
<211> 308
<212> DNA
<213> Homo sapiens

<400> 1397
caattgcgcg ggttactgca ggcgaagatg cagatgatgt cggacaccaa tttcctcgac
60
ctggcccgcg tcgcgattgc cgccactatc cattctccgg aacgcgcgca agacatggtc
120
aaccgcttga gcaaacgcga agaaggcttc acgcaatggg tacgtgccgc acaggacgat
180
ggtcgactgt cctgcagcga cccggcgttc gctgcccacc agatacaaag cctgctcaag
240

gcgttcgcct tttggccgca aatcaccctg ggccagccgg tgctggatgc cgccagccag
300
gccaacgt
308

<210> 1398
<211> 93
<212> PRT
<213> Homo sapiens

<400> 1398
Met Gln Met Met Ser Asp Thr Asn Phe Leu Asp Leu Ala Arg Val Ala
1 5 10 15
Ile Ala Ala Thr Ile His Ser Pro Glu Arg Ala Gln Asp Met Val Asn
20 25 30
Arg Leu Ser Lys Arg Glu Glu Gly Phe Thr Gln Trp Val Arg Ala Ala
35 40 45
Gln Asp Asp Gly Arg Leu Ser Cys Ser Asp Pro Ala Phe Ala Ala His
50 55 60
Gln Ile Gln Ser Leu Leu Lys Ala Phe Ala Phe Trp Pro Gln Ile Thr
65 70 75 80
Leu Gly Gln Pro Val Leu Asp Ala Ala Ser Gln Ala Asn
85 90

<210> 1399
<211> 539
<212> DNA
<213> Homo sapiens

<400> 1399
gctagctaac atttattttt gtttttatta ttgttatcta gtggtaaaaa tttcttaagc
60
aatgaactga agtctagatt tttgagatgt agtcctttac tgattataaa gcaaatgcct
120
ttagatattt taacttcatc agtactatct gtagtaggag gctgatttta ctaaaattag
180
ataattatat acatctgttc ctattccttt ggtaggacct ttaagaaagt catgctgaat
240
ctgagaatgc caggacattt cacgtggtat gaatgtagga tattcattta cacatcgctg
300
cacagacagc ctctatataa cccaccctgt tggggtattg aatttttttct tttcccgccc
360
tacttttaaa tcttgtcatg taatttcaac acataatttg tggcacttta gttttttttac
420
cctttatagt ttaataactt atacatgtac atgcttaaaa tgtcaaacaa tacaaatggg
480
aacaaagaaa attgcttcac catctgtgaa cccctccttt tgtagtcccc ttcacgcgt
539

<210> 1400
<211> 90
<212> PRT
<213> Homo sapiens

<400> 1400
Met Asn Val Gly Tyr Ser Phe Thr His Arg Cys Thr Asp Ser Leu Tyr
1 5 10 15
Ile Thr His Pro Val Gly Val Leu Asn Phe Phe Phe Ser Arg Pro Thr
20 25 30
Phe Lys Ser Cys His Val Ile Ser Thr His Asn Leu Trp His Phe Ser
35 40 45
Phe Phe Thr Leu Tyr Ser Leu Ile Thr Tyr Thr Cys Thr Cys Leu Lys
50 55 60
Cys Gln Thr Ile Gln Met Gly Thr Lys Lys Ile Ala Ser Pro Ser Val
65 70 75 80
Asn Pro Ser Phe Cys Ser Pro Leu His Ala
85 90

<210> 1401
<211> 653
<212> DNA
<213> Homo sapiens

<400> 1401
ttcgaggggt cacttggact caagcttcgc gaagtccggg acctcggacg accgattttt
60
cggctgtgca ccgtcaccgc aaggctggcg tgggttnnct catcaccggc gcggcgatgg
120
ncattggggt ttgatggccg cgtttccctg ctgctgggcg cgatcctcat cgtcaccggc
180
ccaacggtga ttaacccgat cctgcgtcag ttgcgtccta cccggcgagt gagtgctctg
240
ttgaggtggg aaggaatcgt cgtcgatccg ctcggcgcca tcctggcatt actggtgtat
300
caggccataa ccagcatcga ccgatcttcc atcggacaag gcgtcttgaa tctggggctc
360
accctattgg tcgggctgct cttcgctggc cccatcgggt ggatcgtcac cgcgatgatg
420
aaacggcacc tcatcccgga cttcctacaa ggcgtgattt tcgttggggt cgccgttgga
480
acgtgtgttg gcgctaacgt cattcgggag gaatcgggcc tggtcgccgt tacgatgctc
540
ggcatctacc tggcgaacca gcgcaacctc gagcttgagc ccgtcatcga gttcaaggaa
600
cacctgcagg tgctcctcgt tggcgtccta ttcatcatgc ttgcaggacg cgt
653

<210> 1402
<211> 217
<212> PRT
<213> Homo sapiens

<400> 1402
Phe Glu Gly Ser Leu Gly Leu Lys Leu Arg Glu Val Arg Asp Leu Gly
1 5 10 15
Arg Pro Ile Phe Arg Leu Cys Thr Val Thr Ala Arg Leu Ala Trp Val
20 25 30
Xaa Ser Ser Pro Ala Arg Arg Trp Xaa Leu Gly Phe Asp Gly Arg Val

```
        35                  40                  45
Ser Leu Leu Leu Gly Ala Ile Leu Ile Val Thr Gly Pro Thr Val Ile
    50                  55                  60
Asn Pro Ile Leu Arg Gln Leu Arg Pro Thr Arg Arg Val Ser Ala Leu
65                  70                  75                  80
Leu Arg Trp Glu Gly Ile Val Val Asp Pro Leu Gly Ala Ile Leu Ala
                85                  90                  95
Leu Leu Val Tyr Gln Ala Ile Thr Ser Ile Asp Arg Ser Ser Ile Gly
            100                 105                 110
Gln Gly Val Leu Asn Leu Gly Leu Thr Leu Leu Val Gly Leu Leu Phe
        115                 120                 125
Ala Gly Pro Ile Gly Trp Ile Val Thr Ala Met Met Lys Arg His Leu
    130                 135                 140
Ile Pro Asp Phe Leu Gln Gly Val Ile Phe Val Gly Val Ala Val Gly
145                 150                 155                 160
Thr Cys Val Gly Ala Asn Val Ile Arg Glu Glu Ser Gly Leu Val Ala
                165                 170                 175
Val Thr Met Leu Gly Ile Tyr Leu Ala Asn Gln Arg Asn Leu Glu Leu
            180                 185                 190
Glu Pro Val Ile Glu Phe Lys Glu His Leu Gln Val Leu Leu Val Gly
        195                 200                 205
Val Leu Phe Ile Met Leu Ala Gly Arg
    210                 215
```

<210> 1403
<211> 393
<212> DNA
<213> Homo sapiens

<400> 1403
aagctttgca gtttcttggt atccaaatcc aggcgttctt ggtctttttc cacaacagtg
60
tgtgccacat gaaatggaac acgggcaaac atatctgatc caggaaacat tagccaagta
120
tgttccttgg ggtcatgatc tccacaagtt gggcatatct cctttatcag ctgcttgcca
180
gagcttcctt ccatctcttt cattatgacc tcaaagggag atggcacgct agtcttggac
240
gtcctagctt gtttccgaag ggctgtcaga gcctccctgt taccatttct tatcttatca
300
ttttccacca actgatgtct agccagaaga actttttctg catcagtctc aatatcaacc
360
agagcctctt gaagctgctt catgttggga tcc
393

<210> 1404
<211> 127
<212> PRT
<213> Homo sapiens

<400> 1404
Met Lys Gln Leu Gln Glu Ala Leu Val Asp Ile Glu Thr Asp Ala Glu
 1   5   10   15
Lys Val Leu Leu Ala Arg His Gln Leu Val Glu Asn Asp Lys Ile Arg

```
            20                  25                  30
Asn Gly Asn Arg Glu Ala Leu Thr Ala Leu Arg Lys Gln Ala Arg Thr
        35                  40                  45
Ser Lys Thr Ser Val Pro Ser Pro Phe Glu Val Ile Met Lys Glu Met
    50                  55                  60
Glu Gly Ser Ser Gly Lys Gln Leu Ile Lys Glu Ile Cys Pro Thr Cys
65                  70                  75                  80
Gly Asp His Asp Pro Lys Glu His Thr Trp Leu Met Phe Pro Gly Ser
                85                  90                  95
Asp Met Phe Ala Arg Val Pro Phe His Val Ala His Thr Val Val Glu
            100                 105                 110
Lys Asp Gln Glu Arg Leu Asp Leu Asp Thr Lys Lys Leu Gln Ser
        115                 120                 125
```

<210> 1405
<211> 421
<212> DNA
<213> Homo sapiens

<400> 1405
nnccgactgc acaaggccct gggcatcgaa ctgcccggcg cactgcaggt catcgtcaaa
60
ggcgaaacca gcctgcaatg gctcggcccg gacgaatggc tgctgatcgt gcccagcggt
120
gaagagttcg ccgccgagca aaacctgcgt gccgccctgg gcgagttgca tatccaggtc
180
gtcaacgtca gcggtggcca gcagatcctc gaactcagcg gcccgaacgt gcgcgacgtg
240
ctgatgaaat ccaccagcta cgacgtacac cccaacaact tcccggtggg caaggcggtg
300
ggcacggtgt tcgccaagtc gcaactggtg atccgccata ccgccgaaga cacctgggaa
360
ctgctgatcc gtcgcagctt ctcggattac tggtggctgt ggttgcagga cgcggctgca
420
t
421

<210> 1406
<211> 140
<212> PRT
<213> Homo sapiens

<400> 1406

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Xaa Arg Leu His Lys Ala Leu Gly Ile Glu Leu Pro Gly Ala Leu Gln
 1               5                  10                  15
Val Ile Val Lys Gly Glu Thr Ser Leu Gln Trp Leu Gly Pro Asp Glu
            20                  25                  30
Trp Leu Leu Ile Val Pro Ser Gly Glu Glu Phe Ala Ala Glu Gln Asn
        35                  40                  45
Leu Arg Ala Ala Leu Gly Glu Leu His Ile Gln Val Val Asn Val Ser
    50                  55                  60
Gly Gly Gln Gln Ile Leu Glu Leu Ser Gly Pro Asn Val Arg Asp Val
65                  70                  75                  80
Leu Met Lys Ser Thr Ser Tyr Asp Val His Pro Asn Asn Phe Pro Val
```

```
                85                  90                  95
Gly Lys Ala Val Gly Thr Val Phe Ala Lys Ser Gln Leu Val Ile Arg
            100                 105                 110
His Thr Ala Glu Asp Thr Trp Glu Leu Leu Ile Arg Arg Ser Phe Ser
        115                 120                 125
Asp Tyr Trp Trp Leu Trp Leu Gln Asp Ala Ala Ala
    130                 135                 140
```

<210> 1407
<211> 1006
<212> DNA
<213> Homo sapiens

<400> 1407
nncggccggg agaagctgga gctcgtcctg tctaacctgc aggcagacgt cctggagttg
60
ctgctggagt ttgtctacac gggctccctg gtcatcgact cggccaacgc caagacactg
120
ctggaggcgg ccagcaagtt ccagttccac accttctgca aagtctgcgt gtcctttctt
180
gagaagcagc tgacggccag caactgcctg ggcgttgctg ccatggccga ggccatgcag
240
tgcagcgagc tctaccacat ngccaaggcc ttcgcgctgc agatcttccc cgaggtggcc
300
gcccaggagg agatcctcag catctccaag gacgacttca tcgcctacgt ctccaacgac
360
agcctcaaca ccaaggctga ggagctggtg tacgagacag tcatcaagtg gatcaagaag
420
gaccccgcga cacgcacaca gtacgcggct gagctcctgg ccgtggtccg cctccccttc
480
atccacccca gctacctgct caatgtggtt gacaatgaag agctgatcaa gtcatcagaa
540
gcctgccggg acctggtgaa cgaggccaaa cgctaccata tgctgcccca cgcccgccag
600
gagatgcaga cgccccgaac ccggccgcgc ctctctgcag gtgtggctga ggtcatcgtc
660
ttggttgggg gccgtcagat ggtggggatg acccagcgct cgctggtggc cgtcacctgc
720
tggaacccgc agaacaacaa gtggtacccc ttggcctcgg tgccctttt aggcccggga
780
ttcttcagtg tagtgagtgc aggggccaac atctacctct caggtgggat ggaatcaggg
840
gtgccgctgg ctgatgtctg gtgctacatg tccctgcttg ataactggaa cctcgtctcc
900
agaatgccag tcccccgctg tcggccccat agcctcgtct acgatgggaa gatttacacc
960
ctcgggggac ttggcgtggc aggcaacgtg gaccacgtgg agagga
1006

<210> 1408
<211> 335
<212> PRT
<213> Homo sapiens

<400> 1408
Xaa Gly Arg Glu Lys Leu Glu Leu Val Leu Ser Asn Leu Gln Ala Asp
1 5 10 15
Val Leu Glu Leu Leu Leu Glu Phe Val Tyr Thr Gly Ser Leu Val Ile
20 25 30
Asp Ser Ala Asn Ala Lys Thr Leu Leu Glu Ala Ala Ser Lys Phe Gln
35 40 45
Phe His Thr Phe Cys Lys Val Cys Val Ser Phe Leu Glu Lys Gln Leu
50 55 60
Thr Ala Ser Asn Cys Leu Gly Val Ala Ala Met Ala Glu Ala Met Gln
65 70 75 80
Cys Ser Glu Leu Tyr His Xaa Ala Lys Ala Phe Ala Leu Gln Ile Phe
85 90 95
Pro Glu Val Ala Ala Gln Glu Glu Ile Leu Ser Ile Ser Lys Asp Asp
100 105 110
Phe Ile Ala Tyr Val Ser Asn Asp Ser Leu Asn Thr Lys Ala Glu Glu
115 120 125
Leu Val Tyr Glu Thr Val Ile Lys Trp Ile Lys Lys Asp Pro Ala Thr
130 135 140
Arg Thr Gln Tyr Ala Ala Glu Leu Leu Ala Val Val Arg Leu Pro Phe
145 150 155 160
Ile His Pro Ser Tyr Leu Leu Asn Val Val Asp Asn Glu Glu Leu Ile
165 170 175
Lys Ser Ser Glu Ala Cys Arg Asp Leu Val Asn Glu Ala Lys Arg Tyr
180 185 190
His Met Leu Pro His Ala Arg Gln Glu Met Gln Thr Pro Arg Thr Arg
195 200 205
Pro Arg Leu Ser Ala Gly Val Ala Glu Val Ile Val Leu Val Gly Gly
210 215 220
Arg Gln Met Val Gly Met Thr Gln Arg Ser Leu Val Ala Val Thr Cys
225 230 235 240
Trp Asn Pro Gln Asn Asn Lys Trp Tyr Pro Leu Ala Ser Val Pro Phe
245 250 255
Leu Gly Pro Gly Phe Phe Ser Val Val Ser Ala Gly Ala Asn Ile Tyr
260 265 270
Leu Ser Gly Gly Met Glu Ser Gly Val Pro Leu Ala Asp Val Trp Cys
275 280 285
Tyr Met Ser Leu Leu Asp Asn Trp Asn Leu Val Ser Arg Met Pro Val
290 295 300
Pro Arg Cys Arg Pro His Ser Leu Val Tyr Asp Gly Lys Ile Tyr Thr
305 310 315 320
Leu Gly Gly Leu Gly Val Ala Gly Asn Val Asp His Val Glu Arg
325 330 335

<210> 1409
<211> 279
<212> DNA
<213> Homo sapiens

<400> 1409
nnnatgaagt tcttggtttt ttcagaaaaa cgcgcttttt gctatgctgg ccgccccgcg
60
gcacgagata gcaccatgca actgatcgat atcggcgtca acctgaccaa cagcagtttc
120

cacgaccaac aggccgcaat cgtcgagcgc gcgctggagg ccggcgttac gcaaatgctg
180
ctgacaggca ccagcctggc ggtcagcgaa caagccctgg aactgtgcca tcaactggat
240
gcaagcggcg cccacctgtt cgccacggcc ggcgtgcac
279

<210> 1410
<211> 93
<212> PRT
<213> Homo sapiens

<400> 1410
Xaa Met Lys Phe Leu Val Phe Ser Glu Lys Arg Ala Phe Cys Tyr Ala
1 5 10 15
Gly Arg Pro Ala Ala Arg Asp Ser Thr Met Gln Leu Ile Asp Ile Gly
20 25 30
Val Asn Leu Thr Asn Ser Ser Phe His Asp Gln Gln Ala Ala Ile Val
35 40 45
Glu Arg Ala Leu Glu Ala Gly Val Thr Gln Met Leu Leu Thr Gly Thr
50 55 60
Ser Leu Ala Val Ser Glu Gln Ala Leu Glu Leu Cys His Gln Leu Asp
65 70 75 80
Ala Ser Gly Ala His Leu Phe Ala Thr Ala Gly Val His
85 90

<210> 1411
<211> 321
<212> DNA
<213> Homo sapiens

<400> 1411
nnncgtattt caggaatgaa gaacgaacct gaatggatgc ttgaatggcg cttgagtgca
60
tttcgtgaat ggttagaaat ggaagagcct agctgggctc atgtcgatta ccctaaaatt
120
gattttcaat ctatttctta ctattccgcg ccaaaaagca tgaaggataa gcctaagtcg
180
ttagacgaag tcgatcctga attgttacgt acttatgaaa aactgggcat tcctctcata
240
gaacagcaaa tgcttgctgg tatcgccgta gatgctgtct ttgactcagt gtctgtcgtt
300
actacttttc gtcaaaagct t
321

<210> 1412
<211> 107
<212> PRT
<213> Homo sapiens

<400> 1412
Xaa Arg Ile Ser Gly Met Lys Asn Glu Pro Glu Trp Met Leu Glu Trp
1 5 10 15
Arg Leu Ser Ala Phe Arg Glu Trp Leu Glu Met Glu Glu Pro Ser Trp

```
            20                  25                  30
Ala His Val Asp Tyr Pro Lys Ile Asp Phe Gln Ser Ile Ser Tyr Tyr
        35                  40                  45
Ser Ala Pro Lys Ser Met Lys Asp Lys Pro Lys Ser Leu Asp Glu Val
    50                  55                  60
Asp Pro Glu Leu Leu Arg Thr Tyr Glu Lys Leu Gly Ile Pro Leu Ile
65                  70                  75                  80
Glu Gln Gln Met Leu Ala Gly Ile Ala Val Asp Ala Val Phe Asp Ser
                85                  90                  95
Val Ser Val Val Thr Thr Phe Arg Gln Lys Leu
            100                 105
```

<210> 1413
<211> 385
<212> DNA
<213> Homo sapiens

<400> 1413
atgacccatg acgtcagcga agccgtggcg attgccgacc gggtgatcct gatcgaagac
60
ggcgaaatcg gcctcgacct gatcatcgac ctgccacgtc cgcgtgcccg tggttcacac
120
cgcctggccg cgttggaagc cgaagtgata aaccgtgtgc tgtcataacc cngcacgaag
180
ccggaacccg aacatgttaa accgctgcct acgaaattgc gttgggctca ataactcata
240
gaggaacacc atcatgacta taaaagccat caacgtgcgt aaccagttaa aaggcaccat
300
caaggaaatc gtagtcggca acgtgctctc ggaaatcgac gtgcagaccg cctccgggat
360
cgtcacttct gtgatcacta cgcgt
385

<210> 1414
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1414
Met Thr His Asp Val Ser Glu Ala Val Ala Ile Ala Asp Arg Val Ile
 1   5   10   15
Leu Ile Glu Asp Gly Glu Ile Gly Leu Asp Leu Ile Ile Asp Leu Pro
            20   25   30
Arg Pro Arg Ala Arg Gly Ser His Arg Leu Ala Ala Leu Glu Ala Glu
        35   40   45
Val Ile Asn Arg Val Leu Ser
    50   55

<210> 1415
<211> 420
<212> DNA
<213> Homo sapiens

<400> 1415

acgcgtgcag gcaaacatta atatgagtta acaccacaca ggatgagact gtttgtacct
60
gtaactgtcc ttgtcatctg tcttgcagat ttagaagagg aatcagaaag ctgggacaac
120
tctgaggctg aagaggagga gaaagcccct gtgttgccag agagtacaga agggcgggag
180
ctgacccagg gcccggcaga gtcctcctct ctctcaggct gtgggagctg gcagccccgg
240
aagctgccag tcttcaagtc cctccggcac atgaggcagg tcctgggtgc cccttctttc
300
cgcatgctgg cctggcacgt tctcatgggg aaccaggtga tctggaaaag cagagacgtg
360
gacctcgtcc agtcagcttt tgaagtactt cgggtgagaa catcttttcc ttaggtgtgc
420

<210> 1416
<211> 123
<212> PRT
<213> Homo sapiens

<400> 1416
Met Arg Leu Phe Val Pro Val Thr Val Leu Val Ile Cys Leu Ala Asp
 1   5   10   15
Leu Glu Glu Glu Ser Glu Ser Trp Asp Asn Ser Glu Ala Glu Glu Glu
            20   25   30
Glu Lys Ala Pro Val Leu Pro Glu Ser Thr Glu Gly Arg Glu Leu Thr
        35   40   45
Gln Gly Pro Ala Glu Ser Ser Ser Leu Ser Gly Cys Gly Ser Trp Gln
    50   55   60
Pro Arg Lys Leu Pro Val Phe Lys Ser Leu Arg His Met Arg Gln Val
65   70   75   80
Leu Gly Ala Pro Ser Phe Arg Met Leu Ala Trp His Val Leu Met Gly
                85   90   95
Asn Gln Val Ile Trp Lys Ser Arg Asp Val Asp Leu Val Gln Ser Ala
            100   105   110
Phe Glu Val Leu Arg Val Arg Thr Ser Phe Pro
        115   120

<210> 1417
<211> 5058
<212> DNA
<213> Homo sapiens

<400> 1417
nngtacagcc ccaaggtcgc tccctctggg ccctttcttc cccattcttc ccagcagccc
60
aaagctctgg tgggacaggg gcagcccctg gggagggagg agaggaccca ggaacccggc
120
taggagggtg gcccacccat ttccagtgtg acctgttccc attcccccat gtctcctccc
180
atccctcccg ccactcagct caggctgatg agaagcagag caacgggtgt atcggtgttt
240
tctttcctgg tggggtagtg gggtggggct gaggagagaa aagggtgatt agcgtggggc
300

cccgccctct tttgtcctct tcccaggttc cctggcccct tcggagaaac gcacttggtt
360
cgggccagcc gcctgagggg acgggctcac gtctgctcct cacactgcag ctgctgggcc
420
gtggagcttc cccagggagc caggggact tttgccgcag ccatgaaggg ggcacgctgg
480
aggagggtcc cctgggtgtc cctgagctgc ctgtgtctct gcctccttcc gcatgtggtc
540
ccaggaacca cagaggacac attaataact ggaagtaaaa ctcctgcccc agtcacctca
600
acaggctcaa caacagcgac actagaggga caatcaactg cagcttcttc aaggacctct
660
aatcaggaca tatcagcttc atctcagaac caccagacta agagcacgga gaccaccagc
720
aaagctcaaa ccgacaccct cacgcagatg atgacatcaa ctctttttc ttccccaagt
780
gtacacaatg tgatggagac tgttacgcag gagacagctc ctccagatga aatgaccaca
840
tcatttccct ccagtgtcac caacacactc atgatgacat caaagactat aacaatgaca
900
acctccacag actccactct tggaaacaca gaagagacat caacagcagg aactgaaagt
960
tctaccccag tgacctcagc agtctcaata acagctggac aggaaggaca atcacgaaaa
1020
acttcctgga ggacctctat ccaagacaca tcagcttctt ctcagaacca ctggactcgg
1080
agcacgcaga ccaccaggga atctcaaacc agcaccctaa cacacagaac cacttcaact
1140
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<210> 1418

<211> 1532
<212> PRT
<213> Homo sapiens

<400> 1418

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            20                  25                  30
Thr Leu Ile Thr Gly Ser Lys Thr Pro Ala Pro Val Thr Ser Thr Gly
        35                  40                  45
Ser Thr Thr Ala Thr Leu Glu Gly Gln Ser Thr Ala Ala Ser Ser Arg
    50                  55                  60
Thr Ser Asn Gln Asp Ile Ser Ala Ser Ser Gln Asn His Gln Thr Lys
65                  70                  75                  80
Ser Thr Glu Thr Thr Ser Lys Ala Gln Thr Asp Thr Leu Thr Gln Met
                85                  90                  95
Met Thr Ser Thr Leu Phe Ser Ser Pro Ser Val His Asn Val Met Glu
            100                 105                 110
Thr Val Thr Gln Glu Thr Ala Pro Pro Asp Glu Met Thr Thr Ser Phe
        115                 120                 125
Pro Ser Ser Val Thr Asn Thr Leu Met Met Thr Ser Lys Thr Ile Thr
    130                 135                 140
Met Thr Thr Ser Thr Asp Ser Thr Leu Gly Asn Thr Glu Glu Thr Ser
145                 150                 155                 160
Thr Ala Gly Thr Glu Ser Ser Thr Pro Val Thr Ser Ala Val Ser Ile
                165                 170                 175
Thr Ala Gly Gln Glu Gly Gln Ser Arg Lys Thr Ser Trp Arg Thr Ser
            180                 185                 190
Ile Gln Asp Thr Ser Ala Ser Ser Gln Asn His Trp Thr Arg Ser Thr
        195                 200                 205
Gln Thr Thr Arg Glu Ser Gln Thr Ser Thr Leu Thr His Arg Thr Thr
    210                 215                 220
Ser Thr Pro Ser Phe Ser Pro Ser Val His Asn Val Thr Gly Thr Val
225                 230                 235                 240
Ser Gln Lys Thr Ser Pro Ser Gly Glu Thr Ala Thr Ser Ser Leu Cys
                245                 250                 255
Ser Val Thr Asn Thr Ser Met Met Thr Ser Glu Lys Ile Thr Val Thr
            260                 265                 270
Thr Ser Thr Gly Ser Thr Leu Gly Asn Pro Gly Glu Thr Ser Ser Val
        275                 280                 285
Pro Val Thr Gly Ser Leu Met Pro Val Thr Ser Ala Ala Leu Val Thr
    290                 295                 300
Val Asp Pro Glu Gly Gln Ser Pro Ala Thr Phe Ser Arg Thr Ser Thr
305                 310                 315                 320
Gln Asp Thr Thr Ala Phe Ser Lys Asn His Gln Thr Gln Ser Val Glu
                325                 330                 335
Thr Thr Arg Val Ser Gln Ile Asn Thr Leu Asn Thr Leu Thr Pro Val
            340                 345                 350
Thr Thr Ser Thr Val Leu Ser Ser Pro Ser Gly Phe Asn Pro Ser Gly
        355                 360                 365
Thr Val Ser Gln Glu Thr Phe Pro Ser Gly Glu Thr Thr Ile Ser Ser
    370                 375                 380
Pro Ser Ser Val Ser Asn Thr Phe Leu Val Thr Ser Lys Val Phe Arg
```

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385                 390                 395                 400
Met Pro Ile Ser Arg Asp Ser Thr Leu Gly Asn Thr Glu Glu Thr Ser
                405                 410                 415
Leu Ser Val Ser Gly Thr Ile Ser Ala Ile Thr Ser Lys Val Ser Thr
            420                 425                 430
Ile Trp Trp Ser Asp Thr Leu Ser Thr Ala Leu Ser Pro Ser Ser Leu
        435                 440                 445
Pro Pro Lys Ile Ser Thr Ala Phe His Thr Gln Gln Ser Glu Gly Ala
    450                 455                 460
Glu Thr Thr Gly Arg Pro His Glu Arg Ser Ser Phe Ser Pro Gly Val
465                 470                 475                 480
Ser Gln Glu Ile Phe Thr Leu His Glu Thr Thr Thr Trp Pro Ser Ser
                485                 490                 495
Phe Ser Ser Lys Gly His Thr Thr Trp Ser Gln Thr Glu Leu Pro Ser
            500                 505                 510
Thr Ser Thr Gly Ala Ala Thr Arg Leu Val Thr Gly Asn Pro Ser Thr
        515                 520                 525
Gly Ala Ala Gly Thr Ile Pro Arg Val Pro Ser Lys Val Ser Ala Ile
    530                 535                 540
Gly Glu Pro Gly Glu Pro Thr Thr Tyr Ser Ser His Ser Thr Thr Leu
545                 550                 555                 560
Pro Lys Thr Thr Gly Ala Gly Ala Gln Thr Gln Trp Thr Gln Glu Thr
                565                 570                 575
Gly Thr Thr Gly Glu Ala Leu Leu Ser Ser Pro Ser Tyr Ser Val Thr
            580                 585                 590
Gln Met Ile Lys Thr Ala Thr Ser Pro Ser Ser Ser Pro Met Leu Asp
        595                 600                 605
Arg His Thr Ser Gln Gln Ile Thr Thr Ala Pro Ser Thr Asn His Ser
    610                 615                 620
Thr Ile His Ser Thr Ser Thr Ser Pro Gln Glu Ser Pro Ala Val Ser
625                 630                 635                 640
Gln Arg Gly His Thr Gln Ala Pro Gln Thr Thr Gln Glu Ser Gln Thr
                645                 650                 655
Thr Arg Ser Val Ser Pro Met Thr Asp Thr Lys Thr Val Thr Thr Pro
            660                 665                 670
Gly Ser Ser Phe Thr Ala Ser Gly His Ser Pro Ser Glu Ile Val Pro
        675                 680                 685
Gln Asp Ala Pro Thr Ile Ser Ala Ala Thr Thr Phe Ala Pro Ala Pro
    690                 695                 700
Thr Gly Asp Gly His Thr Thr Gln Ala Pro Thr Thr Ala Leu Gln Ala
705                 710                 715                 720
Thr Pro Ser Ser His Asp Ala Thr Leu Gly Pro Ser Gly Gly Thr Ser
                725                 730                 735
Leu Ser Lys Thr Gly Ala Leu Thr Leu Ala Asn Ser Val Val Ser Thr
            740                 745                 750
Pro Gly Gly Pro Glu Gly Gln Trp Thr Ser Ala Ser Ala Ser Thr Ser
        755                 760                 765
Pro Asp Thr Ala Ala Ala Met Thr His Thr His Gln Ala Glu Ser Thr
    770                 775                 780
Glu Ala Ser Gly Gln Thr Gln Thr Ser Glu Pro Ala Ser Ser Gly Ser
785                 790                 795                 800
Arg Thr Thr Ser Ala Gly Thr Ala Thr Pro Ser Ser Ser Gly Ala Ser
                805                 810                 815
Gly Thr Thr Pro Ser Gly Ser Glu Gly Ile Ser Thr Ser Gly Glu Thr
```

```
            820                 825                 830
Thr Arg Phe Ser Ser Asn Pro Ser Arg Asp Ser His Thr Thr Gln Ser
        835                 840                 845
Thr Thr Glu Leu Leu Ser Ala Ser Ala Ser His Gly Ala Ile Pro Val
    850                 855                 860
Ser Thr Gly Met Ala Ser Ser Ile Val Pro Gly Thr Phe His Pro Thr
865                 870                 875                 880
Leu Ser Glu Ala Ser Thr Ala Gly Arg Pro Thr Gly Gln Ser Ser Pro
                885                 890                 895
Thr Ser Pro Ser Ala Ser Pro Gln Glu Thr Ala Ala Ile Ser Arg Met
            900                 905                 910
Ala Gln Thr Gln Arg Thr Arg Thr Ser Arg Gly Ser Asp Thr Ile Ser
        915                 920                 925
Leu Ala Ser Gln Ala Thr Asp Thr Phe Ser Thr Val Pro Pro Thr Pro
    930                 935                 940
Pro Ser Ile Thr Ser Ser Gly Leu Thr Ser Pro Gln Thr Gln Thr His
945                 950                 955                 960
Thr Leu Ser Pro Ser Gly Ser Gly Lys Thr Phe Thr Thr Ala Leu Ile
                965                 970                 975
Ser Asn Ala Thr Pro Leu Pro Val Thr Tyr Ala Ser Ser Ala Ser Thr
            980                 985                 990
Gly His Thr Thr Pro Leu His Val Thr Asp Ala Ser Ser Val Ser Thr
        995                 1000                1005
Gly His Ala Thr Pro Leu Pro Val Thr Ser Pro Ser Ser Val Ser Thr
    1010                1015                1020
Gly Asp Thr Thr Pro Leu Pro Val Thr Ser Pro Ser Ser Ala Ser Ser
1025                1030                1035                1040
Gly His Ala Thr Ser Leu Pro Val Thr Asp Ala Ser Ser Leu Ser Thr
                1045                1050                1055
Gly His Ala Thr Ser Leu His Val Thr Asp Ala Ser Ser Val Ser Thr
            1060                1065                1070
Gly His Ala Thr Leu Leu His Val Thr Asp Ala Ser Ser Ala Ser Thr
        1075                1080                1085
Gly His Thr Thr Ser Leu Pro Val Thr Asp Ala Ser Ser Val Ser Thr
    1090                1095                1100
Gly Asp Thr Thr Pro Leu Pro Val Thr Asp Thr Ser Ser Ala Ser Thr
1105                1110                1115                1120
Gly Asp Thr Thr Pro Leu His Val Thr Asp Ala Ser Ser Val Ser Thr
                1125                1130                1135
Gly His Ala Thr Pro Leu His Val Thr Ser Leu Ser Ser Val Ser Thr
            1140                1145                1150
Gly Asp Thr Thr Pro Leu Pro Val Thr Ser Pro Ser Ser Ala Ser Ser
        1155                1160                1165
Gly His Ala Thr Ser Leu Pro Val Thr Asp Ala Ser Ser Val Ser Thr
    1170                1175                1180
Gly His Ala Thr Ser Leu Pro Val Thr Ile Pro Ser Ser Ala Ser Ser
1185                1190                1195                1200
Gly Asp Ala Thr Ser Leu Pro Val Thr Ser Leu Ser Ser Leu Ser Thr
                1205                1210                1215
Gly His Ala Thr Pro Leu Pro Val Thr Ser Leu Ser Ser Ala Ser Thr
            1220                1225                1230
Gly His Ala Thr Pro Leu Pro Val Thr Asp Thr Ser Ser Val Ser Thr
        1235                1240                1245
Gly His Ala Thr Ser Leu Leu Val Thr Asp Ala Ser Ser Val Ser Thr
```

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    1250                1255                1260
Gly His Ala Thr Pro Leu His Val Thr Asp Ala Ser Ser Val Ser Thr
1265                1270                1275                1280
Gly Asp Thr Thr Pro Leu Pro Val Thr Ser Pro Ser Ser Ala Ser Thr
                1285                1290                1295
Gly Asp Thr Thr Pro Leu Pro Val Thr Asp Thr Ser Ser Val Ser Thr
            1300                1305                1310
Gly Asp Thr Thr Pro Leu Leu Val Thr Asp Thr Ser Ser Val Ser Thr
        1315                1320                1325
Ser His Ala Thr Ser Leu Pro Val Thr Asp Thr Ser Ser Val Ser Thr
    1330                1335                1340
Ser His Ala Thr Ser Leu Pro Val Thr Asp Pro Ser Ser Ala Ser Thr
1345                1350                1355                1360
Gly Asp Thr Thr Pro Leu Pro Val Thr Asp Thr Ser Ser Val Ser Thr
                1365                1370                1375
Gly His Ala Thr Ser Leu Pro Val Thr Asp Thr Ser Ser Ala Ser Thr
            1380                1385                1390
Gly Asp Thr Thr Ser Leu Pro Val Thr Asp Thr Ser Ser Ala Ser Thr
        1395                1400                1405
Gly His Ala Thr Pro Leu Pro Val Thr Asp Thr Ser Ser Ala Ser Thr
    1410                1415                1420
Gly His Ala Thr Pro Leu Leu Val Thr Asp Thr Ser Ser Ala Ser Thr
1425                1430                1435                1440
Gly His Thr Thr Pro Leu His Val Thr Ser Pro Ser Ser Ala Ser Thr
                1445                1450                1455
Gly His Ala Thr Pro Leu Pro Val Thr Ser Pro Ser Ser Ala Ser Thr
            1460                1465                1470
Ser His Ala Thr Ser Leu Pro Val Thr Asp Thr Ser Ser Ala Ser Thr
        1475                1480                1485
Gly His Ala Thr Pro Leu Leu Val Thr Asp Thr Ser Ser Ala Ser Thr
    1490                1495                1500
Gly His Ala Thr Pro Leu Leu Val Thr Asp Thr Ser Ser Ala Ser Thr
1505                1510                1515                1520
Gly His Ala Thr Pro Leu Pro Val Thr Asp Thr Ser
                1525                1530
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<210> 1419
<211> 309
<212> DNA
<213> Homo sapiens

<400> 1419
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gaggttccct tgatggaaat caagtattgt actggtaaat ttattcagga cagtggtctg
120
gattatatca tcatccgttt gtgtggtttc atgcagggtc ttattgggca atatgctgtt
180
cctatactag aagagaagtc cgtctgggga actgatgctc caactcggat tgcttacatg
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gatacccagg acgtagctcg actaacgttt atagctatgc ggaatgagaa ggccaacaag
300
aaactcatg
309

<210> 1420
<211> 103
<212> PRT
<213> Homo sapiens

<400> 1420
Lys Ala Met Gly Ile Gln Lys Tyr Val Phe Tyr Ser Ile His Asn Cys
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Asp Lys Gln Pro Glu Val Pro Leu Met Glu Ile Lys Tyr Cys Thr Gly
20 25 30
Lys Phe Ile Gln Asp Ser Gly Leu Asp Tyr Ile Ile Ile Arg Leu Cys
35 40 45
Gly Phe Met Gln Gly Leu Ile Gly Gln Tyr Ala Val Pro Ile Leu Glu
50 55 60
Glu Lys Ser Val Trp Gly Thr Asp Ala Pro Thr Arg Ile Ala Tyr Met
65 70 75 80
Asp Thr Gln Asp Val Ala Arg Leu Thr Phe Ile Ala Met Arg Asn Glu
85 90 95
Lys Ala Asn Lys Lys Leu Met
100

<210> 1421
<211> 385
<212> DNA
<213> Homo sapiens

<400> 1421
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120
gatgttagag caaagccgag cccagctgct ggcgaatgca tctgtgatgc ccatgagcag
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ccaggatttc agctccgctc tacttcttga ctgctgcaga actcagcacc agctccagtg
240
ccctcagagc cctgattttt cacaaaccga ctcctccaag cctcccctgt gggcgggata
300
cacaagccag agtcgccttg tcacatctct tctctctcca ccaggtcatg ggcaaacctt
360
cctgacatac tttacgacat tacag
385

<210> 1422
<211> 125
<212> PRT
<213> Homo sapiens

<400> 1422
Met Gly Gly Glu Arg Ser Trp Gly Glu Glu Met Met Gln Arg Ser Arg
1 5 10 15
Gln Ala Arg Glu Leu Gly Trp Ala Ala Arg Ser Arg Glu Thr Thr Leu
20 25 30
Pro Glu Glu Gly Arg Met Leu Glu Gln Ser Arg Ala Gln Leu Leu Ala

```
        35                  40                  45
Asn Ala Ser Val Met Pro Met Ser Ser Gln Asp Phe Ser Ser Ala Leu
    50                  55                  60
Leu Leu Asp Cys Cys Arg Thr Gln His Gln Leu Gln Cys Pro Gln Ser
65                  70                  75                  80
Pro Asp Phe Ser Gln Thr Asp Ser Ser Lys Pro Pro Leu Trp Ala Gly
                85                  90                  95
Tyr Thr Ser Gln Ser Arg Leu Val Thr Ser Leu Leu Ser Pro Pro Gly
            100                 105                 110
His Gly Gln Thr Phe Leu Thr Tyr Phe Thr Thr Leu Gln
        115                 120                 125
```

<210> 1423
<211> 336
<212> DNA
<213> Homo sapiens

<400> 1423
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ctctattttg tggaccatgt cggtgaccgg atctttgttt gtaattccaa cggttctgta
120
tgtgtcaccc tgattgatct ggagcttcac aatcctaaag caatagcagt agatccaata
180
gcaggaaaac ttttctttac tgactacggg aatgtcgcca aagtggagag atgtgacatg
240
gatgggatga accgaacaag gataattgat tcaaagacag agcagccagc tgcactggca
300
ctagacctag tcaacaaatt ggtttactgg gtagat
336

<210> 1424
<211> 112
<212> PRT
<213> Homo sapiens

<400> 1424

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Xaa Ile Leu Gln Ser Phe His Asn Val Gln Gln Met Ala Ile Asp Trp
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Leu Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile Phe
            20                  25                  30
Val Cys Asn Ser Asn Gly Ser Val Cys Val Thr Leu Ile Asp Leu Glu
        35                  40                  45
Leu His Asn Pro Lys Ala Ile Ala Val Asp Pro Ile Ala Gly Lys Leu
    50                  55                  60
Phe Phe Thr Asp Tyr Gly Asn Val Ala Lys Val Glu Arg Cys Asp Met
65                  70                  75                  80
Asp Gly Met Asn Arg Thr Arg Ile Ile Asp Ser Lys Thr Glu Gln Pro
                85                  90                  95
Ala Ala Leu Ala Leu Asp Leu Val Asn Lys Leu Val Tyr Trp Val Asp
            100                 105                 110
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<210> 1425
<211> 672

<212> DNA
<213> Homo sapiens

<400> 1425
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gcccggcatg tcgaagacct ggccttggcg ctacaggtca ttgccggtga agatggggtc
120
gatgccgggg tgattccgat gccgctgcgc cgtatgcaaa ctcaaacgct gaaggggttg
180
cgagtcgcct ggtacagcga tggtggcatt gagcccgttg acgcgctcac gcacaccaca
240
ttgcaggcgg tcgccgatct attggacgct gaaggcgcct tgatccgccc ggccttcccc
300
tcggcgttga gcaatgcccg tgacattacc gaacgctatt gggcaatgag tcaaagctcc
360
ggcgcgcagt cgatccagct gttttcagat tgggatcagt tccgtacagc catgctgggg
420
ttcatggccg actacgacat tatcctgtgc cctgtcgatg ccgcgccggc gacccaactg
480
ggagagacgc ggccagggct gttcagttcc ccccttccta atggcttggc gggttggcct
540
tgtgtggtgg tccgggccgg aacggatagc gcgggtttgc cggttggcgt gcagattgtc
600
gcgcgacctt ggcacgagcc tgtcgcgttg gcggcagcag cggccattga gcgcgcgctg
660
ccgttcacgc gt
672

<210> 1426
<211> 224
<212> PRT
<213> Homo sapiens

<400> 1426
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Ile Gly Pro Met Ala Arg His Val Glu Asp Leu Ala Leu Ala Leu Gln
            20   25   30
Val Ile Ala Gly Glu Asp Gly Val Asp Ala Gly Val Ile Pro Met Pro
        35   40   45
Leu Arg Arg Met Gln Thr Gln Thr Leu Lys Gly Leu Arg Val Ala Trp
    50   55   60
Tyr Ser Asp Gly Gly Ile Glu Pro Val Asp Ala Leu Thr His Thr Thr
65   70   75   80
Leu Gln Ala Val Ala Asp Leu Leu Asp Ala Glu Gly Ala Leu Ile Arg
                85   90   95
Pro Ala Phe Pro Ser Ala Leu Ser Asn Ala Arg Asp Ile Thr Glu Arg
            100   105   110
Tyr Trp Ala Met Ser Gln Ser Ser Gly Ala Gln Ser Ile Gln Leu Phe
        115   120   125
Ser Asp Trp Asp Gln Phe Arg Thr Ala Met Leu Gly Phe Met Ala Asp
    130   135   140
Tyr Asp Ile Ile Leu Cys Pro Val Asp Ala Ala Pro Ala Thr Gln Leu

```
145                 150                 155                 160
Gly Glu Thr Arg Pro Gly Leu Phe Ser Ser Pro Leu Pro Asn Gly Leu
                165                 170                 175
Ala Gly Trp Pro Cys Val Val Val Arg Ala Gly Thr Asp Ser Ala Gly
            180                 185                 190
Leu Pro Val Gly Val Gln Ile Val Ala Arg Pro Trp His Glu Pro Val
        195                 200                 205
Ala Leu Ala Ala Ala Ala Ala Ile Glu Arg Ala Leu Pro Phe Thr Arg
    210                 215                 220
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<210> 1427
<211> 270
<212> DNA
<213> Homo sapiens

<400> 1427
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tttgatgttc cactaagata cggggatctg gtggtgacac ccatgcgact ggcttcggaa
120
ttgatgcaag tccatccctc aggggctgta cgcttccgtc actgttcagt tccccagaat
180
aaactcaact cacaaaagat acttccggtg gaaaaggccc aagggaagat cctcttcatt
240
gcaggagaga atgacgaaag cttggctagc
270

<210> 1428
<211> 90
<212> PRT
<213> Homo sapiens

<400> 1428
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Met Ala Cys Tyr Leu Lys Gln Val Ala Ala Thr Val Cys Ile Asn Gly
 1               5                  10                  15
Pro Ser Ala Val Phe Asp Val Pro Leu Arg Tyr Gly Asp Leu Val Val
            20                  25                  30
Thr Pro Met Arg Leu Ala Ser Glu Leu Met Gln Val His Pro Ser Gly
        35                  40                  45
Ala Val Arg Phe Arg His Cys Ser Val Pro Gln Asn Lys Leu Asn Ser
    50                  55                  60
Gln Lys Ile Leu Pro Val Glu Lys Ala Gln Gly Lys Ile Leu Phe Ile
65                  70                  75                  80
Ala Gly Glu Asn Asp Glu Ser Leu Ala Ser
                85                  90
```

<210> 1429
<211> 384
<212> DNA
<213> Homo sapiens

<400> 1429
ncctagggga ttatcgacat aaacgcgact gcgtaaggtt ggtgactcat cccccagcga
60

catgaggcaa acgccatgac atccgagaat gcaccgccgc gaggcaagat catcatgatg
120
gcggtgatcg ccggcgcggt ggtcaccaac atttactgca cccagccggt gctgccgttg
180
atcgcctcgg acatgggcgt cgcagtgtcg acggtcaacc tggtggcagg cgcggccttg
240
ctggggtttg ccaccgggtt ggcgttttta ttgcccatgg gcgaccgctt tgaccggcgc
300
aagctggtac tcgggcagat tgcgctggcg ttctgctttg ccttggcggc ggcttttgcg
360
ccgaggatct gggcgttgat cggc
384

<210> 1430
<211> 103
<212> PRT
<213> Homo sapiens

<400> 1430
Met Thr Ser Glu Asn Ala Pro Pro Arg Gly Lys Ile Ile Met Met Ala
 1   5   10   15
Val Ile Ala Gly Ala Val Val Thr Asn Ile Tyr Cys Thr Gln Pro Val
            20   25   30
Leu Pro Leu Ile Ala Ser Asp Met Gly Val Ala Val Ser Thr Val Asn
        35   40   45
Leu Val Ala Gly Ala Ala Leu Leu Gly Phe Ala Thr Gly Leu Ala Phe
    50   55   60
Leu Leu Pro Met Gly Asp Arg Phe Asp Arg Arg Lys Leu Val Leu Gly
65   70   75   80
Gln Ile Ala Leu Ala Phe Cys Phe Ala Leu Ala Ala Ala Phe Ala Pro
                85   90   95
Arg Ile Trp Ala Leu Ile Gly
            100

<210> 1431
<211> 414
<212> DNA
<213> Homo sapiens

<400> 1431
aagcttcagg gcaggtgtcc cctgaagtca agcctgattc tgcatcatct tgtatagcac
60
aaactggcga cacctgtgac tttgcctttc ccagggtccc tgctctccgc tccaggtagg
120
ctcagcctga gggaggtgct ggcaggagcc tcggaggcag gaggggctgg cgtgcttcac
180
tccttcagct tgtcttggga gagctgtggg ctgcatcccc ctggctcctc gtcccacagg
240
cagccccgct gtgtgtctgg tcttgcaggt tggctgcagc ttctgggccc tgcttccagc
300
ccctcttccc atgatcctcc agccttggaa ggtgtaatag tttcccatgt tgctgatctt
360
tagtttgcct ccctctcctt ggctgttctt tctgctgttc catcctctgt gcac
414

<210> 1432
<211> 106
<212> PRT
<213> Homo sapiens

<400> 1432
Met Gly Asn Tyr Tyr Thr Phe Gln Gly Trp Arg Ile Met Gly Arg Gly
1 5 10 15
Ala Gly Ser Arg Ala Gln Lys Leu Gln Pro Thr Cys Lys Thr Arg His
20 25 30
Thr Ala Gly Leu Pro Val Gly Arg Gly Ala Arg Gly Met Gln Pro Thr
35 40 45
Ala Leu Pro Arg Gln Ala Glu Gly Val Lys His Ala Ser Pro Ser Cys
50 55 60
Leu Arg Gly Ser Cys Gln His Leu Pro Gln Ala Glu Pro Thr Trp Ser
65 70 75 80
Gly Glu Gln Gly Pro Trp Glu Arg Gln Ser His Arg Cys Arg Gln Phe
85 90 95
Val Leu Tyr Lys Met Met Gln Asn Gln Ala
100 105

<210> 1433
<211> 294
<212> DNA
<213> Homo sapiens

<400> 1433
aaattttcga tggaactggg cggcaatgca ccgtttattg tatttgatga tgcggatgtg
60
gacgcggccg tcagcaatgc tgtggcttgc aagttccgct gtggtggaca aacgtgcatt
120
tcggccaacc gaatctacgt gcacgaacaa gtgcacgacg agtttgtctc taagtttggc
180
gagagagtca agaagcttcg cgtgggctac ggtctggacg aaaacatcaa cattggaccg
240
ctagtgaatg aggctagtca ggacaaagca gagtcacatg tccgtgcgat gcaa
294

<210> 1434
<211> 98
<212> PRT
<213> Homo sapiens

<400> 1434
Lys Phe Ser Met Glu Leu Gly Gly Asn Ala Pro Phe Ile Val Phe Asp
1 5 10 15
Asp Ala Asp Val Asp Ala Ala Val Ser Asn Ala Val Ala Cys Lys Phe
20 25 30
Arg Cys Gly Gly Gln Thr Cys Ile Ser Ala Asn Arg Ile Tyr Val His
35 40 45
Glu Gln Val His Asp Glu Phe Val Ser Lys Phe Gly Glu Arg Val Lys
50 55 60
Lys Leu Arg Val Gly Tyr Gly Leu Asp Glu Asn Ile Asn Ile Gly Pro

65 70 75 80
Leu Val Asn Glu Ala Ser Gln Asp Lys Ala Glu Ser His Val Arg Ala
85 90 95
Met Gln

<210> 1435
<211> 1772
<212> DNA
<213> Homo sapiens

<400> 1435
ntttctggct tatgtggttt ccccgtgtgt gaggtgggat ccactccccg catagtctct
60
cgtggcgatg ggacacctgg aaagtgctgt gatgtctttg aatgtgttaa tgatacaaag
120
ccagcctgcg tatttaacaa tgtggaatat tatgatggag acatgtttcg aatggacaac
180
tgtcggttct gtcgatgcca agggggcgtt gccatctgct tcactgccca gtgtggtgag
240
ataaactgcg agaggtacta cgtgcccgaa ggagagtgct gcccagtgtg tgaaatccag
300
tgtatccttt taataatccc gctggctgct gccaatggcc tgatccttgc ccacggagac
360
cggtggcggg aagacgactg cacattctgc cagtgcgtca acggtgaacg ccactgcgtt
420
gcgaccgtct gcggacagac ctgcacaaac cctgtgaaag tgcctgggga gtgttgccct
480
gtgtgcgaag aaccaaccat catcacagtt gatccacctg catgtgggga gttatcaaac
540
tgcactctga cagggaagga ctgcattaat ggtttcaaac gcgatcacaa tggttgtcgg
600
acctgtcagt gcataaacac cgaggaacta tgttcagaac gtaaacaagg ctgcaccttg
660
aactgtccct tcggtttcct tactgatgcc caaaactgtg agatctgtga gtgccgccca
720
aggcccaaga agtgcagacc cataatctgt gacaagtatt gtccacttgg attgctgaag
780
aataagcacg gctgtgacat ctgtcgctgt aagaaatgtc cagagctctc atgcagtaag
840
natctgcccc ttgggtttcc agcaggacag tcacggctgt cttatctgca agtgcagaga
900
ggcctctgct tcagctgggc cacccatcct gtcgggcact tgtctcaccg tggatggtca
960
tcatcataaa aatgaggaga gctggcacga tgggtgccgg gaatgctact gtctcaatgg
1020
acgggaaatg tgtgccctga tcacctgccc ggtgcctgcc tgtggcaacc ccaccattca
1080
ccctggacag tgctgcccat catgtgcaga tgactttgtg gtgcagaagc cagagctcag
1140
tactccnnct ccatttgcca cgcccctgga ggagaatact ttgtggaagg agaaacgtgg
1200
aacattgact cctgtactca gtgcacctgc cacagcggac gggtgctgtg tgagacagag
1260

gtgtgcccac cgctgctctg ccagaacccc tcacgcaccc aggattcctg ctgcccacag
1320
tgtacagatc aacctttttcg gccttccttg tcccgcaata acagcgtacc taattactgc
1380
aaaaatgatg aaggggatat attcctggca gctgagtcct ggaagcctga cgtttgtacc
1440
agctgcatct gcattgatag cgtaattagc tgtttctctg agtcctgccc ttctgtatcc
1500
tgtgaaaaac ctgtcttgag aaaaggccag tgttgtccct actgcataga agacacaatt
1560
ccaaagaagg tggtgtgcca cttcagtggg aaggcctatg ccgacgagga gcggtgggac
1620
cttgacagct gcacccactg ctactgcctg cagggccaga ccttctgctc gaccgtcagc
1680
tgccccctc tgccctgtgt tgagcccatc aacgtggaag gaagttgctg cccaatgtgt
1740
ccagaaatgt atgtcccagt cccttcacgc gt
1772

<210> 1436
<211> 322
<212> PRT
<213> Homo sapiens

<400> 1436
Xaa Ser Gly Leu Cys Gly Phe Pro Val Cys Glu Val Gly Ser Thr Pro
1 5 10 15
Arg Ile Val Ser Arg Gly Asp Gly Thr Pro Gly Lys Cys Cys Asp Val
20 25 30
Phe Glu Cys Val Asn Asp Thr Lys Pro Ala Cys Val Phe Asn Asn Val
35 40 45
Glu Tyr Tyr Asp Gly Asp Met Phe Arg Met Asp Asn Cys Arg Phe Cys
50 55 60
Arg Cys Gln Gly Gly Val Ala Ile Cys Phe Thr Ala Gln Cys Gly Glu
65 70 75 80
Ile Asn Cys Glu Arg Tyr Tyr Val Pro Glu Gly Glu Cys Cys Pro Val
85 90 95
Cys Glu Ile Gln Cys Ile Leu Leu Ile Ile Pro Leu Ala Ala Ala Asn
100 105 110
Gly Leu Ile Leu Ala His Gly Asp Arg Trp Arg Glu Asp Asp Cys Thr
115 120 125
Phe Cys Gln Cys Val Asn Gly Glu Arg His Cys Val Ala Thr Val Cys
130 135 140
Gly Gln Thr Cys Thr Asn Pro Val Lys Val Pro Gly Glu Cys Cys Pro
145 150 155 160
Val Cys Glu Glu Pro Thr Ile Ile Thr Val Asp Pro Pro Ala Cys Gly
165 170 175
Glu Leu Ser Asn Cys Thr Leu Thr Gly Lys Asp Cys Ile Asn Gly Phe
180 185 190
Lys Arg Asp His Asn Gly Cys Arg Thr Cys Gln Cys Ile Asn Thr Glu
195 200 205
Glu Leu Cys Ser Glu Arg Lys Gln Gly Cys Thr Leu Asn Cys Pro Phe
210 215 220
Gly Phe Leu Thr Asp Ala Gln Asn Cys Glu Ile Cys Glu Cys Arg Pro

225 230 235 240
Arg Pro Lys Lys Cys Arg Pro Ile Ile Cys Asp Lys Tyr Cys Pro Leu
245 250 255
Gly Leu Leu Lys Asn Lys His Gly Cys Asp Ile Cys Arg Cys Lys Lys
260 265 270
Cys Pro Glu Leu Ser Cys Ser Lys Xaa Leu Pro Leu Gly Phe Pro Ala
275 280 285
Gly Gln Ser Arg Leu Ser Tyr Leu Gln Val Gln Arg Gly Leu Cys Phe
290 295 300
Ser Trp Ala Thr His Pro Val Gly His Leu Ser His Arg Gly Trp Ser
305 310 315 320
Ser Ser

<210> 1437
<211> 372
<212> DNA
<213> Homo sapiens

<400> 1437
cgggaactgt gctcgcccac catccggtga ccggtgtcgg gcagtggcaa ctcaacaccc
60
aggccatgac cggagccatc ccgagcagca ggtgcacggc ccgggccgtt gactcgtgga
120
cccgtaccct catgacctcg atgcaacttc cacggtggtc caccgatcac atcgaccgct
180
cggtccatgt cgatgctgag cagttcgacc ggttgcgcag cgagttcctg tcccgtgggc
240
acagttctgg ccctgccgca catggggtcc tgggacttgg ccggggcctg ggtggccaga
300
cgcggcttct ccccgagttc cgtcgcggag aatcttccga gggcacagtt cgagttgttc
360
tgccgcacgc gt
372

<210> 1438
<211> 62
<212> PRT
<213> Homo sapiens

<400> 1438
Met Ser Met Leu Ser Ser Ser Thr Gly Cys Ala Ala Ser Ser Cys Pro
1 5 10 15
Val Gly Thr Val Leu Ala Leu Pro His Met Gly Ser Trp Asp Leu Ala
20 25 30
Gly Ala Trp Val Ala Arg Arg Gly Phe Ser Pro Ser Ser Val Ala Glu
35 40 45
Asn Leu Pro Arg Ala Gln Phe Glu Leu Phe Cys Arg Thr Arg
50 55 60

<210> 1439
<211> 471
<212> DNA
<213> Homo sapiens

<400> 1439
accggtttgc tttccacaag gagagctaaa atgccggttg ctaagcagca tacatgccgc
60
tgcttctttc cacaatgtag acttaaaaaa atcgccgtaa acattttacc atatgattga
120
gtcaggtgtg gggagtcgca gtaaacattt taccatgtga ttgagtcatg ggtggggagt
180
cgcggaaata cacagggcag gcagttcgct atcacgatgt tctctctcat ttctgtcttt
240
ggtctgtctt cctgggtaat gtcacatgga gacccagggg atctgccatc agctgtgtgc
300
agtgggttaa caagacgacg gggaacttca gagtgcaggc agtcctcatc tttggcagat
360
tctgtatttg cacattcacc cactcactga aatgcatttg taaccccaaa atcaatacag
420
cggtttcaca gtcattttcc gacacgggca gaggggtgaa gatactgagt c
471

<210> 1440
<211> 101
<212> PRT
<213> Homo sapiens

<400> 1440
Met Gly Gly Glu Ser Arg Lys Tyr Thr Gly Gln Ala Val Arg Tyr His
 1   5   10   15
Asp Val Leu Ser His Phe Cys Leu Trp Ser Val Phe Leu Gly Asn Val
            20   25   30
Thr Trp Arg Pro Arg Gly Ser Ala Ile Ser Cys Val Gln Trp Val Asn
        35   40   45
Lys Thr Thr Gly Asn Phe Arg Val Gln Ala Val Leu Ile Phe Gly Arg
    50   55   60
Phe Cys Ile Cys Thr Phe Thr His Ser Leu Lys Cys Ile Cys Asn Pro
65   70   75   80
Lys Ile Asn Thr Ala Val Ser Gln Ser Phe Ser Asp Thr Gly Arg Gly
                85   90   95
Val Lys Ile Leu Ser
            100

<210> 1441
<211> 376
<212> DNA
<213> Homo sapiens

<400> 1441
nnngagtcgc ggggaccttc atggactctc tcgtgctccg tagctcacac tcaccgcacg
60
gcagctcaca ttcaccacac gggaactcac tctcaccaca cggcagctca ctctctctgc
120
accgcagctc acactcaccg cacggcagct cactctcacc gcacggcagc tcacactcac
180
cacacagcag ctcactctta ccggacgggg aacctaaact taccggacgg gaagcctcac
240

tctcaccgca cggaaagctc acactcaccg caccgcagcc actctcaccg cacggcagct
300
cactctcacc gcaccgcagc tcactctcac cggacgggag ctcactctca ccacacggca
360
cctcactctc acgcgt
376

<210> 1442
<211> 125
<212> PRT
<213> Homo sapiens

<400> 1442
Xaa Glu Ser Arg Gly Pro Ser Trp Thr Leu Ser Cys Ser Val Ala His
1 5 10 15
Thr His Arg Thr Ala Ala His Ile His His Thr Gly Thr His Ser His
20 25 30
His Thr Ala Ala His Ser Leu Cys Thr Ala Ala His Thr His Arg Thr
35 40 45
Ala Ala His Ser His Arg Thr Ala Ala His Thr His His Thr Ala Ala
50 55 60
His Ser Tyr Arg Thr Gly Asn Leu Asn Leu Pro Asp Gly Lys Pro His
65 70 75 80
Ser His Arg Thr Glu Ser Ser His Ser Pro His Arg Ser His Ser His
85 90 95
Arg Thr Ala Ala His Ser His Arg Thr Ala Ala His Ser His Arg Thr
100 105 110
Gly Ala His Ser His His Thr Ala Pro His Ser His Ala
115 120 125

<210> 1443
<211> 286
<212> DNA
<213> Homo sapiens

<400> 1443
atggcagccc tgcgtcccaa ggagctgcca caactaatgg tcgccatcgg caatgcgagc
60
ataaaacgga caacacgctg cctgatcgaa tggcaactcc acaccatgac ccgtcctgcg
120
gaagccgcta cgacttcctg ggctgacatc gactgcgaca agaaaacctg gacgatccca
180
gcggagcgta tgaaaaagcg acgtgcccat gtcataccgc taaccgagca cgcacttgcc
240
ttgcttgaga caatcaaacc ctacagcggn cacagagagt acgcgt
286

<210> 1444
<211> 95
<212> PRT
<213> Homo sapiens

<400> 1444
Met Ala Ala Leu Arg Pro Lys Glu Leu Pro Gln Leu Met Val Ala Ile

```
 1               5                  10                  15
Gly Asn Ala Ser Ile Lys Arg Thr Thr Arg Cys Leu Ile Glu Trp Gln
            20                  25                  30
Leu His Thr Met Thr Arg Pro Ala Glu Ala Ala Thr Thr Ser Trp Ala
        35                  40                  45
Asp Ile Asp Cys Asp Lys Lys Thr Trp Thr Ile Pro Ala Glu Arg Met
    50                  55                  60
Lys Lys Arg Arg Ala His Val Ile Pro Leu Thr Glu His Ala Leu Ala
65                  70                  75                  80
Leu Leu Glu Thr Ile Lys Pro Tyr Ser Gly His Arg Glu Tyr Ala
                85                  90                  95
```

<210> 1445
<211> 294
<212> DNA
<213> Homo sapiens

<400> 1445
naccggttca ccggggaggc cttcgatggg ggcaaggtca gcatggttgg cccgattccc
60
atgtacctgt atggcacctt cgtcgttccg gacttcgacg cattcatctc cggcaagcag
120
actccctacc gggagacggt ctccaagcgg accactactt ggttctttcg agccggctca
180
gaggtttatg agctggccnt cccccgagga gtcgtgttcg ccatgcaaag cgcctcgttg
240
agggtggacc ccgacaacac cgtcgacaag ctgccaacac tcggcgagcg cctg
294

<210> 1446
<211> 98
<212> PRT
<213> Homo sapiens

<400> 1446
```
Xaa Arg Phe Thr Gly Glu Ala Phe Asp Gly Gly Lys Val Ser Met Val
 1               5                  10                  15
Gly Pro Ile Pro Met Tyr Leu Tyr Gly Thr Phe Val Val Pro Asp Phe
            20                  25                  30
Asp Ala Phe Ile Ser Gly Lys Gln Thr Pro Tyr Arg Glu Thr Val Ser
        35                  40                  45
Lys Arg Thr Thr Thr Trp Phe Phe Arg Ala Gly Ser Glu Val Tyr Glu
    50                  55                  60
Leu Ala Xaa Pro Arg Gly Val Val Phe Ala Met Gln Ser Ala Ser Leu
65                  70                  75                  80
Arg Val Asp Pro Asp Asn Thr Val Asp Lys Leu Pro Thr Leu Gly Glu
                85                  90                  95
Arg Leu
```

<210> 1447
<211> 363
<212> DNA
<213> Homo sapiens

<400> 1447
nnncagaacc agaagatcaa cctgcatgac ggctcgttct ccgacgttgg cggcatggtg
60
ggtaatatct ccattgccca gggtgtcacg atcgagaacg ccgtcggcgg ttcgggcaac
120
gacctgctga tcggcaacga tgcggccaac gaactgcgcg gcggtgccgg caacgatatc
180
ctctacgggg ctggcggtgc cgaccaggtt tgggttggtt cgggcaacaa taccttcgtg
240
ttcgccgccg tttccgactc ggcgccgaaa gcggccgacc ggatcatgga cttcaccagt
300
ggccaggaca agatcgatct gtccgggatc acccatggtt cgggcctgac cttcgtcaac
360
gcg
363

<210> 1448
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1448
Xaa Gln Asn Gln Lys Ile Asn Leu His Asp Gly Ser Phe Ser Asp Val
 1   5   10   15
Gly Gly Met Val Gly Asn Ile Ser Ile Ala Gln Gly Val Thr Ile Glu
            20   25   30
Asn Ala Val Gly Gly Ser Gly Asn Asp Leu Leu Ile Gly Asn Asp Ala
        35   40   45
Ala Asn Glu Leu Arg Gly Gly Ala Gly Asn Asp Ile Leu Tyr Gly Ala
    50   55   60
Gly Gly Ala Asp Gln Val Trp Val Gly Ser Gly Asn Asn Thr Phe Val
65   70   75   80
Phe Ala Ala Val Ser Asp Ser Ala Pro Lys Ala Ala Asp Arg Ile Met
                85   90   95
Asp Phe Thr Ser Gly Gln Asp Lys Ile Asp Leu Ser Gly Ile Thr His
            100   105   110
Gly Ser Gly Leu Thr Phe Val Asn Ala
        115   120

<210> 1449
<211> 541
<212> DNA
<213> Homo sapiens

<400> 1449
aggcgctacc agattatggg ctgcccgacc tcaatgacat gcgcttgagc ctgcatgaat
60
cactcagcca atcgcgcttg gcgattgaac gctttatcca ggcgtacgag cctcggttgg
120
ggaatgtacg tgtcaggagg agggagggtg cctacaaccc tttggtactg gcgtttgtga
180
ttgaggcaac cgtcgtcatc gatggtgtca tccaacctgt ggtgtttaac gcacacctgg
240

tgggggggg gacgggtcga gtgtgttacc tgatgttctt tgagctcttt taccagagtg
300
aactcagtgc attgcgcacg cttgggcggc gtttttctga acgcaatccc gccctggcac
360
cctttcttgc cgattccagg ccaggacccg gacgtcgagg gtctattgaa agtctttgcc
420
tttctccccg ggcgcctgcg ccagaagctt gctgacgagc ttctgaggtt gacccattca
480
ttgatgcact tggtgtggcc caattacatg cggccattgc cggccttcag tattttgcag
540
t
541

<210> 1450
<211> 138
<212> PRT
<213> Homo sapiens

<400> 1450
Met Arg Leu Ser Leu His Glu Ser Leu Ser Gln Ser Arg Leu Ala Ile
 1   5   10   15
Glu Arg Phe Ile Gln Ala Tyr Glu Pro Arg Leu Gly Asn Val Arg Val
            20   25   30
Arg Arg Arg Glu Gly Ala Tyr Asn Pro Leu Val Leu Ala Phe Val Ile
        35   40   45
Glu Ala Thr Val Val Ile Asp Gly Val Ile Gln Pro Val Val Phe Asn
    50   55   60
Ala His Leu Val Gly Gly Gly Thr Gly Arg Val Cys Tyr Leu Met Phe
65   70   75   80
Phe Glu Leu Phe Tyr Gln Ser Glu Leu Ser Ala Leu Arg Thr Leu Gly
                85   90   95
Arg Arg Phe Ser Glu Arg Asn Pro Ala Leu Ala Pro Phe Leu Ala Asp
            100   105   110
Ser Arg Pro Gly Pro Gly Arg Arg Gly Ser Ile Glu Ser Leu Cys Leu
        115   120   125
Ser Pro Arg Ala Pro Ala Pro Glu Ala Cys
    130   135

<210> 1451
<211> 326
<212> DNA
<213> Homo sapiens

<400> 1451
aggcctctgg cgagttgatc tacagcttcg gacccggtgc tatggctact ggcgtcaagt
60
acacgaacac agtttgcact cctgtgggcg actacgaggt ggtgctgacg gattcttggg
120
gtgatggctg gaacccgggt tcttacctga acatgtacga cagctcggac aacttgatcc
180
aggagttcac gatggattac gacgcctctt ctcgtaacat taaggagaag cacggcttct
240
tcacggtggc ttccaccacg agcagcggca ctgtctggaa gattatggcg aacaagaagg
300

tggacaagga gtggaactct gtggac
326

<210> 1452
<211> 95
<212> PRT
<213> Homo sapiens

<400> 1452
Met Ala Thr Gly Val Lys Tyr Thr Asn Thr Val Cys Thr Pro Val Gly
1 5 10 15
Asp Tyr Glu Val Val Leu Thr Asp Ser Trp Gly Asp Gly Trp Asn Pro
20 25 30
Gly Ser Tyr Leu Asn Met Tyr Asp Ser Ser Asp Asn Leu Ile Gln Glu
35 40 45
Phe Thr Met Asp Tyr Asp Ala Ser Ser Arg Asn Ile Lys Glu Lys His
50 55 60
Gly Phe Phe Thr Val Ala Ser Thr Thr Ser Ser Gly Thr Val Trp Lys
65 70 75 80
Ile Met Ala Asn Lys Lys Val Asp Lys Glu Trp Asn Ser Val Asp
85 90 95

<210> 1453
<211> 326
<212> DNA
<213> Homo sapiens

<400> 1453
cggccgcgcg gccccacgtg caccgcgtgc atggtccctc gaggacgcgc atctgcagcc
60
cccgctcccc gcaaacctcc aggccggaga gctccggcca aggccgctgc atcacatgat
120
acaggagggg catgcacacg ctcacgtgca cacagcctca aacacgctca tccgtacata
180
caggagtgtg tgaacgcact gaggtgcaca ggacaaagac acagacacct gtttgcacac
240
cgactcgcct atagaaatgt gcaaaccacc cgtgcgcaca ggcccctcca cccatgcagg
300
cgtgtgcaca tcacccacac ggacac
326

<210> 1454
<211> 98
<212> PRT
<213> Homo sapiens

<400> 1454
Met Val Pro Arg Gly Arg Ala Ser Ala Ala Pro Ala Pro Arg Lys Pro
1 5 10 15
Pro Gly Arg Arg Ala Pro Ala Lys Ala Ala Ala Ser His Asp Thr Gly
20 25 30
Gly Ala Cys Thr Arg Ser Arg Ala His Ser Leu Lys His Ala His Pro
35 40 45
Tyr Ile Gln Glu Cys Val Asn Ala Leu Arg Cys Thr Gly Gln Arg His

```
    50                  55                  60
Arg His Leu Phe Ala His Arg Leu Ala Tyr Arg Asn Val Gln Thr Thr
65                  70                  75                  80
Arg Ala His Arg Pro Leu His Pro Cys Arg Arg Val His Ile Thr His
                85                  90                  95
Thr Asp
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<210> 1455
<211> 314
<212> DNA
<213> Homo sapiens

<400> 1455
gatccagtca aaaaagcatg tggggttgct cacgctggtt ggaaaggtac tttgttgggt
60
gttgctatgg ctacagtgaa tgctatgata gcagaatatg gctgccgttt ggaaaaactt
120
tggtggacct tggacccttc agtgggacct ggctgtttta ctcttccagg ggaatcagca
180
gaggcatttc ataatcttca tcctgcatgt gtacaactat ttgattcacc aaatcccctgt
240
atcgacatcc gtaaagccac aagatacttg actggatttt tgtataactg cttcctgcct
300
ccttccaaac tgac
314

<210> 1456
<211> 104
<212> PRT
<213> Homo sapiens

<400> 1456
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Asp Pro Val Lys Lys Ala Cys Gly Val Ala His Ala Gly Trp Lys Gly
 1               5                  10                  15
Thr Leu Leu Gly Val Ala Met Ala Thr Val Asn Ala Met Ile Ala Glu
            20                  25                  30
Tyr Gly Cys Arg Leu Glu Lys Leu Trp Trp Thr Leu Asp Pro Ser Val
        35                  40                  45
Gly Pro Gly Cys Phe Thr Leu Pro Gly Glu Ser Ala Glu Ala Phe His
    50                  55                  60
Asn Leu His Pro Ala Cys Val Gln Leu Phe Asp Ser Pro Asn Pro Cys
65                  70                  75                  80
Ile Asp Ile Arg Lys Ala Thr Arg Tyr Leu Thr Gly Phe Leu Tyr Asn
                85                  90                  95
Cys Phe Leu Pro Pro Ser Lys Leu
            100
```

<210> 1457
<211> 437
<212> DNA
<213> Homo sapiens

<400> 1457

nattcaccag aatccccaga atcccccaaa tactacattg cactttaggg ttccttttcta
60
gcacatgcat tgctaaaatc ggcgcccaga accttctctg ccccctctccc atgggatgca
120
atgtcagcgg agaaacagac caagtctgca ctagcctgtc cctacaccct ccccaggaaa
180
aggtcccccc gcgccaagtc aacagctccc agaggaagcc cactgactgc tctcttcagg
240
gtgggggaca caggaagtcc acgcttgcac ggaggggacg ggcacaccta ccgtgactgc
300
cagagcccat tttgggagtc tgattggaat ttatacagca ggagcactgg gcactcggac
360
aactccagcc cacaaccaag tcactgggct gcctacccac tgcccaagtg cctcaagtca
420
acacattcct gcactgn
437

<210> 1458
<211> 105
<212> PRT
<213> Homo sapiens

<400> 1458
Met Ser Ala Glu Lys Gln Thr Lys Ser Ala Leu Ala Cys Pro Tyr Thr
1 5 10 15
Leu Pro Arg Lys Arg Ser Pro Cys Ala Lys Ser Thr Ala Pro Arg Gly
20 25 30
Ser Pro Leu Thr Ala Leu Phe Arg Val Gly Asp Thr Gly Ser Pro Arg
35 40 45
Leu His Gly Gly Asp Gly His Thr Tyr Arg Asp Cys Gln Ser Pro Phe
50 55 60
Trp Glu Ser Asp Trp Asn Leu Tyr Ser Arg Ser Thr Gly His Ser Asp
65 70 75 80
Asn Ser Ser Pro Gln Pro Ser His Trp Ala Ala Tyr Pro Leu Pro Lys
85 90 95
Cys Leu Lys Ser Thr His Ser Cys Thr
100 105

<210> 1459
<211> 295
<212> DNA
<213> Homo sapiens

<400> 1459
ngagaggtca ccggccacga gattcccgcg gaggtcgcgc cccgccgcgc gggcgacccg
60
gccgtactca tcgcttcttc ggagaagatc aagcgggagc tgggctggaa cccgacgcgc
120
acggatctgc gccgcatcgt cgaggacgcc tgggccttta cggctggggg ggccgaacgg
180
taaacccttg gtaaggcgac gcagttatcc tcgatctcct cccagagcag gcggcagccc
240
gccactgcgg tgtcgagcat gccctcccac tccccgatcg ccatgagctg gcgan
295

<210> 1460
<211> 60
<212> PRT
<213> Homo sapiens

<400> 1460
Xaa Glu Val Thr Gly His Glu Ile Pro Ala Glu Val Ala Pro Arg Arg
1 5 10 15
Ala Gly Asp Pro Ala Val Leu Ile Ala Ser Ser Glu Lys Ile Lys Arg
20 25 30
Glu Leu Gly Trp Asn Pro Thr Arg Thr Asp Leu Arg Arg Ile Val Glu
35 40 45
Asp Ala Trp Ala Phe Thr Ala Gly Gly Ala Glu Arg
50 55 60

<210> 1461
<211> 432
<212> DNA
<213> Homo sapiens

<400> 1461
nnaagcttac gtgaaatgaa acgtcaatgg caacaggcga caatcgtgcc agagaaattg
60
gttgaagcac agtcaattgc gggttctaaa tgcgaacacg cctggcgctt acaacgttca
120
gaaaatgact gggtaggctt tgaaaaaaat tggaaagagg ttgttgcatt atcccgtgaa
180
gaagcacaaa ttcgcggtga agcgcttaat ctaacgcctt atgatgcgat gcttgataag
240
tttgaaccag gcacgacaac ggtttcgctc aatactttgt tttcaaaggt aaagacgtgg
300
ttacctacgt taattgaaaa agcgttagaa aagcagcaat cagaatctat cattatgcca
360
tcaggcacct tttccacggc gaatcaaaaa gcccttggat tagaaataat gaaattgtta
420
aaattcgact tt
432

<210> 1462
<211> 144
<212> PRT
<213> Homo sapiens

<400> 1462
Xaa Ser Leu Arg Glu Met Lys Arg Gln Trp Gln Gln Ala Thr Ile Val
1 5 10 15
Pro Glu Lys Leu Val Glu Ala Gln Ser Ile Ala Gly Ser Lys Cys Glu
20 25 30
His Ala Trp Arg Leu Gln Arg Ser Glu Asn Asp Trp Val Gly Phe Glu
35 40 45
Lys Asn Trp Lys Glu Val Val Ala Leu Ser Arg Glu Glu Ala Gln Ile
50 55 60
Arg Gly Glu Ala Leu Asn Leu Thr Pro Tyr Asp Ala Met Leu Asp Lys

65 70 75 80
Phe Glu Pro Gly Thr Thr Thr Val Ser Leu Asn Thr Leu Phe Ser Lys
85 90 95
Val Lys Thr Trp Leu Pro Thr Leu Ile Glu Lys Ala Leu Glu Lys Gln
100 105 110
Gln Ser Glu Ser Ile Ile Met Pro Ser Gly Thr Phe Ser Thr Ala Asn
115 120 125
Gln Lys Ala Leu Gly Leu Glu Ile Met Lys Leu Leu Lys Phe Asp Phe
130 135 140

<210> 1463
<211> 421
<212> DNA
<213> Homo sapiens

<400> 1463
nacgcgttcc agagcaagct ggacctgacc gccttcgaat tcttctccga caaggccctg
60
gccaaagtca tgggccgtgg cgacgtaccg gcaccgttcg aaaccgaatg cccgttctac
120
gcgctgctgg aattcgaagc caccaccgaa gaagtcgcca accacgccct ggaaaccttc
180
gagcactgcg ttgagcaggg ctgggtgctg gacggcgtga tgagccagag cgaaacccaa
240
ctgcacaacc tgtggaaact gcgcgagtac atctcggaga ctatttccca ctggacgccc
300
tacaagaacg acatctccgt gaccgtttcc aaagtccccg cgttcttgaa ggaaattgac
360
gcgatcgtcg tgagcattac ccggacttcg aaattgttgg tcggccacat cggcgacgca
420
a
421

<210> 1464
<211> 140
<212> PRT
<213> Homo sapiens

<400> 1464
Xaa Ala Phe Gln Ser Lys Leu Asp Leu Thr Ala Phe Glu Phe Phe Ser
1 5 10 15
Asp Lys Ala Leu Ala Lys Val Met Gly Arg Gly Asp Val Pro Ala Pro
20 25 30
Phe Glu Thr Glu Cys Pro Phe Tyr Ala Leu Leu Glu Phe Glu Ala Thr
35 40 45
Thr Glu Glu Val Ala Asn His Ala Leu Glu Thr Phe Glu His Cys Val
50 55 60
Glu Gln Gly Trp Val Leu Asp Gly Val Met Ser Gln Ser Glu Thr Gln
65 70 75 80
Leu His Asn Leu Trp Lys Leu Arg Glu Tyr Ile Ser Glu Thr Ile Ser
85 90 95
His Trp Thr Pro Tyr Lys Asn Asp Ile Ser Val Thr Val Ser Lys Val
100 105 110
Pro Ala Phe Leu Lys Glu Ile Asp Ala Ile Val Val Ser Ile Thr Arg

115 120 125
Thr Ser Lys Leu Leu Val Gly His Ile Gly Asp Ala
130 135 140

<210> 1465
<211> 424
<212> DNA
<213> Homo sapiens

<400> 1465
gtgcacggtc tttgagctgc aattcccagg aatcaggggc cataggcggt agatggcatg
60
cagcctctcg ggcgggaaag tggtctacag tgcctgcttg cccgggcagg cagctcgtag
120
gcttatatgc ttagtggtta tggcccctac cactgttttt gaccgcgcta ccattcgcca
180
caacctcacc gaattcaaac tccggtggat ttcccacgcc gagcagtgga aggcggaaaa
240
ccgtcctgca acagagtcta aagccgctga gacggactgc tcagtacatg gggatctctg
300
gaccttggcc acggaagttt tcggtcaagc acccgaattc gacttcccat atatgaaact
360
cactcggcag gaatgtaggt tccttttct gccgagaaac gacatcagct tgagctgctt
420
cacg
424

<210> 1466
<211> 124
<212> PRT
<213> Homo sapiens

<400> 1466
Met Ala Cys Ser Leu Ser Gly Gly Lys Val Val Tyr Ser Ala Cys Leu
1 5 10 15
Pro Gly Gln Ala Ala Arg Arg Leu Ile Cys Leu Val Val Met Ala Pro
20 25 30
Thr Thr Val Phe Asp Arg Ala Thr Ile Arg His Asn Leu Thr Glu Phe
35 40 45
Lys Leu Arg Trp Ile Ser His Ala Glu Gln Trp Lys Ala Glu Asn Arg
50 55 60
Pro Ala Thr Glu Ser Lys Ala Ala Glu Thr Asp Cys Ser Val His Gly
65 70 75 80
Asp Leu Trp Thr Leu Ala Thr Glu Val Phe Gly Gln Ala Pro Glu Phe
85 90 95
Asp Phe Pro Tyr Met Lys Leu Thr Arg Gln Glu Cys Arg Phe Leu Phe
100 105 110
Leu Pro Arg Asn Asp Ile Ser Leu Ser Cys Phe Thr
115 120

<210> 1467
<211> 441
<212> DNA
<213> Homo sapiens

<400> 1467
nacgcgtgac ggcgaatgag cggcggaggc atgacaacga gcgcaccgtt ccgcagcttg
60
gtgccgtgca tcatggctca agtgccgcgc aactttcggc tgctcgagga gctggagaaa
120
ggcgaaaagg ggctaggaaa tggctcgtgc tcttacggcc ttgcgaacag tgatgacatt
180
cgtacgtatg cgcctgtgct gatggtcatg acaacgtgga atgccacgat cctaggcccg
240
gccaactcgg tgcatgagaa ccgcatatac tgcctgcgcc tcgtgtgtgg cgactcgtac
300
cctcttgtgc cgcctgagat ttggttccag acgcgcatca acttgccgtg cgtcgatgcc
360
cacacgggcc gcgtcatgcc cgatcagttc tcgcccctct tgcattggcg tgatgagtac
420
actatggaaa gctgctgcat g
441

<210> 1468
<211> 123
<212> PRT
<213> Homo sapiens

<400> 1468
Met Ala Gln Val Pro Arg Asn Phe Arg Leu Leu Glu Glu Leu Glu Lys
1 5 10 15
Gly Glu Lys Gly Leu Gly Asn Gly Ser Cys Ser Tyr Gly Leu Ala Asn
20 25 30
Ser Asp Asp Ile Arg Thr Tyr Ala Pro Val Leu Met Val Met Thr Thr
35 40 45
Trp Asn Ala Thr Ile Leu Gly Pro Ala Asn Ser Val His Glu Asn Arg
50 55 60
Ile Tyr Cys Leu Arg Leu Val Cys Gly Asp Ser Tyr Pro Leu Val Pro
65 70 75 80
Pro Glu Ile Trp Phe Gln Thr Arg Ile Asn Leu Pro Cys Val Asp Ala
85 90 95
His Thr Gly Arg Val Met Pro Asp Gln Phe Ser Pro Leu Leu His Trp
100 105 110
Arg Asp Glu Tyr Thr Met Glu Ser Cys Cys Met
115 120

<210> 1469
<211> 468
<212> DNA
<213> Homo sapiens

<400> 1469
nngctcgatc tagtctatgg gctaaatgat cgaccgaacc cttttattgc ttttttagcg
60
gcgcttcaac atcttttagc gattttagtg ccaattgtca ccnctggatt attgatttgt
120
ttggcattag gcgtgtctcg cgaagacacc aatatgattc tttctatgtc attaattatt
180

tcagggatcg cgactttctt gcaatgtaaa aaagttggtc catttggcgc tggattactt
240
attgttcaag gaactagctt taatttcatt ggtcctatca ttggtatagg tagctcaatg
300
gtggctgctg gcacacctgt cgaacaagtt atggctgcga tttttggtgt cgtaatcgca
360
ggttcattta tcgaaatggg cgtatctcaa attttacctt gggtaaaaaa gctgattact
420
cctctcgtta caggaatcgt cgttctgttg attggtctac cattaatg
468

<210> 1470
<211> 156
<212> PRT
<213> Homo sapiens

<400> 1470
Xaa Leu Asp Leu Val Tyr Gly Leu Asn Asp Arg Pro Asn Pro Phe Ile
1 5 10 15
Ala Phe Leu Ala Ala Leu Gln His Leu Leu Ala Ile Leu Val Pro Ile
20 25 30
Val Thr Xaa Gly Leu Leu Ile Cys Leu Ala Leu Gly Val Ser Arg Glu
35 40 45
Asp Thr Asn Met Ile Leu Ser Met Ser Leu Ile Ile Ser Gly Ile Ala
50 55 60
Thr Phe Leu Gln Cys Lys Lys Val Gly Pro Phe Gly Ala Gly Leu Leu
65 70 75 80
Ile Val Gln Gly Thr Ser Phe Asn Phe Ile Gly Pro Ile Ile Gly Ile
85 90 95
Gly Ser Ser Met Val Ala Ala Gly Thr Pro Val Glu Gln Val Met Ala
100 105 110
Ala Ile Phe Gly Val Val Ile Ala Gly Ser Phe Ile Glu Met Gly Val
115 120 125
Ser Gln Ile Leu Pro Trp Val Lys Lys Leu Ile Thr Pro Leu Val Thr
130 135 140
Gly Ile Val Val Leu Leu Ile Gly Leu Pro Leu Met
145 150 155

<210> 1471
<211> 341
<212> DNA
<213> Homo sapiens

<400> 1471
gcgtggatgg ggatcctgaa aaacaatggc gtgctgaata acttcttgct gtggctcggc
60
gttatcgatc agccgctgac gattttgcac accaatctgg cggtgtatat cggcattgtg
120
tacgcttatc tgccgtttat ggtactgccc atttatacgg cgctgacgcg cattgattac
180
tcgctggtgg aggcctcact ggatctcggt gcccgtccgc tgaaaacgtt tttcaatgtg
240
attgtcccgc tcaccaaagg cggcattatc gcggggtcga tgctggtgtt tatcccggcg
300

gtcggtgagt ttgttatccc ggaactgctc ggcggcggcc g
341

<210> 1472
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1472
Ala Trp Met Gly Ile Leu Lys Asn Asn Gly Val Leu Asn Asn Phe Leu
1 5 10 15
Leu Trp Leu Gly Val Ile Asp Gln Pro Leu Thr Ile Leu His Thr Asn
20 25 30
Leu Ala Val Tyr Ile Gly Ile Val Tyr Ala Tyr Leu Pro Phe Met Val
35 40 45
Leu Pro Ile Tyr Thr Ala Leu Thr Arg Ile Asp Tyr Ser Leu Val Glu
50 55 60
Ala Ser Leu Asp Leu Gly Ala Arg Pro Leu Lys Thr Phe Phe Asn Val
65 70 75 80
Ile Val Pro Leu Thr Lys Gly Gly Ile Ile Ala Gly Ser Met Leu Val
85 90 95
Phe Ile Pro Ala Val Gly Glu Phe Val Ile Pro Glu Leu Leu Gly Gly
100 105 110
Gly

<210> 1473
<211> 352
<212> DNA
<213> Homo sapiens

<400> 1473
tccggaactg ctcaatgtct gtccagcaca taagatccat gcttgaagaa tgagtctcaa
60
gaaactgacg gaaatgttca aactccagtt tgttgttaag cagatcacta aacttaaaat
120
gcttgtattc tgcaggaaca ttatcccaat attctgttcg tttagagacg ttagagagtg
180
ataaaatgcc agttccaatt tcacaagtgg tgtcctcagc tttcttggaa aatgtctctt
240
tatgcaaagc ctgtagcttt ctgaagtatg tggagtctaa ctgtcgagtt tcttccacca
300
gctccacctt tttataagca atttggtccg attttaccat ctttgtccat gg
352

<210> 1474
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1474
Met Val Lys Ser Asp Gln Ile Ala Tyr Lys Lys Val Glu Leu Val Glu
1 5 10 15
Glu Thr Arg Gln Leu Asp Ser Thr Tyr Phe Arg Lys Leu Gln Ala Leu

```
            20                  25                  30
His Lys Glu Thr Phe Ser Lys Lys Ala Glu Asp Thr Thr Cys Glu Ile
        35                  40                  45
Gly Thr Gly Ile Leu Ser Leu Ser Asn Val Ser Lys Arg Thr Glu Tyr
    50                  55                  60
Trp Asp Asn Val Pro Ala Glu Tyr Lys His Phe Lys Phe Ser Asp Leu
65                  70                  75                  80
Leu Asn Asn Lys Leu Glu Phe Glu His Phe Arg Gln Phe Leu Glu Thr
                85                  90                  95
His Ser Ser Ser Met Asp Leu Met Cys Trp Thr Asp Ile Glu Gln Phe
            100                 105                 110
Arg
```

<210> 1475
<211> 389
<212> DNA
<213> Homo sapiens

<400> 1475
accggtgccg gagccgatct ccacgatggt cttggcgccg gtgcggccga accactcatc
60
gacatcgata agctcatcgc ttaagacgcg gcccagctcg ggccagcatt gctcaaaaag
120
ctggtgctgg ttgtccgtga gcgtgccgcg ggggaaaggg acctttgccc aggcgcgggt
180
agtccaggtc attatcaaag accgcattga agtccgtttg cggcgggcga cccggcggca
240
tttctccggc agggggtgtt ttgagaatta tccgtgctat acatcgcgcc ctatttttcc
300
ctgtccaggc atggcaagca atatgccgcg ccgggtattt tccccgccgt atggggaggg
360
ggataaccgg agcttgacgg ggtggtgtc
389

<210> 1476
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1476
```
Met Val Leu Ala Pro Val Arg Pro Asn His Ser Ser Thr Ser Ile Ser
 1               5                  10                  15
Ser Ser Leu Lys Thr Arg Pro Ser Ser Gly Gln His Cys Ser Lys Ser
            20                  25                  30
Trp Cys Trp Leu Ser Val Ser Val Pro Arg Gly Lys Gly Thr Phe Ala
        35                  40                  45
Gln Ala Arg Val Val Gln Val Ile Ile Lys Asp Arg Ile Glu Val Arg
    50                  55                  60
Leu Arg Arg Ala Thr Arg Arg His Phe Ser Gly Arg Gly Cys Phe Glu
65                  70                  75                  80
Asn Tyr Pro Cys Tyr Thr Ser Arg Pro Ile Phe Pro Cys Pro Gly Met
                85                  90                  95
Ala Ser Asn Met Pro Arg Arg Val Phe Ser Pro Pro Tyr Gly Glu Gly
```

```
            100                 105                 110
Asp Asn Arg Ser Leu Thr Gly Trp Cys
        115                 120
```

<210> 1477
<211> 500
<212> DNA
<213> Homo sapiens

<400> 1477
tacagcgaga atctgcacga tacccacttc ctcaaaacct attgcgttgg cttcgagcaa
60
ttcctccctt atttgctggg ccaaacggac ggccaaccta aagatgccca atgggcatcg
120
gcgctgtgtg gtattgatgc cgaaatcatc cgggcactgg cccgccaaat ggcggccaac
180
cgtacgcaaa tcattgcggg ctggtgcgtg caacgtatgc aacacggcga acaatgggcg
240
tggatgacgg tagtgctggc ggcgatgctt ggccaaatcg gcttaccggg cggcgggttc
300
ggttttggtt ggccctccaa cggcgcaggt acccccgagc cgcaaggggt gatcctgagc
360
ggtttctccg gttcccccgc tacgccggca cgccatgcca agggggattt caaaggttac
420
agcagtacca ttccgatcgc gcgctttatc gatgccatgc tggagccggg caaggagatc
480
gattggaatg gcaaacgcgt
500

<210> 1478
<211> 166
<212> PRT
<213> Homo sapiens

<400> 1478
```
Tyr Ser Glu Asn Leu His Asp Thr His Phe Leu Lys Thr Tyr Cys Val
 1               5                  10                  15
Gly Phe Glu Gln Phe Leu Pro Tyr Leu Leu Gly Gln Thr Asp Gly Gln
            20                  25                  30
Pro Lys Asp Ala Gln Trp Ala Ser Ala Leu Cys Gly Ile Asp Ala Glu
        35                  40                  45
Ile Ile Arg Ala Leu Ala Arg Gln Met Ala Ala Asn Arg Thr Gln Ile
    50                  55                  60
Ile Ala Gly Trp Cys Val Gln Arg Met Gln His Gly Glu Gln Trp Ala
65                  70                  75                  80
Trp Met Thr Val Val Leu Ala Ala Met Leu Gly Gln Ile Gly Leu Pro
                85                  90                  95
Gly Gly Gly Phe Gly Phe Gly Trp Pro Ser Asn Gly Ala Gly Thr Pro
            100                 105                 110
Glu Pro Gln Gly Val Ile Leu Ser Gly Phe Ser Gly Ser Pro Ala Thr
        115                 120                 125
Pro Ala Arg His Ala Lys Gly Asp Phe Lys Gly Tyr Ser Ser Thr Ile
    130                 135                 140
Pro Ile Ala Arg Phe Ile Asp Ala Met Leu Glu Pro Gly Lys Glu Ile
```

145 150 155 160
Asp Trp Asn Gly Lys Arg
165

<210> 1479
<211> 421
<212> DNA
<213> Homo sapiens

<400> 1479
acgcgtgtgg agctggcacc atgaaagcac gatgtgcatc actcatagag gcaggcacac
60
ttaagtatgt tctttacatt gaaacagaaa ggaaagaaga taggaaaaat ggtgccagca
120
cgctgggctt tttttgtttg ctgttttggg tggggtgtgc tagtgcagtg tccggtgtac
180
gcttttgtcc tcaaacaggc ttgttccccg gtcagagttt cattattgtt gctggtaaac
240
aaatgccaag tttgacaaaa aacagtgaaa taaagcaaaa gattttgaaa aatgcttcat
300
catgtcagaa ggaaagaacc cttttcacgg gtgcctgccc acatttcctt gcccagcctg
360
agaccctatt gactttgaat tatcttttgc tgttttattt ctatgaaaat tatatacgcg
420
t
421

<210> 1480
<211> 133
<212> PRT
<213> Homo sapiens

<400> 1480
Met Lys Ala Arg Cys Ala Ser Leu Ile Glu Ala Gly Thr Leu Lys Tyr
1 5 10 15
Val Leu Tyr Ile Glu Thr Glu Arg Lys Glu Asp Arg Lys Asn Gly Ala
20 25 30
Ser Thr Leu Gly Phe Phe Cys Leu Leu Phe Trp Val Gly Cys Ala Ser
35 40 45
Ala Val Ser Gly Val Arg Phe Cys Pro Gln Thr Gly Leu Phe Pro Gly
50 55 60
Gln Ser Phe Ile Ile Val Ala Gly Lys Gln Met Pro Ser Leu Thr Lys
65 70 75 80
Asn Ser Glu Ile Lys Gln Lys Ile Leu Lys Asn Ala Ser Ser Cys Gln
85 90 95
Lys Glu Arg Thr Leu Phe Thr Gly Ala Cys Pro His Phe Leu Ala Gln
100 105 110
Pro Glu Thr Leu Leu Thr Leu Asn Tyr Leu Leu Leu Phe Tyr Phe Tyr
115 120 125
Glu Asn Tyr Ile Arg
130

<210> 1481
<211> 545

<212> DNA
<213> Homo sapiens

<400> 1481
gtcgggtcgc cgcccagtct cgtgccgaca tgcagttcct ggcccgggag gtcgcatcca
60
tccggatgca gatgggcgag ttggccacgc gcgattattt gcgctcggag ctacgcgacg
120
agttgcgctc cctgctcgag gagatcgagg cctcaccggc ctcccactaa ctgacccggt
180
tcgcgacgag cgagttgtcg catcgggcca acggtgtgta gacaagtcag catgagcacc
240
gagaacccag tggttaaggc cattgccgat gcgttgtcgc acgtcaatga ccccgagatc
300
aaacgcccca ttaccgatct caacatgatt gatgagatta ccgtcgacga gcaaggacgc
360
gctttcgtcc gcatcctgct gaccgtcgcc gggtgtcccc tcaagaccga gctgcgtgag
420
caggccaccg aggctgtgcg cagcgttgac ggggtgacca gtgtttccgt cgaactcggc
480
accatgaccg acgaacagcg cgatgctctc aaagttcagc tgcgcggtga cgtccccgaa
540
cgcgt
545

<210> 1482
<211> 104
<212> PRT
<213> Homo sapiens

<400> 1482
Met Ser Thr Glu Asn Pro Val Val Lys Ala Ile Ala Asp Ala Leu Ser
 1   5   10   15
His Val Asn Asp Pro Glu Ile Lys Arg Pro Ile Thr Asp Leu Asn Met
            20   25   30
Ile Asp Glu Ile Thr Val Asp Glu Gln Gly Arg Ala Phe Val Arg Ile
        35   40   45
Leu Leu Thr Val Ala Gly Cys Pro Leu Lys Thr Glu Leu Arg Glu Gln
    50   55   60
Ala Thr Glu Ala Val Arg Ser Val Asp Gly Val Thr Ser Val Ser Val
65   70   75   80
Glu Leu Gly Thr Met Thr Asp Glu Gln Arg Asp Ala Leu Lys Val Gln
                85   90   95
Leu Arg Gly Asp Val Pro Glu Arg
            100

<210> 1483
<211> 625
<212> DNA
<213> Homo sapiens

<400> 1483
gtacggcttc gagagggcta cagtgtccga gaggtcacac tggccaaagg agggtcccaa
60

ttggaggtaa agctggtgct gctgtggaaa cacaacatgc gcattgagta tgtggctatg
120
gcatcctggc ccctggagcc tgagggccct cgagtaacac gggtggaagt gacgatggaa
180
ggcggctacg acattttgca tgatgtgtcc tgtgcactaa ggcagcccat tcgttcattg
240
tatcgtaccc atgttatccg gcgtttctgg aacacgctgc agagcatcaa ccagacagac
300
cagatgcttg cccaccttca gtccttctcc tcagtgcctg agcatttcac gcttcctgac
360
agcaccaaga gcggagtgcc actcttctac atccctccag gctccaccac cccggtgctc
420
tccctccagc ccagtggttc tgactcatcc catgcccagt ttgctgccta ctggaagccc
480
agtgctgtcc atggatgcaa attcctggca gcgatggctg cacatgcatc gcctggtgct
540
aatcctggag catgacacac caatccccaa gcacttgcac accccgggca gcaatgggcg
600
ctactacgga gagaagacaa cgcgt
625

<210> 1484
<211> 184
<212> PRT
<213> Homo sapiens

<400> 1484
Val Arg Leu Arg Glu Gly Tyr Ser Val Arg Glu Val Thr Leu Ala Lys
1 5 10 15
Gly Gly Ser Gln Leu Glu Val Lys Leu Val Leu Leu Trp Lys His Asn
20 25 30
Met Arg Ile Glu Tyr Val Ala Met Ala Ser Trp Pro Leu Glu Pro Glu
35 40 45
Gly Pro Arg Val Thr Arg Val Glu Val Thr Met Glu Gly Gly Tyr Asp
50 55 60
Ile Leu His Asp Val Ser Cys Ala Leu Arg Gln Pro Ile Arg Ser Leu
65 70 75 80
Tyr Arg Thr His Val Ile Arg Arg Phe Trp Asn Thr Leu Gln Ser Ile
85 90 95
Asn Gln Thr Asp Gln Met Leu Ala His Leu Gln Ser Phe Ser Ser Val
100 105 110
Pro Glu His Phe Thr Leu Pro Asp Ser Thr Lys Ser Gly Val Pro Leu
115 120 125
Phe Tyr Ile Pro Pro Gly Ser Thr Thr Pro Val Leu Ser Leu Gln Pro
130 135 140
Ser Gly Ser Asp Ser Ser His Ala Gln Phe Ala Ala Tyr Trp Lys Pro
145 150 155 160
Ser Ala Val His Gly Cys Lys Phe Leu Ala Ala Met Ala Ala His Ala
165 170 175
Ser Pro Gly Ala Asn Pro Gly Ala
180

<210> 1485
<211> 2058

<212> DNA
<213> Homo sapiens

<400> 1485
ntatgttcag cgttcaacga tattggctac cactatggtg ccatggtcgt cgatgctgcg
60
ctgttcctgc cacagtcacg acccagacta tttatcattg gtgtcagaaa cgatattttt
120
gttggcgata ttacttctga atcaccgtct aaaatgtggc ataccagaac tttattgaat
180
gcctacagca atctgaaaga tgatgccaag tccaattggg tatggtggga ccttcctatg
240
ccagcccaga gaaaatctgc tttcgccgat ttgattgaag aaaatcctag cagcgttaag
300
tggcataccc ggaaggaaac acagcagctc ttggatatga tgactgatgt taacttagct
360
aaggttgagg ctgcaaaaaa gctatcgatc gagtctaagg aaaatgttgt agggacaatt
420
tataaaagaa ctcgcaccga tagctttgga gttaaagcgc agcgtgctga agtgcggttt
480
gatgatgttg ccggttgtct tcgcacccct ggaggggggt caagtcggca agtcataatg
540
gtcgttgata acgggactgt aaaaacgagg ttgatctcaa gtagagaaac tgcaaggctt
600
atggggttac ccgacgaata catattgcca aaaaattata atgaggcgta tcacttaacg
660
ggtgatggtg ttgtagtgcc ggttgtatcc cacatagcca ctcatatttt tgacccagtg
720
atggagcgtg tgtttgagga tgcggcggga ctgcttaagc aaatcgcata gcatcgtttt
780
ggcaggaaga tatgagcgtt attccgtgta aaaaggacct tcagctaaaa aaattgattg
840
aatcctatgc agaagccttg aaagttgagg cccataagct aggagagcat ggattaactg
900
aagctgaatt ttatgatagc ggcctctttc ggggggctat cgagcgaatt cgaggacagt
960
tctccgcgac catgcgggag aaaagaaatt tcgttaagca tgttttaaat tacatgcagg
1020
ataacgacta cattgctgat tgggagtcgg ctggtgaatc gaatcgccat gattatatgg
1080
taactctcaa ttctgggcgc aaagctgcta ttgagctgaa agggtgcctt gatggcaata
1140
acactaacat ctttgatcgc ccccctcagg cagaagaatt tgttatctgg agtgtatgca
1200
caaatcctgg tgctgaccct cagcataatg tttggtctgg gcttcacacc agactaagtg
1260
ctgaaatcat ttcacgggag caaaggattg atggaatggt catttgggac tgggcttgtg
1320
gaacagtcgg aaggccatgc cccaaaatag caactgaacc tgagcgggct gtaacatttg
1380
ggccgttcaa attgccgcca ccatgtttgt atcttttacc ttcgacgatt ccaagcccaa
1440
gaaacaaccc gtctccaaga gctcagcaga ttgaagacgt gcagctaatc aaagcgtttc
1500

acgattgttt tgggtgccgg tctgaagaag ttaatttcgt taactttgat gttggttatc
1560
atggtaaaga taccgtccgt aaaacgacta tcattcgaaa cggcatggtg gagcgtgaat
1620
cggaaatgac ggcaataagg cggtcttaat ttgtgcatgc ctatgctgca tgaatccgca
1680
tgatcgtttg aggatcgttt ttgctgaggc ccgccagttc tggtgggctt ttgcttatgt
1740
catgcacctg catgaaaacc gctacataaa gcgggcaggc gtggcgggga tacgagcgcg
1800
cgcaacgggg tgaaatggtg aatatcaggg gcaatctccg gcacgctggc ggcttgaatc
1860
gggtagggtg agtgagaggc agcaataaag aagcgccccg cagaatgctg ctggggcgct
1920
gtgagaggtg gtcttgttgt cgcggtgcgg tgggtcagtc gtagcgattg tcttctgtca
1980
gccccagcgt gtacggctca aagcggatca cttcttcgcc cagccagtca ttaagctccc
2040
gcagtcgctt ctgcaggc
2058

<210> 1486
<211> 256
<212> PRT
<213> Homo sapiens

<400> 1486
Xaa Cys Ser Ala Phe Asn Asp Ile Gly Tyr His Tyr Gly Ala Met Val
 1   5   10   15
Val Asp Ala Ala Leu Phe Leu Pro Gln Ser Arg Pro Arg Leu Phe Ile
            20   25   30
Ile Gly Val Arg Asn Asp Ile Phe Val Gly Asp Ile Thr Ser Glu Ser
        35   40   45
Pro Ser Lys Met Trp His Thr Arg Thr Leu Leu Asn Ala Tyr Ser Asn
    50   55   60
Leu Lys Asp Asp Ala Lys Ser Asn Trp Val Trp Trp Asp Leu Pro Met
65   70   75   80
Pro Ala Gln Arg Lys Ser Ala Phe Ala Asp Leu Ile Glu Glu Asn Pro
                85   90   95
Ser Ser Val Lys Trp His Thr Arg Lys Glu Thr Gln Gln Leu Leu Asp
            100   105   110
Met Met Thr Asp Val Asn Leu Ala Lys Val Glu Ala Ala Lys Lys Leu
        115   120   125
Ser Ile Glu Ser Lys Glu Asn Val Val Gly Thr Ile Tyr Lys Arg Thr
    130   135   140
Arg Thr Asp Ser Phe Gly Val Lys Ala Gln Arg Ala Glu Val Arg Phe
145   150   155   160
Asp Asp Val Ala Gly Cys Leu Arg Thr Pro Gly Gly Gly Ser Ser Arg
                165   170   175
Gln Val Ile Met Val Val Asp Asn Gly Thr Val Lys Thr Arg Leu Ile
            180   185   190
Ser Ser Arg Glu Thr Ala Arg Leu Met Gly Leu Pro Asp Glu Tyr Ile
        195   200   205
Leu Pro Lys Asn Tyr Asn Glu Ala Tyr His Leu Thr Gly Asp Gly Val

```
    210                 215                 220
Val Val Pro Val Val Ser His Ile Ala Thr His Ile Phe Asp Pro Val
225                 230                 235                 240
Met Glu Arg Val Phe Glu Asp Ala Ala Gly Leu Leu Lys Gln Ile Ala
                245                 250                 255
```

<210> 1487
<211> 823
<212> DNA
<213> Homo sapiens

<400> 1487
acgcgtgagg ggaggggatg ctgggcagat cttgtgaggg aaaattcagg aaggacctct
60
ccgagcaggt gacatttcag ctaaggctgg gaaggatgag gagaagtcag gaactccagg
120
catcagggaa tgctggggaa aaaaagcact ccaggcccag ggatcagcaa agcacaggat
180
gcctgggggа acacacagcc tcagagcatt tgaggaacag aaaaggcaac gtgactaagc
240
ttcctggggc ggtgaggtca ggcagggagg tgggtgcgag gtcatggggc cgcaggcaaa
300
cggccctccc tcccagtgcc ccacatgcag gccctggagc accaggagcg gggaggctcc
360
gtggtgtgtc ttcctgcaag tggcctgcct ttgggagcat cagccctttc tcctggggac
420
tgggagaggc cggcagtgag ggaagaatgg ccctcggtcg tgcgtagaga atgtagggga
480
cacagggcct ctcacggacc cagatcctga tcttgtcaga tctgcacgcc cgtgggaggg
540
tgctggcggc agaaacgcgt tgccataagc cttctcccca ctgcaggcag gtgtggtcag
600
gggacctcct tggagaacaa ggtgggggaa tttggcagct ttctcagcat ggcgtccatc
660
ccccctacat tcctggggca cccactgtag gccaggccct gtgccggatc tgatgataca
720
gtgatgacta agtcacagtc cctgcctctg aggcccccat gatgtgccgg gacagccaag
780
caacccaata tgttaaaatc cagtgtcagg acccnaggag aag
823

<210> 1488
<211> 149
<212> PRT
<213> Homo sapiens

<400> 1488
```
Met Leu Gly Arg Ser Cys Glu Gly Lys Phe Arg Lys Asp Leu Ser Glu
 1               5                  10                  15
Gln Val Thr Phe Gln Leu Arg Leu Gly Arg Met Arg Arg Ser Gln Glu
            20                  25                  30
Leu Gln Ala Ser Gly Asn Ala Gly Glu Lys Lys His Ser Arg Pro Arg
        35                  40                  45
Asp Gln Gln Ser Thr Gly Cys Leu Gly Glu His Thr Ala Ser Glu His
```

```
    50                  55                  60
Leu Arg Asn Arg Lys Gly Asn Val Thr Lys Leu Pro Gly Ala Val Arg
65                  70                  75                  80
Ser Gly Arg Glu Val Gly Ala Arg Ser Trp Gly Arg Arg Gln Thr Ala
                85                  90                  95
Leu Pro Pro Ser Ala Pro His Ala Gly Pro Gly Ala Pro Gly Ala Gly
            100                 105                 110
Arg Leu Arg Gly Val Ser Ser Cys Lys Trp Pro Ala Phe Gly Ser Ile
        115                 120                 125
Ser Pro Phe Ser Trp Gly Leu Gly Glu Ala Gly Ser Glu Gly Arg Met
    130                 135                 140
Ala Leu Gly Arg Ala
145
```

<210> 1489
<211> 342
<212> DNA
<213> Homo sapiens

<400> 1489
nnccagttca ccgtcaagct ggccgcggcc ggcgaacaca atgtgcgcaa tgcgctggcc
60
gcgattgcct gcgccgtggg tgccggcatc aaccaggacg ccatcgtgcg cggcctcgaa
120
gccttcgccc cggtcggcgg acgtttgcag cgcaagcagg ccgccagcgg cgcgcccgtc
180
attgacgaca cccacaaccc caatcccaat tcaatgcgcc cggcgatcga cgtgctggcc
240
cgcgtacccg cgccgcgcat cctggtggtg ggcgacatgg gcgaagtcgg cgcacaggga
300
aaagaatttc acgaagaaat cggggcttac gcacacacgc gt
342

<210> 1490
<211> 114
<212> PRT
<213> Homo sapiens

<400> 1490
```
Xaa Gln Phe Thr Val Lys Leu Ala Ala Ala Gly Glu His Asn Val Arg
 1               5                  10                  15
Asn Ala Leu Ala Ala Ile Ala Cys Ala Val Gly Ala Gly Ile Asn Gln
            20                  25                  30
Asp Ala Ile Val Arg Gly Leu Glu Ala Phe Ala Pro Val Gly Gly Arg
        35                  40                  45
Leu Gln Arg Lys Gln Ala Ala Ser Gly Ala Pro Val Ile Asp Asp Thr
    50                  55                  60
His Asn Pro Asn Pro Asn Ser Met Arg Pro Ala Ile Asp Val Leu Ala
65                  70                  75                  80
Arg Val Pro Ala Pro Arg Ile Leu Val Val Gly Asp Met Gly Glu Val
                85                  90                  95
Gly Ala Gln Gly Lys Glu Phe His Glu Glu Ile Gly Ala Tyr Ala His
            100                 105                 110
Thr Arg
```

<210> 1491
<211> 333
<212> DNA
<213> Homo sapiens

<400> 1491
ncctcgttgt tctcatagag ggctacggca tcgcgtttga actgttcgga gtacctggac
60
atgggggtag attacctttc ttcccagctc gactgggctg gatatcaggt gtccaccaca
120
tgggggtcag gtcccactcc caaaggagta gccatcaccc acgagtcggc ggtcaatacg
180
attgtcgatg tcaacgaacg cctcggggtg actccgaccg accggatatt ggggatttca
240
gagctaaact tcgatctatc ggtatacgac atcttcggga tgttcgcgcg gggtgctacc
300
ttggtgttgc catctccagc agacaaacgt gat
333

<210> 1492
<211> 91
<212> PRT
<213> Homo sapiens

<400> 1492
Met Gly Val Asp Tyr Leu Ser Ser Gln Leu Asp Trp Ala Gly Tyr Gln
 1   5   10   15
Val Ser Thr Thr Trp Gly Ser Gly Pro Thr Pro Lys Gly Val Ala Ile
            20   25   30
Thr His Glu Ser Ala Val Asn Thr Ile Val Asp Val Asn Glu Arg Leu
        35   40   45
Gly Val Thr Pro Thr Asp Arg Ile Leu Gly Ile Ser Glu Leu Asn Phe
    50   55   60
Asp Leu Ser Val Tyr Asp Ile Phe Gly Met Phe Ala Arg Gly Ala Thr
65   70   75   80
Leu Val Leu Pro Ser Pro Ala Asp Lys Arg Asp
                85   90

<210> 1493
<211> 1316
<212> DNA
<213> Homo sapiens

<400> 1493
nggtaccagg gcaaagaagg ctgggccccc gcctcctacc taaagaagaa cagtggggag
60
cccttgcccc cgaagccagg ccctggctca ccctcccacc cgggtgccct tgacttggat
120
ggtgtttccc ggcagcagaa cgcggtgggc agggagaagg agctgctcag cagccagagg
180
gacgggcggt ttgaaggccg cccggtgccc gacggtgacg ccaagcagag atcaccaaag
240

atgaggcaga gacccctcc tcgccgggac atgaccattc ctcgaggcct caacctgccg
300
aagccgccca tcccgcccca agtggaggaa gagtattaca ccatcgccga attccagaca
360
accatcccag acggcatcag cttccaggca ggcctgaagg tcgaggtgat cgagaaaaac
420
ttgagtggct ggtggtacat tcagattgaa gataaggaag ggtgggcccc ggccaccttc
480
attgacaagt acaagaagac gagcaacgcg tcgagaccca actttctggc tcccctgccc
540
cacgaggtga cccagctccg gctgggggaa gcagcagcgc tggagaacaa cacgggcagc
600
gaagccacgg gcccctcccg gcccctgcct gacgcaccgc atggtgtcat ggactcgggg
660
ttgccatggt ctaaagactg gaagggcagt aaggatgtcc tgaggaaggc atcttcagac
720
atgtctgcgt cagcaggcta cgaggagatc tcagaccccg acatggagga gaagcccagc
780
ctccctccgc ggaaagaatc catcatcaag tcggaggggg agctgctgga gcgggagcgg
840
gagcggcaga ggacggagca gctccggggc cccactccca agcctccggg cgtgattttg
900
ccgatgatgc cagccaaaca catccctcca gcccgggaca gcaggaggcc agagcccaaa
960
cctgacaaaa gcagactgtt ccagctgaaa aatgacatgg ggctggagtg tggccacaag
1020
gtcttggcca aggaagtgaa gaagcccaac ctccggccca tctccaaatc caaaactgac
1080
ctgccagagg agaagccaga tgccactccc cagaatccct tcttgaagtc cagacctcag
1140
gttaggccaa aaccagctcc ttcccccaaa acggagccac ctcagggcga agaccaagtc
1200
gacatctgca acctcaggag taagctcagg cctgccaagt cccaagacaa gtccttgttg
1260
gatggggagg gcccccaggc agtaggggggc caagacgtgg ccttcagccg aagctt
1316

<210> 1494
<211> 438
<212> PRT
<213> Homo sapiens

<400> 1494
Xaa Tyr Gln Gly Lys Glu Gly Trp Ala Pro Ala Ser Tyr Leu Lys Lys
1 5 10 15
Asn Ser Gly Glu Pro Leu Pro Pro Lys Pro Gly Pro Gly Ser Pro Ser
20 25 30
His Pro Gly Ala Leu Asp Leu Asp Gly Val Ser Arg Gln Gln Asn Ala
35 40 45
Val Gly Arg Glu Lys Glu Leu Leu Ser Ser Gln Arg Asp Gly Arg Phe
50 55 60
Glu Gly Arg Pro Val Pro Asp Gly Asp Ala Lys Gln Arg Ser Pro Lys
65 70 75 80
Met Arg Gln Arg Pro Pro Pro Arg Arg Asp Met Thr Ile Pro Arg Gly

```
                85                  90                  95
Leu Asn Leu Pro Lys Pro Pro Ile Pro Pro Gln Val Glu Glu Glu Tyr
            100                 105                 110
Tyr Thr Ile Ala Glu Phe Gln Thr Thr Ile Pro Asp Gly Ile Ser Phe
        115                 120                 125
Gln Ala Gly Leu Lys Val Glu Val Ile Glu Lys Asn Leu Ser Gly Trp
    130                 135                 140
Trp Tyr Ile Gln Ile Glu Asp Lys Glu Gly Trp Ala Pro Ala Thr Phe
145                 150                 155                 160
Ile Asp Lys Tyr Lys Lys Thr Ser Asn Ala Ser Arg Pro Asn Phe Leu
                165                 170                 175
Ala Pro Leu Pro His Glu Val Thr Gln Leu Arg Leu Gly Glu Ala Ala
            180                 185                 190
Ala Leu Glu Asn Asn Thr Gly Ser Glu Ala Thr Gly Pro Ser Arg Pro
        195                 200                 205
Leu Pro Asp Ala Pro His Gly Val Met Asp Ser Gly Leu Pro Trp Ser
    210                 215                 220
Lys Asp Trp Lys Gly Ser Lys Asp Val Leu Arg Lys Ala Ser Ser Asp
225                 230                 235                 240
Met Ser Ala Ser Ala Gly Tyr Glu Glu Ile Ser Asp Pro Asp Met Glu
                245                 250                 255
Glu Lys Pro Ser Leu Pro Pro Arg Lys Glu Ser Ile Ile Lys Ser Glu
            260                 265                 270
Gly Glu Leu Leu Glu Arg Glu Arg Glu Arg Gln Arg Thr Glu Gln Leu
        275                 280                 285
Arg Gly Pro Thr Pro Lys Pro Pro Gly Val Ile Leu Pro Met Met Pro
    290                 295                 300
Ala Lys His Ile Pro Pro Ala Arg Asp Ser Arg Arg Pro Glu Pro Lys
305                 310                 315                 320
Pro Asp Lys Ser Arg Leu Phe Gln Leu Lys Asn Asp Met Gly Leu Glu
                325                 330                 335
Cys Gly His Lys Val Leu Ala Lys Glu Val Lys Lys Pro Asn Leu Arg
            340                 345                 350
Pro Ile Ser Lys Ser Lys Thr Asp Leu Pro Glu Glu Lys Pro Asp Ala
        355                 360                 365
Thr Pro Gln Asn Pro Phe Leu Lys Ser Arg Pro Gln Val Arg Pro Lys
    370                 375                 380
Pro Ala Pro Ser Pro Lys Thr Glu Pro Pro Gln Gly Glu Asp Gln Val
385                 390                 395                 400
Asp Ile Cys Asn Leu Arg Ser Lys Leu Arg Pro Ala Lys Ser Gln Asp
                405                 410                 415
Lys Ser Leu Leu Asp Gly Glu Gly Pro Gln Ala Val Gly Gly Gln Asp
            420                 425                 430
Val Ala Phe Ser Arg Ser
        435
```

<210> 1495
<211> 329
<212> DNA
<213> Homo sapiens

<400> 1495
agatctctgt cccgtagagg tgccacctca tcctccatga gagctgtgct ttgctttctt
60

ctggaggctg caaggaggat ggcccccatc acggcggacc tacatgctgg gagtccggga
120
gagggcaggc cgcggacatg gggcatgtgg cgatgtgttt caccacccac tcccgcctga
180
agtgccactg tgagcccaac ccacggtgcc aggctgggct gcactccagg ctcctgcagc
240
agacccacct cctcagcctc cttcccctga aggctgggca tggcctggac aaagggtgtc
300
ctcctctgct gtgccatgct gacgtggca
329

<210> 1496
<211> 105
<212> PRT
<213> Homo sapiens

<400> 1496
Met Ala Gln Gln Arg Arg Thr Pro Phe Val Gln Ala Met Pro Ser Leu
1 5 10 15
Gln Gly Lys Glu Ala Glu Glu Val Gly Leu Leu Gln Glu Pro Gly Val
20 25 30
Gln Pro Ser Leu Ala Pro Trp Val Gly Leu Thr Val Ala Leu Gln Ala
35 40 45
Gly Val Gly Gly Glu Thr His Arg His Met Pro His Val Arg Gly Leu
50 55 60
Pro Ser Pro Gly Leu Pro Ala Cys Arg Ser Ala Val Met Gly Ala Ile
65 70 75 80
Leu Leu Ala Ala Ser Arg Arg Lys Gln Ser Thr Ala Leu Met Glu Asp
85 90 95
Glu Val Ala Pro Leu Arg Asp Arg Asp
100 105

<210> 1497
<211> 345
<212> DNA
<213> Homo sapiens

<400> 1497
naacttcttg cactcactca ggcgcacggt tggcggccga cttggaagcc gctgcagcac
60
ttgacgcggg gcgatctcga agcgttcggt cttggcctga cggtcgatgg ctgcggcgtg
120
ccgttgatcg cgcgaatgcg acgggtgggg cagggcgtgc ggccgacacc accgcaagaa
180
cgcaactcac ggcagatgaa tctgttttga aacgcaagga agggtaatga caggcaccga
240
caagaagcgg atcccgcagc tgctgcgtgt tgagctcact gaacttaccg gcccgatcga
300
gcagccttac gcgcccgatg cacgtcattc tttcgggcca cgcgt
345

<210> 1498
<211> 104
<212> PRT

<213> Homo sapiens

<400> 1498
Met Thr Cys Ile Gly Arg Val Arg Leu Leu Asp Arg Ala Gly Lys Phe
1 5 10 15
Ser Glu Leu Asn Thr Gln Gln Leu Arg Asp Pro Leu Leu Val Gly Ala
20 25 30
Cys His Tyr Pro Ser Leu Arg Phe Lys Thr Asp Ser Ser Ala Val Ser
35 40 45
Cys Val Leu Ala Val Val Ser Ala Ala Arg Pro Ala Pro Pro Val Ala
50 55 60
Phe Ala Arg Ser Thr Ala Arg Arg Ser His Arg Pro Ser Gly Gln Asp
65 70 75 80
Arg Thr Leu Arg Asp Arg Pro Ala Ser Ser Ala Ala Ala Ala Ser Lys
85 90 95
Ser Ala Ala Asn Arg Ala Pro Glu
100

<210> 1499
<211> 402
<212> DNA
<213> Homo sapiens

<400> 1499
aaatatattc tgccagagtt tgaacacgac accatgctct ggcatttggg catgtcgggg
60
agtttccgtc tatgcgagag caatgaagaa ttacgcaaac atgaccatct aatcattcag
120
tttgaagata tcgaactgcg ttatcatgat cctcgccgtt ttggttgcat tctttggctg
180
gatgcacaat cacaaagcaa attaatagat acgctggggc cagaaccctt aagcgagaac
240
tttaatgcgg agtatttatt tgaaaaattg aagaataaaa aggttggcac caaagttgca
300
attatggata accatgtggt ggtgggcgta ggcaatattt atgcgaccga aagtctgttt
360
aatctgggga ttcatccagc acaaccggcc tcgactttaa gc
402

<210> 1500
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1500
Lys Tyr Ile Leu Pro Glu Phe Glu His Asp Thr Met Leu Trp His Leu
1 5 10 15
Gly Met Ser Gly Ser Phe Arg Leu Cys Glu Ser Asn Glu Glu Leu Arg
20 25 30
Lys His Asp His Leu Ile Ile Gln Phe Glu Asp Ile Glu Leu Arg Tyr
35 40 45
His Asp Pro Arg Arg Phe Gly Cys Ile Leu Trp Leu Asp Ala Gln Ser
50 55 60
Gln Ser Lys Leu Ile Asp Thr Leu Gly Pro Glu Pro Leu Ser Glu Asn

65 70 75 80
Phe Asn Ala Glu Tyr Leu Phe Glu Lys Leu Lys Asn Lys Lys Val Gly
85 90 95
Thr Lys Val Ala Ile Met Asp Asn His Val Val Val Gly Val Gly Asn
100 105 110
Ile Tyr Ala Thr Glu Ser Leu Phe Asn Leu Gly Ile His Pro Ala Gln
115 120 125
Pro Ala Ser Thr Leu Ser
130

<210> 1501
<211> 362
<212> DNA
<213> Homo sapiens

<400> 1501
nnacgcgtgc atgctgcagg catcatccat cgcgatctga agccccaaaa catcttcctg
60
gtgccgagcg cgcgcgagcg cgacttcgtg aagatcttcg acttcggcgc atgccagatg
120
gtcacaccga aggtatcgaa cggcgtgccc gagctgaaga cgagcgcggg aaatctcttc
180
ggcacggtgc cgtacatggc gccggagtgc ttcgaggacg gctcgcaccg gctggatgcg
240
cgcgcggaca tctactccac gggcatcatc atgtaccgct gcgtgacggg gacgctcccc
300
ttcaaggcga acaccgtctt cgagatgctc atccatctgc gcgagggccg cccatcaagc
360
tt
362

<210> 1502
<211> 120
<212> PRT
<213> Homo sapiens

<400> 1502
Xaa Arg Val His Ala Ala Gly Ile Ile His Arg Asp Leu Lys Pro Gln
1 5 10 15
Asn Ile Phe Leu Val Pro Ser Ala Arg Glu Arg Asp Phe Val Lys Ile
20 25 30
Phe Asp Phe Gly Ala Cys Gln Met Val Thr Pro Lys Val Ser Asn Gly
35 40 45
Val Pro Glu Leu Lys Thr Ser Ala Gly Asn Leu Phe Gly Thr Val Pro
50 55 60
Tyr Met Ala Pro Glu Cys Phe Glu Asp Gly Ser His Arg Leu Asp Ala
65 70 75 80
Arg Ala Asp Ile Tyr Ser Thr Gly Ile Ile Met Tyr Arg Cys Val Thr
85 90 95
Gly Thr Leu Pro Phe Lys Ala Asn Thr Val Phe Glu Met Leu Ile His
100 105 110
Leu Arg Glu Gly Arg Pro Ser Ser
115 120

<210> 1503
<211> 623
<212> DNA
<213> Homo sapiens

<400> 1503
gccggcgtga ggcagagaaa cgtcctcgcc ctgtcattcc accctgaaga gactgacgac
60
gaccgggtac accgcacctg gttgcgccag gtgtctgagg aggtctgaca gttaccgcaa
120
gggctcatga cgacccctcc tgaacactgt tcaaagggcg acggcttacc attcctcgct
180
gtgagtcctg aacagcagct tctcgaatat gaccgacgtc atgtctggca cccctacgcc
240
ccgacgatcg gggcagaccc aatgcttgca gtgacggctg ccaacggagt ctggctgcag
300
ctgcatgatg gggaacaccg ccacgaggtc atcgatgcga tggcctcgtg gtggtgccag
360
attcacggtt accgaaaccc ggtcctcgac gaggccctca accgtcaaag ctcccagttc
420
agtcacgtca tgtttggcgg actcacccat aaggccgcgg ttgacgccgt catatcccta
480
gtgcgcctgg ccccggggcc cctcgaccgg atcttcctgg ctgattccgg gtctgtcggc
540
gtcgaggtga gtctcaaatt ggctcgtcag gtgcaaatcg ctcgcaccgc agcgcgcggc
600
ggcactttga cgaggacacg cgt
623

<210> 1504
<211> 165
<212> PRT
<213> Homo sapiens

<400> 1504
Met Thr Thr Pro Pro Glu His Cys Ser Lys Gly Asp Gly Leu Pro Phe
 1   5   10   15
Leu Ala Val Ser Pro Glu Gln Gln Leu Leu Glu Tyr Asp Arg Arg His
            20   25   30
Val Trp His Pro Tyr Ala Pro Thr Ile Gly Ala Asp Pro Met Leu Ala
        35   40   45
Val Thr Ala Ala Asn Gly Val Trp Leu Gln Leu His Asp Gly Glu His
    50   55   60
Arg His Glu Val Ile Asp Ala Met Ala Ser Trp Trp Cys Gln Ile His
65   70   75   80
Gly Tyr Arg Asn Pro Val Leu Asp Glu Ala Leu Asn Arg Gln Ser Ser
                85   90   95
Gln Phe Ser His Val Met Phe Gly Gly Leu Thr His Lys Ala Ala Val
            100   105   110
Asp Ala Val Ile Ser Leu Val Arg Leu Ala Pro Gly Pro Leu Asp Arg
        115   120   125
Ile Phe Leu Ala Asp Ser Gly Ser Val Gly Val Glu Val Ser Leu Lys
    130   135   140
Leu Ala Arg Gln Val Gln Ile Ala Arg Thr Ala Ala Arg Gly Gly Thr

145 150 155 160
Leu Thr Arg Thr Arg
165

<210> 1505
<211> 556
<212> DNA
<213> Homo sapiens

<400> 1505
nngcgcgccg gtccctcaac accaccctga cttcgaaata tctggagaat gtctacgttg
60
gtttcaatcg gtttgccgaa cagatggcca ggatggccgg cgcctcggcg aaactggacg
120
acgggggccc cgaaactcgc tgacggcact aaaccttctt cccccggcgc aaccaccttg
180
gcttccngca tgacgaagct cagcgggggа gctcagcggt tgtcagctaa cggcggcaag
240
ctcaccgacg gtgtctccca gctctccgga gggctcacaa ccttgtctca caagggccag
300
cagctcagcc aaggggccga tgggctggcc agcggggtgg cgacctacac cgatggcacg
360
gggaaggtcg tcgacggcat cgggcagctg tcggctggtt tgacgacgat ggatgagaag
420
atcgctgcgg ctaccgggaa aatcgatccc tcccagctcg acaaactcgc cggtggggcc
480
ggacagcttg ctgatggcat cgaccagttc accggcaatc tggtgggtta tcgtactgag
540
atccgccagt acgcgt
556

<210> 1506
<211> 169
<212> PRT
<213> Homo sapiens

<400> 1506
Met Ser Thr Leu Val Ser Ile Gly Leu Pro Asn Arg Trp Pro Gly Trp
1 5 10 15
Pro Ala Pro Arg Arg Asn Trp Thr Thr Gly Ala Pro Lys Leu Ala Asp
20 25 30
Gly Thr Lys Pro Ser Ser Pro Gly Ala Thr Thr Leu Ala Ser Xaa Met
35 40 45
Thr Lys Leu Ser Gly Gly Ala Gln Arg Leu Ser Ala Asn Gly Gly Lys
50 55 60
Leu Thr Asp Gly Val Ser Gln Leu Ser Gly Gly Leu Thr Thr Leu Ser
65 70 75 80
His Lys Gly Gln Gln Leu Ser Gln Gly Ala Asp Gly Leu Ala Ser Gly
85 90 95
Val Ala Thr Tyr Thr Asp Gly Thr Gly Lys Val Val Asp Gly Ile Gly
100 105 110
Gln Leu Ser Ala Gly Leu Thr Thr Met Asp Glu Lys Ile Ala Ala Ala
115 120 125
Thr Gly Lys Ile Asp Pro Ser Gln Leu Asp Lys Leu Ala Gly Gly Ala

```
    130                 135                 140
Gly Gln Leu Ala Asp Gly Ile Asp Gln Phe Thr Gly Asn Leu Val Gly
145                 150                 155                 160
Tyr Arg Thr Glu Ile Arg Gln Tyr Ala
                165
```

<210> 1507
<211> 667
<212> DNA
<213> Homo sapiens

<400> 1507
agatctctta agatgtgctc attatcatga gaacagcgtg gaggaaacca cccccaggat
60
ccagttacct ccacttgtcc tgcccttggc acgtggggct tatggggatt acaattcaag
120
gtgagacttg ggtggggaca cagtggaaca tgaagtgtgc cacgctgggt ggatgacgcc
180
ctcctccccc cgccaccgag agctgcaggc cacatgattc cttttgggta gcactcggga
240
aagggcagaa tgtacaggaa cagagtgaga ttcgcagggc ctggggctga gggaggggac
300
gcactagagg aaggcaaagg ggagcctcct gggtgtgggg agcactttct gtcttggttt
360
tggtggtggc tgcacagtgg cccacacccg tcagagctca cctgcctgca cccaggccct
420
ccgtgcaccc tggcagccca gatgactgca ccagcccagg ggaggtggag gaatgccaca
480
cgcaccggta cctggggacc gggggtcctc ggtgatcatc ccgagctcca agacagaagc
540
tggactacag ccgtgctgag tggaggggtt tggtggctgg gtgcccgcct cctattgctc
600
ctgcagactc tggggtctcg ggcgccccca gtggggcaat gtgggctgct gcagggaact
660
cacgcgt
667

<210> 1508
<211> 139
<212> PRT
<213> Homo sapiens

<400> 1508
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Met Tyr Arg Asn Arg Val Arg Phe Ala Gly Pro Gly Ala Glu Gly Gly
 1               5                  10                  15
Asp Ala Leu Glu Glu Gly Lys Gly Glu Pro Pro Gly Cys Gly Glu His
            20                  25                  30
Phe Leu Ser Trp Phe Trp Trp Trp Leu His Ser Gly Pro His Pro Ser
        35                  40                  45
Glu Leu Thr Cys Leu His Pro Gly Pro Pro Cys Thr Leu Ala Ala Gln
    50                  55                  60
Met Thr Ala Pro Ala Gln Gly Arg Trp Arg Asn Ala Thr Arg Thr Gly
65                  70                  75                  80
Thr Trp Gly Pro Gly Val Leu Gly Asp His Pro Glu Leu Gln Asp Arg
```

```
                85                  90                  95
Ser Trp Thr Thr Ala Val Leu Ser Gly Gly Val Trp Trp Leu Gly Ala
            100                 105                 110
Arg Leu Leu Leu Leu Leu Gln Thr Leu Gly Ser Arg Ala Pro Pro Val
        115                 120                 125
Gly Gln Cys Gly Leu Leu Gln Gly Thr His Ala
    130                 135
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<210> 1509
<211> 463
<212> DNA
<213> Homo sapiens

<400> 1509
tgatcagagt ggctgagcaa cttgctcaag atcacagttt cagaagtacg ctctaagctg
60
ggtctggctg actccaaagt tgtggctttt gttggttttc ttgttctgtc gcgttttaga
120
aagggctagg aaccgagcac tgggcgttgg gcttactctc ctcctatggt gacctgggag
180
tggtgcccaa ggcgctctct tcccagcacc tcagggtcct cactggtaaa ggagggagtg
240
attggaatgt cgccaaagtt acttggctct ggaattctgt ggctattcac gtggactctg
300
gatggcggtc accaagtaga agaggggccc tgggatagag agaagtctcc tctcctgctc
360
ctgatttccc aggcctctcc ctctcctggc cctccctcct ttcttccact tccccggatt
420
cccttcgagt ttggttgcaa ctttaatttt nngttccgat tca
463

<210> 1510
<211> 99
<212> PRT
<213> Homo sapiens

<400> 1510

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Met Val Thr Trp Glu Trp Cys Pro Arg Arg Ser Leu Pro Ser Thr Ser
 1               5                  10                  15
Gly Ser Ser Leu Val Lys Glu Gly Val Ile Gly Met Ser Pro Lys Leu
            20                  25                  30
Leu Gly Ser Gly Ile Leu Trp Leu Phe Thr Trp Thr Leu Asp Gly Gly
        35                  40                  45
His Gln Val Glu Glu Gly Pro Trp Asp Arg Glu Lys Ser Pro Leu Leu
    50                  55                  60
Leu Leu Ile Ser Gln Ala Ser Pro Ser Pro Gly Pro Pro Ser Phe Leu
65                  70                  75                  80
Pro Leu Pro Arg Ile Pro Phe Glu Phe Gly Cys Asn Phe Asn Phe Xaa
                85                  90                  95
Phe Arg Phe
```

<210> 1511
<211> 633

<212> DNA
<213> Homo sapiens

<400> 1511
gccggcaccg gcgtcaaggc catggcgctg ggcccgggat gggtacacac cgaattccac
60
tcacgcgcca acgtcaccgg caaccatctg ccggactttt tctggatcga cgccgaagtt
120
ctggtacgcg aggctctcaa cgaccttgac catgacaagg tagtatccat tcctaccccg
180
ctctggaagt tcttcatcgc agtggccaca catacccccac gttccgctat gagattcctg
240
tcacgaactc tgtcctcgtc tcgagacaag gacgaccatc ctcgacacac tccgggaggc
300
gaggcctgag atggccagcg tcaaacccac taaggaccgg ggccggtaca ccaatgatct
360
gtccgccgcg acgcggcagg cagcgaacat gcttctgctg cgtcctttgg tgtggaaagt
420
cgtcaaagtg agcgtccacg gagccgacaa cctcgacggg ctcgacggtg ccttacgtcg
480
ccgtcgctaa ccattcctcc cacctcgacg cgccgctcgt ttttggggcc cttcccaagc
540
ggctgtcaaa gtacctagct accggggccg ctgctgacta tttcttcacc gtctggtgga
600
aggccatcgc tccggtgctc ttcttcaacg cgt
633

<210> 1512
<211> 102
<212> PRT
<213> Homo sapiens

<400> 1512
Ala Gly Thr Gly Val Lys Ala Met Ala Leu Gly Pro Gly Trp Val His
1 5 10 15
Thr Glu Phe His Ser Arg Ala Asn Val Thr Gly Asn His Leu Pro Asp
20 25 30
Phe Phe Trp Ile Asp Ala Glu Val Leu Val Arg Glu Ala Leu Asn Asp
35 40 45
Leu Asp His Asp Lys Val Val Ser Ile Pro Thr Pro Leu Trp Lys Phe
50 55 60
Phe Ile Ala Val Ala Thr His Thr Pro Arg Ser Ala Met Arg Phe Leu
65 70 75 80
Ser Arg Thr Leu Ser Ser Ser Arg Asp Lys Asp Asp His Pro Arg His
85 90 95
Thr Pro Gly Gly Glu Ala
100

<210> 1513
<211> 401
<212> DNA
<213> Homo sapiens

<400> 1513

acgcgtgaag gggtggaatt tcaccacaga ggggacgccg gggttcctgt tcagaaatat
60
ttggtcgtcc aatctcgtaa tgcccttctg aatgacttgc tgggcctgcc tcctgacacg
120
gctgtttcgc aggaaccgcc actcccgctc cttgcggatc tgactctcca ggtcgtgctc
180
ttctgggatc ttcatgacgg gctgggtaaa atagccgggc gctccagtcg cagaaccccg
240
tctgcaccgt ggcggagatg aaacttttgt gtccagcagc atcgtccgcg tcgtccgcag
300
tctgctctgg gcccttgtcg aacatcttcc gtgtccgggg gaactggtgg gagtgagggg
360
tgtactgcgc cccagcgggg cctgtggtgc ccggccggcc g
401

<210> 1514
<211> 108
<212> PRT
<213> Homo sapiens

<400> 1514
Met Phe Asp Lys Gly Pro Glu Gln Thr Ala Asp Asp Ala Asp Asp Ala
1 5 10 15
Ala Gly His Lys Ser Phe Ile Ser Ala Thr Val Gln Thr Gly Phe Cys
20 25 30
Asp Trp Ser Ala Arg Leu Phe Tyr Pro Ala Arg His Glu Asp Pro Arg
35 40 45
Arg Ala Arg Pro Gly Glu Ser Asp Pro Gln Gly Ala Gly Val Ala Val
50 55 60
Pro Ala Lys Gln Pro Cys Gln Glu Ala Gly Pro Ala Ser His Ser Glu
65 70 75 80
Gly His Tyr Glu Ile Gly Arg Pro Asn Ile Ser Glu Gln Glu Pro Arg
85 90 95
Arg Pro Leu Cys Gly Glu Ile Pro Pro Leu His Ala
100 105

<210> 1515
<211> 720
<212> DNA
<213> Homo sapiens

<400> 1515
nnggatcctg accgcggcat gaggttcaac cctgccaagc tattgctcga cccttatgcc
60
agggccatca cggcaggagt cgattatcac ggcccgatta tggaccacac gccggaatcc
120
aactacgagc ctgacctgac cgacgatgcg acgtcggtcc cgctcgccgt cgtcattgac
180
gatcccggcc cgcctacgcc tattgcgcgc cgccacgaca tcagcgaatc gggcatctat
240
gagacccatg tcaaagggct aacccgcctt caccccctcg ttcctgagca tcttcgcagc
300
acctatgccg ggcttgccta tccggctgtt atcgaacacc tcaagtcaat cggagtaaca
360

gccatcgaac tactacccgt ccagcagttc gtctccgaac cattcatcgt tgggcgcggc
420
ttatccgatt actggggtta caacaccctg gggttctttg cgccgcatgc tgcctactgc
480
tccgtcggct cgatgggaac ccaggtgcgc gagttcaagg acatggtgac gtctttccac
540
gaagccggca tcgaggtttt cctcgatgtc gtctacaacc acactggtga gggcggccat
600
gaaggaccga ctctgtcttt ccgcggcatc gatcacgagt cttattaccg cctcaccaac
660
gatcaccgca atgactatga cgtcaccggt tgtggcaatt ctgtcgacac ctcccatccg
720

<210> 1516
<211> 240
<212> PRT
<213> Homo sapiens

<400> 1516
Xaa Asp Pro Asp Arg Gly Met Arg Phe Asn Pro Ala Lys Leu Leu Leu
 1   5   10   15
Asp Pro Tyr Ala Arg Ala Ile Thr Ala Gly Val Asp Tyr His Gly Pro
            20   25   30
Ile Met Asp His Thr Pro Glu Ser Asn Tyr Glu Pro Asp Leu Thr Asp
        35   40   45
Asp Ala Thr Ser Val Pro Leu Ala Val Val Ile Asp Asp Pro Gly Pro
    50   55   60
Pro Thr Pro Ile Ala Arg Arg His Asp Ile Ser Glu Ser Gly Ile Tyr
65   70   75   80
Glu Thr His Val Lys Gly Leu Thr Arg Leu His Pro Leu Val Pro Glu
                85   90   95
His Leu Arg Ser Thr Tyr Ala Gly Leu Ala Tyr Pro Ala Val Ile Glu
            100   105   110
His Leu Lys Ser Ile Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln
        115   120   125
Gln Phe Val Ser Glu Pro Phe Ile Val Gly Arg Gly Leu Ser Asp Tyr
    130   135   140
Trp Gly Tyr Asn Thr Leu Gly Phe Phe Ala Pro His Ala Ala Tyr Cys
145   150   155   160
Ser Val Gly Ser Met Gly Thr Gln Val Arg Glu Phe Lys Asp Met Val
                165   170   175
Thr Ser Phe His Glu Ala Gly Ile Glu Val Phe Leu Asp Val Val Tyr
            180   185   190
Asn His Thr Gly Glu Gly Gly His Glu Gly Pro Thr Leu Ser Phe Arg
        195   200   205
Gly Ile Asp His Glu Ser Tyr Tyr Arg Leu Thr Asn Asp His Arg Asn
    210   215   220
Asp Tyr Asp Val Thr Gly Cys Gly Asn Ser Val Asp Thr Ser His Pro
225   230   235   240

<210> 1517
<211> 497
<212> DNA
<213> Homo sapiens

<400> 1517
nnacgcgtga agggggttcg ggaggaggac gccctgctgg agaacgggag ccagagcaac
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gaaagtgacg acgtcagcac agaccgtggc cctgcgccac cttccccgct caaggagacc
120
tccttttcca tcgggctgca agtactgttt ccattcctcc tggcaggctt tgggaccgtg
180
gctgctggca tggtgttgga catcgtgcag cactgggaag tcttccagaa ggtgacagag
240
gtcttcatcc tagtgcctgc gctgctgggg ctcaaaggga acctggaaat gaccctggca
300
tcaaggcttt ccactgcagc caacattgga cacatggaca cacccaagga gctctggcgg
360
atgatcactg ggaacatggc cctcatccag gtgcaggccc cggtggtggg cttcctggcg
420
tccatcgcag ccgtcgtctt tggctggatc cctgatggcc acttcagtat tccgcacgcc
480
ttcctgctct gtggtag
497

<210> 1518
<211> 165
<212> PRT
<213> Homo sapiens

<400> 1518
Xaa Arg Val Lys Gly Val Arg Glu Glu Asp Ala Leu Leu Glu Asn Gly
1 5 10 15
Ser Gln Ser Asn Glu Ser Asp Asp Val Ser Thr Asp Arg Gly Pro Ala
20 25 30
Pro Pro Ser Pro Leu Lys Glu Thr Ser Phe Ser Ile Gly Leu Gln Val
35 40 45
Leu Phe Pro Phe Leu Leu Ala Gly Phe Gly Thr Val Ala Ala Gly Met
50 55 60
Val Leu Asp Ile Val Gln His Trp Glu Val Phe Gln Lys Val Thr Glu
65 70 75 80
Val Phe Ile Leu Val Pro Ala Leu Leu Gly Leu Lys Gly Asn Leu Glu
85 90 95
Met Thr Leu Ala Ser Arg Leu Ser Thr Ala Ala Asn Ile Gly His Met
100 105 110
Asp Thr Pro Lys Glu Leu Trp Arg Met Ile Thr Gly Asn Met Ala Leu
115 120 125
Ile Gln Val Gln Ala Pro Val Val Gly Phe Leu Ala Ser Ile Ala Ala
130 135 140
Val Val Phe Gly Trp Ile Pro Asp Gly His Phe Ser Ile Pro His Ala
145 150 155 160
Phe Leu Leu Cys Gly
165

<210> 1519
<211> 2076
<212> DNA
<213> Homo sapiens

<400> 1519
nnagatcttt gggggattca acgagtggaa aatgcacgat ttctttcacc agaagaaaat
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gtgtgcaatg agatgttggt aaaatcccag tttgttgctt gtatggctac ttgtcattca
120
cttacaaaaa ttgaaggagt gctctctggt gatccacttg atctgaaaat gtttgaggct
180
attggatgga ttctggaaga agcaactgaa gaagaaacag cacttcataa tcgaattatg
240
cccacagtgg ttcgtcctcc caaacaactg cttcctgaat ctacccctgc aggaaaccaa
300
gaaatggagc tgtttgaact tccagctact tatgagatag gaattgttcg ccagttccca
360
ttttcttctg ctttgcaacg tatgagtgtg gttgccaggg tgctggggga taggaaaatg
420
gacgcctaca tgaagggagc gcccgaggcc attgccggtc tctgtaaacc tgaaacagtt
480
cctgtcgatt ttcaaaacgt tttggaagac ttcactaaac agggcttccg tgtgattgct
540
cttgcacaca gaaaattgga gtcaaaactg acatggcata aagtacagaa tattagcaga
600
gatgcaattg agaacaacat ggattttatg ggattaatta taatgcagaa caaattaaag
660
caagaaaccc ctgcagtact tgaagatttg cataaagcca acattcgcac cgtcatggtc
720
acaggtgaca gtatgttgac tgctgtctct gtggccagag attgtggaat gattctacct
780
caggataaag tgattattgc tgaagcatta cctccaaagg atgggaaagt tgccaaaata
840
aattggcatt atgcagactc cctcacgcag tgcagtcatc catcagcaat tgacccagag
900
gctattccgg ttaaattggt ccatgatagc ttagaggatc ttcaaatgac tcgttatcat
960
tttgcaatga atggaaaatc attctcagtg atactggagc attttcaaga ccttgttcct
1020
aagttgatgt tgcatggcac cgtgtttgcc cgtatggcac ctgatcagaa gacacagttg
1080
atagaagcat tgcaaaatgt tgattatttt gttgggatgt gtggtgatgg cgcaaatgat
1140
tgtggtgctt tgaagagggc acacggaggc atttccttat cggagctcga agcttcagtg
1200
gcatctccct ttacctctaa gactcctagt atttcctgtg tgccaaacct tatcagggaa
1260
ggccgtgctg ctttaataac ttccttctgt gtgtttaaat tcatggcatt gtacagcatt
1320
atccagtact tcagtgttac tctgctgtat tctatcttaa gtaacctagg agacttccag
1380
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1440
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1500
ttctccgttt tgtctcagat tatcatctgc attggatttc aatctttggg ttttttttgg
1560

gtcaaacagc aaccttggta tgaagtgtgg catccaaaat cagatgcttg taatacaaca
1620
ggaagcgggt tttggaattc ttcacacgta gacaatgaaa ccgaacttga tgaacataat
1680
atacaaaatt atgaaaatac cacagtgttt tttatttcca gttttcagta cctcatagtg
1740
gcaattgcct tttcaaaagg aaaacccttc aggcaacctt gctacaaaaa ttatttttt
1800
gtttttttctg tgatttttt atatattttt atattattca tcatgttgta tccagttgcc
1860
tctgttgacc aggttcttca gatagtgtgt gtaccatatc agtggcgtgt aactatgctc
1920
atcattgttc ttgtcaatgc ctttgtgtct atcacagtgg agaacttctt ccttgacatg
1980
gtcctttgga aagttgtgtt caaccgagac aaacaaggag agtatcggtt cagcaccaca
2040
cagccaccgc aggagtcagt ggatcggtgg ggaaaa
2076

<210> 1520
<211> 692
<212> PRT
<213> Homo sapiens

<400> 1520
Xaa Asp Leu Trp Gly Ile Gln Arg Val Glu Asn Ala Arg Phe Leu Ser
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Pro Glu Glu Asn Val Cys Asn Glu Met Leu Val Lys Ser Gln Phe Val
20 25 30
Ala Cys Met Ala Thr Cys His Ser Leu Thr Lys Ile Glu Gly Val Leu
35 40 45
Ser Gly Asp Pro Leu Asp Leu Lys Met Phe Glu Ala Ile Gly Trp Ile
50 55 60
Leu Glu Glu Ala Thr Glu Glu Glu Thr Ala Leu His Asn Arg Ile Met
65 70 75 80
Pro Thr Val Val Arg Pro Pro Lys Gln Leu Leu Pro Glu Ser Thr Pro
85 90 95
Ala Gly Asn Gln Glu Met Glu Leu Phe Glu Leu Pro Ala Thr Tyr Glu
100 105 110
Ile Gly Ile Val Arg Gln Phe Pro Phe Ser Ser Ala Leu Gln Arg Met
115 120 125
Ser Val Val Ala Arg Val Leu Gly Asp Arg Lys Met Asp Ala Tyr Met
130 135 140
Lys Gly Ala Pro Glu Ala Ile Ala Gly Leu Cys Lys Pro Glu Thr Val
145 150 155 160
Pro Val Asp Phe Gln Asn Val Leu Glu Asp Phe Thr Lys Gln Gly Phe
165 170 175
Arg Val Ile Ala Leu Ala His Arg Lys Leu Glu Ser Lys Leu Thr Trp
180 185 190
His Lys Val Gln Asn Ile Ser Arg Asp Ala Ile Glu Asn Asn Met Asp
195 200 205
Phe Met Gly Leu Ile Ile Met Gln Asn Lys Leu Lys Gln Glu Thr Pro
210 215 220
Ala Val Leu Glu Asp Leu His Lys Ala Asn Ile Arg Thr Val Met Val

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225                 230                 235                 240
Thr Gly Asp Ser Met Leu Thr Ala Val Ser Val Ala Arg Asp Cys Gly
                245                 250                 255
Met Ile Leu Pro Gln Asp Lys Val Ile Ile Ala Glu Ala Leu Pro Pro
            260                 265                 270
Lys Asp Gly Lys Val Ala Lys Ile Asn Trp His Tyr Ala Asp Ser Leu
        275                 280                 285
Thr Gln Cys Ser His Pro Ser Ala Ile Asp Pro Glu Ala Ile Pro Val
    290                 295                 300
Lys Leu Val His Asp Ser Leu Glu Asp Leu Gln Met Thr Arg Tyr His
305                 310                 315                 320
Phe Ala Met Asn Gly Lys Ser Phe Ser Val Ile Leu Glu His Phe Gln
                325                 330                 335
Asp Leu Val Pro Lys Leu Met Leu His Gly Thr Val Phe Ala Arg Met
            340                 345                 350
Ala Pro Asp Gln Lys Thr Gln Leu Ile Glu Ala Leu Gln Asn Val Asp
        355                 360                 365
Tyr Phe Val Gly Met Cys Gly Asp Gly Ala Asn Asp Cys Gly Ala Leu
    370                 375                 380
Lys Arg Ala His Gly Gly Ile Ser Leu Ser Glu Leu Glu Ala Ser Val
385                 390                 395                 400
Ala Ser Pro Phe Thr Ser Lys Thr Pro Ser Ile Ser Cys Val Pro Asn
                405                 410                 415
Leu Ile Arg Glu Gly Arg Ala Ala Leu Ile Thr Ser Phe Cys Val Phe
            420                 425                 430
Lys Phe Met Ala Leu Tyr Ser Ile Ile Gln Tyr Phe Ser Val Thr Leu
        435                 440                 445
Leu Tyr Ser Ile Leu Ser Asn Leu Gly Asp Phe Gln Phe Leu Phe Ile
    450                 455                 460
Asp Leu Ala Ile Ile Leu Val Val Val Phe Thr Met Ser Leu Asn Pro
465                 470                 475                 480
Ala Trp Lys Glu Leu Val Ala Gln Arg Pro Pro Ser Gly Leu Ile Ser
                485                 490                 495
Gly Ala Leu Leu Phe Ser Val Leu Ser Gln Ile Ile Ile Cys Ile Gly
            500                 505                 510
Phe Gln Ser Leu Gly Phe Phe Trp Val Lys Gln Gln Pro Trp Tyr Glu
        515                 520                 525
Val Trp His Pro Lys Ser Asp Ala Cys Asn Thr Thr Gly Ser Gly Phe
    530                 535                 540
Trp Asn Ser Ser His Val Asp Asn Glu Thr Glu Leu Asp Glu His Asn
545                 550                 555                 560
Ile Gln Asn Tyr Glu Asn Thr Thr Val Phe Phe Ile Ser Ser Phe Gln
                565                 570                 575
Tyr Leu Ile Val Ala Ile Ala Phe Ser Lys Gly Lys Pro Phe Arg Gln
            580                 585                 590
Pro Cys Tyr Lys Asn Tyr Phe Phe Val Phe Ser Val Ile Phe Leu Tyr
        595                 600                 605
Ile Phe Ile Leu Phe Ile Met Leu Tyr Pro Val Ala Ser Val Asp Gln
    610                 615                 620
Val Leu Gln Ile Val Cys Val Pro Tyr Gln Trp Arg Val Thr Met Leu
625                 630                 635                 640
Ile Ile Val Leu Val Asn Ala Phe Val Ser Ile Thr Val Glu Asn Phe
                645                 650                 655
Phe Leu Asp Met Val Leu Trp Lys Val Val Phe Asn Arg Asp Lys Gln
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660 665 670
Gly Glu Tyr Arg Phe Ser Thr Thr Gln Pro Pro Gln Glu Ser Val Asp
675 680 685
Arg Trp Gly Lys
690

<210> 1521
<211> 373
<212> DNA
<213> Homo sapiens

<400> 1521
acgcgtcaca gctgaagccc gcagtgatag ccgacgcaca agccgaatca ataacttgtg
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tctgcacgcg ctgggcctca acgagtagtt cagcaaaagt aggcggaaca ggcgcaacga
120
gcgtaccatc cgatacacgc cagccttgac tgctgataca ccccagccac tgcgcatcag
180
tgatttcaat ggcggttaca cagtctggta tcggactgtc gatatcatcg taataggcga
240
tcacattccc atttgcatcg tatgctgcga acttttgacc catgattatt atttcccgaa
300
tgcaaaccaa taaacagtgt tggcgcttga tgaatagccg ttctgcacca cggcggtaga
360
gagtggcgtc gac
373

<210> 1522
<211> 94
<212> PRT
<213> Homo sapiens

<400> 1522
Met Gly Gln Lys Phe Ala Ala Tyr Asp Ala Asn Gly Asn Val Ile Ala
1 5 10 15
Tyr Tyr Asp Asp Ile Asp Ser Pro Ile Pro Asp Cys Val Thr Ala Ile
20 25 30
Glu Ile Thr Asp Ala Gln Trp Leu Gly Cys Ile Ser Ser Gln Gly Trp
35 40 45
Arg Val Ser Asp Gly Thr Leu Val Ala Pro Val Pro Pro Thr Phe Ala
50 55 60
Glu Leu Leu Val Glu Ala Gln Arg Val Gln Thr Gln Val Ile Asp Ser
65 70 75 80
Ala Cys Ala Ser Ala Ile Thr Ala Gly Phe Ser Cys Asp Ala
85 90

<210> 1523
<211> 525
<212> DNA
<213> Homo sapiens

<400> 1523
nnacgcgtgc ggtcaatatg ccgccattcc cataagcgct tggtggcatg tttccagggc
60

cagcatggca ccgatgccga gaggagacac aaaaaactgc ctctgacagc tcttgctcaa
120
aatatgcaag aagcatcgac tcagctggaa gactctctcc tggggaagat gctggagacg
180
tgtggagatg ctgagaatca gctggctctc gagctctccc agcacgaagt ctttgttgag
240
aaggagatcg tggaccctct gtacggcata gctgaggtgg agattcccaa catccagaag
300
cagaggaagc agcttgcaag attggtgtta gactgggatt cagtcagagc caggtggaac
360
caagctcaca aatcctcagg aaccaacttt caggggcttc catcaaaaat agatactcta
420
aaggaaggga tggatgaagc tggaaataaa gtagaacagt gcaaggatca acttgcagca
480
gacatgtaca actttatggc caaagaaggg gagtatggca aattt
525

<210> 1524
<211> 175
<212> PRT
<213> Homo sapiens

<400> 1524
Xaa Arg Val Arg Ser Ile Cys Arg His Ser His Lys Arg Leu Val Ala
1 5 10 15
Cys Phe Gln Gly Gln His Gly Thr Asp Ala Glu Arg Arg His Lys Lys
20 25 30
Leu Pro Leu Thr Ala Leu Ala Gln Asn Met Gln Glu Ala Ser Thr Gln
35 40 45
Leu Glu Asp Ser Leu Leu Gly Lys Met Leu Glu Thr Cys Gly Asp Ala
50 55 60
Glu Asn Gln Leu Ala Leu Glu Leu Ser Gln His Glu Val Phe Val Glu
65 70 75 80
Lys Glu Ile Val Asp Pro Leu Tyr Gly Ile Ala Glu Val Glu Ile Pro
85 90 95
Asn Ile Gln Lys Gln Arg Lys Gln Leu Ala Arg Leu Val Leu Asp Trp
100 105 110
Asp Ser Val Arg Ala Arg Trp Asn Gln Ala His Lys Ser Ser Gly Thr
115 120 125
Asn Phe Gln Gly Leu Pro Ser Lys Ile Asp Thr Leu Lys Glu Gly Met
130 135 140
Asp Glu Ala Gly Asn Lys Val Glu Gln Cys Lys Asp Gln Leu Ala Ala
145 150 155 160
Asp Met Tyr Asn Phe Met Ala Lys Glu Gly Glu Tyr Gly Lys Phe
165 170 175

<210> 1525
<211> 294
<212> DNA
<213> Homo sapiens

<400> 1525
gtgcacgagc gcatggatct catccgccaa agcgtggatg cgcgcattaa cgtggactac
60

tggtccggcc tgctcgtgga ctatacctcg cagcacggcg tcgacgtttt ggtcaagggg
120
ctgcgttctt ccctggacta tgaatatgaa ctgccgatgg cccagatgaa ccggcgttta
180
tctggcatcg atacggtctt tttgcttacc gatgaaaagt acggctacat cagctcatcg
240
ctgtgcaaac aggtcgcgca attcggcggt gaggtcaccg ggatgcttcg gatc
294

<210> 1526
<211> 98
<212> PRT
<213> Homo sapiens

<400> 1526
Val His Glu Arg Met Asp Leu Ile Arg Gln Ser Val Asp Ala Arg Ile
1 5 10 15
Asn Val Asp Tyr Trp Ser Gly Leu Leu Val Asp Tyr Thr Ser Gln His
20 25 30
Gly Val Asp Val Leu Val Lys Gly Leu Arg Ser Ser Leu Asp Tyr Glu
35 40 45
Tyr Glu Leu Pro Met Ala Gln Met Asn Arg Arg Leu Ser Gly Ile Asp
50 55 60
Thr Val Phe Leu Leu Thr Asp Glu Lys Tyr Gly Tyr Ile Ser Ser Ser
65 70 75 80
Leu Cys Lys Gln Val Ala Gln Phe Gly Gly Glu Val Thr Gly Met Leu
85 90 95
Arg Ile

<210> 1527
<211> 371
<212> DNA
<213> Homo sapiens

<400> 1527
tgtacaaacc cgcctatgag caagtgcaaa ccaacatgga aatgctcaag gccggacgca
60
gcttcaagga atacgccgag atggcctgga agattcccga gcattacaaa aacaaccgct
120
acttcgccct ggtgcacggg gttggcatga ccggcgagta cccttgggtg gtgcaccgcg
180
aagacattga cgcgctgggt tacgacggtg tgttcgaggc cggcatgacc atctgtgtgg
240
aaagctacat cggccacgac gacggcggcg aaggcgtgaa gctcgaagaa cagatctaca
300
tccacgaaca cagcatcgag ttgctctccg attatccgtt cgacccacgc ctgttgccgc
360
gctgaacgcg t
371

<210> 1528
<211> 109
<212> PRT

<213> Homo sapiens

<400> 1528
Met Glu Met Leu Lys Ala Gly Arg Ser Phe Lys Glu Tyr Ala Glu Met
1 5 10 15
Ala Trp Lys Ile Pro Glu His Tyr Lys Asn Asn Arg Tyr Phe Ala Leu
20 25 30
Val His Gly Val Gly Met Thr Gly Glu Tyr Pro Trp Val Val His Arg
35 40 45
Glu Asp Ile Asp Ala Leu Gly Tyr Asp Gly Val Phe Glu Ala Gly Met
50 55 60
Thr Ile Cys Val Glu Ser Tyr Ile Gly His Asp Asp Gly Gly Glu Gly
65 70 75 80
Val Lys Leu Glu Glu Gln Ile Tyr Ile His Glu His Ser Ile Glu Leu
85 90 95
Leu Ser Asp Tyr Pro Phe Asp Pro Arg Leu Leu Pro Arg
100 105

<210> 1529
<211> 609
<212> DNA
<213> Homo sapiens

<400> 1529
nacgcgtggt gctcaccctc cgtgtgactc gcgctctgtc cggctcaggg ctcgccctcc
60
gtgggacttg cgctctgtcc ggctcagggc tcgccctccg tgggacttgc gctctgtccg
120
gctcagggct cgccctccgt gggacttgcg ctctgtccgg ctcagggctc gccctccgtg
180
ggacttgcgc tctgtccggc tcagggctcg ccctccgtgg gacttgcgct ctgtccggct
240
cagggctcgc cctccgtggg acttgcgctc tgtccggctc agggctcgcc ctccgtggga
300
tttgcgctct gtctggctca ggctgcgcag ggcaatggag gaacctcccg agcaggccca
360
gcggctcctt ccacccagcc cccatctccg gccggccatt tgtgaggccc tctgccactg
420
aggtgcactg tttccaattc ctcattcaca agctctacct tccacgagcc cagagcatga
480
acgcattcgg ccatggtcct caccactctg cgaggagcac agcctcttct ccaccgtcca
540
atagcgtgtt cctcctttcc caggcctcac agaatgctct gtccgcatcc tcccagcatt
600
ccattcacg
609

<210> 1530
<211> 125
<212> PRT
<213> Homo sapiens

<400> 1530
Leu Ala Leu Cys Pro Ala Gln Gly Ser Pro Ser Val Gly Leu Ala Leu

```
 1               5                  10                  15
Cys Pro Ala Gln Gly Ser Pro Ser Val Gly Leu Ala Leu Cys Pro Ala
            20                  25                  30
Gln Gly Ser Pro Ser Val Gly Leu Ala Leu Cys Pro Ala Gln Gly Ser
        35                  40                  45
Pro Ser Val Gly Leu Ala Leu Cys Pro Ala Gln Gly Ser Pro Ser Val
    50                  55                  60
Gly Leu Ala Leu Cys Pro Ala Gln Gly Ser Pro Ser Val Gly Leu Ala
65                  70                  75                  80
Leu Cys Pro Ala Gln Gly Ser Pro Ser Val Gly Phe Ala Leu Cys Leu
                85                  90                  95
Ala Gln Ala Ala Gln Gly Asn Gly Gly Thr Ser Arg Ala Gly Pro Ala
            100                 105                 110
Ala Pro Ser Thr Gln Pro Pro Ser Pro Ala Gly His Leu
        115                 120                 125
```

<210> 1531
<211> 726
<212> DNA
<213> Homo sapiens

<400> 1531
accggtcgcc ggcttgtcga gggtaacctt ctggccacag ttggtgatgg tgataggtcc
60
agcgttggac tgggacgccg acgctgaaaa agaagctgac gagtccttgg gggcgcccgc
120
acattcggca agcatgagga cggggagcat cgagaccgcg acagctcggc gaaggaattt
180
cggggtggca ggcatggcga aactagcttt ctgtgatcgg cgtgcgcggc cgggcaacaa
240
cagggcgtcg tcaggtggtc ttcgggctcg acttcgtctc cgttcccggc accttcccag
300
tgcgcatggc caggtggttc aagtcggggc ggatcagtca taccgctgcg ctcagctccg
360
gcttttcacc ggattccagc gctggtgtgg tcaccagcaa cctgacgcga ggattttagc
420
acccccttcg cataccgcta tccagggcct ccacgacagc ggcaccgatg acgatcgcgt
480
tcaccgagcg cggcgttttc ggcagcttcc acatggggat cagaccatat tgatgcactg
540
gcgatccctt catacgcgag ccgccgatat ggcccccgag tgaggcccct cagttcgcgc
600
tgacgcatgc cgctctgcgc agcctgccaa cgctttcccg caacctcacc acacgtttgc
660
cgggttcggg gctggcgacg tgagccgtgt cacaagttca cgagctggct cacccgtccg
720
cgagag
726

<210> 1532
<211> 178
<212> PRT
<213> Homo sapiens

<400> 1532
Met Val Ile Gly Pro Ala Leu Asp Trp Asp Ala Asp Ala Glu Lys Glu
1 5 10 15
Ala Asp Glu Ser Leu Gly Ala Pro Ala His Ser Ala Ser Met Arg Thr
20 25 30
Gly Ser Ile Glu Thr Ala Thr Ala Arg Arg Arg Asn Phe Gly Val Ala
35 40 45
Gly Met Ala Lys Leu Ala Phe Cys Asp Arg Arg Ala Arg Pro Gly Asn
50 55 60
Asn Arg Ala Ser Ser Gly Gly Leu Arg Ala Arg Leu Arg Leu Arg Ser
65 70 75 80
Arg His Leu Pro Ser Ala His Gly Gln Val Val Gln Val Gly Ala Asp
85 90 95
Gln Ser Tyr Arg Cys Ala Gln Leu Arg Leu Phe Thr Gly Phe Gln Arg
100 105 110
Trp Cys Gly His Gln Gln Pro Asp Ala Arg Ile Leu Ala Pro Pro Ser
115 120 125
His Thr Ala Ile Gln Gly Leu His Asp Ser Gly Thr Asp Asp Asp Arg
130 135 140
Val His Arg Ala Arg Arg Phe Arg Gln Leu Pro His Gly Asp Gln Thr
145 150 155 160
Ile Leu Met His Trp Arg Ser Leu His Thr Arg Ala Ala Asp Met Ala
165 170 175
Pro Glu

<210> 1533
<211> 364
<212> DNA
<213> Homo sapiens

<400> 1533
natatgctgg tcgatcatgt gcatcagatc gtccagtggc cggagcgcgg ctggctggcg
60
gagattattc acagcgaacg ggcgaccggc ggtgcgccgc ttaacgtcct gctgacgctg
120
gttaaaatgc acgtcggctt gccgttgcag gcggtcggtc ttatcggcga agacagcgat
180
ggcgattaca ttatggcgat gctcgaccag taccacgtca atcgccagcg ggtacagcgc
240
accacgtttg cccccacgtc gatgtcgcag gtgatgaccg atcccactgg gcagcgcacc
300
tttttccatt cgcctgccgc caatcgcctg ctcgatctcc ccgcctttga tcgactcgac
360
gcgt
364

<210> 1534
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1534
Xaa Met Leu Val Asp His Val His Gln Ile Val Gln Trp Pro Glu Arg

```
 1               5                  10                  15
Gly Trp Leu Ala Glu Ile Ile His Ser Glu Arg Ala Thr Gly Gly Ala
            20                  25                  30
Pro Leu Asn Val Leu Leu Thr Leu Val Lys Met His Val Gly Leu Pro
        35                  40                  45
Leu Gln Ala Val Gly Leu Ile Gly Glu Asp Ser Asp Gly Asp Tyr Ile
    50                  55                  60
Met Ala Met Leu Asp Gln Tyr His Val Asn Arg Gln Arg Val Gln Arg
65                  70                  75                  80
Thr Thr Phe Ala Pro Thr Ser Met Ser Gln Val Met Thr Asp Pro Thr
                85                  90                  95
Gly Gln Arg Thr Phe Phe His Ser Pro Ala Ala Asn Arg Leu Leu Asp
            100                 105                 110
Leu Pro Ala Phe Asp Arg Leu Asp Ala
        115                 120
```

<210> 1535
<211> 369
<212> DNA
<213> Homo sapiens

<400> 1535
gaattcgggg ggctccggga atgaagtttc catttcgcaa gccttctgaa gcaaatccgc
60
caatccctgg ggcccgcggt gcgtgccggc cagcggccag tcctggcccg gaatgatcca
120
ctcgatatct tcggcagaca acgccagcag accgggccta tcgccgcggc ccatggctgc
180
aaaaaaactc ttcacagtct ggacattccc ttgtgtgctc atcgaaatct ctccatgtcc
240
tttacctggg atcgtgtccg atctcatcgg acgcgttgag gacctgctgg tgaggacggg
300
gtgtcggtga ttcagccgat atcgactttg catggcgatg tcccagctgc cggagccgtt
360
actggccac
369

<210> 1536
<211> 111
<212> PRT
<213> Homo sapiens

<400> 1536
```
Met Gln Ser Arg Tyr Arg Leu Asn His Arg His Pro Val Leu Thr Ser
 1               5                  10                  15
Arg Ser Ser Thr Arg Pro Met Arg Ser Asp Thr Ile Pro Gly Lys Gly
            20                  25                  30
His Gly Glu Ile Ser Met Ser Thr Gln Gly Asn Val Gln Thr Val Lys
        35                  40                  45
Ser Phe Phe Ala Ala Met Gly Arg Gly Asp Arg Pro Gly Leu Leu Ala
    50                  55                  60
Leu Ser Ala Glu Asp Ile Glu Trp Ile Ile Pro Gly Gln Asp Trp Pro
65                  70                  75                  80
Leu Ala Gly Thr His Arg Gly Pro Gln Gly Leu Ala Asp Leu Leu Gln
```

```
                85                  90                  95
Lys Ala Cys Glu Met Glu Thr Ser Phe Pro Glu Pro Pro Glu Phe
            100                 105                 110

<210> 1537
<211> 294
<212> DNA
<213> Homo sapiens

<400> 1537
ccactcgcgg cgcctcctga gccctctcgt gtgtcaggac gccagcatcc tgttcgtgtt
60
ctcggggctg ctgcacgtgt accagcggaa gatcggcagc caggaggaca cctgcttgtt
120
cctcacgcgc cccggggaga tggtgggcca gctggccgtg ctcaccgagg agacctcgtc
180
ggcgtggtgg agacactgac ccaccaggcc cgggcgacca cggtgcatgc cgttcgggac
240
tcagaattgg ccaagctgcc ggcaggagcc ctcacgtcca tcaagcgcag gtac
294

<210> 1538
<211> 98
<212> PRT
<213> Homo sapiens

<400> 1538
Pro Leu Ala Ala Pro Pro Glu Pro Ser Arg Val Ser Gly Arg Gln His
 1               5                  10                  15
Pro Val Arg Val Leu Gly Ala Ala Ala Arg Val Pro Ala Glu Asp Arg
            20                  25                  30
Gln Pro Gly Gly His Leu Leu Val Pro His Ala Pro Arg Gly Asp Gly
        35                  40                  45
Gly Pro Ala Gly Arg Ala His Arg Gly Asp Leu Val Gly Val Val Glu
    50                  55                  60
Thr Leu Thr His Gln Ala Arg Ala Thr Thr Val His Ala Val Arg Asp
65                  70                  75                  80
Ser Glu Leu Ala Lys Leu Pro Ala Gly Ala Leu Thr Ser Ile Lys Arg
                85                  90                  95
Arg Tyr


<210> 1539
<211> 1015
<212> DNA
<213> Homo sapiens

<400> 1539
acgcgttcgg gcgtcaggca cacgcatctc aacagatgtg gctgacaccc aaggcagtcg
60
gcctcagtgc cctgtcaccc acctagaacc tgttcacagc atgtcatccg ggctgctctg
120
gccttgactg gacatgatta tttatcctta cacaccgtgg ctgctctaca ggccaagaaa
180
```

caggctgctc agccagggtc aggagaaggt gggtcaggct ccccggggac ctcaggccct
240
gacgcatcct ggcctcaccc taggcctcct ctgtcggggc agcctggctc agcagagccc
300
gggacacacg gctgaggcca cccaggctgg gccatcttgc ccctgttttg tgcccctac
360
tcagttctcc ttctgtcctg gctcaggtct aggccagtca agagggtggc tgagaagcag
420
gaggagcctc agagaccctc ccctcgaaag cactggggct tccacctcac aagcggcagg
480
ttcgctttgg gagctgctgg tccatcgccc aggcctggcc aggggcaggc gaggatcctg
540
gttgccgatc catcgtccag gcctggccca ggagccggtg aggaacctgg ggctgttgtg
600
caggggtcgc cgtctccagc tctctgccgt ggtgagggga ttgtgctgtg tgcacaccac
660
ctggctgcat cgaatcccac catggcccag agggtggacc tgtggctcct tgggggggca
720
gcatccccag tctaatgggt gcccctgcca ctctcctgag ttcccgtgca gagctccccc
780
caacacctca gccttcacct ttctcagtta atcaaaagat tccaaaaaaa gcaaacccat
840
cagaacggct tcctccaccg agtgttcagg ataaataatc atgtccagtc aaggccagag
900
cagcccggat gacatgctat gaacaggttt taggtgggtg acagggcact gaggccgact
960
gccttgggtg tcagccacat ctgttgagat gcgtgtgcct gacgcccgaa cgcgt
1015

<210> 1540
<211> 89
<212> PRT
<213> Homo sapiens

<400> 1540
His Pro Arg Gln Ser Ala Ser Val Pro Cys His Pro Pro Arg Thr Cys
1 5 10 15
Ser Gln His Val Ile Arg Ala Ala Leu Ala Leu Thr Gly His Asp Tyr
20 25 30
Leu Ser Leu His Thr Val Ala Ala Leu Gln Ala Lys Lys Gln Ala Ala
35 40 45
Gln Pro Gly Ser Gly Glu Gly Gly Ser Gly Ser Pro Gly Thr Ser Gly
50 55 60
Pro Asp Ala Ser Trp Pro His Pro Arg Pro Pro Leu Ser Gly Gln Pro
65 70 75 80
Gly Ser Ala Glu Pro Gly Thr His Gly
85

<210> 1541
<211> 1482
<212> DNA
<213> Homo sapiens

<400> 1541

cgccgatcac ggggagcccc tcgactgcct cccagaacaa agtgggaaag ggaagcttag
60
cccgccgctg ccgcctccga gcagcccgcc aggactctgg ctactggaga tgggcgcccg
120
gctatcgcgg cgacgggtgc cggcggaccc gtccctggcc ctggacgcgc tgcccccgga
180
gctgctggtg caggtgctga gccacgtgcc ggccacgctc cttggacacg cgatgccgcc
240
cagtgtgccg cgcctggcgc gacatagtgg acgggcccac tgggaggctg ctgcaactgg
300
cccgcgaccg cagcgccgag ggccgagcac tctacgcagt ggctcaacgc tgcctgccca
360
acaacgaaga caaagaggag ttcccgctgt gcgccctggc gcgctactga ctgcgcgcgc
420
ccttcggccg caatctcatc ttcaactcct gcggagagca gggcttcaga ggctgggagg
480
tggagcatgg cgggaacggc tgggccatag aaaagaacct aacaccggtg cctggggctc
540
cttcgcagac ctgcttcgtg acctctttcg aatggtgctc caagaggcag cttgtggacc
600
tggtgatgga aggggtgtgg caggagctgc tggacagcgc ccagattgag atctgtgtgg
660
ctgactggtg gggcgctcga gagaactgcg gctgcgtcta ccagctccgg gtccgccttc
720
tggatgtgta tgaaaaggaa gtggtcaagt tctcagcctc acctgacccg gtccttcagt
780
ggactgagag gggctgccga caggtctccc acgtcttcac caactttggc aagggcatcc
840
gctacgtatc ttttgagcag tacgggagag acgtgagttc ctgggtgggg cactatggcg
900
cccttgtgac ccactccagt gtgagggtca ggatccgtct gtcctagcga ctggactact
960
gcctgacgtt gtcagtcaag accagccttg cagccaggtg cagtggctca cacctgtggg
1020
atcctcccac tttggccttc caaaatgttg cgattatagg cgtgagccac tgtggctggc
1080
ctgaaatttt ctagtatcca cattcataaa gtaaaaagaa aataaaaagg catagaatgt
1140
caagctaacc aggcgtccgc tacttcagaa gagtgtactg tcgcatgggg agtctgtaac
1200
catgcttttc acttccactg catctctcgc tggctcaaaa cacgacaggt gtgtccattg
1260
gacaacagag agtgggaatt ccaaaagtat gggcactagg aaaagacttc ttccatcaag
1320
cttaattgtt ttgttattca tttaatgact ttccctgctg ttacctaatt acaaattgga
1380
tggaactgtg tttttttctg ctttgttttt tcagtttgct gtttctgtag ccatattgta
1440
ttctgtgtca aataaagtcc agttggattc tggaaaaaaa aa
1482

<210> 1542
<211> 57
<212> PRT

<213> Homo sapiens

<400> 1542
Lys Gly Ile Glu Cys Gln Ala Asn Gln Ala Ser Ala Thr Ser Glu Glu
1 5 10 15
Cys Thr Val Ala Trp Gly Val Cys Asn His Ala Phe His Phe His Cys
20 25 30
Ile Ser Arg Trp Leu Lys Thr Arg Gln Val Cys Pro Leu Asp Asn Arg
35 40 45
Glu Trp Glu Phe Gln Lys Tyr Gly His
50 55

<210> 1543
<211> 311
<212> DNA
<213> Homo sapiens

<400> 1543
gctagcgatg ctactttaag gtatgcgaag ttggatgctg acgttgcctc ctatcggttg
60
gagtcaaacg gacgaacaag cgttcgaggt agctttaaat gcgggcgacg ccagaaagtt
120
accaaagtcg gtgccgcgcc ttatgtttct cgaatggctc acgcgccgag gctacttgct
180
ccacggctcg agccgagccg acctcgtttg ttttgaacct cgagcaccca aagacttcag
240
ccctgacgag ttcagcaaac gcaccgccgt tttcgcctct tcagatgggg tgtggccccc
300
cnccncccnc c
311

<210> 1544
<211> 96
<212> PRT
<213> Homo sapiens

<400> 1544
Met Arg Ser Trp Met Leu Thr Leu Pro Pro Ile Gly Trp Ser Gln Thr
1 5 10 15
Asp Glu Gln Ala Phe Glu Val Ala Leu Asn Ala Gly Asp Ala Arg Lys
20 25 30
Leu Pro Lys Ser Val Pro Arg Leu Met Phe Leu Glu Trp Leu Thr Arg
35 40 45
Arg Gly Tyr Leu Leu His Gly Ser Ser Arg Ala Asp Leu Val Cys Phe
50 55 60
Glu Pro Arg Ala Pro Lys Asp Phe Ser Pro Asp Glu Phe Ser Lys Arg
65 70 75 80
Thr Ala Val Phe Ala Ser Ser Asp Gly Val Trp Pro Pro Xaa Xaa Xaa
85 90 95

<210> 1545
<211> 362
<212> DNA
<213> Homo sapiens

<400> 1545
ccatggtgcg gccgtctggt aacgataggc aaatccttgc catgccacca attcttcctt
60
caacagtagt tggcgaatcc ttcgatggtc aagtcctgtg agcttgctca tctgacggat
120
cgtctctgtc tcaagcacct cgcctgtttc caggttcaag gcctggatag tgcgagtgtc
180
gtactggtcg atcacttcca ccgagtggtc tgggtagccc cttgccattc gctttatgat
240
ctcaaccata gatgcatttg gcatgttcca gagcttgtac tccttaacga tctctctggc
300
gtcgtagaaa accttcacgc tatcgtcagg atgggtcact gtggtgatgt accgtccaga
360
ac
362

<210> 1546
<211> 92
<212> PRT
<213> Homo sapiens

<400> 1546
Met Val Lys Ser Cys Glu Leu Ala His Leu Thr Asp Arg Leu Cys Leu
1 5 10 15
Lys His Leu Ala Cys Phe Gln Val Gln Gly Leu Asp Ser Ala Ser Val
20 25 30
Val Leu Val Asp His Phe His Arg Val Val Trp Val Ala Pro Cys His
35 40 45
Ser Leu Tyr Asp Leu Asn His Arg Cys Ile Trp His Val Pro Glu Leu
50 55 60
Val Leu Leu Asn Asp Leu Ser Gly Val Val Glu Asn Leu His Ala Ile
65 70 75 80
Val Arg Met Gly His Cys Gly Asp Val Pro Ser Arg
85 90

<210> 1547
<211> 429
<212> DNA
<213> Homo sapiens

<400> 1547
cgcgttgcca caccggaaga cccggccagc tcacgcctgg gtgaaagttt ctgggcgttc
60
ctgccgcgtt cggtgtggtt cagcgccgtg tcggcgtgga acctggagcg cgagcgcctg
120
cgcaaactcg gcctgccggc ctggcactgg aagaacgccg tgctcagtgc ctggatgtac
180
agcgtggtgt tgtgggggt gatgattgtc tggttgggcg cggcggtgat tccgttcctg
240
atcattcagg gtgtctacgg gttctcgttg ctggaagtgg tcaactacgt cgagcactac
300
gggcttaaac gccagaagtt gcccaacggt cgttatgaac ggtgttcgcc tcggcactcg
360

tggaacagca accggattgt caccaatatc tttctgttcc aacttcagcg gcattccgac
420
caccatgcc
429

<210> 1548
<211> 143
<212> PRT
<213> Homo sapiens

<400> 1548
Arg Val Ala Thr Pro Glu Asp Pro Ala Ser Ser Arg Leu Gly Glu Ser
1 5 10 15
Phe Trp Ala Phe Leu Pro Arg Ser Val Trp Phe Ser Ala Val Ser Ala
20 25 30
Trp Asn Leu Glu Arg Glu Arg Leu Arg Lys Leu Gly Leu Pro Ala Trp
35 40 45
His Trp Lys Asn Ala Val Leu Ser Ala Trp Met Tyr Ser Val Val Leu
50 55 60
Trp Gly Val Met Ile Val Trp Leu Gly Ala Ala Val Ile Pro Phe Leu
65 70 75 80
Ile Ile Gln Gly Val Tyr Gly Phe Ser Leu Leu Glu Val Val Asn Tyr
85 90 95
Val Glu His Tyr Gly Leu Lys Arg Gln Lys Leu Pro Asn Gly Arg Tyr
100 105 110
Glu Arg Cys Ser Pro Arg His Ser Trp Asn Ser Asn Arg Ile Val Thr
115 120 125
Asn Ile Phe Leu Phe Gln Leu Gln Arg His Ser Asp His His Ala
130 135 140

<210> 1549
<211> 443
<212> DNA
<213> Homo sapiens

<400> 1549
gtcgacaggc tccagggttc tgttttgtag tgcacccgct gtggtgcaac atgcgtctgg
60
gcacaccagc gtcgcccgtt tcctgttgta gtctttcctc tctgactcca ggggtattgg
120
gtctttctgc cagcgcccat gcaactttgg cagcctggcc tgtctgctgg taagtggggc
180
agaatccctg cactccacca ttcttgggca acactccctc taggattttg gtctcccttt
240
tctctctggt ctttgaccac cgctacccag caaactcctc catctagacc agccagcatt
300
ggtttcttcc actcccccag ctgccgcgtg ggaggcgcca ctgcaaactt ccctggggtc
360
tcccagctgc tcagagatcc ccatgcccct ccctgatcag ctccctgccc ggttctcatc
420
ccgacgcggc tgcatggata ttc
443

<210> 1550

<211> 139
<212> PRT
<213> Homo sapiens

<400> 1550
Met Arg Thr Gly Gln Gly Ala Asp Gln Gly Arg Ala Trp Gly Ser Leu
1 5 10 15
Ser Ser Trp Glu Thr Pro Gly Lys Phe Ala Val Ala Pro Pro Thr Arg
20 25 30
Gln Leu Gly Glu Trp Lys Lys Pro Met Leu Ala Gly Leu Asp Gly Gly
35 40 45
Val Cys Trp Val Ala Val Val Lys Asp Gln Arg Glu Lys Gly Asp Gln
50 55 60
Asn Pro Arg Gly Ser Val Ala Gln Glu Trp Trp Ser Ala Gly Ile Leu
65 70 75 80
Pro His Leu Pro Ala Asp Arg Pro Gly Cys Gln Ser Cys Met Gly Ala
85 90 95
Gly Arg Lys Thr Gln Tyr Pro Trp Ser Gln Arg Gly Lys Thr Thr Thr
100 105 110
Gly Asn Gly Arg Arg Trp Cys Ala Gln Thr His Val Ala Pro Gln Arg
115 120 125
Val His Tyr Lys Thr Glu Pro Trp Ser Leu Ser
130 135

<210> 1551
<211> 306
<212> DNA
<213> Homo sapiens

<400> 1551
ccatggatac cccacctctg gcactcaaca tgacttggct gccacacacc aggaaacctc
60
agaggagcag ccagctggcc aagcacccct gcccctgccc tgcgggctcc acaaaagctg
120
gaggagcaaa cgcagctcac ctctttttct gtccactgct tcagggccta cccctgtgct
180
ttggagatgg aacaaaagtg agagagctcc ctgacacacc ctcccagggc gaggatggca
240
gctccttcct ccatttggtc ctaacacagc ctccccagga gaccaggggc atcccnnnnc
300
cccnnc
306

<210> 1552
<211> 101
<212> PRT
<213> Homo sapiens

<400> 1552
Met Asp Thr Pro Pro Leu Ala Leu Asn Met Thr Trp Leu Pro His Thr
1 5 10 15
Arg Lys Pro Gln Arg Ser Ser Gln Leu Ala Lys His Pro Cys Pro Cys
20 25 30
Pro Ala Gly Ser Thr Lys Ala Gly Gly Ala Asn Ala Ala His Leu Phe

```
        35                  40                  45
Phe Cys Pro Leu Leu Gln Gly Leu Pro Leu Cys Phe Gly Asp Gly Thr
    50                  55                  60
Lys Val Arg Glu Leu Pro Asp Thr Pro Ser Gln Gly Glu Asp Gly Ser
65                  70                  75                  80
Ser Phe Leu His Leu Val Leu Thr Gln Pro Pro Gln Glu Thr Arg Gly
                85                  90                  95
Ile Pro Xaa Pro Xaa
            100
```

<210> 1553
<211> 657
<212> DNA
<213> Homo sapiens

<400> 1553
atcctgcaga atgatggcgt ggtcaccagc ccctattccc ggccacgcaa ggcgggccac
60
acgctactca tcctgggggg ccagaccttc atgtgtgaca agatctacca ggtggaccac
120
aaggccaagg agatcatccc caaggccgac ctgcccagcc cccggaagga gttcagcgcc
180
tcagcgatcg gctgcaaggt ctatgtgacg gggggcaggg gctccgagaa cggggtctcc
240
aaggatgtct gggtgtacga caccgtacat gaggaatggt ccaaggcggc gcccatgctg
300
attgcccgct ttggccatgg ctcagctgag ctggagaact gcctctatgt ggtgggggga
360
cacacatccc tggcaggggt cttcccggcc tcgccttctg tctccctgaa acaagtggag
420
aaatacgacc ctggggccaa caagtggatg atggtggccc ccttgcggga tggcgtcagc
480
aatgccgcag tggtgagtgc caagctgaag ctctttgttt ttggaggaac cagcatccac
540
cgggacatgg tgtccaaggt ccagtgctat gacccctcgg agaacaggtg gacgatcaag
600
gccgagtgcc cccagccttg gcggtacaca gccgctgccg tcctgggcag ccagatc
657

<210> 1554
<211> 219
<212> PRT
<213> Homo sapiens

<400> 1554
```
Ile Leu Gln Asn Asp Gly Val Val Thr Ser Pro Tyr Ser Arg Pro Arg
 1               5                  10                  15
Lys Ala Gly His Thr Leu Leu Ile Leu Gly Gly Gln Thr Phe Met Cys
            20                  25                  30
Asp Lys Ile Tyr Gln Val Asp His Lys Ala Lys Glu Ile Ile Pro Lys
        35                  40                  45
Ala Asp Leu Pro Ser Pro Arg Lys Glu Phe Ser Ala Ser Ala Ile Gly
    50                  55                  60
Cys Lys Val Tyr Val Thr Gly Gly Arg Gly Ser Glu Asn Gly Val Ser
```

65 70 75 80
Lys Asp Val Trp Val Tyr Asp Thr Val His Glu Glu Trp Ser Lys Ala
85 90 95
Ala Pro Met Leu Ile Ala Arg Phe Gly His Gly Ser Ala Glu Leu Glu
100 105 110
Asn Cys Leu Tyr Val Val Gly Gly His Thr Ser Leu Ala Gly Val Phe
115 120 125
Pro Ala Ser Pro Ser Val Ser Leu Lys Gln Val Glu Lys Tyr Asp Pro
130 135 140
Gly Ala Asn Lys Trp Met Met Val Ala Pro Leu Arg Asp Gly Val Ser
145 150 155 160
Asn Ala Ala Val Val Ser Ala Lys Leu Lys Leu Phe Val Phe Gly Gly
165 170 175
Thr Ser Ile His Arg Asp Met Val Ser Lys Val Gln Cys Tyr Asp Pro
180 185 190
Ser Glu Asn Arg Trp Thr Ile Lys Ala Glu Cys Pro Gln Pro Trp Arg
195 200 205
Tyr Thr Ala Ala Ala Val Leu Gly Ser Gln Ile
210 215

<210> 1555
<211> 328
<212> DNA
<213> Homo sapiens

<400> 1555
acgcgtggga gctcgggaga gaggactctg cttctggggt ttgaaggtga gcgtgattct
60
ggaggagcct gccttgcggc gagcgtgtgt tgtggagagg atgcaggaca tgagtgatcc
120
tgtaagggtg atcgagtgtg cctcgtgaag tctggaagtc agcgagtgtg ggccgtggag
180
gtgagccacc ggtttgtgat ttgaaactga gtgagagtgc tgtggagcgc gaaatatgtg
240
tgtgtgtaga gtggaggtga gcgaatttgt gtgcatgtga gacggacgca atggcagagt
300
gtagcatcct gtgttgggat tgggattn
328

<210> 1556
<211> 102
<212> PRT
<213> Homo sapiens

<400> 1556
Met Leu His Ser Ala Ile Ala Ser Val Ser His Ala His Lys Phe Ala
1 5 10 15
His Leu His Ser Thr His Thr His Ile Ser Arg Ser Thr Ala Leu Ser
20 25 30
Leu Ser Phe Lys Ser Gln Thr Gly Gly Ser Pro Pro Arg Pro Thr Leu
35 40 45
Ala Asp Phe Gln Thr Ser Arg Gly Thr Leu Asp His Pro Tyr Arg Ile
50 55 60
Thr His Val Leu His Pro Leu His Asn Thr Arg Ser Pro Gln Gly Arg

65 70 75 80
Leu Leu Gln Asn His Ala His Leu Gln Thr Pro Glu Ala Glu Ser Ser
85 90 95
Leu Pro Ser Ser His Ala
100

<210> 1557
<211> 390
<212> DNA
<213> Homo sapiens

<400> 1557
gtgcacagac ttttcgagcg ggccattaag tggtttacgt ctgggatcgg ctccgctttc
60
tcgcattttt cggatcaggt caaattctgt gctcggcatt gacaggaaat tgacgtgtat
120
cagtcgattc tttgcagtgt ctggacggca ggctgaatag gctgaaagca ggacaactac
180
gaccatgccg caccatgtgg atcgtctacc gttttggcct tgccgccatt gccttgatcg
240
ccctgattgc gctgttcgtg tgccagtacc ggctatcggc caggctggcg cgccggaagc
300
gaagctcgat gggcagcagg cgcatgagga acccggcgcc attgaatcgt gaggcgctgg
360
cggagcgcgg cccgttcaaa tgcgacgcgt
390

<210> 1558
<211> 114
<212> PRT
<213> Homo sapiens

<400> 1558
Met Ala Pro Gly Ser Ser Cys Ala Cys Cys Pro Ser Ser Phe Ala Ser
1 5 10 15
Gly Ala Pro Ala Trp Pro Ile Ala Gly Thr Gly Thr Arg Thr Ala Gln
20 25 30
Ser Gly Arg Ser Arg Gln Trp Arg Gln Gly Gln Asn Gly Arg Arg Ser
35 40 45
Thr Trp Cys Gly Met Val Val Val Val Leu Leu Ser Ala Tyr Ser Ala
50 55 60
Cys Arg Pro Asp Thr Ala Lys Asn Arg Leu Ile His Val Asn Phe Leu
65 70 75 80
Ser Met Pro Ser Thr Glu Phe Asp Leu Ile Arg Lys Met Arg Glu Ser
85 90 95
Gly Ala Asp Pro Arg Arg Lys Pro Leu Asn Gly Pro Leu Glu Lys Ser
100 105 110
Val His

<210> 1559
<211> 556
<212> DNA
<213> Homo sapiens

<400> 1559
accggtggcg acggtatcgg tggcgcgtcg atccttgcct cggaatcctt cgctgcagag
60
ggtgagtcga agcgacccag cgtccaggtg ggcgacccgt tcatggagaa gctgctcatc
120
gagtgcaccc ttgacctctt caacgccggg gtagttgagg ccttgcagga tttcggtgcc
180
gccggaatct cctgtgccac ctccgagctg gccagtgctg gcgacggtgg catgcacgtc
240
gagctcgacc gcgttccgct gcgcgacccg aacctcgccc ctgaagagat cctcatgagc
300
gagtcccagg agcggatggc cgcggtggtg cgccccgatc agcttgaccg cttcatggag
360
atctgcgccc attggggtgt cgctgccact gtcattggcg aggtcaccga caccggtcga
420
cttcacattg attggcaggg cgagcggatt gtcgacgtcg atccgcggac ggttgctcac
480
gacggaccgg ttctcgacat gccggccgcc cgtccgtggt ggattgatga gctcaacgag
540
aacgacgcta acgcgt
556

<210> 1560
<211> 185
<212> PRT
<213> Homo sapiens

<400> 1560
Thr Gly Gly Asp Gly Ile Gly Gly Ala Ser Ile Leu Ala Ser Glu Ser
 1   5   10   15
Phe Ala Ala Glu Gly Glu Ser Lys Arg Pro Ser Val Gln Val Gly Asp
            20   25   30
Pro Phe Met Glu Lys Leu Leu Ile Glu Cys Thr Leu Asp Leu Phe Asn
        35   40   45
Ala Gly Val Val Glu Ala Leu Gln Asp Phe Gly Ala Ala Gly Ile Ser
    50   55   60
Cys Ala Thr Ser Glu Leu Ala Ser Ala Gly Asp Gly Gly Met His Val
65   70   75   80
Glu Leu Asp Arg Val Pro Leu Arg Asp Pro Asn Leu Ala Pro Glu Glu
                85   90   95
Ile Leu Met Ser Glu Ser Gln Glu Arg Met Ala Ala Val Val Arg Pro
            100   105   110
Asp Gln Leu Asp Arg Phe Met Glu Ile Cys Ala His Trp Gly Val Ala
        115   120   125
Ala Thr Val Ile Gly Glu Val Thr Asp Thr Gly Arg Leu His Ile Asp
    130   135   140
Trp Gln Gly Glu Arg Ile Val Asp Val Asp Pro Arg Thr Val Ala His
145   150   155   160
Asp Gly Pro Val Leu Asp Met Pro Ala Ala Arg Pro Trp Trp Ile Asp
                165   170   175
Glu Leu Asn Glu Asn Asp Ala Asn Ala
            180   185

<210> 1561
<211> 466
<212> DNA
<213> Homo sapiens

<400> 1561
acgcgtgaaa ggtttgagag aagagagatg ccgctattga atctgctgga gttttacatc
60
ccaagatgaa gacagcattc agaattgatg tgatttcctt gaatgtggct taggaaatgt
120
ggacacttaa aactctcact tgaaattggg cacaggtttg atgtagagat aaggacgggg
180
tgcggaatgg agacccattt tgtcattgat tcatctgacc gataaggcca tagtgcagtt
240
aggtgatatt cgaaagcttc tttgatgctc tttatgtata tgttggaagg aactaccagg
300
cgttgcttta aattcccaat gtgttgtttc gttactacta atttaatacc gtaagctcta
360
ggtaaagttc catgttgttg aactctgact gttctctttg gaattgaacg ttttgcatcc
420
tcctcctgtg gctttaggtc tgacattgta tttgaccttt actagt
466

<210> 1562
<211> 130
<212> PRT
<213> Homo sapiens

<400> 1562
Met Ser Asp Leu Lys Pro Gln Glu Glu Asp Ala Lys Arg Ser Ile Pro
1 5 10 15
Lys Arg Thr Val Arg Val Gln Gln His Gly Thr Leu Pro Arg Ala Tyr
20 25 30
Gly Ile Lys Leu Val Val Thr Lys Gln His Ile Gly Asn Leu Lys Gln
35 40 45
Arg Leu Val Val Pro Ser Asn Ile Tyr Ile Lys Ser Ile Lys Glu Ala
50 55 60
Phe Glu Tyr His Leu Thr Ala Leu Trp Pro Tyr Arg Ser Asp Glu Ser
65 70 75 80
Met Thr Lys Trp Val Ser Ile Pro His Pro Val Leu Ile Ser Thr Ser
85 90 95
Asn Leu Cys Pro Ile Ser Ser Glu Ser Phe Lys Cys Pro His Phe Leu
100 105 110
Ser His Ile Gln Gly Asn His Ile Asn Ser Glu Cys Cys Leu His Leu
115 120 125
Gly Met
130

<210> 1563
<211> 434
<212> DNA
<213> Homo sapiens

<400> 1563

ctgggggtg tgttcggcct gctgtcggtg tacttgccgc gttggctgca tgaaacaccg
60
atcttcgctg agatgcagca gcgcaaaacc ctggctgccg agttgccatt gcgcgcggta
120
ttgcgtgacc accgtggcgc catcgtgctg tcgatgctgt tgacgtggtt gctgtcggcg
180
ggtgtggttg tggtcatcct gatgaccccg accgtgctgc aaaccgtcta ccacttcagc
240
ccgacggttg cgctgcaagc caacagcctg gcgatcgtta cgctgagcct gggctgcatt
300
gcgtccggcg cgctggctga ccgttttggt gccggtcgcg ttttggtcac cggttggcgt
360
tgctgctggc cacttcctgg acgctgtatc acagcctgat ggcccagacg gaatggttga
420
ataagtgtac gcgt
434

<210> 1564
<211> 132
<212> PRT
<213> Homo sapiens

<400> 1564
Leu Gly Gly Val Phe Gly Leu Leu Ser Val Tyr Leu Pro Arg Trp Leu
1 5 10 15
His Glu Thr Pro Ile Phe Ala Glu Met Gln Gln Arg Lys Thr Leu Ala
20 25 30
Ala Glu Leu Pro Leu Arg Ala Val Leu Arg Asp His Arg Gly Ala Ile
35 40 45
Val Leu Ser Met Leu Leu Thr Trp Leu Leu Ser Ala Gly Val Val Val
50 55 60
Val Ile Leu Met Thr Pro Thr Val Leu Gln Thr Val Tyr His Phe Ser
65 70 75 80
Pro Thr Val Ala Leu Gln Ala Asn Ser Leu Ala Ile Val Thr Leu Ser
85 90 95
Leu Gly Cys Ile Ala Ser Gly Ala Leu Ala Asp Arg Phe Gly Ala Gly
100 105 110
Arg Val Leu Val Thr Gly Trp Arg Cys Cys Trp Pro Leu Pro Gly Arg
115 120 125
Cys Ile Thr Ala
130

<210> 1565
<211> 373
<212> DNA
<213> Homo sapiens

<400> 1565
ccatggtcgt agcccttggt tcaacaagag ccgtctactg acgctaaccc accatgagcc
60
agagggtgag cggttctggc acctactgga ccatgaaagc aataaagagg acaagggagc
120
ctgcattcgg ccatttcttc ccaagaatca ccataaaggt tgtcaaaatc aaggaccctg
180

atccggtgat tctcgaagtc atcgatgagc agaacaagtt tacccccgag ggagaaaagc
240
gggtggtgct cttgatgctc gacaacctct accgtcccag tacccaccgt gcattggcga
300
acgggggcgt cccttatctg cggtcgaaga gtgtcactgt tgacctcgta gacagccggg
360
acaacacggg tac
373

<210> 1566
<211> 106
<212> PRT
<213> Homo sapiens

<400> 1566
Met Ser Gln Arg Val Ser Gly Ser Gly Thr Tyr Trp Thr Met Lys Ala
 1   5   10   15
Ile Lys Arg Thr Arg Glu Pro Ala Phe Gly His Phe Phe Pro Arg Ile
            20   25   30
Thr Ile Lys Val Val Lys Ile Lys Asp Pro Asp Pro Val Ile Leu Glu
        35   40   45
Val Ile Asp Glu Gln Asn Lys Phe Thr Pro Glu Gly Glu Lys Arg Val
    50   55   60
Val Leu Leu Met Leu Asp Asn Leu Tyr Arg Pro Ser Thr His Arg Ala
65   70   75   80
Leu Ala Asn Gly Gly Val Pro Tyr Leu Arg Ser Lys Ser Val Thr Val
                85   90   95
Asp Leu Val Asp Ser Arg Asp Asn Thr Gly
            100   105

<210> 1567
<211> 917
<212> DNA
<213> Homo sapiens

<400> 1567
agctttttcg accgctgaag gagtgggata cccgctcccc agacactccc tttctagggg
60
aagccgctgc actcctgggg gacccagttt gatgcctcca ggaggataag tctgaagccg
120
ggttgggaag ggagcggaga ggcccaaaca gagcagcagg cagcgccctc tgctggcacc
180
ctggagacag cttcggctgc ggggcccctg ccttctagtc ctccccagct ttcaggacac
240
cttgacaacc tggggtccct gcagaagtgg cccggctgtc ccccaagtct cctgaagcta
300
tctgggtagg gtgggaggca gtgctgtgag ccacaaatgc aaagcagagg ggacagatgt
360
tgggactcaa agacatgagg tagagctggc cccatgggta ggtgccacca ccagagccca
420
tgaggcttcg tgttctagaa ggtggtgggt tagtgccgca ctgagggcgt gtccgggagg
480
gagcatgtgt caccagggct caggaaacag catgagtcat gacgcggggg tgtttaaggc
540

attcgtgcca cagcggggac ctcggagcta tgccttgata aggcaagtga ggttacatgt
600
acgatgatgc ggtttgtgct gcagactgga aaaaagcagg ggctttgtcc tctcctgacc
660
ccctcacact ctgccttcac ggtaggctcc tgagaggggg gtctccaagg agggtgtcag
720
tactgcagct tcagctggcg tggatggggt gcttacagga gcagcagggc tgagggagat
780
gacagcagta cgaatcgtgg ctctcctgag gcctgggttt cctcatatgt aaaatggggg
840
ttgcattaga ccataccctt ggcctgtgtt taggcaaata gggatgaaag tggggccaag
900
ggctgaagag ctgggtc
917

<210> 1568
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1568
Met Gly Pro Ala Leu Pro His Val Phe Glu Ser Gln His Leu Ser Pro
1 5 10 15
Leu Leu Cys Ile Cys Gly Ser Gln His Cys Leu Pro Pro Tyr Pro Asp
20 25 30
Ser Phe Arg Arg Leu Gly Gly Gln Pro Gly His Phe Cys Arg Asp Pro
35 40 45
Arg Leu Ser Arg Cys Pro Glu Ser Trp Gly Gly Leu Glu Gly Arg Gly
50 55 60
Pro Ala Ala Glu Ala Val Ser Arg Val Pro Ala Glu Gly Ala Ala Cys
65 70 75 80
Cys Ser Val Trp Ala Ser Pro Leu Pro Ser Gln Pro Gly Phe Arg Leu
85 90 95
Ile Leu Leu Glu Ala Ser Asn Trp Val Pro Gln Glu Cys Ser Gly Phe
100 105 110
Pro

<210> 1569
<211> 379
<212> DNA
<213> Homo sapiens

<400> 1569
ggagggcctg tgattctact gcaggcaggc acccccaca acctcacatg ccgggccttc
60
aatgcgaagc ctgctgccac catcatctgg ttccgggacg ggacgcagca ggagggcgct
120
gtggccagca cggaattgct gaaggatggg aagagggaga ccaccgtgag ccaactgctt
180
attaacccca cggacctgga catagggcgt gtcttcactt gccgaagcat gaacgaagcc
240
atccctagtg gcaaggagac ttccatcgag ctggatgtgc accacccctcc tacagtgacc
300

ctgtccattg agccacagac ggtgcaggag ggtgagcgtg ttgtctttac ctgccaggcc
360
acagccaacc cggagatct
379

<210> 1570
<211> 126
<212> PRT
<213> Homo sapiens

<400> 1570
Gly Gly Pro Val Ile Leu Leu Gln Ala Gly Thr Pro His Asn Leu Thr
1 5 10 15
Cys Arg Ala Phe Asn Ala Lys Pro Ala Ala Thr Ile Ile Trp Phe Arg
20 25 30
Asp Gly Thr Gln Gln Glu Gly Ala Val Ala Ser Thr Glu Leu Leu Lys
35 40 45
Asp Gly Lys Arg Glu Thr Thr Val Ser Gln Leu Leu Ile Asn Pro Thr
50 55 60
Asp Leu Asp Ile Gly Arg Val Phe Thr Cys Arg Ser Met Asn Glu Ala
65 70 75 80
Ile Pro Ser Gly Lys Glu Thr Ser Ile Glu Leu Asp Val His His Pro
85 90 95
Pro Thr Val Thr Leu Ser Ile Glu Pro Gln Thr Val Gln Glu Gly Glu
100 105 110
Arg Val Val Phe Thr Cys Gln Ala Thr Ala Asn Pro Glu Ile
115 120 125

<210> 1571
<211> 357
<212> DNA
<213> Homo sapiens

<400> 1571
tgcgcacttt tccgctcccg atgggtcccc tggncgttga tcatgcccca gatgttcatc
60
atcggcatct tcttcttcct gccaagcggc caagccgtgc tccagtcttt ccagatggaa
120
gatgcgttcg gcatgtcgac cgaatgggtc ggattggaca acttccgcaa cctgctggat
180
gaccccacct acctgaattc cttccagcgc accgccgtgt tctcggtgct ggtggcaggg
240
gtcgggatcg ccgtgtcact gggtctggcg atctttgccg accccatcac tccgtcgcca
300
tgtgtacaag acacactgct gatcgtgccc tacgccgtgg cacccatgat cgccggc
357

<210> 1572
<211> 119
<212> PRT
<213> Homo sapiens

<400> 1572
Cys Ala Leu Phe Arg Ser Arg Trp Val Pro Trp Xaa Leu Ile Met Pro

```
 1               5                  10                  15
Gln Met Phe Ile Ile Gly Ile Phe Phe Phe Leu Pro Ser Gly Gln Ala
            20                  25                  30
Val Leu Gln Ser Phe Gln Met Glu Asp Ala Phe Gly Met Ser Thr Glu
        35                  40                  45
Trp Val Gly Leu Asp Asn Phe Arg Asn Leu Leu Asp Asp Pro Thr Tyr
    50                  55                  60
Leu Asn Ser Phe Gln Arg Thr Ala Val Phe Ser Val Leu Val Ala Gly
65                  70                  75                  80
Val Gly Ile Ala Val Ser Leu Gly Leu Ala Ile Phe Ala Asp Pro Ile
                85                  90                  95
Thr Pro Ser Pro Cys Val Gln Asp Thr Leu Leu Ile Val Pro Tyr Ala
            100                 105                 110
Val Ala Pro Met Ile Ala Gly
        115
```

<210> 1573
<211> 337
<212> DNA
<213> Homo sapiens

<400> 1573
gaattcccat tgtcatctga ttccatgtct ggaaagaggg aagagagaca tcatgcagaa
60
tattgtacag attttggaat cggtacagtt gaaatgggaa ctttttcaga gctggacaga
120
cttttcaagg ctccatcttt ctaataaact ggccattttt ggaattggtt ataacacccg
180
ttggaaagag gatatccgtt accattatgc tgagatcagc tcccaggtgc cccttggcaa
240
gcgacttcgg gagtacttca actctgagaa gcctgaagga cggatcatta tgacccgagt
300
gcagaaaatg aactggaaaa atgtttacta caaattt
337

<210> 1574
<211> 95
<212> PRT
<213> Homo sapiens

<400> 1574

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Met Gln Asn Ile Val Gln Ile Leu Glu Ser Val Gln Leu Lys Trp Glu
 1               5                  10                  15
Leu Phe Gln Ser Trp Thr Asp Phe Ser Arg Leu His Leu Ser Asn Lys
            20                  25                  30
Leu Ala Ile Phe Gly Ile Gly Tyr Asn Thr Arg Trp Lys Glu Asp Ile
        35                  40                  45
Arg Tyr His Tyr Ala Glu Ile Ser Ser Gln Val Pro Leu Gly Lys Arg
    50                  55                  60
Leu Arg Glu Tyr Phe Asn Ser Glu Lys Pro Glu Gly Arg Ile Ile Met
65                  70                  75                  80
Thr Arg Val Gln Lys Met Asn Trp Lys Asn Val Tyr Tyr Lys Phe
                85                  90                  95
```

<210> 1575
<211> 471
<212> DNA
<213> Homo sapiens

<400> 1575
nnacgcgtca gagagatctg tgtgtcggga ggggtgcccc tcatcattga tgaccgcgta
60
catctcgttg ccgaaattgg ggccgatggt gtccatgttg ggcagtctga catgccggtc
120
gaccaggccc gtgcgattct gggcgacgat ctactcatcg gcttgtccgc tcagactccc
180
gcccatgtgg aggccgccct gtcccagggg cgtgacatcg tcgactatct gggagttggg
240
gccctgcatg gtactggaac caaacctgag gctggggagc tcggcctggc tgagattcgt
300
gatgtcgtca acgccagccc gtggccggtg tgcgtcatcg gtggggtgag cgcatccgat
360
gctcaagacg tagcccgggt gggatgtgac ggcctgagcg tcgtctcggc gatttgccgg
420
agtaccgacc ccaagtccag tgcacgggaa cttgcggagg cgtggcgtac g
471

<210> 1576
<211> 157
<212> PRT
<213> Homo sapiens

<400> 1576
Xaa Arg Val Arg Glu Ile Cys Val Ser Gly Gly Val Pro Leu Ile Ile
 1   5   10   15
Asp Asp Arg Val His Leu Val Ala Glu Ile Gly Ala Asp Gly Val His
            20   25   30
Val Gly Gln Ser Asp Met Pro Val Asp Gln Ala Arg Ala Ile Leu Gly
        35   40   45
Asp Asp Leu Leu Ile Gly Leu Ser Ala Gln Thr Pro Ala His Val Glu
    50   55   60
Ala Ala Leu Ser Gln Gly Arg Asp Ile Val Asp Tyr Leu Gly Val Gly
65   70   75   80
Ala Leu His Gly Thr Gly Thr Lys Pro Glu Ala Gly Glu Leu Gly Leu
                85   90   95
Ala Glu Ile Arg Asp Val Val Asn Ala Ser Pro Trp Pro Val Cys Val
            100   105   110
Ile Gly Gly Val Ser Ala Ser Asp Ala Gln Asp Val Ala Arg Val Gly
        115   120   125
Cys Asp Gly Leu Ser Val Val Ser Ala Ile Cys Arg Ser Thr Asp Pro
    130   135   140
Lys Ser Ser Ala Arg Glu Leu Ala Glu Ala Trp Arg Thr
145   150   155

<210> 1577
<211> 287
<212> DNA
<213> Homo sapiens

<400> 1577
ctcgtcctcc agcgtccgat cagtgcgctc aggatgctga tcggcggccc cttgcgcatc
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ccccatcctg cgggcttgcg cacggttgcg ctcgaacccg gcgtcgcgca cgcgcgcacc
120
ttgcgcgttg ccggggcagg cttccccgct cgcggccagc gcgccgccgg cgatctggtg
180
atcgagctgg agccgatgct gccgcaggcg cccgacaagc aactgcacgc gctgatcgag
240
cagctcgacg tggcgctcgg gaagagcgcg acacgccatt ttccgga
287

<210> 1578
<211> 95
<212> PRT
<213> Homo sapiens

<400> 1578
Leu Val Leu Gln Arg Pro Ile Ser Ala Leu Arg Met Leu Ile Gly Gly
1 5 10 15
Pro Leu Arg Ile Pro His Pro Ala Gly Leu Arg Thr Val Ala Leu Glu
20 25 30
Pro Gly Val Ala His Ala Arg Thr Leu Arg Val Ala Gly Ala Gly Phe
35 40 45
Pro Ala Arg Gly Gln Arg Ala Ala Gly Asp Leu Val Ile Glu Leu Glu
50 55 60
Pro Met Leu Pro Gln Ala Pro Asp Lys Gln Leu His Ala Leu Ile Glu
65 70 75 80
Gln Leu Asp Val Ala Leu Gly Lys Ser Ala Thr Arg His Phe Pro
85 90 95

<210> 1579
<211> 2829
<212> DNA
<213> Homo sapiens

<400> 1579
nggggcgggg agcggacttc ctcctctgag ggccgtgccg cgctgccaga tttgttcttc
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cgcccctgcc tccgcggctc ggaggcgagc ggaaggtgcc ccggggccga ggcccgtgac
120
ggggcgggcg ggagccccgg cagtccgggg tcgccggcga gggccatgtc gctgttgggg
180
gacccgctac aggccctgcc gccctcggcc gcccccacgg ggccgctgct cgcccctccg
240
gccggcgcga ccctcaaccg cctgcgggag ccgctgctgc ggaggctcag cgagctcctg
300
gatcaggcgc ccgagggccg gggctggagg agactggcgg agctggcggg gagtcgcggg
360
cgcctccgcc tcagttgcct agacctggag cagtgttctc ttaaggtact ggagcctgaa
420
ggaagcccca gcctgtgtct gctgaagtta atgggtgaaa aaggttgcac agtcacagaa
480

ttgagtgatt tcctgcaggc tatggaacac actgaagttc ttcagcttct cagcccccca
540
ggaataaaga ttactgtaaa cccagagtca aaggcagtct tggctggaca gtttgtgaaa
600
ctgtgttgcc gggcaactgg acatcctttt gttcaatatc agtggttcaa aatgaataaa
660
gagattccaa atggaaatac atcagagctt atttttaatg cagtgcatgt aaaagatgca
720
ggcttttatg tctgtcgagt taataacaat ttcacctttg aattcagcca gtggtcacag
780
ctggatgttt gcgacatccc agagagcttc cagagaagtg ttgatggcgt ctctgaatcc
840
aagttgcaaa tctgtgttga accaacttcc caaaagctga tgccaggcag cacattggtt
900
ttacagtgtg ttgctgttgg aagccctatt cctcactacc agtggttcaa aaatgaatta
960
ccattaacac atgagaccaa aaagctatac atggtgcctt atgcggattt ggaacaccaa
1020
ggaacctact ggtgtcatgt atataatgat cgagacagtc aagatagcaa gaaggtagaa
1080
atcatcatag gaagaacaga tgaggcagtg gagtgcactg aagatgaatt aaataatctt
1140
ggtcatcctg ataataaaga gcaaacaact gaccagcctt tggcgaagga caaggttgcc
1200
cttttgatag gaaatatgaa ttaccgggag caccccaagc tcaaagctcc tttggtggat
1260
gtgtacgaat tgactaactt actgagacag ctggacttca aagtggtttc actgttggat
1320
cttactgaat atgagatgcg taatgctgtg gatgagtttt tactcctttt agacaaggga
1380
gtatatgggt tattatatta tgcaggacat ggttatgaaa attttgggaa cagcttcatg
1440
gtccccgttg atgctccaaa tccatatagg tctgaaaatt gtctgtgtgt acaaaatata
1500
ctgaaattga tgcaagaaaa agaaactgga cttaatgtgt tcttattgga tatgtgtagg
1560
aaaagaaatg actacgatga taccattcca atcttggatg cactaaaagt caccgccaat
1620
attgtgtttg gatatgccac gtgtcaagga gcagaagctt ttgaaatcca gcattctgga
1680
ttggcaaatg gaatctttat gaaattttta aaagacagat tattagaaga taagaaaatc
1740
actgtgttac tggatgaagt tgcagaagat atgggtaagt gtcaccttac caaaggcaaa
1800
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1860
ggaacagaat attctgctga atctcttgtg cggaatctac agtgggccaa ggctcatgaa
1920
cttccagaaa gtatgtgtct taagtttgac tgtggtgttc agattcaatt aggatttgca
1980
gctgagtttt ccaatgtcat gatcatctat acaagtatag tttacaaacc accggagata
2040
ataatgtgtg atgcctacgt tactgatttt ccacttgatc tagatattga tccaaaagat
2100

gcaaataaag gcacacctga agaaactggc agctacttgg tatcaaagga tcttcccaag
2160
cattgcctct ataccagact cagttcactg caaaaattaa aggaacatct agtcttcaca
2220
gtatgtttat catatcagta ctcaggattg gaagatactg tagaggacaa gcaggaagtg
2280
aatgttggga aacctctcat tgctaaatta gacatgcatc gaggtttggg aaggaagact
2340
tgctttcaaa cttgtcttat gtctaatggt ccttaccaga gttctgcagc cacctcagga
2400
ggagcagggc attatcactc attgcaagac ccattccatg gtgtttacca ttcacatcct
2460
ggtaatccaa gtaatgttac accagcagat agctgtcatt gcagccggac tccagatgca
2520
tttatttcaa gtttcgctca ccatgcttca tgtcatttta gtagaagtaa tgtgccagta
2580
gagacaactg atgaaatacc atttagtttc tctgacaggc tcagaatttc tgaaaaatga
2640
cctccttgtt tttgaaagtt agcataattt tagatgcctg tgaaatagta ctgcacttac
2700
ataaagtgag acattgtgaa aaggcaaatt tgtatatgta gagaaagaat agtagtaact
2760
gtttcatagc aaacttcagg actttgagat gttgaaatta cattatttaa ttacagactt
2820
cctctttct
2829

<210> 1580
<211> 824
<212> PRT
<213> Homo sapiens

<400> 1580
Met Ser Leu Leu Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala
1 5 10 15
Pro Thr Gly Pro Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg
20 25 30
Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala
35 40 45
Pro Glu Gly Arg Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg
50 55 60
Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys
65 70 75 80
Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met
85 90 95
Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala
100 105 110
Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys
115 120 125
Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val
130 135 140
Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp
145 150 155 160
Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile

```
                165                 170                 175
Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val
            180                 185                 190
Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val
        195                 200                 205
Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu
    210                 215                 220
Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro
225                 230                 235                 240
Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro
                245                 250                 255
His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys
            260                 265                 270
Lys Leu Tyr Met Val Pro Tyr Ala Asp Leu Glu His Gln Gly Thr Tyr
        275                 280                 285
Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val
    290                 295                 300
Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp
305                 310                 315                 320
Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp
                325                 330                 335
Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn
            340                 345                 350
Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu
        355                 360                 365
Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu
    370                 375                 380
Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu
385                 390                 395                 400
Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly
                405                 410                 415
Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn
            420                 425                 430
Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu
        435                 440                 445
Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys
    450                 455                 460
Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu
465                 470                 475                 480
Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala
                485                 490                 495
Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met
            500                 505                 510
Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu
        515                 520                 525
Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly
    530                 535                 540
Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu
545                 550                 555                 560
Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg
                565                 570                 575
Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu
            580                 585                 590
Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe
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595 600 605
Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu
610 615 620
Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp
625 630 635 640
Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser
645 650 655
Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu
660 665 670
Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu
675 680 685
Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu
690 695 700
Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly
705 710 715 720
Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro
725 730 735
Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser
740 745 750
Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro
755 760 765
Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp
770 775 780
Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg
785 790 795 800
Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser
805 810 815
Asp Arg Leu Arg Ile Ser Glu Lys
820

<210> 1581
<211> 426
<212> DNA
<213> Homo sapiens

<400> 1581
gatccgcatc gcccgtttat tgacgaggtg accttcaccc gagagggcca tacctatcac
60
cgggtgcccg aggtggctga cgcctggctc gattcgggct cgatgccctt cgcccagtgg
120
ggatacccgc atgtgcccgg ttcgaaggag aagttcgagt cccactaccc gggtgacttc
180
atctgtgagg ccatcgacca gacccgcggg tggttttaca ccatgatggc cgtcggaacc
240
ctggtgtttg acgagtcctc gtaccgcaat gtgctgtgtc tgggccacat cttggccgag
300
gacggtcgca agatgagcaa gcaccttggc aacatcctgt tgcctatccc gctcatggat
360
tcccacggtg ccgacgcgct gcgttggttc atggcggccg acggctcccc atggagtgca
420
cgacgc
426

<210> 1582

<211> 142
<212> PRT
<213> Homo sapiens

<400> 1582
Asp Pro His Arg Pro Phe Ile Asp Glu Val Thr Phe Thr Arg Glu Gly
1 5 10 15
His Thr Tyr His Arg Val Pro Glu Val Ala Asp Ala Trp Leu Asp Ser
20 25 30
Gly Ser Met Pro Phe Ala Gln Trp Gly Tyr Pro His Val Pro Gly Ser
35 40 45
Lys Glu Lys Phe Glu Ser His Tyr Pro Gly Asp Phe Ile Cys Glu Ala
50 55 60
Ile Asp Gln Thr Arg Gly Trp Phe Tyr Thr Met Met Ala Val Gly Thr
65 70 75 80
Leu Val Phe Asp Glu Ser Ser Tyr Arg Asn Val Leu Cys Leu Gly His
85 90 95
Ile Leu Ala Glu Asp Gly Arg Lys Met Ser Lys His Leu Gly Asn Ile
100 105 110
Leu Leu Pro Ile Pro Leu Met Asp Ser His Gly Ala Asp Ala Leu Arg
115 120 125
Trp Phe Met Ala Ala Asp Gly Ser Pro Trp Ser Ala Arg Arg
130 135 140

<210> 1583
<211> 450
<212> DNA
<213> Homo sapiens

<400> 1583
nnacgcgtga agggttatgg agatggttca gggagtaagg aaggtttcag ggatggttta
60
gggggttctg aggaaatggg gtcaatggat gaggcaggtt ataggaagga tttgggggct
120
cctaagggaa taggttcagg gagtaaggca ggtttcaggg atggtttagg gagttctggg
180
gaaatggggt caatggatga ggcagattat aggaaggatt tgggagctcc tgaggaaatg
240
ggttcaggca gttacacaga ttacaggaat ggtttaggca gttctggaaa aatcagttca
300
ggggatgagg caggttataa gaatgtttta gggggttctg ggaggaatcc attagggagc
360
gaggcaggtt ctaggggtag tttggaggat tctgggtaca tcttgtcatg gaatgaggca
420
ggttctaggc aaggctttgg gggaactagt
450

<210> 1584
<211> 150
<212> PRT
<213> Homo sapiens

<400> 1584
Xaa Arg Val Lys Gly Tyr Gly Asp Gly Ser Gly Ser Lys Glu Gly Phe

```
 1               5                  10                  15
Arg Asp Gly Leu Gly Gly Ser Glu Glu Met Gly Ser Met Asp Glu Ala
            20                  25                  30
Gly Tyr Arg Lys Asp Leu Gly Ala Pro Lys Gly Ile Gly Ser Gly Ser
        35                  40                  45
Lys Ala Gly Phe Arg Asp Gly Leu Gly Ser Ser Gly Glu Met Gly Ser
    50                  55                  60
Met Asp Glu Ala Asp Tyr Arg Lys Asp Leu Gly Ala Pro Glu Glu Met
65                  70                  75                  80
Gly Ser Gly Ser Tyr Thr Asp Tyr Arg Asn Gly Leu Gly Ser Ser Gly
                85                  90                  95
Lys Ile Ser Ser Gly Asp Glu Ala Gly Tyr Lys Asn Val Leu Gly Gly
            100                 105                 110
Ser Gly Arg Asn Pro Leu Gly Ser Glu Ala Gly Ser Arg Gly Ser Leu
        115                 120                 125
Glu Asp Ser Gly Tyr Ile Leu Ser Trp Asn Glu Ala Gly Ser Arg Gln
    130                 135                 140
Gly Phe Gly Gly Thr Ser
145                 150
```

<210> 1585
<211> 596
<212> DNA
<213> Homo sapiens

<400> 1585
tgatcatctg taattcttgt ccgtgggcgt ttgaactgag aatgtcttaa gaagttggga
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tctaatccga gctgctgctg gcaaagttgg gtgaggtctg cagagagtgc gtccatctgt
120
ggcagctgca gggcaagctg gggaggaagc gcagggtgtt gcacaggttg catcataatg
180
gaaggaaaga gcggcaggtc cagagaaacc ggcctctccc aaaaagttat caaacactgg
240
tttagaaata cgctttttaa ggaacgacag agaaataaag attcaccata caacttcagt
300
aaccctccta taacggtttt agaagatatc agaattgatc cacagcccac ctctttagaa
360
cattacaaat ctgatgcatc attcagtaaa aggtcttcta gaacgagatt tactgactac
420
cagcttaggg ttctgcaaga ctttttttgac acaaacgctt acccaaaaga tgatgaaata
480
gaacaactct ccactgttct caatctgcct acccgggtta ttgttgtatg gttccagaat
540
gctcgtcaga aagcacgaaa gagttatgag aatcaagcag aaacccccttc acgcgt
596

<210> 1586
<211> 139
<212> PRT
<213> Homo sapiens

<400> 1586
Met Glu Gly Lys Ser Gly Arg Ser Arg Glu Thr Gly Leu Ser Gln Lys

```
 1               5                  10                  15
Val Ile Lys His Trp Phe Arg Asn Thr Leu Phe Lys Glu Arg Gln Arg
            20                  25                  30
Asn Lys Asp Ser Pro Tyr Asn Phe Ser Asn Pro Pro Ile Thr Val Leu
        35                  40                  45
Glu Asp Ile Arg Ile Asp Pro Gln Pro Thr Ser Leu Glu His Tyr Lys
    50                  55                  60
Ser Asp Ala Ser Phe Ser Lys Arg Ser Ser Arg Thr Arg Phe Thr Asp
65                  70                  75                  80
Tyr Gln Leu Arg Val Leu Gln Asp Phe Phe Asp Thr Asn Ala Tyr Pro
                85                  90                  95
Lys Asp Asp Glu Ile Glu Gln Leu Ser Thr Val Leu Asn Leu Pro Thr
            100                 105                 110
Arg Val Ile Val Val Trp Phe Gln Asn Ala Arg Gln Lys Ala Arg Lys
        115                 120                 125
Ser Tyr Glu Asn Gln Ala Glu Thr Pro Ser Arg
    130                 135
```

<210> 1587
<211> 501
<212> DNA
<213> Homo sapiens

<400> 1587
tgtacacaca gtgatttggg gtccttttc ctaaaacagc ttctttatca ggactttgga
60
attctgggtg agatagaaac actgaaaaca gggcggaagt ttttttcttct ggcttcttag
120
tccacggagg gctcagcgtg gagaggatat gccgtggcat tctccctggg agaccacaca
180
tgttcccgac agctcagacc ccagaccgca tgtgctcctg acagctcaga ccccagaccg
240
cgcgtgctcc tgacagctca gaccccagac cgcaggtgct cccgacagct cagaccccag
300
accgcgggtg ctcctgacag ctcagacccc agaccgcgcg tgctcccgac agctcagacc
360
ccagaccgcg ggtgctcctg acagctcaga ccccagaccg cgcgtgctcc cgacagctca
420
gaccccagac cgcgggtgct cctgacagct cagaccccag accgcgggtg ctcctgacag
480
ctcagacccc agaccacgcg t
501

<210> 1588
<211> 86
<212> PRT
<213> Homo sapiens

<400> 1588
```
Ser Thr Glu Gly Ser Ala Trp Arg Gly Tyr Ala Val Ala Phe Ser Leu
 1               5                  10                  15
Gly Asp His Thr Cys Ser Arg Gln Leu Arg Pro Gln Thr Ala Cys Ala
            20                  25                  30
Pro Asp Ser Ser Asp Pro Arg Pro Arg Val Leu Leu Thr Ala Gln Thr
```

```
        35                  40                  45
Pro Asp Arg Arg Cys Ser Arg Gln Leu Arg Pro Gln Thr Ala Gly Ala
    50                  55                  60
Pro Asp Ser Ser Asp Pro Arg Pro Arg Val Leu Pro Thr Ala Gln Thr
65                  70                  75                  80
Pro Asp Arg Gly Cys Ser
                85
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<210> 1589
<211> 407
<212> DNA
<213> Homo sapiens

<400> 1589
aagcttgctg gggacaccct ttttacgggg cctcgtgggg gaggagttac ctgcattgac
60
tccaccggtt ccactaacgc cgacatggct gctttcgtgc gagcaggggg aacgtctttc
120
tgcctactcg ttgctgacca ccaagagggc gggcgtggac ggttcacgcg cagttggcag
180
gatgtccccg gtacgagttt ggcgatctca gcgttggtgc ccaatgatcg tccgtcgcag
240
gactggggct ggctgtcgat ggttgcgggg ctcgctgttg tcaaggtcat caaggaggtc
300
ggtggggctg accgttcccg agtgacgctg aagtggccca atgatgtgct cgtggatctg
360
gacactgacc agggcggcaa agtgtgcgga attctctcag aacgcgt
407

<210> 1590
<211> 135
<212> PRT
<213> Homo sapiens

<400> 1590

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Lys Leu Ala Gly Asp Thr Leu Phe Thr Gly Pro Arg Gly Gly Gly Val
 1               5                  10                  15
Thr Cys Ile Asp Ser Thr Gly Ser Thr Asn Ala Asp Met Ala Ala Phe
            20                  25                  30
Val Arg Ala Gly Gly Thr Ser Phe Cys Leu Leu Val Ala Asp His Gln
        35                  40                  45
Glu Gly Gly Arg Gly Arg Phe Thr Arg Ser Trp Gln Asp Val Pro Gly
    50                  55                  60
Thr Ser Leu Ala Ile Ser Ala Leu Val Pro Asn Asp Arg Pro Ser Gln
65                  70                  75                  80
Asp Trp Gly Trp Leu Ser Met Val Ala Gly Leu Ala Val Val Lys Val
                85                  90                  95
Ile Lys Glu Val Gly Gly Ala Asp Arg Ser Arg Val Thr Leu Lys Trp
            100                 105                 110
Pro Asn Asp Val Leu Val Asp Leu Asp Thr Asp Gln Gly Gly Lys Val
        115                 120                 125
Cys Gly Ile Leu Ser Glu Arg
    130                 135
```

<210> 1591
<211> 424
<212> DNA
<213> Homo sapiens

<400> 1591
agatctctct ccctgagata acccaggctt tagaaccaaa gagctgagag accctgtccc
60
ttcagagagg cacttgcacc tagaggagtc tctgggaagc agatggggat atgggacaga
120
cgcatcttga aaaagccccc agatgcctcc ctatggagga cctcacccac ccacatcacc
180
agtagggagc ttgggactta ccctaaccac agggggggtga ctgttgtcgt ccctgcacag
240
aacgtccagc gagtcctgac tttccagccg ctgcgcttca tccaggagca cgtcctgatc
300
cctgtctttg acctcagcgg ccccagcagt ctggcccagc ctgtccagta ctcccttgac
360
tgtgggatcc ctggctgctc acgcccctga ggacccctcg gatctgctcc agcacgtgaa
420
attt
424

<210> 1592
<211> 95
<212> PRT
<213> Homo sapiens

<400> 1592
Met Gly Ile Trp Asp Arg Arg Ile Leu Lys Lys Pro Pro Asp Ala Ser
 1   5   10   15
Leu Trp Arg Thr Ser Pro Thr His Ile Thr Ser Arg Glu Leu Gly Thr
            20   25   30
Tyr Pro Asn His Arg Gly Val Thr Val Val Val Pro Ala Gln Asn Val
        35   40   45
Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln Glu His Val
    50   55   60
Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro
65   70   75   80
Val Gln Tyr Ser Leu Asp Cys Gly Ile Pro Gly Cys Ser Arg Pro
                85   90   95

<210> 1593
<211> 1678
<212> DNA
<213> Homo sapiens

<400> 1593
cttgaatcta aaataaatga ataaaacaca gaaattaacc agttgattga aaagaaaatg
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atgagaaatg agcccattga aggcaaactc tcactgtata ggcaacaggc atctatcatt
120
tcccgtaaaa aagaagccaa agctgaggaa cttcaggagg ccaaggagaa gttagccagc
180

ctagagagag aagcatcagt aaagagaaat cagacccgtg aatttgatgg tactgaagtt
240
ttaaagggag atgagttcaa acgatatgtc aataaacttc gaagcaagag tacagttttc
300
aaaaagaagc atcacataat agctgaactt aaagctgaat tcggtctttt gcagaggact
360
gaagaacttc ttaagcaacg tcatgaaaat attcaacaac aactgcaaac tatggaggag
420
aaaaagggta tatctggata tagttacacc caagaagagc tagaaagagt atctgcactg
480
aagagtgaag ttgatgaaat gaaaggacga acattggatg atatgtctga aatggtgaaa
540
aaactgtatt cattggtatc tgaaaagaag tcagctcttg cctcagttat aaaagagcta
600
cgacagttgc gtcaaaaata tcaagaactg acccaggagt gtgatgaaaa gaaatcccag
660
tatgatagct gtgcagcagg cctcgaaagc aatcggtcca aattagaaca ggaagttaga
720
agactccgtg aagaatgtct tcaagaagaa agtagatacc attatacaaa ttgtatgatt
780
aagaacctag aagttcaact tcgtcgtgct actgatgaga tgaaggcata tatctcttct
840
gatcaacaag aaaaaagaaa ggcaattagg gaacagtata ccaaaaatac tgctgaacaa
900
gaaaaccttg gaaagaaact tcgggaaaaa caaaaagtta tacgagaaag tcatggtcca
960
aatatgaaac aagcaaaaat gtggcgtgat ttggaacaat taatggaatg taagaaacag
1020
tgctttctga aacaacaaag ccaaacttcc attggtcagg taattcagga gggtggggag
1080
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1140
tataagccta atctcataat gtatttcttt tttgaaactg atttgtttag cattttgttt
1200
tcagaagagc cattctttat taagttttca tagaaaataa tgttaaggta gatttagttt
1260
gaatgttttt tcatatgaaa aagaggcttt tattcttttc catagtttag acatcactgg
1320
cgtcttctga gttttatgag acaggaaact aagtttacta tctgtaaatg taaacatatg
1380
tccattaaga aacatgtagt tttttttag aatgtaataa cccagtggct tactgttttt
1440
cttaatctct tttaaaaaaa ctttagaaga atcttttagg aactaatatc tcttgttctg
1500
aagaaacatt tatctgacgt tcagcagttc ctacagtttt acttcagttt atttttcttc
1560
tgtaaaatgc aagaaaattt aatattttga ctaacatgtc ttttctgttt gtatcattta
1620
aaggcaaata aacttggtac gtatttcata tctatttaaa aaatgaaaaa aaaaaaaa
1678

<210> 1594
<211> 365
<212> PRT

<213> Homo sapiens

<400> 1594

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Leu Glu Ser Lys Ile Asn Glu Ile Asn Thr Glu Ile Asn Gln Leu Ile
 1               5                  10                  15
Glu Lys Lys Met Met Arg Asn Glu Pro Ile Glu Gly Lys Leu Ser Leu
            20                  25                  30
Tyr Arg Gln Gln Ala Ser Ile Ile Ser Arg Lys Lys Glu Ala Lys Ala
        35                  40                  45
Glu Glu Leu Gln Glu Ala Lys Glu Lys Leu Ala Ser Leu Glu Arg Glu
    50                  55                  60
Ala Ser Val Lys Arg Asn Gln Thr Arg Glu Phe Asp Gly Thr Glu Val
65                  70                  75                  80
Leu Lys Gly Asp Glu Phe Lys Arg Tyr Val Asn Lys Leu Arg Ser Lys
                85                  90                  95
Ser Thr Val Phe Lys Lys Lys His His Ile Ile Ala Glu Leu Lys Ala
            100                 105                 110
Glu Phe Gly Leu Leu Gln Arg Thr Glu Glu Leu Leu Lys Gln Arg His
        115                 120                 125
Glu Asn Ile Gln Gln Gln Leu Gln Thr Met Glu Glu Lys Lys Gly Ile
    130                 135                 140
Ser Gly Tyr Ser Tyr Thr Gln Glu Glu Leu Glu Arg Val Ser Ala Leu
145                 150                 155                 160
Lys Ser Glu Val Asp Glu Met Lys Gly Arg Thr Leu Asp Asp Met Ser
                165                 170                 175
Glu Met Val Lys Lys Leu Tyr Ser Leu Val Ser Glu Lys Lys Ser Ala
            180                 185                 190
Leu Ala Ser Val Ile Lys Glu Leu Arg Gln Leu Arg Gln Lys Tyr Gln
        195                 200                 205
Glu Leu Thr Gln Glu Cys Asp Glu Lys Lys Ser Gln Tyr Asp Ser Cys
    210                 215                 220
Ala Ala Gly Leu Glu Ser Asn Arg Ser Lys Leu Glu Gln Glu Val Arg
225                 230                 235                 240
Arg Leu Arg Glu Glu Cys Leu Gln Glu Glu Ser Arg Tyr His Tyr Thr
                245                 250                 255
Asn Cys Met Ile Lys Asn Leu Glu Val Gln Leu Arg Arg Ala Thr Asp
            260                 265                 270
Glu Met Lys Ala Tyr Ile Ser Ser Asp Gln Gln Glu Lys Arg Lys Ala
        275                 280                 285
Ile Arg Glu Gln Tyr Thr Lys Asn Thr Ala Glu Gln Glu Asn Leu Gly
    290                 295                 300
Lys Lys Leu Arg Glu Lys Gln Lys Val Ile Arg Glu Ser His Gly Pro
305                 310                 315                 320
Asn Met Lys Gln Ala Lys Met Trp Arg Asp Leu Glu Gln Leu Met Glu
                325                 330                 335
Cys Lys Lys Gln Cys Phe Leu Lys Gln Gln Ser Gln Thr Ser Ile Gly
            340                 345                 350
Gln Val Ile Gln Glu Gly Gly Glu Asp Arg Leu Ile Leu
        355                 360                 365
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<210> 1595
<211> 559
<212> DNA
<213> Homo sapiens

<400> 1595
accggtcccg ctcacaggcc cacacctgct tctcctcctg gggcagggca gcctggtggg
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gcatggccgg ggagccgccc acttggcgag gaacaggctc catagcgacc tcagaacact
120
ggtgctgggg cccagccagg gagagcatct tcccgctggg accttccccg gggcggctca
180
tcccttggag atgtagggtg cagctgagat ggtggcggcc ccattcctgc tgttcgccag
240
cctgggctgg gggtactagg atcacccttg ggctgatgag gagcccgggt cttgggcagt
300
taccaagtgg ggggtcacag tctggaaagt ggtggaacca agggagcggc ctcgcccagg
360
ccacactctc aaatactggc cctcgacaaa aggcagctgg gctctcaaga cagggccacc
420
tcctctctgc tgggcccgcg cccgtggaga gcaagtggga actgacccta tcttctgtcc
480
cagcttggag agccagcatc aaggtcaggc ctcacttgcc caagaaagag gagtgaggag
540
gcccactgga ggaacgcgt
559

<210> 1596
<211> 166
<212> PRT
<213> Homo sapiens

<400> 1596
Met Leu Ala Leu Gln Ala Gly Thr Glu Asp Arg Val Ser Ser His Leu
1 5 10 15
Leu Ser Thr Gly Ala Gly Pro Ala Glu Arg Arg Trp Pro Cys Leu Glu
20 25 30
Ser Pro Ala Ala Phe Cys Arg Gly Pro Val Phe Glu Ser Val Ala Trp
35 40 45
Ala Arg Pro Leu Pro Trp Phe His His Phe Pro Asp Cys Asp Pro Pro
50 55 60
Leu Gly Asn Cys Pro Arg Pro Gly Leu Leu Ile Ser Pro Arg Val Ile
65 70 75 80
Leu Val Pro Pro Ala Gln Ala Gly Glu Gln Gln Glu Trp Gly Arg His
85 90 95
His Leu Ser Cys Thr Leu His Leu Gln Gly Met Ser Arg Pro Gly Glu
100 105 110
Gly Pro Ser Gly Lys Met Leu Ser Leu Ala Gly Pro Gln His Gln Cys
115 120 125
Ser Glu Val Ala Met Glu Pro Val Pro Arg Gln Val Gly Gly Ser Pro
130 135 140
Ala Met Pro His Gln Ala Ala Leu Pro Gln Glu Glu Lys Gln Val Trp
145 150 155 160
Ala Cys Glu Arg Asp Arg
165

<210> 1597
<211> 609

<212> DNA
<213> Homo sapiens

<400> 1597
tcgtcaacgg aaacttcggc cttcgggcct acccataatc cttgggacct tgaacgggta
60
ccgggtggtt ccggtggtgg ttcagcagct agcttggctt cctttcaggc cccgttggct
120
ttgggcactg ataccggggg ctcgatccgc caacctggag cggtgaccgg caccgtcggg
180
atcaagccga cctacggttc gacctcccga tacggcgtta tcgctatggc ttcatctttg
240
gatactcctg ggccctgcgc ccgtaccgtc cttgacgccg cgttgctcca tcaggccatt
300
gccggtcacg acgctatgga ccagaccacg attaatcagc ccaccccggc ggtcgttgag
360
gctgcgcggc aggcagacgt ttccggggtg cgcattggcg ttgtcacgga gttgagcggg
420
cagggttacg accctcaggt cgaggcccgg ttccacgagg ctgtcgagat gctaatagag
480
gcgggggctg aggtcgttga ggtctcttgc ccgaactttg acctcgcctt acctgcttat
540
taccttattc agcctgccga ggtgtctagc aacctggctc gttacgacgc catgcgttac
600
ggcttacgc
609

<210> 1598
<211> 203
<212> PRT
<213> Homo sapiens

<400> 1598
Ser Ser Thr Glu Thr Ser Ala Phe Gly Pro Thr His Asn Pro Trp Asp
 1   5   10   15
Leu Glu Arg Val Pro Gly Gly Ser Gly Gly Gly Ser Ala Ala Ser Leu
            20   25   30
Ala Ser Phe Gln Ala Pro Leu Ala Leu Gly Thr Asp Thr Gly Gly Ser
        35   40   45
Ile Arg Gln Pro Gly Ala Val Thr Gly Thr Val Gly Ile Lys Pro Thr
    50   55   60
Tyr Gly Ser Thr Ser Arg Tyr Gly Val Ile Ala Met Ala Ser Ser Leu
65   70   75   80
Asp Thr Pro Gly Pro Cys Ala Arg Thr Val Leu Asp Ala Ala Leu Leu
                85   90   95
His Gln Ala Ile Ala Gly His Asp Ala Met Asp Gln Thr Thr Ile Asn
            100   105   110
Gln Pro Thr Pro Ala Val Val Glu Ala Ala Arg Gln Ala Asp Val Ser
        115   120   125
Gly Val Arg Ile Gly Val Val Thr Glu Leu Ser Gly Gln Gly Tyr Asp
    130   135   140
Pro Gln Val Glu Ala Arg Phe His Glu Ala Val Glu Met Leu Ile Glu
145   150   155   160
Ala Gly Ala Glu Val Val Glu Val Ser Cys Pro Asn Phe Asp Leu Ala

```
                165                 170                 175
Leu Pro Ala Tyr Tyr Leu Ile Gln Pro Ala Glu Val Ser Ser Asn Leu
            180                 185                 190
Ala Arg Tyr Asp Ala Met Arg Tyr Gly Leu Arg
        195                 200
```

<210> 1599
<211> 526
<212> DNA
<213> Homo sapiens

<400> 1599
gcgtggccga cggctgctgt gtggtcagcg atctttattt ttcttgatcg attcagaacc
60
cggcacctgc acgtgtggtt tctctgcttt tgttggggag cgtgcgtcgc gacctggatt
120
agcatgcacg tgaacacgtg gatggccggg atgctctcgg tgacaggtgg ggttgatcca
180
gcatcgggcg ccggtccggc agtgtattcg gctccctttg ttgaggaatc atgcaaggcg
240
cttgtgcttt tcgcgctggc catcggcatg gggcgacgga tgacctcggt agttcagacg
300
gtgagcatgg ccgggctctc ggcaattggt ttcgcctttg ttgagaacat tatgtactac
360
gcccgtgcag ataactacgc ccgtgtgacg gcttcgggtg gggaccccaa acaaggcgtt
420
gatgaagttg gtgctgttgc ggggagtgta tgcctcgttt gggcatccgc tgttcaccag
480
catgacgggt atcggtctgg cccttgggct gaggtcacga agttga
526

<210> 1600
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1600
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Met His Val Asn Thr Trp Met Ala Gly Met Leu Ser Val Thr Gly Gly
 1               5                  10                  15
Val Asp Pro Ala Ser Gly Ala Gly Pro Ala Val Tyr Ser Ala Pro Phe
            20                  25                  30
Val Glu Glu Ser Cys Lys Ala Leu Val Leu Phe Ala Leu Ala Ile Gly
        35                  40                  45
Met Gly Arg Arg Met Thr Ser Val Val Gln Thr Val Ser Met Ala Gly
    50                  55                  60
Leu Ser Ala Ile Gly Phe Ala Phe Val Glu Asn Ile Met Tyr Tyr Ala
65                  70                  75                  80
Arg Ala Asp Asn Tyr Ala Arg Val Thr Ala Ser Gly Gly Asp Pro Lys
                85                  90                  95
Gln Gly Val Asp Glu Val Gly Ala Val Ala Gly Ser Val Cys Leu Val
            100                 105                 110
Trp Ala Ser Ala Val His Gln His Asp Gly Tyr Arg Ser Gly Pro Trp
        115                 120                 125
Ala Glu Val Thr Lys Leu
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130

<210> 1601
<211> 447
<212> DNA
<213> Homo sapiens

<400> 1601
gccggccgcc ccgtttccgc agattctgga ggagtgccga tggccgagtt catctacacc
60
atgcacaacg tccgaaaggc ggtgggtgac aaagttatcc ttgacaatgt cacgctgtcg
120
ttcttcccgg gcgccaagat tggtgttgtc ggaccgaatg gcgctggcaa atcgacgatg
180
ctcaagctca tggctggtct cgataagccc aataacggcg atgccaactt ggctaaaggc
240
gccaccgtcg gaatcttgct tcaggagccc ccgctcaccg aggacaaaac tgttcgcgag
300
aacgtcgaag aggccgtcgg cgacatcaaa gccaagctgg cacggttcga ggaagtctcc
360
gccgagatgg ccaaccctga cgccgacttt gacgccctga tggcggagat gggtgagctg
420
cagaccgagc tcgataacgc caacgcg
447

<210> 1602
<211> 136
<212> PRT
<213> Homo sapiens

<400> 1602
Met Ala Glu Phe Ile Tyr Thr Met His Asn Val Arg Lys Ala Val Gly
1 5 10 15
Asp Lys Val Ile Leu Asp Asn Val Thr Leu Ser Phe Phe Pro Gly Ala
20 25 30
Lys Ile Gly Val Val Gly Pro Asn Gly Ala Gly Lys Ser Thr Met Leu
35 40 45
Lys Leu Met Ala Gly Leu Asp Lys Pro Asn Asn Gly Asp Ala Asn Leu
50 55 60
Ala Lys Gly Ala Thr Val Gly Ile Leu Leu Gln Glu Pro Pro Leu Thr
65 70 75 80
Glu Asp Lys Thr Val Arg Glu Asn Val Glu Glu Ala Val Gly Asp Ile
85 90 95
Lys Ala Lys Leu Ala Arg Phe Glu Glu Val Ser Ala Glu Met Ala Asn
100 105 110
Pro Asp Ala Asp Phe Asp Ala Leu Met Ala Glu Met Gly Glu Leu Gln
115 120 125
Thr Glu Leu Asp Asn Ala Asn Ala
130 135

<210> 1603
<211> 540
<212> DNA
<213> Homo sapiens

<400> 1603
acgcgtaagc tcaccgaagc catgatggca atgctgctgg aactgcatta cagcaagcag
60
gaaatccttg aggcgtacct caacgaggtc ttcgtcggtc aggatggcca gcgcgccgtg
120
cacgggtttg gcttggccag tcagttcttc tttggccagc ctttgtccga gctgaagttg
180
catcaagtcg cgttgttggt cgggatggtc aagggcccgt cctattacaa cccgcggcgc
240
aatccggaac gtgcgctcga gcgtcgtaac ctggtgctgg atgtgctgga acagcagggt
300
gtagccactg ccgaacaagt cgctgccgca aagaaaatgc cgctgggtgt aaccactcgc
360
ggcaagctgg cggacagctc cttcccaggc tttatcgacc tggtcaaacg ccagttgcgt
420
gaagattacc gcgacgaaga cttgaccgaa gaaggcctgc ggattttcac cagtttcgac
480
ccgattctgc agatgaaagc cgaagcatcg gtgaacgaca cattcaagcg cctgaccggc
540

<210> 1604
<211> 180
<212> PRT
<213> Homo sapiens

<400> 1604
Thr Arg Lys Leu Thr Glu Ala Met Met Ala Met Leu Leu Glu Leu His
 1   5   10   15
Tyr Ser Lys Gln Glu Ile Leu Glu Ala Tyr Leu Asn Glu Val Phe Val
            20   25   30
Gly Gln Asp Gly Gln Arg Ala Val His Gly Phe Gly Leu Ala Ser Gln
        35   40   45
Phe Phe Phe Gly Gln Pro Leu Ser Glu Leu Lys Leu His Gln Val Ala
    50   55   60
Leu Leu Val Gly Met Val Lys Gly Pro Ser Tyr Tyr Asn Pro Arg Arg
65   70   75   80
Asn Pro Glu Arg Ala Leu Glu Arg Arg Asn Leu Val Leu Asp Val Leu
                85   90   95
Glu Gln Gln Gly Val Ala Thr Ala Glu Gln Val Ala Ala Ala Lys Lys
            100   105   110
Met Pro Leu Gly Val Thr Thr Arg Gly Lys Leu Ala Asp Ser Ser Phe
        115   120   125
Pro Gly Phe Ile Asp Leu Val Lys Arg Gln Leu Arg Glu Asp Tyr Arg
    130   135   140
Asp Glu Asp Leu Thr Glu Glu Gly Leu Arg Ile Phe Thr Ser Phe Asp
145   150   155   160
Pro Ile Leu Gln Met Lys Ala Glu Ala Ser Val Asn Asp Thr Phe Lys
                165   170   175
Arg Leu Thr Gly
            180

<210> 1605
<211> 427

<212> DNA
<213> Homo sapiens

<400> 1605
acgcgttggt gcggtcggtc gcacgcagtc cgtccaagag gtacaggcca gcgttgccgc
60
cattctttgc gggcgggatc tgcactggga tattgcggcc catcgcctgt gaccacacat
120
cgcagcgctg gacccaccag cccacctggt cccactcgca cgtgccagta ctgtccgcac
180
gcaagaaatc gcggtgagct gcgtgcgcct gctgggtgcc gcctgccact acggcaagac
240
ccagcgctac ggcgactgcc atgatgaccg aaaggacgcg acccctaata gatgcagtca
300
tctttctcct tcacaaagta tttggtaatt gtcacttagc tttatcgctc ggaatctgtg
360
aaccgttaac atcccgacgc ggaagctaac tagcaagcag tctaatgcac tcccgggcca
420
aatgttg
427

<210> 1606
<211> 100
<212> PRT
<213> Homo sapiens

<400> 1606
Met Thr Ala Ser Ile Arg Gly Arg Val Leu Ser Val Ile Met Ala Val
 1   5   10   15
Ala Val Ala Leu Gly Leu Ala Val Val Ala Gly Gly Thr Gln Gln Ala
            20   25   30
His Ala Ala His Arg Asp Phe Leu Arg Ala Asp Ser Thr Gly Thr Cys
        35   40   45
Glu Trp Asp Gln Val Gly Trp Trp Val Gln Arg Cys Asp Val Trp Ser
    50   55   60
Gln Ala Met Gly Arg Asn Ile Pro Val Gln Ile Pro Pro Ala Lys Asn
65   70   75   80
Gly Gly Asn Ala Gly Leu Tyr Leu Leu Asp Gly Leu Arg Ala Thr Asp
                85   90   95
Arg Thr Asn Ala
            100

<210> 1607
<211> 396
<212> DNA.
<213> Homo sapiens

<400> 1607
gcacggctcc gctcgcggcc gccgtgatgg tacataccgg cgcgaccgtg atcgattctt
60
tgccgcaagg caatttactt ccacgtcacg gccgatgcga tgaagatgac gattcgtcaa
120
cggatgggac tgatcccgta cgaggcgatc gtgggcggga cgatgatgat cgtggcgacg
180

ttgctgtacg gattcatttt gtagcataaa taaggagggg ttcgatgaac aggaaaaccc
240
tttctgttgg cacccgattc gttcaaggaa agcatgacgg caaaagaagt ctgtatcgcg
300
atggaaaaag gactgagccg cgtctacccc gacgcccggt ttatccatgt gccgatggcg
360
gacggaggcg aaggcacggt gcagtcgctg gtcgac
396

<210> 1608
<211> 56
<212> PRT
<213> Homo sapiens

<400> 1608
Thr Gly Lys Pro Phe Leu Leu Ala Pro Asp Ser Phe Lys Glu Ser Met
1 5 10 15
Thr Ala Lys Glu Val Cys Ile Ala Met Glu Lys Gly Leu Ser Arg Val
20 25 30
Tyr Pro Asp Ala Arg Phe Ile His Val Pro Met Ala Asp Gly Gly Glu
35 40 45
Gly Thr Val Gln Ser Leu Val Asp
50 55

<210> 1609
<211> 505
<212> DNA
<213> Homo sapiens

<400> 1609
acgcgtagat gccacagcgc caggacacac gccaccgcgg agccgaggat gatccacatg
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ggctcgactc acatggacgc catggattcg gcagtggaga gcaggccgcg agcttcgcac
120
gcggcccgac tgcgtagtcg cgtcatctca gtgcacatct gttcttcccc gctcatgagg
180
ttcgcggcgt aggacatcgt tacgtccagc atggtggcga tctcagcaat gtcacagccg
240
gccttgtgga gggcgaggag ccgagcgcgc gtgcttcctg ctggcacgat gcgttcacgt
300
gctgcgttga tgtcgtcgat actgatatgc aggatgcgcc cggggtcgaa gacggggaat
360
ggggtgaatt ggacggtccc ccctggccag cgagtcgttg gacgattcga ctggggacat
420
gcgcgagcag ggcgacgaca cgccacggaa cgcggcattc atggacgagg gaacggacat
480
ggagcgagaa aaagcgggcg tcgac
505

<210> 1610
<211> 129
<212> PRT
<213> Homo sapiens

<400> 1610
Met Pro Arg Ser Val Ala Cys Arg Arg Pro Ala Arg Ala Cys Pro Gln
1 5 10 15
Ser Asn Arg Pro Thr Thr Arg Trp Pro Gly Gly Thr Val Gln Phe Thr
20 25 30
Pro Phe Pro Val Phe Asp Pro Gly Arg Ile Leu His Ile Ser Ile Asp
35 40 45
Asp Ile Asn Ala Ala Arg Glu Arg Ile Val Pro Ala Gly Ser Thr Arg
50 55 60
Ala Arg Leu Leu Ala Leu His Lys Ala Gly Cys Asp Ile Ala Glu Ile
65 70 75 80
Ala Thr Met Leu Asp Val Thr Met Ser Tyr Ala Ala Asn Leu Met Ser
85 90 95
Gly Glu Glu Gln Met Cys Thr Glu Met Thr Arg Leu Arg Ser Arg Ala
100 105 110
Ala Cys Glu Ala Arg Gly Leu Leu Ser Thr Ala Glu Ser Met Ala Ser
115 120 125
Met

<210> 1611
<211> 532
<212> DNA
<213> Homo sapiens

<400> 1611
acgcgtgctg cgtttacagt tgcgtctatt gatttaggtg cgcatccaga atttttagga
60
aaaaatgata ttcaattagg caaaaaagaa tctgtagagg atactgcgaa agtattaggt
120
agaatgttcg atggtattga attccgtggt ttttcacaac aagctggtga agatttagcg
180
aagttctctg gtgtaccggg gtggaatgga ttaacagacg attggcatcc tacacaaatg
240
ttagctgatt ttatgacaat aaaagagaat tttggatatc tagaaggaat aaacttaact
300
tacgttggag atggacgtaa taatattgcg cattcattaa tggtagcagg tgctatgtta
360
ggtgttaatg taagaatttg tacacctaaa tcattaaatc caaaagaggc atatgttgat
420
attgcaaaag aaaaagcgag tcaatatggt ggttcagtca tgattacgga taatattgca
480
gaagcagttg aaaatacaga tgctatatat acagatgttt gggtatcgac gg
532

<210> 1612
<211> 177
<212> PRT
<213> Homo sapiens

<400> 1612
Thr Arg Ala Ala Phe Thr Val Ala Ser Ile Asp Leu Gly Ala His Pro
1 5 10 15
Glu Phe Leu Gly Lys Asn Asp Ile Gln Leu Gly Lys Lys Glu Ser Val

```
            20                  25                  30
Glu Asp Thr Ala Lys Val Leu Gly Arg Met Phe Asp Gly Ile Glu Phe
        35                  40                  45
Arg Gly Phe Ser Gln Gln Ala Gly Glu Asp Leu Ala Lys Phe Ser Gly
    50                  55                  60
Val Pro Gly Trp Asn Gly Leu Thr Asp Asp Trp His Pro Thr Gln Met
65                  70                  75                  80
Leu Ala Asp Phe Met Thr Ile Lys Glu Asn Phe Gly Tyr Leu Glu Gly
                85                  90                  95
Ile Asn Leu Thr Tyr Val Gly Asp Gly Arg Asn Asn Ile Ala His Ser
            100                 105                 110
Leu Met Val Ala Gly Ala Met Leu Gly Val Asn Val Arg Ile Cys Thr
        115                 120                 125
Pro Lys Ser Leu Asn Pro Lys Glu Ala Tyr Val Asp Ile Ala Lys Glu
    130                 135                 140
Lys Ala Ser Gln Tyr Gly Gly Ser Val Met Ile Thr Asp Asn Ile Ala
145                 150                 155                 160
Glu Ala Val Glu Asn Thr Asp Ala Ile Tyr Thr Asp Val Trp Val Ser
                165                 170                 175
Thr
```

<210> 1613
<211> 584
<212> DNA
<213> Homo sapiens

<400> 1613
nnacgcgttc agccgagaaa tatgctgctt tttgcctgcc acctcacaaa tgctacggca
60
cagggcgtcc aggttttgcg cctcctggta cgttgctaca cacttgctca cctcccagcg
120
gtatcaatac aacttgcgaa atgcagacaa ggcccaggcc taagacatgg tagacataca
180
tatatacaag gaattcacta tatattgggt gaaaggagat cttcccgttc ctgttcttcc
240
tctgccgcat cctgtgaagc gttcagggag gtcgacatgg ataatgtgcg tatgcctggc
300
acggtaaagt gtcgcgggct tgtagatgcg tgtgaacgtt ttcgtgactt gaagaggtcg
360
aagctgatgt gttcgcgtga gctcgatgca gcgcgctgcg ttgcgtgcct tgtggtcgat
420
cgtcgccccg atccgataga atgcggagtt gtatttttcgt agtactgctc gacaatgcca
480
gtgggcgagg cgatgagttc ctcatttgcg tctttctcga ggtcttggtc catgtccata
540
aacataccaa agctggatgg gtcatacgac ggcgcagcat gcat
584

<210> 1614
<211> 153
<212> PRT
<213> Homo sapiens

<400> 1614
Xaa Arg Val Gln Pro Arg Asn Met Leu Leu Phe Ala Cys His Leu Thr
1 5 10 15
Asn Ala Thr Ala Gln Gly Val Gln Val Leu Arg Leu Leu Val Arg Cys
20 25 30
Tyr Thr Leu Ala His Leu Pro Ala Val Ser Ile Gln Leu Ala Lys Cys
35 40 45
Arg Gln Gly Pro Gly Leu Arg His Gly Arg His Thr Tyr Ile Gln Gly
50 55 60
Ile His Tyr Ile Leu Gly Glu Arg Arg Ser Ser Arg Ser Cys Ser Ser
65 70 75 80
Ser Ala Ala Ser Cys Glu Ala Phe Arg Glu Val Asp Met Asp Asn Val
85 90 95
Arg Met Pro Gly Thr Val Lys Cys Arg Gly Leu Val Asp Ala Cys Glu
100 105 110
Arg Phe Arg Asp Leu Lys Arg Ser Lys Leu Met Cys Ser Arg Glu Leu
115 120 125
Asp Ala Ala Arg Cys Val Ala Cys Leu Val Val Asp Arg Arg Pro Asp
130 135 140
Pro Ile Glu Cys Gly Val Val Phe Ser
145 150

<210> 1615
<211> 363
<212> DNA
<213> Homo sapiens

<400> 1615
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60
tcggtgcttg tcagtgctgg tgtcatcatt tccctgcttg gggctctact ggcctggatc
120
ctactgtgcg gtgagacgat gcaggtgccg ggtgaggacg gcaccatgcc gaaactgttc
180
ggacggatca acaaacatga ggctccagct cccgctttgt ggatcaccaa catcgtctcc
240
cagatatgcc ttgtcatgac ggtgttgtgg gacggtgctt acttggcgat ggcgaccctg
300
gctgccgccc tcatcctggt gccgtacctg ctgtcagccg cattcgccct gaagatggtg
360
atc
363

<210> 1616
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1616
Ala Gly Leu Pro Asp Ala Ser Met Gly Asp Val Leu Ser Ser Val Val
1 5 10 15
Gly Pro Trp Gly Ser Val Leu Val Ser Ala Gly Val Ile Ile Ser Leu
20 25 30
Leu Gly Ala Leu Leu Ala Trp Ile Leu Leu Cys Gly Glu Thr Met Gln

```
        35                  40                  45
Val Pro Gly Glu Asp Gly Thr Met Pro Lys Leu Phe Gly Arg Ile Asn
    50                  55                  60
Lys His Glu Ala Pro Ala Pro Ala Leu Trp Ile Thr Asn Ile Val Ser
65                  70                  75                  80
Gln Ile Cys Leu Val Met Thr Val Leu Trp Asp Gly Ala Tyr Leu Ala
                85                  90                  95
Met Ala Thr Leu Ala Ala Ala Leu Ile Leu Val Pro Tyr Leu Leu Ser
            100                 105                 110
Ala Ala Phe Ala Leu Lys Met Val Ile
        115                 120
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<210> 1617
<211> 447
<212> DNA
<213> Homo sapiens

<400> 1617
accggtgact acctgtggga gaagaagggc atcgttccca tcctcaagat tgataagggc
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ctggctgacg agggctgcca cgttcgtctc atgaagccga ttcccggcct cgacgagttg
120
gtgcaccgcg ccgtcgagga gaagcacatc ttcggtacca aggagcgctc tgtcatcctg
180
gatgacgaca aagctggcat cgaaaagatt gtcgaccagc agttcgaact ggccgaacag
240
gtgcgcgctg cgggtcttgt gccgatcctc gaacccgagg tcgacatcca cgctccacat
300
aaggagaagg ctgaggaaag gctgcacaac ctcatccgcg agcacatcga ctctctgccg
360
ctcgacgcca agatcatgtt gaagctgacg atcccgagtt ccgaagacct gtatgccgac
420
ctcattgcgg atccgaaggt cctacgc
447

<210> 1618
<211> 149
<212> PRT
<213> Homo sapiens

<400> 1618
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Thr Gly Asp Tyr Leu Trp Glu Lys Lys Gly Ile Val Pro Ile Leu Lys
 1               5                  10                  15
Ile Asp Lys Gly Leu Ala Asp Glu Gly Cys His Val Arg Leu Met Lys
            20                  25                  30
Pro Ile Pro Gly Leu Asp Glu Leu Val His Arg Ala Val Glu Glu Lys
        35                  40                  45
His Ile Phe Gly Thr Lys Glu Arg Ser Val Ile Leu Asp Asp Asp Lys
    50                  55                  60
Ala Gly Ile Glu Lys Ile Val Asp Gln Gln Phe Glu Leu Ala Glu Gln
65                  70                  75                  80
Val Arg Ala Ala Gly Leu Val Pro Ile Leu Glu Pro Glu Val Asp Ile
                85                  90                  95
His Ala Pro His Lys Glu Lys Ala Glu Glu Arg Leu His Asn Leu Ile
```

```
            100                 105                 110
Arg Glu His Ile Asp Ser Leu Pro Leu Asp Ala Lys Ile Met Leu Lys
        115                 120                 125
Leu Thr Ile Pro Ser Ser Glu Asp Leu Tyr Ala Asp Leu Ile Ala Asp
    130                 135                 140
Pro Lys Val Leu Arg
145

<210> 1619
<211> 355
<212> DNA
<213> Homo sapiens

<400> 1619
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acaacaaatg gtgcctccat tcccgccctt ggccttggca ctttccgtat gcccggcgaa
120
gatgtgcttc gcatcgtccc ttacgcgctc aaggctggtt ttcgccatgt cgataccgcg
180
cagatttatg gcaatgaagt cgaggtcggt gaagcaattg cgacttccgg cgttcagcgt
240
ggcgacatct ttctgaccac aaaagtctgg gtagataatt ataagcatga tgctttcatc
300
gcatctgtcg atgaaagcct taccaagctt aagaccgact atgtcgatct gctgc
355

<210> 1620
<211> 118
<212> PRT
<213> Homo sapiens

<400> 1620
Xaa Val Pro Lys Pro Val Ser Leu Pro His Lys Ile Lys Gly Thr Ser
 1               5                  10                  15
Met His Asn Val Thr Thr Asn Gly Ala Ser Ile Pro Ala Leu Gly Leu
            20                  25                  30
Gly Thr Phe Arg Met Pro Gly Glu Asp Val Leu Arg Ile Val Pro Tyr
        35                  40                  45
Ala Leu Lys Ala Gly Phe Arg His Val Asp Thr Ala Gln Ile Tyr Gly
    50                  55                  60
Asn Glu Val Glu Val Gly Glu Ala Ile Ala Thr Ser Gly Val Gln Arg
65                  70                  75                  80
Gly Asp Ile Phe Leu Thr Thr Lys Val Trp Val Asp Asn Tyr Lys His
                85                  90                  95
Asp Ala Phe Ile Ala Ser Val Asp Glu Ser Leu Thr Lys Leu Lys Thr
            100                 105                 110
Asp Tyr Val Asp Leu Leu
        115

<210> 1621
<211> 386
<212> DNA
<213> Homo sapiens
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<400> 1621
gcgcgccatg gaggcgcccc gggtcgcgcc aggatgctcc aggccaagtg aagcggtccg
60
gctggggtcg gcgggacccg cgggccatgt acggcgacat attcaacgcc acggggcggg
120
cccccgaggc ggcggtaggc agcgcgctgg ccccaggagc cacggtcaag gcagaaggcg
180
ctttgccgct ggagctggcc actgcgcgcg gtatgaggga cggcgcggcc acaaagcccg
240
acctgcccac ctacctgctg ctcttcttcc tgctgctgct ctcgggggcg ctcggcggcc
300
tcttcatcgg ttgccagctg cgccattcgg ccttcgccgc gctgccccac gaccgcttcg
360
ctcgcgacgc ccgcgcgccc ggaagg
386

<210> 1622
<211> 126
<212> PRT
<213> Homo sapiens

<400> 1622
Met Glu Ala Pro Arg Val Ala Pro Gly Cys Ser Arg Pro Ser Glu Ala
 1   5   10   15
Val Arg Leu Gly Ser Ala Gly Pro Ala Gly His Val Arg Arg His Ile
            20   25   30
Gln Arg His Gly Ala Gly Pro Arg Gly Gly Gly Arg Gln Arg Ala Gly
        35   40   45
Pro Arg Ser His Gly Gln Gly Arg Arg Arg Phe Ala Ala Gly Ala Gly
    50   55   60
His Cys Ala Arg Tyr Glu Gly Arg Arg Gly His Lys Ala Arg Pro Ala
65   70   75   80
His Leu Pro Ala Ala Leu Leu Pro Ala Ala Ala Leu Gly Gly Ala Arg
                85   90   95
Arg Pro Leu His Arg Leu Pro Ala Ala Pro Phe Gly Leu Arg Arg Ala
            100   105   110
Ala Pro Arg Pro Leu Arg Ser Arg Arg Pro Arg Ala Arg Lys
        115   120   125

<210> 1623
<211> 314
<212> DNA
<213> Homo sapiens

<400> 1623
nctggtgccc agagcctcgt cggggtccag ccccagggcc tttgcgagtc agacacttgg
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ggcccttgct tgtggttttt ctgggagctt tgggccgagg gttccccgga cccttccctg
120
aacttttccg cagtttcaga ggagagtctg caagtgagag ctgcagtgac tgtgccttgt
180
gcttggcacc caagcagggc atgggagtct taagtggaac cagggcctca aggacaacag
240

agagccgcat ggcagggtag acacctggat aaaagtgggt gggggaagcc cactgctgca
300
ccccgggcat tgct
314

<210> 1624
<211> 103
<212> PRT
<213> Homo sapiens

<400> 1624
Met Pro Gly Val Gln Gln Trp Ala Ser Pro Thr His Phe Tyr Pro Gly
1 5 10 15
Val Tyr Pro Ala Met Arg Leu Ser Val Val Leu Glu Ala Leu Val Pro
20 25 30
Leu Lys Thr Pro Met Pro Cys Leu Gly Ala Lys His Lys Ala Gln Ser
35 40 45
Leu Gln Leu Ser Leu Ala Asp Ser Pro Leu Lys Leu Arg Lys Ser Ser
50 55 60
Gly Lys Gly Pro Gly Asn Pro Arg Pro Lys Ala Pro Arg Lys Thr Thr
65 70 75 80
Ser Lys Gly Pro Lys Cys Leu Thr Arg Lys Gly Pro Gly Ala Gly Pro
85 90 95
Arg Arg Gly Ser Gly His Gln
100

<210> 1625
<211> 619
<212> DNA
<213> Homo sapiens

<400> 1625
acgcgtactc agcagcaagt tctgctgagc cccaaatcca cacagactga gcctggacca
60
gggctgggcc ctccttatcc aagccaatcc agggaaacac tgtgctgact tcaaggcaga
120
agggacaaga aagcatgact gtgcacaaat tggctttgca gccatctcca ccaggtagcc
180
ctgggagcac ctgggaagaa gccgggccat gcagggagcc caacctcacc ctgcattcag
240
aaccgggcct tggaatggcc tgatctgagc cctagcaccc ctgggaagcc gcccaccttt
300
cttctggcct ctgggaagaa gatgggaatt ttaaggccat gggagaagac actcctggat
360
tctttcagct tctccaccca ccccctgctc cagatgtaat ctgggaagac tggggagtca
420
ggggcacagt gagttggagc aggggattgg agggtttgtg ggacagcctt ccagggcacc
480
tcaggagctg aattatttaa gccagctgcc cgtgggcccc gctcccagcc cttcctgttt
540
acacagactc cgtccatagc agacaccttc ccagagcctg ggtgacaata ggctgggtgt
600
gttttctgca atcttatag
619

<210> 1626
<211> 106
<212> PRT
<213> Homo sapiens

<400> 1626
Met Asp Gly Val Cys Val Asn Arg Lys Gly Trp Glu Arg Gly Pro Arg
1 5 10 15
Ala Ala Gly Leu Asn Asn Ser Ala Pro Glu Val Pro Trp Lys Ala Val
20 25 30
Pro Gln Thr Leu Gln Ser Pro Ala Pro Thr His Cys Ala Pro Asp Ser
35 40 45
Pro Val Phe Pro Asp Tyr Ile Trp Ser Arg Gly Trp Val Glu Lys Leu
50 55 60
Lys Glu Ser Arg Ser Val Phe Ser His Gly Leu Lys Ile Pro Ile Phe
65 70 75 80
Phe Pro Glu Ala Arg Arg Lys Val Gly Gly Phe Pro Gly Val Leu Gly
85 90 95
Leu Arg Ser Gly His Ser Lys Ala Arg Phe
100 105

<210> 1627
<211> 481
<212> DNA
<213> Homo sapiens

<400> 1627
naccggtgcg ttgtgcccat gccttgtcga acaaggccat ataggccgta ccgacgtgag
60
gatcaccagt gggcgagggg gcaacgcgcg tgcgcgcggg atgcaaatca gtcatgatga
120
cacgaagtct atcgggatcc gctgacagac tccggtaaag ttcccgccat ggcagaacct
180
actggaaacc cggctgagtc cagctcggac ttcattcatc aggttgttcg cgcggacatc
240
caacaggaca cctacggcgg gcgcgtccag acccggttcc cacctgagcc taacggctac
300
ctccacattg gccacgcgaa ggccatcgtc accgatttcg gcgttgccga ggatttcggc
360
ggcacctgca acctgagact tgatgatact aatccaggca ccgaggaaac cgagtatgtc
420
gagtcgatcg ttgcagacat tgagtggtta ggttactccc cggcccacgt tgtccacgcg
480
t
481

<210> 1628
<211> 104
<212> PRT
<213> Homo sapiens

<400> 1628
Met Ala Glu Pro Thr Gly Asn Pro Ala Glu Ser Ser Ser Asp Phe Ile

```
 1               5                  10                  15
His Gln Val Val Arg Ala Asp Ile Gln Gln Asp Thr Tyr Gly Gly Arg
            20                  25                  30
Val Gln Thr Arg Phe Pro Pro Glu Pro Asn Gly Tyr Leu His Ile Gly
        35                  40                  45
His Ala Lys Ala Ile Val Thr Asp Phe Gly Val Ala Glu Asp Phe Gly
    50                  55                  60
Gly Thr Cys Asn Leu Arg Leu Asp Asp Thr Asn Pro Gly Thr Glu Glu
65                  70                  75                  80
Thr Glu Tyr Val Glu Ser Ile Val Ala Asp Ile Glu Trp Leu Gly Tyr
                85                  90                  95
Ser Pro Ala His Val Val His Ala
            100
```

<210> 1629
<211> 4519
<212> DNA
<213> Homo sapiens

<400> 1629

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ccaaattgct gggaatgtcc aaagtgctac caggaggaca gctcggagaa agcccagaag
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cggaaaatgg aagagagtga cgaagaagct gtgcaagcca aagtcctgcg gcccctgcgg
120
agctgcgatg agcctctcac gcccccgcct cattcaccca cttccatgct gcagctcatc
180
catgacccgg tttccccccg gggtatggtg actcggtcat cccctggggc tggccccagc
240
gaccaccaca gtgccagccg cgatgagcgc ttcaaacggc ggcagttgct gcggctgcag
300
gccacagagc gcaccatggt acgggaaaag gagaacaatc ccagcggcaa aaaggagctg
360
tctgaagttg agaaagccaa gatccgggga tcgtacctca ctgtcacgct acagaggccc
420
accaaagagc tccacgggac atccattgtg cccaagctgc aggccatcac ggcctcctct
480
gccaaccttc gccattcccc ccgtgtgcta gtgcagcact gcccagcccg aacccccccag
540
cgtggggatg aggaggggct gggggagag gaggaggaag aggaggagga ggaggaggaa
600
gatgacagtg cagaggaggg gggtgcagcc aggctgaatg gccggggcag ttgggctcag
660
gatggagacg aaagctggat gcagcgggag gtctggatgt ctgtcttccg ctacctcagc
720
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780
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840
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900
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960
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1020
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gatcttcggt gggcagtagg aatcaaggac cctcaaattc gggacttgct tactccaccg
1080
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1140
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1200
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1320
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1440
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1620
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1680
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1740
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1980
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2100
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2160
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2220
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2280
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3180
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4020
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4080
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4140
aatattgtaa atatatattt ttttgttgct gatttagagt caatctccaa tgttgtgcta
4200
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4260

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4320
aagttctcca ctattggttt tagagagagc aaggacatct ttcctctgac acgtgggaat
4380
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4500
aggctttaaa aacaaaaaa
4519

<210> 1630
<211> 496
<212> PRT
<213> Homo sapiens

<400> 1630
Pro Asn Cys Trp Glu Cys Pro Lys Cys Tyr Gln Glu Asp Ser Ser Glu
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Lys Ala Gln Lys Arg Lys Met Glu Glu Ser Asp Glu Glu Ala Val Gln
20 25 30
Ala Lys Val Leu Arg Pro Leu Arg Ser Cys Asp Glu Pro Leu Thr Pro
35 40 45
Pro Pro His Ser Pro Thr Ser Met Leu Gln Leu Ile His Asp Pro Val
50 55 60
Ser Pro Arg Gly Met Val Thr Arg Ser Ser Pro Gly Ala Gly Pro Ser
65 70 75 80
Asp His His Ser Ala Ser Arg Asp Glu Arg Phe Lys Arg Arg Gln Leu
85 90 95
Leu Arg Leu Gln Ala Thr Glu Arg Thr Met Val Arg Glu Lys Glu Asn
100 105 110
Asn Pro Ser Gly Lys Lys Glu Leu Ser Glu Val Glu Lys Ala Lys Ile
115 120 125
Arg Gly Ser Tyr Leu Thr Val Thr Leu Gln Arg Pro Thr Lys Glu Leu
130 135 140
His Gly Thr Ser Ile Val Pro Lys Leu Gln Ala Ile Thr Ala Ser Ser
145 150 155 160
Ala Asn Leu Arg His Ser Pro Arg Val Leu Val Gln His Cys Pro Ala
165 170 175
Arg Thr Pro Gln Arg Gly Asp Glu Glu Gly Leu Gly Gly Glu Glu Glu
180 185 190
Glu Glu Glu Glu Glu Glu Glu Glu Asp Asp Ser Ala Glu Glu Gly Gly
195 200 205
Ala Ala Arg Leu Asn Gly Arg Gly Ser Trp Ala Gln Asp Gly Asp Glu
210 215 220
Ser Trp Met Gln Arg Glu Val Trp Met Ser Val Phe Arg Tyr Leu Ser
225 230 235 240
Arg Arg Glu Leu Cys Glu Cys Met Arg Val Cys Lys Thr Trp Tyr Lys
245 250 255
Trp Cys Cys Asp Lys Arg Leu Trp Thr Lys Ile Asp Leu Ser Arg Cys
260 265 270
Lys Ala Ile Val Pro Gln Ala Leu Ser Gly Ile Ile Lys Arg Gln Pro
275 280 285
Val Ser Leu Asp Leu Ser Trp Thr Asn Ile Ser Lys Lys Gln Leu Thr

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    290                 295                 300
Trp Leu Val Asn Arg Leu Pro Gly Leu Lys Asp Leu Leu Leu Ala Gly
305                 310                 315                 320
Cys Ser Trp Ser Ala Val Ser Ala Leu Ser Thr Ser Ser Cys Pro Leu
                325                 330                 335
Leu Arg Thr Leu Asp Leu Arg Trp Ala Val Gly Ile Lys Asp Pro Gln
            340                 345                 350
Ile Arg Asp Leu Leu Thr Pro Pro Ala Asp Lys Pro Gly Gln Asp Asn
        355                 360                 365
Arg Ser Lys Leu Arg Asn Met Thr Asp Phe Arg Leu Ala Gly Leu Asp
    370                 375                 380
Ile Thr Asp Ala Thr Leu Arg Leu Ile Ile Arg His Met Pro Leu Leu
385                 390                 395                 400
Ser Arg Leu Asp Leu Ser His Cys Ser His Leu Thr Asp Gln Ser Ser
                405                 410                 415
Asn Leu Leu Thr Ala Val Gly Ser Ser Thr Arg Tyr Ser Leu Thr Glu
            420                 425                 430
Leu Asn Met Ala Gly Cys Asn Lys Leu Thr Asp Gln Thr Leu Ile Tyr
        435                 440                 445
Leu Arg Arg Ile Ala Asn Val Thr Leu Ile Asp Leu Arg Gly Cys Lys
    450                 455                 460
Gln Ile Thr Arg Lys Ala Cys Glu His Phe Ile Ser Asp Leu Ser Ile
465                 470                 475                 480
Asn Ser Leu Tyr Cys Leu Ser Asp Glu Lys Leu Ile Gln Lys Ile Ser
                485                 490                 495
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<210> 1631
<211> 330
<212> DNA
<213> Homo sapiens

<400> 1631
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tcagaacccg aacacacgtg cttcagacat ggcgggatgg aagacacttc agactctttt
120
ccatgttgac tctcgcgacg agcttgttga gttgcttggc ttttcgaaag acgacattac
180
caaccaagtt cagcaagctg tgggcgcctt gggtttaccg ccactagaag atgaaaacgc
240
acaaggtgaa gatccggcgt cgcaggtccc gccagtcacc gacgaggacc ccactgcttt
300
cttcgatcaa gttccagatg tgcctctaga
330

<210> 1632
<211> 92
<212> PRT
<213> Homo sapiens

<400> 1632
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Met Gln Cys Gln Asn Pro Asn Thr Arg Ala Ser Asp Met Ala Gly Trp
 1               5                  10                  15
Lys Thr Leu Gln Thr Leu Phe His Val Asp Ser Arg Asp Glu Leu Val
```

```
            20                  25                  30
Glu Leu Leu Gly Phe Ser Lys Asp Asp Ile Thr Asn Gln Val Gln Gln
        35                  40                  45
Ala Val Gly Ala Leu Gly Leu Pro Pro Leu Glu Asp Glu Asn Ala Gln
    50                  55                  60
Gly Glu Asp Pro Ala Ser Gln Val Pro Pro Val Thr Asp Glu Asp Pro
65                  70                  75                  80
Thr Ala Phe Phe Asp Gln Val Pro Asp Val Pro Leu
                85                  90
```

<210> 1633
<211> 259
<212> DNA
<213> Homo sapiens

<400> 1633
nggggggacgt tggctatcaa tcttgtcgga gctttcgtac tggcgacttt gctcgagctg
60
ctcgtccacg ctggccctgg cccaggggtt cgtcgagcgg tgcggctatg catcggtacc
120
ggattgttag gtggatttac gacttattcc gccctcacgg tggaaaccgg ccaacgtgtg
180
atgtcagggc agtggttatg gggtattgcc tatcttttga cgagtgtcgt ggcaggtgca
240
ttgttggcat gggtcatga
259

<210> 1634
<211> 86
<212> PRT
<213> Homo sapiens

<400> 1634
```
Xaa Gly Thr Leu Ala Ile Asn Leu Val Gly Ala Phe Val Leu Ala Thr
 1               5                  10                  15
Leu Leu Glu Leu Leu Val His Ala Gly Pro Gly Pro Gly Val Arg Arg
            20                  25                  30
Ala Val Arg Leu Cys Ile Gly Thr Gly Leu Leu Gly Gly Phe Thr Thr
        35                  40                  45
Tyr Ser Ala Leu Thr Val Glu Thr Gly Gln Arg Val Met Ser Gly Gln
    50                  55                  60
Trp Leu Trp Gly Ile Ala Tyr Leu Leu Thr Ser Val Val Ala Gly Ala
65                  70                  75                  80
Leu Leu Ala Trp Val Met
                85
```

<210> 1635
<211> 792
<212> DNA
<213> Homo sapiens

<400> 1635
nngtcctttt ttatgaaccg gcggactcgg ttggcgttgt ggggcagggg gtggtggagc
60

aagatggcgg ctcatctgtc ctacggccga gtgaacctaa acgtgttgcg cgaggcggtg
120
cgtcgcgagc tgcgcgagtt cctggacaag tgcgcaggaa gcaaggcaat agtttgggat
180
gaatacctaa ctggaccctt tggcctgatt gcacagtatt cactattgaa ggaacatgaa
240
gtggaaaaaa tgttcacact taaaggaaat cgtttgccgg cagctgatgt gaagaatata
300
attttttttg tcagacccag gctagagttg atggatataa tcgctgaaaa cgtgctcagt
360
gaagatagac gaggcccaac gagagatttt catattctgt ttgtgccacg ccgtagcctg
420
ttgtgcgaac agcggttgaa ggatctgggt gtcttgggat cctttattca cagggaggag
480
tacagcttag atctcattcc attcgatggg gatctcttat ccatggaatc agagggtgca
540
ttcaaagagt gctacctgga gggtgaccag acgagcctgt accacgcagc caaggggctg
600
atgaccctgc aagctctgta tggaacgatc ccccagatct ttgggaaagg agaatgcgct
660
cgggtgagaa ccggctgctt tgtggtggta aaggagggcc cttcacaccc caaaagggag
720
gaggaacggg aagctcctta caaacaaatt cagttgatct taattattta tgaatactgt
780
actcatgaat tc
792

<210> 1636
<211> 243
<212> PRT
<213> Homo sapiens

<400> 1636
Met Ala Ala His Leu Ser Tyr Gly Arg Val Asn Leu Asn Val Leu Arg
1 5 10 15
Glu Ala Val Arg Arg Glu Leu Arg Glu Phe Leu Asp Lys Cys Ala Gly
20 25 30
Ser Lys Ala Ile Val Trp Asp Glu Tyr Leu Thr Gly Pro Phe Gly Leu
35 40 45
Ile Ala Gln Tyr Ser Leu Leu Lys Glu His Glu Val Glu Lys Met Phe
50 55 60
Thr Leu Lys Gly Asn Arg Leu Pro Ala Ala Asp Val Lys Asn Ile Ile
65 70 75 80
Phe Phe Val Arg Pro Arg Leu Glu Leu Met Asp Ile Ile Ala Glu Asn
85 90 95
Val Leu Ser Glu Asp Arg Arg Gly Pro Thr Arg Asp Phe His Ile Leu
100 105 110
Phe Val Pro Arg Arg Ser Leu Leu Cys Glu Gln Arg Leu Lys Asp Leu
115 120 125
Gly Val Leu Gly Ser Phe Ile His Arg Glu Glu Tyr Ser Leu Asp Leu
130 135 140
Ile Pro Phe Asp Gly Asp Leu Leu Ser Met Glu Ser Glu Gly Ala Phe
145 150 155 160
Lys Glu Cys Tyr Leu Glu Gly Asp Gln Thr Ser Leu Tyr His Ala Ala

```
                165                 170                 175
Lys Gly Leu Met Thr Leu Gln Ala Leu Tyr Gly Thr Ile Pro Gln Ile
            180                 185                 190
Phe Gly Lys Gly Glu Cys Ala Arg Val Arg Thr Gly Cys Phe Val Val
        195                 200                 205
Val Lys Glu Gly Pro Ser His Pro Lys Arg Glu Glu Glu Arg Glu Ala
    210                 215                 220
Pro Tyr Lys Gln Ile Gln Leu Ile Leu Ile Ile Tyr Glu Tyr Cys Thr
225                 230                 235                 240
His Glu Phe
```

<210> 1637
<211> 357
<212> DNA
<213> Homo sapiens

<400> 1637
ntcatgatga cacagacccc cgcgcaccca ggcttgatct ccctgcaagg catcggcaaa
60
cgttatcagt tggccgggca aaagctgtcc attctcaatg acgtgtgcct gtccatctcc
120
cgcggtgaca gctgcggcat cctcggcgcc tccggttccg gcaagagcac cctgctcaat
180
atccttggcc tgctggacct gcccaacagc ggccagtacc actttgccgg ccacgatatt
240
ttggcgctca ccccggacga actgtcggcg atccgcaact cagntnnaat ggttgtgttc
300
cagagcttca acctgctgcc gcgcctcagc gccctggaca acgtcgccct gcccctg
357

<210> 1638
<211> 119
<212> PRT
<213> Homo sapiens

<400> 1638
```
Xaa Met Met Thr Gln Thr Pro Ala His Pro Gly Leu Ile Ser Leu Gln
 1               5                  10                  15
Gly Ile Gly Lys Arg Tyr Gln Leu Ala Gly Gln Lys Leu Ser Ile Leu
            20                  25                  30
Asn Asp Val Cys Leu Ser Ile Ser Arg Gly Asp Ser Cys Gly Ile Leu
        35                  40                  45
Gly Ala Ser Gly Ser Gly Lys Ser Thr Leu Leu Asn Ile Leu Gly Leu
    50                  55                  60
Leu Asp Leu Pro Asn Ser Gly Gln Tyr His Phe Ala Gly His Asp Ile
65                  70                  75                  80
Leu Ala Leu Thr Pro Asp Glu Leu Ser Ala Ile Arg Asn Ser Xaa Xaa
                85                  90                  95
Met Val Val Phe Gln Ser Phe Asn Leu Leu Pro Arg Leu Ser Ala Leu
            100                 105                 110
Asp Asn Val Ala Leu Pro Leu
        115
```

<210> 1639
<211> 396
<212> DNA
<213> Homo sapiens

<400> 1639
acgcgtgtac gtgcgcgtgt gatttcacat gccctcaaag atattcttac tgaaggcgat
60
aaagttatcg ttatgggaca taagcgacca gatttagatg ctataggtgc agctatcgga
120
gtttcgcgct ttgcatcaat gaataattta gaggcattta tcgttcttaa tgattctgat
180
attgatccga cattacgtcg tgttatggat gagattgata agaaaccgga actaaaagaa
240
cgctttgtaa catcggatga ggcttgggat atgatgactt ctaagacgac tgtcgttgtt
300
gtagatacac ataaacctga aatggtctta gatgaaaatg tcttaaataa agcaaaccgc
360
aaagtagtca ttgatcatca tagacgtggc gaaact
396

<210> 1640
<211> 132
<212> PRT
<213> Homo sapiens

<400> 1640
Thr Arg Val Arg Ala Arg Val Ile Ser His Ala Leu Lys Asp Ile Leu
1 5 10 15
Thr Glu Gly Asp Lys Val Ile Val Met Gly His Lys Arg Pro Asp Leu
20 25 30
Asp Ala Ile Gly Ala Ala Ile Gly Val Ser Arg Phe Ala Ser Met Asn
35 40 45
Asn Leu Glu Ala Phe Ile Val Leu Asn Asp Ser Asp Ile Asp Pro Thr
50 55 60
Leu Arg Arg Val Met Asp Glu Ile Asp Lys Lys Pro Glu Leu Lys Glu
65 70 75 80
Arg Phe Val Thr Ser Asp Glu Ala Trp Asp Met Met Thr Ser Lys Thr
85 90 95
Thr Val Val Val Val Asp Thr His Lys Pro Glu Met Val Leu Asp Glu
100 105 110
Asn Val Leu Asn Lys Ala Asn Arg Lys Val Val Ile Asp His His Arg
115 120 125
Arg Gly Glu Thr
130

<210> 1641
<211> 376
<212> DNA
<213> Homo sapiens

<400> 1641
ttatcagcaa acgacagcag acaagagctc ctggggctct ggggaaatgc tgctgcctgc
60

tggccaaacg aactgatgga tgggctcttg gagtgggaga gactgggcag aagctgtgtg
120
gggtgggtga ctcccaacct aaagaaccca ctgagacata tgtggcttcc ctcttccacc
180
ttcattgcct ctttccgtct agatgctggc aaggggggac ttggtggaca aagagagcta
240
ctattcattc aggagctatg ttacaccagt cactttacat gtgccacttg ctctgggtta
300
aactgtgcct cccctcactc atatgttgaa gtcctaaccc taactacctc agaatgggac
360
gttatttgga aaaaag
376

<210> 1642
<211> 100
<212> PRT
<213> Homo sapiens

<400> 1642
Met Asp Gly Leu Leu Glu Trp Glu Arg Leu Gly Arg Ser Cys Val Gly
1 5 10 15
Trp Val Thr Pro Asn Leu Lys Asn Pro Leu Arg His Met Trp Leu Pro
20 25 30
Ser Ser Thr Phe Ile Ala Ser Phe Arg Leu Asp Ala Gly Lys Gly Gly
35 40 45
Leu Gly Gly Gln Arg Glu Leu Leu Phe Ile Gln Glu Leu Cys Tyr Thr
50 55 60
Ser His Phe Thr Cys Ala Thr Cys Ser Gly Leu Asn Cys Ala Ser Pro
65 70 75 80
His Ser Tyr Val Glu Val Leu Thr Leu Thr Thr Ser Glu Trp Asp Val
85 90 95
Ile Trp Lys Lys
100

<210> 1643
<211> 494
<212> DNA
<213> Homo sapiens

<400> 1643
aagcttccag aattccatag gaacccagct gcccttctgg tacctcagtg aggtggagcc
60
gagtgtctga gagcaggtgc aggagaaggt gtgggctcca cctgggcctc tgaagccagg
120
ggccagaatc cccagatcta ggtccaagag ggggctccat gacctcccca tgctgctcct
180
ctgcttggat ccaggatata agaaaggagg ggcacacact gtgggggaac tctggggtcc
240
cctgtgtgca tcagcgagtc ccgggtctgc cccaccagga tgcaaagggc ctggctgctc
300
cagccccatg ctcacagccc tataagtgca cgatggcacc ctatatcatc taagcggggc
360
tgtgcctcct gaggctttag ggacaccaga atgagccccc ctcggcggag tctggctctg
420

ggtgtgtgga gatgccacct gggacgggaa ccccaggtgc atggagcccc actgcagaca
480
ccatcccccg tgtg
494

<210> 1644
<211> 103
<212> PRT
<213> Homo sapiens

<400> 1644
Met Gly Leu Glu Gln Pro Gly Pro Leu His Pro Gly Gly Ala Asp Pro
1 5 10 15
Gly Leu Ala Asp Ala His Arg Gly Pro Gln Ser Ser Pro Thr Val Cys
20 25 30
Ala Pro Pro Phe Leu Tyr Pro Gly Ser Lys Gln Arg Ser Ser Met Gly
35 40 45
Arg Ser Trp Ser Pro Leu Leu Asp Leu Asp Leu Gly Ile Leu Ala Pro
50 55 60
Gly Phe Arg Gly Pro Gly Gly Ala His Thr Phe Ser Cys Thr Cys Ser
65 70 75 80
Gln Thr Leu Gly Ser Thr Ser Leu Arg Tyr Gln Lys Gly Ser Trp Val
85 90 95
Pro Met Glu Phe Trp Lys Leu
100

<210> 1645
<211> 330
<212> DNA
<213> Homo sapiens

<400> 1645
nnagatctgt cggataatgg ctttggctcc gacatggtga cactggtgct tgccatcggg
60
aggagccggt ctctgaaaca cgtggcccct ggaaggaact tcaacgttcg gtgcaaggag
120
accctggacg atgtcctgca tcggatagcc cagctaatgc aggatgacga ctgtcctttg
180
cagtcactat ccgtggctga gtcgcggttg aagcagggtg ccagcatcct gatccgggct
240
ttgggcacca atcctaaact gacagcgctg gatatcagtg gcaatgccat aggggatgct
300
ggggccaaga tgctagccaa ggctctacgc
330

<210> 1646
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1646
Xaa Asp Leu Ser Asp Asn Gly Phe Gly Ser Asp Met Val Thr Leu Val
1 5 10 15
Leu Ala Ile Gly Arg Ser Arg Ser Leu Lys His Val Ala Leu Gly Arg

```
            20                  25                  30
Asn Phe Asn Val Arg Cys Lys Glu Thr Leu Asp Asp Val Leu His Arg
        35                  40                  45
Ile Ala Gln Leu Met Gln Asp Asp Asp Cys Pro Leu Gln Ser Leu Ser
    50                  55                  60
Val Ala Glu Ser Arg Leu Lys Gln Gly Ala Ser Ile Leu Ile Arg Ala
65                  70                  75                  80
Leu Gly Thr Asn Pro Lys Leu Thr Ala Leu Asp Ile Ser Gly Asn Ala
                85                  90                  95
Ile Gly Asp Ala Gly Ala Lys Met Leu Ala Lys Ala Leu Arg
            100                 105                 110
```

<210> 1647
<211> 501
<212> DNA
<213> Homo sapiens

<400> 1647
aggccgctcg gtgatccgcg gcggcggcag cggcgcttcc tgctaggacc ggccggggcc
60
gtaccggagg ctcgggctcc accgaccctc ctcccacccc ctcccactca ccctctgggc
120
cgcgactgcg cagggcgggg ccggccgaac catgggccgc ggtgtgggct aagctggtgg
180
ccccggcttt agactggacc ccacaatgtt tgcagagatg ttcaggcacg cgggagctga
240
ttacacacaa tgaatggggg caatgagagc agtggagcag acagagctgg gggccctgtg
300
gccacatctg tccccatcgg ctggcagcgc tgtgtgcgag agggtgctgt gctctacatc
360
agtccaagtg gcacagagct gtcttccttg gagcaaaccc ggagctacct cctcagcgat
420
gggacctgca agtgcggtct ggagtgtcca cttaatgtcc ccaaggtttt caactttgac
480
cctttggccc cggtgacccc g
501

<210> 1648
<211> 84
<212> PRT
<213> Homo sapiens

<400> 1648
```
Met Asn Gly Gly Asn Glu Ser Ser Gly Ala Asp Arg Ala Gly Gly Pro
 1               5                  10                  15
Val Ala Thr Ser Val Pro Ile Gly Trp Gln Arg Cys Val Arg Glu Gly
            20                  25                  30
Ala Val Leu Tyr Ile Ser Pro Ser Gly Thr Glu Leu Ser Ser Leu Glu
        35                  40                  45
Gln Thr Arg Ser Tyr Leu Leu Ser Asp Gly Thr Cys Lys Cys Gly Leu
    50                  55                  60
Glu Cys Pro Leu Asn Val Pro Lys Val Phe Asn Phe Asp Pro Leu Ala
65                  70                  75                  80
Pro Val Thr Pro
```

<210> 1649
<211> 441
<212> DNA
<213> Homo sapiens

<400> 1649
gcgtcggcag ctgaacgggt gctactggca atcggcgaac ccgaactgct ggatacgtcc
60
accaactcac ggttgtcgcg catcttctcc aacaaggtga tccggcgcta tccggccttt
120
gaagacttcc acgggatgga agaatgcatc gatcagatcg tttcgtattt ccgccacgcc
180
gcccaaggcc tggaagagaa gaaacagatc ctttacctgc tcggccccgt cggcggcggt
240
aaatcgtccc tggccgaaaa gctgaaacag ctgatcgaga aggtcccctt ctacgccatc
300
aagggctcgc cggtcttcga gtcgcccctg gggttgttca acgccactga agacggcgcg
360
atcctcgagg aagacttcgg gattccacgg cgttacctga acaccatcat gtcgccctgg
420
gcgaccaagc gcctggccga a
441

<210> 1650
<211> 147
<212> PRT
<213> Homo sapiens

<400> 1650
Ala Ser Ala Ala Glu Arg Val Leu Leu Ala Ile Gly Glu Pro Glu Leu
1 5 10 15
Leu Asp Thr Ser Thr Asn Ser Arg Leu Ser Arg Ile Phe Ser Asn Lys
20 25 30
Val Ile Arg Arg Tyr Pro Ala Phe Glu Asp Phe His Gly Met Glu Glu
35 40 45
Cys Ile Asp Gln Ile Val Ser Tyr Phe Arg His Ala Ala Gln Gly Leu
50 55 60
Glu Glu Lys Lys Gln Ile Leu Tyr Leu Leu Gly Pro Val Gly Gly Gly
65 70 75 80
Lys Ser Ser Leu Ala Glu Lys Leu Lys Gln Leu Ile Glu Lys Val Pro
85 90 95
Phe Tyr Ala Ile Lys Gly Ser Pro Val Phe Glu Ser Pro Leu Gly Leu
100 105 110
Phe Asn Ala Thr Glu Asp Gly Ala Ile Leu Glu Glu Asp Phe Gly Ile
115 120 125
Pro Arg Arg Tyr Leu Asn Thr Ile Met Ser Pro Trp Ala Thr Lys Arg
130 135 140
Leu Ala Glu
145

<210> 1651
<211> 408

<212> DNA
<213> Homo sapiens

<400> 1651
nccgcggatc cctccggcat cctggttatc gctccctcga aggaatccgg agcccgactg
60
cgccgcgagc tttccgaacg cctcgaggat tacgccgcac aaacttccat ggtgcgttcc
120
gtacactccc tcgcattcgc gttgctgcgc acagcggccg aggaggagct gcgccttatt
180
accggtgcgg acnaagacgc cgttatccgc gagctgctca cgggccaagc agaagacgga
240
catggctcgt ggcccgcgga gatgcgcccc gcgtggaatn natgtgggct ttcgcggcag
300
ctgcgcgatt tccttttgcg ttccattgaa cgcggcctgg gaccgggtga cctagagagc
360
ctcggtgccg agcacggccg ccccatgtgg tctgcggcgg gtgaattc
408

<210> 1652
<211> 136
<212> PRT
<213> Homo sapiens

<400> 1652
Xaa Ala Asp Pro Ser Gly Ile Leu Val Ile Ala Pro Ser Lys Glu Ser
 1   5   10   15
Gly Ala Arg Leu Arg Arg Glu Leu Ser Glu Arg Leu Glu Asp Tyr Ala
            20   25   30
Ala Gln Thr Ser Met Val Arg Ser Val His Ser Leu Ala Phe Ala Leu
        35   40   45
Leu Arg Thr Ala Ala Glu Glu Glu Leu Arg Leu Ile Thr Gly Ala Asp
    50   55   60
Xaa Asp Ala Val Ile Arg Glu Leu Leu Thr Gly Gln Ala Glu Asp Gly
65   70   75   80
His Gly Ser Trp Pro Ala Glu Met Arg Pro Ala Trp Asn Xaa Cys Gly
                85   90   95
Leu Ser Arg Gln Leu Arg Asp Phe Leu Leu Arg Ser Ile Glu Arg Gly
            100   105   110
Leu Gly Pro Gly Asp Leu Glu Ser Leu Gly Ala Glu His Gly Arg Pro
        115   120   125
Met Trp Ser Ala Ala Gly Glu Phe
    130   135

<210> 1653
<211> 398
<212> DNA
<213> Homo sapiens

<400> 1653
ccagcctctc tccgaccgcg tccttcttcc ggccatacgg cacccaatgt cgcgtcacca
60
tcacccgcgc acatggccat cgctccaccg gacgagttga gtgacaagat ccggtgcatt
120

ctgcgcaccc ttgaacctgg tgacagtgtg aaggagattc tcaacacgtc gcgtgtcgtc
180
ggcattgacg tccagagcag cctgcttatt gctggtgctc agcatctgta cttgttggac
240
gattacttcc agcgtccgaa cggtgaaatc gtcaatgtct gggaagctcc gccacacgag
300
cgcgatgcct tgatcgtggc ggccggtgtc gcacaggtgg cacaaagcag cacacccgtg
360
cagatatggc gctgggaaca gctccgactt tgtctaga
398

<210> 1654
<211> 132
<212> PRT
<213> Homo sapiens

<400> 1654
Pro Ala Ser Leu Arg Pro Arg Pro Ser Ser Gly His Thr Ala Pro Asn
 1   5   10   15
Val Ala Ser Pro Ser Pro Ala His Met Ala Ile Ala Pro Pro Asp Glu
            20   25   30
Leu Ser Asp Lys Ile Arg Cys Ile Leu Arg Thr Leu Glu Pro Gly Asp
        35   40   45
Ser Val Lys Glu Ile Leu Asn Thr Ser Arg Val Val Gly Ile Asp Val
    50   55   60
Gln Ser Ser Leu Leu Ile Ala Gly Ala Gln His Leu Tyr Leu Leu Asp
65   70   75   80
Asp Tyr Phe Gln Arg Pro Asn Gly Glu Ile Val Asn Val Trp Glu Ala
                85   90   95
Pro Pro His Glu Arg Asp Ala Leu Ile Val Ala Ala Gly Val Ala Gln
            100   105   110
Val Ala Gln Ser Ser Thr Pro Val Gln Ile Trp Arg Trp Glu Gln Leu
        115   120   125
Arg Leu Cys Leu
    130

<210> 1655
<211> 1115
<212> DNA
<213> Homo sapiens

<400> 1655
nccctgacct gacctgtcct cgccatggcc gaggccgcct ccggcgccgg gggcacgtcc
60
ctggagggcg agcgtggcaa gaggcccccg ccggagggcg agcctgcagc cccggcgtcc
120
ggagttctgg ataagctttt cggaaagcgg ctcctgcagg ctggtcgcta cctggtgtcc
180
cacaaggcgt ggatgaagac ggtgcctaca gagaactgcg acgtgctgat gaccttccca
240
gacacgaccg atgaccacac gctgctatgg ctgctgaacc acatccgcgt gggcattccc
300
gagctcatcg tgcaagtccg ccaccaccgc cacacgcgtg cctacgcctt ctttgtcacc
360

gccacgtatg agagcctact ccgaggggcc gacgagctgg gtctgcgcaa agcagtgaag
420
gccgagtttg gcgggggcac ccgcggcttc tcctgcgagg aggactttat ctatgagaat
480
gtggagagcg agctacgctt cttcacctcc caggaacgcc agagcatcat ccgcttctgg
540
ctgcagaatt tgcgtgccaa gcagggagaa gcactccaca acgtgcgctt cctggaggac
600
cagccaatca tcccggagct ggcagcacgt gggatcatcc agcaggtgtt ccctgtccac
660
gagcagcgta ttctgaaccg cctcatgaag tcatgggtgc aggccgtgtg tgaaaaccag
720
cctctagatg acatctgtga ttactttggt gtgaaaattg ccatgtactt cgcctggctg
780
ggcttctaca cgtcggctat ggtataccca gctgtcttcg ggtctgtcct gtacacattc
840
acagaggctg atcagacaag ccgggatgtt tcctgcgtgg tctttgccct cttcaacgtg
900
atctggtcga cgctgttcct ataggaatgg aagcgtatag gggctgagct gggatataat
960
tgggggacgc tggactcatc ctgggaagcc gtggaggagc cacgccccca gttcaggtgc
1020
gtgcgacgta tcatccccat cactcgggcc gaggagttct actacccgcc ctggaagcgg
1080
ctgctcttcc agctgcttgt tagcctccgc ctgtg
1115

<210> 1656
<211> 299
<212> PRT
<213> Homo sapiens

<400> 1656
Met Ala Glu Ala Ala Ser Gly Ala Gly Gly Thr Ser Leu Glu Gly Glu
1 5 10 15
Arg Gly Lys Arg Pro Pro Pro Glu Gly Glu Pro Ala Ala Pro Ala Ser
20 25 30
Gly Val Leu Asp Lys Leu Phe Gly Lys Arg Leu Leu Gln Ala Gly Arg
35 40 45
Tyr Leu Val Ser His Lys Ala Trp Met Lys Thr Val Pro Thr Glu Asn
50 55 60
Cys Asp Val Leu Met Thr Phe Pro Asp Thr Thr Asp Asp His Thr Leu
65 70 75 80
Leu Trp Leu Leu Asn His Ile Arg Val Gly Ile Pro Glu Leu Ile Val
85 90 95
Gln Val Arg His His Arg His Thr Arg Ala Tyr Ala Phe Phe Val Thr
100 105 110
Ala Thr Tyr Glu Ser Leu Leu Arg Gly Ala Asp Glu Leu Gly Leu Arg
115 120 125
Lys Ala Val Lys Ala Glu Phe Gly Gly Gly Thr Arg Gly Phe Ser Cys
130 135 140
Glu Glu Asp Phe Ile Tyr Glu Asn Val Glu Ser Glu Leu Arg Phe Phe
145 150 155 160
Thr Ser Gln Glu Arg Gln Ser Ile Ile Arg Phe Trp Leu Gln Asn Leu

```
                165                 170                 175
Arg Ala Lys Gln Gly Glu Ala Leu His Asn Val Arg Phe Leu Glu Asp
            180                 185                 190
Gln Pro Ile Ile Pro Glu Leu Ala Ala Arg Gly Ile Ile Gln Gln Val
        195                 200                 205
Phe Pro Val His Glu Gln Arg Ile Leu Asn Arg Leu Met Lys Ser Trp
    210                 215                 220
Val Gln Ala Val Cys Glu Asn Gln Pro Leu Asp Asp Ile Cys Asp Tyr
225                 230                 235                 240
Phe Gly Val Lys Ile Ala Met Tyr Phe Ala Trp Leu Gly Phe Tyr Thr
                245                 250                 255
Ser Ala Met Val Tyr Pro Ala Val Phe Gly Ser Val Leu Tyr Thr Phe
            260                 265                 270
Thr Glu Ala Asp Gln Thr Ser Arg Asp Val Ser Cys Val Val Phe Ala
        275                 280                 285
Leu Phe Asn Val Ile Trp Ser Thr Leu Phe Leu
    290                 295
```

<210> 1657
<211> 333
<212> DNA
<213> Homo sapiens

<400> 1657
tgtagaggct cgaggtcatc cggaccatgt ggtccaggac gcccccgtcc tccgggcccc
60
gcacggagac gcggcgtcag cacggacagc acgcagtctg tgagcctctg caggcagttc
120
ttggagcccg cgggcttccc gcgccgcttc agggggcggg cggcagctcg ggccggtact
180
tctcccaaaa ctgctccggg caggggcgct ccagcagcct ctgcatgaga cggacggcat
240
ccacgcggcc cgtgtaagtg gcccactcct gcggcgacat tccacggcgg gggtaccctc
300
gcgtggacat ccgcccctgc tagcatcagg gct
333

<210> 1658
<211> 108
<212> PRT
<213> Homo sapiens

<400> 1658
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Met Leu Ala Gly Ala Asp Val His Ala Arg Val Pro Pro Pro Trp Asn
 1               5                  10                  15
Val Ala Ala Gly Val Gly His Leu His Gly Pro Arg Gly Cys Arg Pro
            20                  25                  30
Ser His Ala Glu Ala Ala Gly Ala Pro Leu Pro Gly Ala Val Leu Gly
        35                  40                  45
Glu Val Pro Ala Arg Ala Ala Ala Arg Pro Leu Lys Arg Arg Gly Lys
    50                  55                  60
Pro Ala Gly Ser Lys Asn Cys Leu Gln Arg Leu Thr Asp Cys Val Leu
65                  70                  75                  80
Ser Val Leu Thr Pro Arg Leu Arg Ala Gly Pro Gly Gly Arg Gly Arg
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                85                  90                  95
Pro Gly Pro His Gly Pro Asp Asp Leu Glu Pro Leu
            100                 105

<210> 1659
<211> 382
<212> DNA
<213> Homo sapiens

<400> 1659
nnaagcttat ttgttattac taatattttc cgtgaccaga tgggccgcta tggtgagatt
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tacacaactt acaagatgat tttggatgct attcgtaagg tgcctactgc cactgttctc
120
cttaatggag acagtccact tttctacaag ccagctattc caaatcctgt acagtatttt
180
ggttttgact tggagaaagg cccagcccaa ctggctcact ataataccga aggaattctc
240
tgtcccgact gccaaggcat cctcaaatat gagcataata cctatgcaaa cttgggcgcc
300
tatatctgtg aagactgtgg atgtaaacgt cctgatctcg actatcgctt gacagaactg
360
gttgagttaa ccaacaatcg cn
382

<210> 1660
<211> 127
<212> PRT
<213> Homo sapiens

<400> 1660
Xaa Ser Leu Phe Val Ile Thr Asn Ile Phe Arg Asp Gln Met Gly Arg
 1               5                  10                  15
Tyr Gly Glu Ile Tyr Thr Thr Tyr Lys Met Ile Leu Asp Ala Ile Arg
            20                  25                  30
Lys Val Pro Thr Ala Thr Val Leu Leu Asn Gly Asp Ser Pro Leu Phe
        35                  40                  45
Tyr Lys Pro Ala Ile Pro Asn Pro Val Gln Tyr Phe Gly Phe Asp Leu
    50                  55                  60
Glu Lys Gly Pro Ala Gln Leu Ala His Tyr Asn Thr Glu Gly Ile Leu
65                  70                  75                  80
Cys Pro Asp Cys Gln Gly Ile Leu Lys Tyr Glu His Asn Thr Tyr Ala
                85                  90                  95
Asn Leu Gly Ala Tyr Ile Cys Glu Asp Cys Gly Cys Lys Arg Pro Asp
            100                 105                 110
Leu Asp Tyr Arg Leu Thr Glu Leu Val Glu Leu Thr Asn Asn Arg
        115                 120                 125

<210> 1661
<211> 524
<212> DNA
<213> Homo sapiens

<400> 1661
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acgcgtcgat gatcatggag aagacgcggg ccggctcctt gcctgtgacc ttcttgtaca
60
gctgcgggta gtagagctcc aggctctcga ggaaggccac gtagcccttg tggccggtcc
120
gctgcaggat gtccaggagc acacccactt tccgtttgcg gatgaccagg ttggggtcgc
180
tgagcacctg ctcctcatca tcagggttca ggaccttgca ctgccgcagg taaggtgtga
240
tgcgtgaggg gtcgatgacc gaggtgagcg tcacccggaa gccctccagg acgttccagc
300
actcgtcatc gttctcgtag tccgacatgg cctcagcagg caggctgggg agtgtggggc
360
agtgctgaga gcgatgccgg ctcctgcccc cacccgggcc cagctcccac tccttctcag
420
acgctgggcc agggctctcg tcagggcatc gaggggggatc agcccaggcg catccaggag
480
aggtgcccag ctccgtgtcc catcccacgc ttgatcgctg catg
524

<210> 1662
<211> 174
<212> PRT
<213> Homo sapiens

<400> 1662
Met Gln Arg Ser Ser Val Gly Trp Asp Thr Glu Leu Gly Thr Ser Pro
 1   5   10   15
Gly Cys Ala Trp Ala Asp Pro Pro Arg Cys Pro Asp Glu Ser Pro Gly
            20   25   30
Pro Ala Ser Glu Lys Glu Trp Glu Leu Gly Pro Gly Gly Gly Arg Ser
        35   40   45
Arg His Arg Ser Gln His Cys Pro Thr Leu Pro Ser Leu Pro Ala Glu
    50   55   60
Ala Met Ser Asp Tyr Glu Asn Asp Asp Glu Cys Trp Asn Val Leu Glu
65   70   75   80
Gly Phe Arg Val Thr Leu Thr Ser Val Ile Asp Pro Ser Arg Ile Thr
                85   90   95
Pro Tyr Leu Arg Gln Cys Lys Val Leu Asn Pro Asp Asp Glu Glu Gln
            100   105   110
Val Leu Ser Asp Pro Asn Leu Val Ile Arg Lys Arg Lys Val Gly Val
        115   120   125
Leu Leu Asp Ile Leu Gln Arg Thr Gly His Lys Gly Tyr Val Ala Phe
    130   135   140
Leu Glu Ser Leu Glu Leu Tyr Tyr Pro Gln Leu Tyr Lys Lys Val Thr
145   150   155   160
Gly Lys Glu Pro Ala Arg Val Phe Ser Met Ile Ile Asp Ala
                165   170

<210> 1663
<211> 321
<212> DNA
<213> Homo sapiens

<400> 1663

nnagtacttg tcatgattac gcctagtttg ggtatctatt tctctcagcg ttctcagatc
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tcccgaaccc aagacgacga ggctcggaca cgcgcttcta tctcgaccct tcaagacgag
120
gtcaagaggt ggcacgatcc cgactacgtc cgtgctcagg cgcgctccca gctcggctgg
180
gtgatgccgg gcgaaactgg gtatcaggtc attggagaaa acggtaaggt cattggatcg
240
acgacttctt tggacgaaaa agatccggcg agtgaagcca gcgctgacgc tcggtggtgg
300
caagaggctt gcggatcagt c
321

<210> 1664
<211> 107
<212> PRT
<213> Homo sapiens

<400> 1664
Xaa Val Leu Val Met Ile Thr Pro Ser Leu Gly Ile Tyr Phe Ser Gln
 1   5   10   15
Arg Ser Gln Ile Ser Arg Thr Gln Asp Asp Glu Ala Arg Thr Arg Ala
            20   25   30
Ser Ile Ser Thr Leu Gln Asp Glu Val Lys Arg Trp His Asp Pro Asp
        35   40   45
Tyr Val Arg Ala Gln Ala Arg Ser Gln Leu Gly Trp Val Met Pro Gly
    50   55   60
Glu Thr Gly Tyr Gln Val Ile Gly Glu Asn Gly Lys Val Ile Gly Ser
65   70   75   80
Thr Thr Ser Leu Asp Glu Lys Asp Pro Ala Ser Glu Ala Ser Ala Asp
                85   90   95
Ala Arg Trp Trp Gln Glu Ala Cys Gly Ser Val
            100   105

<210> 1665
<211> 431
<212> DNA
<213> Homo sapiens

<400> 1665
gcttccgaac tcatcaagaa gctcaagagg tataaaatgg ttttgcgctc taccggcggc
60
ggcccgacta tctccggtgg tgaagtactc atgcaacgcg cttttgcgtg gaacttgctc
120
atgagtgcta agtcgatggg cattcatacc tgtatcgata cctccggttt tttgggggct
180
gcggcaacag atgacttttt agagtctgtt gatttggtgt tgctcgacgt caaatcggga
240
gatgaagaaa tctaccgtgc cctcaccggc agagcgttgc aacctaccat cgattttggt
300
gatcgtctca ccgcgctcgg taaagaaatc tggattcggt tcgttgtggt ccccggatac
360
accgactcgg tagagaacgt ggaaaaggtt gccgatatcg tccgcagatg gcgcaccgct
420

gtttcacgcg t
431

<210> 1666
<211> 143
<212> PRT
<213> Homo sapiens

<400> 1666
Ala Ser Glu Leu Ile Lys Lys Leu Lys Arg Tyr Lys Met Val Leu Arg
1 5 10 15
Ser Thr Gly Gly Gly Pro Thr Ile Ser Gly Gly Glu Val Leu Met Gln
20 25 30
Arg Ala Phe Ala Trp Asn Leu Leu Met Ser Ala Lys Ser Met Gly Ile
35 40 45
His Thr Cys Ile Asp Thr Ser Gly Phe Leu Gly Ala Ala Ala Thr Asp
50 55 60
Asp Phe Leu Glu Ser Val Asp Leu Val Leu Leu Asp Val Lys Ser Gly
65 70 75 80
Asp Glu Glu Ile Tyr Arg Ala Leu Thr Gly Arg Ala Leu Gln Pro Thr
85 90 95
Ile Asp Phe Gly Asp Arg Leu Thr Ala Leu Gly Lys Glu Ile Trp Ile
100 105 110
Arg Phe Val Val Val Pro Gly Tyr Thr Asp Ser Val Glu Asn Val Glu
115 120 125
Lys Val Ala Asp Ile Val Arg Arg Trp Arg Thr Ala Val Ser Arg
130 135 140

<210> 1667
<211> 370
<212> DNA
<213> Homo sapiens

<400> 1667
tccgctgaga ccagcgttgg tgacttccca ggtgagactg tccgcaccat ggccaagatc
60
gttgagtcta ctgaggcccg tggcttggac aagatcgcca agatcgactg ggatccgcac
120
accaccagtg gcatcatgtc gaaggcagct gctgagatcg ctgagcgcgc cgaggccaag
180
ttcatcgtgg cctttaccaa gtccggtgac accgcccgtc gtatcgctcg tctgcgtccg
240
agcaccccgc tcatcgtttt cacctctgat gagaccacga ccaagaccct cgcctgggtc
300
tggggcgctc acgccgtcgt taccccggtg tttaagaatg cggaggagct gtaccgctgg
360
gttaacgcgt
370

<210> 1668
<211> 123
<212> PRT
<213> Homo sapiens

<400> 1668
Ser Ala Glu Thr Ser Val Gly Asp Phe Pro Gly Glu Thr Val Arg Thr
1 5 10 15
Met Ala Lys Ile Val Glu Ser Thr Glu Ala Arg Gly Leu Asp Lys Ile
20 25 30
Ala Lys Ile Asp Trp Asp Pro His Thr Thr Ser Gly Ile Met Ser Lys
35 40 45
Ala Ala Ala Glu Ile Ala Glu Arg Ala Glu Ala Lys Phe Ile Val Ala
50 55 60
Phe Thr Lys Ser Gly Asp Thr Ala Arg Arg Ile Ala Arg Leu Arg Pro
65 70 75 80
Ser Thr Pro Leu Ile Val Phe Thr Ser Asp Glu Thr Thr Thr Lys Thr
85 90 95
Leu Ala Trp Val Trp Gly Ala His Ala Val Val Thr Pro Val Phe Lys
100 105 110
Asn Ala Glu Glu Leu Tyr Arg Trp Val Asn Ala
115 120

<210> 1669
<211> 1491
<212> DNA
<213> Homo sapiens

<400> 1669
ggatcctgca gtggtgatct gtcatcgtca cgtcacagaa ctgaacatgg aaatgaacaa
60
cgaaaactcc acccccttct caaacgagtt attcctagct ccgcccccag tccttgcctc
120
tcccagcctt ggtggtaatt agcttgaaag tgggaacgag agtgcggtcc gcaaagaaag
180
gacttctggt tagacactga aatacaaaca gactgccaac gagctctggg caaagctgcc
240
ccgtcttctt ttttcgaaag accctcaaaa actgcctttc cttctgctac caaaacttgg
300
gccctagaaa gtggctgcgg agtggagcag atggacatca ctgagaatgg tagaggaggg
360
gctgtgtttt ctgaggggga gtcatggcag cttgtgctgg gggccaggaa gggaaaaaac
420
caatctggca ttcaggttgt ggaaggcaaa gtgaaacaag aagtcatttg ggaaaatatt
480
atattataaa cacatagaat aatatgtaca cgctcatata catcccaaag agaagcctca
540
aggagttccg tttcttctca aaagaaactt cactatgata aagcattcct atagtgggaa
600
ttaactacaa tgaaataatt taacaatttc atttatgcta tatctgtgtc cactacagag
660
tctacggtga aggctgtgtg gagcgagtgt gtctagtgga ctcgaacacc aacgcgttct
720
tcaaaaatag gcaatgacct gtttttttct attcacattt acaatagcta cacagtgatg
780
aaacgcagac tgaaaaatca aatggcagga cgatggaact gtcgtcaagg ttctcagact
840
tgtggcttct gcacctgtta tacttttgga tacgagtgag ctccacttag cttcgttaag
900

attagaaatt tccatgaaac acttacccac atataaattc tgtgtaaagc tttatttttt
960
tccccaccta ctttaatttt ttttaaaaag tgaaataaga ggaaaaactc ttataaaata
1020
taaggtttaa catacgagag agcgaggaac accccggagg ctgccggtgc gtgtggcttc
1080
atgtttctgt gctacatgag tctagtgtcc tcatcttcca ttgtgacaac ccttctcccc
1140
ccatcacact gtcaatgagc tctaggcaaa gctgccccgt ttgcttttaa cctaagggat
1200
gctgtggttt ggttgactac atttgactac caccactgaa ggcggcggac gtctgaagcg
1260
gctggatacc gcaacgatgg aaaatcaggc gaggtactag cgtggagggc cgggctgcca
1320
ggtcaaggtc gtctgggttc tcaggagcca gtctgtgcca cagaaccatc ggcagctgcc
1380
ttcgtaaggc acctcggtct ggcattcgga aaaccacccc atcttgccag agtcccttgg
1440
tccttgggta gcaaaagccg tatgcgatct aaatcaagct ttcaatcatg a
1491

<210> 1670
<211> 132
<212> PRT
<213> Homo sapiens

<400> 1670
Met Pro Asp Trp Phe Phe Pro Phe Leu Ala Pro Ser Thr Ser Cys His
1 5 10 15
Asp Ser Pro Ser Glu Asn Thr Ala Pro Pro Leu Pro Phe Ser Val Met
20 25 30
Ser Ile Cys Ser Thr Pro Gln Pro Leu Ser Arg Ala Gln Val Leu Val
35 40 45
Ala Glu Gly Lys Ala Val Phe Glu Gly Leu Ser Lys Lys Glu Asp Gly
50 55 60
Ala Ala Leu Pro Arg Ala Arg Trp Gln Ser Val Cys Ile Ser Val Ser
65 70 75 80
Asn Gln Lys Ser Phe Leu Cys Gly Pro His Ser Arg Ser His Phe Gln
85 90 95
Ala Asn Tyr His Gln Gly Trp Glu Arg Gln Gly Leu Gly Ala Glu Leu
100 105 110
Gly Ile Thr Arg Leu Arg Arg Gly Trp Ser Phe Arg Cys Ser Phe Pro
115 120 125
Cys Ser Val Leu
130

<210> 1671
<211> 432
<212> DNA
<213> Homo sapiens

<400> 1671
gcgcgccggg gcgggaggac gccagtcgtc ttcccgcccc tcaccacgac acgaccatta
60

tcgcgacgaa ggaagcccat ggctgaaacc acatcgccgg cacagcggaa acccacggcg
120
gcatcccgca tgaagccggt gtcgcgggtc ggggacacga ttttcgctgg cgcctcgtcg
180
gttattgcca tagccctggc cgtcatcgtc atcctgatgt tcgtcttcct catgaagacg
240
gcagccccga cgttgttggc taacaccgat aacttttttca cgtcccgggc ttggacaacg
300
gatcagaacc cgccggcctt tggtatccag gccctgctat ggacgacagt catctcatcc
360
ctgcttgccc tgctcatcgc agtgccgctc tcggtgggca tcgctctgtt tatcacccag
420
ctcgcaccta gg
432

<210> 1672
<211> 144
<212> PRT
<213> Homo sapiens

<400> 1672
Ala Arg Arg Gly Gly Arg Thr Pro Val Val Phe Pro Pro Leu Thr Thr
 1   5   10   15
Thr Arg Pro Leu Ser Arg Arg Arg Lys Pro Met Ala Glu Thr Thr Ser
            20   25   30
Pro Ala Gln Arg Lys Pro Thr Ala Ala Ser Arg Met Lys Pro Val Ser
        35   40   45
Arg Val Gly Asp Thr Ile Phe Ala Gly Ala Ser Ser Val Ile Ala Ile
    50   55   60
Ala Leu Ala Val Ile Val Ile Leu Met Phe Val Phe Leu Met Lys Thr
65   70   75   80
Ala Ala Pro Thr Leu Leu Ala Asn Thr Asp Asn Phe Phe Thr Ser Arg
                85   90   95
Ala Trp Thr Thr Asp Gln Asn Pro Pro Ala Phe Gly Ile Gln Ala Leu
            100   105   110
Leu Trp Thr Thr Val Ile Ser Ser Leu Leu Ala Leu Leu Ile Ala Val
        115   120   125
Pro Leu Ser Val Gly Ile Ala Leu Phe Ile Thr Gln Leu Ala Pro Arg
    130   135   140

<210> 1673
<211> 401
<212> DNA
<213> Homo sapiens

<400> 1673
tcgcgagcac actccagcct ctggggcgtc tgccagggcc tctgtgtttt gatatactct
60
gacctggcag tgaagctgct gatgaatgca cgacaaagac cagtttgctc cgtaacccca
120
ggctcccagc gtcttttcca tgagccaaag gcctggtcct ggaggggggt gccctgcagc
180
tctgctggcc ttcttccagg ggagttcatt gctgggggtg gccctgcagg gacctccact
240

gtgctgggga ggggaagaag aaggatgcaa caggggggagg ggagaatttg agaaaatagg
300
atgcaaattc tccacttgtg aataaagaaa tagagagcca ttgctaagaa ctatgtttac
360
gcagggttag tgctgggacc cagaaccagt caactggttt t
401

<210> 1674
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1674
Met Ala Leu Tyr Phe Phe Ile His Lys Trp Arg Ile Cys Ile Leu Phe
1 5 10 15
Ser Gln Ile Leu Pro Ser Pro Cys Cys Ile Leu Leu Leu Pro Leu Pro
20 25 30
Ser Thr Val Glu Val Pro Ala Gly Pro Pro Pro Ala Met Asn Ser Pro
35 40 45
Gly Arg Arg Pro Ala Glu Leu Gln Gly Thr Pro Leu Gln Asp Gln Ala
50 55 60
Phe Gly Ser Trp Lys Arg Arg Trp Glu Pro Gly Val Thr Glu Gln Thr
65 70 75 80
Gly Leu Cys Arg Ala Phe Ile Ser Ser Phe Thr Ala Arg Ser Glu Tyr
85 90 95
Ile Lys Thr Gln Arg Pro Trp Gln Thr Pro Gln Arg Leu Glu Cys Ala
100 105 110
Arg

<210> 1675
<211> 500
<212> DNA
<213> Homo sapiens

<400> 1675
gccggcgcac ccacctggga cgtggtgaaa tcggcaaaac tcacctcttt agctacctgc
60
gcgccaaccg cacgggcagc ctcccacacg ccctctagag cgctgctgga cagaatggct
120
tgattgtttg gcatgctctc aggatacccg tttagccagg aaacaccggt aggcttgcta
180
ctatgcgagc agccgacgca cgggtagagg gaattcccac cacagtccct cgcactccac
240
ccgcacacgc cctgggaacc gtcacccgcg gtaccaccgg gtcaatcggc tccgcaaatg
300
cgaccgctgg atgtgccacc accccgcnca tccgcagtgc gctccgtaac gccgtctgca
360
acaccgtccc ctccgtatct gccgacacct gtgccaacac ttgtaccgat gcatgcaccg
420
atgcagcaac aggcgctccg ctcgctatcg atctgggata cggcgccgcc ccctggacca
480
ctgttgagat ggctacgcgt
500

<210> 1676
<211> 97
<212> PRT
<213> Homo sapiens

<400> 1676
Arg Glu Phe Pro Pro Gln Ser Leu Ala Leu His Pro His Thr Pro Trp
1 5 10 15
Glu Pro Ser Pro Ala Val Pro Pro Gly Gln Ser Ala Pro Gln Met Arg
20 25 30
Pro Leu Asp Val Pro Pro Pro Arg Xaa Ser Ala Val Arg Ser Val Thr
35 40 45
Pro Ser Ala Thr Pro Ser Pro Pro Tyr Leu Pro Thr Pro Val Pro Thr
50 55 60
Leu Val Pro Met His Ala Pro Met Gln Gln Gln Ala Leu Arg Ser Leu
65 70 75 80
Ser Ile Trp Asp Thr Ala Pro Pro Pro Gly Pro Leu Leu Arg Trp Leu
85 90 95
Arg

<210> 1677
<211> 631
<212> DNA
<213> Homo sapiens

<400> 1677
nntcatgatt tcctcaatga tgccaaggtg atggaggccg gctatacctg ggtgcaggtg
60
gatttgcgcg gtacgggtgc ttctactggg tgtttgngac tggaatggtc cnncggggag
120
cagcaggatg ttgtgaccgc cgtggaatgg gcggcggtac agccgtggtc gaatggtcgg
180
gtggggcttt tcggtaaatc ctacgatggg gggacggggt cttattgctg caggtaatca
240
gccgcggggg ttggctgctg tggtggcgca ggagccagct atggagccct acacttacct
300
gtataacaat gaggtccttt actacaacgc tattggtacg agcctttctt atgatgagat
360
tgctgcctcc cccggccgtg tccttcacga cactcccgaa tatatgaaga acagtgtcta
420
cgaggtggcc cacccgcatt gcctgtccga caatttgcgt aattctttag accccatccg
480
tagccacaaa taatgggcgg gatcggtctt tccctcacca agacgcataa tttcccccgt
540
gcccttgttt atttccgctg gccttattga ggacaatacg gagcctgatg gtttggtgga
600
attgttgaag gaccgtaagg ctccgacgcg t
631

<210> 1678
<211> 78
<212> PRT

<213> Homo sapiens

<400> 1678
Xaa His Asp Phe Leu Asn Asp Ala Lys Val Met Glu Ala Gly Tyr Thr
1 5 10 15
Trp Val Gln Val Asp Leu Arg Gly Thr Gly Ala Ser Thr Gly Cys Leu
20 25 30
Xaa Leu Glu Trp Ser Xaa Gly Glu Gln Gln Asp Val Val Thr Ala Val
35 40 45
Glu Trp Ala Ala Val Gln Pro Trp Ser Asn Gly Arg Val Gly Leu Phe
50 55 60
Gly Lys Ser Tyr Asp Gly Gly Thr Gly Ser Tyr Cys Cys Arg
65 70 75

<210> 1679
<211> 531
<212> DNA
<213> Homo sapiens

<400> 1679
nctacttaga gcaaaggtag gaaaagaagg cagctaggcg tggctctcat tccttcccac
60
agaatggatt ataagtcgag cctgatccag gatgggaatc ccatggagaa cttggagaag
120
cagctgatct gccctatctg cctggagatg tttaccaagc cagtggtcat cttgccgtgc
180
cagcacaacc tgtgccggaa gtgtgccaat gacatcttcc aggctgcaaa tccctactgg
240
accagccggg gcagctcagt gtccatgtct ggaggccgtt tccgctgccc tacctgccgc
300
cacgaggtga tcatggatcg tcacggagtg tacggcctgc agaggaacct gctggtggag
360
aacatcatcg acatctacaa acaggagtgc tccagtcggc cgctgcagaa gggcagtcac
420
cccatgtaca aggagcacga agatgagaaa atcaacatct actgtctcac gtgtgaggtg
480
cccacctgct ccatgtgcaa ggtgtttggg atccacaagg cctgcgaggt g
531

<210> 1680
<211> 143
<212> PRT
<213> Homo sapiens

<400> 1680
Met Glu Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met
1 5 10 15
Phe Thr Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg
20 25 30
Lys Cys Ala Asn Asp Ile Phe Gln Ala Ala Asn Pro Tyr Trp Thr Ser
35 40 45
Arg Gly Ser Ser Val Ser Met Ser Gly Gly Arg Phe Arg Cys Pro Thr
50 55 60
Cys Arg His Glu Val Ile Met Asp Arg His Gly Val Tyr Gly Leu Gln

65 70 75 80
Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Cys
85 90 95
Ser Ser Arg Pro Leu Gln Lys Gly Ser His Pro Met Tyr Lys Glu His
100 105 110
Glu Asp Glu Lys Ile Asn Ile Tyr Cys Leu Thr Cys Glu Val Pro Thr
115 120 125
Cys Ser Met Cys Lys Val Phe Gly Ile His Lys Ala Cys Glu Val
130 135 140

<210> 1681
<211> 396
<212> DNA
<213> Homo sapiens

<400> 1681
gagttccaca actgcaggac agatgacaag acgttccaat gtgagatgtg tttcagattc
60
ttttccacca acagcaacct ctccaagcac aagaagaagc acggcgacaa gaagtttgcc
120
tgtgaggtct gcagcaagat gttctaccgc aaggacgtca tgctggacca ccagcgccgg
180
cacnctggaa ggagtgcggc gagtgaagcg nnagaggacc tggaggccgg tggggagaac
240
ctggtccgtt acaagaagga gccttccggg tgcccggtgt gtggcaaggt gttctcctgc
300
cggagcaata tgaacaagca cctgctcacc cacggcgaca agaagtacac ctgcgagatc
360
tgcgggcgca agttcttccg cgtggatgtg ctcagg
396

<210> 1682
<211> 132
<212> PRT
<213> Homo sapiens

<400> 1682
Glu Phe His Asn Cys Arg Thr Asp Asp Lys Thr Phe Gln Cys Glu Met
1 5 10 15
Cys Phe Arg Phe Phe Ser Thr Asn Ser Asn Leu Ser Lys His Lys Lys
20 25 30
Lys His Gly Asp Lys Lys Phe Ala Cys Glu Val Cys Ser Lys Met Phe
35 40 45
Tyr Arg Lys Asp Val Met Leu Asp His Gln Arg Arg His Xaa Gly Arg
50 55 60
Ser Ala Ala Ser Glu Ala Xaa Glu Asp Leu Glu Ala Gly Gly Glu Asn
65 70 75 80
Leu Val Arg Tyr Lys Lys Glu Pro Ser Gly Cys Pro Val Cys Gly Lys
85 90 95
Val Phe Ser Cys Arg Ser Asn Met Asn Lys His Leu Leu Thr His Gly
100 105 110
Asp Lys Lys Tyr Thr Cys Glu Ile Cys Gly Arg Lys Phe Phe Arg Val
115 120 125
Asp Val Leu Arg

130

<210> 1683
<211> 676
<212> DNA
<213> Homo sapiens

<400> 1683
nncggccgga caggtcccga gcagccccgc ccaacatgga cccagacccc caggcgggcg
60
tgcaggtggg catgcgggtg gtgcgcggcg tggaccggaa gtggggccag caggacggcg
120
gcgagggcgg cgtgggcacg gtggtggagc ttggccgcca cggcagcccc tcgacacccg
180
accgcacagt ggtcgtgcag tgggaccagg gcacgcgcac caactaccgc gccggctacc
240
agggcgcgca cgacctgctg ctgtacgaca acgcccagat cggcgtccgg caccccaaca
300
tcatctgtga ctgctgcaag aagcacgggc tgcgggggat gcgctggaag tgccgtgtgt
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420
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480
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540
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660
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676

<210> 1684
<211> 154
<212> PRT
<213> Homo sapiens

<400> 1684
Xaa Gly Arg Thr Gly Pro Glu Gln Pro Arg Pro Thr Trp Thr Gln Thr
 1   5   10   15
Pro Arg Arg Ala Cys Arg Trp Ala Cys Gly Trp Cys Ala Ala Trp Thr
            20   25   30
Gly Ser Gly Ala Ser Arg Thr Ala Ala Arg Ala Ala Trp Ala Arg Trp
        35   40   45
Trp Ser Leu Ala Ala Thr Ala Ala Pro Arg His Pro Thr Ala Gln Trp
    50   55   60
Ser Cys Ser Gly Thr Arg Ala Arg Ala Pro Thr Thr Ala Pro Ala Thr
65   70   75   80
Arg Ala Arg Thr Thr Cys Cys Cys Thr Thr Thr Pro Arg Ser Ala Ser
                85   90   95
Gly Thr Pro Thr Ser Ser Val Thr Ala Ala Arg Ser Thr Gly Cys Gly
            100   105   110
Gly Cys Ala Gly Ser Ala Val Cys Ala Trp Thr Thr Thr Ser Ala Arg

115 120 125
Ser Ala Thr Cys Thr Thr Ser Met Ser Ser Pro Thr Pro Ser Thr Ala
130 135 140
Thr Arg Pro Leu Thr Arg Ala Leu Ser His
145 150

<210> 1685
<211> 2740
<212> DNA
<213> Homo sapiens

<400> 1685
ngaggaggag ccggcggcgg ctccggggaa agggaggggg gcgctccgca gccgccgccg
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cccaggggct ggcgagggaa aggcgtacgc gctcagcaga ggggcggcag cggcggggag
120
ggggcctccc cttctccatc ctcctcttct gcgggcaaaa ccccaggaac cggcagcaga
180
aactccggaa gcggcgttgc ggggggcggc agcggtggtg gagggagcta ctggaaagaa
240
ggatgtctgc agtctgagct catccagttc catctcaaga aggagcgggc ggcagcggcg
300
gcggccgcgg ctcagatgca cgctaagaac ggcggcggca gcagtagccg cagctccccg
360
gtgtctggcc cccctgccgt ttgcgagacc ctggccgtcg cctccgcctc cccaatggcg
420
gcggcggcgg agggccccca gcagagcgca gagggcagcg cgagcggcgg gggcatgcag
480
gcggcagcgc ccccttcgtc gcagccgcac ccgcagcagc tccaagagca ggaagaaatg
540
caagaggaga tggagaagct gcgagaggaa aacgagactc tcaagaacga gatcgatgag
600
ctgagaaccg agatggacga gatgagggac actttcttcg aggaggatgc ctgtcaactg
660
caggaaatgc gccacgagtt ggagagagcc aacaaaaact gccggatcct gcagtaccgc
720
ctccgcaaag ccgagcgcaa aaggctccgc tacgcccaga ccggggaaat cgacggggag
780
ctgttgcgca gcctggagca ggacctcaag gttgcaaagg atgtatctgt gagacttcac
840
catgaattag aaaatgtgga agaaaagaga acaacaacag aagatgaaaa tgagaaactg
900
aggcaacagc tcatagaagt tgaaattgca aagcaagctt tacagaatga actggaaaaa
960
atgaaagagt tatccttaaa aagaagagga agcaaagatt tgccaaaatc tgaaaaaaag
1020
gctcaacaga ctcccacaga ggaggacaat gaagatctga agtgccagct gcagtttgtt
1080
aaggaagaag ccgctttgat gagaaagaaa atggccaaga ttgataaaga aaaggacaga
1140
tttgaacacg agctccagaa gtacagatcc ttttatgggg atctggacag tcctttgccc
1200
aaaggagaag ccggaggccc tcccagcact agggaggccg agctcaagct acggctaagg
1260

ctggtggagg aagaagccaa catcctgggc aggaaaatcg tcgaactgga ggtggagaac
1320
agaggcctga aggcggaact ggacgacctt aggggcgatg acnnttcaac ggctcggcca
1380
acccgctcat gagggnagca gagcgaatcc ctgtcggagc tgcggcagca cctgcagctg
1440
gtggaagacg agacggagct gctgcggagg aacgtggccg acctggagga gcagaacaag
1500
cgcatcacgg cggagctcaa caagtacaag tacaagnntc cggcggccac gacagcgcgc
1560
ggcaccacga caacgccana gaccgaggcc ctgcaggagg agctgaaggc ggcgcgcctg
1620
cagatcaacg agctcagcgg caaggtcatg cagctgcagt acgagaaccg cgtgcttatg
1680
tccaacatgc agcgctacga cctggcctcg cacctgggca tccgcggcag cccccgcgac
1740
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1800
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1860
gctgcctcan cgcccactcg ctccttctac ccggcgcccg ggccctggcc caagagcttc
1920
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1980
gaccggctca tcgccgacac gagcaccatc atcaccgagg cgcgcatcnt acgtggccaa
2040
cggggacctg ttnncggact catggacgag gaggacgacg gcagccgcat ccgggagcac
2100
gagctgctct accgcatcaa cgctcagatg aaggccttcc gcaaggagct gcagaccttc
2160
atcgaccgcc tcgaggtgcc caagtctgcg gacgaccgcg gcgccgagga gcccatttcc
2220
gtgagtcaga tgttccagcc tatcatttta cttattctca ttcttgtatt attttcatca
2280
ctttcttaca caacaatatt taaacttgtc ttccttttta cactgttttt tgtactgtaa
2340
atctttcatc atttaccatt cattgtagta ttttcagttt gtttattttg ttcacccttc
2400
aagacaagaa gtaaaagaag tataatttct gtagtaacca atgctataaa aacactgaag
2460
actgcttatt tctttacaaa gatacaactc atcttaccaa gaccaaattc aataagaagc
2520
ccaaacacta aaatatttca ggtaagaaag tgtgacattt ttctgtatga attgttttaa
2580
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2640
ataaaaatgg actacatgtc tcataattat ttctcagtag ttcactatta ttattcaaaa
2700
gctggacgga cattcacaat ttggtcacat ttccaaaaag
2740

<210> 1686
<211> 463
<212> PRT

<213> Homo sapiens

<400> 1686

```
Xaa Gly Gly Ala Gly Gly Gly Ser Gly Glu Arg Glu Gly Gly Ala Pro
 1               5                  10                  15
Gln Pro Pro Pro Pro Arg Gly Trp Arg Gly Lys Gly Val Arg Ala Gln
            20                  25                  30
Gln Arg Gly Gly Ser Gly Gly Glu Gly Ala Ser Pro Ser Pro Ser Ser
        35                  40                  45
Ser Ser Ala Gly Lys Thr Pro Gly Thr Gly Ser Arg Asn Ser Gly Ser
    50                  55                  60
Gly Val Ala Gly Gly Gly Ser Gly Gly Gly Gly Ser Tyr Trp Lys Glu
65                  70                  75                  80
Gly Cys Leu Gln Ser Glu Leu Ile Gln Phe His Leu Lys Lys Glu Arg
                85                  90                  95
Ala Ala Ala Ala Ala Ala Ala Ala Gln Met His Ala Lys Asn Gly Gly
            100                 105                 110
Gly Ser Ser Ser Arg Ser Ser Pro Val Ser Gly Pro Pro Ala Val Cys
        115                 120                 125
Glu Thr Leu Ala Val Ala Ser Ala Ser Pro Met Ala Ala Ala Ala Glu
    130                 135                 140
Gly Pro Gln Gln Ser Ala Glu Gly Ser Ala Ser Gly Gly Gly Met Gln
145                 150                 155                 160
Ala Ala Ala Pro Pro Ser Ser Gln Pro His Pro Gln Gln Leu Gln Glu
                165                 170                 175
Gln Glu Glu Met Gln Glu Glu Met Glu Lys Leu Arg Glu Glu Asn Glu
            180                 185                 190
Thr Leu Lys Asn Glu Ile Asp Glu Leu Arg Thr Glu Met Asp Glu Met
        195                 200                 205
Arg Asp Thr Phe Phe Glu Glu Asp Ala Cys Gln Leu Gln Glu Met Arg
    210                 215                 220
His Glu Leu Glu Arg Ala Asn Lys Asn Cys Arg Ile Leu Gln Tyr Arg
225                 230                 235                 240
Leu Arg Lys Ala Glu Arg Lys Arg Leu Arg Tyr Ala Gln Thr Gly Glu
                245                 250                 255
Ile Asp Gly Glu Leu Leu Arg Ser Leu Glu Gln Asp Leu Lys Val Ala
            260                 265                 270
Lys Asp Val Ser Val Arg Leu His His Glu Leu Glu Asn Val Glu Glu
        275                 280                 285
Lys Arg Thr Thr Thr Glu Asp Glu Asn Glu Lys Leu Arg Gln Gln Leu
    290                 295                 300
Ile Glu Val Glu Ile Ala Lys Gln Ala Leu Gln Asn Glu Leu Glu Lys
305                 310                 315                 320
Met Lys Glu Leu Ser Leu Lys Arg Arg Gly Ser Lys Asp Leu Pro Lys
                325                 330                 335
Ser Glu Lys Lys Ala Gln Gln Thr Pro Thr Glu Glu Asp Asn Glu Asp
            340                 345                 350
Leu Lys Cys Gln Leu Gln Phe Val Lys Glu Glu Ala Ala Leu Met Arg
        355                 360                 365
Lys Lys Met Ala Lys Ile Asp Lys Glu Lys Asp Arg Phe Glu His Glu
    370                 375                 380
Leu Gln Lys Tyr Arg Ser Phe Tyr Gly Asp Leu Asp Ser Pro Leu Pro
385                 390                 395                 400
Lys Gly Glu Ala Gly Gly Pro Pro Ser Thr Arg Glu Ala Glu Leu Lys
```

```
                405                 410                 415
Leu Arg Leu Arg Leu Val Glu Glu Glu Ala Asn Ile Leu Gly Arg Lys
            420                 425                 430
Ile Val Glu Leu Glu Val Glu Asn Arg Gly Leu Lys Ala Glu Leu Asp
        435                 440                 445
Asp Leu Arg Gly Asp Asp Xaa Ser Thr Ala Arg Pro Thr Arg Ser
    450                 455                 460
```

<210> 1687
<211> 326
<212> DNA
<213> Homo sapiens

<400> 1687
gtgcacacag gtgagcgtcc ctacaagtgt ccacactgcg actatgcagg tacccagtcg
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ggctcgctca agtatcacct tcagcgtcac caccgagagc agaagaacag tgcgggttcc
120
tgggcctccc ccagaacccc cgccaccttc ccagcggggc tcactgcagc cgcagtcagg
180
agccaagcca actcaggcct cagccacctg ggtagagggc actgcaagta cccggcctcc
240
ttcgagcagc accggaccag ggtcccgtag gaagcctgct agccctggga ggaccctgcg
300
aaacggcgat gtggtgaagc cgaact
326

<210> 1688
<211> 89
<212> PRT
<213> Homo sapiens

<400> 1688

```
Val His Thr Gly Glu Arg Pro Tyr Lys Cys Pro His Cys Asp Tyr Ala
 1               5                  10                  15
Gly Thr Gln Ser Gly Ser Leu Lys Tyr His Leu Gln Arg His His Arg
            20                  25                  30
Glu Gln Lys Asn Ser Ala Gly Ser Trp Ala Ser Pro Arg Thr Pro Ala
        35                  40                  45
Thr Phe Pro Ala Gly Leu Thr Ala Ala Ala Val Arg Ser Gln Ala Asn
    50                  55                  60
Ser Gly Leu Ser His Leu Gly Arg Gly His Cys Lys Tyr Pro Ala Ser
65                  70                  75                  80
Phe Glu Gln His Arg Thr Arg Val Pro
                85
```

<210> 1689
<211> 301
<212> DNA
<213> Homo sapiens

<400> 1689
nggggaagcc atggctgctt aaggacaatg cactgtcagc tcggtgatgt cttgatttgg
60

tctgggattc tgcacttagt aattgcagat aatactcatg tggcgccaag gaaaaaaaaa
120
ttggcctttt cccagtccat taagcctaaa caaaccacat cactttacat caggcagatc
180
atgtggtacc agaattttcc agtttggcgg actatcttga tcaaatcaac taaattattg
240
ccactgtggc tatctgtgaa agaacacaat gaagaaaatc tggagcctta tctcatactc
300
a
301

<210> 1690
<211> 91
<212> PRT
<213> Homo sapiens

<400> 1690
Met His Cys Gln Leu Gly Asp Val Leu Ile Trp Ser Gly Ile Leu His
1 5 10 15
Leu Val Ile Ala Asp Asn Thr His Val Ala Pro Arg Lys Lys Lys Leu
20 25 30
Ala Phe Ser Gln Ser Ile Lys Pro Lys Gln Thr Thr Ser Leu Tyr Ile
35 40 45
Arg Gln Ile Met Trp Tyr Gln Asn Phe Pro Val Trp Arg Thr Ile Leu
50 55 60
Ile Lys Ser Thr Lys Leu Leu Pro Leu Trp Leu Ser Val Lys Glu His
65 70 75 80
Asn Glu Glu Asn Leu Glu Pro Tyr Leu Ile Leu
85 90

<210> 1691
<211> 483
<212> DNA
<213> Homo sapiens

<400> 1691
nacgcgttcc ggtatgccga tgggccggtg ctgctgggcg tccgccggcg gcgcggtgag
60
ttgtgccttg aagtgtggga ccgcggcccc ggcattcctc aagacaaaca aaagtcattc
120
ttcgaagaat tcaaacgcct ggacagtcac cagacccgcg ccgagaaagg cctgggcctg
180
ggcctggcga ttgccgacgg cttgtgccgc gtgctcgggc atcgcttgag cgtgcgttcg
240
tggccgggca agggcagcgt gttcagcgtg cgcgtgccgt tggcgcgcac ccaggtcagc
300
gcgcctgcca agccggcgca ggaaagcggc cagccgttga gtggcgcgca ggtgctgtgt
360
gtgaataaca aagaaagcat cctgatcggc atgcgcagct tgctcccgcg ctggggctgc
420
gaagtctggc ccgcgcgcga ccaggcgcaa tgtgccgcgc tgttggctga gggtgtgcgg
480
ccg
483

<210> 1692
<211> 161
<212> PRT
<213> Homo sapiens

<400> 1692
Xaa Ala Phe Arg Tyr Ala Asp Gly Pro Val Leu Leu Gly Val Arg Arg
1 5 10 15
Arg Arg Gly Glu Leu Cys Leu Glu Val Trp Asp Arg Gly Pro Gly Ile
20 25 30
Pro Gln Asp Lys Gln Lys Ser Phe Phe Glu Glu Phe Lys Arg Leu Asp
35 40 45
Ser His Gln Thr Arg Ala Glu Lys Gly Leu Gly Leu Gly Leu Ala Ile
50 55 60
Ala Asp Gly Leu Cys Arg Val Leu Gly His Arg Leu Ser Val Arg Ser
65 70 75 80
Trp Pro Gly Lys Gly Ser Val Phe Ser Val Arg Val Pro Leu Ala Arg
85 90 95
Thr Gln Val Ser Ala Pro Ala Lys Pro Ala Gln Glu Ser Gly Gln Pro
100 105 110
Leu Ser Gly Ala Gln Val Leu Cys Val Asn Asn Lys Glu Ser Ile Leu
115 120 125
Ile Gly Met Arg Ser Leu Leu Pro Arg Trp Gly Cys Glu Val Trp Pro
130 135 140
Ala Arg Asp Gln Ala Gln Cys Ala Ala Leu Leu Ala Glu Gly Val Arg
145 150 155 160
Pro

<210> 1693
<211> 333
<212> DNA
<213> Homo sapiens

<400> 1693
acgcgtgttc catctgcagc cgtgcgaaaa ctctcccacc atgtcgcaga ctggatactt
60
cgaggattca agctactaca agtgtgacac agatgacacc ttcgaagccc gagaggagat
120
actgggggg atgaggcctt cgacactgcc aactcctcca tcgtgtctgg cgagagtatc
180
cgttttttg tcaatgtcaa ccttgagatg caggccacca acactgagaa tgaagcgact
240
tccggtggct gtgtgctcct gcacacctcc cgaaaggcca gcatcgtcct gaacgagacg
300
gccacctccc tggataacgt gctgcggacc atg
333

<210> 1694
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1694
Met Val Arg Ser Thr Leu Ser Arg Glu Val Ala Val Ser Phe Arg Thr
1 5 10 15
Met Leu Ala Phe Arg Glu Val Cys Arg Ser Thr Gln Pro Pro Glu Val
20 25 30
Ala Ser Phe Ser Val Leu Val Ala Cys Ile Ser Arg Leu Thr Leu Thr
35 40 45
Lys Lys Arg Ile Leu Ser Pro Asp Thr Met Glu Glu Leu Ala Val Ser
50 55 60
Lys Ala Ser Ser Pro Pro Val Ser Pro Leu Gly Leu Arg Arg Cys His
65 70 75 80
Leu Cys His Thr Cys Ser Ser Leu Asn Pro Arg Ser Ile Gln Ser Ala
85 90 95
Thr Trp Trp Glu Ser Phe Arg Thr Ala Ala Asp Gly Thr Arg
100 105 110

<210> 1695
<211> 485
<212> DNA
<213> Homo sapiens

<400> 1695
tgatcagctt tatcaggagt ttttgcaagt accgcagatt tatgttgaat cctagtaagc
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gccaggaatt tgaagactat cttcaccagg aaatgcaaaa tagcaaggaa aatttcacca
120
cagcacacaa cacatcggga cgttcagctc caccctccac aaatgtccgg agtgcagacc
180
aagagaatgg agaaataacc cttgtaaagc gtcgtatatt tggccacagg attatcactg
240
tcaactttgc gatcaatgat ctatatttct tttctgaaat ggagaaattt aatgatctgg
300
tcagttcagc ccacatgctg caggtcaacc gggcatataa tgagaatgat gtgatcctaa
360
tgcggtccaa aatgaacatt atccaaaaac tcttcctgaa ttctgacatc cctccaaagc
420
tgagggtgaa tgtccctgag ttccagaagg atgccatcct tgctgccatc acagagggct
480
accta
485

<210> 1696
<211> 148
<212> PRT
<213> Homo sapiens

<400> 1696
Met Leu Asn Pro Ser Lys Arg Gln Glu Phe Glu Asp Tyr Leu His Gln
1 5 10 15
Glu Met Gln Asn Ser Lys Glu Asn Phe Thr Thr Ala His Asn Thr Ser
20 25 30
Gly Arg Ser Ala Pro Pro Ser Thr Asn Val Arg Ser Ala Asp Gln Glu
35 40 45
Asn Gly Glu Ile Thr Leu Val Lys Arg Arg Ile Phe Gly His Arg Ile

```
    50                  55                  60
Ile Thr Val Asn Phe Ala Ile Asn Asp Leu Tyr Phe Phe Ser Glu Met
65                  70                  75                  80
Glu Lys Phe Asn Asp Leu Val Ser Ser Ala His Met Leu Gln Val Asn
                85                  90                  95
Arg Ala Tyr Asn Glu Asn Asp Val Ile Leu Met Arg Ser Lys Met Asn
            100                 105                 110
Ile Ile Gln Lys Leu Phe Leu Asn Ser Asp Ile Pro Pro Lys Leu Arg
        115                 120                 125
Val Asn Val Pro Glu Phe Gln Lys Asp Ala Ile Leu Ala Ala Ile Thr
    130                 135                 140
Glu Gly Tyr Leu
145
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<210> 1697
<211> 337
<212> DNA
<213> Homo sapiens

<400> 1697
accaggttcc caccatcctc aggggaatca caggttactg gctttggaga ccgagatgtc
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ttcccgcctc ccaggggcct gtggatggga ctccctgcga attcgactcc caggggaaaa
120
gccaagagct gcctccttgg gacaactggg gcggcagctg tgatcgcaca tggcttcagc
180
agaggcctga gcggctgcct ccgttggcca gcaggctctg agagcactcg cccggcctga
240
ctgttcatcc atcctttcac ccggaggcca gctgtggctg tctgtgctct cagaggggag
300
gcgatgggca aggcgcctgc catgcagatg ggtggtg
337

<210> 1698
<211> 107
<212> PRT
<213> Homo sapiens

<400> 1698

```
Met Ala Gly Ala Leu Pro Ile Ala Ser Pro Leu Arg Ala Gln Thr Ala
 1               5                  10                  15
Thr Ala Gly Leu Arg Val Lys Gly Trp Met Asn Ser Gln Ala Gly Arg
            20                  25                  30
Val Leu Ser Glu Pro Ala Gly Gln Arg Arg Gln Pro Leu Arg Pro Leu
        35                  40                  45
Leu Lys Pro Cys Ala Ile Thr Ala Ala Ala Pro Val Val Pro Arg Arg
    50                  55                  60
Gln Leu Leu Ala Phe Pro Leu Gly Val Glu Phe Ala Gly Ser Pro Ile
65                  70                  75                  80
His Arg Pro Leu Gly Gly Gly Lys Thr Ser Arg Ser Pro Lys Pro Val
                85                  90                  95
Thr Cys Asp Ser Pro Glu Asp Gly Gly Asn Leu
            100                 105
```

<210> 1699
<211> 442
<212> DNA
<213> Homo sapiens

<400> 1699
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aatggtgtgg tgcgcggcaa gcgcatcgaa cgcaccagcc tccacaaggt ttacgagaag
120
ggcattaacc tgcctgcctc tctatttgcc ctggatatca atggctcaac ggtggaaagc
180
accggcctgg gtctggacat cggtgatgct gaccgaatct gttatccaat ccccgacacc
240
ctgtgcaatg aaccctggca aaagcgccca accgcgcaac tgctgatgac catgcacgaa
300
cttgaagggg aacctttttt cgccgatcct cgcgaagtac tccgccaagt tgtaagcaaa
360
tttgacgacc tcggtctgac catctgcgcc gcattcgagc tggagttcta cctgattgac
420
caggagaacg tgaatggccg gc
442

<210> 1700
<211> 147
<212> PRT
<213> Homo sapiens

<400> 1700
Xaa Ala Phe Leu Lys Asp His Pro Glu Val Leu Tyr Val Asp Leu Leu
1 5 10 15
Ile Ala Asp Met Asn Gly Val Val Arg Gly Lys Arg Ile Glu Arg Thr
20 25 30
Ser Leu His Lys Val Tyr Glu Lys Gly Ile Asn Leu Pro Ala Ser Leu
35 40 45
Phe Ala Leu Asp Ile Asn Gly Ser Thr Val Glu Ser Thr Gly Leu Gly
50 55 60
Leu Asp Ile Gly Asp Ala Asp Arg Ile Cys Tyr Pro Ile Pro Asp Thr
65 70 75 80
Leu Cys Asn Glu Pro Trp Gln Lys Arg Pro Thr Ala Gln Leu Leu Met
85 90 95
Thr Met His Glu Leu Glu Gly Glu Pro Phe Phe Ala Asp Pro Arg Glu
100 105 110
Val Leu Arg Gln Val Val Ser Lys Phe Asp Asp Leu Gly Leu Thr Ile
115 120 125
Cys Ala Ala Phe Glu Leu Glu Phe Tyr Leu Ile Asp Gln Glu Asn Val
130 135 140
Asn Gly Arg
145

<210> 1701
<211> 8265
<212> DNA
<213> Homo sapiens

<400> 1701
nacgcgtgaa gggagggcga ggccggagcc cgagggcgac ccgagaagcg gcggggcggc
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gggccggcgg gcggggcgca gagccaggca gcgcaggtat agccaggctg gagaaaagaa
120
gctgccacca tggttgcact ttcactgaag atcagcattg ggaatgtggt gaagacgatg
180
cagtttgagc cgtctaccat ggtgtacgac gcctgccgca tcattcgtga gcggatccca
240
gaggccccag ctggtcctcc cagcgacttt gggctctttc tgtcagatga tgaccccaaa
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360
actatggagt acaggaagaa acagagaccc ctgaagatcc gtatgctgga tggaactgtg
420
aagacgatca tggtggatga ctctaagact gtcactgaca tgctcatgac catctgtgcc
480
cgcattggca tcaccaatca tgatgaatat tcattggttc gagagctgat ggaagaaaag
540
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600
atggagaaac taaagcagaa attgcacaca gatgatgagt tgaactggct ggaccatggt
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cggacactga gggagcaggg tgtagaggag cacgagacgc tgctgctgcg gaggaagttc
720
ttttactcag accagaatgt ggattcccgg gaccctgtac agctgaacct cctgtatgtg
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840
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900
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960
aagatcttcc aggcacacaa gaattgtggg cagatgagtg agattgaggc caaggtccgc
1020
tacgtgaagc tagcccgttc tctcaagact tacggtgtct ccttcttcct ggtgaaggaa
1080
aaaatgaaag ggaagaacaa gctagtgccc aggcttctgg gcatcaccaa ggagtgtgtg
1140
atgcgagtgg atgagaagac caaggaagtg atccaggagt ggaacctcac caacatcaaa
1200
cgctgggctg cgtctcccaa aagcttcacc ctggattttg gagattacca agatggctat
1260
tactcagtac agacaactga aggggagcag attgcacagc tcattgccgg ctacatcgat
1320
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1380
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1440
cgggtgggga aagtggagca tggctctgtg gccctgcctg ccatcatgcg ctctggagcc
1500
tctggtcctg agaatttcca ggtgggcagc atgccccctg cccagcagca gattaccagc
1560

ggccagatgc accgaggaca catgcctcct ctgacttcag cccagcaggc actcactgga
1620
accattaact ccagcatgca ggccgtgcag gctgcccagg ccaccctgga tgactttgac
1680
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Leu Phe Leu Ser Asp Asp Asp Pro Lys Lys Gly Ile Trp Leu Glu Ala
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Gly Lys Ala Leu Asp Tyr Tyr Met Leu Arg Asn Gly Asp Thr Met Glu
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Tyr Arg Lys Lys Gln Arg Pro Leu Lys Ile Arg Met Leu Asp Gly Thr
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            2020                2025                2030
Leu Val Gln Asn Ala Ala Gly Ser Gln Glu Lys Leu Ala Gln Ala Ala
```

```
        2035                2040                2045
Gln Ser Ser Val Ala Thr Ile Thr Arg Leu Ala Asp Val Val Lys Leu
    2050                2055                2060
Gly Ala Ala Ser Leu Gly Ala Glu Asp Pro Glu Thr Gln Val Val Leu
2065                2070                2075                2080
Ile Asn Ala Val Lys Asp Val Ala Lys Ala Leu Gly Asp Leu Ile Ser
                2085                2090                2095
Ala Thr Lys Ala Ala Ala Gly Lys Val Gly Asp Asp Pro Ala Val Trp
            2100                2105                2110
Gln Leu Lys Asn Ser Ala Lys Val Met Val Thr Asn Val Thr Ser Leu
        2115                2120                2125
Leu Lys Thr Val Lys Ala Val Glu Asp Glu Ala Thr Lys Gly Thr Arg
    2130                2135                2140
Ala Leu Glu Ala Thr Thr Glu His Ile Arg Gln Glu Leu Ala Val Phe
2145                2150                2155                2160
Cys Ser Pro Glu Pro Pro Ala Lys Thr Ser Thr Pro Glu Asp Phe Ile
                2165                2170                2175
Arg Met Thr Lys Gly Ile Thr Met Ala Thr Ala Lys Ala Val Ala Ala
            2180                2185                2190
Gly Asn Ser Cys Arg Gln Glu Asp Val Ile Ala Thr Ala Asn Leu Ser
        2195                2200                2205
Arg Arg Ala Ile Ala Asp Met Leu Arg Ala Cys Lys Glu Ala Ala Tyr
    2210                2215                2220
His Pro Glu Val Ala Pro Asp Val Arg Leu Arg Ala Leu His Tyr Gly
2225                2230                2235                2240
Arg Glu Cys Ala Asn Gly Tyr Leu Glu Leu Leu Asp His Val Leu Leu
                2245                2250                2255
Thr Leu Gln Lys Pro Ser Pro Glu Leu Lys Gln Gln Leu Thr Gly His
            2260                2265                2270
Ser Lys Arg Val Ala Gly Ser Val Thr Glu Leu Ile Gln Ala Ala Glu
        2275                2280                2285
Ala Met Lys Gly Thr Glu Trp Val Asp Pro Glu Asp Pro Thr Val Ile
    2290                2295                2300
Ala Glu Asn Glu Leu Leu Gly Ala Ala Ala Ala Ile Glu Ala Ala Ala
2305                2310                2315                2320
Lys Lys Leu Glu Gln Leu Lys Pro Arg Ala Lys Pro Lys Glu Ala Asp
                2325                2330                2335
Glu Ser Leu Asn Phe Glu Glu Gln Ile Leu Glu Ala Ala Lys Ser Ile
            2340                2345                2350
Ala Ala Ala Thr Ser Ala Leu Val Lys Ala Ala Ser Ala Ala Gln Arg
        2355                2360                2365
Glu Leu Val Ala Gln Gly Lys Val Gly Ala Ile Pro Ala Asn Ala Leu
    2370                2375                2380
Asp Asp Gly Gln Trp Ser Gln Gly Leu Ile Ser Ala Ala Arg Met Val
2385                2390                2395                2400
Ala Ala Ala Thr Asn Asn Leu Cys Glu Ala Ala Asn Ala Ala Val Gln
                2405                2410                2415
Gly His Ala Ser Gln Glu Lys Leu Ile Ser Ser Ala Lys Gln Val Ala
            2420                2425                2430
Ala Ser Thr Ala Gln Leu Leu Val Ala Cys Lys Val Lys Ala Asp Gln
        2435                2440                2445
Asp Ser Glu Ala Met Lys Arg Leu Gln Ala Ala Gly Asn Ala Val Lys
    2450                2455                2460
Arg Ala Ser Asp Asn Leu Val Lys Ala Ala Gln Lys Ala Ala Ala Phe
```

2465 2470 2475 2480
Glu Glu Gln Glu Asn Glu Thr Val Val Val Lys Glu Lys Met Val Gly
2485 2490 2495
Gly Ile Ala Gln Ile Ile Ala Ala Gln Glu Glu Met Leu Arg Lys Glu
2500 2505 2510
Arg Glu Leu Glu Glu Ala Arg Lys Lys Leu Ala Gln Ile Arg Gln Gln
2515 2520 2525
Gln Tyr Lys Phe Leu Pro Ser Glu Leu Arg Asp Glu His
2530 2535 2540

<210> 1703
<211> 346
<212> DNA
<213> Homo sapiens

<400> 1703
ggatcccgag gagaaaaatc ctctgttact tcatgggtca tgtgactgag aatcttttta
60
ggaatctgtg atggagaaga atgactcctc ttcttctctg agtcctgtag taatgcattc
120
tctgctctac ccttctccat gactgctgcc tggtctgtcc tagccttgct ctgatccaca
180
ctgagctggc cttgagcagg gtcgcacctg tacatgaaga caatggctgg tttctcactg
240
gactctcctt tcgcctctgt gaaccagtga tggcgctgaa ctggaggaag aggcagcatg
300
tgaatgactg tgccatccat ggccaccaag ttccctttct ctcgct
346

<210> 1704
<211> 106
<212> PRT
<213> Homo sapiens

<400> 1704
Met Asp Gly Thr Val Ile His Met Leu Pro Leu Pro Pro Val Gln Arg
1 5 10 15
His His Trp Phe Thr Glu Ala Lys Gly Glu Ser Ser Glu Lys Pro Ala
20 25 30
Ile Val Phe Met Tyr Arg Cys Asp Pro Ala Gln Gly Gln Leu Ser Val
35 40 45
Asp Gln Ser Lys Ala Arg Thr Asp Gln Ala Ala Val Met Glu Lys Gly
50 55 60
Arg Ala Glu Asn Ala Leu Leu Gln Asp Ser Glu Lys Lys Arg Ser His
65 70 75 80
Ser Ser Pro Ser Gln Ile Pro Lys Lys Ile Leu Ser His Met Thr His
85 90 95
Glu Val Thr Glu Asp Phe Ser Pro Arg Asp
100 105

<210> 1705
<211> 377
<212> DNA
<213> Homo sapiens

<400> 1705
gtgcaccttt tctcaggact cgctcagaag gtccttctgg gaggacaatg gacaagacta
60
aaccatcaaa tccattctca atgggtcaaa ttccaaattt tcctgaaggg ctggcttcta
120
ctggtgctcc aatcgagttg cagaaaggta tacagggtgg agcaagttta tttaatcctg
180
gttttggctg gaaccaaaat ccacaagttc aaaccttgaa gaattctcaa ggttctattc
240
ataatttagt gaggtctgga gttactgttg aaaggaaagt taatgtaggg gcacaaggag
300
cttttaactc tgcccctgca ccacagatgg aatttcccac agttcctcca tacaacccct
360
cttccttcgg agctagc
377

<210> 1706
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1706
Met Asp Lys Thr Lys Pro Ser Asn Pro Phe Ser Met Gly Gln Ile Pro
1 5 10 15
Asn Phe Pro Glu Gly Leu Ala Ser Thr Gly Ala Pro Ile Glu Leu Gln
20 25 30
Lys Gly Ile Gln Gly Gly Ala Ser Leu Phe Asn Pro Gly Phe Gly Trp
35 40 45
Asn Gln Asn Pro Gln Val Gln Thr Leu Lys Asn Ser Gln Gly Ser Ile
50 55 60
His Asn Leu Val Arg Ser Gly Val Thr Val Glu Arg Lys Val Asn Val
65 70 75 80
Gly Ala Gln Gly Ala Phe Asn Ser Ala Pro Ala Pro Gln Met Glu Phe
85 90 95
Pro Thr Val Pro Pro Tyr Asn Pro Ser Ser Phe Gly Ala Ser
100 105 110

<210> 1707
<211> 427
<212> DNA
<213> Homo sapiens

<400> 1707
nnttcggtga acccgaagcc cggacgcagc gccgataccc atgtgcgccc agtactacgc
60
catcacgcca agcgagtgct catcatcggg gccgggctag ccggcatgga ggctgcgcga
120
gttctcagcg aacgcgcaca cgaacctctc atcgtcgagg ccagcgacca cattggcgga
180
gtcatccttg cgggtggtca accttccttc aaggaggacg acctagctct gctggagtgg
240
taccgcacca ccctggagga gttgggcgtg gagattcgac tcaacaccac cgtaacggct
300

gatcttatcg cttccttcgg ggccgatcac gtcgtcctgg cgaccggatc gaggccgcgt
360
cgactcgacc taggtgatga tgccaaggtc attgacgcca ccgacgctct gctcaaccgc
420
gacgcgt
427

<210> 1708
<211> 142
<212> PRT
<213> Homo sapiens

<400> 1708
Xaa Ser Val Asn Pro Lys Pro Gly Arg Ser Ala Asp Thr His Val Arg
1 5 10 15
Pro Val Leu Arg His His Ala Lys Arg Val Leu Ile Ile Gly Ala Gly
20 25 30
Leu Ala Gly Met Glu Ala Ala Arg Val Leu Ser Glu Arg Ala His Glu
35 40 45
Pro Leu Ile Val Glu Ala Ser Asp His Ile Gly Gly Val Ile Leu Ala
50 55 60
Gly Gly Gln Pro Ser Phe Lys Glu Asp Asp Leu Ala Leu Leu Glu Trp
65 70 75 80
Tyr Arg Thr Thr Leu Glu Glu Leu Gly Val Glu Ile Arg Leu Asn Thr
85 90 95
Thr Val Thr Ala Asp Leu Ile Ala Ser Phe Gly Ala Asp His Val Val
100 105 110
Leu Ala Thr Gly Ser Arg Pro Arg Arg Leu Asp Leu Gly Asp Asp Ala
115 120 125
Lys Val Ile Asp Ala Thr Asp Ala Leu Leu Asn Arg Asp Ala
130 135 140

<210> 1709
<211> 446
<212> DNA
<213> Homo sapiens

<400> 1709
acgcgtgaag gggaccagga ggttggacac agaccattgc aatggaaatg atgatttaga
60
ctgttctttt ctgactgatg actgggagtc agggaagatg aatgcagagt ctgtgatcac
120
ctcctcttcc agccacatca tatctcagcc tcctggagga aactcccata gcttgtctct
180
tcagtcccag ttgacagctt ctgaacgttt ccaagagaat agttcggatc attcagaaac
240
caggttgttg caagaggtct tctttcaggc aatcctgctt gctgtgtgct taatcatttc
300
tgcatgtgca agatgggtta tgggagaaat attagccagt gtcttcacat gctcattgat
360
gataactgta gcttatgtga aatcattgtt tctcagcctt gccagctatt tcaaaaccac
420
tgcctgtgct cggtttgtca aaattt
446

<210> 1710
<211> 116
<212> PRT
<213> Homo sapiens

<400> 1710
Met Asn Ala Glu Ser Val Ile Thr Ser Ser Ser Ser His Ile Ile Ser
1 5 10 15
Gln Pro Pro Gly Gly Asn Ser His Ser Leu Ser Leu Gln Ser Gln Leu
20 25 30
Thr Ala Ser Glu Arg Phe Gln Glu Asn Ser Ser Asp His Ser Glu Thr
35 40 45
Arg Leu Leu Gln Glu Val Phe Phe Gln Ala Ile Leu Leu Ala Val Cys
50 55 60
Leu Ile Ile Ser Ala Cys Ala Arg Trp Val Met Gly Glu Ile Leu Ala
65 70 75 80
Ser Val Phe Thr Cys Ser Leu Met Ile Thr Val Ala Tyr Val Lys Ser
85 90 95
Leu Phe Leu Ser Leu Ala Ser Tyr Phe Lys Thr Thr Ala Cys Ala Arg
100 105 110
Phe Val Lys Ile
115

<210> 1711
<211> 426
<212> DNA
<213> Homo sapiens

<400> 1711
nggggggattc atgttagtat ttgtcagaaa aggcttttga aagagccaaa ttaaaaagag
60
cactagaaca tgaacaggga aagcagagga aatacttgta gaaagtattt tttacagctc
120
cctcaataca attcagtaat gttcattcct ggtgagaagt ctgtccgcac acacagcatc
180
agccaagcag cagaagcagt ggtgtctggg gggctgggaa gtttttcccc caaataccca
240
ccccatgcac tgcccagtcc ccagacccca aagactttgt cctcgcctca cgcacctttt
300
gcaggctcac actgtctgtg tgcgcaagag gtagcgacag gagacaatgg ggaaagagct
360
gaaggaggca aacaaggcca gggggaaagc ctacctcgag gcacagaggg gccccaagat
420
ggatat
426

<210> 1712
<211> 119
<212> PRT
<213> Homo sapiens

<400> 1712
Met Asn Arg Glu Ser Arg Gly Asn Thr Cys Arg Lys Tyr Phe Leu Gln

```
 1               5                  10                  15
Leu Pro Gln Tyr Asn Ser Val Met Phe Ile Pro Gly Glu Lys Ser Val
            20                  25                  30
Arg Thr His Ser Ile Ser Gln Ala Ala Glu Ala Val Val Ser Gly Gly
        35                  40                  45
Leu Gly Ser Phe Ser Pro Lys Tyr Pro Pro His Ala Leu Pro Ser Pro
    50                  55                  60
Gln Thr Pro Lys Thr Leu Ser Ser Pro His Ala Pro Phe Ala Gly Ser
65                  70                  75                  80
His Cys Leu Cys Ala Gln Glu Val Ala Thr Gly Asp Asn Gly Glu Arg
                85                  90                  95
Ala Glu Gly Gly Lys Gln Gly Gln Gly Glu Ser Leu Pro Arg Gly Thr
            100                 105                 110
Glu Gly Pro Gln Asp Gly Tyr
        115
```

<210> 1713
<211> 328
<212> DNA
<213> Homo sapiens

<400> 1713
tctagaaagg tttatttcat gggccaaggc ttgtgtttcc aaagccagga agggctgaag
60
ccagaattgg ccctggctgc ttgccacaga gtctggccgg gggaccctgg acctcagcag
120
ggtcatgatg aggtcagctt tggaggagca gggccagcgt gtcctgcttt ctgctcctgg
180
aatgagcctc actccctccc tgctcaaggc agcccttcac ccagccgccg ggacaggtgc
240
cctgtgccac ctgccatccc tgggattctc catctcagtg agtgctccct ggggcctggg
300
aacgcatctg gctggtgact cctggggg
328

<210> 1714
<211> 99
<212> PRT
<213> Homo sapiens

<400> 1714

```
Met Gly Gln Gly Leu Cys Phe Gln Ser Gln Glu Gly Leu Lys Pro Glu
 1               5                  10                  15
Leu Ala Leu Ala Ala Cys His Arg Val Trp Pro Gly Asp Pro Gly Pro
            20                  25                  30
Gln Gln Gly His Asp Glu Val Ser Phe Gly Gly Ala Gly Pro Ala Cys
        35                  40                  45
Pro Ala Phe Cys Ser Trp Asn Glu Pro His Ser Leu Pro Ala Gln Gly
    50                  55                  60
Ser Pro Ser Pro Ser Arg Arg Asp Arg Cys Pro Val Pro Pro Ala Ile
65                  70                  75                  80
Pro Gly Ile Leu His Leu Ser Glu Cys Ser Leu Gly Pro Gly Asn Ala
                85                  90                  95
Ser Gly Trp
```

<210> 1715
<211> 489
<212> DNA
<213> Homo sapiens

<400> 1715
gttgccagcg atgggccgca tttgtacatc ccggtatttc gtgttcggtg tggtgtaaaa
60
gatgccccat gtgtgacatt ctgtggatag ttattgttag cattatttga caagttctag
120
aaatcgatcc acccaggcgt gtagctgcgg tatttcatca gagttgatcg ttgcgatgag
180
ttgatcatgg cctgtcatgg cgtagtcttc tacgtcgtaa agtatgagac aatccacggt
240
aatatggtgt tttttggcca actcggaagc cggggtgtcg gggaagtcgg tccctgtaag
300
gtatgggcct gtcccaatga cgacgtgtgc tgggtccatg aggagttcgt ccaaggttcg
360
aactcattac cgtcgaatac gacgctgtcg ccatcggcgg tgtcgaatcg aatcctcaaa
420
gtgtatccgt actcggtgtc gcgcaacagg tgcctaacct cagcgctagt gggctgtgca
480
ctgacgcgt
489

<210> 1716
<211> 101
<212> PRT
<213> Homo sapiens

<400> 1716
Met Ala Cys His Gly Val Val Phe Tyr Val Val Lys Tyr Glu Thr Ile
 1   5   10   15
His Gly Asn Met Val Phe Phe Gly Gln Leu Gly Ser Arg Gly Val Gly
            20   25   30
Glu Val Gly Pro Cys Lys Val Trp Ala Cys Pro Asn Asp Asp Val Cys
        35   40   45
Trp Val His Glu Glu Phe Val Gln Gly Ser Asn Ser Leu Pro Ser Asn
    50   55   60
Thr Thr Leu Ser Pro Ser Ala Val Ser Asn Arg Ile Leu Lys Val Tyr
65   70   75   80
Pro Tyr Ser Val Ser Arg Asn Arg Cys Leu Thr Ser Ala Leu Val Gly
                85   90   95
Cys Ala Leu Thr Arg
            100

<210> 1717
<211> 312
<212> DNA
<213> Homo sapiens

<400> 1717

nggcatacaa cggagtaaaa accacatcaa cagaagtgga aacaggccca gagagcgtga
60
gaggtttctg gtttcaagaa ggcacactga gtccctgcac ccgatgcctc tccttcccca
120
aatcccactg gaatacacag agagacataa aaacaaggag tgtcctgtag cagagcagcc
180
aggctggctc atgagacaga gggagcagtc ttctgggaga catggctctt gctgctgcgg
240
atcagccaac agatccatgg aaagcaaagg gcccttctcc ggaggcttcc tggggcctgc
300
catgaatgtg tc
312

<210> 1718
<211> 101
<212> PRT
<213> Homo sapiens

<400> 1718
Met Ala Gly Pro Arg Lys Pro Pro Glu Lys Gly Pro Leu Leu Ser Met
1 5 10 15
Asp Leu Leu Ala Asp Pro Gln Gln Gln Glu Pro Cys Leu Pro Glu Asp
20 25 30
Cys Ser Leu Cys Leu Met Ser Gln Pro Gly Cys Ser Ala Thr Gly His
35 40 45
Ser Leu Phe Leu Cys Leu Ser Val Tyr Ser Ser Gly Ile Trp Gly Arg
50 55 60
Arg Gly Ile Gly Cys Arg Asp Ser Val Cys Leu Leu Glu Thr Arg Asn
65 70 75 80
Leu Ser Arg Ser Leu Gly Leu Phe Pro Leu Leu Leu Met Trp Phe Leu
85 90 95
Leu Arg Cys Met Pro
100

<210> 1719
<211> 404
<212> DNA
<213> Homo sapiens

<400> 1719
tgatcaccac ggccctgcca ttttttgtcg ggaccgcaga ccgtatgctg cccctcgaag
60
tcagagacaa tccaaccggc ctgcaaaact gcggtcttgc ccggggcaac gtcgtagggt
120
ccaacagttt ctccaacctc ataggtagaa gaagtgctat agctgctgga aatggagatg
180
tggatcacat cgagcagtgg gaagtcaatg cctgccgaaa ccgaccagtt cttcgtctta
240
gtttctgtga tggatcgcgt gaccggctgc ggagtgtcgt tgagttggaa atcgtcacgt
300
cccagcagag ccatcgaagt agctgcgcac cacatgaacg ggctgtccgt gtcacccgga
360
ttcgagcagg gagcacccat tggtgngtgg tgtccccggg ggtt
404

<210> 1720
<211> 126
<212> PRT
<213> Homo sapiens

<400> 1720
Met Gly Ala Pro Cys Ser Asn Pro Gly Asp Thr Asp Ser Pro Phe Met
1 5 10 15
Trp Cys Ala Ala Thr Ser Met Ala Leu Leu Gly Arg Asp Asp Phe Gln
20 25 30
Leu Asn Asp Thr Pro Gln Pro Val Thr Arg Ser Ile Thr Glu Thr Lys
35 40 45
Thr Lys Asn Trp Ser Val Ser Ala Gly Ile Asp Phe Pro Leu Leu Asp
50 55 60
Val Ile His Ile Ser Ile Ser Ser Ser Tyr Ser Thr Ser Ser Thr Tyr
65 70 75 80
Glu Val Gly Glu Thr Val Gly Pro Tyr Asp Val Ala Pro Gly Lys Thr
85 90 95
Ala Val Leu Gln Ala Gly Trp Ile Val Ser Asp Phe Glu Gly Gln His
100 105 110
Thr Val Cys Gly Pro Asp Lys Lys Trp Gln Gly Arg Gly Asp
115 120 125

<210> 1721
<211> 529
<212> DNA
<213> Homo sapiens

<400> 1721
ccatggccac cctttcagga cagagctgcc cttcccatgc tggaggagcc acagggcctg
60
gtcgctgtgg cttcagcctc ccagctcctc ctgtcctctg ctgggcactt gtaatgtcca
120
ggcactccct gcttggatca ggggatctgg gtttcatctt cccagctcct cctgtcctct
180
gctgggcacc tgtgatgtcc aggcactccc tgcttggatt gggggatctg ggtttcatct
240
tcccagctcc tcctgtcctc cgctgggcac ctgtgatgtc caggcactcc ctgcttggat
300
cgggggtct gggttttgtg ctatacttgg tgctcccttt cactcaggcc ccttcttgac
360
tctgcagagc taccctcgc catctctttc acgcgggcct cctgcagtct ctgtgctcac
420
cctgtgactc tgcttccggt gttgtcaaat gggggtcatc ccaggacccg caccactggg
480
tcgtgtgcag gtttctgggg tggcagagtg cggatgagtg ggcacgcgt
529

<210> 1722
<211> 118
<212> PRT
<213> Homo sapiens

<400> 1722
Met Ala Thr Leu Ser Gly Gln Ser Cys Pro Ser His Ala Gly Gly Ala
1 5 10 15
Thr Gly Pro Gly Arg Cys Gly Phe Ser Leu Pro Ala Pro Pro Val Leu
20 25 30
Cys Trp Ala Leu Val Met Ser Arg His Ser Leu Leu Gly Ser Gly Asp
35 40 45
Leu Gly Phe Ile Phe Pro Ala Pro Pro Val Leu Cys Trp Ala Pro Val
50 55 60
Met Ser Arg His Ser Leu Leu Gly Leu Gly Asp Leu Gly Phe Ile Phe
65 70 75 80
Pro Ala Pro Pro Val Leu Arg Trp Ala Pro Val Met Ser Arg His Ser
85 90 95
Leu Leu Gly Ser Gly Gly Leu Gly Phe Val Leu Tyr Leu Val Leu Pro
100 105 110
Phe Thr Gln Ala Pro Ser
115

<210> 1723
<211> 371
<212> DNA
<213> Homo sapiens

<400> 1723
acgcgtttga agctggatgc atggatatcc agcgccgcca tcgggtcaaa tgggttgacg
60
ctgcccttga tggtcaccgg ggcgtagcga tctaccttac cgttgatgtc gacgctcgcc
120
ggtttggcct ggcggctgtc aatggtgcca atcttcccgt tgagttgttg aatggcagtg
180
gcaaagttgg gcgtgaggct gaagtcggcg aagttggccg agccatcatt gatcgcaacc
240
tgcccaatgt gaatgcccag tggcttctct ttgctggccg ccggctgtct tgttgccagt
300
gtcggccggg tgcgggatca gcaagtcatc gatgttggtg gggcggtcat cggtgatcgc
360
tgcattcaat a
371

<210> 1724
<211> 111
<212> PRT
<213> Homo sapiens

<400> 1724
Met Asp Ile Gln Arg Arg His Arg Val Lys Trp Val Asp Ala Ala Leu
1 5 10 15
Asp Gly His Arg Gly Val Ala Ile Tyr Leu Thr Val Asp Val Asp Ala
20 25 30
Arg Arg Phe Gly Leu Ala Ala Val Asn Gly Ala Asn Leu Pro Val Glu
35 40 45
Leu Leu Asn Gly Ser Gly Lys Val Gly Arg Glu Ala Glu Val Gly Glu
50 55 60
Val Gly Arg Ala Ile Ile Asp Arg Asn Leu Pro Asn Val Asn Ala Gln

65 70 75 80
Trp Leu Leu Phe Ala Gly Arg Arg Leu Ser Cys Cys Gln Cys Arg Pro
85 90 95
Gly Ala Gly Ser Ala Ser His Arg Cys Trp Trp Gly Gly His Arg
100 105 110

<210> 1725
<211> 807
<212> DNA
<213> Homo sapiens

<400> 1725
ngtgcacctg gtatggtgcc ctctgggtct aagcctgtcc ttgtacacac tcacactttg
60
atttgaagtg acctcttccc tctgagcctt ctggtgtcca actctcccct tctctaggac
120
catgcagtgc tggaggccga gaggcagaag atgtcagccc ttgtgcgagg gctgcagagg
180
gagctggagg agacttcaga ggagacaggg cattggcaga gtatgttcca gaagaacaag
240
gaggatctta gagccaccaa gcaggaactc ctgcagctgc gaatggagaa ggaggagatg
300
gaagaggagc ttggagagaa gatagaggtc ttgcagaggg aattagagca ggcccgagct
360
agtgctggag atactcgcca ggttgaggtg ctcaagaagg agctgctccg gacacaggag
420
gagcttaagg aactgcaggc agaacggcag agccaggagg tggctgggcg acaccgggac
480
cgggagttgg agaagcagct ggcggtcctg agggtcgagg ctgatcgagg tcgggagctg
540
gaagaacaga acctccagct acaaaagacc ctccagcaat tgcgacagga ctgtgaagag
600
gcttccaagg ctaagatggt ggccgaggca gaggcaacag tgctggggca gcggcgggcc
660
gcagtggaga cgacgcttcg ggagacccag gaggaaaatg acgaattccg ccggcgcatc
720
ctgggtttgg agcagcagct gaaggagact cgaggtctgg tggatggtgg ggaagcggtg
780
gaggcacgac tacgggacaa gctgcag
807

<210> 1726
<211> 230
<212> PRT
<213> Homo sapiens

<400> 1726
Asp His Ala Val Leu Glu Ala Glu Arg Gln Lys Met Ser Ala Leu Val
1 5 10 15
Arg Gly Leu Gln Arg Glu Leu Glu Glu Thr Ser Glu Glu Thr Gly His
20 25 30
Trp Gln Ser Met Phe Gln Lys Asn Lys Glu Asp Leu Arg Ala Thr Lys
35 40 45
Gln Glu Leu Leu Gln Leu Arg Met Glu Lys Glu Glu Met Glu Glu Glu

```
    50                  55                  60
Leu Gly Glu Lys Ile Glu Val Leu Gln Arg Glu Leu Glu Gln Ala Arg
65                  70                  75                  80
Ala Ser Ala Gly Asp Thr Arg Gln Val Glu Val Leu Lys Lys Glu Leu
                85                  90                  95
Leu Arg Thr Gln Glu Glu Leu Lys Glu Leu Gln Ala Glu Arg Gln Ser
            100                 105                 110
Gln Glu Val Ala Gly Arg His Arg Asp Arg Glu Leu Glu Lys Gln Leu
        115                 120                 125
Ala Val Leu Arg Val Glu Ala Asp Arg Gly Arg Glu Leu Glu Glu Gln
    130                 135                 140
Asn Leu Gln Leu Gln Lys Thr Leu Gln Gln Leu Arg Gln Asp Cys Glu
145                 150                 155                 160
Glu Ala Ser Lys Ala Lys Met Val Ala Glu Ala Glu Ala Thr Val Leu
                165                 170                 175
Gly Gln Arg Arg Ala Ala Val Glu Thr Thr Leu Arg Glu Thr Gln Glu
            180                 185                 190
Glu Asn Asp Glu Phe Arg Arg Arg Ile Leu Gly Leu Glu Gln Gln Leu
        195                 200                 205
Lys Glu Thr Arg Gly Leu Val Asp Gly Gly Glu Ala Val Glu Ala Arg
    210                 215                 220
Leu Arg Asp Lys Leu Gln
225                 230
```

<210> 1727
<211> 474
<212> DNA
<213> Homo sapiens

<400> 1727
aaccaactct ccacaacatc gccagaaaca gtcgctgcca agaggctcca ccatgtttta
60
gcagcttcag aagacaaaga taagatgaaa aaggaagttt tacaaagctc aagggacatt
120
atgcaatcca aatcagcttg cgaaattaaa caaagtcacc aagaatgtag tacccaacaa
180
acacaacaga agaagtattt ggagcagttg cacttgcccc aaagcaaacc aatttcccca
240
aatttcaaag ttaaaaccat caaacttcca actctagatc atacattaaa tgaaacagac
300
cacagctatg aaagtcataa acagcaatct gagattgatg ttcaaacctt taccaaaaaa
360
caatatctga aaaccaagaa aactgaagca agcactgaat gtagtcataa gcaatctctg
420
gctgaaagac attatcagtt acctaagaag gagaaaagag tgacagtaca attg
474

<210> 1728
<211> 130
<212> PRT
<213> Homo sapiens

<400> 1728
Met Lys Lys Glu Val Leu Gln Ser Ser Arg Asp Ile Met Gln Ser Lys

```
 1               5                  10                  15
Ser Ala Cys Glu Ile Lys Gln Ser His Gln Glu Cys Ser Thr Gln Gln
            20                  25                  30
Thr Gln Gln Lys Lys Tyr Leu Glu Gln Leu His Leu Pro Gln Ser Lys
        35                  40                  45
Pro Ile Ser Pro Asn Phe Lys Val Lys Thr Ile Lys Leu Pro Thr Leu
    50                  55                  60
Asp His Thr Leu Asn Glu Thr Asp His Ser Tyr Glu Ser His Lys Gln
65                  70                  75                  80
Gln Ser Glu Ile Asp Val Gln Thr Phe Thr Lys Lys Gln Tyr Leu Lys
                85                  90                  95
Thr Lys Lys Thr Glu Ala Ser Thr Glu Cys Ser His Lys Gln Ser Leu
            100                 105                 110
Ala Glu Arg His Tyr Gln Leu Pro Lys Lys Glu Lys Arg Val Thr Val
        115                 120                 125
Gln Leu
    130
```

<210> 1729
<211> 470
<212> DNA
<213> Homo sapiens

<400> 1729
acgcgtgact cgccataaca ttgctgacac gttttccacg gcaagggagg catcatgacg
60
aggatcgacg tgtggctgtg gtcggtgcgc gtctataagt cccggtcgtt ggctaccgcc
120
gccgtcaagg gcggccacat tcgcctcaat ggagacccgg ttaaaccctc ccacgacgtg
180
aaacccggcg ataccgtcac catccacacc cccggatggg accgggtcct caaggtcatc
240
aacccgatca cgaaaagagt cggcgccaaa ctcgcggtcg aggcttacga agatctgtca
300
nngccccccg acccgcctac ctctctgnct cccctcgccc gccgcgaccg tggggctgga
360
cgacccacca agaaggatcg tcgcgagatc gatcggctcc gaggccggga ctctcgctat
420
tgaggactct tcgcccggcc caacacacca cggctcgcgg ccgaattggc
470

<210> 1730
<211> 131
<212> PRT
<213> Homo sapiens

<400> 1730
```
His Val Phe His Gly Lys Gly Gly Ile Met Thr Arg Ile Asp Val Trp
 1               5                  10                  15
Leu Trp Ser Val Arg Val Tyr Lys Ser Arg Ser Leu Ala Thr Ala Ala
            20                  25                  30
Val Lys Gly Gly His Ile Arg Leu Asn Gly Asp Pro Val Lys Pro Ser
        35                  40                  45
His Asp Val Lys Pro Gly Asp Thr Val Thr Ile His Thr Pro Gly Trp
```

```
    50                  55                  60
Asp Arg Val Leu Lys Val Ile Asn Pro Ile Thr Lys Arg Val Gly Ala
65                  70                  75                  80
Lys Leu Ala Val Glu Ala Tyr Glu Asp Leu Ser Xaa Pro Pro Asp Pro
                85                  90                  95
Pro Thr Ser Leu Xaa Pro Leu Ala Arg Arg Asp Arg Gly Ala Gly Arg
            100                 105                 110
Pro Thr Lys Lys Asp Arg Arg Glu Ile Asp Arg Leu Arg Gly Arg Asp
        115                 120                 125
Ser Arg Tyr
    130
```

<210> 1731
<211> 534
<212> DNA
<213> Homo sapiens

<400> 1731
agcgctccct gcctgctgct gggcggaggg aaggcggcaa gagctgcgga gcccctggaa
60
gagcttccag gaaccctgcg ctgtgggata aaggaatgag gttcagaaag gggcagggag
120
ttgcccgcag ccgcaccgca cgtcttcagc ccgaccgttg tcctgacctc tctgtcccgt
180
cccctgccca gtctcaccat ggccttctgg acacagctga tgctgctgct ctggaagaat
240
ttcatgtatc gccggagaca gccggtccag ctcctggtcg aattgctgtg gcctctcttc
300
ctcttcttca tcctggtggc tgttcgccac tcccacccgc ccctggagca ccatgaatgc
360
cacttcccaa acaagccact gccatcggcg ggcaccgtgc cctggctcca gggtctcatc
420
tgtaatgtga acaacacctg ctttccgcag ctgacaccgg gcgaggagcc cgggcgcctg
480
agcaacttca acgactccct ggtctcccgg ctgctacgtc ggagagaggc tgga
534

<210> 1732
<211> 112
<212> PRT
<213> Homo sapiens

<400> 1732
```
Met Ala Phe Trp Thr Gln Leu Met Leu Leu Leu Trp Lys Asn Phe Met
 1               5                  10                  15
Tyr Arg Arg Arg Gln Pro Val Gln Leu Leu Val Glu Leu Leu Trp Pro
            20                  25                  30
Leu Phe Leu Phe Phe Ile Leu Val Ala Val Arg His Ser His Pro Pro
        35                  40                  45
Leu Glu His His Glu Cys His Phe Pro Asn Lys Pro Leu Pro Ser Ala
    50                  55                  60
Gly Thr Val Pro Trp Leu Gln Gly Leu Ile Cys Asn Val Asn Asn Thr
65                  70                  75                  80
Cys Phe Pro Gln Leu Thr Pro Gly Glu Glu Pro Gly Arg Leu Ser Asn
```

```
                85                  90                  95
Phe Asn Asp Ser Leu Val Ser Arg Leu Leu Arg Arg Arg Glu Ala Gly
            100                 105                 110
```

<210> 1733
<211> 409
<212> DNA
<213> Homo sapiens

<400> 1733
acgcgtgatg gccgatccga ctgtgcccgg tcacgacccg cggcgtccga gtcctgaccc
60
ggacatgccg tggctgatcc gcgacatcac cctcggcaac aacgtgatcg cgggcagcac
120
gggcaactgc accctctgcg tcgaggacta ctcgcgcagg tacgcggcga ggatcctcaa
180
catcgtctcc gacggcaacg tcctgcagcg cgcatcggcc gcacagccag cgtggctggt
240
tggtgtggtc gcggggatca gcgaactccg atccgtacgt attctccagc ctcgacgctt
300
accgggcgac cactggtttt taggaccttc gctcggtctc gatcgatggc gtgctgtcac
360
cgcggccgga gcgctgctcc cgggcattga tctcaaggcg gtcacgagg
409

<210> 1734
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1734
```
Met Ala Asp Pro Thr Val Pro Gly His Asp Pro Arg Arg Pro Ser Pro
 1               5                  10                  15
Asp Pro Asp Met Pro Trp Leu Ile Arg Asp Ile Thr Leu Gly Asn Asn
            20                  25                  30
Val Ile Ala Gly Ser Thr Gly Asn Cys Thr Leu Cys Val Glu Asp Tyr
        35                  40                  45
Ser Arg Arg Tyr Ala Ala Arg Ile Leu Asn Ile Val Ser Asp Gly Asn
    50                  55                  60
Val Leu Gln Arg Ala Ser Ala Ala Gln Pro Ala Trp Leu Val Gly Val
65                  70                  75                  80
Val Ala Gly Ile Ser Glu Leu Arg Ser Val Arg Ile Leu Gln Pro Arg
                85                  90                  95
Arg Leu Pro Gly Asp His Trp Phe Leu Gly Pro Ser Leu Gly Leu Asp
            100                 105                 110
Arg Trp Arg Ala Val Thr Ala Ala Gly Ala Leu Leu Pro Gly Ile Asp
        115                 120                 125
Leu Lys Ala Val Thr Arg
    130
```

<210> 1735
<211> 342
<212> DNA
<213> Homo sapiens

<400> 1735
ggcgccatgg tcatcagcat catgtgttcg gcgcccgctg cacgaatgtt cgtgcgatca
60
agcgcgcctt ttagttcgac gcacggtaaa gcccgtgcgc atcgatgtag gccaggaccg
120
cgtcaggcac caggaaacgt accgacttcc cgctggccgg cagttgacgg atctgggtgg
180
cggacaccgc aagcggggtc tgccagacga atgcaatatt cccgttcggc ccggtcaggg
240
ccaaggggtc acttaccgac cgcgcggcca gcaggttgcg caaggcatcc ggcggttcgc
300
tggcggcatc cgggcgttgc aaaaccagga tgtggcaatg ct
342

<210> 1736
<211> 112
<212> PRT
<213> Homo sapiens

<400> 1736
Met Val Ile Ser Ile Met Cys Ser Ala Pro Ala Ala Arg Met Phe Val
1 5 10 15
Arg Ser Ser Ala Pro Phe Ser Ser Thr His Gly Lys Ala Arg Ala His
20 25 30
Arg Cys Arg Pro Gly Pro Arg Gln Ala Pro Gly Asn Val Pro Thr Ser
35 40 45
Arg Trp Pro Ala Val Asp Gly Ser Gly Trp Arg Thr Pro Gln Ala Gly
50 55 60
Ser Ala Arg Arg Met Gln Tyr Ser Arg Ser Ala Arg Ser Gly Pro Arg
65 70 75 80
Gly His Leu Pro Thr Ala Arg Pro Ala Gly Cys Ala Arg His Pro Ala
85 90 95
Val Arg Trp Arg His Pro Gly Val Ala Lys Pro Gly Cys Gly Asn Ala
100 105 110

<210> 1737
<211> 506
<212> DNA
<213> Homo sapiens

<400> 1737
acgcgtgttc accatgacct ggaccgccca gcggcccgac gggtcgagcg cggaggagtc
60
ggacgagacg actgtggtgg tccctgccat ctcagcgccc cacgggtacg acgtgcaggc
120
gtccggcgcc cacgtcacct cccacccagg cgaccgggtg gcgcggttgc acctcaacca
180
aggcagtacc acggcgaagg tcacgatcac cctgcgctaa cccttcaagc gtcttcagca
240
ccgacctata agtctcccag acacttttac gaccggccct ccccttgggg gtgggccccg
300
tccttttcgt gtcgtgggat gcacctggca gcaccacctc cggcccccat ggagaacagt
360

aggtatcctc gcagggtact acggccaagg catatttgac gttccacgct tgccactgcc
420
gtcttagggc catactgccg ccacgcagct gagacggtga ccaatcgggt aaggtgactg
480
gttgccgtag tccatgcgag gccggc
506

<210> 1738
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1738
Met Ala Leu Arg Arg Gln Trp Gln Ala Trp Asn Val Lys Tyr Ala Leu
1 5 10 15
Ala Val Val Pro Cys Glu Asp Thr Tyr Cys Ser Pro Trp Gly Pro Glu
20 25 30
Val Val Leu Pro Gly Ala Ser His Asp Thr Lys Arg Thr Gly Pro Thr
35 40 45
Pro Arg Gly Arg Ala Gly Arg Lys Ser Val Trp Glu Thr Tyr Arg Ser
50 55 60
Val Leu Lys Thr Leu Glu Gly Leu Ala Gln Gly Asp Arg Asp Leu Arg
65 70 75 80
Arg Gly Thr Ala Leu Val Glu Val Gln Pro Arg His Pro Val Ala Trp
85 90 95
Val Gly Gly Asp Val Gly Ala Gly Arg Leu His Val Val Pro Val Gly
100 105 110
Arg

<210> 1739
<211> 420
<212> DNA
<213> Homo sapiens

<400> 1739
cgcgttattg aaaatgctgc ttttttttact aaattaggac agcgtttaat cggcgcatta
60
catcaagtga cggttgatgg atttgtttac cgtgttgata tgcggttacg ccctttttgga
120
gagtctgggc cattggttag cacgtttaat tcaatagagg actattatca aacccatggt
180
cgagagtggg agtgttatgc catggttaaa gcccgtgtta ttggtgttga ggacgagtat
240
aaacaagcgt tagaaaggat gttaaggcct ttcgtattta gacgttacat tgattttagc
300
gctattgatt ctttgcgaaa aatgaaaacg atgatcagtg ctgaagttcg tcgcaagggg
360
ttaaaagaca atattaagtt gggaatggga gggatccgtg aaattgaatt tgtggctcaa
420

<210> 1740
<211> 140
<212> PRT

<213> Homo sapiens

<400> 1740
Arg Val Ile Glu Asn Ala Ala Phe Phe Thr Lys Leu Gly Gln Arg Leu
1 5 10 15
Ile Gly Ala Leu His Gln Val Thr Val Asp Gly Phe Val Tyr Arg Val
20 25 30
Asp Met Arg Leu Arg Pro Phe Gly Glu Ser Gly Pro Leu Val Ser Thr
35 40 45
Phe Asn Ser Ile Glu Asp Tyr Tyr Gln Thr His Gly Arg Glu Trp Glu
50 55 60
Cys Tyr Ala Met Val Lys Ala Arg Val Ile Gly Val Glu Asp Glu Tyr
65 70 75 80
Lys Gln Ala Leu Glu Arg Met Leu Arg Pro Phe Val Phe Arg Arg Tyr
85 90 95
Ile Asp Phe Ser Ala Ile Asp Ser Leu Arg Lys Met Lys Thr Met Ile
100 105 110
Ser Ala Glu Val Arg Arg Lys Gly Leu Lys Asp Asn Ile Lys Leu Gly
115 120 125
Met Gly Gly Ile Arg Glu Ile Glu Phe Val Ala Gln
130 135 140

<210> 1741
<211> 378
<212> DNA
<213> Homo sapiens

<400> 1741
nnacgcgtcg aggtgattca ggccgacgcc actgacccgc tggtccttca cagtctcaat
60
gggcaggtcg acgtcgtcgt ctccaacccg ccctacgtgc cagccggcgc cgtggaggac
120
accgagacgg cccagcacga gcccacggtg gcgctctatg gcgggggccc ggacgggtga
180
gagattccga ttgacgtcct gngtgcgctc agtcgcgctg ctgccaccgg cggagtgctc
240
gtcatggagc acgaccacga gcagggggcg ctgctgccgg cggccgcttc gtgagccggg
300
ttcaagcagg ccgagaccgg tcaggacctc accggccgcg accgctacct gcgcgcggtg
360
cgtaaacccc gctggtag
378

<210> 1742
<211> 59
<212> PRT
<213> Homo sapiens

<400> 1742
Xaa Arg Val Glu Val Ile Gln Ala Asp Ala Thr Asp Pro Leu Val Leu
1 5 10 15
His Ser Leu Asn Gly Gln Val Asp Val Val Val Ser Asn Pro Pro Tyr
20 25 30
Val Pro Ala Gly Ala Val Glu Asp Thr Glu Thr Ala Gln His Glu Pro

35 40 45
Thr Val Ala Leu Tyr Gly Gly Gly Pro Asp Gly
50 55

<210> 1743
<211> 4121
<212> DNA
<213> Homo sapiens

<400> 1743
atcacgtaca actgcaagga ggagttccag atccatgatg agctgctcaa ggctcattac
60
acgttgggcc ggctctcgga caacacccct gagcactacc tggtgcaagg ccgctacttc
120
ctggtgcggg atgtcactga gaagatggat gtgctgggca ccgtgggaag ctgtggggcc
180
cccaacttcc ggcaggtgca gggtgggctc actgtgttcg gcatgggaca gcccagcctc
240
tcagggttca ggcgggtcct ccagaaactc cagaaggacg gacataggga gtgtgtcatc
300
ttctgtgtgc gggaggaacc tgtgcttttc ctgcgtgcag atgaggactt tgtgtcctac
360
acacctcgag acaagcagaa ccttcatgag aacctccagg gccttggacc cggggtccgg
420
gtggagagcc tggagctggc catccggaaa gagatccacg actttgccca gctgagcgag
480
aacacatacc atgtgtacca taacaccgag gacctgtggg gggagcccca tgctgtggcc
540
atccatggtg aggacgactt gcatgtgacg gaggaggtgt acaagcggcc cctcttcctg
600
cagcccacct acaggtacca ccgcctgccc ctgcccgagc aagggagtcc cctggaggcc
660
cagttggacg cctttgtcag tgttctccgg gagaccccca gcctgctgca gctccgtgat
720
gcccacgggc ctcccccagc cctcgtcttc agctgccaga tgggcgtggg caggaccaac
780
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840
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900
tttctccgca tggtgcccca gggaaggagg atggtggaag aggtggacag agccatcact
960
gcctgtgccg agttgcatga cctgaaagaa gtggtcttgg aaaaccagaa gaagttagaa
1020
ggtatccgac cggagagccc agcccaggga agcggcagcc gacacagcgt ctggcagagg
1080
gcgctgtgga gcctggagcg atacttctac ctgatcctgt ttaactacta ccttcatgag
1140
cagtacccgc tggcctttgc cctcagtttc agccgctggc tgtgtgccca ccctgagctg
1200
taccgcctgc ccgtgacgct gagctcagca ggccctgtgg ctccgaggga cctcatcgcc
1260
aggggctccc tacgggagga cgatctggtc tccccggacg cgctcagcac tgtcagagag
1320

atggatgtgg ccaacttccg gcgggtgccc cgcatgccca tctacggcac ggcccagccc
1380
agcgccaagg ccctggggag catcctggcc tacctgacgg acgccaagag gaggctgcgg
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1680
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1740
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1920
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1980
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2040
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2160
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2280
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2520
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2580
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2640
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2700
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2820
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3060
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3180
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3420
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3480
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3540
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3660
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3720
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3780
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3840
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3900
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3960
cacatcacct ctctgcctca gtttccccat ctgtaaaatg ggagaataat acttgcctac
4020
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4080
gcttttaagc attaaaaaca gctaaatgtg aaaaaaaaaa a
4121

<210> 1744
<211> 796
<212> PRT
<213> Homo sapiens

<400> 1744
Ile Thr Tyr Asn Cys Lys Glu Glu Phe Gln Ile His Asp Glu Leu Leu
1 5 10 15
Lys Ala His Tyr Thr Leu Gly Arg Leu Ser Asp Asn Thr Pro Glu His
20 25 30
Tyr Leu Val Gln Gly Arg Tyr Phe Leu Val Arg Asp Val Thr Glu Lys
35 40 45
Met Asp Val Leu Gly Thr Val Gly Ser Cys Gly Ala Pro Asn Phe Arg

```
    50                  55                  60
Gln Val Gln Gly Gly Leu Thr Val Phe Gly Met Gly Gln Pro Ser Leu
65                  70                  75                  80
Ser Gly Phe Arg Arg Val Leu Gln Lys Leu Gln Lys Asp Gly His Arg
                85                  90                  95
Glu Cys Val Ile Phe Cys Val Arg Glu Glu Pro Val Leu Phe Leu Arg
            100                 105                 110
Ala Asp Glu Asp Phe Val Ser Tyr Thr Pro Arg Asp Lys Gln Asn Leu
        115                 120                 125
His Glu Asn Leu Gln Gly Leu Gly Pro Gly Val Arg Val Glu Ser Leu
    130                 135                 140
Glu Leu Ala Ile Arg Lys Glu Ile His Asp Phe Ala Gln Leu Ser Glu
145                 150                 155                 160
Asn Thr Tyr His Val Tyr His Asn Thr Glu Asp Leu Trp Gly Glu Pro
                165                 170                 175
His Ala Val Ala Ile His Gly Glu Asp Asp Leu His Val Thr Glu Glu
            180                 185                 190
Val Tyr Lys Arg Pro Leu Phe Leu Gln Pro Thr Tyr Arg Tyr His Arg
        195                 200                 205
Leu Pro Leu Pro Glu Gln Gly Ser Pro Leu Glu Ala Gln Leu Asp Ala
    210                 215                 220
Phe Val Ser Val Leu Arg Glu Thr Pro Ser Leu Leu Gln Leu Arg Asp
225                 230                 235                 240
Ala His Gly Pro Pro Pro Ala Leu Val Phe Ser Cys Gln Met Gly Val
                245                 250                 255
Gly Arg Thr Asn Leu Gly Met Val Leu Gly Thr Leu Ile Leu Leu His
            260                 265                 270
Arg Ser Gly Thr Thr Ser Gln Pro Glu Ala Ala Pro Thr Gln Ala Lys
        275                 280                 285
Pro Leu Pro Met Glu Gln Phe Gln Val Ile Gln Ser Phe Leu Arg Met
    290                 295                 300
Val Pro Gln Gly Arg Arg Met Val Glu Glu Val Asp Arg Ala Ile Thr
305                 310                 315                 320
Ala Cys Ala Glu Leu His Asp Leu Lys Glu Val Val Leu Glu Asn Gln
                325                 330                 335
Lys Lys Leu Glu Gly Ile Arg Pro Glu Ser Pro Ala Gln Gly Ser Gly
            340                 345                 350
Ser Arg His Ser Val Trp Gln Arg Ala Leu Trp Ser Leu Glu Arg Tyr
        355                 360                 365
Phe Tyr Leu Ile Leu Phe Asn Tyr Tyr Leu His Glu Gln Tyr Pro Leu
    370                 375                 380
Ala Phe Ala Leu Ser Phe Ser Arg Trp Leu Cys Ala His Pro Glu Leu
385                 390                 395                 400
Tyr Arg Leu Pro Val Thr Leu Ser Ser Ala Gly Pro Val Ala Pro Arg
                405                 410                 415
Asp Leu Ile Ala Arg Gly Ser Leu Arg Glu Asp Asp Leu Val Ser Pro
            420                 425                 430
Asp Ala Leu Ser Thr Val Arg Glu Met Asp Val Ala Asn Phe Arg Arg
        435                 440                 445
Val Pro Arg Met Pro Ile Tyr Gly Thr Ala Gln Pro Ser Ala Lys Ala
    450                 455                 460
Leu Gly Ser Ile Leu Ala Tyr Leu Thr Asp Ala Lys Arg Arg Leu Arg
465                 470                 475                 480
Lys Val Val Trp Val Ser Leu Arg Glu Glu Ala Val Leu Glu Cys Asp
```

```
                485                 490                 495
Gly His Thr Tyr Ser Leu Arg Trp Pro Gly Pro Pro Val Ala Pro Asp
            500                 505                 510
Gln Leu Glu Thr Leu Glu Ala Gln Leu Lys Ala His Leu Ser Glu Pro
        515                 520                 525
Pro Pro Gly Lys Glu Gly Pro Leu Thr Tyr Arg Phe Gln Thr Cys Leu
    530                 535                 540
Thr Met Gln Glu Val Phe Ser Gln His Arg Arg Ala Cys Pro Gly Leu
545                 550                 555                 560
Thr Tyr His Arg Ile Pro Met Pro Asp Phe Cys Ala Pro Arg Glu Glu
                565                 570                 575
Asp Phe Asp Gln Leu Leu Glu Ala Leu Arg Ala Ala Leu Ser Lys Asp
            580                 585                 590
Pro Gly Thr Gly Phe Val Phe Ser Cys Leu Ser Gly Gln Gly Arg Thr
        595                 600                 605
Thr Thr Ala Met Val Val Ala Val Leu Ala Phe Trp His Ile Gln Gly
    610                 615                 620
Phe Pro Glu Val Gly Glu Glu Glu Leu Val Ser Val Pro Asp Ala Lys
625                 630                 635                 640
Phe Thr Lys Gly Glu Phe Gln Val Val Met Lys Val Val Gln Leu Leu
                645                 650                 655
Pro Asp Gly His Arg Val Lys Lys Glu Val Asp Ala Ala Leu Asp Thr
            660                 665                 670
Val Ser Glu Thr Met Thr Pro Met His Tyr His Leu Arg Glu Ile Ile
        675                 680                 685
Ile Cys Thr Tyr Arg Gln Ala Lys Ala Ala Lys Glu Ala Gln Glu Met
    690                 695                 700
Arg Arg Leu Gln Leu Arg Ser Leu Gln Tyr Leu Glu Arg Tyr Val Cys
705                 710                 715                 720
Leu Ile Leu Phe Asn Ala Tyr Leu His Leu Glu Lys Ala Asp Ser Trp
                725                 730                 735
Gln Arg Pro Phe Ser Thr Trp Met Gln Glu Val Ala Ser Lys Ala Gly
            740                 745                 750
Ile Tyr Glu Ile Leu Asn Glu Leu Gly Phe Pro Glu Leu Glu Ser Gly
        755                 760                 765
Glu Asp Gln Pro Phe Ser Arg Leu Arg Tyr Arg Trp Gln Glu Gln Ser
    770                 775                 780
Cys Ser Leu Glu Pro Ser Ala Pro Glu Asp Leu Leu
785                 790                 795
```

<210> 1745
<211> 426
<212> DNA
<213> Homo sapiens

<400> 1745
ntcatgaaaa ttaaaaaatg gcttggtgta gcagcccttg ctacagtcgc aggtttggct
60
cttgcagctt gcggaaactc agaaaagaaa gcagacaatg caacaactat caaaatcgca
120
actgttaacc gtagcggttc tgaagaaaaa cgttgggaca aaatccaaga attggttaaa
180
aaagacggta tcactttgga atttacggag ttcacaggct actcacaacc aaacaaggca
240

actgctgatg gcgaagtaga tttgaacgct ttccaacact ataacttctt gaacaactgg
300
aacaaagaaa acgggaaaga ccttgtagcg attgcagata cttacatctc tccaatccgt
360
ctttactcag gtttgaatgg aagtgacaac aagtacacta aagtagaggc tggagtgtgc
420
tcgcga
426

<210> 1746
<211> 142
<212> PRT
<213> Homo sapiens

<400> 1746
Xaa Met Lys Ile Lys Lys Trp Leu Gly Val Ala Ala Leu Ala Thr Val
 1   5   10   15
Ala Gly Leu Ala Leu Ala Ala Cys Gly Asn Ser Glu Lys Lys Ala Asp
            20   25   30
Asn Ala Thr Thr Ile Lys Ile Ala Thr Val Asn Arg Ser Gly Ser Glu
        35   40   45
Glu Lys Arg Trp Asp Lys Ile Gln Glu Leu Val Lys Lys Asp Gly Ile
    50   55   60
Thr Leu Glu Phe Thr Glu Phe Thr Gly Tyr Ser Gln Pro Asn Lys Ala
65   70   75   80
Thr Ala Asp Gly Glu Val Asp Leu Asn Ala Phe Gln His Tyr Asn Phe
                85   90   95
Leu Asn Asn Trp Asn Lys Glu Asn Gly Lys Asp Leu Val Ala Ile Ala
            100   105   110
Asp Thr Tyr Ile Ser Pro Ile Arg Leu Tyr Ser Gly Leu Asn Gly Ser
        115   120   125
Asp Asn Lys Tyr Thr Lys Val Glu Ala Gly Val Cys Ser Arg
    130   135   140

<210> 1747
<211> 373
<212> DNA
<213> Homo sapiens

<400> 1747
nnaagctttt gtccacacag ataggaagta atcatggtca ctcaccgccc agaactgcat
60
atcaccgccc ctgaaggcgt gttggaggca ccggcggggt cgctcctcaa ggacggcacg
120
tggcacatca tgtaccagta cgaaccacac gcggatgggc acggcctctg gggacatgtc
180
acttccccca acttctctcc ctttaactgg acagacggag aagacattct ggttccagag
240
ggcgaggaaa ccgacctgtg ggcaggttct gttattagca acgctggaaa agtgacgctg
300
ttttttacct ccgtcaaggg cgacnaagac ggaaatccat cgggcagatg tcgccgacgg
360
caaagctacg cgt
373

<210> 1748
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1748
Met Val Thr His Arg Pro Glu Leu His Ile Thr Ala Pro Glu Gly Val
1 5 10 15
Leu Glu Ala Pro Ala Gly Ser Leu Leu Lys Asp Gly Thr Trp His Ile
20 25 30
Met Tyr Gln Tyr Glu Pro His Ala Asp Gly His Gly Leu Trp Gly His
35 40 45
Val Thr Ser Pro Asn Phe Ser Pro Phe Asn Trp Thr Asp Gly Glu Asp
50 55 60
Ile Leu Val Pro Glu Gly Glu Glu Thr Asp Leu Trp Ala Gly Ser Val
65 70 75 80
Ile Ser Asn Ala Gly Lys Val Thr Leu Phe Phe Thr Ser Val Lys Gly
85 90 95
Asp Xaa Asp Gly Asn Pro Ser Gly Arg Cys Arg Arg Arg Gln Ser Tyr
100 105 110
Ala

<210> 1749
<211> 853
<212> DNA
<213> Homo sapiens

<400> 1749
cccagcaggc aaagagagag gcctccctgg cttcgagtgt caggggagcc gcgttccctc
60
ccagggctgg agcagaggac cacaaggcag cagaaagcgc gggtccagat gagggccagg
120
aaggggagga gagtgagggc caagaacgag ccttaaggga gcagtcccaa gctggagcca
180
cccagggctg ggtctgggag tcctcagtgt ccacttgtcc caggttaggg ggcttgcctt
240
gctctctcca gggccagtct ctgtgtgtgg ggactcagcc cgtggccggc agatgccatc
300
caggatgtac aaggtgcagc caaggcaggc catgcagggg ccgggcctgt ctgcagctgg
360
tggatgcctg tgggcatggc tttctctggg gaccccattc ctgtcagtag caaccctggc
420
agtgtccgga gcggctctag acaactttgg tcataggaac tctggaggtg ggttctggtc
480
atctgaggtg gctactcaac aggtttgagg ccccacagca acagaagtcc aggacccact
540
aggttgcctc agaagcccta agactgatga gctggagcgc gcatttgaga gaagcctcgc
600
acccactgtg tactggcccc gctcaggccg gcctggcaca ccgttgcctg ctggcggctc
660
tcatggggaa gcgcctgggc actggggatt gcttgtggcc cactcaactc ttggggcagt
720

ggccgtaacc ctagtttgcc tgaggccctt atgtcccctt atgttcctgg tactggagct
780
tgagctcttg cctggcacgc tgcagctgca cccaccctgc ttgatcccac ctgggaggcc
840
aggacactga gga
853

<210> 1750
<211> 64
<212> PRT
<213> Homo sapiens

<400> 1750
Glu Lys Pro Arg Thr His Cys Val Leu Ala Pro Leu Arg Pro Ala Trp
1 5 10 15
His Thr Val Ala Cys Trp Arg Leu Ser Trp Gly Ser Ala Trp Ala Leu
20 25 30
Gly Ile Ala Cys Gly Pro Leu Asn Ser Trp Gly Ser Gly Arg Asn Pro
35 40 45
Ser Leu Pro Glu Ala Leu Met Ser Pro Tyr Val Pro Gly Thr Gly Ala
50 55 60

<210> 1751
<211> 531
<212> DNA
<213> Homo sapiens

<400> 1751
ggccgcatcc cgcatctggg ccgatggcga atgggcaatt tcagtcgcag acagggacat
60
gacgatgccg ttgtcgagaa ggccatggcg acgaccgggg tctccgagct tactgatagg
120
gcatggtctt ccctgtcagg aggagagagg caacgggtac agctggctcg tgccttggca
180
caggagcccg agatcttatt tcttgacgag ccgacaaatc accttgactt gccacaccag
240
atcgacctcc tggagcgggt ccgaggactc ggcctgacga cggtcaccgt cattcatgac
300
ctcgacttgg ctgccgccta cgccgacgac ctcatcgtgc tcgactcggg tcgcatggtt
360
gctggcggac cggcgagcac agtgctgacg cctggccttg tccgtgacca ctttggtgtc
420
gacggtgagg tttggtcctc ctcgaggcgc ggcttcacct ggaacgggct gcagacatga
480
cgacgcgtat cgcagtatcc ctccgatggg acgacgccat tgacttgagc c
531

<210> 1752
<211> 159
<212> PRT
<213> Homo sapiens

<400> 1752
Gly Arg Ile Pro His Leu Gly Arg Trp Arg Met Gly Asn Phe Ser Arg

```
 1               5                  10                  15
Arg Gln Gly His Asp Asp Ala Val Val Glu Lys Ala Met Ala Thr Thr
            20                  25                  30
Gly Val Ser Glu Leu Thr Asp Arg Ala Trp Ser Ser Leu Ser Gly Gly
        35                  40                  45
Glu Arg Gln Arg Val Gln Leu Ala Arg Ala Leu Ala Gln Glu Pro Glu
    50                  55                  60
Ile Leu Phe Leu Asp Glu Pro Thr Asn His Leu Asp Leu Pro His Gln
65                  70                  75                  80
Ile Asp Leu Leu Glu Arg Val Arg Gly Leu Gly Leu Thr Thr Val Thr
                85                  90                  95
Val Ile His Asp Leu Asp Leu Ala Ala Ala Tyr Ala Asp Asp Leu Ile
            100                 105                 110
Val Leu Asp Ser Gly Arg Met Val Ala Gly Gly Pro Ala Ser Thr Val
        115                 120                 125
Leu Thr Pro Gly Leu Val Arg Asp His Phe Gly Val Asp Gly Glu Val
    130                 135                 140
Trp Ser Ser Ser Arg Arg Gly Phe Thr Trp Asn Gly Leu Gln Thr
145                 150                 155
```

<210> 1753
<211> 920
<212> DNA
<213> Homo sapiens

<400> 1753
gagacagtgg agaggctggg tcagtcccct gcccaggaca ccccggtcct ggggccttgc
60
tgggacccga tggctctggg gactcagggc cgcctgctgc tggacaggga ttccaaggac
120
acacagacca ggatcagcca aaagggccgc cgtctgcagc ccccggggac tccctcggcc
180
ccaccccaga gaaggccccg gaaacagctg aacccctgcc ggggcaccga gagagtggac
240
cctgggttcg agggggtgac tctgaagttt cagataaagc cggactccag cctgcagatc
300
atccccacgt acagcctgcc ctgcagtagc cgttctcagg aatcccctgc agatgctgtt
360
gggggccntg cagccatccc agagggcacc gagggccact cagcaggcag cgaggccctg
420
gagccccggc gctgtgcttc ctgtcggacc cagaggaccc cgctctggag agacgctgaa
480
gatgggaccc ttctctgcaa cgcctgtggg atcaggtaca agaaatacgg cactcgctgc
540
tccagctgct ggctggtgcc caggaaaaat gtccagccca agaggctatg tggcagatgt
600
ggagtgtccc tggaccccat tcaggaaggt taaacccagc ttcaccctgc tgagctgctg
660
cttctgcctc cgtttcacca gtgggagaat gggcagaagc agctctccta ggaggattgg
720
ggaaagagcc ggcctgcctc ctctctgcca tctccagatt caaggatccc gggggaagac
780
ccaggcctca ggtggcagag cctgctaggg gtcaccagcc ccttctccag tcagccttgg
840

ccgaggcccc ctcaggagac gctctcagga aggatgagca ttgttacagc agggacaata
900
aagtacagag atatgccgag
920

<210> 1754
<211> 210
<212> PRT
<213> Homo sapiens

<400> 1754
Glu Thr Val Glu Arg Leu Gly Gln Ser Pro Ala Gln Asp Thr Pro Val
1 5 10 15
Leu Gly Pro Cys Trp Asp Pro Met Ala Leu Gly Thr Gln Gly Arg Leu
20 25 30
Leu Leu Asp Arg Asp Ser Lys Asp Thr Gln Thr Arg Ile Ser Gln Lys
35 40 45
Gly Arg Arg Leu Gln Pro Pro Gly Thr Pro Ser Ala Pro Pro Gln Arg
50 55 60
Arg Pro Arg Lys Gln Leu Asn Pro Cys Arg Gly Thr Glu Arg Val Asp
65 70 75 80
Pro Gly Phe Glu Gly Val Thr Leu Lys Phe Gln Ile Lys Pro Asp Ser
85 90 95
Ser Leu Gln Ile Ile Pro Thr Tyr Ser Leu Pro Cys Ser Ser Arg Ser
100 105 110
Gln Glu Ser Pro Ala Asp Ala Val Gly Gly Xaa Ala Ala Ile Pro Glu
115 120 125
Gly Thr Glu Gly His Ser Ala Gly Ser Glu Ala Leu Glu Pro Arg Arg
130 135 140
Cys Ala Ser Cys Arg Thr Gln Arg Thr Pro Leu Trp Arg Asp Ala Glu
145 150 155 160
Asp Gly Thr Leu Leu Cys Asn Ala Cys Gly Ile Arg Tyr Lys Lys Tyr
165 170 175
Gly Thr Arg Cys Ser Ser Cys Trp Leu Val Pro Arg Lys Asn Val Gln
180 185 190
Pro Lys Arg Leu Cys Gly Arg Cys Gly Val Ser Leu Asp Pro Ile Gln
195 200 205
Glu Gly
210

<210> 1755
<211> 437
<212> DNA
<213> Homo sapiens

<400> 1755
nnttctgcag agtagggaga cagtcttggg cctggatggc cattagtgct tggagtcatg
60
ggagcaatca gaaatgatca aggagaatcc ttgatacgaa ctgcattcca gtgtcttcag
120
ttggttgtga cagattttct accaacaatg ccttgtactt gcctgcaaat agttgtagat
180
gttgcaggta gctttggcct ccataaccaa gaactcaata ttagtttaac ttcaataggt
240

ttattgtgga atatttcaga ttatttttc caaagagggg aaactattga aaaagaacta
300
aataaggaag aggcagcaca gcaaaagcag gcagaagaga aaggagttgt tttaaatcgg
360
ccattccacc ctgcaccgcc atttgattgc ttgtggttat gtctttatgc aaaattgggt
420
gaactatgtg tggatcc
437

<210> 1756
<211> 126
<212> PRT
<213> Homo sapiens

<400> 1756
Met Gly Ala Ile Arg Asn Asp Gln Gly Glu Ser Leu Ile Arg Thr Ala
1 5 10 15
Phe Gln Cys Leu Gln Leu Val Val Thr Asp Phe Leu Pro Thr Met Pro
20 25 30
Cys Thr Cys Leu Gln Ile Val Val Asp Val Ala Gly Ser Phe Gly Leu
35 40 45
His Asn Gln Glu Leu Asn Ile Ser Leu Thr Ser Ile Gly Leu Leu Trp
50 55 60
Asn Ile Ser Asp Tyr Phe Phe Gln Arg Gly Glu Thr Ile Glu Lys Glu
65 70 75 80
Leu Asn Lys Glu Glu Ala Ala Gln Gln Lys Gln Ala Glu Glu Lys Gly
85 90 95
Val Val Leu Asn Arg Pro Phe His Pro Ala Pro Pro Phe Asp Cys Leu
100 105 110
Trp Leu Cys Leu Tyr Ala Lys Leu Gly Glu Leu Cys Val Asp
115 120 125

<210> 1757
<211> 1297
<212> DNA
<213> Homo sapiens

<400> 1757
nggatccgac ggaaatagaa ttgaaggcat tctaaaatgg ctaaccgtac agtgaaggat
60
gcgcacagca tccatggcac caaccctcaa tatctggtgg agaagatcat tcgaacgcga
120
atctatgagt ccaagtactg gaaagaggag tgctttggac ttacagctga acttgtagtc
180
gataaagcca tggagttaag gtttgtgggt ggcgtctatg gtggcaacat aaaaccaaca
240
ccctttctgt gtttaacctt gaagatgctt caaattcaac ccgagaagga tatcattgta
300
gagtttatca aaaatgaaga tttcaagtat gtccgcatgc tgggggcact ttacatgagg
360
ctgacaggca ctgcaattga ttgctacaag tacttggaac ctttgtacaa tgactatcga
420
aaaatcaaga gccagaaccg aaatggggag tttgaattga tgcatgttga tgagtttatt
480

gatgaactat tgcacagtga gagagtctgt gatatcattc tgccccgact acagaaacgc
540
tatgtattag aggaagctga gcaactggag cctcgagtta gtgctctgga agaggacatg
600
gatgatgtgg agtccagtga agaggaagaa gaggaggatg agaagttgga aagagtgcca
660
tcacctgatc accgccggag aagctaccga gacttggaca agccccgtcg ctctcccaca
720
ctgcgctaca ggaggagtag gagccggtct cccagaaggc ggagtcgatc tcccaaaagg
780
agaagcccct cccctcgccg agaaaggcat cggagcaaga gtccaagacg tcaccgcagc
840
aggtcccgag atcggcggca cagatcccgt tccaagtccc caggtcatca ccgtagtcac
900
agacacagga gccactcaaa gtctcccgaa aggtctaaga agagccacaa gaagagccgg
960
agagggaatg agtaatggac tcagtttggt tttagtccac atggcctcct gtggatataa
1020
ggatatctgt atgtggaagg attaagatct cccccaggca gctataagaa tattttagtt
1080
ttttttcttat caagtttctc aacctttatt tttaatgaag gaggtgctga gttttgtatc
1140
tttttaatca taatcaacat cagtttttga cccaactaac cttgactgta ttcaaactta
1200
tgagagtata aaggatctgg aggttgggga tatgactgac aaggaaaggc tgtggccacc
1260
tgatgaccct ttccctttt attaaaccgg acacacc
1297

<210> 1758
<211> 312
<212> PRT
<213> Homo sapiens

<400> 1758
Met Ala Asn Arg Thr Val Lys Asp Ala His Ser Ile His Gly Thr Asn
1 5 10 15
Pro Gln Tyr Leu Val Glu Lys Ile Ile Arg Thr Arg Ile Tyr Glu Ser
20 25 30
Lys Tyr Trp Lys Glu Glu Cys Phe Gly Leu Thr Ala Glu Leu Val Val
35 40 45
Asp Lys Ala Met Glu Leu Arg Phe Val Gly Gly Val Tyr Gly Gly Asn
50 55 60
Ile Lys Pro Thr Pro Phe Leu Cys Leu Thr Leu Lys Met Leu Gln Ile
65 70 75 80
Gln Pro Glu Lys Asp Ile Ile Val Glu Phe Ile Lys Asn Glu Asp Phe
85 90 95
Lys Tyr Val Arg Met Leu Gly Ala Leu Tyr Met Arg Leu Thr Gly Thr
100 105 110
Ala Ile Asp Cys Tyr Lys Tyr Leu Glu Pro Leu Tyr Asn Asp Tyr Arg
115 120 125
Lys Ile Lys Ser Gln Asn Arg Asn Gly Glu Phe Glu Leu Met His Val
130 135 140
Asp Glu Phe Ile Asp Glu Leu Leu His Ser Glu Arg Val Cys Asp Ile

```
145                 150                 155                 160
Ile Leu Pro Arg Leu Gln Lys Arg Tyr Val Leu Glu Glu Ala Glu Gln
                165                 170                 175
Leu Glu Pro Arg Val Ser Ala Leu Glu Glu Asp Met Asp Asp Val Glu
            180                 185                 190
Ser Ser Glu Glu Glu Glu Glu Glu Asp Glu Lys Leu Glu Arg Val Pro
        195                 200                 205
Ser Pro Asp His Arg Arg Arg Ser Tyr Arg Asp Leu Asp Lys Pro Arg
    210                 215                 220
Arg Ser Pro Thr Leu Arg Tyr Arg Arg Ser Arg Ser Arg Ser Pro Arg
225                 230                 235                 240
Arg Arg Ser Arg Ser Pro Lys Arg Arg Ser Pro Ser Pro Arg Arg Glu
                245                 250                 255
Arg His Arg Ser Lys Ser Pro Arg Arg His Arg Ser Arg Ser Arg Asp
            260                 265                 270
Arg Arg His Arg Ser Arg Ser Lys Ser Pro Gly His His Arg Ser His
        275                 280                 285
Arg His Arg Ser His Ser Lys Ser Pro Glu Arg Ser Lys Lys Ser His
    290                 295                 300
Lys Lys Ser Arg Arg Gly Asn Glu
305                 310
```

<210> 1759
<211> 324
<212> DNA
<213> Homo sapiens

<400> 1759
aattccatag tcctcatggg caagagttac acagcgtgga ggaccaactc ccaggcactc
60
ggcctgggca gacacaatta ttgtcggaat ccagatggtg atgccagacc ttggtgccat
120
gtgatgaagg accgaaagct gacgtgggaa tactgtgaca tgtccccatg ctccacctgt
180
ggcctgaggc agtgcaaacg gcctcagttt agaactaaag gaggactcta cacagacatc
240
acctcacacc cttggcaggc tgccatcttt gtcagcaaca agaggtctcc tggagagaga
300
ttcctttgtg gaggggtgct gatc
324

<210> 1760
<211> 108
<212> PRT
<213> Homo sapiens

<400> 1760
```
Asn Ser Ile Val Leu Met Gly Lys Ser Tyr Thr Ala Trp Arg Thr Asn
 1               5                  10                  15
Ser Gln Ala Leu Gly Leu Gly Arg His Asn Tyr Cys Arg Asn Pro Asp
            20                  25                  30
Gly Asp Ala Arg Pro Trp Cys His Val Met Lys Asp Arg Lys Leu Thr
        35                  40                  45
Trp Glu Tyr Cys Asp Met Ser Pro Cys Ser Thr Cys Gly Leu Arg Gln
```

```
    50                  55                  60
Cys Lys Arg Pro Gln Phe Arg Thr Lys Gly Gly Leu Tyr Thr Asp Ile
65                  70                  75                  80
Thr Ser His Pro Trp Gln Ala Ala Ile Phe Val Ser Asn Lys Arg Ser
                85                  90                  95
Pro Gly Glu Arg Phe Leu Cys Gly Gly Val Leu Ile
            100                 105
```

<210> 1761
<211> 351
<212> DNA
<213> Homo sapiens

<400> 1761
ngcgatctcg gctcactaca acctcggtga cagagcgaga ctctatccca aaaaaataaa
60
aataaaaatc aactggagaa ggaaatgggg ttggggagca tcctctgaat atataaaggc
120
agccattcat tgtaggagag gaggtagaag gaaatgctgt ttgtcgatgg ttcttttcca
180
gagaggaaga gaggagaaag gaagagcggg gagcaggtgg ggagcccgca gtaagacccc
240
acagtggggc caggtggtct tgcaccctgt attcccactt tggctggggc agcccagagt
300
ccaggccagc aggtaatgcc ccagccatgc ccactcggtc ctattggatc c
351

<210> 1762
<211> 109
<212> PRT
<213> Homo sapiens

<400> 1762
```
Met Ala Gly Ala Leu Pro Ala Gly Leu Asp Ser Gly Leu Pro Gln Pro
 1               5                  10                  15
Lys Trp Glu Tyr Arg Val Gln Asp His Leu Ala Pro Leu Trp Gly Leu
            20                  25                  30
Thr Ala Gly Ser Pro Pro Ala Pro Arg Ser Ser Phe Leu Leu Ser Ser
        35                  40                  45
Ser Leu Glu Lys Asn His Arg Gln Thr Ala Phe Pro Ser Thr Ser Ser
    50                  55                  60
Pro Thr Met Asn Gly Cys Leu Tyr Ile Phe Arg Gly Cys Ser Pro Thr
65                  70                  75                  80
Pro Phe Pro Ser Pro Val Asp Phe Tyr Phe Tyr Phe Phe Gly Ile Glu
                85                  90                  95
Ser Arg Ser Val Thr Glu Val Val Val Ser Arg Asp Arg
            100                 105
```

<210> 1763
<211> 356
<212> DNA
<213> Homo sapiens

<400> 1763

gcgcgccggg ggcgcgatgt ggagcgggca cttacccgtt tcatggccaa gacaggcgag
60
actcagagtc ttttcaaaga tgacgtcagc acatttccat tgattgctgc cagacctttc
120
accatcccct acctgacagc tcttcttccg tctgaactgg agatgcaaca aatggaagag
180
acagattcct cggagcagga tgaacagaca gacacagaga accttgctct tcatatcagc
240
atggaggatt ctggagccga gaaagagaac acctctgtcc tgcagcagaa cccctccttg
300
tcgggtagcc ggaatgggga ggagaacatc atcgataacc cttatctgcg accggt
356

<210> 1764
<211> 118
<212> PRT
<213> Homo sapiens

<400> 1764
Ala Arg Arg Gly Arg Asp Val Glu Arg Ala Leu Thr Arg Phe Met Ala
1 5 10 15
Lys Thr Gly Glu Thr Gln Ser Leu Phe Lys Asp Asp Val Ser Thr Phe
20 25 30
Pro Leu Ile Ala Ala Arg Pro Phe Thr Ile Pro Tyr Leu Thr Ala Leu
35 40 45
Leu Pro Ser Glu Leu Glu Met Gln Gln Met Glu Glu Thr Asp Ser Ser
50 55 60
Glu Gln Asp Glu Gln Thr Asp Thr Glu Asn Leu Ala Leu His Ile Ser
65 70 75 80
Met Glu Asp Ser Gly Ala Glu Lys Glu Asn Thr Ser Val Leu Gln Gln
85 90 95
Asn Pro Ser Leu Ser Gly Ser Arg Asn Gly Glu Glu Asn Ile Ile Asp
100 105 110
Asn Pro Tyr Leu Arg Pro
115

<210> 1765
<211> 357
<212> DNA
<213> Homo sapiens

<400> 1765
cggccgcatt cttcgtgact ggcgtcccgc cgccggtgca aaagtgtcag gaaataccag
60
tcatgactat gtttagccgc acctctctgc agtatgcgat cgttctggca gcgctgggcg
120
gtgccggtct ggcgctctgg gccatgtcga gtgcgacgga ggccaatcag gcggaaattg
180
cccaggccag gccaggcatt attgcggcgg cgcgcggtgt cgtggatgtc gagggcggcc
240
tgctgcggct ctccacccag cgcgacgggg tgattcagga tgtgccggtg aaggaaggac
300
agcgggtcaa agccggcgat atcctcgccg cgctcgacaa tcgccgcgaa ctgatcg
357

<210> 1766
<211> 98
<212> PRT
<213> Homo sapiens

<400> 1766
Met Thr Met Phe Ser Arg Thr Ser Leu Gln Tyr Ala Ile Val Leu Ala
1 5 10 15
Ala Leu Gly Gly Ala Gly Leu Ala Leu Trp Ala Met Ser Ser Ala Thr
20 25 30
Glu Ala Asn Gln Ala Glu Ile Ala Gln Ala Arg Pro Gly Ile Ile Ala
35 40 45
Ala Ala Arg Gly Val Val Asp Val Glu Gly Gly Leu Leu Arg Leu Ser
50 55 60
Thr Gln Arg Asp Gly Val Ile Gln Asp Val Pro Val Lys Glu Gly Gln
65 70 75 80
Arg Val Lys Ala Gly Asp Ile Leu Ala Ala Leu Asp Asn Arg Arg Glu
85 90 95
Leu Ile

<210> 1767
<211> 297
<212> DNA
<213> Homo sapiens

<400> 1767
nnncgccgac ggccgccatg acgcaccgca ttgacgtgaa ccagggcgac gatgccaacc
60
ccggccaaca cgccaggctg cttgacgccg ccagccaacc cgacgaacgc cccaccaaga
120
acgagcccga gccatccccg gccaatcaac gccagacgta tggccacaac gagtgcgacg
180
agggacaaac ccacctggag tccgtcgttg tgcatgcccc ccaccacgct caacgtcgtc
240
aatggacagc acaccgccag ccagagggca tgatccggat cggttccggc gtagcgn
297

<210> 1768
<211> 73
<212> PRT
<213> Homo sapiens

<400> 1768
Met Pro Thr Pro Ala Asn Thr Pro Glv Cys Leu Thr Pro Pro Ala Asn
1 5 10 15
Pro Thr Asn Ala Pro Pro Arg Thr Ser Pro Ser His Pro Arg Pro Ile
20 25 30
Asn Ala Arg Arg Met Ala Thr Thr Ser Ala Thr Arg Asp Lys Pro Thr
35 40 45
Trp Ser Pro Ser Leu Cys Met Pro Pro Thr Thr Leu Asn Val Val Asn
50 55 60
Gly Gln His Thr Ala Ser Gln Arg Ala

65 70

<210> 1769
<211> 474
<212> DNA
<213> Homo sapiens

<400> 1769
caccatgctg gctcggttcg acgcattcgg gtgggtgagt ctgttctcgt caccgacggg
60
cagggtcatg ccgttcgtgg ccctgccatt gaggtgacga aagggtcagt tagcgtcgag
120
accgttgaga tcctccatac tcccgcgacc acgcatcgat gggtcgccgt ccaggcattg
180
ccgaagtccg atagagctga gctggcggtg gcgaccctca ccgagatggg agttcacgaa
240
atcctcgcct ggcaggctga tcggagcatc gtgcgatgga agggcgacaa gcaagccaag
300
ggcgtcgcga ggtggcaagc ggctgcccgt gaggccacca aacagtctcg acgttttctt
360
gtgccacagg tagaactagc gcaaacccgt gaagttgtta agcggatttg caatgcccag
420
gccgcctacg ttttgcacga gtcggccagt gaaccgctgg tgcatcagga gctc
474

<210> 1770
<211> 158
<212> PRT
<213> Homo sapiens

<400> 1770
His His Ala Gly Ser Val Arg Arg Ile Arg Val Gly Glu Ser Val Leu
1 5 10 15
Val Thr Asp Gly Gln Gly His Ala Val Arg Gly Pro Ala Ile Glu Val
20 25 30
Thr Lys Gly Ser Val Ser Val Glu Thr Val Glu Ile Leu His Thr Pro
35 40 45
Ala Thr Thr His Arg Trp Val Ala Val Gln Ala Leu Pro Lys Ser Asp
50 55 60
Arg Ala Glu Leu Ala Val Ala Thr Leu Thr Glu Met Gly Val His Glu
65 70 75 80
Ile Leu Ala Trp Gln Ala Asp Arg Ser Ile Val Arg Trp Lys Gly Asp
85 90 95
Lys Gln Ala Lys Gly Val Ala Arg Trp Gln Ala Ala Ala Arg Glu Ala
100 105 110
Thr Lys Gln Ser Arg Arg Phe Leu Val Pro Gln Val Glu Leu Ala Gln
115 120 125
Thr Arg Glu Val Val Lys Arg Ile Cys Asn Ala Gln Ala Ala Tyr Val
130 135 140
Leu His Glu Ser Ala Ser Glu Pro Leu Val His Gln Glu Leu
145 150 155

<210> 1771
<211> 287

<212> DNA
<213> Homo sapiens

<400> 1771
acgcgtgatg ggtaattcta atacatgcaa agaattatct ctgcaagtat actcagatat
60
taataacagc gggtgtcgca gaggaagaag cctgggagaa tggaagtcag ggaaggagag
120
caacaggctt ctcactctgt gccatgagca tgtgctagcc atggagacac tctgcatgtt
180
acctagaact gctgattcat tgctctggaa ttattcagct attcaagacc cagtgaaata
240
cagcaagcag ctttcattca tacacacaca tgtgcatcca tgtgcac
287

<210> 1772
<211> 93
<212> PRT
<213> Homo sapiens

<400> 1772
Met Gly Asn Ser Asn Thr Cys Lys Glu Leu Ser Leu Gln Val Tyr Ser
1 5 10 15
Asp Ile Asn Asn Ser Gly Cys Arg Arg Gly Arg Ser Leu Gly Glu Trp
20 25 30
Lys Ser Gly Lys Glu Ser Asn Arg Leu Leu Thr Leu Cys His Glu His
35 40 45
Val Leu Ala Met Glu Thr Leu Cys Met Leu Pro Arg Thr Ala Asp Ser
50 55 60
Leu Leu Trp Asn Tyr Ser Ala Ile Gln Asp Pro Val Lys Tyr Ser Lys
65 70 75 80
Gln Leu Ser Phe Ile His Thr His Val His Pro Cys Ala
85 90

<210> 1773
<211> 393
<212> DNA
<213> Homo sapiens

<400> 1773
accggtgagt tctacgtccc ggttaaccac ctcggaggtg aacaggcgca cctcgacgtc
60
ttcgattctc cgcttaacga gtacgcagcg atgggatttg agtacggcta ctctgttgcc
120
cgtccggatt ctctggtatt gtgggaagcc caattcggcg atttcaccaa cggtgcccag
180
acgatcatcg atgagttcat cgcctcggct ggctccaagt ggggtcagaa gtcgggagtc
240
gtgctgctgc tgccgcacgg ttacgaaggt caggggcctg atcactcgtc ggcccgtctg
300
gagcgcttcc tcaatctatg cagtgaagac gctttggccg tctgccagcc ctcgaccccg
360
gcaagctaca gccatttatt gcgtcagcac gcg
393

<210> 1774
<211> 131
<212> PRT
<213> Homo sapiens

<400> 1774
Thr Gly Glu Phe Tyr Val Pro Val Asn His Leu Gly Gly Glu Gln Ala
1 5 10 15
His Leu Asp Val Phe Asp Ser Pro Leu Asn Glu Tyr Ala Ala Met Gly
20 25 30
Phe Glu Tyr Gly Tyr Ser Val Ala Arg Pro Asp Ser Leu Val Leu Trp
35 40 45
Glu Ala Gln Phe Gly Asp Phe Thr Asn Gly Ala Gln Thr Ile Ile Asp
50 55 60
Glu Phe Ile Ala Ser Ala Gly Ser Lys Trp Gly Gln Lys Ser Gly Val
65 70 75 80
Val Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His Ser
85 90 95
Ser Ala Arg Leu Glu Arg Phe Leu Asn Leu Cys Ser Glu Asp Ala Leu
100 105 110
Ala Val Cys Gln Pro Ser Thr Pro Ala Ser Tyr Ser His Leu Leu Arg
115 120 125
Gln His Ala
130

<210> 1775
<211> 369
<212> DNA
<213> Homo sapiens

<400> 1775
nncctccgag cagctctccg gggcagaccc cagctgcaag ccacagcccg gccctggtaa
60
cgggagggca tcgctaggga ggggtggggc ggcccggctt cgatgcagcc atgtgggagg
120
gccactctca gagacccccc gccttccttg ccacccccac cccagagggg aagctggagc
180
tgggaggctg cagacccagg ccaaggtgtg gccagggctg gctttcttgg gaggctttga
240
gcatcctgct tcctggccac ccagctctgg ggctgctgtc aactcttgat ttgtagacat
300
cactccagcc tctggcctgt caccctgaac ctcccccatg tctgtgtctt ttctcactgg
360
aacaccggt
369

<210> 1776
<211> 59
<212> PRT
<213> Homo sapiens

<400> 1776
Arg Glu Gly Ile Ala Arg Glu Gly Trp Gly Gly Pro Ala Ser Met Gln

```
 1               5                  10                  15
Pro Cys Gly Arg Ala Thr Leu Arg Asp Pro Pro Pro Ser Leu Pro Pro
            20                  25                  30
Pro Pro Gln Arg Gly Ser Trp Ser Trp Glu Ala Ala Asp Pro Gly Gln
        35                  40                  45
Gly Val Ala Arg Ala Gly Phe Leu Gly Arg Leu
    50                  55
```

<210> 1777
<211> 370
<212> DNA
<213> Homo sapiens

<400> 1777
agcttcttat cactatcctt tagtgctttt tggtctacct tagcggtaat gctccatcaa
60
gaatatggtt ttggtagtgc aactgcggga ttttttggcc tcgctggtgc cgccggagct
120
ttagcagcac cactgtccgg taaactaaca gataaacaag gaccgacacg ggtcacgcag
180
ctgggtgctg ccttagttgt cgtctctttc gcatctatgt tgttattgcc ttacttcagt
240
atcagtaccc aagttataat gattattgtt gctaccatag tgtttgactt tggtgttcag
300
gcggcactta ttgctcatca aaccttagtg tataacattg actctaccgc tcgtggacgc
360
cttaacgcgt
370

<210> 1778
<211> 123
<212> PRT
<213> Homo sapiens

<400> 1778
```
Ser Phe Leu Ser Leu Ser Phe Ser Ala Phe Trp Ser Thr Leu Ala Val
 1               5                  10                  15
Met Leu His Gln Glu Tyr Gly Phe Gly Ser Ala Thr Ala Gly Phe Phe
            20                  25                  30
Gly Leu Ala Gly Ala Ala Gly Ala Leu Ala Ala Pro Leu Ser Gly Lys
        35                  40                  45
Leu Thr Asp Lys Gln Gly Pro Thr Arg Val Thr Gln Leu Gly Ala Ala
    50                  55                  60
Leu Val Val Val Ser Phe Ala Ser Met Leu Leu Leu Pro Tyr Phe Ser
65                  70                  75                  80
Ile Ser Thr Gln Val Ile Met Ile Ile Val Ala Thr Ile Val Phe Asp
                85                  90                  95
Phe Gly Val Gln Ala Ala Leu Ile Ala His Gln Thr Leu Val Tyr Asn
            100                 105                 110
Ile Asp Ser Thr Ala Arg Gly Arg Leu Asn Ala
        115                 120
```

<210> 1779
<211> 345

<212> DNA
<213> Homo sapiens

<400> 1779
ccatgtgtgt gtatatgctc gtgtgtgatg gtatgtatat gtgtatatgt gnntatatgt
60
atacacgtgt gttatggtgt gtatatatgt atatacgtgt gtgtatatat atgtatatgg
120
gtatgtgtgt gcatgtgcgt atgggtgtgt atatgtgtat atatgtaggt gtgtatatct
180
gggaatatat gggtgtgtat atgtgtgtat aggtttttat atgtggggaa atatttaaac
240
ctgtgtatat tggaatgtgt gtgtatatgt gtgtatatat ggnggtgtgt atgtacatgt
300
atgtgtgtat atatgtgtgt atatacgtag gtgtgcatat gtgtg
345

<210> 1780
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1780
Pro Cys Val Cys Ile Cys Ser Cys Val Met Val Cys Ile Cys Val Tyr
 1   5   10   15
Val Xaa Ile Cys Ile His Val Cys Tyr Gly Val Tyr Ile Cys Ile Tyr
            20   25   30
Val Cys Val Tyr Ile Cys Ile Trp Val Cys Val Cys Met Cys Val Trp
        35   40   45
Val Cys Ile Cys Val Tyr Met
    50   55

<210> 1781
<211> 349
<212> DNA
<213> Homo sapiens

<400> 1781
nacgcgtcat gctaaatttt gccctttatg gcaacatttt cgtcagaaca agcggaagag
60
aagctactat ccaagtttca tacgccggtt aaaagaaaac atgatgatac gagatcatct
120
gatgtgaaca caacgcaaac tggttcaagc gccacgccca ttacacctgt acccttactg
180
cccagtgcac aagagcccag ttatctttgc cagtggtgcg ctccccagac acgaaagcac
240
aagacatggg agggtgatgc tattcttata ttgcatggaa ataaaactac ttgttcgcta
300
cgatccgcac atgatggcag catgctagtg acgaatgctg ccttccgga
349

<210> 1782
<211> 107
<212> PRT

<213> Homo sapiens

<400> 1782
Met Ala Thr Phe Ser Ser Glu Gln Ala Glu Glu Lys Leu Leu Ser Lys
1 5 10 15
Phe His Thr Pro Val Lys Arg Lys His Asp Asp Thr Arg Ser Ser Asp
20 25 30
Val Asn Thr Thr Gln Thr Gly Ser Ser Ala Thr Pro Ile Thr Pro Val
35 40 45
Pro Leu Leu Pro Ser Ala Gln Glu Pro Ser Tyr Leu Cys Gln Trp Cys
50 55 60
Ala Pro Gln Thr Arg Lys His Lys Thr Trp Glu Gly Asp Ala Ile Leu
65 70 75 80
Ile Leu His Gly Asn Lys Thr Thr Cys Ser Leu Arg Ser Ala His Asp
85 90 95
Gly Ser Met Leu Val Thr Asn Ala Ala Phe Arg
100 105

<210> 1783
<211> 1829
<212> DNA
<213> Homo sapiens

<400> 1783
gtgcacgact tcgacgccag cctctcgggc atcgggcagg aactgggcgc cggcgcttac
60
agcatgagtg atgtcttggc attgcccatt ttcaagcagg aagattccag ccttccattg
120
gatggtgaaa cagagcaccc acccttttcag tatgtgatgt gtgctgcaac gtcaccagca
180
gtaaaactgc atgatgaaac gcttacttat ttgaaccaag gtcagtcata tgaaattcgg
240
atgctggata atcggaaaat gggtgatatg cctgagatca atggaaaatt agtaaagagc
300
atcataaggg ttgtattcca tgacagacgg ctacaataca cagagcatca gcaacttgaa
360
ggatggaagt ggaatcgccc aggagacaga cttcttgatt tagatattcc aatgtctgtg
420
ggaataattg acacaaggac gaatccaggc cagttaaatg cggttgaatt tctgtgggac
480
ccagcaaaac gcacctctgc tttcattcag gtacactgca tcagcacaga atttactcca
540
cggaagcacg gaggtgaaaa gggagtgccc tttaggatcc aggttgacac ctttaagcag
600
aatgaaaatg gagaatacac agatcatcta cactcagcta gctgccaaat caaagttttt
660
aagcctaaag gtgcagacag gaaacaaaaa actgaccgag agaagatgga gaagagaaca
720
gctcatgaaa aagaaaagta tcagccgtcc tatgatacca caatcctcac agagatgagg
780
cttgagccta taattgaaga tgcagttgaa catgagcaga aanaagtcca gcaagcggac
840
tttgccgcag actacggtga ttctctggca aagcgaggca gttgttctcc gtggcccgat
900

gcccccacag cctatgtgaa taacagccct tccccagcgc ccactttcac ctccccacag
960
cagagcactt gcagtgtccc agacagcaat tcttcttccc caaatcatca gggagatgga
1020
gcttcacaga cctctggtga acaaattcag ccttcagcta cgatccagga aacacagcaa
1080
tggctgctca aaaacagatt ctcttcctac acaagactgt tctctaattt ttcaggtgcc
1140
gacttattaa aactgacaaa ggaggattta gttcaaattt gtggtgcagc cgatggaatt
1200
cggctctata attcactgaa gtcaaggtcg gttagacccc gtttaaccat ctatgtctgc
1260
cgggagcagc caagcagcac agtgctgcaa gggcagcagc aagctgcaag cagtgcaagc
1320
gagaatggca gtggggcacc ctatgtttat catgcaatct acttggaaga aatgattgcc
1380
tcagaagttg ctcgaaaact tgcgctggtg tttaatatcc ctctccacca aattaatcag
1440
gtttacagac agggtcccac cggtattcac attcttgtta gtgatcaggt aaatcaaatc
1500
atttgttttt ccttttcaga ctggtattta cttttataca tgtaattgta gaactgtaga
1560
aaaattctgt gacctctttt gaaaatactt atgagaatca ttttcagaga gttgggaatc
1620
actttggaag aacttataac caagagtttc aggcatccta gtgataatat ggaatacaag
1680
ccaaggaaaa ctggcttagc ctccccccag ccctttagga tgcagccaat cactggggca
1740
ctctagggat agtggcaggc tttggccctt tttatgaggt gagtcactgg atgtgttttc
1800
cttttgtcta ttatttgatg actaattta
1829

<210> 1784
<211> 514
<212> PRT
<213> Homo sapiens

<400> 1784
Val His Asp Phe Asp Ala Ser Leu Ser Gly Ile Gly Gln Glu Leu Gly
1 5 10 15
Ala Gly Ala Tyr Ser Met Ser Asp Val Leu Ala Leu Pro Ile Phe Lys
20 25 30
Gln Glu Asp Ser Ser Leu Pro Leu Asp Gly Glu Thr Glu His Pro Pro
35 40 45
Phe Gln Tyr Val Met Cys Ala Ala Thr Ser Pro Ala Val Lys Leu His
50 55 60
Asp Glu Thr Leu Thr Tyr Leu Asn Gln Gly Gln Ser Tyr Glu Ile Arg
65 70 75 80
Met Leu Asp Asn Arg Lys Met Gly Asp Met Pro Glu Ile Asn Gly Lys
85 90 95
Leu Val Lys Ser Ile Ile Arg Val Val Phe His Asp Arg Arg Leu Gln
100 105 110
Tyr Thr Glu His Gln Gln Leu Glu Gly Trp Lys Trp Asn Arg Pro Gly

```
        115                 120                 125
Asp Arg Leu Leu Asp Leu Asp Ile Pro Met Ser Val Gly Ile Ile Asp
    130                 135                 140
Thr Arg Thr Asn Pro Gly Gln Leu Asn Ala Val Glu Phe Leu Trp Asp
145                 150                 155                 160
Pro Ala Lys Arg Thr Ser Ala Phe Ile Gln Val His Cys Ile Ser Thr
                165                 170                 175
Glu Phe Thr Pro Arg Lys His Gly Gly Glu Lys Gly Val Pro Phe Arg
            180                 185                 190
Ile Gln Val Asp Thr Phe Lys Gln Asn Glu Asn Gly Glu Tyr Thr Asp
        195                 200                 205
His Leu His Ser Ala Ser Cys Gln Ile Lys Val Phe Lys Pro Lys Gly
    210                 215                 220
Ala Asp Arg Lys Gln Lys Thr Asp Arg Glu Lys Met Glu Lys Arg Thr
225                 230                 235                 240
Ala His Glu Lys Glu Lys Tyr Gln Pro Ser Tyr Asp Thr Thr Ile Leu
                245                 250                 255
Thr Glu Met Arg Leu Glu Pro Ile Ile Glu Asp Ala Val Glu His Glu
            260                 265                 270
Gln Lys Xaa Val Gln Gln Ala Asp Phe Ala Ala Asp Tyr Gly Asp Ser
        275                 280                 285
Leu Ala Lys Arg Gly Ser Cys Ser Pro Trp Pro Asp Ala Pro Thr Ala
    290                 295                 300
Tyr Val Asn Asn Ser Pro Ser Pro Ala Pro Thr Phe Thr Ser Pro Gln
305                 310                 315                 320
Gln Ser Thr Cys Ser Val Pro Asp Ser Asn Ser Ser Ser Pro Asn His
                325                 330                 335
Gln Gly Asp Gly Ala Ser Gln Thr Ser Gly Glu Gln Ile Gln Pro Ser
            340                 345                 350
Ala Thr Ile Gln Glu Thr Gln Gln Trp Leu Leu Lys Asn Arg Phe Ser
        355                 360                 365
Ser Tyr Thr Arg Leu Phe Ser Asn Phe Ser Gly Ala Asp Leu Leu Lys
    370                 375                 380
Leu Thr Lys Glu Asp Leu Val Gln Ile Cys Gly Ala Ala Asp Gly Ile
385                 390                 395                 400
Arg Leu Tyr Asn Ser Leu Lys Ser Arg Ser Val Arg Pro Arg Leu Thr
                405                 410                 415
Ile Tyr Val Cys Arg Glu Gln Pro Ser Ser Thr Val Leu Gln Gly Gln
            420                 425                 430
Gln Gln Ala Ala Ser Ser Ala Ser Glu Asn Gly Ser Gly Ala Pro Tyr
        435                 440                 445
Val Tyr His Ala Ile Tyr Leu Glu Glu Met Ile Ala Ser Glu Val Ala
    450                 455                 460
Arg Lys Leu Ala Leu Val Phe Asn Ile Pro Leu His Gln Ile Asn Gln
465                 470                 475                 480
Val Tyr Arg Gln Gly Pro Thr Gly Ile His Ile Leu Val Ser Asp Gln
                485                 490                 495
Val Asn Gln Ile Ile Cys Phe Ser Phe Ser Asp Trp Tyr Leu Leu Leu
            500                 505                 510
Tyr Met
```

<210> 1785
<211> 381

<212> DNA
<213> Homo sapiens

<400> 1785
atcacggacg cagaggagaa agggctgatt actccaggcg tgagtgttct gattgaacca
60
actagcggca acacaggcat tggactggcc tttatggctg ctgccaaggg ctacaaactt
120
acactcacaa tgcctgcctc catgagcatg gagaggagga tcatattgaa ggcttttggt
180
gctgaacttg tccttactga cccactcttg ggaatgaaag gagctgtcaa gaaagcggaa
240
gagatacaag caaagacacc caactcgtac atccttcaac aatttgaaaa tccagctaac
300
ccaaagattc actatgagac tactgggcct gaaatctgga aagctacagc aggaaaaatt
360
gatggccttg tatctggtat c
381

<210> 1786
<211> 127
<212> PRT
<213> Homo sapiens

<400> 1786
Ile Thr Asp Ala Glu Glu Lys Gly Leu Ile Thr Pro Gly Val Ser Val
 1   5   10   15
Leu Ile Glu Pro Thr Ser Gly Asn Thr Gly Ile Gly Leu Ala Phe Met
            20   25   30
Ala Ala Ala Lys Gly Tyr Lys Leu Thr Leu Thr Met Pro Ala Ser Met
        35   40   45
Ser Met Glu Arg Arg Ile Ile Leu Lys Ala Phe Gly Ala Glu Leu Val
    50   55   60
Leu Thr Asp Pro Leu Leu Gly Met Lys Gly Ala Val Lys Lys Ala Glu
65   70   75   80
Glu Ile Gln Ala Lys Thr Pro Asn Ser Tyr Ile Leu Gln Gln Phe Glu
                85   90   95
Asn Pro Ala Asn Pro Lys Ile His Tyr Glu Thr Thr Gly Pro Glu Ile
            100   105   110
Trp Lys Ala Thr Ala Gly Lys Ile Asp Gly Leu Val Ser Gly Ile
        115   120   125

<210> 1787
<211> 294
<212> DNA
<213> Homo sapiens

<400> 1787
gtgcacacag caattcaata tgccaagaca ccaggttgca gcagagaaag atttaattgt
60
agggtcacct aacaaggaga tgagaacaaa ctttaaatct atctctctaa ggaatttgga
120
cttcgggttt ttaaggttta gaatgggcca aaacatggac attattgatt ggtcaaagag
180

tacagggtca tggaacctgg agatgaaaaa gccatattct catgctgatc ctgttcctct
240
gtggaaggtc ttcaaattgg ttgccggaat aaaagatctg tcaaacatct tagg
294

<210> 1788
<211> 91
<212> PRT
<213> Homo sapiens

<400> 1788
Met Pro Arg His Gln Val Ala Ala Glu Lys Asp Leu Ile Val Gly Ser
1 5 10 15
Pro Asn Lys Glu Met Arg Thr Asn Phe Lys Ser Ile Ser Leu Arg Asn
20 25 30
Leu Asp Phe Gly Phe Leu Arg Phe Arg Met Gly Gln Asn Met Asp Ile
35 40 45
Ile Asp Trp Ser Lys Ser Thr Gly Ser Trp Asn Leu Glu Met Lys Lys
50 55 60
Pro Tyr Ser His Ala Asp Pro Val Pro Leu Trp Lys Val Phe Lys Leu
65 70 75 80
Val Ala Gly Ile Lys Asp Leu Ser Asn Ile Leu
85 90

<210> 1789
<211> 353
<212> DNA
<213> Homo sapiens

<400> 1789
ttcccacata cacccacgcg gcatgtcctg acagagatgc acacccctag cacatattca
60
cacacacaga catgccacac cccgccatcc ccccacactc gtacacgccc accacccctc
120
gcaggcacac atgcacacac gcgcgcgcac acgcacacac acccccagcc cggaccggcc
180
gacctgctcc ccggggtctc tcccgcaggc aggtctcctc gccgagtctc cgaaaagggg
240
cggtcgtggc ggccctggcg cccagctggg caacgcttcg tggtatctca ccgcttctct
300
ctgttgtgcc cagcgccccg actgaagatc cggatcttca gtccctggcg cgc
353

<210> 1790
<211> 105
<212> PRT
<213> Homo sapiens

<400> 1790
Met His Thr Pro Ser Thr Tyr Ser His Thr Gln Thr Cys His Thr Pro
1 5 10 15
Pro Ser Pro His Thr Arg Thr Arg Pro Pro Pro Leu Ala Gly Thr His
20 25 30
Ala His Thr Arg Ala His Thr His Thr His Pro Gln Pro Gly Pro Ala

```
        35                  40                  45
Asp Leu Leu Pro Gly Val Ser Pro Ala Gly Arg Ser Pro Arg Arg Val
    50                  55                  60
Ser Glu Lys Gly Arg Ser Trp Arg Pro Trp Arg Pro Ala Gly Gln Arg
65                  70                  75                  80
Phe Val Val Ser His Arg Phe Ser Leu Leu Cys Pro Ala Pro Arg Leu
                85                  90                  95
Lys Ile Arg Ile Phe Ser Pro Trp Arg
            100                 105
```

<210> 1791
<211> 355
<212> DNA
<213> Homo sapiens

<400> 1791
aaatttcagt tagagattag ggaaaataaa gatgttattt tttcccatcc tagtttacag
60
acccccccaga aacccactca tggattctcc cgagtctttg gacctggctc agacaccctt
120
gctttggatc aagccaatgc atgtatcccc taacacaccc atgctttatg tggtccctgc
180
ccctccctgc tcaggggact gcttgttaac ttcattgggt tggggacata tatattatag
240
gagagagaca gagaaaaaga aagagaggaa atgttattct ccttgtctgt atctgtatct
300
ccactccgat tcccattccc tctgctgctc tcctctctct cctcccttca cgcgt
355

<210> 1792
<211> 108
<212> PRT
<213> Homo sapiens

<400> 1792
```
Met Leu Phe Phe Pro Ile Leu Val Tyr Arg Pro Pro Arg Asn Pro Leu
 1               5                  10                  15
Met Asp Ser Pro Glu Ser Leu Asp Leu Ala Gln Thr Pro Leu Leu Trp
            20                  25                  30
Ile Lys Pro Met His Val Ser Pro Asn Thr Pro Met Leu Tyr Val Val
        35                  40                  45
Pro Ala Pro Pro Cys Ser Gly Asp Cys Leu Leu Thr Ser Leu Gly Trp
    50                  55                  60
Gly His Ile Tyr Tyr Arg Arg Glu Thr Glu Lys Lys Lys Glu Arg Lys
65                  70                  75                  80
Cys Tyr Ser Pro Cys Leu Tyr Leu Tyr Leu His Ser Asp Ser His Ser
                85                  90                  95
Leu Cys Cys Ser Pro Leu Ser Pro Pro Phe Thr Arg
            100                 105
```

<210> 1793
<211> 510
<212> DNA
<213> Homo sapiens

<400> 1793
tgggttccag cccgtagatg accttggcct gggaggcctt ccgaaggcca cacccatatc
60
caccccctcg gagctcctcg cttaccagtc gcccaaagag cttgtccccc cagcagccag
120
agtcagccag acccttagca aacaccatag gggtcatctc aatctcttct ccaacttcac
180
cttcttctct ggagatgaat cctgacaaca cctcagggct gaggcagaag tcggtggagg
240
ccgagccgtg ctcattgtgg atggtgcacc gatacacacc gcagtctacg ggggaggcct
300
gcacgatggc caaggccgcc ggcccctcat cccctgcgct cctgcccacc tcgcccactg
360
ggcgctgatc cttggcccat gtcaagactg agtcactaag aatgttgaaa aactggcacc
420
acagcttcag gctaccggag gcatcaggaa actgctccac ccgaatcttc cggatcacct
480
gtggggcttt cagcaggtct ttggctttcc
510

<210> 1794
<211> 116
<212> PRT
<213> Homo sapiens

<400> 1794
Met Thr Leu Ala Trp Glu Ala Phe Arg Arg Pro His Pro Tyr Pro Pro
 1   5   10   15
Pro Arg Ser Ser Ser Leu Thr Ser Arg Pro Lys Ser Leu Ser Pro Gln
            20   25   30
Gln Pro Glu Ser Ala Arg Pro Leu Ala Asn Thr Ile Gly Val Ile Ser
        35   40   45
Ile Ser Ser Pro Thr Ser Pro Ser Ser Leu Glu Met Asn Pro Asp Asn
    50   55   60
Thr Ser Gly Leu Arg Gln Lys Ser Val Glu Ala Glu Pro Cys Ser Leu
65   70   75   80
Trp Met Val His Arg Tyr Thr Pro Gln Ser Thr Gly Glu Ala Cys Thr
                85   90   95
Met Ala Lys Ala Ala Gly Pro Ser Ser Pro Ala Leu Leu Pro Thr Ser
            100   105   110
Pro Thr Gly Arg
        115

<210> 1795
<211> 386
<212> DNA
<213> Homo sapiens

<400> 1795
ctatgctctg agtcacttct ccaagcattc ctttctgttc ttccttccct gggctgatca
60
tttcaagaag tcctacattc cagaaaactt gagaggtgct tcttctctgg aagccccttt
120

tcttttctgt gagctcaggg agcattctac atacctcagc tgtgtctgct atcttttgct
180
taattatcaa tctttccata taaacagtaa aggaccacag tttattcatc agattcccca
240
tccaaacctg cacctgcata cataaacgca ctggataaat gtaccgcagt agacagaggc
300
tctccaggtt gagagctcca tgagggcacc aatttttgtc tgtttagctg tgtcctcaaa
360
gcaaggaagg gttgatccgg tctaga
386

<210> 1796
<211> 86
<212> PRT
<213> Homo sapiens

<400> 1796
Met Gln Val Gln Val Trp Met Gly Asn Leu Met Asn Lys Leu Trp Ser
1 5 10 15
Phe Thr Val Tyr Met Glu Arg Leu Ile Ile Lys Gln Lys Ile Ala Asp
20 25 30
Thr Ala Glu Val Cys Arg Met Leu Pro Glu Leu Thr Glu Lys Lys Arg
35 40 45
Gly Phe Gln Arg Arg Ser Thr Ser Gln Val Phe Trp Asn Val Gly Leu
50 55 60
Leu Glu Met Ile Ser Pro Gly Lys Glu Glu Gln Lys Gly Met Leu Gly
65 70 75 80
Glu Val Thr Gln Ser Ile
85

<210> 1797
<211> 348
<212> DNA
<213> Homo sapiens

<400> 1797
aagcttcact atgttgccca ttccatgggc ggcgtgctgg tgcgtgacct gctggcggac
60
cggaatttgc cgatgtcatt gatcaggtca tctgtctggg ctcgccgcag cagggctcgc
120
gtgccgctaa tttgttggcg ccatttgctg gcggcgcatc cgtcaaatgg tgtatcacag
180
cgactatgtg atgccgcttg cgcccacgcc cggcagcgcg cgttggagcg ccatcaactc
240
acagatggac aacctggtgt tgccggtgac ctcggcaatt ttaccgggaa tgacccatgt
300
ggcggtggat tacctggggc attgttcgtt attgtacagc ccacgcgt
348

<210> 1798
<211> 108
<212> PRT
<213> Homo sapiens

<400> 1798
Met Gly Gly Val Leu Val Arg Asp Leu Leu Ala Asp Arg Asn Leu Pro
1 5 10 15
Met Ser Leu Ile Arg Ser Ser Val Trp Ala Arg Arg Ser Arg Ala Arg
20 25 30
Val Pro Leu Ile Cys Trp Arg His Leu Leu Ala Ala His Pro Ser Asn
35 40 45
Gly Val Ser Gln Arg Leu Cys Asp Ala Ala Cys Ala His Ala Arg Gln
50 55 60
Arg Ala Leu Glu Arg His Gln Leu Thr Asp Gly Gln Pro Gly Val Ala
65 70 75 80
Gly Asp Leu Gly Asn Phe Thr Gly Asn Asp Pro Cys Gly Gly Gly Leu
85 90 95
Pro Gly Ala Leu Phe Val Ile Val Gln Pro Thr Arg
100 105

<210> 1799
<211> 366
<212> DNA
<213> Homo sapiens

<400> 1799
acgcgtcgcc tcctgctggt cgggattttc cttgctgtag ttaaccaaac caccggcgtc
60
aataccgtca tgtattacgc gcccaaggtg ttggagttcg caggaatgag cacccaggcg
120
tcgattattt cagaggtggc taatggagtc atgtctgtta ttggtgccgc tgcaggcttg
180
tggctcatcg aacggtttga tcgtcgtcac ctgcttatct tcgatgtcac ggcggtcggt
240
gtgtgtctcc ttggtattgc ggctactttc gggctggcaa ttgctcctca tgtgggtcaa
300
ggggtaccga agtgggcgcc tattctcgtg ctcgtcctga tgagtatctt catgcttatc
360
gtgcac
366

<210> 1800
<211> 122
<212> PRT
<213> Homo sapiens

<400> 1800
Thr Arg Arg Leu Leu Leu Val Gly Ile Phe Leu Ala Val Val Asn Gln
1 5 10 15
Thr Thr Gly Val Asn Thr Val Met Tyr Tyr Ala Pro Lys Val Leu Glu
20 25 30
Phe Ala Gly Met Ser Thr Gln Ala Ser Ile Ile Ser Glu Val Ala Asn
35 40 45
Gly Val Met Ser Val Ile Gly Ala Ala Ala Gly Leu Trp Leu Ile Glu
50 55 60
Arg Phe Asp Arg Arg His Leu Leu Ile Phe Asp Val Thr Ala Val Gly
65 70 75 80
Val Cys Leu Leu Gly Ile Ala Ala Thr Phe Gly Leu Ala Ile Ala Pro

```
                85                  90                  95
His Val Gly Gln Gly Val Pro Lys Trp Ala Pro Ile Leu Val Leu Val
            100                 105                 110
Leu Met Ser Ile Phe Met Leu Ile Val His
        115                 120
```

<210> 1801
<211> 597
<212> DNA
<213> Homo sapiens

<400> 1801
aatttctcct tcggtgacta cttcaagaac gaggccattc agtacgcatg ggagctcgtc
60
actaagccgg cagaacaggg cggattgggt ttcgatcctg ccagcatctg ggtgacggtc
120
cttggacctg ggtttcaccc tgactatccg gagggcgaca ttgaggcgcg cgaggcgtgg
180
cgtgctgcgg gtatccctga cgagcagatt cagggtcgct cccttaagga caactactgg
240
catatggggg ttcccggccc cggcggcccg tgctcggaaa tctacatcga tcgtggccca
300
gcctatggtc ccgacggtgg tccagaagca gatgaggacc gttaccttga gatctggaac
360
ctcgtattcg agaccgagga tctctcagcg gtgcgcgcta aagatgactt cgacatcgca
420
ggcccattgc gcagccttaa catcgacact ggtgccggtc tcgaacgtat tgcctaccta
480
ctccagggcg tcgacaatat gtacgagact gaccaggtat tccctgtcat tgagaaagcg
540
tccgagatgt cgggcaagcg gtacggcgtt cgccacgacg acgacgtccg actacgc
597

<210> 1802
<211> 199
<212> PRT
<213> Homo sapiens

<400> 1802
```
Asn Phe Ser Phe Gly Asp Tyr Phe Lys Asn Glu Ala Ile Gln Tyr Ala
 1               5                  10                  15
Trp Glu Leu Val Thr Lys Pro Ala Glu Gln Gly Gly Leu Gly Phe Asp
            20                  25                  30
Pro Ala Ser Ile Trp Val Thr Val Leu Gly Pro Gly Phe His Pro Asp
        35                  40                  45
Tyr Pro Glu Gly Asp Ile Glu Ala Arg Glu Ala Trp Arg Ala Ala Gly
    50                  55                  60
Ile Pro Asp Glu Gln Ile Gln Gly Arg Ser Leu Lys Asp Asn Tyr Trp
65                  70                  75                  80
His Met Gly Val Pro Gly Pro Gly Gly Pro Cys Ser Glu Ile Tyr Ile
                85                  90                  95
Asp Arg Gly Pro Ala Tyr Gly Pro Asp Gly Gly Pro Glu Ala Asp Glu
            100                 105                 110
Asp Arg Tyr Leu Glu Ile Trp Asn Leu Val Phe Glu Thr Glu Asp Leu
```

```
        115                 120                 125
Ser Ala Val Arg Ala Lys Asp Asp Phe Asp Ile Ala Gly Pro Leu Arg
    130                 135                 140
Ser Leu Asn Ile Asp Thr Gly Ala Gly Leu Glu Arg Ile Ala Tyr Leu
145                 150                 155                 160
Leu Gln Gly Val Asp Asn Met Tyr Glu Thr Asp Gln Val Phe Pro Val
                165                 170                 175
Ile Glu Lys Ala Ser Glu Met Ser Gly Lys Arg Tyr Gly Val Arg His
            180                 185                 190
Asp Asp Asp Val Arg Leu Arg
        195
```

<210> 1803
<211> 708
<212> DNA
<213> Homo sapiens

<400> 1803
cccacaacga tggccgtcat ggtggatggg gaagtgcctg aggaggtcac acctaaggac
60
ctcatcctgg ccctcatctc cgagatcggc accggtgggg gacaaggtca tatggtcgag
120
tatcgcggcg aggccatcga gaagatgtcg atggagggtc gcatgacgat ctgcaatatg
180
tcgattgagt ggggagctcg cgtcggcatg gttgcttctg atgagaccac cttcacctac
240
ctcaaggatc gtccgcacgc tccgcgtggt gcacagtggg acaaggctgt cgcgtactgg
300
cgcactctgc gtactgacga cgatgcgacc tttgacgctg agatccatgt ggacgcctcg
360
aatctcgccc ccttcgttac ctggggtacc aacccggggc agggatcccc cctaggcggt
420
gtggtgccgg ccgtcgaaga ctttgaggac gaggtagctc gcagcgcagc gtttggagta
480
catggatttg accccgacga gatcggttcc cggtttgctg acatctttcg caataactct
540
gcgaacaacg gcttgttact ggctcaggtt gatcccaagg tcgtcggaga gttgtgggac
600
tttgccgagc agcatcctgg tgagcagctc accctctccc tcgagaatcg gacgattaac
660
cttccgggtc gcacgaccta cccgttccat attgatgacg tcacgcgt
708

<210> 1804
<211> 236
<212> PRT
<213> Homo sapiens

<400> 1804
```
Pro Thr Thr Met Ala Val Met Val Asp Gly Glu Val Pro Glu Glu Val
 1               5                  10                  15
Thr Pro Lys Asp Leu Ile Leu Ala Leu Ile Ser Glu Ile Gly Thr Gly
            20                  25                  30
Gly Gly Gln Gly His Met Val Glu Tyr Arg Gly Glu Ala Ile Glu Lys
```

```
        35                  40                  45
Met Ser Met Glu Gly Arg Met Thr Ile Cys Asn Met Ser Ile Glu Trp
    50                  55                  60
Gly Ala Arg Val Gly Met Val Ala Ser Asp Glu Thr Thr Phe Thr Tyr
65                  70                  75                  80
Leu Lys Asp Arg Pro His Ala Pro Arg Gly Ala Gln Trp Asp Lys Ala
                85                  90                  95
Val Ala Tyr Trp Arg Thr Leu Arg Thr Asp Asp Asp Ala Thr Phe Asp
            100                 105                 110
Ala Glu Ile His Val Asp Ala Ser Asn Leu Ala Pro Phe Val Thr Trp
        115                 120                 125
Gly Thr Asn Pro Gly Gln Gly Ser Pro Leu Gly Gly Val Val Pro Ala
    130                 135                 140
Val Glu Asp Phe Glu Asp Glu Val Ala Arg Ser Ala Ala Phe Gly Val
145                 150                 155                 160
His Gly Phe Asp Pro Asp Glu Ile Gly Ser Arg Phe Ala Asp Ile Phe
                165                 170                 175
Arg Asn Asn Ser Ala Asn Asn Gly Leu Leu Leu Ala Gln Val Asp Pro
            180                 185                 190
Lys Val Val Gly Glu Leu Trp Asp Phe Ala Glu Gln His Pro Gly Glu
        195                 200                 205
Gln Leu Thr Leu Ser Leu Glu Asn Arg Thr Ile Asn Leu Pro Gly Arg
    210                 215                 220
Thr Thr Tyr Pro Phe His Ile Asp Asp Val Thr Arg
225                 230                 235
```

<210> 1805
<211> 833
<212> DNA
<213> Homo sapiens
<400> 1805

```
nccgcagtgg tgtgggacaa gaacaccggt gagccggttt ataacgccat cgtgtggcag
60
gacacgcgca ctcaaaagat ctgtaacgaa ctagctggtg acaagggcgc cgaccgctac
120
aaggagatct gtggtctggg cctgtcgacc tatttctctg gcccgaaggt caaatggatt
180
ctcgacaacg ttgagggagc ccgtgcgagg gccgaggccg gcgatctgct cttcggtaac
240
atggacactt gggtgctgtg gaacctgact ggcggtacta acggtggcgt gcacatcacc
300
gatccgacca acgcgtcccg aaccatgctc atggacgtcc gaaagctgca gtgggacgac
360
tcgatgtgcg aggtcatggg aattccaaag tccatgcttc ctgagatcaa gtcctcctcc
420
gagatctacg gctatggtcg caagaacggc ctgctgatcg ataccccgat ctccggcatt
480
cttggcgatc agcaggccgc cacctttggc caggcttgct tccaaaaggg catggcgaag
540
aacacgtacg gcaccggctg cttcatgctc atgaacacag gtgaggaggc catcttctcc
600
gagaacggtc tgctgaccac cgtctgctac aagattggtg accagcccac cgtctatgcc
660
```

ctggaaggtt cgatcgccgt cgctggatcg ctggtacagt ggctgcgcga caacctcaag
720
atgttcgaga ccgccccgca aatcgaagcc ctcgccaaca ccgtcgagga caatggtggc
780
gcctactttg tgccggcctt ctctggcctg ttcgcgccgt actggcgtcc gga
833

<210> 1806
<211> 277
<212> PRT
<213> Homo sapiens

<400> 1806
Xaa Ala Val Val Trp Asp Lys Asn Thr Gly Glu Pro Val Tyr Asn Ala
1 5 10 15
Ile Val Trp Gln Asp Thr Arg Thr Gln Lys Ile Cys Asn Glu Leu Ala
20 25 30
Gly Asp Lys Gly Ala Asp Arg Tyr Lys Glu Ile Cys Gly Leu Gly Leu
35 40 45
Ser Thr Tyr Phe Ser Gly Pro Lys Val Lys Trp Ile Leu Asp Asn Val
50 55 60
Glu Gly Ala Arg Ala Arg Ala Glu Ala Gly Asp Leu Leu Phe Gly Asn
65 70 75 80
Met Asp Thr Trp Val Leu Trp Asn Leu Thr Gly Gly Thr Asn Gly Gly
85 90 95
Val His Ile Thr Asp Pro Thr Asn Ala Ser Arg Thr Met Leu Met Asp
100 105 110
Val Arg Lys Leu Gln Trp Asp Asp Ser Met Cys Glu Val Met Gly Ile
115 120 125
Pro Lys Ser Met Leu Pro Glu Ile Lys Ser Ser Ser Glu Ile Tyr Gly
130 135 140
Tyr Gly Arg Lys Asn Gly Leu Leu Ile Asp Thr Pro Ile Ser Gly Ile
145 150 155 160
Leu Gly Asp Gln Gln Ala Ala Thr Phe Gly Gln Ala Cys Phe Gln Lys
165 170 175
Gly Met Ala Lys Asn Thr Tyr Gly Thr Gly Cys Phe Met Leu Met Asn
180 185 190
Thr Gly Glu Glu Ala Ile Phe Ser Glu Asn Gly Leu Leu Thr Thr Val
195 200 205
Cys Tyr Lys Ile Gly Asp Gln Pro Thr Val Tyr Ala Leu Glu Gly Ser
210 215 220
Ile Ala Val Ala Gly Ser Leu Val Gln Trp Leu Arg Asp Asn Leu Lys
225 230 235 240
Met Phe Glu Thr Ala Pro Gln Ile Glu Ala Leu Ala Asn Thr Val Glu
245 250 255
Asp Asn Gly Gly Ala Tyr Phe Val Pro Ala Phe Ser Gly Leu Phe Ala
260 265 270
Pro Tyr Trp Arg Pro
275

<210> 1807
<211> 420
<212> DNA
<213> Homo sapiens

<400> 1807
nnntatcggc aaggtggtcg aaatggctct tgactatgtc aacggtgaca cgtgcgccgc
60
gaccgcccca ttcatttgtc gtttgacgtc gacgcgatgg accctagcgt ggccccgagc
120
acaggcacac cggtgcgtgg tggtctcaca ttccgagaag gccactacat atgcgaggcg
180
gtagctgaga ccggctcgtt ggtggctatg gatatggtag aagtcaaccc ccatcttgaa
240
aagcatgcgg ctgagcagac gatcgccgtg ggttgttccc tcattcgttc ggcgctgggg
300
gagacgcttc tgtaatgggt gcatgatggg ccggtggtcc atagccatgc atagacactc
360
cgggcgctga tatgatgagt gacatagcac gtacgataaa tctcggtttt gagcacgcgt
420

<210> 1808
<211> 88
<212> PRT
<213> Homo sapiens

<400> 1808
His Val Arg Arg Asp Arg Pro Ile His Leu Ser Phe Asp Val Asp Ala
 1   5   10   15
Met Asp Pro Ser Val Ala Pro Ser Thr Gly Thr Pro Val Arg Gly Gly
            20   25   30
Leu Thr Phe Arg Glu Gly His Tyr Ile Cys Glu Ala Val Ala Glu Thr
        35   40   45
Gly Ser Leu Val Ala Met Asp Met Val Glu Val Asn Pro His Leu Glu
    50   55   60
Lys His Ala Ala Glu Gln Thr Ile Ala Val Gly Cys Ser Leu Ile Arg
65   70   75   80
Ser Ala Leu Gly Glu Thr Leu Leu
                85

<210> 1809
<211> 340
<212> DNA
<213> Homo sapiens

<400> 1809
nnaccggtga tcgcatcggt gagcctcggc gcgatgcgcg tgttcgacct tcgccatcgc
60
cagaccggtg tcacgcatgc gtatcgcctc gggcatggca gcctcctcgt gatgcggggc
120
cccacccagg ccgaatggca gcatcgcgtg ccgaaagcgc cgggtgtgca gggcgagcgc
180
gtgaacctga cgtttcggcg cgtgatgccg gtcggtatgg gccggtaaca accggcgtcg
240
ccgaggtgcc cggatcgccg ggcgattcgc gccccgtttt cgcgattcat gcgcgatcga
300
tacgggcagg cggtcgcatg tgcggcacgt tgccgcacgn
340

<210> 1810
<211> 75
<212> PRT
<213> Homo sapiens

<400> 1810
Xaa Pro Val Ile Ala Ser Val Ser Leu Gly Ala Met Arg Val Phe Asp
1 5 10 15
Leu Arg His Arg Gln Thr Gly Val Thr His Ala Tyr Arg Leu Gly His
20 25 30
Gly Ser Leu Leu Val Met Arg Gly Pro Thr Gln Ala Glu Trp Gln His
35 40 45
Arg Val Pro Lys Ala Pro Gly Val Gln Gly Glu Arg Val Asn Leu Thr
50 55 60
Phe Arg Arg Val Met Pro Val Gly Met Gly Arg
65 70 75

<210> 1811
<211> 500
<212> DNA
<213> Homo sapiens

<400> 1811
nnacgcgtgc taggaatagc catggactca tcatcagata catgctggat ttatacttca
60
ctgggtggat tgtatgagct gctcgtaaaa gatgaggctc gcgatatgtg gcatttgttg
120
ctgaaacggt gcgactttga gaaggcacta acattttgtc gtgatgagac gtgtcggaag
180
caggtactgg aaaagaaggg cgatgcactg ctacacgcag gtcagctcat ggaggccgtc
240
gagtgctatg ctcaggccca gacaccggcc tttgaacagg ttgtgctttc tttgatggac
300
gtctgtgccg acaaggcatt gcgtcgatat gtcagactgc gtctcgacaa gatgccgaaa
360
caagctcgcg tgcctcgtct catgctggct acttggctca ttgaattgta tgtggccgcc
420
attcaagcgc atgaacccac ctccgaacat tatcagacac ttttgctgga agcccaggag
480
acacttgagc ggcatcatga
500

<210> 1812
<211> 166
<212> PRT
<213> Homo sapiens

<400> 1812
Xaa Arg Val Leu Gly Ile Ala Met Asp Ser Ser Ser Asp Thr Cys Trp
1 5 10 15
Ile Tyr Thr Ser Leu Gly Gly Leu Tyr Glu Leu Leu Val Lys Asp Glu
20 25 30
Ala Arg Asp Met Trp His Leu Leu Leu Lys Arg Cys Asp Phe Glu Lys

```
        35                  40                  45
Ala Leu Thr Phe Cys Arg Asp Glu Thr Cys Arg Lys Gln Val Leu Glu
    50                  55                  60
Lys Lys Gly Asp Ala Leu Leu His Ala Gly Gln Leu Met Glu Ala Val
65                  70                  75                  80
Glu Cys Tyr Ala Gln Ala Gln Thr Pro Ala Phe Glu Gln Val Val Leu
                85                  90                  95
Ser Leu Met Asp Val Cys Ala Asp Lys Ala Leu Arg Arg Tyr Val Arg
            100                 105                 110
Leu Arg Leu Asp Lys Met Pro Lys Gln Ala Arg Val Pro Arg Leu Met
        115                 120                 125
Leu Ala Thr Trp Leu Ile Glu Leu Tyr Val Ala Ala Ile Gln Ala His
    130                 135                 140
Glu Pro Thr Ser Glu His Tyr Gln Thr Leu Leu Leu Glu Ala Gln Glu
145                 150                 155                 160
Thr Leu Glu Arg His His
                165
```

<210> 1813
<211> 426
<212> DNA
<213> Homo sapiens

<400> 1813
tctagagccg ttgtgatcgg tatccatggt tggatggggt tcatctcgat ggaggagtgt
60
gtcctgaggg gtggcagtga cctggtaggg gtgcctgcgg cgtcgcggct tgcgatcgct
120
ggttctcggg gatgactctc ggatgaatat agatctgcta agacgtcatt agattcgctt
180
ggcgcttggt tgggaacggg tgtgaagcag ccttctgatg gatgtatttt tgcgttgttg
240
aataaggttt caatattaat tgaatatggc gctagatgct ggtttaggat cagttgacgt
300
ccgctgtaga tcctccctat ggtcattctg gggccaggcg cttcgccagc tggccatcgc
360
aacaatggtg tggcgaaggg ttatgaggtg agtatggctg agcaagtcgt tggacaggcg
420
tctaca
426

<210> 1814
<211> 108
<212> PRT
<213> Homo sapiens

<400> 1814
```
Met Thr Ile Gly Arg Ile Tyr Ser Gly Arg Gln Leu Ile Leu Asn Gln
 1               5                  10                  15
His Leu Ala Pro Tyr Ser Ile Asn Ile Glu Thr Leu Phe Asn Asn Ala
            20                  25                  30
Lys Ile His Pro Ser Glu Gly Cys Phe Thr Pro Val Pro Asn Gln Ala
        35                  40                  45
Pro Ser Glu Ser Asn Asp Val Leu Ala Asp Leu Tyr Ser Ser Glu Ser
```

```
    50                  55                  60
His Pro Arg Glu Pro Ala Ile Ala Ser Arg Asp Ala Ala Gly Thr Pro
65                  70                  75                  80
Thr Arg Ser Leu Pro Pro Leu Arg Thr His Ser Ser Ile Glu Met Asn
                85                  90                  95
Pro Ile Gln Pro Trp Ile Pro Ile Thr Thr Ala Leu
            100                 105
```

<210> 1815
<211> 303
<212> DNA
<213> Homo sapiens

<400> 1815
ggcgcccaca tggctacgct cgcaccgcgg cacaaggtaa gccgtagcgg cgggatcgag
60
cgccaggccg cgcatctcgg catggagcgc gatcagttcg gccatcatcg cgtcgtcggg
120
cgtgccgatc tcgaggggca acgccgcgcc gagccgcgaa gccagatcgg gcagcgcgat
180
ccgccagcca tcggcaaatt cgcgagtgat gacgagcaag ggccgcctgg tctcctgcgc
240
ccggttccag cagtggaaca cgttcgcctc gggcagacgg gcggcatcgg cgatcacggt
300
acc
303

<210> 1816
<211> 98
<212> PRT
<213> Homo sapiens

<400> 1816
```
Met Ala Thr Leu Ala Pro Arg His Lys Val Ser Arg Ser Gly Gly Ile
 1               5                  10                  15
Glu Arg Gln Ala Ala His Leu Gly Met Glu Arg Asp Gln Phe Gly His
            20                  25                  30
His Arg Val Val Gly Arg Ala Asp Leu Glu Gly Gln Arg Arg Ala Glu
        35                  40                  45
Pro Arg Ser Gln Ile Gly Gln Arg Asp Pro Pro Ala Ile Gly Lys Phe
    50                  55                  60
Ala Ser Asp Asp Glu Gln Gly Pro Pro Gly Leu Leu Arg Pro Val Pro
65                  70                  75                  80
Ala Val Glu His Val Arg Leu Gly Gln Thr Gly Gly Ile Gly Asp His
                85                  90                  95
Gly Thr
```

<210> 1817
<211> 413
<212> DNA
<213> Homo sapiens

<400> 1817

nncagcttgc aagaccgcgg ccacacagtg tacatcttaa catcacattt cgatgcgtcg
60
catgcgtttg agcccacacg cgatggcaca cttcaggtca ttcacgcaaa gacatggatc
120
ccgcgctcct tatttcacat gctgcatctg cgatggccat tcgcagcagt tttttctctt
180
gtgatgcagg tcgtggtagc agcgtatgga tcgtcactcg cacgccactt gccgcatgtg
240
tacagggcgt gacgcatgtc ccgtcaaact cgctcccaga cgtgtttgtt attgaccaac
300
ttccagcagc gataccccta atcaaactcc tgtgtgggcg gcgtgtcatg tactactgtc
360
acttccctga caaagaaatc agcgctgctc tggctcgaca gcgaggcacg cgt
413

<210> 1818
<211> 83
<212> PRT
<213> Homo sapiens

<400> 1818
Xaa Ser Leu Gln Asp Arg Gly His Thr Val Tyr Ile Leu Thr Ser His
1 5 10 15
Phe Asp Ala Ser His Ala Phe Glu Pro Thr Arg Asp Gly Thr Leu Gln
20 25 30
Val Ile His Ala Lys Thr Trp Ile Pro Arg Ser Leu Phe His Met Leu
35 40 45
His Leu Arg Trp Pro Phe Ala Ala Val Phe Ser Leu Val Met Gln Val
50 55 60
Val Val Ala Ala Tyr Gly Ser Ser Leu Ala Arg His Leu Pro His Val
65 70 75 80
Tyr Arg Ala

<210> 1819
<211> 343
<212> DNA
<213> Homo sapiens

<400> 1819
ggatccaaga gtggggcatc aggaacatgc catggttgtc gtggtgctgg aatgagaaca
60
atcacaagac agataggcct tggcatgatc caacagatga acactgtttg ccctgaatgc
120
aaaggatcag gtgagatcat aagtgacaag gacaaatgcc caagctgtaa aggaaacaaa
180
gtagtccagg agaagaaggt gttagaggtt catgtggaga aaggaatgca acataaccaa
240
aagattgtat tccagggtca ggctgatgaa gctcctgata cgggtacagg agacattgtt
300
tttgtcttgc aacttaaaga ccatccaaaa tttaagagga tgt
343

<210> 1820

<211> 114
<212> PRT
<213> Homo sapiens

<400> 1820
Gly Ser Lys Ser Gly Ala Ser Gly Thr Cys His Gly Cys Arg Gly Ala
1 5 10 15
Gly Met Arg Thr Ile Thr Arg Gln Ile Gly Leu Gly Met Ile Gln Gln
20 25 30
Met Asn Thr Val Cys Pro Glu Cys Lys Gly Ser Gly Glu Ile Ile Ser
35 40 45
Asp Lys Asp Lys Cys Pro Ser Cys Lys Gly Asn Lys Val Val Gln Glu
50 55 60
Lys Lys Val Leu Glu Val His Val Glu Lys Gly Met Gln His Asn Gln
65 70 75 80
Lys Ile Val Phe Gln Gly Gln Ala Asp Glu Ala Pro Asp Thr Gly Thr
85 90 95
Gly Asp Ile Val Phe Val Leu Gln Leu Lys Asp His Pro Lys Phe Lys
100 105 110
Arg Met

<210> 1821
<211> 285
<212> DNA
<213> Homo sapiens

<400> 1821
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120
gcccgggaaa agttgctcgc caaggaggcc gcccagcgga tgacctagat tgtctactgc
180
tgtgtctgcc ctgtagtttg acggggaaga actgatgaac tcgtattgtg gttttccgaa
240
tctagtttca tatgtttctg tccaccagac catgtttaga agctt
285

<210> 1822
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1822
Lys Leu Glu Phe Ser Lys Ile Leu Glu Ala Ile Lys Ala Asn Phe Asn
1 5 10 15
Asp Lys Phe Asp Glu Val Gly Lys Lys Trp Gly Gly Gly Ile Met Gly
20 25 30
Ser Lys Ser Gln Ala Lys Thr Lys Ala Arg Glu Lys Leu Leu Ala Lys
35 40 45
Glu Ala Ala Gln Arg Met Thr
50 55

<210> 1823
<211> 387
<212> DNA
<213> Homo sapiens

<400> 1823
ngttggctgc tgttgctggg cgttctgtcc ctgacgggct gcgcccgttc cgatgcgctg
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tggggcgtgg tcgataagct ctgcatggcc aactatcagc aaaagcgcga tccggccccg
120
tgtgagcaga tttatatgcc gcagggtaaa gcgcagggct ttagcgtgct gcaaaacccg
180
cgttatccct atcatttcat tctggtgccg acggcgccgc tttccggcat tgaaagcccg
240
ctgctgctgg ccggagagcg aacggactat tttggctatg catggctgat gcgttaccgg
300
ctggccgccg agtatggcgg gccggtgccg gacgacaggc tgggcatggc gatcaactcc
360
gcttacggcc gcagccagaa ccaattg
387

<210> 1824
<211> 129
<212> PRT
<213> Homo sapiens

<400> 1824
Xaa Trp Leu Leu Leu Leu Gly Val Leu Ser Leu Thr Gly Cys Ala Arg
 1   5   10   15
Ser Asp Ala Leu Trp Gly Val Val Asp Lys Leu Cys Met Ala Asn Tyr
            20   25   30
Gln Gln Lys Arg Asp Pro Ala Pro Cys Glu Gln Ile Tyr Met Pro Gln
        35   40   45
Gly Lys Ala Gln Gly Phe Ser Val Leu Gln Asn Pro Arg Tyr Pro Tyr
    50   55   60
His Phe Ile Leu Val Pro Thr Ala Pro Leu Ser Gly Ile Glu Ser Pro
65   70   75   80
Leu Leu Leu Ala Gly Glu Arg Thr Asp Tyr Phe Gly Tyr Ala Trp Leu
                85   90   95
Met Arg Tyr Arg Leu Ala Ala Glu Tyr Gly Gly Pro Val Pro Asp Asp
            100   105   110
Arg Leu Gly Met Ala Ile Asn Ser Ala Tyr Gly Arg Ser Gln Asn Gln
        115   120   125
Leu

<210> 1825
<211> 413
<212> DNA
<213> Homo sapiens

<400> 1825
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120
ttggcacgtc gtgattgggc gcctaggcac catgtcgcag gccgacatgg acatgtgggc
180
gtcgtgcctc gatacgcgcg acccttcctg ctctcggtgg gccttgtgtg cctggagcgc
240
gatgcctggc ctacgggcac gcgatgcatc ggtggtctac ctgtcggaca tgccgctggg
300
tctggcctca ggtgcgtggc cgatccgcgt gcctcgctcg gcgttatgtg tctgccggcg
360
cctatgccat tcatctcgtg cagctacgtc acctggctga tctcgacgcg gct
413

<210> 1826
<211> 124
<212> PRT
<213> Homo sapiens

<400> 1826
Met Gly Arg Arg Arg Cys Val Cys Val His Thr Ala Ala Leu Ala Gly
 1   5   10   15
Arg Ala Cys Asp Cys Arg Arg His Ile Gly Gly Leu Ala Arg Arg Asp
            20   25   30
Trp Ala Pro Arg His His Val Ala Gly Arg His Gly His Val Gly Val
        35   40   45
Val Pro Arg Tyr Ala Arg Pro Phe Leu Leu Ser Val Gly Leu Val Cys
    50   55   60
Leu Glu Arg Asp Ala Trp Pro Thr Gly Thr Arg Cys Ile Gly Gly Leu
65   70   75   80
Pro Val Gly His Ala Ala Gly Ser Gly Leu Arg Cys Val Ala Asp Pro
                85   90   95
Arg Ala Ser Leu Gly Val Met Cys Leu Pro Ala Pro Met Pro Phe Ile
            100   105   110
Ser Cys Ser Tyr Val Thr Trp Leu Ile Ser Thr Arg
        115   120

<210> 1827
<211> 345
<212> DNA
<213> Homo sapiens

<400> 1827
ctggccaact gggtgccgga cctgttcatg aagcgcgtcg aagccgacca ggaatggtcg
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120
gcctacctgc aggccgaagc gcagggcaag gccaaccgca cgatctctgc ccgcaagctg
180
tacgcccgca tgatgcgtac gctggccgag accggcaacg gctggatgac cttcaaggac
240
aagtgcaacc gcgccagcaa ccagaccctg cgtccgggca acgtgatcca cctgtccaac
300
ctgtgcaccg aaatcctgga agtcacttcc aacgatgaaa ccgcg
345

<210> 1828
<211> 115
<212> PRT
<213> Homo sapiens

<400> 1828
Leu Ala Asn Trp Val Pro Asp Leu Phe Met Lys Arg Val Glu Ala Asp
1 5 10 15
Gln Glu Trp Ser Leu Phe Asp Pro Arg Val Val Pro Glu Phe Thr Asp
20 25 30
Leu Phe Gly Glu Ala Phe Glu Ala Ala Tyr Leu Gln Ala Glu Ala Gln
35 40 45
Gly Lys Ala Asn Arg Thr Ile Ser Ala Arg Lys Leu Tyr Ala Arg Met
50 55 60
Met Arg Thr Leu Ala Glu Thr Gly Asn Gly Trp Met Thr Phe Lys Asp
65 70 75 80
Lys Cys Asn Arg Ala Ser Asn Gln Thr Leu Arg Pro Gly Asn Val Ile
85 90 95
His Leu Ser Asn Leu Cys Thr Glu Ile Leu Glu Val Thr Ser Asn Asp
100 105 110
Glu Thr Ala
115

<210> 1829
<211> 4457
<212> DNA
<213> Homo sapiens

<400> 1829
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120
gaaaccgtga atgcccaaga ggattctcaa atgcccaagg aaagctcccc agatgatgat
180
gttcaacagg tagtatttga cctgatatgt aaagttgtaa gtggcctcga agtggaatct
240
gcatcagtta catctcaatt agaaattgaa gctatgcccc caaagtgcag tgatatagat
300
ccagatgaag agacgattaa aattgaagat gactccattc gacagagtca gaatgctttg
360
ctgagtaatg aaagttctca gtttctgtct gtgtctgcag agggaggcca tgagtgtgtg
420
gcaaatggaa tctccaggaa tagctcctca ccttgtattt caggaaccac acacactctt
480
catgactctt ctgttgcttc catagaaacc aaatctagac aaaggagtca cagtagtatt
540
caattcagct tcaaagaaaa attatcagaa aaagtttcgg agaaggaaac aatagttaag
600
gagtcaggta aacaaccagg agcaaaacct aaagtaaaac ttgccagaaa aaaggatgat
660
gacaagaaaa aatcttcaaa tgaaaaactc aaacaaacca gtgtattctt cagtgatggt
720

ctggatttag agaactggta tagctgtgga gagggagaca tttctgaaat tgagagtgac
780
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840
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900
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1080
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2340

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4320
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4440
aaaaaaaaaa aaaaaaa
4457

<210> 1830
<211> 1377
<212> PRT
<213> Homo sapiens

<400> 1830
Ile Pro Met Val Val Ser Asp Phe Asp Leu Pro Asp Gln Gln Ile Glu
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Ile Leu Gln Ser Ser Asp Ser Gly Cys Ser Gln Ser Ser Ala Gly Asp
20 25 30
Asn Leu Ser Tyr Glu Val Asp Pro Glu Thr Val Asn Ala Gln Glu Asp
35 40 45
Ser Gln Met Pro Lys Glu Ser Ser Pro Asp Asp Asp Val Gln Gln Val
50 55 60
Val Phe Asp Leu Ile Cys Lys Val Val Ser Gly Leu Glu Val Glu Ser
65 70 75 80
Ala Ser Val Thr Ser Gln Leu Glu Ile Glu Ala Met Pro Pro Lys Cys
85 90 95
Ser Asp Ile Asp Pro Asp Glu Glu Thr Ile Lys Ile Glu Asp Asp Ser
100 105 110
Ile Arg Gln Ser Gln Asn Ala Leu Leu Ser Asn Glu Ser Ser Gln Phe
115 120 125
Leu Ser Val Ser Ala Glu Gly Gly His Glu Cys Val Ala Asn Gly Ile
130 135 140
Ser Arg Asn Ser Ser Ser Pro Cys Ile Ser Gly Thr Thr His Thr Leu
145 150 155 160
His Asp Ser Ser Val Ala Ser Ile Glu Thr Lys Ser Arg Gln Arg Ser
165 170 175
His Ser Ser Ile Gln Phe Ser Phe Lys Glu Lys Leu Ser Glu Lys Val
180 185 190
Ser Glu Lys Glu Thr Ile Val Lys Glu Ser Gly Lys Gln Pro Gly Ala
195 200 205
Lys Pro Lys Val Lys Leu Ala Arg Lys Lys Asp Asp Asp Lys Lys Lys
210 215 220
Ser Ser Asn Glu Lys Leu Lys Gln Thr Ser Val Phe Phe Ser Asp Gly

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225                 230                 235                 240
Leu Asp Leu Glu Asn Trp Tyr Ser Cys Gly Glu Gly Asp Ile Ser Glu
                245                 250                 255
Ile Glu Ser Asp Met Gly Ser Pro Gly Ser Arg Lys Ser Pro Asn Phe
            260                 265                 270
Asn Ile His Pro Leu Tyr Gln His Val Leu Leu Tyr Leu Gln Leu Tyr
        275                 280                 285
Asp Ser Ser Arg Thr Leu Tyr Ala Phe Ser Ala Ile Lys Ala Ile Leu
    290                 295                 300
Lys Thr Asn Pro Ile Ala Phe Val Asn Ala Ile Ser Thr Thr Ser Val
305                 310                 315                 320
Asn Asn Ala Tyr Thr Pro Gln Leu Ser Leu Leu Gln Asn Leu Leu Ala
                325                 330                 335
Arg His Arg Ile Ser Val Met Gly Lys Asp Phe Tyr Ser His Ile Pro
            340                 345                 350
Val Asp Ser Asn His Asn Phe Arg Ser Ser Met Tyr Ile Glu Ile Leu
        355                 360                 365
Ile Ser Leu Cys Leu Tyr Tyr Met Arg Ser His Tyr Pro Thr His Val
    370                 375                 380
Lys Val Thr Ala Gln Asp Leu Ile Gly Asn Arg Asn Met Gln Met Met
385                 390                 395                 400
Ser Ile Glu Ile Leu Thr Leu Leu Phe Thr Glu Leu Ala Lys Val Ile
                405                 410                 415
Glu Ser Ser Ala Lys Gly Phe Pro Ser Phe Ile Ser Asp Met Leu Ser
            420                 425                 430
Lys Cys Lys Val Gln Lys Val Ile Leu His Cys Leu Leu Ser Ser Ile
        435                 440                 445
Phe Ser Ala Gln Lys Trp His Ser Glu Lys Met Ala Gly Lys Asn Leu
    450                 455                 460
Val Ala Val Glu Glu Gly Phe Ser Glu Asp Ser Leu Ile Asn Phe Ser
465                 470                 475                 480
Glu Asp Glu Phe Asp Asn Gly Ser Thr Leu Gln Ser Gln Leu Leu Lys
                485                 490                 495
Val Leu Gln Arg Leu Ile Val Leu Glu His Arg Val Met Thr Ile Pro
            500                 505                 510
Glu Glu Asn Glu Thr Gly Phe Asp Phe Val Val Ser Asp Leu Glu His
        515                 520                 525
Ile Ser Pro His Gln Pro Met Thr Ser Leu Gln Tyr Leu His Ala Gln
    530                 535                 540
Pro Ile Thr Cys Gln Gly Met Phe Leu Cys Ala Val Ile Arg Ala Leu
545                 550                 555                 560
His Gln His Cys Ala Cys Lys Met His Pro Gln Trp Ile Gly Leu Ile
                565                 570                 575
Thr Ser Thr Leu Pro Tyr Met Gly Lys Val Leu Gln Arg Val Val Val
            580                 585                 590
Ser Val Thr Leu Gln Leu Cys Arg Asn Leu Asp Asn Leu Ile Gln Gln
        595                 600                 605
Tyr Lys Tyr Glu Thr Gly Leu Ser Asp Ser Arg Pro Leu Trp Met Ala
    610                 615                 620
Ser Ile Ile Pro Pro Asp Met Ile Leu Thr Leu Leu Glu Gly Ile Thr
625                 630                 635                 640
Ala Ile Ile His Tyr Cys Leu Leu Asp Pro Thr Thr Gln Tyr His Gln
                645                 650                 655
Leu Leu Val Ser Val Asp Gln Lys His Leu Phe Glu Ala Arg Ser Gly
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660 665 670
Ile Leu Ser Ile Leu His Met Ile Met Ser Ser Val Thr Leu Leu Trp
675 680 685
Ser Ile Leu His Gln Ala Asp Ser Ser Glu Lys Met Thr Ile Ala Ala
690 695 700
Ser Ala Ser Leu Thr Thr Ile Asn Leu Gly Ala Thr Lys Asn Leu Arg
705 710 715 720
Gln Gln Ile Leu Glu Leu Leu Gly Pro Ile Ser Met Asn His Gly Val
725 730 735
His Phe Met Ala Ala Ile Ala Phe Val Trp Asn Glu Arg Arg Gln Asn
740 745 750
Lys Thr Thr Thr Arg Thr Lys Val Ile Pro Ala Ala Ser Glu Glu Gln
755 760 765
Leu Leu Leu Val Glu Leu Val Arg Ser Ile Ser Val Met Arg Ala Glu
770 775 780
Thr Val Ile Gln Thr Val Lys Glu Val Leu Lys Gln Pro Pro Ala Ile
785 790 795 800
Ala Lys Asp Lys Lys His Leu Ser Leu Glu Val Cys Met Leu Gln Phe
805 810 815
Phe Tyr Ala Tyr Ile Gln Arg Ile Pro Val Pro Asn Leu Val Asp Ser
820 825 830
Trp Ala Ser Leu Leu Ile Leu Leu Lys Asp Ser Ile Gln Leu Ser Leu
835 840 845
Pro Ala Pro Gly Gln Phe Leu Ile Leu Gly Val Leu Asn Glu Phe Ile
850 855 860
Met Lys Asn Pro Ser Leu Glu Asn Lys Lys Asp Gln Arg Asp Leu Gln
865 870 875 880
Asp Val Thr His Lys Ile Val Asp Ala Ile Gly Ala Ile Ala Gly Ser
885 890 895
Ser Leu Glu Gln Thr Thr Trp Leu Arg Arg Asn Leu Glu Val Lys Pro
900 905 910
Ser Pro Lys Ile Met Val Asp Gly Thr Asn Leu Glu Ser Asp Val Glu
915 920 925
Asp Met Leu Ser Pro Ala Met Glu Thr Ala Asn Ile Thr Pro Ser Val
930 935 940
Tyr Ser Val His Ala Leu Thr Leu Leu Ser Glu Val Leu Ala His Leu
945 950 955 960
Leu Asp Met Val Phe Tyr Ser Asp Glu Lys Glu Arg Val Ile Pro Leu
965 970 975
Leu Val Asn Ile Met His Tyr Val Val Pro Tyr Leu Arg Asn His Ser
980 985 990
Ala His Asn Ala Pro Ser Tyr Arg Ala Cys Val Gln Leu Leu Ser Ser
995 1000 1005
Leu Ser Gly Tyr Gln Tyr Thr Arg Arg Ala Trp Lys Lys Glu Ala Phe
1010 1015 1020
Asp Leu Phe Met Asp Pro Ser Phe Phe Gln Met Asp Ala Ser Cys Val
1025 1030 1035 1040
Asn His Trp Arg Ala Ile Met Asp Asn Leu Met Thr His Asp Lys Thr
1045 1050 1055
Thr Phe Arg Asp Leu Met Thr Arg Val Ala Val Ala Gln Ser Ser Ser
1060 1065 1070
Leu Asn Leu Phe Ala Asn Arg Asp Val Glu Leu Glu Gln Arg Ala Met
1075 1080 1085
Leu Leu Lys Arg Leu Ala Phe Ala Ile Phe Ser Ser Glu Ile Asp Gln

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    1090                1095                1100
Tyr Gln Lys Tyr Leu Pro Asp Ile Gln Glu Arg Leu Val Glu Ser Leu
1105                1110                1115                1120
Arg Leu Pro Gln Val Pro Thr Leu His Ser Gln Val Phe Leu Phe Phe
                1125                1130                1135
Arg Val Leu Leu Leu Arg Met Ser Pro Gln His Leu Thr Ser Leu Trp
            1140                1145                1150
Pro Thr Met Ile Thr Glu Leu Val Gln Val Phe Leu Leu Met Glu Gln
        1155                1160                1165
Glu Leu Thr Ala Asp Glu Asp Ile Ser Arg Thr Ser Gly Pro Ser Val
    1170                1175                1180
Ala Gly Leu Glu Thr Thr Tyr Thr Gly Gly Asn Gly Phe Ser Thr Ser
1185                1190                1195                1200
Tyr Asn Ser Gln Arg Trp Leu Asn Leu Tyr Leu Ser Ala Cys Lys Phe
                1205                1210                1215
Leu Asp Leu Ala Leu Ala Leu Pro Ser Glu Asn Leu Pro Gln Phe Gln
            1220                1225                1230
Met Tyr Arg Trp Ala Phe Ile Pro Glu Ala Ser Asp Asp Ser Gly Leu
        1235                1240                1245
Glu Val Arg Arg Gln Gly Ile His Gln Arg Glu Phe Lys Pro Tyr Val
    1250                1255                1260
Val Arg Leu Ala Lys Leu Leu Arg Lys Arg Ala Lys Lys Asn Pro Glu
1265                1270                1275                1280
Glu Asp Asn Ser Gly Arg Thr Leu Gly Trp Glu Pro Gly His Leu Leu
                1285                1290                1295
Leu Thr Ile Cys Thr Val Arg Ser Met Glu Gln Leu Leu Pro Phe Phe
            1300                1305                1310
Asn Val Leu Ser Gln Val Phe Asn Ser Lys Val Thr Ser Arg Cys Gly
        1315                1320                1325
Gly His Ser Gly Ser Pro Ile Leu Tyr Ser Asn Ala Phe Pro Asn Lys
    1330                1335                1340
Asp Met Lys Leu Glu Asn His Lys Pro Cys Ser Ser Lys Ala Arg Gln
1345                1350                1355                1360
Lys Ile Glu Glu Met Val Glu Lys Asp Phe Leu Glu Gly Met Ile Lys
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Thr
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<210> 1831
<211> 508
<212> DNA
<213> Homo sapiens

<400> 1831
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240
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300

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360
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508

<210> 1832
<211> 169
<212> PRT
<213> Homo sapiens

<400> 1832
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Phe Val Arg Glu Ala Val Cys Pro Pro Gly Lys Ser Lys Val Asp Tyr
20 25 30
Tyr Asp Asn Ala Leu Lys Gly Phe Ile Leu Glu Ala Arg Pro Ser Gly
35 40 45
Gly Lys Thr Phe Tyr Leu Arg Tyr His Asp Ser His Gly Lys Leu Arg
50 55 60
Gln Cys Lys Ile Gly Asp Ala Ala Ala Val Ser Tyr Asp Lys Ala Arg
65 70 75 80
Gln Lys Ala Met Arg Leu Arg Trp Lys Val Glu Trp Gly Gly Asn Pro
85 90 95
Leu Glu Glu Arg Gln Ala Leu Arg Ala Val Pro Thr Leu Ala Glu Phe
100 105 110
Ile Arg Glu Thr Tyr Val Pro His Ile His Leu His Arg Arg Asn Phe
115 120 125
Gln Ser Thr Leu Ser Phe Leu Lys Cys His Val Leu Pro Arg Phe Gly
130 135 140
Ala Lys His Leu Asp Glu Ile Thr Thr Asn Met Leu Ala Glu Ala His
145 150 155 160
Gln Asp Leu Arg Thr Lys Gly Tyr Ala
165

<210> 1833
<211> 430
<212> DNA
<213> Homo sapiens

<400> 1833
acgcgtgcga tgttgaagga gcgcttcggc atcgggcatg cgacgctgca ggttgaactg
60
tccggtgccg aggcagacga tgccgaggcg ggcggctgct aagggtcgcc gtcgttcagt
120
ggcgcaaagc ggcgatgatc gcgtcgaaca gcgttactcc agccagcggg ccaaccaaca
180
gcatcaccag gttgaaaccg atgatccacg ccgcgatgct ttctcggcgc gggtttggca
240
gcggcttggg ctcggcttcc cagcgttccg gcggcggcca gccattttgg aaatcgacga
300

acatctccgg cgctcctgct gtcaggcgct gaaggtatcg aaagtcatgc gccgtgacaa
360
aggaagatcg gcgacacagg agccgaagcg ccgccgcctg caataagcgc gcgcgatcgc
420
aattgtcggn
430

<210> 1834
<211> 122
<212> PRT
<213> Homo sapiens

<400> 1834
Met Arg Arg Cys Arg Leu Asn Cys Pro Val Pro Arg Gln Thr Met Pro
1 5 10 15
Arg Arg Ala Ala Ala Lys Gly Arg Arg Arg Ser Val Ala Gln Ser Gly
20 25 30
Asp Asp Arg Val Glu Gln Arg Tyr Ser Ser Gln Arg Ala Asn Gln Gln
35 40 45
His His Gln Val Glu Thr Asp Asp Pro Arg Arg Asp Ala Phe Ser Ala
50 55 60
Arg Val Trp Gln Arg Leu Gly Leu Gly Phe Pro Ala Phe Arg Arg Arg
65 70 75 80
Pro Ala Ile Leu Glu Ile Asp Glu His Leu Arg Arg Ser Cys Cys Gln
85 90 95
Ala Leu Lys Val Ser Lys Val Met Arg Arg Asp Lys Gly Arg Ser Ala
100 105 110
Thr Gln Glu Pro Lys Arg Arg Arg Leu Gln
115 120

<210> 1835
<211> 677
<212> DNA
<213> Homo sapiens

<400> 1835
natactcaag gactttgacg gcacccgagc ccggttgctc cctgaggcca tcatgaaccc
60
cccagtggca ccctatgcta ctgtggcacc cagcacttta gcccaccccc aggcccaggc
120
tctggcccgc cagcaggccc tgcagcatgc acagaccctg gcccatgccc ctccccagac
180
gctgcagcac cctcagggta tcccgccacc ccaggcactg tcccaccctc agagcctcca
240
gcagcctcag ggcctgggcc accctcagcc catggcccaa acccagggct tggtccaccc
300
tcaggccctg gctcaccagg gtctccagca cccccacaat cccttgctgc atggaggccg
360
gaagatgcca gactcagatg cccccccgaa tgtgaccgtg tctacctcaa ctatcccccc
420
ttcaatggcg gccactctgc agcacagcca gcctccggac ctgagtagca tcgtgcacca
480
gatcaaccag ttttgccaga cgagggcagg catcagcact acctcagtgt gtgagggcca
540

gatcgccaac cccagcccca ttagtcgcag tctgctcatc aatgcaagca cccgggtgtc
600
gacccacagc gtccccacac caatgccttc atgtgtggtc aatcccatgg agcacaccca
660
cgcggccacc gccgcgg
677

<210> 1836
<211> 140
<212> PRT
<213> Homo sapiens

<400> 1836
Gly His His Glu Pro Pro Ser Gly Thr Leu Cys Tyr Cys Gly Thr Gln
1 5 10 15
His Phe Ser Pro Pro Pro Gly Pro Gly Ser Gly Pro Pro Ala Gly Pro
20 25 30
Ala Ala Cys Thr Asp Pro Gly Pro Cys Pro Ser Pro Asp Ala Ala Ala
35 40 45
Pro Ser Gly Tyr Pro Ala Thr Pro Gly Thr Val Pro Pro Ser Glu Pro
50 55 60
Pro Ala Ala Ser Gly Pro Gly Pro Pro Ser Ala His Gly Pro Asn Pro
65 70 75 80
Gly Leu Gly Pro Pro Ser Gly Pro Gly Ser Pro Gly Ser Pro Ala Pro
85 90 95
Pro Gln Ser Leu Ala Ala Trp Arg Pro Glu Asp Ala Arg Leu Arg Cys
100 105 110
Pro Pro Glu Cys Asp Arg Val Tyr Leu Asn Tyr Pro Pro Phe Asn Gly
115 120 125
Gly His Ser Ala Ala Gln Pro Ala Ser Gly Pro Glu
130 135 140

<210> 1837
<211> 564
<212> DNA
<213> Homo sapiens

<400> 1837
nntctagaac actctgcccc tgaatctgta ccgggattgt ttggcccgtc acgaactcgt
60
acggtcgata tcaatatcac tgggttttct tcacagtatt tacccgcccc ctatggacca
120
attgctgcgg acgtcaaaca aacctgggcg tgggacccac aggatctgac gattgtctca
180
acttctgctg atcacgacca taacctccga tatgcagtac agcatttcgg cgcaagcccg
240
accccgatcc agtaaccttc gataacgcga aagccggcac cccacataac tcggntgtac
300
accgaagtcc ctgccaacgt tccatccgac ataggggagt taactaaccg aattatcaag
360
gggaaatcta ccccccgtaac caaggccatc gcgattcaaa actggcttcg tgacagcgct
420
cgattccatt acgacatcaa cgcacccgaa ggtgacggct atcaggtact ggaaaacttc
480

ctgctgcaca cccaccgcgg ttattgcatc catttcgcgg cgtcaatggc actcatggca
540
cgacttgaag gtattccgtc acgc
564

<210> 1838
<211> 84
<212> PRT
<213> Homo sapiens

<400> 1838
Xaa Leu Glu His Ser Ala Pro Glu Ser Val Pro Gly Leu Phe Gly Pro
1 5 10 15
Ser Arg Thr Arg Thr Val Asp Ile Asn Ile Thr Gly Phe Ser Ser Gln
20 25 30
Tyr Leu Pro Ala Pro Tyr Gly Pro Ile Ala Ala Asp Val Lys Gln Thr
35 40 45
Trp Ala Trp Asp Pro Gln Asp Leu Thr Ile Val Ser Thr Ser Ala Asp
50 55 60
His Asp His Asn Leu Arg Tyr Ala Val Gln His Phe Gly Ala Ser Pro
65 70 75 80
Thr Pro Ile Gln

<210> 1839
<211> 300
<212> DNA
<213> Homo sapiens

<400> 1839
ncaatacggc tgaacaccgc tgatatcacc cgtactttcc ccgtcaacgg aaaatttcc
60
gaagttcagg caaaggctta tcaggcggtg ctggacgctg cagatgcggc atttaaggca
120
gccgttcctg gcaataaatt ccgcgacgtc catgctgcag cgatgaatgt tctcgcctcc
180
cgccttgagg actgggggct tatgccggtc agcgcgaagg tcgctctttc ggacgagggc
240
gggcaacacc gtcgttggat gccgcacggc accagccacc atctagggct ggatgtgcac
300

<210> 1840
<211> 100
<212> PRT
<213> Homo sapiens

<400> 1840
Xaa Ile Arg Leu Asn Thr Ala Asp Ile Thr Arg Thr Phe Pro Val Asn
1 5 10 15
Gly Lys Phe Ser Glu Val Gln Ala Lys Ala Tyr Gln Ala Val Leu Asp
20 25 30
Ala Ala Asp Ala Ala Phe Lys Ala Ala Val Pro Gly Asn Lys Phe Arg
35 40 45
Asp Val His Ala Ala Ala Met Asn Val Leu Ala Ser Arg Leu Glu Asp

```
    50                  55                  60
Trp Gly Leu Met Pro Val Ser Ala Lys Val Ala Leu Ser Asp Glu Gly
65                  70                  75                  80
Gly Gln His Arg Arg Trp Met Pro His Gly Thr Ser His His Leu Gly
                85                  90                  95
Leu Asp Val His
            100

<210> 1841
<211> 330
<212> DNA
<213> Homo sapiens

<400> 1841
nnctccaaga acgtcccgga gtggggcccc agggcgctcg aactccccgg cgggcccggt
60
gtcgatccgg tggtcgagat cggcggtccc ggtacgctag cccaatcgat ggtcgccccg
120
cgcgtcggcg cccatgtcgc cttgatcggc gtgcttnacg gggattgtcg ggcggtgagg
180
acggcgctgc tgatgagcaa gaatctgcgc gtgcaagggc tgccggtcgg cagccgcgcg
240
cagcaactcg cgatgatcgc gggggtcgag gcgaacggca tccgtccgat cctcgaccag
300
catttcccgc tcgaaaatct ccccgacgcg
330

<210> 1842
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1842
Xaa Ser Lys Asn Val Pro Glu Trp Gly Pro Arg Ala Leu Glu Leu Pro
 1               5                  10                  15
Gly Gly Pro Gly Val Asp Pro Val Val Glu Ile Gly Gly Pro Gly Thr
            20                  25                  30
Leu Ala Gln Ser Met Val Ala Pro Arg Val Gly Ala His Val Ala Leu
        35                  40                  45
Ile Gly Val Leu Xaa Gly Asp Cys Arg Ala Val Arg Thr Ala Leu Leu
    50                  55                  60
Met Ser Lys Asn Leu Arg Val Gln Gly Leu Pro Val Gly Ser Arg Ala
65                  70                  75                  80
Gln Gln Leu Ala Met Ile Ala Gly Val Glu Ala Asn Gly Ile Arg Pro
                85                  90                  95
Ile Leu Asp Gln His Phe Pro Leu Glu Asn Leu Pro Asp Ala
            100                 105                 110

<210> 1843
<211> 473
<212> DNA
<213> Homo sapiens

<400> 1843
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aagctttggc atctccagca aaagatgtgc tatttactga taccatcacc atgaaggcca
60
acagttttga gtccagatta acaccaagca ggttcatgaa agccttaagt tatgcatcat
120
tagataaaga agatttattg agtcctatta atcaaaatac cctgcaacga tcttcctcag
180
tgcggtccat ggtgtccagt gccacatatg ggggttcaga tgattacatt ggtcttgctc
240
tcccggtgga tataaatgat atattccagg taaaggatat tccctatttt cagacaaaaa
300
acataccacc acatgatgat cgaggtgcaa gagcatttgc ccatgatgca ggaggtcttc
360
catctggaac tggaggtctt gtaaaaaatt cttttcactt gctacgacag cagatgagtc
420
ttacggaaat aatgaattca atccattcag atgcctctcn cnnccncncc ccc
473

<210> 1844
<211> 141
<212> PRT
<213> Homo sapiens

<400> 1844

Met	Lys	Ala	Asn	Ser	Phe	Glu	Ser	Arg	Leu	Thr	Pro	Ser	Arg	Phe	Met
1				5					10					15	
Lys	Ala	Leu	Ser	Tyr	Ala	Ser	Leu	Asp	Lys	Glu	Asp	Leu	Leu	Ser	Pro
			20					25					30		
Ile	Asn	Gln	Asn	Thr	Leu	Gln	Arg	Ser	Ser	Ser	Val	Arg	Ser	Met	Val
		35					40					45			
Ser	Ser	Ala	Thr	Tyr	Gly	Gly	Ser	Asp	Asp	Tyr	Ile	Gly	Leu	Ala	Leu
	50					55					60				
Pro	Val	Asp	Ile	Asn	Asp	Ile	Phe	Gln	Val	Lys	Asp	Ile	Pro	Tyr	Phe
65					70					75					80
Gln	Thr	Lys	Asn	Ile	Pro	Pro	His	Asp	Asp	Arg	Gly	Ala	Arg	Ala	Phe
				85					90					95	
Ala	His	Asp	Ala	Gly	Gly	Leu	Pro	Ser	Gly	Thr	Gly	Gly	Leu	Val	Lys
			100					105					110		
Asn	Ser	Phe	His	Leu	Leu	Arg	Gln	Gln	Met	Ser	Leu	Thr	Glu	Ile	Met
		115					120					125			
Asn	Ser	Ile	His	Ser	Asp	Ala	Ser	Xaa	Xaa	Xaa	Xaa	Pro			
	130					135					140				

<210> 1845
<211> 390
<212> DNA
<213> Homo sapiens

<400> 1845
aagcttacga cgcctagctt tggagacctg aaccacttga tcagtgcaac aatgagtgga
60
gtgacttgct gcctccgctt cccggggcag ctcaactcgg accttcggaa acttgcagtg
120
aacctgattc cattccctcg cctgcacttt tttatggtcg gctttgcgcc actcacctcg
180

cgtggctccc agcagtaccg tgctctcact gtccctgagc tgacccagca gatgtgggac
240
tccaagaaca tgatgtgtgc tgctgacccg cgtcatggcc gctacctcac agtatctgcc
300
atgttccgtg gaaagatgag caccaaggag gtggacgagc agatgctgaa cgtgcagaac
360
aagaactctt cctacttcgt ggagtggatc
390

<210> 1846
<211> 130
<212> PRT
<213> Homo sapiens

<400> 1846
Lys Leu Thr Thr Pro Ser Phe Gly Asp Leu Asn His Leu Ile Ser Ala
1 5 10 15
Thr Met Ser Gly Val Thr Cys Cys Leu Arg Phe Pro Gly Gln Leu Asn
20 25 30
Ser Asp Leu Arg Lys Leu Ala Val Asn Leu Ile Pro Phe Pro Arg Leu
35 40 45
His Phe Phe Met Val Gly Phe Ala Pro Leu Thr Ser Arg Gly Ser Gln
50 55 60
Gln Tyr Arg Ala Leu Thr Val Pro Glu Leu Thr Gln Gln Met Trp Asp
65 70 75 80
Ser Lys Asn Met Met Cys Ala Ala Asp Pro Arg His Gly Arg Tyr Leu
85 90 95
Thr Val Ser Ala Met Phe Arg Gly Lys Met Ser Thr Lys Glu Val Asp
100 105 110
Glu Gln Met Leu Asn Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu
115 120 125
Trp Ile
130

<210> 1847
<211> 343
<212> DNA
<213> Homo sapiens

<400> 1847
cagccgtgct ttcctgcgtc aactcgggaa cggctatatc gcgcagatcc aacagttcca
60
tggctcgaag agtagtaaaa atatcaataa ctggcagagc atcgcgtcaa gctggcgacc
120
ctggccgccg ccgcgttggc cgatcacgcc atgttggagc aggccttcca gctgttccag
180
caaaaaagtt gcggacaatc tcctgccgga tggctcggtg ttcgacttca gggagcgcga
240
tgcactgcac tacgtcgtct atgacctgga gccgctggtt caggcggccc tggcgggcaa
300
gccctaacgg tggcaactgg ctgacttaca ccgcccccac cgn
343

<210> 1848

<211> 94
<212> PRT
<213> Homo sapiens

<400> 1848
Met Ala Arg Arg Val Val Lys Ile Ser Ile Thr Gly Arg Ala Ser Arg
1 5 10 15
Gln Ala Gly Asp Pro Gly Arg Arg Arg Val Gly Arg Ser Arg His Val
20 25 30
Gly Ala Gly Leu Pro Ala Val Pro Ala Lys Lys Leu Arg Thr Ile Ser
35 40 45
Cys Arg Met Ala Arg Cys Ser Thr Ser Gly Ser Ala Met His Cys Thr
50 55 60
Thr Ser Ser Met Thr Trp Ser Arg Trp Phe Arg Arg Pro Trp Arg Ala
65 70 75 80
Ser Pro Asn Gly Gly Asn Trp Leu Thr Tyr Thr Ala Pro Thr
85 90

<210> 1849
<211> 390
<212> DNA
<213> Homo sapiens

<400> 1849
cggaaagaac aggttcagca aagagcaata gaatgttccc gggctctcag tgcgattctt
60
gacattgaac atggagaccc aaaagagaat gtactaggtt cagcttttga catgaaacag
120
ctgaaggatg ctattgatga gactaaaata gctttgatgg gacattcttt tggaggagca
180
acagttcttc aagcccttag tgaggaccag agattcagat gtggagttgc tcttgatcca
240
tggatgtatc cggtgaacga agagctgtac tccagaaccc tccagcctct cctctttatc
300
aactctgcca aattccagac tccaaaggac atcgcaaaaa tgaaaaagtt ctaccagcct
360
gacaaggaaa ggaaanatga ttacaatcaa
390

<210> 1850
<211> 130
<212> PRT
<213> Homo sapiens

<400> 1850
Arg Lys Glu Gln Val Gln Gln Arg Ala Ile Glu Cys Ser Arg Ala Leu
1 5 10 15
Ser Ala Ile Leu Asp Ile Glu His Gly Asp Pro Lys Glu Asn Val Leu
20 25 30
Gly Ser Ala Phe Asp Met Lys Gln Leu Lys Asp Ala Ile Asp Glu Thr
35 40 45
Lys Ile Ala Leu Met Gly His Ser Phe Gly Gly Ala Thr Val Leu Gln
50 55 60
Ala Leu Ser Glu Asp Gln Arg Phe Arg Cys GIy Val Ala Leu Asp Pro

65 70 75 80
Trp Met Tyr Pro Val Asn Glu Glu Leu Tyr Ser Arg Thr Leu Gln Pro
85 90 95
Leu Leu Phe Ile Asn Ser Ala Lys Phe Gln Thr Pro Lys Asp Ile Ala
100 105 110
Lys Met Lys Lys Phe Tyr Gln Pro Asp Lys Glu Arg Lys Xaa Asp Tyr
115 120 125
Asn Gln
130

<210> 1851
<211> 574
<212> DNA
<213> Homo sapiens

<400> 1851
ncgatcggag aggctttccg cactggtgac ttggactcta agcccgaccc cagccggagc
60
ttcaggcctt accgagctga agacaatgat tcctatgcct ctgagatcaa ggagctgcag
120
ctggtgctgg ctgaggccca cgacagcctc cggggcttgc aagagcagct ctcccaggag
180
cggcagctac gaaaggagga ggccgacaat ttcaaccaga aaatggtcca gctgaaggag
240
gaccagcaga gggcgctcct gaggcgggag tttgagctgc agagtctgag cctccagcgg
300
aggctggagc agaaattctg gagccaggag aagaacatgc tggtgcagga gtcccagcaa
360
ttcaagcaca acttcctgct gctcttcatg aagctcaggt ggttcctcaa gcgctggcgg
420
cagggcaagg ttttgcccag cgaaggggat gacttcctcg aggtgaacag catgaaggac
480
ctgtacttgc tgatggagga agacgagata aacgctcagc attctgataa caaggcctgc
540
acgggggaca gctggaccca gaacacgccc aatg
574

<210> 1852
<211> 191
<212> PRT
<213> Homo sapiens

<400> 1852
Xaa Ile Gly Glu Ala Phe Arg Thr Gly Asp Leu Asp Ser Lys Pro Asp
1 5 10 15
Pro Ser Arg Ser Phe Arg Pro Tyr Arg Ala Glu Asp Asn Asp Ser Tyr
20 25 30
Ala Ser Glu Ile Lys Glu Leu Gln Leu Val Leu Ala Glu Ala His Asp
35 40 45
Ser Leu Arg Gly Leu Gln Glu Gln Leu Ser Gln Glu Arg Gln Leu Arg
50 55 60
Lys Glu Glu Ala Asp Asn Phe Asn Gln Lys Met Val Gln Leu Lys Glu
65 70 75 80
Asp Gln Gln Arg Ala Leu Leu Arg Arg Glu Phe Glu Leu Gln Ser Leu

```
                85                  90                  95
Ser Leu Gln Arg Arg Leu Glu Gln Lys Phe Trp Ser Gln Glu Lys Asn
            100                 105                 110
Met Leu Val Gln Glu Ser Gln Gln Phe Lys His Asn Phe Leu Leu Leu
        115                 120                 125
Phe Met Lys Leu Arg Trp Phe Leu Lys Arg Trp Arg Gln Gly Lys Val
    130                 135                 140
Leu Pro Ser Glu Gly Asp Asp Phe Leu Glu Val Asn Ser Met Lys Asp
145                 150                 155                 160
Leu Tyr Leu Leu Met Glu Glu Asp Glu Ile Asn Ala Gln His Ser Asp
                165                 170                 175
Asn Lys Ala Cys Thr Gly Asp Ser Trp Thr Gln Asn Thr Pro Asn
            180                 185                 190
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<210> 1853
<211> 338
<212> DNA
<213> Homo sapiens

<400> 1853
gccggcgccg accaagccac ggcatgcccc acccaccttg gaagaggtgt cgttccgcca
60
cgtcattgag gagcgcgccg tcgaagctga cttgttcgtc cgctcgctca atacactcga
120
gcctgcgacg ggcatggcac ttctgcgcat ctcgcaccac atggatggca aggtcggcac
180
gacgttttac ctggatgacg atgtcatttt tgtcgcgcca cagaagcagc gctcagccga
240
gggccagcga ctcgaatacg agcccgtctc tttggccgag ttgctcgagc gcgctgctgc
300
atagaataca tatacccaag ctatgatgat gccgtcgt
338

<210> 1854
<211> 100
<212> PRT
<213> Homo sapiens

<400> 1854

```
Met Pro His Pro Pro Trp Lys Arg Cys Arg Ser Ala Thr Ser Leu Arg
 1               5                  10                  15
Ser Ala Pro Ser Lys Leu Thr Cys Ser Ser Ala Arg Ser Ile His Ser
            20                  25                  30
Ser Leu Arg Arg Ala Trp His Phe Cys Ala Ser Arg Thr Thr Trp Met
        35                  40                  45
Ala Arg Ser Ala Arg Arg Phe Thr Trp Met Thr Met Ser Phe Leu Ser
    50                  55                  60
Arg His Arg Ser Ser Ala Gln Pro Arg Ala Ser Asp Ser Asn Thr Ser
65                  70                  75                  80
Pro Ser Leu Trp Pro Ser Cys Ser Ser Ala Leu Leu His Arg Ile His
                85                  90                  95
Ile Pro Lys Leu
            100
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<210> 1855
<211> 429
<212> DNA
<213> Homo sapiens

<400> 1855
gcgtccttcg cgtacgtgga cgagggcggg caggtgttcg tccagtgcag cacccagcac
60
ccgagcgaaa cgcaggaaat cgtggcgcac gtcctggacc tggacaacca cgaggtcacg
120
gtgcagtgct tgcgcatggg cggtggcttt ggcggtaagg aaatgcagcc gcacgggttc
180
gccgcgatcg cagcactcgg cgcgaccctg accgggcgac cggttcgact gcgactgacc
240
cgaaaccagg acatcaccat ctccggaaag cgccacccat acctcgcgga gtgggacgtg
300
gccttcgacg acgacggccg cctccaggct ctgcgcgcca ccgtcaccag cgacggcggg
360
tggagcctgg acctctcgga gccggtgatg cagcggacgg tgtgtcacat cgataactcc
420
tattggatc
429

<210> 1856
<211> 143
<212> PRT
<213> Homo sapiens

<400> 1856
Ala Ser Phe Ala Tyr Val Asp Glu Gly Gly Gln Val Phe Val Gln Cys
 1   5   10   15
Ser Thr Gln His Pro Ser Glu Thr Gln Glu Ile Val Ala His Val Leu
            20   25   30
Asp Leu Asp Asn His Glu Val Thr Val Gln Cys Leu Arg Met Gly Gly
        35   40   45
Gly Phe Gly Gly Lys Glu Met Gln Pro His Gly Phe Ala Ala Ile Ala
    50   55   60
Ala Leu Gly Ala Thr Leu Thr Gly Arg Pro Val Arg Leu Arg Leu Thr
65   70   75   80
Arg Asn Gln Asp Ile Thr Ile Ser Gly Lys Arg His Pro Tyr Leu Ala
                85   90   95
Glu Trp Asp Val Ala Phe Asp Asp Asp Gly Arg Leu Gln Ala Leu Arg
            100   105   110
Ala Thr Val Thr Ser Asp Gly Gly Trp Ser Leu Asp Leu Ser Glu Pro
        115   120   125
Val Met Gln Arg Thr Val Cys His Ile Asp Asn Ser Tyr Trp Ile
    130   135   140

<210> 1857
<211> 393
<212> DNA
<213> Homo sapiens

<400> 1857

gtgcacgccg ctgccccagc cgtcgcctac cgatcaacag acgcagccgc cgtgcgttga
60
gataccagcc gagcacgatc atgctcagca tggtcagcag cagccagaac ggaaatcgca
120
gcaggcgctc gaacagctca ctgccaccca gcaccagcgg gattgccccg gccacgacca
180
gtgcgccgag gagcagccac catcgcccgc tcatgctgcg gcactcgata ccaatacgtt
240
gcgcttcaac caatcgatct tggtcgaggc atgccgccca tcttccaaca ggcgagtcac
300
cagactcagc cagtaacacc gcgaaaaatc gtggcgcatg tcgacagggt gcaaaccgag
360
acgcagcacg ggtgcctgtc ggtggcgggc gag
393

<210> 1858
<211> 104
<212> PRT
<213> Homo sapiens

<400> 1858
Met Leu Ser Met Val Ser Ser Ser Gln Asn Gly Asn Arg Ser Arg Arg
1 5 10 15
Ser Asn Ser Ser Leu Pro Pro Ser Thr Ser Gly Ile Ala Pro Ala Thr
20 25 30
Thr Ser Ala Pro Arg Ser Ser His His Arg Pro Leu Met Leu Arg His
35 40 45
Ser Ile Pro Ile Arg Cys Ala Ser Thr Asn Arg Ser Trp Ser Arg His
50 55 60
Ala Ala His Leu Pro Thr Gly Glu Ser Pro Asp Ser Ala Ser Asn Thr
65 70 75 80
Ala Lys Asn Arg Gly Ala Cys Arg Gln Gly Ala Asn Arg Asp Ala Ala
85 90 95
Arg Val Pro Val Gly Gly Gly Arg
100

<210> 1859
<211> 345
<212> DNA
<213> Homo sapiens

<400> 1859
nagatctggc gcctcgtcac caacttcctc tacttccgca agatggattt ggattttctg
60
ttccacatgt tttttctcgc acgatactgc aagcttctgg aggagaactc atttagagga
120
agaactgccg actttttttta catgctcttg tttggtgcta ctgtcctaac tagcattgtt
180
ctgatcggag ggatgatacc ttacatttcc gagacatttg ccagaattct gttcctgagc
240
aattcattga cgtttatgat ggtttatgtc tggagcaagc acaatcctat catccatatg
300
agcaatctgg gcctgttcac ctttacggct gcatacttac catgg
345

<210> 1860
<211> 115
<212> PRT
<213> Homo sapiens

<400> 1860
Xaa Ile Trp Arg Leu Val Thr Asn Phe Leu Tyr Phe Arg Lys Met Asp
1 5 10 15
Leu Asp Phe Leu Phe His Met Phe Phe Leu Ala Arg Tyr Cys Lys Leu
20 25 30
Leu Glu Glu Asn Ser Phe Arg Gly Arg Thr Ala Asp Phe Phe Tyr Met
35 40 45
Leu Leu Phe Gly Ala Thr Val Leu Thr Ser Ile Val Leu Ile Gly Gly
50 55 60
Met Ile Pro Tyr Ile Ser Glu Thr Phe Ala Arg Ile Leu Phe Leu Ser
65 70 75 80
Asn Ser Leu Thr Phe Met Met Val Tyr Val Trp Ser Lys His Asn Pro
85 90 95
Ile Ile His Met Ser Asn Leu Gly Leu Phe Thr Phe Thr Ala Ala Tyr
100 105 110
Leu Pro Trp
115

<210> 1861
<211> 435
<212> DNA
<213> Homo sapiens

<400> 1861
gcgttgactg tagtgagtga cgaagctgat atacaaaatg cgccgggcgt tagaaaagcc
60
aatagtgagc ttcattcagt cggcttaggt gttatgaact tacatggcta tcttgctaaa
120
aacaaaattg gctatgagtc ggaagaagct aaagattttg ctaatatatt ctttatgatg
180
atgaattact attcacttga aagatcaatg caaatagcaa aagaaagaca ggaaacgttt
240
aaagactttg ataagtcaga ttatgcaaat ggaaaatatt tcgaatttta tacttcgcaa
300
tcatttgaac cgaaatacga aaaagtacgt aaattatttg atggtttaga aatcccaacg
360
cctgaagatt ggaaagcatt gcaaaaagaa gttgaaactc acggtttatt ccatgcttat
420
cgtttagcga ttgca
435

<210> 1862
<211> 145
<212> PRT
<213> Homo sapiens

<400> 1862
Ala Leu Thr Val Val Ser Asp Glu Ala Asp Ile Gln Asn Ala Pro Gly

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 1               5                  10                  15
Val Arg Lys Ala Asn Ser Glu Leu His Ser Val Gly Leu Gly Val Met
            20                  25                  30
Asn Leu His Gly Tyr Leu Ala Lys Asn Lys Ile Gly Tyr Glu Ser Glu
        35                  40                  45
Glu Ala Lys Asp Phe Ala Asn Ile Phe Phe Met Met Met Asn Tyr Tyr
    50                  55                  60
Ser Leu Glu Arg Ser Met Gln Ile Ala Lys Glu Arg Gln Glu Thr Phe
65                  70                  75                  80
Lys Asp Phe Asp Lys Ser Asp Tyr Ala Asn Gly Lys Tyr Phe Glu Phe
                85                  90                  95
Tyr Thr Ser Gln Ser Phe Glu Pro Lys Tyr Glu Lys Val Arg Lys Leu
            100                 105                 110
Phe Asp Gly Leu Glu Ile Pro Thr Pro Glu Asp Trp Lys Ala Leu Gln
        115                 120                 125
Lys Glu Val Glu Thr His Gly Leu Phe His Ala Tyr Arg Leu Ala Ile
    130                 135                 140
Ala
145
```

<210> 1863
<211> 792
<212> DNA
<213> Homo sapiens

<400> 1863

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nggatcctca cgcccgccat catacgtggg atatcgttga gcaaatgcgt catgacgggg
60
tctccgtcgt gctcactacc cacaacatgg atgaggctca acggctggct gatcacgtct
120
ggatcgtcga tcgcggcagg gtcgcaactc atggaactgt gccagagctc accgctgagt
180
cgagtttgga agatgtgttc ctcactcaca ctagtgaccg cgcagcaggg aggaattgac
240
atgacgacac tcgatctccg ccccgcacct caggccgcac cggctgctgc acgcgtgcgt
300
aaccacgctc tcaccgaggt gcgtctggtg atgcgcaacg gtgagcagct gctactagct
360
ctcgtcattc ccatcgggat catcgtcgcc gggcgcttcc tgggcggccg ggtcggactg
420
acgatggacg tcttagcacc ctcagtgctg gcgctcgcca tctggtcgac atgtttcact
480
tcccaagcga tcatgaccgg ttttgaacgc cgttacgggg tgctcgaacg attgtccgca
540
accccgttag gtcggtcggg tctgctagct ggcaaggcga tggcttattc cgttatcagt
600
ctcgctcagg tgatactgct tgtcatcatc tctttagcgc tgggctggca cccccacggt
660
tccggcctgg cctggctccc aaccctggtg agcgttgtgc tcgccatgat gacattcggg
720
ctcgcagcac tggcaatggc cggcgctggc aaagctgaag tcactctcgg actggccaac
780
ttggtataca tc
792
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<210> 1864
<211> 264
<212> PRT
<213> Homo sapiens

<400> 1864
Xaa Ile Leu Thr Pro Ala Ile Ile Arg Gly Ile Ser Leu Ser Lys Cys
1 5 10 15
Val Met Thr Gly Ser Pro Ser Cys Ser Leu Pro Thr Thr Trp Met Arg
20 25 30
Leu Asn Gly Trp Leu Ile Thr Ser Gly Ser Ser Ile Ala Ala Gly Ser
35 40 45
Gln Leu Met Glu Leu Cys Gln Ser Ser Pro Leu Ser Arg Val Trp Lys
50 55 60
Met Cys Ser Ser Leu Thr Leu Val Thr Ala Gln Gln Gly Gly Ile Asp
65 70 75 80
Met Thr Thr Leu Asp Leu Arg Pro Ala Pro Gln Ala Ala Pro Ala Ala
85 90 95
Ala Arg Val Arg Asn His Ala Leu Thr Glu Val Arg Leu Val Met Arg
100 105 110
Asn Gly Glu Gln Leu Leu Leu Ala Leu Val Ile Pro Ile Gly Ile Ile
115 120 125
Val Ala Gly Arg Phe Leu Gly Gly Arg Val Gly Leu Thr Met Asp Val
130 135 140
Leu Ala Pro Ser Val Leu Ala Leu Ala Ile Trp Ser Thr Cys Phe Thr
145 150 155 160
Ser Gln Ala Ile Met Thr Gly Phe Glu Arg Arg Tyr Gly Val Leu Glu
165 170 175
Arg Leu Ser Ala Thr Pro Leu Gly Arg Ser Gly Leu Leu Ala Gly Lys
180 185 190
Ala Met Ala Tyr Ser Val Ile Ser Leu Ala Gln Val Ile Leu Leu Val
195 200 205
Ile Ile Ser Leu Ala Leu Gly Trp His Pro His Gly Ser Gly Leu Ala
210 215 220
Trp Leu Pro Thr Leu Val Ser Val Val Leu Ala Met Met Thr Phe Gly
225 230 235 240
Leu Ala Ala Leu Ala Met Ala Gly Ala Gly Lys Ala Glu Val Thr Leu
245 250 255
Gly Leu Ala Asn Leu Val Tyr Ile
260

<210> 1865
<211> 717
<212> DNA
<213> Homo sapiens

<400> 1865
ngccggctga tcaaacaact cacagacatg ggcttcccga gagagccagc tgaggaggcc
60
ttgaagagta acaatatgaa tcttgatcag gccatgagcg ctctgctgga aaagaaggtg
120
gacgtggaca agcgtgggct gggagtgacc gaccataatg gaatggccgc caagcccctc
180

ggctgccgcc cgccaatctc caaagagtct tccgtggacc gccccaccct tcttgacaag
240
gatggcggcc tcgtggaaga gcccacgcct tcaccgttct tgccttcccc aagcctgaag
300
ctcccccttt cacacagtgc actccccagt caggccctgg gtggggttgc ctccgggctg
360
ggcatgcaaa acttgaattc ttctagacag ataccgagtg gcaatctggg tatgtttggc
420
aatagtggag cagcacaagc caggaccatg cagcagccgc cacagccacc agtgcagcct
480
cttaactctt cccagcccag tctccgtgct caagtgcctc agtttctatc ccctcaggtt
540
caagcacagc ttttgcagtt tgcagcaaaa aacattggtc tcaaccctgc actattaacc
600
tcgccaatta atcctcaaca tatgacgatg ttgaaccagc tctatcagct gcagctggca
660
taccaacgtt tacaaatcca gcagcagatg ttacaggccc agcgtaatgt gtccgga
717

<210> 1866
<211> 239
<212> PRT
<213> Homo sapiens

<400> 1866
Xaa Arg Leu Ile Lys Gln Leu Thr Asp Met Gly Phe Pro Arg Glu Pro
 1   5   10   15
Ala Glu Glu Ala Leu Lys Ser Asn Asn Met Asn Leu Asp Gln Ala Met
            20   25   30
Ser Ala Leu Leu Glu Lys Lys Val Asp Val Asp Lys Arg Gly Leu Gly
        35   40   45
Val Thr Asp His Asn Gly Met Ala Ala Lys Pro Leu Gly Cys Arg Pro
    50   55   60
Pro Ile Ser Lys Glu Ser Ser Val Asp Arg Pro Thr Leu Leu Asp Lys
65   70   75   80
Asp Gly Gly Leu Val Glu Glu Pro Thr Pro Ser Pro Phe Leu Pro Ser
                85   90   95
Pro Ser Leu Lys Leu Pro Leu Ser His Ser Ala Leu Pro Ser Gln Ala
            100   105   110
Leu Gly Gly Val Ala Ser Gly Leu Gly Met Gln Asn Leu Asn Ser Ser
        115   120   125
Arg Gln Ile Pro Ser Gly Asn Leu Gly Met Phe Gly Asn Ser Gly Ala
    130   135   140
Ala Gln Ala Arg Thr Met Gln Gln Pro Pro Gln Pro Pro Val Gln Pro
145   150   155   160
Leu Asn Ser Ser Gln Pro Ser Leu Arg Ala Gln Val Pro Gln Phe Leu
                165   170   175
Ser Pro Gln Val Gln Ala Gln Leu Leu Gln Phe Ala Ala Lys Asn Ile
            180   185   190
Gly Leu Asn Pro Ala Leu Leu Thr Ser Pro Ile Asn Pro Gln His Met
        195   200   205
Thr Met Leu Asn Gln Leu Tyr Gln Leu Gln Leu Ala Tyr Gln Arg Leu
    210   215   220
Gln Ile Gln Gln Gln Met Leu Gln Ala Gln Arg Asn Val Ser Gly

225 230 235

<210> 1867
<211> 518
<212> DNA
<213> Homo sapiens

<400> 1867
nngggcacg gttagggcca gtgggcagag gggtgaggga tatgcaggac cttccactgt
60
tccatgcatg ggacggcact tgggtccgcg atcaggtagc caggcatgga aggaacatgg
120
gaggaaggga actgtctggt gcgccagtgt tgttcaagga ggatgtgaca agacaggcca
180
tctggttggc tggccctgtt acccaacaac gtggtggcca aggccttgtg cccggagagg
240
ttcttggggg ccagcagggg gctacatagg acatgggtgg ggaccccagc tccgagccca
300
cctctcctgc ctccacccct tccacccnng cagcccccgc ctctcccgca gaactctccc
360
caagccagac cgcctggacc ggctgcttaa gtcaggcttt gggacatacc ctgggaggaa
420
gcgaggtgct ttgcaccccc aagtgatcat gttcccgtgc ccagcctgcc aaggtgatgt
480
ggagcttggg gagcggggtc tggcagggct tttccgga
518

<210> 1868
<211> 73
<212> PRT
<213> Homo sapiens

<400> 1868
Gln Asp Arg Pro Ser Gly Trp Leu Ala Leu Leu Pro Asn Asn Val Val
1 5 10 15
Ala Lys Ala Leu Cys Pro Glu Arg Phe Leu Gly Ala Ser Arg Gly Leu
20 25 30
His Arg Thr Trp Val Gly Thr Pro Ala Pro Ser Pro Pro Leu Leu Pro
35 40 45
Pro Pro Leu Pro Pro Xaa Gln Pro Pro Pro Leu Pro Gln Asn Ser Pro
50 55 60
Gln Ala Arg Pro Pro Gly Pro Ala Ala
65 70

<210> 1869
<211> 436
<212> DNA
<213> Homo sapiens

<400> 1869
acgcgtcacc ttcctgctgg agctactggg agccctcgga cacctgcgtg cattgcccga
60
ccgtgacatg ccgagcaccg aaacccacct gtggattcgc gagctgagcc gcatcgaccg
120

cgacgtgtcg actgccaccc actttcgttg gagcgacgac ggcaccgtgc taggtcagac
180
gaccgacgat ggcaccgagc ctgaggttgt tgccctgcca gcggtctact gccgtcgttg
240
cggccgcagc ggatggggag tccagctcgc cagcaccggc aataacctca gcgagaacaa
300
cgacagcatc cgacggaccc acgcggcaca cgacggtcgc ttccgagcct tgctttcggc
360
ccctcgagag ggagccagcg cggtcgacac cggcgaggcg acactgtcct tacgctggtt
420
cgacaccgtc aacagg
436

<210> 1870
<211> 123
<212> PRT
<213> Homo sapiens

<400> 1870
Met Pro Ser Thr Glu Thr His Leu Trp Ile Arg Glu Leu Ser Arg Ile
 1   5   10   15
Asp Arg Asp Val Ser Thr Ala Thr His Phe Arg Trp Ser Asp Asp Gly
            20   25   30
Thr Val Leu Gly Gln Thr Thr Asp Asp Gly Thr Glu Pro Glu Val Val
        35   40   45
Ala Leu Pro Ala Val Tyr Cys Arg Arg Cys Gly Arg Ser Gly Trp Gly
    50   55   60
Val Gln Leu Ala Ser Thr Gly Asn Asn Leu Ser Glu Asn Asn Asp Ser
65   70   75   80
Ile Arg Arg Thr His Ala Ala His Asp Gly Arg Phe Arg Ala Leu Leu
                85   90   95
Ser Ala Pro Arg Glu Gly Ala Ser Ala Val Asp Thr Gly Glu Ala Thr
            100   105   110
Leu Ser Leu Arg Trp Phe Asp Thr Val Asn Arg
        115   120

<210> 1871
<211> 474
<212> DNA
<213> Homo sapiens

<400> 1871
nntgcagcgc cccgaggtcg atgtctccaa cgtctttgcc agccttgaca tggctagcga
60
gcccgacctc gtccgtaccc tgctgaggca agcccaacaa tgaccgggga acagctcgcg
120
cattggatcg aggagtcgac gtcgacggtg tttttcggcg gcgccggaat gtccaccgaa
180
tcaggtattc cggactttcg ctcggctggc gggctttaca ccactcagca tgacctgccc
240
ttccccgcgg agtacatgct cagtcacagc tgtttggttg agcatcccgc ggagttcttc
300
gacttctacc gcacctacct catccatcct caggccaggc ccaatgctgg tcatcgtgcg
360

ttggttgcct tggagcaggc tggggaactt tcgacgatca ttacccagaa tattgacggc
420
ctgcaccaag aagctgggtc tcgtcaggtc attgagttgc atgggtcggt gcac
474

<210> 1872
<211> 125
<212> PRT
<213> Homo sapiens

<400> 1872
Met Thr Gly Glu Gln Leu Ala His Trp Ile Glu Glu Ser Thr Ser Thr
1 5 10 15
Val Phe Phe Gly Gly Ala Gly Met Ser Thr Glu Ser Gly Ile Pro Asp
20 25 30
Phe Arg Ser Ala Gly Gly Leu Tyr Thr Thr Gln His Asp Leu Pro Phe
35 40 45
Pro Ala Glu Tyr Met Leu Ser His Ser Cys Leu Val Glu His Pro Ala
50 55 60
Glu Phe Phe Asp Phe Tyr Arg Thr Tyr Leu Ile His Pro Gln Ala Arg
65 70 75 80
Pro Asn Ala Gly His Arg Ala Leu Val Ala Leu Glu Gln Ala Gly Glu
85 90 95
Leu Ser Thr Ile Ile Thr Gln Asn Ile Asp Gly Leu His Gln Glu Ala
100 105 110
Gly Ser Arg Gln Val Ile Glu Leu His Gly Ser Val His
115 120 125

<210> 1873
<211> 338
<212> DNA
<213> Homo sapiens

<400> 1873
nacgcgtaga aatgaagccc cagctggtca gagaccggaa atccggtagt gcacgggacg
60
ggttccctcg gggatctcgg aggggagacc cccacccggg aggactggag gcagcgcctc
120
tcccgccccg gcgcgcgcag cctatttccc tctttccaag gggccaatcc ccaccgcggc
180
ccgcaggggg cgcgctcaag gcaaggtccg cggcgagaac ggtgcccagt gggagcgaag
240
ggcgaggcca gcccttggtc cttggccggc agttcgggtc ccgcctccaa attttagtat
300
gcatatgagt caccaggaaa gttttttgaa acaaattt
338

<210> 1874
<211> 93
<212> PRT
<213> Homo sapiens

<400> 1874
Ser Pro Ser Trp Ser Glu Thr Gly Asn Pro Val Val His Gly Thr Gly

```
 1               5                  10                  15
Ser Leu Gly Asp Leu Gly Gly Glu Thr Pro Thr Arg Glu Asp Trp Arg
            20                  25                  30
Gln Arg Leu Ser Arg Pro Gly Ala Arg Ser Leu Phe Pro Ser Phe Gln
        35                  40                  45
Gly Ala Asn Pro His Arg Gly Pro Gln Gly Ala Arg Ser Arg Gln Gly
    50                  55                  60
Pro Arg Arg Glu Arg Cys Pro Val Gly Ala Lys Gly Glu Ala Ser Pro
65                  70                  75                  80
Trp Ser Leu Ala Gly Ser Ser Gly Pro Ala Ser Lys Phe
                85                  90
```

<210> 1875
<211> 366
<212> DNA
<213> Homo sapiens

<400> 1875
aagcttggcg tacaagtggt tcgtcgtttc tcaggtggtg gagccgtgta tcacgatatg
60
ggcaatatct gcttctgctt cattacagaa gatgatggcg atagcttccg tgattttgga
120
aaattcacag aacccgtgat tgaagcactc cataaaatgg gagcaacagg ggcagagtta
180
caaggacgta acgaccttct catcgacgga aagaaattct ctggaaatgc gatgtactca
240
aacaatggcc gtttaacagc gcacggaaca ttaatgttgg atttagatgt gagcattttg
300
ccacaaattt tacgtccaaa acaagagaaa atcgagtcaa aaggaatcaa gtcggttcgt
360
tcacgc
366

<210> 1876
<211> 122
<212> PRT
<213> Homo sapiens

<400> 1876
```
Lys Leu Gly Val Gln Val Val Arg Arg Phe Ser Gly Gly Gly Ala Val
 1               5                  10                  15
Tyr His Asp Met Gly Asn Ile Cys Phe Cys Phe Ile Thr Glu Asp Asp
            20                  25                  30
Gly Asp Ser Phe Arg Asp Phe Gly Lys Phe Thr Glu Pro Val Ile Glu
        35                  40                  45
Ala Leu His Lys Met Gly Ala Thr Gly Ala Glu Leu Gln Gly Arg Asn
    50                  55                  60
Asp Leu Leu Ile Asp Gly Lys Lys Phe Ser Gly Asn Ala Met Tyr Ser
65                  70                  75                  80
Asn Asn Gly Arg Leu Thr Ala His Gly Thr Leu Met Leu Asp Leu Asp
                85                  90                  95
Val Ser Ile Leu Pro Gln Ile Leu Arg Pro Lys Gln Glu Lys Ile Glu
            100                 105                 110
Ser Lys Gly Ile Lys Ser Val Arg Ser Arg
```

115 120

<210> 1877
<211> 357
<212> DNA
<213> Homo sapiens

<400> 1877
acgcgtgagt ggtcgcaaat atgacgggca agaaacgctt agaaagaaac tacccattaa
60
cgaggttatg caaattgcag aaatctctct atcggattgt ggctatatta tttcatcttt
120
ccaagctgct ggaccaaggg ctgtagggtt gcaacgacct attatatctg aacatttttt
180
tcaatttgac ccatttgata aacgacattg ggttgtctca catcatttac cacacgctgc
240
gacagctgct ttcacttccg gatttgaaga ttgcgctgga ttagtttcag atactgccgg
300
atcgaacact cttgatggaa aggactatgt tgaaagctgc tgcaatgcta ttccacg
357

<210> 1878
<211> 96
<212> PRT
<213> Homo sapiens

<400> 1878
Met Gln Ile Ala Glu Ile Ser Leu Ser Asp Cys Gly Tyr Ile Ile Ser
1 5 10 15
Ser Phe Gln Ala Ala Gly Pro Arg Ala Val Gly Leu Gln Arg Pro Ile
20 25 30
Ile Ser Glu His Phe Phe Gln Phe Asp Pro Phe Asp Lys Arg His Trp
35 40 45
Val Val Ser His His Leu Pro His Ala Ala Thr Ala Ala Phe Thr Ser
50 55 60
Gly Phe Glu Asp Cys Ala Gly Leu Val Ser Asp Thr Ala Gly Ser Asn
65 70 75 80
Thr Leu Asp Gly Lys Asp Tyr Val Glu Ser Cys Cys Asn Ala Ile Pro
85 90 95

<210> 1879
<211> 1062
<212> DNA
<213> Homo sapiens

<400> 1879
nacgcgtgga tgctccttgg acggcttttt cgtggtagag ggttcccggt gcgcgccgca
60
tccctgggaa gtagctgaag agaaggcaca ggaagagtcg cctccactga tggtctccct
120
gtccctccca caggctctga cgcccgctct gcggcttcgg tgtttgaaca ggccacagtc
180
caggagcgct tacattcagg agctccgcgt agcacctgcc caaccaaact cagccctccg
240

ttaagatcct ggttccatgc cgcagtagga cagcaggccc aagtctgcac atcccagtga
300
tgcaccatgc caatagtgga taagttgaag gaggccctga aacccggccg caaggactcg
360
gctgatgatg gagaactggg gaagcttctt gcctcctctg ccaagaaggt ccttttacag
420
aaaatcgagt tcgagccagc cagcaagagc ttctcctacc agctggaggc cttaaagagc
480
aaatatgtgt tgctcaaccc caaaacagag ggagctagtc gccacaagag tggagatgac
540
ccaccggcca ggagacaggg cagtgaacac acgtatgaga gctgtggtga cggagtccca
600
gccccgcaga aagtgctttt ccccacggag cgactgtctc tgaggtggga gcgggtcttc
660
cgcgtgggcg caggactcca caaccttggc aacacctgct ttctcaatgc caccatccag
720
tgcttgacct acacaccacc tctagccaac tacctgctct ccaaggagca tgctcgcagc
780
tgccaccagg gaagcttctg catgctgtgt gtcatgcaga accacattgt ccaggccttc
840
gccaacagcg gcaacgccat caagcccgtc tccttcatcc gagacctgaa aaagatcgcc
900
cgacacttcc gctttgggaa ccaggaggac gcgcatgagt tcctgcggta caccatcgac
960
gccatgcaga aagcctgcct gaatggctgt gccaagttgg atcgtcaaac gcaggctact
1020
accttggtcc atcaaatttt tggagggtat ctcagatcac gc
1062

<210> 1880
<211> 252
<212> PRT
<213> Homo sapiens

<400> 1880
Met Pro Ile Val Asp Lys Leu Lys Glu Ala Leu Lys Pro Gly Arg Lys
1 5 10 15
Asp Ser Ala Asp Asp Gly Glu Leu Gly Lys Leu Leu Ala Ser Ser Ala
20 25 30
Lys Lys Val Leu Leu Gln Lys Ile Glu Phe Glu Pro Ala Ser Lys Ser
35 40 45
Phe Ser Tyr Gln Leu Glu Ala Leu Lys Ser Lys Tyr Val Leu Leu Asn
50 55 60
Pro Lys Thr Glu Gly Ala Ser Arg His Lys Ser Gly Asp Asp Pro Pro
65 70 75 80
Ala Arg Arg Gln Gly Ser Glu His Thr Tyr Glu Ser Cys Gly Asp Gly
85 90 95
Val Pro Ala Pro Gln Lys Val Leu Phe Pro Thr Glu Arg Leu Ser Leu
100 105 110
Arg Trp Glu Arg Val Phe Arg Val Gly Ala Gly Leu His Asn Leu Gly
115 120 125
Asn Thr Cys Phe Leu Asn Ala Thr Ile Gln Cys Leu Thr Tyr Thr Pro
130 135 140
Pro Leu Ala Asn Tyr Leu Leu Ser Lys Glu His Ala Arg Ser Cys His

```
145                 150                 155                 160
Gln Gly Ser Phe Cys Met Leu Cys Val Met Gln Asn His Ile Val Gln
                165                 170                 175
Ala Phe Ala Asn Ser Gly Asn Ala Ile Lys Pro Val Ser Phe Ile Arg
            180                 185                 190
Asp Leu Lys Lys Ile Ala Arg His Phe Arg Phe Gly Asn Gln Glu Asp
        195                 200                 205
Ala His Glu Phe Leu Arg Tyr Thr Ile Asp Ala Met Gln Lys Ala Cys
    210                 215                 220
Leu Asn Gly Cys Ala Lys Leu Asp Arg Gln Thr Gln Ala Thr Thr Leu
225                 230                 235                 240
Val His Gln Ile Phe Gly Gly Tyr Leu Arg Ser Arg
                245                 250
```

<210> 1881
<211> 358
<212> DNA
<213> Homo sapiens

<400> 1881
natcaccatg gatggacgcc ggcaaagcaa catcaatcga tgtcaagcca cagacatctc
60
aaatcccctgc agaaccgcaa agtttggcag agaagaagga tgaatgggag atcgcataca
120
tcaacacgaa gattaacgac gtctacaacc ctctcaacaa caatgtggac tggttaagca
180
cgagaattga tctgctacag caagatttgg acaccactcg caagaaggat ctaaaaccag
240
ccacatcgat cgatatctgc accatcacat cgatcgatag caagttcgta gccatggaag
300
ataggttaca atcttataag gatatgcacg accgtttcac ctcacctatc aggcgata
358

<210> 1882
<211> 115
<212> PRT
<213> Homo sapiens

<400> 1882
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Met Asp Ala Gly Lys Ala Thr Ser Ile Asp Val Lys Pro Gln Thr Ser
 1               5                  10                  15
Gln Ile Pro Ala Glu Pro Gln Ser Leu Ala Glu Lys Lys Asp Glu Trp
            20                  25                  30
Glu Ile Ala Tyr Ile Asn Thr Lys Ile Asn Asp Val Tyr Asn Pro Leu
        35                  40                  45
Asn Asn Asn Val Asp Trp Leu Ser Thr Arg Ile Asp Leu Leu Gln Gln
    50                  55                  60
Asp Leu Asp Thr Thr Arg Lys Lys Asp Leu Lys Pro Ala Thr Ser Ile
65                  70                  75                  80
Asp Ile Cys Thr Ile Thr Ser Ile Asp Ser Lys Phe Val Ala Met Glu
                85                  90                  95
Asp Arg Leu Gln Ser Tyr Lys Asp Met His Asp Arg Phe Thr Ser Pro
            100                 105                 110
Ile Arg Arg
```

115

<210> 1883
<211> 367
<212> DNA
<213> Homo sapiens

<400> 1883
ggatcctatc atgaatctgc actctgacca gggaagtaac tcccttggct gctcagactt
60
gggctgggag aatgatacta agacaccaga catcacatcc attgctccca ttcccactat
120
tgctgaaggc gatgagtctg tatttgtcaa ctccaattca aacagctcga tggtgcctcc
180
tgtcctggag aacaatgctg ttgatctcac tgatgggctg acagatttgg aatcctatat
240
gaggtttctt atggatggcg gngcaagtga ttcaattgat agccttctga accttgatgg
300
atcacaggat cttggtagca atatggacct ctggaccttc gatgacatgc ccatcgctgg
360
cgatttn
367

<210> 1884
<211> 119
<212> PRT
<213> Homo sapiens

<400> 1884
Met Asn Leu His Ser Asp Gln Gly Ser Asn Ser Leu Gly Cys Ser Asp
1 5 10 15
Leu Gly Trp Glu Asn Asp Thr Lys Thr Pro Asp Ile Thr Ser Ile Ala
20 25 30
Pro Ile Pro Thr Ile Ala Glu Gly Asp Glu Ser Val Phe Val Asn Ser
35 40 45
Asn Ser Asn Ser Ser Met Val Pro Pro Val Leu Glu Asn Asn Ala Val
50 55 60
Asp Leu Thr Asp Gly Leu Thr Asp Leu Glu Ser Tyr Met Arg Phe Leu
65 70 75 80
Met Asp Gly Gly Ala Ser Asp Ser Ile Asp Ser Leu Leu Asn Leu Asp
85 90 95
Gly Ser Gln Asp Leu Gly Ser Asn Met Asp Leu Trp Thr Phe Asp Asp
100 105 110
Met Pro Ile Ala Gly Asp Xaa
115

<210> 1885
<211> 392
<212> DNA
<213> Homo sapiens

<400> 1885
nacgcgtatt cgcaaagaat gtctttgcgg cacagagaca gtcgtcgtcc tcgacaccat
60

gttcgacgat ctcggcatgt tgggaacccg gtgatttctc gcctgcggcg cacctcgtgg
120
ctgcgtagta cagctgctgt tgccgccggg gccgcgaccg gtaccgggtt ccaaccactg
180
aactggtgga tcctcgtcat tcccggtctc gctgcgctca tcctgctggt gcgcaacgcc
240
actggtcggg ccgcggcagg actggggtat ctcttcggca tcggtctgtt taccaccacc
300
atttcctggg taggcgtcat cggcccgccg gtggcgatac ttctcatcgc tgtcatggcg
360
ttgtggtgtc tgctggccgg gtggacgatt cg
392

<210> 1886
<211> 130
<212> PRT
<213> Homo sapiens

<400> 1886
Xaa Ala Tyr Ser Gln Arg Met Ser Leu Arg His Arg Asp Ser Arg Arg
 1   5   10   15
Pro Arg His His Val Arg Arg Ser Arg His Val Gly Asn Pro Val Ile
            20   25   30
Ser Arg Leu Arg Arg Thr Ser Trp Leu Arg Ser Thr Ala Ala Val Ala
        35   40   45
Ala Gly Ala Ala Thr Gly Thr Gly Phe Gln Pro Leu Asn Trp Trp Ile
    50   55   60
Leu Val Ile Pro Gly Leu Ala Ala Leu Ile Leu Leu Val Arg Asn Ala
65   70   75   80
Thr Gly Arg Ala Ala Ala Gly Leu Gly Tyr Leu Phe Gly Ile Gly Leu
                85   90   95
Phe Thr Thr Thr Ile Ser Trp Val Gly Val Ile Gly Pro Pro Val Ala
            100   105   110
Ile Leu Leu Ile Ala Val Met Ala Leu Trp Cys Leu Leu Ala Gly Trp
        115   120   125
Thr Ile
    130

<210> 1887
<211> 363
<212> DNA
<213> Homo sapiens

<400> 1887
cgcgagttca ttcggacctt tgaggacgtt gccaagcgtc tcaatgggga ccagccgatc
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gacttcttgg tgcagggaac tttatatccc gatgtcgtcg agtctggtgg cggtgagggc
120
gctgccaata tcaagagtca ccataatgtt ggtgggctcc ctgacgacct ccagttcagt
180
ctcgttgagc cattgcgcac cctctttaag gacgaggtgc gagccgtcgg actcgaactt
240
ggtctgcccg aggacatcgt ctggcgtcag cccttcccgg gcccggggct ggctatccgc
300

attattggcg aagtcaccgc ggagcgtctg gaggtgctac gcactgccga tgccatcacg
360
cgt
363

<210> 1888
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1888
Arg Glu Phe Ile Arg Thr Phe Glu Asp Val Ala Lys Arg Leu Asn Gly
 1   5   10   15
Asp Gln Pro Ile Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val
            20   25   30
Val Glu Ser Gly Gly Gly Glu Gly Ala Ala Asn Ile Lys Ser His His
        35   40   45
Asn Val Gly Gly Leu Pro Asp Asp Leu Gln Phe Ser Leu Val Glu Pro
    50   55   60
Leu Arg Thr Leu Phe Lys Asp Glu Val Arg Ala Val Gly Leu Glu Leu
65   70   75   80
Gly Leu Pro Glu Asp Ile Val Trp Arg Gln Pro Phe Pro Gly Pro Gly
                85   90   95
Leu Ala Ile Arg Ile Ile Gly Glu Val Thr Ala Glu Arg Leu Glu Val
            100   105   110
Leu Arg Thr Ala Asp Ala Ile Thr Arg
        115   120

<210> 1889
<211> 530
<212> DNA
<213> Homo sapiens

<400> 1889
gcaccagatc tgctcatggc gcgcattgcg acggcaacgc agtcgatccg gcttgggtct
60
ggtggggtga tggccatgca ctacgggtcg ctgcaaatag cggaacggtt ttcgaccctc
120
acagcgctct tcggtgatcg tatcgacatg gggctgggcc gggctcccgg cggtgacatg
180
ctctccgccc atgccctcaa tcaggggcag gtcatccgcc ctgaggccat taattccctc
240
atcgccgaaa cggtagggtt cgtgcgcgaa atgctaccgt cgaagcatcc gtacgcaaag
300
gtcgtcgtga ccccggcagg tcagatccag ccacagacgt ggctgctggg atcgtcgggc
360
cagtcagcag cgtgggctgg tgagcagggt atggactacg cctacgccca gtttttcacc
420
gggcgccagg acaccgggat catggatcac taccgcgcgc acctgtccga cggcttcccc
480
ggcaggaccc tctcagcagt gtgtgtatcg gctgctccga cgcgtccgga
530

<210> 1890

<211> 176
<212> PRT
<213> Homo sapiens

<400> 1890
Ala Pro Asp Leu Leu Met Ala Arg Ile Ala Thr Ala Thr Gln Ser Ile
1 5 10 15
Arg Leu Gly Ser Gly Gly Val Met Ala Met His Tyr Gly Ser Leu Gln
20 25 30
Ile Ala Glu Arg Phe Ser Thr Leu Thr Ala Leu Phe Gly Asp Arg Ile
35 40 45
Asp Met Gly Leu Gly Arg Ala Pro Gly Gly Asp Met Leu Ser Ala His
50 55 60
Ala Leu Asn Gln Gly Gln Val Ile Arg Pro Glu Ala Ile Asn Ser Leu
65 70 75 80
Ile Ala Glu Thr Val Gly Phe Val Arg Glu Met Leu Pro Ser Lys His
85 90 95
Pro Tyr Ala Lys Val Val Val Thr Pro Ala Gly Gln Ile Gln Pro Gln
100 105 110
Thr Trp Leu Leu Gly Ser Ser Gly Gln Ser Ala Ala Trp Ala Gly Glu
115 120 125
Gln Gly Met Asp Tyr Ala Tyr Ala Gln Phe Phe Thr Gly Arg Gln Asp
130 135 140
Thr Gly Ile Met Asp His Tyr Arg Ala His Leu Ser Asp Gly Phe Pro
145 150 155 160
Gly Arg Thr Leu Ser Ala Val Cys Val Ser Ala Ala Pro Thr Arg Pro
165 170 175

<210> 1891
<211> 423
<212> DNA
<213> Homo sapiens

<400> 1891
agatctcagg gagacagagg ggcccgggat aggaagaata tgtgggcacc tctcccacag
60
tcctccatct gcacaaggct acccactctg cagatggccc ctgcttgcag agagatccag
120
cgtcaattta cagaggcagc ccagcttcct atcaactttc tggcctggct taacggtgta
180
atgggcaggg ggcaaggcct tgaccacact catgtttctc ccccggcctc ctccactctg
240
ggattttgta ccggtatggg gaggcactac ggttgcagat ttagcttttc agcgtggata
300
caagcaccca agtgtcccag accacagcag aaaccgtgtt gctgccgttt ccaacctgct
360
gatttggtct cttgctgccg ttctgaccaa cagaattgct actgactgac aaatcccttg
420
tgc
423

<210> 1892
<211> 121
<212> PRT

<213> Homo sapiens

<400> 1892

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Met Trp Ala Pro Leu Pro Gln Ser Ser Ile Cys Thr Arg Leu Pro Thr
 1               5                  10                  15
Leu Gln Met Ala Pro Ala Cys Arg Glu Ile Gln Arg Gln Phe Thr Glu
            20                  25                  30
Ala Ala Gln Leu Pro Ile Asn Phe Leu Ala Trp Leu Asn Gly Val Met
        35                  40                  45
Gly Arg Gly Gln Gly Leu Asp His Thr His Val Ser Pro Pro Ala Ser
    50                  55                  60
Ser Thr Leu Gly Phe Cys Thr Gly Met Gly Arg His Tyr Gly Cys Arg
65                  70                  75                  80
Phe Ser Phe Ser Ala Trp Ile Gln Ala Pro Lys Cys Pro Arg Pro Gln
                85                  90                  95
Gln Lys Pro Cys Cys Cys Arg Phe Gln Pro Ala Asp Leu Val Ser Cys
            100                 105                 110
Cys Arg Ser Asp Gln Gln Asn Cys Tyr
        115                 120
```

<210> 1893
<211> 886
<212> DNA
<213> Homo sapiens

<400> 1893

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accggtggtg ctgaaccggc ccgagttgcc cttcctagcc ggatatacgt cgagggacgt
60
catgacgctg aactcgtcga aaagatatgg ggcgacgacc tgcgccacgt cggggtcgtt
120
gtggaataca tgggtggcat ggacgacctc gtcgggatcg tcgccgagtt taagcctggt
180
ccggggcatc gccttggcgt gttggttgac cacctcgttg ccgacaccaa agagtcacgg
240
gtagcggacg aagtacgtcg tggtgggtat agcgagtatg tcatgattac cggtcatcgc
300
tttattgaca tctggcaggc catcaaacct caacgaattg gccgtcaaga atggcctgag
360
gtcccgatgg acgaagactt caaactcggc accctgaagc gtctgggcct gcctcactcg
420
acccaagctg acgtcggtaa ggcctggcag gccatgctgg cacgagtgcg cgactggcac
480
gatttagacc cccgctttaa cacggagatg gagaaactta tcgatttcgt cacgcgtgac
540
catgtcgacg agctggacaa tggggagatg gcatgagtat tgacgtcgac acggtgtctg
600
acctcatccg ggatgtgagt gccagggtta tcgatccccg gttccggacc ctccacgatc
660
atcaaatcca ccagaaaaag cccggggact tcgttactga tgccgatcgt caggccgagt
720
gcgagctggg tgccgctgtg accaagtatg ccggcggtat tgtcgtgggg gaggaatcag
780
ccttcgccga cccaaccatc cttgatgccg tttccgatgc tgacctggcc tgggtcatcg
840
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accccattga tggcactaag aacttcgtgc acgggtctgt tgatca
886

<210> 1894
<211> 191
<212> PRT
<213> Homo sapiens

<400> 1894
Thr Gly Gly Ala Glu Pro Ala Arg Val Ala Leu Pro Ser Arg Ile Tyr
1 5 10 15
Val Glu Gly Arg His Asp Ala Glu Leu Val Glu Lys Ile Trp Gly Asp
20 25 30
Asp Leu Arg His Val Gly Val Val Val Glu Tyr Met Gly Gly Met Asp
35 40 45
Asp Leu Val Gly Ile Val Ala Glu Phe Lys Pro Gly Pro Gly His Arg
50 55 60
Leu Gly Val Leu Val Asp His Leu Val Ala Asp Thr Lys Glu Ser Arg
65 70 75 80
Val Ala Asp Glu Val Arg Arg Gly Gly Tyr Ser Glu Tyr Val Met Ile
85 90 95
Thr Gly His Arg Phe Ile Asp Ile Trp Gln Ala Ile Lys Pro Gln Arg
100 105 110
Ile Gly Arg Gln Glu Trp Pro Glu Val Pro Met Asp Glu Asp Phe Lys
115 120 125
Leu Gly Thr Leu Lys Arg Leu Gly Leu Pro His Ser Thr Gln Ala Asp
130 135 140
Val Gly Lys Ala Trp Gln Ala Met Leu Ala Arg Val Arg Asp Trp His
145 150 155 160
Asp Leu Asp Pro Arg Phe Asn Thr Glu Met Glu Lys Leu Ile Asp Phe
165 170 175
Val Thr Arg Asp His Val Asp Glu Leu Asp Asn Gly Glu Met Ala
180 185 190

<210> 1895
<211> 2555
<212> DNA
<213> Homo sapiens

<400> 1895
nntcatgatt tttggaggtg ggttgtacct cctgaacttc tagctttcaa gttgtggctg
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ttttttgttt ttgtttttgt ttttgttttc tttagaattt ttccctgttt cccaccttct
120
cttcccctgt tgccaaggtc taactcactg tagtctggat gtgggtgtat gttcatgtac
180
acaactttag aaagttgctt gcagaacaaa aaggctacac aaaagcccac tggctctcaa
240
taccctcaag tggatggcag aggctcttgt tgaaagtggg caatttgcaa tctttgcatt
300
aggatttcag atgcatgcca ggtttccact gattgccaga actcgagatc actacacatg
360
gatccccaaa atcaacatgg cagtggcagt tcgttagttg tgatccagca gccttctttg
420

gatagccgtc agagattaga ctatgagaga gagattcagc ctactgctat tttgtcctta
480
gaccagatca aggccataag aggcagcaat gaatacacag aagggccttc ggtggtgaaa
540
agacctgctc ctcggacagc accaagacaa gaaaagcatg aaaggactca tgaaatcata
600
ccaattaatg tgaataataa ctacgagcac agacacacaa gccacctggg acatgcagta
660
ctcccaagta atgccagggg ccccattttg agcagatcaa ccagcactgg aagtgcagcc
720
agctctggga gcaacagcag tgcctcttct gaacagggac tgttaggaag gtcaccacca
780
accagaccag tccctggtca taggtctgaa agggcaatcc ggacccagcc caagcaactg
840
attgtggatg acttgaaggg ttccttgaaa gaggacctga cacagcacaa gttcatttgt
900
gaacagtgtg ggaagtgcaa gtgtggagaa tgcactgctc ccaggaccct accatcctgt
960
ttggcctgta accggcagtg cctttgctct gctgagagca tggtggaata tggaacctgc
1020
atgtgcttag tcaagggcat cttctaccac tgctccaatg acgacgaagg ggattcctat
1080
tcagataatc cttgctcctg ttcacaatca cactgctgct ctagatacct gtgtatggga
1140
gccatgtctt tatttttacc ttgcttactc tgttatcctc ctgctaaagg atgcctgaag
1200
ctgtgcagga ggtgttatga ctggatccat cgcccagggt gcagatgtaa gaactccaac
1260
actgtctatt gtaagctgga gagctgcccc tcccggggtc agggtaaacc atcatgattt
1320
ttggaggtgg gttgtacctc ctgaacttct agctttcaag ttgtggctgt tttttgtttt
1380
tgtttttgtt tttgttttct ttagaatttt tccctgtttc ccaccttctc ttcccctgtt
1440
gccaaggtct aactcatgga ttttttctctt tcctcatgga tgatcttcag caagagtgga
1500
ctgggaagct gcacctggct cccactttca acaagagcct ctgccatcca cttgagggta
1560
ttgagagcca gtgggctttt gtgtagcctt tttgttctgc aagcaacttt ctaaagttgt
1620
gtacatgaac atacacccac atccagacta cagtgattta gagttgtttt gattgggtac
1680
cgtgggagca gggaaattgg ttttttaaaa agcaactgtt taattgctta aataagctat
1740
gtattaaatc tgtctccagt tagggctatc ttcctagcat aggcccctta agtagcatgg
1800
gggatatatt ttttgctata acgtaaaaat tttcctttaa ccactgccct ctcctttctc
1860
cttcaaggtt ctttcccccc cagttttgtt gttgtcttac tctggagatg ccaagtgtat
1920
ttttttcttc tatgtaattt tagattcgcc ttacaatgta aatcttcaca ttggagataa
1980
tattggttgg accttgccca tcttcactct agccttcgta tttgtgaagg actcagccac
2040

cttccttctt caccccatgc ttctcaccaa atttttgttg tcattgaggg cacttggata
2100
actcaagttg atatttatag ctgatcaatc tatatgtgtc acagaactat gctgcctaaa
2160
gtgatcttgg ctccttaatg gtccttttgg ccccttggat agttaacagc tgagtaattc
2220
taatctcttc tgtgttttcc ttgccttaac cacaaattgt ggtgcttttt gtatatttta
2280
tgtataaatc acaaagttga attctgacta tttttaagac aaaagtctgt taaacttttt
2340
tattgtaaag aatatttatt atgcgaatct ctattatttt atggtattta ttgcaaaaga
2400
ctgttgaaat gtactcatgt ttgaatataa caaaatatca atacttaacg gaaaataagg
2460
tgacacgaag aaagtacata tgttaactat aatgcagaaa atatattaat taatgaaaaa
2520
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa
2555

<210> 1896
<211> 139
<212> PRT
<213> Homo sapiens

<400> 1896
Cys Glu Gln Cys Gly Lys Cys Lys Cys Gly Glu Cys Thr Ala Pro Arg
1 5 10 15
Thr Leu Pro Ser Cys Leu Ala Cys Asn Arg Gln Cys Leu Cys Ser Ala
20 25 30
Glu Ser Met Val Glu Tyr Gly Thr Cys Met Cys Leu Val Lys Gly Ile
35 40 45
Phe Tyr His Cys Ser Asn Asp Asp Glu Gly Asp Ser Tyr Ser Asp Asn
50 55 60
Pro Cys Ser Cys Ser Gln Ser His Cys Cys Ser Arg Tyr Leu Cys Met
65 70 75 80
Gly Ala Met Ser Leu Phe Leu Pro Cys Leu Leu Cys Tyr Pro Pro Ala
85 90 95
Lys Gly Cys Leu Lys Leu Cys Arg Arg Cys Tyr Asp Trp Ile His Arg
100 105 110
Pro Gly Cys Arg Cys Lys Asn Ser Asn Thr Val Tyr Cys Lys Leu Glu
115 120 125
Ser Cys Pro Ser Arg Gly Gln Gly Lys Pro Ser
130 135

<210> 1897
<211> 938
<212> DNA
<213> Homo sapiens

<400> 1897
cgtcatggct gctacgtgtg cggnaagagc tttgcctggc gctccacact ggtggagcac
60
gtctacagtc acactggcga gaagcccttc cactgcactg actgcggcaa gggcttcggc
120

cacgcttcct ccctgagcaa acaccgggcc atccatcgtg gggagcggcc ccaccgctgt
180
ctggagtgtg gccgggcctt cacgcagcgc tcggcgctga cttcgcacct gcgcgtccac
240
accggcgaga aaccctatgg ctgcgccgac tgtggccgcc gcttcagcca gagctctgcc
300
ctctaccagc accggcgcgt gcacagcggc gagacccccc tcccctgccc ggactgtggc
360
cgcgccttcg cctacccctc ggacctgcgg cgccacgtgc gcatccacac gggcgagaag
420
ccctaccctt gcccagactg tgggcgccgc ttttcctcct cctccctgct ggtcagtcac
480
cggcgggcac actccggcga gtgcccctat gtttgtgacc agtgtggcaa acgtttctcc
540
cagcgcaaga acctctccca gcaccaggtc atccatacag gggagaagcc ctatcactgc
600
cctgactgtg gtcgctgctt ccggaggagc cggtccttgg ccaatcaccg gaccacacac
660
acaggtgaaa aaccccacca gtgccctagc tgtggacgtc gcttcgccta cccctccctg
720
ctggccagcc accggcgcgt gcactcgggc gagcggccct atgcctgcga cctttgctcc
780
aagcgttttg ctcagtggag ccacctggcc cagcaccagc tgctgcacac gggggagaag
840
cctttccccc gcctcgagtg tggccgggct tccgccagag gtggtctctg gctgtccaca
900
agtgtagccc caaggcccca aactgtagcc ctagatct
938

<210> 1898
<211> 312
<212> PRT
<213> Homo sapiens

<400> 1898
Arg His Gly Cys Tyr Val Cys Gly Lys Ser Phe Ala Trp Arg Ser Thr
1 5 10 15
Leu Val Glu His Val Tyr Ser His Thr Gly Glu Lys Pro Phe His Cys
20 25 30
Thr Asp Cys Gly Lys Gly Phe Gly His Ala Ser Ser Leu Ser Lys His
35 40 45
Arg Ala Ile His Arg Gly Glu Arg Pro His Arg Cys Leu Glu Cys Gly
50 55 60
Arg Ala Phe Thr Gln Arg Ser Ala Leu Thr Ser His Leu Arg Val His
65 70 75 80
Thr Gly Glu Lys Pro Tyr Gly Cys Ala Asp Cys Gly Arg Arg Phe Ser
85 90 95
Gln Ser Ser Ala Leu Tyr Gln His Arg Arg Val His Ser Gly Glu Thr
100 105 110
Pro Phe Pro Cys Pro Asp Cys Gly Arg Ala Phe Ala Tyr Pro Ser Asp
115 120 125
Leu Arg Arg His Val Arg Ile His Thr Gly Glu Lys Pro Tyr Pro Cys
130 135 140
Pro Asp Cys Gly Arg Arg Phe Ser Ser Ser Ser Leu Leu Val Ser His

```
145                 150                 155                 160
Arg Arg Ala His Ser Gly Glu Cys Pro Tyr Val Cys Asp Gln Cys Gly
                165                 170                 175
Lys Arg Phe Ser Gln Arg Lys Asn Leu Ser Gln His Gln Val Ile His
            180                 185                 190
Thr Gly Glu Lys Pro Tyr His Cys Pro Asp Cys Gly Arg Cys Phe Arg
        195                 200                 205
Arg Ser Arg Ser Leu Ala Asn His Arg Thr Thr His Thr Gly Glu Lys
    210                 215                 220
Pro His Gln Cys Pro Ser Cys Gly Arg Arg Phe Ala Tyr Pro Ser Leu
225                 230                 235                 240
Leu Ala Ser His Arg Arg Val His Ser Gly Glu Arg Pro Tyr Ala Cys
                245                 250                 255
Asp Leu Cys Ser Lys Arg Phe Ala Gln Trp Ser His Leu Ala Gln His
            260                 265                 270
Gln Leu Leu His Thr Gly Glu Lys Pro Phe Pro Cys Leu Glu Cys Gly
        275                 280                 285
Arg Ala Ser Ala Arg Gly Gly Leu Trp Leu Ser Thr Ser Val Ala Pro
    290                 295                 300
Arg Pro Gln Thr Val Ala Leu Asp
305                 310
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<210> 1899
<211> 508
<212> DNA
<213> Homo sapiens

<400> 1899
aaatttgcct ccctaattgg caaggtgcaa gccctggaac agcgcgacca gctgctggag
60
acacgctgga gcttcctgca gggccaggac tcagccatct tcgacctcgg gcatctctat
120
gaggaaatat caggccggct gcggagggaa ctgggccaaa gggacaggaa ccgggggcag
180
ctggaggcca ccctgctgca ggtgttgaaa aaggtggagg agtttcgaat caggtattga
240
gatgagatct ccaagcgcac agacatggag ttcacctttg ttcagctgaa gaaggacctg
300
gatgcagagt gtcttcatcg gactgaactg gaaaccaagt taaaaagcct ggagagcttc
360
gtggagttga tgaaaaccat ctatgagcag gagctgaagg acctggcagc acaggtgaag
420
gatgtgtcgg tgaccgtcgg catggacagc cgctgccaca tcgacctgag cggcatcgtg
480
gaggaggtga aggcccagta tgacgccg
508

<210> 1900
<211> 79
<212> PRT
<213> Homo sapiens

<400> 1900
Lys Phe Ala Ser Leu Ile Gly Lys Val Gln Ala Leu Glu Gln Arg Asp

```
 1               5                  10                  15
Gln Leu Leu Glu Thr Arg Trp Ser Phe Leu Gln Gly Gln Asp Ser Ala
            20                  25                  30
Ile Phe Asp Leu Gly His Leu Tyr Glu Glu Ile Ser Gly Arg Leu Arg
        35                  40                  45
Arg Glu Leu Gly Gln Arg Asp Arg Asn Arg Gly Gln Leu Glu Ala Thr
    50                  55                  60
Leu Leu Gln Val Leu Lys Lys Val Glu Glu Phe Arg Ile Arg Tyr
65                  70                  75
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<210> 1901
<211> 453
<212> DNA
<213> Homo sapiens

<400> 1901
acgcgtggac cacgatgcgc cggatcgggc tcggcgccat gcacacctcg gacctggcgg
60
cggtgttcgg cgatgcgaag gcaacccgcg cttccaagtt cgacccgttc cagccgcgcg
120
aggaattcga cgaggtcagc gccgccatgc agttccactg gggctccttc ttccacaacg
180
cgcatccggg cgagaagtgg ccggtctacg gtttccgcag cgacacggag cccggccgcg
240
cgaccgcgat cttcgcggcg aagtcctccg tggagtacga ccccaaggcg gcgcagcgcc
300
gcgcgtggga gggctttgac atgcgcgaat ggggcatgca caggcaggac ctggtggaaa
360
cgctcaccga ttccatcgcc gacgagggca acgcttagcg acgccagcgc caccgagttt
420
agagaaatga aagaaatttt aatagagggt gga
453

<210> 1902
<211> 151
<212> PRT
<213> Homo sapiens

<400> 1902
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Thr Arg Gly Pro Arg Cys Ala Gly Ser Gly Ser Ala Pro Cys Thr Pro
 1               5                  10                  15
Arg Thr Trp Arg Arg Cys Ser Ala Met Arg Arg Gln Pro Ala Leu Pro
            20                  25                  30
Ser Ser Thr Arg Ser Ser Arg Ala Arg Asn Ser Thr Arg Ser Ala Pro
        35                  40                  45
Pro Cys Ser Ser Thr Gly Ala Pro Ser Ser Thr Thr Arg Ile Arg Ala
    50                  55                  60
Arg Ser Gly Arg Ser Thr Val Ser Ala Ala Thr Arg Ser Pro Ala Ala
65                  70                  75                  80
Arg Pro Arg Ser Ser Arg Arg Ser Pro Pro Trp Ser Thr Thr Pro Arg
                85                  90                  95
Arg Arg Ser Ala Ala Arg Gly Arg Ala Leu Thr Cys Ala Asn Gly Ala
            100                 105                 110
Cys Thr Gly Arg Thr Trp Trp Lys Arg Ser Pro Ile Pro Ser Pro Thr
```

```
        115                 120                 125
Arg Ala Thr Leu Ser Asp Ala Ser Ala Thr Glu Phe Arg Glu Met Lys
    130                 135                 140
Glu Ile Leu Ile Glu Gly Gly
145                 150
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<210> 1903
<211> 531
<212> DNA
<213> Homo sapiens

<400> 1903
ccggcgaggg agctgttccg ggacgccgcc ttccccgccg cggactcctc gctcttctgc
60
gacttgtcta cgccgctggc ccagttccgc gaggacatca cgtggaggcg gccccagaga
120
atttgtgcca acccccgctt gtttccaaat gaccaacggg aagggcaggt gaagcagggg
180
ctgctggggg attgctggtt cctgtgtgcc tgcgccgcgc tgcagaagag caggcacctc
240
ctggaccagg tcattcctgc gggacagccg agctgggccg accaggagta ccggggctcc
300
ttcacctgtc gcttttggca gtttggacgg tgggtggagg gtccatgggt cccttcgagc
360
ccctgtgggc ggggcaggtg gcggatgccc tggtggacct gaccggcggc ctggcagaaa
420
gatggaacct gaagggcgta gcaggaagcg gaggccagca ggacaggcca ggccgctggg
480
agcacaggac ttgtcggcag ctgctccacc tgaaggacca gtgtctgatc a
531

<210> 1904
<211> 133
<212> PRT
<213> Homo sapiens

<400> 1904
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Pro Ala Arg Glu Leu Phe Arg Asp Ala Ala Phe Pro Ala Ala Asp Ser
 1               5                  10                  15
Ser Leu Phe Cys Asp Leu Ser Thr Pro Leu Ala Gln Phe Arg Glu Asp
            20                  25                  30
Ile Thr Trp Arg Arg Pro Gln Arg Ile Cys Ala Asn Pro Arg Leu Phe
        35                  40                  45
Pro Asn Asp Gln Arg Glu Gly Gln Val Lys Gln Gly Leu Leu Gly Asp
    50                  55                  60
Cys Trp Phe Leu Cys Ala Cys Ala Ala Leu Gln Lys Ser Arg His Leu
65                  70                  75                  80
Leu Asp Gln Val Ile Pro Ala Gly Gln Pro Ser Trp Ala Asp Gln Glu
                85                  90                  95
Tyr Arg Gly Ser Phe Thr Cys Arg Phe Trp Gln Phe Gly Arg Trp Val
            100                 105                 110
Glu Gly Pro Trp Val Pro Ser Ser Pro Cys Gly Arg Gly Arg Trp Arg
        115                 120                 125
Met Pro Trp Trp Thr
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130

<210> 1905
<211> 387
<212> DNA
<213> Homo sapiens

<400> 1905
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120
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240
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360
gggccgacct ggactttcag catcgtt
387

<210> 1906
<211> 129
<212> PRT
<213> Homo sapiens

<400> 1906
Thr Arg Gly Leu Ile Gly Met Leu Trp Ala Leu Gly Val Val Ala Glu
1 5 10 15
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20 25 30
Arg Arg Val Leu Leu Ala Ser Phe Leu Leu Ala Ala Val Arg Trp Leu
35 40 45
Leu Leu Gly Ala Leu Ala Asp His Leu Ala Val Leu Leu Phe Ala Gln
50 55 60
Val Leu His Ala Ala Thr Phe Ala Ser Phe His Ala Ser Ala Ile His
65 70 75 80
Phe Val Gln Arg Ser Phe Gly Ala Arg Xaa Ala Arg Pro Gly Gln Ala
85 90 95
Leu Tyr Ala Ala Leu Ala Gly Thr Gly Gly Ala Leu Gly Ala Leu Tyr
100 105 110
Ala Gly Tyr Ser Trp Asn Ser Leu Gly Pro Thr Trp Thr Phe Ser Ile
115 120 125
Val

<210> 1907
<211> 333
<212> DNA
<213> Homo sapiens

<400> 1907

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120
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180
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240
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atgcccgcga tccaggccga cgacctgtct nnc
333

<210> 1908
<211> 111
<212> PRT
<213> Homo sapiens

<400> 1908
Thr Arg Phe Asp Gln Arg Ile Arg Val Gly Gly Met Ala Glu Ile Val
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Gly Phe Asp Lys Lys Leu Arg Ala Ala Arg Arg Glu Thr Leu Glu Met
20 25 30
Cys Val Asn Asp Leu Phe Pro Gly Gly Gly Asp Thr Ser Lys Ala Thr
35 40 45
Phe Trp Thr Gly Leu Arg Pro Met Thr Pro Asp Gly Thr Pro Ile Val
50 55 60
Gly Arg Thr Pro Val Ser Asn Leu Phe Leu Asn Thr Gly His Gly Thr
65 70 75 80
Leu Gly Trp Thr Met Val Cys Gly Ser Gly Gln Leu Leu Ala Asp Leu
85 90 95
Ile Ser Gly Lys Met Pro Ala Ile Gln Ala Asp Asp Leu Ser Xaa
100 105 110

<210> 1909
<211> 2767
<212> DNA
<213> Homo sapiens

<400> 1909
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actccggagg agctggcagc cctctttgcg ccctacggca cggtcatgag ctgcgccgtc
180
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240
gccctgcacg gccacgagct gcggccgggg cgcgcgctcg tggtggaaat gtcgcgccca
300
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360
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420

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540
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720
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1260
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1380
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1440
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1560
gccactggct cctatggtgc cgcagcagcc tacggggccc aaccttctgc cactctggca
1620
gctccttacc gcactcagtc atcagcctca ttggctgctt cctatgctgc ccagcagcat
1680
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1800
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1860
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1920
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1980
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2040

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2100
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2160
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2280
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2340
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2400
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2460
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2520
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2580
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2700
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2760
tggaaaa
2767

<210> 1910
<211> 669
<212> PRT
<213> Homo sapiens

<400> 1910

Met	Lys	Ile	Phe	Val	Gly	Asn	Val	Asp	Gly	Ala	Asp	Thr	Thr	Pro	Glu
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Glu	Leu	Ala	Ala	Leu	Phe	Ala	Pro	Tyr	Gly	Thr	Val	Met	Ser	Cys	Ala
		20					25					30			
Val	Met	Lys	Gln	Phe	Ala	Phe	Val	His	Met	Arg	Glu	Asn	Ala	Gly	Ala
	35					40					45				
Leu	Arg	Ala	Ile	Glu	Ala	Leu	His	Gly	His	Glu	Leu	Arg	Pro	Gly	Arg
50					55					60					
Ala	Leu	Val	Val	Glu	Met	Ser	Arg	Pro	Arg	Pro	Leu	Asn	Thr	Trp	Lys
65				70					75					80	
Ile	Phe	Val	Gly	Asn	Val	Ser	Ala	Ala	Cys	Thr	Ser	Gln	Glu	Leu	Arg
			85					90					95		
Ser	Leu	Phe	Glu	Arg	Arg	Gly	Arg	Val	Ile	Glu	Cys	Asp	Val	Val	Lys
		100					105					110			
Asp	Tyr	Ala	Phe	Val	His	Met	Glu	Lys	Glu	Ala	Asp	Ala	Lys	Ala	Ala
	115					120					125				
Ile	Ala	Gln	Leu	Asn	Gly	Lys	Glu	Val	Lys	Gly	Lys	Arg	Ile	Asn	Val
130					135					140					
Glu	Leu	Ser	Thr	Lys	Gly	Gln	Lys	Lys	Gly	Pro	Gly	Leu	Ala	Val	Gln
145				150					155					160	
Ser	Gly	Asp	Lys	Thr	Lys	Lys	Pro	Gly	Ala	Gly	Asp	Thr	Ala	Phe	Pro

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                165                 170                 175
Gly Thr Gly Gly Phe Ser Ala Thr Phe Asp Tyr Gln Gln Ala Phe Gly
            180                 185                 190
Asn Ser Thr Gly Gly Phe Asp Gly Gln Ala Arg Gln Pro Thr Pro Pro
        195                 200                 205
Phe Phe Gly Arg Asp Arg Ser Pro Leu Arg Arg Ser Pro Pro Arg Ala
    210                 215                 220
Ser Tyr Val Ala Pro Leu Thr Ala Gln Pro Ala Thr Tyr Arg Ala Gln
225                 230                 235                 240
Pro Ser Val Ser Leu Gly Ala Ala Tyr Arg Ala Gln Pro Ser Ala Ser
                245                 250                 255
Leu Gly Val Gly Tyr Arg Thr Gln Pro Met Thr Ala Gln Ala Ala Ser
            260                 265                 270
Tyr Arg Ala Gln Pro Ser Val Ser Leu Gly Ala Pro Tyr Arg Gly Gln
        275                 280                 285
Leu Ala Ser Pro Ser Ser Gln Ser Ala Ala Ala Ser Ser Leu Gly Pro
    290                 295                 300
Tyr Gly Gly Ala Gln Pro Ser Ala Ser Ala Leu Ser Ser Tyr Gly Gly
305                 310                 315                 320
Gln Ala Ala Ala Ala Ser Ser Leu Asn Ser Tyr Gly Ala Gln Gly Ser
                325                 330                 335
Ser Leu Ala Ser Tyr Gly Asn Gln Pro Ser Ser Tyr Gly Ala Gln Ala
            340                 345                 350
Ala Ser Ser Tyr Gly Val Arg Ala Ala Ala Ser Ser Tyr Asn Thr Gln
        355                 360                 365
Gly Ala Ala Ser Ser Leu Gly Ser Tyr Gly Ala Gln Ala Ala Ser Tyr
    370                 375                 380
Gly Ala Gln Ser Ala Ala Ser Ser Leu Ala Tyr Gly Ala Gln Ala Ala
385                 390                 395                 400
Ser Tyr Asn Ala Gln Pro Ser Ala Ser Tyr Asn Ala Gln Ser Ala Pro
                405                 410                 415
Tyr Ala Ala Gln Gln Ala Ala Ser Tyr Ser Ser Gln Pro Ala Ala Tyr
            420                 425                 430
Val Ala Gln Pro Ala Thr Ala Ala Ala Tyr Ala Ser Gln Pro Ala Ala
        435                 440                 445
Tyr Ala Ala Gln Ala Thr Thr Pro Met Ala Gly Ser Tyr Gly Ala Gln
    450                 455                 460
Pro Val Val Gln Thr Gln Leu Asn Ser Tyr Gly Ala Gln Ala Ser Met
465                 470                 475                 480
Gly Leu Ser Gly Ser Tyr Gly Ala Gln Ser Ala Ala Ala Ala Thr Gly
                485                 490                 495
Ser Tyr Gly Ala Ala Ala Ala Tyr Gly Ala Gln Pro Ser Ala Thr Leu
            500                 505                 510
Ala Ala Pro Tyr Arg Thr Gln Ser Ser Ala Ser Leu Ala Ala Ser Tyr
        515                 520                 525
Ala Ala Gln Gln His Pro Gln Ala Ala Ala Ser Tyr Arg Gly Gln Pro
    530                 535                 540
Gly Asn Ala Tyr Asp Gly Ala Gly Gln Pro Ser Ala Ala Tyr Leu Ser
545                 550                 555                 560
Met Ser Gln Gly Ala Val Ala Asn Ala Asn Ser Thr Pro Pro Pro Tyr
                565                 570                 575
Glu Arg Thr Arg Leu Ser Pro Pro Arg Ala Ser Tyr Asp Asp Pro Tyr
            580                 585                 590
Lys Lys Ala Val Ala Met Ser Lys Arg Tyr Gly Ser Asp Arg Arg Leu
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595 600 605
Ala Glu Leu Ser Asp Tyr Arg Arg Leu Ser Glu Ser Gln Leu Ser Phe
610 615 620
Arg Arg Ser Pro Thr Lys Ser Ser Leu Asp Tyr Arg Arg Leu Pro Asp
625 630 635 640
Ala His Ser Asp Tyr Ala Arg Tyr Ser Gly Ser Tyr Asn Asp Tyr Leu
645 650 655
Arg Ala Ala Gln Met His Ser Gly Tyr Gln Arg Arg Met
660 665

<210> 1911
<211> 339
<212> DNA
<213> Homo sapiens

<400> 1911
ncggggtggc cggaatctac tcctagtgtc cagcttccct cctcttctgt ctttccctcg
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ggtgcgcgga tgcgtttgcg ccccctgctg cgttccgacg gtcatgagtg gcggcgtcag
120
cgcatcgacg atgaaagctt cctccgccca gttgagccga cccaagccgc accgtgggcg
180
gcagcgcata gccagcaggc gtggtggaat cacctgaagt acctgcgcac cgccgcgcgt
240
gaagcactgg tggtcccgct cgtcattgag gtggagggga aattcgcagg gcaggtaacc
300
ctgggaaaca ttcagcatgg cagcattcgc gattgctgg
339

<210> 1912
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1912
Xaa Gly Trp Pro Glu Ser Thr Pro Ser Val Gln Leu Pro Ser Ser Ser
1 5 10 15
Val Phe Pro Ser Gly Ala Arg Met Arg Leu Arg Pro Leu Leu Arg Ser
20 25 30
Asp Gly His Glu Trp Arg Arg Gln Arg Ile Asp Asp Glu Ser Phe Leu
35 40 45
Arg Pro Val Glu Pro Thr Gln Ala Ala Pro Trp Ala Ala Ala His Ser
50 55 60
Gln Gln Ala Trp Trp Asn His Leu Lys Tyr Leu Arg Thr Ala Ala Arg
65 70 75 80
Glu Ala Leu Val Val Pro Leu Val Ile Glu Val Glu Gly Lys Phe Ala
85 90 95
Gly Gln Val Thr Leu Gly Asn Ile Gln His Gly Ser Ile Arg Asp Cys
100 105 110
Trp

<210> 1913
<211> 767

<212> DNA
<213> Homo sapiens

<400> 1913
gtgcacaccg gttcacagcg atatttcagg caaattgaaa gcgtcagttc gataggctga
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atgcgaaatg ggggatttgt caccctcagg gaccggaagg aagggagcag tccgatggca
120
gcgccagtac tcgatctcgt cctcccagcc ttgtccgaaa cctccgccaa tctcatcggc
180
cagaggttgc gccagggatg tcacacctcc atccccacat cgaatctacg gtgagcttcg
240
tcccagctgt cgggcagtac aaggcacctc ggatcaagct ttcctggcgt gaactggtcc
300
tggtacccat caatgccacc cacctgcact ccaatccccc acaagttgtc caacacgccg
360
cagaattgcg tcgcagccac ccggaccttg ccatcaaggt ggcccgcccc accggaccag
420
caccggtcct cctcaacctc gtcgatacgc gattgcgtct ggcagctcat cgcgtccatg
480
cccaggagct ggactcactc gtattgtctt cccctgatgg cggcgattta cgtggctcgg
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caatgctgtc caggctgacc cggctgtggt cccagcacca ccaccttccg gtccgcatcg
600
ccaccaatcg tggtggggct actgcggtcg aggaggtcgt cgcccgcctg cgacaggagg
660
ggcgccgtca tatcgcagtg ggaagcctgt ggatttgcga cgacgagaat ttccgcattc
720
atactcgcca ggctttgcat gccggtgccg aggttgtcgc cgcaccg
767

<210> 1914
<211> 190
<212> PRT
<213> Homo sapiens

<400> 1914
Met Ser His Leu His Pro His Ile Glu Ser Thr Val Ser Phe Val Pro
 1   5   10   15
Ala Val Gly Gln Tyr Lys Ala Pro Arg Ile Lys Leu Ser Trp Arg Glu
            20   25   30
Leu Val Leu Val Pro Ile Asn Ala Thr His Leu His Ser Asn Pro Pro
        35   40   45
Gln Val Val Gln His Ala Ala Glu Leu Arg Arg Ser His Pro Asp Leu
    50   55   60
Ala Ile Lys Val Ala Arg Pro Thr Gly Pro Ala Pro Val Leu Leu Asn
65   70   75   80
Leu Val Asp Thr Arg Leu Arg Leu Ala Ala His Arg Val His Ala Gln
                85   90   95
Glu Leu Asp Ser Leu Val Leu Ser Ser Pro Asp Gly Gly Asp Leu Arg
            100   105   110
Gly Ser Ala Met Leu Ser Arg Leu Thr Arg Leu Trp Ser Gln His His
        115   120   125
His Leu Pro Val Arg Ile Ala Thr Asn Arg Gly Gly Ala Thr Ala Val

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    130                 135                 140
Glu Glu Val Val Ala Arg Leu Arg Gln Glu Gly Arg Arg His Ile Ala
145                 150                 155                 160
Val Gly Ser Leu Trp Ile Cys Asp Asp Glu Asn Phe Arg Ile His Thr
                165                 170                 175
Arg Gln Ala Leu His Ala Gly Ala Glu Val Val Ala Ala Pro
            180                 185                 190
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<210> 1915
<211> 571
<212> DNA
<213> Homo sapiens

<400> 1915
acgcgtccca ggccccacag gccccctctg gctctcaggc cccccgccca gtggccagga
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aggtgtgagc gcacgatggg cagtcacgcc gcacacacgc tctgctcatg tccctccccа
120
ggaccctctg accgggcaca agggcagctg tgaggacaag gccacagcca caaaccaacc
180
tggcacacac ggctcagggc gaggcactgc cccatggggc tgcatgatcc acgctcacag
240
gtgtcattgt ctatgctcag gggggcttgg caccatggga aacccaccca gaacacatgg
300
agaagccaca gcacaacctc agcgcccgcc atgcaggacc ctgggtctca cccattgcac
360
ccaccgtgcg ggacccctgc gcctcacccg gaacatccac agtgtgggac tgctgcgtct
420
cacccactgc acctgccgtg caggatccct gagtctcacc cgccgcaccc gccgtgcggg
480
atccctgagt ctcacccgcc gcacccgccg tacctgccgc atccgccatg cgggacccct
540
gcgtctcacc caccgcaccc gccgtgcggg a
571

<210> 1916
<211> 119
<212> PRT
<213> Homo sapiens

<400> 1916
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Met Gly Leu His Asp Pro Arg Ser Gln Val Ser Leu Ser Met Leu Arg
 1               5                  10                  15
Gly Ala Trp His His Gly Lys Pro Thr Gln Asn Thr Trp Arg Ser His
            20                  25                  30
Ser Thr Thr Ser Ala Pro Ala Met Gln Asp Pro Gly Ser His Pro Leu
        35                  40                  45
His Pro Pro Cys Gly Thr Pro Ala Pro His Pro Glu His Pro Gln Cys
    50                  55                  60
Gly Thr Ala Ala Ser His Pro Leu His Leu Pro Cys Arg Ile Pro Glu
65                  70                  75                  80
Ser His Pro Pro His Pro Pro Cys Gly Ile Pro Glu Ser His Pro Pro
                85                  90                  95
His Pro Pro Tyr Leu Pro His Pro Pro Cys Gly Thr Pro Ala Ser His
```

100 105 110
Pro Pro His Pro Pro Cys Gly
115

<210> 1917
<211> 360
<212> DNA
<213> Homo sapiens

<400> 1917
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gatatgtctt gggctgccat caccttgtgg cgcggtgtcg ttgcctccgc cttggaccgt
120
catccctatg gcccggtgaa gtcggtaaag gtagcaggtc cggccggcca cccagccccg
180
gatttcgccg ccggatggtt gctcgaccgc ttggcagttc ccgtacatcg cacagtggcc
240
gactccccaa ggagacactt cccggtgact catttgcagt tcaatcggga gacaacccac
300
gtagacgtcg atgtcattga cgagcgcacg gttcgtgtat gtgttccggg ttcgccggaa
360

<210> 1918
<211> 120
<212> PRT
<213> Homo sapiens

<400> 1918
Xaa Arg Val Thr Gly Glu Asp Leu Arg Thr Leu Ser Ala Gly Tyr Thr
1 5 10 15
Pro Gly Asp Ser Asp Met Ser Trp Ala Ala Ile Thr Leu Trp Arg Gly
20 25 30
Val Val Ala Ser Ala Leu Asp Arg His Pro Tyr Gly Pro Val Lys Ser
35 40 45
Val Lys Val Ala Gly Pro Ala Gly His Pro Ala Pro Asp Phe Ala Ala
50 55 60
Gly Trp Leu Leu Asp Arg Leu Ala Val Pro Val His Arg Thr Val Ala
65 70 75 80
Asp Ser Pro Arg Arg His Phe Pro Val Thr His Leu Gln Phe Asn Arg
85 90 95
Glu Thr Thr His Val Asp Val Asp Val Ile Asp Glu Arg Thr Val Arg
100 105 110
Val Cys Val Pro Gly Ser Pro Glu
115 120

<210> 1919
<211> 354
<212> DNA
<213> Homo sapiens

<400> 1919
nncggccgca gctgtgtcca ctgcgctgtc cctgccacct cggccatctg cctctctctt
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ccaggctgca gccatccctc ctgcactgct gaggcctggc cacgcgcatc ncggccacgc
120
ccacctccat cctctttgcc ccttactaaa cactgggagc ccgcccgccc gcgacaggcc
180
aggccagcgg gaaggtgtag acgaacagcc caaaggattc agcagtgtaa gtaccccacc
240
tacgcactta caaagtgcag gccaccgccc agccccacct ccagacacag gcggaggcca
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agctcgcggg caccgtatca tcccgtgccg tctccaccct acccctgcca attg
354

<210> 1920
<211> 118
<212> PRT
<213> Homo sapiens

<400> 1920
Xaa Gly Arg Ser Cys Val His Cys Ala Val Pro Ala Thr Ser Ala Ile
1 5 10 15
Cys Leu Ser Leu Pro Gly Cys Ser His Pro Ser Cys Thr Ala Glu Ala
20 25 30
Trp Pro Arg Ala Ser Arg Pro Arg Pro Pro Pro Ser Ser Leu Pro Leu
35 40 45
Thr Lys His Trp Glu Pro Ala Arg Pro Arg Gln Ala Arg Pro Ala Gly
50 55 60
Arg Cys Arg Arg Thr Ala Gln Arg Ile Gln Gln Cys Lys Tyr Pro Thr
65 70 75 80
Tyr Ala Leu Thr Lys Cys Arg Pro Pro Pro Ser Pro Thr Ser Arg His
85 90 95
Arg Arg Arg Pro Ser Ser Arg Ala Pro Tyr His Pro Val Pro Ser Pro
100 105 110
Pro Tyr Pro Cys Gln Leu
115

<210> 1921
<211> 357
<212> DNA
<213> Homo sapiens

<400> 1921
gaattcatct ggaggcagag agatggggaa gcgggtggga gaagagcaag aacggaaact
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atttttaata caaatccagt catggtattg tatacacagc agcctctgtc ttccagaaac
120
ctacacggcc gccacaccaa agttaatgcc accaggcgtc atcacacaga tgtgaggtgc
180
aggtgccact ccacagccgt gggcagacct gggagcccag ctcctcctgg tttcaccctc
240
cacactgccc accccatcct tctctcccag tctccactcc atcgaagcct cccagatgac
300
ttcatgtggg gacaggagaa ctacagatca tggctgagaa gggcgcngtg tngtcca
357

<210> 1922

<211> 92
<212> PRT
<213> Homo sapiens

<400> 1922
Met Val Leu Tyr Thr Gln Gln Pro Leu Ser Ser Arg Asn Leu His Gly
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Arg His Thr Lys Val Asn Ala Thr Arg Arg His His Thr Asp Val Arg
20 25 30
Cys Arg Cys His Ser Thr Ala Val Gly Arg Pro Gly Ser Pro Ala Pro
35 40 45
Pro Gly Phe Thr Leu His Thr Ala His Pro Ile Leu Leu Ser Gln Ser
50 55 60
Pro Leu His Arg Ser Leu Pro Asp Asp Phe Met Trp Gly Gln Glu Asn
65 70 75 80
Tyr Arg Ser Trp Leu Arg Arg Ala Xaa Cys Xaa Pro
85 90

<210> 1923
<211> 368
<212> DNA
<213> Homo sapiens

<400> 1923
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ggtagtgcac agaagaaaga atggttcagc aacattaaac tctcaggcta tggaatgacc
120
cagtatcaat atactgatca agagggaagc aaaggccatt catttaatct gcgattgttc
180
ccgttgcctt taaacggacg tatcttaaat gacttttatt ggaaggcaca ggcccaattc
240
aatggaaaca catcgacatt gggaagcagt ccacgtcttg tagacctatt tgtagagtgg
300
cagaaatatg attatttcaa ggtgaagtta ggccagttta agcgaccatt cacgtttgaa
360
aatcccag
368

<210> 1924
<211> 119
<212> PRT
<213> Homo sapiens

<400> 1924
Met Val Arg Lys Gly Leu Cys Val Ala Leu Leu Val Leu Val Thr Leu
1 5 10 15
Ser Gly Ser Ala Gln Lys Lys Glu Trp Phe Ser Asn Ile Lys Leu Ser
20 25 30
Gly Tyr Gly Met Thr Gln Tyr Gln Tyr Thr Asp Gln Glu Gly Ser Lys
35 40 45
Gly His Ser Phe Asn Leu Arg Leu Phe Pro Leu Pro Leu Asn Gly Arg
50 55 60
Ile Leu Asn Asp Phe Tyr Trp Lys Ala Gln Ala Gln Phe Asn Gly Asn

65 70 75 80
Thr Ser Thr Leu Gly Ser Ser Pro Arg Leu Val Asp Leu Phe Val Glu
85 90 95
Trp Gln Lys Tyr Asp Tyr Phe Lys Val Lys Leu Gly Gln Phe Lys Arg
100 105 110
Pro Phe Thr Phe Glu Asn Pro
115

<210> 1925
<211> 427
<212> DNA
<213> Homo sapiens

<400> 1925
actagtgttt ccagcaggca gcgatttaat tgttcttgca ttgaaaccca gtgtggcaag
60
ccccccctgtg atttgaggct aatccctccc caccctgttc tggcacatgt gcggtgccca
120
gggctccccc caggctgtga gcagataaag ccctgcgtgg cttcacaaca gtgactggtt
180
ctgagaaaca ggtccttgta caagcgacag ggagtgctca caccagatgt ggcagcccct
240
ccacgccagg ctgtgtggtg cagccgcctg gtatatgtgt ccatcgctga tgaaaacagc
300
gttgtgtggt gcatgactgt tgtctgtttt cttcatggaa acaaggaaac ctaagcatta
360
aaacaacacc atccacgtct ggttccttag agcaaatgga agcaccaggc tctggtgcac
420
ggcgcgc
427

<210> 1926
<211> 104
<212> PRT
<213> Homo sapiens

<400> 1926
Met His His Thr Thr Leu Phe Ser Ser Ala Met Asp Thr Tyr Thr Arg
1 5 10 15
Arg Leu His His Thr Ala Trp Arg Gly Gly Ala Ala Thr Ser Gly Val
20 25 30
Ser Thr Pro Cys Arg Leu Tyr Lys Asp Leu Phe Leu Arg Thr Ser His
35 40 45
Cys Cys Glu Ala Thr Gln Gly Phe Ile Cys Ser Gln Pro Gly Gly Ser
50 55 60
Pro Gly His Arg Thr Cys Ala Arg Thr Gly Trp Gly Gly Ile Ser Leu
65 70 75 80
Lys Ser Gln Gly Gly Leu Pro His Trp Val Ser Met Gln Glu Gln Leu
85 90 95
Asn Arg Cys Leu Leu Glu Thr Leu
100

<210> 1927
<211> 516

<212> DNA
<213> Homo sapiens

<400> 1927
nntctagaag actccaccta cttttcccca gactttcagc tctattctgg gaggcatgaa
60
acatctgctt tgacggtgga ggcaaccagt agcatcaggg aaaaagttgt tgaagatcct
120
ctttgtaact tccactcccc aaacttcctg aggatctcag aggtggaaat gagaggttcc
180
gaggatgcgg cagctggaac agtattgcag cggctgatcc aggaacaact gcggtatggc
240
accccaaccg agaacatgaa cttgctggcc attcagcacc aggccacagg gagtgcagga
300
ccagcccatc ctacaaacaa cttttcttcc acggaaaacc tcactcaaga agacccacaa
360
atggtctacc agtcagcacg ccaagaaccg cagggtcaag aacaccagng tgganncaat
420
acggtgatgg agaaacaggt ccggtccacg cagcctcagc agaacaacga ggaactgccc
480
acttacgagg aggccaaagc acagcccttc acgcgt
516

<210> 1928
<211> 172
<212> PRT
<213> Homo sapiens

<400> 1928
Xaa Leu Glu Asp Ser Thr Tyr Phe Ser Pro Asp Phe Gln Leu Tyr Ser
 1   5   10   15
Gly Arg His Glu Thr Ser Ala Leu Thr Val Glu Ala Thr Ser Ser Ile
            20   25   30
Arg Glu Lys Val Val Glu Asp Pro Leu Cys Asn Phe His Ser Pro Asn
        35   40   45
Phe Leu Arg Ile Ser Glu Val Glu Met Arg Gly Ser Glu Asp Ala Ala
    50   55   60
Ala Gly Thr Val Leu Gln Arg Leu Ile Gln Glu Gln Leu Arg Tyr Gly
65   70   75   80
Thr Pro Thr Glu Asn Met Asn Leu Leu Ala Ile Gln His Gln Ala Thr
                85   90   95
Gly Ser Ala Gly Pro Ala His Pro Thr Asn Asn Phe Ser Ser Thr Glu
            100   105   110
Asn Leu Thr Gln Glu Asp Pro Gln Met Val Tyr Gln Ser Ala Arg Gln
        115   120   125
Glu Pro Gln Gly Gln Glu His Gln Xaa Gly Xaa Asn Thr Val Met Glu
    130   135   140
Lys Gln Val Arg Ser Thr Gln Pro Gln Gln Asn Asn Glu Glu Leu Pro
145   150   155   160
Thr Tyr Glu Glu Ala Lys Ala Gln Pro Phe Thr Arg
                165   170

<210> 1929
<211> 843

<212> DNA
<213> Homo sapiens

<400> 1929
nnccgcggac actcagggtc tggggtccct cttccccaag aggcctgact gcctgggtgt
60
tctccaggta catgtccttc aaggagaaat acacttcctg gcctgggcct gggccagggg
120
ccttctgggc cttgtctgga gtgcccacag cagaggctgg cttcctggta ctatctgtgc
180
cagaggaccc aggcccccgt gcagccctgc ctctgggctg ggtctgaacc tgctccacgc
240
ccacgggccc ctgagtccca caggagtcag gctcgtctga gctggggatg cagttttctg
300
aagaacggcg gctttgggct gccttctcta actctggctt ccgcaccttg cttggattcc
360
tcatctttct ttttcttctt ggccccactc tcctctttga gggctctctg aggccccagc
420
tccatggcgt cacagatgta tgtcagcaag ccatgctctc cgtcctctcc attctcgggg
480
gcagcctccc cgttggtggt cacttctcca gaagcaaact gttgatcagg cccaaacctg
540
agtgctgagc agtctcagtc tctccctcct gccaagccgc cagggtccca ccctcaggct
600
ccctggtagg gaccgagggg cccggcgctt gagccccgct caatcgccgc tttcgctgga
660
agcggtcggg gctgagcttg cgcagagtgt cgacctcccc aggcaccgcc ttctcgtgct
720
tccagctctg ctcgatctcg cgcagctttg ccgcagcctt gcgcttcaac ttggcgaacc
780
agcgctggtg gatcttgtac tcagtcatgg tgcccacctc ccaggaccct gagcaggaca
840
caa
843

<210> 1930
<211> 120
<212> PRT
<213> Homo sapiens

<400> 1930
Leu Pro Gly Cys Ser Pro Gly Thr Cys Pro Ser Arg Arg Asn Thr Leu
 1   5   10   15
Pro Gly Leu Gly Leu Gly Gln Gly Pro Ser Gly Pro Cys Leu Glu Cys
            20   25   30
Pro Gln Gln Arg Leu Ala Ser Trp Tyr Tyr Leu Cys Gln Arg Thr Gln
        35   40   45
Ala Pro Val Gln Pro Cys Leu Trp Ala Gly Ser Glu Pro Ala Pro Arg
    50   55   60
Pro Arg Ala Pro Glu Ser His Arg Ser Gln Ala Arg Leu Ser Trp Gly
65   70   75   80
Cys Ser Phe Leu Lys Asn Gly Gly Phe Gly Leu Pro Ser Leu Thr Leu
                85   90   95
Ala Ser Ala Pro Cys Leu Asp Ser Ser Ser Phe Phe Phe Phe Leu Ala

```
            100                 105                 110
Pro Leu Ser Ser Leu Arg Ala Leu
        115                 120
```

<210> 1931
<211> 719
<212> DNA
<213> Homo sapiens

<400> 1931
acgcgtaggc ctgagccgct ccacagccct ggggagggca gaaaaggagg aaagtaggca
60
gtgcaagaaa caggaggaaa ccccccagag cgcagcctcc tggaagcgga agggagcact
120
gaagaggagg tggttagtgg tgtcagaagc tgctgagaag ccagttagat aaagcggaga
180
agcttcctac taggacagct tcctcccagc ccagtgtggc cacgctggtg tcctcggtga
240
ccagacacgt ggccatgaat ttctcagtgt gctttattgt tgattaaatg cagtcggctc
300
acgaggctga ctttggaaac aggaggtccg tgggtcgtgg aataagaaag ggcatcatgg
360
ttgcagagga agggaaggaa gcccacggct gccttgggga gctttctgaa aggcaggtct
420
gatcatgcct ctctgggcta cggtctcctc acggtggctc ctggttggaa ctgaagtggt
480
ccccttggtc cctctctccc atctcagcat tagccaggac ttttggcttg gcggccccag
540
cagggctgcc cccttgcaac acttcttttc ccacatgatc gtgccttcca aacctacttc
600
cagcgtcgcc ctcttcaggg agcctttcat aaccacctct cccttccact ggctaaagat
660
gaggttgagc aactgcagga cttgggacct tgttcctgcc cctgtggctg cctggatcc
719

<210> 1932
<211> 98
<212> PRT
<213> Homo sapiens

<400> 1932
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Met Pro Leu Trp Ala Thr Val Ser Ser Arg Trp Leu Leu Val Gly Thr
 1               5                  10                  15
Glu Val Val Pro Leu Val Pro Leu Ser His Leu Ser Ile Ser Gln Asp
            20                  25                  30
Phe Trp Leu Gly Gly Pro Ser Arg Ala Ala Pro Leu Gln His Phe Phe
        35                  40                  45
Ser His Met Ile Val Pro Ser Lys Pro Thr Ser Ser Val Ala Leu Phe
    50                  55                  60
Arg Glu Pro Phe Ile Thr Thr Ser Pro Phe His Trp Leu Lys Met Arg
65                  70                  75                  80
Leu Ser Asn Cys Arg Thr Trp Asp Leu Val Pro Ala Pro Val Ala Ala
                85                  90                  95
Trp Ile
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<210> 1933
<211> 295
<212> DNA
<213> Homo sapiens

<400> 1933
ggcgccgagc tgtgggcggc catggagcgc atgcctgccg acctgattat cctcgacctg
60
atgctgccgg gggataacgg cctcttgctg tgccagcgcc tgcgccagca atacgcaaca
120
ccagtgatca tgctgaccgc catgggcgaa ctgagtgatc gcgtgggggg cctggaaatg
180
ggcgccgatg actacctgaa caaacctttc gatgcccgtg aattacttgc ccgggtgcgc
240
gctgtactgc gtccggcgtg tgaaaaccga ccgacgttgg gcgacgtgtc gcgcc
295

<210> 1934
<211> 98
<212> PRT
<213> Homo sapiens

<400> 1934
Gly Ala Glu Leu Trp Ala Ala Met Glu Arg Met Pro Ala Asp Leu Ile
1 5 10 15
Ile Leu Asp Leu Met Leu Pro Gly Asp Asn Gly Leu Leu Leu Cys Gln
20 25 30
Arg Leu Arg Gln Gln Tyr Ala Thr Pro Val Ile Met Leu Thr Ala Met
35 40 45
Gly Glu Leu Ser Asp Arg Val Gly Gly Leu Glu Met Gly Ala Asp Asp
50 55 60
Tyr Leu Asn Lys Pro Phe Asp Ala Arg Glu Leu Leu Ala Arg Val Arg
65 70 75 80
Ala Val Leu Arg Pro Ala Cys Glu Asn Arg Pro Thr Leu Gly Asp Val
85 90 95
Ser Arg

<210> 1935
<211> 298
<212> DNA
<213> Homo sapiens

<400> 1935
accggtgtgg cgggcgcggc cttcaccacc atcggctcca ccgggccgac ggcgggttcg
60
caatacatcg tcgatacctt cctggtagtg gtgttcgggg gggcccaaag cctgttcggc
120
cccatcgcct cggcgttcgt gattgcccag acccaatcgc tgtcggagtt tttcctcagt
180
ggctcgatgg ccaaggtgct gaccttgtcg tcggtgattc tgatcctgat gctgcgcccg
240

caagggttgt tctccatcaa agtgcgcaag taaaggcgag cagataaggg tttaagca
298

<210> 1936
<211> 90
<212> PRT
<213> Homo sapiens

<400> 1936
Thr Gly Val Ala Gly Ala Ala Phe Thr Thr Ile Gly Ser Thr Gly Pro
1 5 10 15
Thr Ala Gly Ser Gln Tyr Ile Val Asp Thr Phe Leu Val Val Val Phe
20 25 30
Gly Gly Ala Gln Ser Leu Phe Gly Pro Ile Ala Ser Ala Phe Val Ile
35 40 45
Ala Gln Thr Gln Ser Leu Ser Glu Phe Phe Leu Ser Gly Ser Met Ala
50 55 60
Lys Val Leu Thr Leu Ser Ser Val Ile Leu Ile Leu Met Leu Arg Pro
65 70 75 80
Gln Gly Leu Phe Ser Ile Lys Val Arg Lys
85 90

<210> 1937
<211> 513
<212> DNA
<213> Homo sapiens

<400> 1937
gcacggcgca cagtaacacc aactcgaaag agaccttatg aatgcaaggt gtgcgggaaa
60
gcctttaatt ctcccaattt atttcaaatc catcaaagaa ctcacactgg aaagaggtcc
120
tataaatgta gggaaatagt gagagccttc acagtttcca gtttctttcg aaaacatgga
180
aaaatgcata ctggagaaaa acgctatgaa tgtaaatact gtggaaaacc tatcgattat
240
cccagtttat ttcaaattca tgttagaact cactctggag aaaaacccta caaatgtaaa
300
caatgtggta aagccttcat ttccgcaggt tacgttcgga cacatgaaat cagatctcac
360
gcgctggaga aatcccacca atgtcaggaa tgtgggaaga aactcagttg ttccagttcc
420
cttcacagac atgaaagaac tcatagtgga ggaaaactct acgaatgtca aaaatgtgac
480
caagtcttta gatgtcccac gtcccttcac gcg
513

<210> 1938
<211> 171
<212> PRT
<213> Homo sapiens

<400> 1938
Ala Arg Arg Thr Val Thr Pro Thr Arg Lys Arg Pro Tyr Glu Cys Lys

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 1               5                  10                  15
Val Cys Gly Lys Ala Phe Asn Ser Pro Asn Leu Phe Gln Ile His Gln
            20                  25                  30
Arg Thr His Thr Gly Lys Arg Ser Tyr Lys Cys Arg Glu Ile Val Arg
        35                  40                  45
Ala Phe Thr Val Ser Ser Phe Phe Arg Lys His Gly Lys Met His Thr
    50                  55                  60
Gly Glu Lys Arg Tyr Glu Cys Lys Tyr Cys Gly Lys Pro Ile Asp Tyr
65                  70                  75                  80
Pro Ser Leu Phe Gln Ile His Val Arg Thr His Ser Gly Glu Lys Pro
                85                  90                  95
Tyr Lys Cys Lys Gln Cys Gly Lys Ala Phe Ile Ser Ala Gly Tyr Val
            100                 105                 110
Arg Thr His Glu Ile Arg Ser His Ala Leu Glu Lys Ser His Gln Cys
        115                 120                 125
Gln Glu Cys Gly Lys Lys Leu Ser Cys Ser Ser Ser Leu His Arg His
    130                 135                 140
Glu Arg Thr His Ser Gly Gly Lys Leu Tyr Glu Cys Gln Lys Cys Asp
145                 150                 155                 160
Gln Val Phe Arg Cys Pro Thr Ser Leu His Ala
                165                 170
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<210> 1939
<211> 1233
<212> DNA
<213> Homo sapiens

<400> 1939

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gccggcagcg ccgctcccca gggagggagt ccgcagcctg aggtcttctc caagaaaaaa
60
aaagaaaaaa aaacaacatg gctgcaaagg agaaactgga ggcagtgtta aatgtggccc
120
tgagggtgcc aagcatcatg ctgttggatg tcctgtacag atgggatgtc agctcctttt
180
tccagcagat ccaaagaagt agccttagta ataaccctct tttccagtat aagtatttgg
240
ctcttaatat gcattatgta ggttatatct taagtgtggt gctgctaaca ttgcccaggc
300
agcatctggt tcagctttat ctatattttt tgactgctct gctcctctat gctggacatc
360
aaatttccag ggactatgtt cggagtgaac tggggtttgc ctatgaggga ccaatgtatt
420
tagaacctct ctctatgaat cggtttacca cagccttaat aggtcagttg gtggtgtgta
480
ctttatgctc ctgtgtcatg aaaacaaagc agatttggct gttttcagct cacatgcttc
540
ctctgctagc acgactctgc cttgttcctt tggagacaat tgctatcatc aataaatttg
600
ctatgatttt tactggattg gaagttctct attttcttgg gtctaatctt ttggtacctt
660
ataaccttgc taaatctgca tacagagaat tggttcaggt agtggaggta tatggccttc
720
tcgccttggg aatgtccctg tggaatcaac tggtagtccc tgttcttttc atggttttct
780
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ggctcgtctt atttgctctt cagatttact cctatttcag tactcgagat cagcctgcat
840
cacgtgagag gcttcttttc ctttttctga caaggtaatt aataagagcc tatgatacta
900
tatataacct tagaaagaga aaactttgat ctaggaatag taagttttgc agattacttt
960
tatcgttcat gttacacaac ttcgtatttt gttaagatag gattttcatt cactggatac
1020
ctaggtttgg caatgcagag aggtgctaac ataataatgt ggtttatttg gctgcactat
1080
ggaccagagt gtagcaaatg atttgtggaa aggtacatag cacatcgtaa aagtattttt
1140
tcaatttcaa gttaaaatta ttgggtcaat cagaaaaaag tatattataa aaataacatt
1200
tattgagtat tttaaatgta ccataccatt naa
1233

<210> 1940
<211> 266
<212> PRT
<213> Homo sapiens

<400> 1940
Met Ala Ala Lys Glu Lys Leu Glu Ala Val Leu Asn Val Ala Leu Arg
1 5 10 15
Val Pro Ser Ile Met Leu Leu Asp Val Leu Tyr Arg Trp Asp Val Ser
20 25 30
Ser Phe Phe Gln Gln Ile Gln Arg Ser Ser Leu Ser Asn Asn Pro Leu
35 40 45
Phe Gln Tyr Lys Tyr Leu Ala Leu Asn Met His Tyr Val Gly Tyr Ile
50 55 60
Leu Ser Val Val Leu Leu Thr Leu Pro Arg Gln His Leu Val Gln Leu
65 70 75 80
Tyr Leu Tyr Phe Leu Thr Ala Leu Leu Leu Tyr Ala Gly His Gln Ile
85 90 95
Ser Arg Asp Tyr Val Arg Ser Glu Leu Gly Phe Ala Tyr Glu Gly Pro
100 105 110
Met Tyr Leu Glu Pro Leu Ser Met Asn Arg Phe Thr Thr Ala Leu Ile
115 120 125
Gly Gln Leu Val Val Cys Thr Leu Cys Ser Cys Val Met Lys Thr Lys
130 135 140
Gln Ile Trp Leu Phe Ser Ala His Met Leu Pro Leu Leu Ala Arg Leu
145 150 155 160
Cys Leu Val Pro Leu Glu Thr Ile Ala Ile Ile Asn Lys Phe Ala Met
165 170 175
Ile Phe Thr Gly Leu Glu Val Leu Tyr Phe Leu Gly Ser Asn Leu Leu
180 185 190
Val Pro Tyr Asn Leu Ala Lys Ser Ala Tyr Arg Glu Leu Val Gln Val
195 200 205
Val Glu Val Tyr Gly Leu Leu Ala Leu Gly Met Ser Leu Trp Asn Gln
210 215 220
Leu Val Val Pro Val Leu Phe Met Val Phe Trp Leu Val Leu Phe Ala
225 230 235 240
Leu Gln Ile Tyr Ser Tyr Phe Ser Thr Arg Asp Gln Pro Ala Ser Arg

245 250 255
Glu Arg Leu Leu Phe Leu Phe Leu Thr Arg
260 265

<210> 1941
<211> 411
<212> DNA
<213> Homo sapiens

<400> 1941
ctggggccct gccccacagc atcatgatgg ggaaactccc cctgggggtc gtctcccctt
60
atgtgaagat gagttcgggg ggctacacgg acccccctgaa attctacgcc accagctact
120
gcacagccta cggtcgggag gatttcaagc cccgtgtggg cagtcacgta ggcaccggct
180
acaaatcaaa tttccagccc gtggtctcat gccaagccag tctggaggcc ttagacaacc
240
cggccagggg ggaacaagcc caggaccatt tccagtctgt ggccagccag agctaccgcc
300
ccctggaggt gcctgacggc aagcatcccc tgccctggag catgcgccag accagctcag
360
gctatgggcg ggagaagccc agtgcgggtc cccccaccaa ggaggtccgg a
411

<210> 1942
<211> 129
<212> PRT
<213> Homo sapiens

<400> 1942
Met Met Gly Lys Leu Pro Leu Gly Val Val Ser Pro Tyr Val Lys Met
1 5 10 15
Ser Ser Gly Gly Tyr Thr Asp Pro Leu Lys Phe Tyr Ala Thr Ser Tyr
20 25 30
Cys Thr Ala Tyr Gly Arg Glu Asp Phe Lys Pro Arg Val Gly Ser His
35 40 45
Val Gly Thr Gly Tyr Lys Ser Asn Phe Gln Pro Val Val Ser Cys Gln
50 55 60
Ala Ser Leu Glu Ala Leu Asp Asn Pro Ala Arg Gly Glu Gln Ala Gln
65 70 75 80
Asp His Phe Gln Ser Val Ala Ser Gln Ser Tyr Arg Pro Leu Glu Val
85 90 95
Pro Asp Gly Lys His Pro Leu Pro Trp Ser Met Arg Gln Thr Ser Ser
100 105 110
Gly Tyr Gly Arg Glu Lys Pro Ser Ala Gly Pro Pro Thr Lys Glu Val
115 120 125
Arg

<210> 1943
<211> 386
<212> DNA
<213> Homo sapiens

<400> 1943
nagaaacatt cagggctcca acagggtgga aaacatgagg ctgcaggatg tttaacagga
60
gtctttgctg cagctcctct tggagccttt aacgagatac tatcatgcct atgaactgcc
120
acacagatgt acatggcata gcactgccca aaagtatcag cccaaggaac cctactttcc
180
ccagcaacat ctaactcaga aatgctgatc tttggcctca atctggtccc aaaatacctc
240
cagggtattt tgggcttcgg tgtgttcaca cacttggtca tgtaaatctg aacacagact
300
ctctctgcct tggcaagaac cccccacacc cccatagata attacaccct ttggttctcc
360
ctctgcaatc tcacctgcta gagacg
386

<210> 1944
<211> 111
<212> PRT
<213> Homo sapiens

<400> 1944
Met Gly Val Trp Gly Val Leu Ala Lys Ala Glu Arg Val Cys Val Gln
 1   5   10   15
Ile Tyr Met Thr Lys Cys Val Asn Thr Pro Lys Pro Lys Ile Pro Trp
            20   25   30
Arg Tyr Phe Gly Thr Arg Leu Arg Pro Lys Ile Ser Ile Ser Glu Leu
        35   40   45
Asp Val Ala Gly Glu Ser Arg Val Pro Trp Ala Asp Thr Phe Gly Gln
    50   55   60
Cys Tyr Ala Met Tyr Ile Cys Val Ala Val His Arg His Asp Ser Ile
65   70   75   80
Ser Leu Lys Ala Pro Arg Gly Ala Ala Ala Lys Thr Pro Val Lys His
                85   90   95
Pro Ala Ala Ser Cys Phe Pro Pro Cys Trp Ser Pro Glu Cys Phe
            100   105   110

<210> 1945
<211> 443
<212> DNA
<213> Homo sapiens

<400> 1945
nacgcgtcac gaagcgcgct cggcccacgt ggctccaagg gcgtccacgc gcccctcctc
60
gaccgattgg tgtcgaacat ggcacggtgg catgcgacgc gcaccaagat ccagctcaag
120
ctcgcgatcc agcgantcgg catgctacag gagaaaaaag ccgcactgca taaaaaagtg
180
cgactggaaa ttgcggacnn tcgtagacgc caaaagcttg aatctgcgcg cgtcaaaacc
240
gaatcgctga tcatggacga tatacatttg gagttgcttg aactgcttga gctctactgt
300

gagacactct atgccagatt cggattacta gaaggacgcg acaatgagcc tgatgatgcg
360
atccgcgagc cgatgatcgc cattattcat gcggctcatc gcacagaggt gaaggaacta
420
catgtgctcc aaaacatgct gaa
443

<210> 1946
<211> 147
<212> PRT
<213> Homo sapiens

<400> 1946
Xaa Ala Ser Arg Ser Ala Leu Gly Pro Arg Gly Ser Lys Gly Val His
1 5 10 15
Ala Pro Leu Leu Asp Arg Leu Val Ser Asn Met Ala Arg Trp His Ala
20 25 30
Thr Arg Thr Lys Ile Gln Leu Lys Leu Ala Ile Gln Arg Xaa Gly Met
35 40 45
Leu Gln Glu Lys Lys Ala Ala Leu His Lys Lys Val Arg Leu Glu Ile
50 55 60
Ala Asp Xaa Arg Arg Arg Gln Lys Leu Glu Ser Ala Arg Val Lys Thr
65 70 75 80
Glu Ser Leu Ile Met Asp Asp Ile His Leu Glu Leu Leu Glu Leu Leu
85 90 95
Glu Leu Tyr Cys Glu Thr Leu Tyr Ala Arg Phe Gly Leu Leu Glu Gly
100 105 110
Arg Asp Asn Glu Pro Asp Asp Ala Ile Arg Glu Pro Met Ile Ala Ile
115 120 125
Ile His Ala Ala His Arg Thr Glu Val Lys Glu Leu His Val Leu Gln
130 135 140
Asn Met Leu
145

<210> 1947
<211> 472
<212> DNA
<213> Homo sapiens

<400> 1947
cggccgtgta ggccgtgacg gtgaccaaca gagccacagc gggcccgctg taggcgggag
60
gactgtgccg caggtgcagg agggtcagat ggaaacaaaa ggcgcaggcg gcctccacaa
120
gcgccccgtg gggcacggat gtgcgcaggg ccgagctgca gctctgggcc atgaggctct
180
gcagcaggtg caggtcactg agctcccagg cccagcagag gcgcgtcagg gtgcaggcgg
240
cctgcatgcc cagcccctgt gccgccagct tcagcagcgt gccaggcaga gactcctcgg
300
ccatgaggaa ctcctgcagg gacacggtgg ggttggccga ggccccgtcc aaggtgaccc
360
cgtgcgccag gaagagcagg aagagcaggg tgagcagcag gtcaggccca aagtccccag
420

cccagggccc gagctcgaac agcgtcctca tctccaggaa gcaggccccg ag
472

<210> 1948
<211> 150
<212> PRT
<213> Homo sapiens

<400> 1948
Met Arg Thr Leu Phe Glu Leu Gly Pro Trp Ala Gly Asp Phe Gly Pro
1 5 10 15
Asp Leu Leu Leu Thr Leu Leu Phe Leu Leu Phe Leu Ala His Gly Val
20 25 30
Thr Leu Asp Gly Ala Ser Ala Asn Pro Thr Val Ser Leu Gln Glu Phe
35 40 45
Leu Met Ala Glu Glu Ser Leu Pro Gly Thr Leu Leu Lys Leu Ala Ala
50 55 60
Gln Gly Leu Gly Met Gln Ala Ala Cys Thr Leu Thr Arg Leu Cys Trp
65 70 75 80
Ala Trp Glu Leu Ser Asp Leu His Leu Leu Gln Ser Leu Met Ala Gln
85 90 95
Ser Cys Ser Ser Ala Leu Arg Thr Ser Val Pro His Gly Ala Leu Val
100 105 110
Glu Ala Ala Cys Ala Phe Cys Phe His Leu Thr Leu Leu His Leu Arg
115 120 125
His Ser Pro Pro Ala Tyr Ser Gly Pro Ala Val Ala Leu Leu Val Thr
130 135 140
Val Thr Ala Tyr Thr Ala
145 150

<210> 1949
<211> 395
<212> DNA
<213> Homo sapiens

<400> 1949
acgcgttgag ggaggcgaca tgcttcatga gcgcttggcg ccactgctca agcgacatct
60
gccccttgct gatgttgcaa ggcggacagg acggcatgta attcgactcg acgtcacgct
120
ccggatgcct cgacgggacg ctcacaagct tccattggcc attcgcgggt cgcttggtct
180
cgaccgcgcg tacaaccggg tctacatggt cgccatgcca ccgatcgggc aatggcattc
240
cacagtacgc gcagcggccg tcgtatttgc gccggagccg atcgcgctgt gctttcgtca
300
gccggctcac gctttatgct ccacggcagg tgtggcagca tcctggcagg cgactccaag
360
atccgcgcct gcgtccagct tgacggcgcc gggtt
395

<210> 1950
<211> 125
<212> PRT

<213> Homo sapiens

<400> 1950
Met Leu His Glu Arg Leu Ala Pro Leu Leu Lys Arg His Leu Pro Leu
1 5 10 15
Ala Asp Val Ala Arg Arg Thr Gly Arg His Val Ile Arg Leu Asp Val
20 25 30
Thr Leu Arg Met Pro Arg Arg Asp Ala His Lys Leu Pro Leu Ala Ile
35 40 45
Arg Gly Ser Leu Gly Leu Asp Arg Ala Tyr Asn Arg Val Tyr Met Val
50 55 60
Ala Met Pro Pro Ile Gly Gln Trp His Ser Thr Val Arg Ala Ala Ala
65 70 75 80
Val Val Phe Ala Pro Glu Pro Ile Ala Leu Cys Phe Arg Gln Pro Ala
85 90 95
His Ala Leu Cys Ser Thr Ala Gly Val Ala Ala Ser Trp Gln Ala Thr
100 105 110
Pro Arg Ser Ala Pro Ala Ser Ser Leu Thr Ala Pro Gly
115 120 125

<210> 1951
<211> 363
<212> DNA
<213> Homo sapiens

<400> 1951
cggccgccgc ctctccgctc ccgggccccc gccgccaccg cgccccccgc gggagatgga
60
acagcggaac cggctcggtg ccctcggata cctgccgcct ctgctgctgc atgccctgct
120
gctcttcgtg gccgacgctg cattcacaga agtccccaaa gatgtgacag tacgggaggg
180
agacgacatc gaaatgccct gcgcgttccg ggccagcgga gccacctcgt attcgctgga
240
gattcagtgg tggtacctca aggagccacc ccgggagctg ctgcacgagc tggcgctcag
300
cgtgccgggc gcccggagca aggtaacaaa taaggatgca actaaaatca gcaccgtacg
360
cgt
363

<210> 1952
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1952
Arg Pro Pro Pro Leu Arg Ser Arg Ala Pro Ala Ala Thr Ala Pro Pro
1 5 10 15
Ala Gly Asp Gly Thr Ala Glu Pro Ala Arg Cys Pro Arg Ile Pro Ala
20 25 30
Ala Ser Ala Ala Ala Cys Pro Ala Ala Leu Arg Gly Arg Arg Cys Ile
35 40 45
His Arg Ser Pro Gln Arg Cys Asp Ser Thr Gly Gly Arg Arg His Arg

```
    50                  55                  60
Asn Ala Leu Arg Val Pro Gly Gln Arg Ser His Leu Val Phe Ala Gly
65                  70                  75                  80
Asp Ser Val Val Val Pro Gln Gly Ala Thr Pro Gly Ala Ala Ala Arg
                85                  90                  95
Ala Gly Ala Gln Arg Ala Gly Arg Pro Glu Gln Gly Asn Lys
            100                 105                 110
```

<210> 1953
<211> 329
<212> DNA
<213> Homo sapiens

<400> 1953
acgcgtcagc ctgagcccaa taactataaa agagtcgcaa ccatgactgt gctattgagt
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gagcgcagcc agattttccg gggtgccgat gcctacgcgg tgtcggacta cgtcaaccag
120
catgtgggca gccactgcat tcgcctgcct cccaagggcc ggccacgggc gagtatcagc
180
catcgcacct ttgccagcct ggacctgtgc cgcatcagct acggcgctcc ggtacgggtc
240
acatcggtgg cgctggagac catctatcac ctgcagatcc tgttgagcgg gcattgccgc
300
tccagctccc gtggtgagga tgacgtggn
329

<210> 1954
<211> 109
<212> PRT
<213> Homo sapiens

<400> 1954
```
Thr Arg Gln Pro Glu Pro Asn Asn Tyr Lys Arg Val Ala Thr Met Thr
 1               5                  10                  15
Val Leu Leu Ser Glu Arg Ser Gln Ile Phe Arg Gly Ala Asp Ala Tyr
            20                  25                  30
Ala Val Ser Asp Tyr Val Asn Gln His Val Gly Ser His Cys Ile Arg
        35                  40                  45
Leu Pro Pro Lys Gly Arg Pro Arg Ala Ser Ile Ser His Arg Thr Phe
    50                  55                  60
Ala Ser Leu Asp Leu Cys Arg Ile Ser Tyr Gly Ala Pro Val Arg Val
65                  70                  75                  80
Thr Ser Val Ala Leu Glu Thr Ile Tyr His Leu Gln Ile Leu Leu Ser
                85                  90                  95
Gly His Cys Arg Ser Ser Ser Arg Gly Glu Asp Asp Val
            100                 105
```

<210> 1955
<211> 415
<212> DNA
<213> Homo sapiens

<400> 1955

acgcgtggct cgacgaaaac caagtacgag acatgcccga caaggtacta tcacacatgg
60
tggaatactg ctgggggcgc ttcacagaca acatcaaata cgctgtagct gcccaatatt
120
ggaaagggcc acacaagccc gatagtgacc atcaacggat cattgtaggc tatttcaaaa
180
ccgccaaaca agccatgaac gcagcaaaac aattccactg gaacacccgg ctacaacaac
240
aatggaaaac atggatactc ccagtccaca acggcaccgt gtccgagttt ttcacccaac
300
aaaaaacttt gctagacgag caagacgata gcaatagcga gctgccggag catctacaaa
360
acgtcatgtg cggcaaaaca ctccaccacc aagacgacac catatcgtgg tgcac
415

<210> 1956
<211> 127
<212> PRT
<213> Homo sapiens

<400> 1956
Met Pro Asp Lys Val Leu Ser His Met Val Glu Tyr Cys Trp Gly Arg
 1   5   10   15
Phe Thr Asp Asn Ile Lys Tyr Ala Val Ala Ala Gln Tyr Trp Lys Gly
            20   25   30
Pro His Lys Pro Asp Ser Asp His Gln Arg Ile Ile Val Gly Tyr Phe
        35   40   45
Lys Thr Ala Lys Gln Ala Met Asn Ala Ala Lys Gln Phe His Trp Asn
    50   55   60
Thr Arg Leu Gln Gln Gln Trp Lys Thr Trp Ile Leu Pro Val His Asn
65   70   75   80
Gly Thr Val Ser Glu Phe Phe Thr Gln Gln Lys Thr Leu Leu Asp Glu
                85   90   95
Gln Asp Asp Ser Asn Ser Glu Leu Pro Glu His Leu Gln Asn Val Met
            100   105   110
Cys Gly Lys Thr Leu His His Gln Asp Asp Thr Ile Ser Trp Cys
        115   120   125

<210> 1957
<211> 526
<212> DNA
<213> Homo sapiens

<400> 1957
acgcgttccg gagagatttt cctaacctct ctccgagctg ctgagccgat cggtgaccac
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caggagctcc tccctgtgag gacaaagttc cagagtcggg gtcacgggcc ttacttattg
120
gggaggaggc ccgccggggc cgcagtgggc gaggggccct tggcgcgctc ctgggaggtc
180
agacctggca cagtgtggcg aaggtttcca gtgcgatccc gagtcgaggg cgcatttcgc
240
ggtgactgcc agcatgaacc gcagccgacc gagttctgcg atcgggcttc tccgcagagt
300

ggggaccctg gggaaggcgc caacttctct cctctgccca cctcactccc cgcgggcgtc
360
cctgggccgc ctgcccgggc cgcactgggc ggcctccatc gtcccttccc tctacctgca
420
ctgccccagg cgggagagag gccttggccc nncgagggac cagctgcagc gggcagcggg
480
gtcctgctcc cccaaccccc gccccatggc acggggctga accggt
526

<210> 1958
<211> 175
<212> PRT
<213> Homo sapiens

<400> 1958
Thr Arg Ser Gly Glu Ile Phe Leu Thr Ser Leu Arg Ala Ala Glu Pro
1 5 10 15
Ile Gly Asp His Gln Glu Leu Leu Pro Val Arg Thr Lys Phe Gln Ser
20 25 30
Arg Gly His Gly Pro Tyr Leu Leu Gly Arg Arg Pro Ala Gly Ala Ala
35 40 45
Val Gly Glu Gly Pro Leu Ala Arg Ser Trp Glu Val Arg Pro Gly Thr
50 55 60
Val Trp Arg Arg Phe Pro Val Arg Ser Arg Val Glu Gly Ala Phe Arg
65 70 75 80
Gly Asp Cys Gln His Glu Pro Gln Pro Thr Glu Phe Cys Asp Arg Ala
85 90 95
Ser Pro Gln Ser Gly Asp Pro Gly Glu Gly Ala Asn Phe Ser Pro Leu
100 105 110
Pro Thr Ser Leu Pro Ala Gly Val Pro Gly Pro Pro Ala Arg Ala Ala
115 120 125
Leu Gly Gly Leu His Arg Pro Phe Pro Leu Pro Ala Leu Pro Gln Ala
130 135 140
Gly Glu Arg Pro Trp Pro Xaa Glu Gly Pro Ala Ala Ala Gly Ser Gly
145 150 155 160
Val Leu Leu Pro Gln Pro Pro Pro His Gly Thr Gly Leu Asn Arg
165 170 175

<210> 1959
<211> 378
<212> DNA
<213> Homo sapiens

<400> 1959
gtgcaccgga cggctcctcc aacggatcat gcgacggccc agcggaaggc tcacccgagt
60
cgtcagaagg atcagggcgc ttgtcgtcgt cagacttcag gacatcccac gacatggtga
120
acggctggga ggagaccttg tccccgtcgg tcttggcgcc gacaacaaca ccgctcatgg
180
tgtattttcc ggcatgagtg aagaaccagt gggcatgctg atgacccttg atcggcagtg
240
aggctccttt gaccacctga tatgtgtcat cagcgaggaa ggtgccgagt ttggcgttct
300

cgtctgcctc gggtgaattg ccgaggaggt acatcttgcc tggacccgta atcgcggtga
360
agtcgacgcg caacgcgt
378

<210> 1960
<211> 111
<212> PRT
<213> Homo sapiens

<400> 1960
Met Tyr Leu Leu Gly Asn Ser Pro Glu Ala Asp Glu Asn Ala Lys Leu
1 5 10 15
Gly Thr Phe Leu Ala Asp Asp Thr Tyr Gln Val Val Lys Gly Ala Ser
20 25 30
Leu Pro Ile Lys Gly His Gln His Ala His Trp Phe Phe Thr His Ala
35 40 45
Gly Lys Tyr Thr Met Ser Gly Val Val Val Gly Ala Lys Thr Asp Gly
50 55 60
Asp Lys Val Ser Ser Gln Pro Phe Thr Met Ser Trp Asp Val Leu Lys
65 70 75 80
Ser Asp Asp Asp Lys Arg Pro Asp Pro Ser Asp Asp Ser Gly Glu Pro
85 90 95
Ser Ala Gly Pro Ser His Asp Pro Leu Glu Glu Pro Ser Gly Ala
100 105 110

<210> 1961
<211> 384
<212> DNA
<213> Homo sapiens

<400> 1961
ggatccaccc cggaaaccgg caggatgaag ggggcaagtg aggagaagct ggcatctgtg
60
tccaacctgg tcactgtgtt tgagaatagc aggaccccag aagcagcacc cagaggccag
120
aggctagagg acgtgcatca ccgccctgag tgcaggcctc ccgagtcccc aggaccacgg
180
gagaagacga atgtcgggga ggccgtgggg tctgagccca ggacagtcag caggaggtac
240
ctgaactccc tgaagaacaa gctgtccagc gaagcctgga ggaaatcttg ccagcctgtg
300
accctctcag gatcggggac gcaggagcca gagaagaaga tcgtccagga gctgctggag
360
acagagcagg cctatgtggc gcgc
384

<210> 1962
<211> 128
<212> PRT
<213> Homo sapiens

<400> 1962
Gly Ser Thr Pro Glu Thr Gly Arg Met Lys Gly Ala Ser Glu Glu Lys

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 1               5                  10                  15
Leu Ala Ser Val Ser Asn Leu Val Thr Val Phe Glu Asn Ser Arg Thr
            20                  25                  30
Pro Glu Ala Ala Pro Arg Gly Gln Arg Leu Glu Asp Val His His Arg
        35                  40                  45
Pro Glu Cys Arg Pro Pro Glu Ser Pro Gly Pro Arg Glu Lys Thr Asn
    50                  55                  60
Val Gly Glu Ala Val Gly Ser Glu Pro Arg Thr Val Ser Arg Arg Tyr
65                  70                  75                  80
Leu Asn Ser Leu Lys Asn Lys Leu Ser Ser Glu Ala Trp Arg Lys Ser
                85                  90                  95
Cys Gln Pro Val Thr Leu Ser Gly Ser Gly Thr Gln Glu Pro Glu Lys
            100                 105                 110
Lys Ile Val Gln Glu Leu Leu Glu Thr Glu Gln Ala Tyr Val Ala Arg
        115                 120                 125
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<210> 1963
<211> 323
<212> DNA
<213> Homo sapiens

<400> 1963
nnnccccttcc taccctccca tactccccac ccctcttcct ccccctgtgc tgagcttgca
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ggcatgaaac acccacctgg cctctctccc tctgttttgc cccttctgtc gtctctctcc
120
cacagctgcc tggctcttcg gcgtcagtcc accaccttct gcagctctcc ctcaccctgg
180
cgaccactca ggcatgcatc tcgcgggccc ccttcagacc tctcggggtc atcttccccct
240
tccctggcca ttatttttct tcatctgggc tgggcccgga ggggcgttcc ccccttcct
300
cttctttctt ttttttctc ttt
323

<210> 1964
<211> 107
<212> PRT
<213> Homo sapiens

<400> 1964
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Xaa Pro Phe Leu Pro Ser His Thr Pro His Pro Ser Ser Ser Pro Cys
 1               5                  10                  15
Ala Glu Leu Ala Gly Met Lys His Pro Pro Gly Leu Ser Pro Ser Val
            20                  25                  30
Leu Pro Leu Leu Ser Ser Leu Ser His Ser Cys Leu Ala Leu Arg Arg
        35                  40                  45
Gln Ser Thr Thr Phe Cys Ser Ser Pro Ser Pro Trp Arg Pro Leu Arg
    50                  55                  60
His Ala Ser Arg Gly Pro Pro Ser Asp Leu Ser Gly Ser Ser Ser Pro
65                  70                  75                  80
Ser Leu Ala Ile Ile Phe Leu His Leu Gly Trp Ala Arg Arg Gly Val
                85                  90                  95
Pro Pro Leu Pro Leu Leu Ser Phe Phe Phe Ser
```

100 105

<210> 1965
<211> 1416
<212> DNA
<213> Homo sapiens

<400> 1965
cggctggggc aggagctgga cgacgccacc atggacctgg agcagcagcg gcagcttgtg
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agcaccctgg agaagaagca gcgcaagttt gaccagcttc tggcagagga gaaggcagct
120
gtacttcggg cagtggagga acgtgagcgg gccgaggcag agggccggga gcgtgaggct
180
cgggccctgt cactgacacg ggcactggag gaggagcagg aggcacgtga ggagctggag
240
cggcagaacc gggccctgcg ggctgagctg gaggcactgc tgagcagcaa ggatgacgtc
300
ggcaagagcg tgcatgagct ggaacgagcc tgccgggtag cagaacaggc agccaatgat
360
ctgcgagcac aggtgacaga actggaggat gagctgacag cggccgagga tgccaagctg
420
cgtctggagg tgactgtgca ggctctcaag actcagcatg agcgtgacct gcagggccgt
480
gatgaggctg gtgaagagag gcggaggcag ctggccaagc agctgagaga tgcagaggtg
540
gagcgggatg aggagcggaa gcagcgcact ctggccgtgg ctgcccgcaa gaagctggag
600
ggagagctgg aggagctgaa ggctcagatg gcctctgccg gccagggcaa ggaggaggcg
660
gtgaagcagc ttcgcaagat gcaggcccag atgaaggagc tatggcggga ggtggaggag
720
acacgcacct cccgggagga gatcttctcc cagaatcggg aaagtgaaaa gcgcctcaag
780
ggcctggagg ctgaggtgct gcggctgcag gaggaactgg ccgcctcgga ccgtgctcgg
840
cggcaggccc agcaggaccg ggatgagatg gcagatgagg tggccaatgg taaccttagc
900
aaggcagcca ttctggagga gaagcgtcag ctggaggggc gcctggggca gttggaggaa
960
gagctggagg aggagcagac anactcagag ctgctcaatg accgctaccg caagctgctc
1020
ctgcaggtag agtcactgac cacagagctg tcagctgagc gcagtttctc agccaaggca
1080
gagagcgggc ggcagcagct ggaacggcag atccaggagc tacggggacg cctgggtgag
1140
gaggatgctg gggcccgtgc ccgccacaag atgaccattg ctgcccttga gtctaagttg
1200
gcccaggctg aggagcagct agagcaagag accagagagc gcatcctctc tggaaagctg
1260
gtgcccaaaa gtaagaagcg gtttaaagag gtggtgctcc aggtggagga ggagcggagg
1320
gtggctgacc agctccggga ccagctggag aagggaaacc ttcgagtcaa gcagctgaag
1380

cggcagctgg aggaggccga ggaggaggca tcccgg
1416

<210> 1966
<211> 472
<212> PRT
<213> Homo sapiens

<400> 1966
Arg Leu Gly Gln Glu Leu Asp Asp Ala Thr Met Asp Leu Glu Gln Gln
1 5 10 15
Arg Gln Leu Val Ser Thr Leu Glu Lys Lys Gln Arg Lys Phe Asp Gln
20 25 30
Leu Leu Ala Glu Glu Lys Ala Ala Val Leu Arg Ala Val Glu Glu Arg
35 40 45
Glu Arg Ala Glu Ala Glu Gly Arg Glu Arg Glu Ala Arg Ala Leu Ser
50 55 60
Leu Thr Arg Ala Leu Glu Glu Glu Gln Glu Ala Arg Glu Glu Leu Glu
65 70 75 80
Arg Gln Asn Arg Ala Leu Arg Ala Glu Leu Glu Ala Leu Leu Ser Ser
85 90 95
Lys Asp Asp Val Gly Lys Ser Val His Glu Leu Glu Arg Ala Cys Arg
100 105 110
Val Ala Glu Gln Ala Ala Asn Asp Leu Arg Ala Gln Val Thr Glu Leu
115 120 125
Glu Asp Glu Leu Thr Ala Ala Glu Asp Ala Lys Leu Arg Leu Glu Val
130 135 140
Thr Val Gln Ala Leu Lys Thr Gln His Glu Arg Asp Leu Gln Gly Arg
145 150 155 160
Asp Glu Ala Gly Glu Glu Arg Arg Arg Gln Leu Ala Lys Gln Leu Arg
165 170 175
Asp Ala Glu Val Glu Arg Asp Glu Glu Arg Lys Gln Arg Thr Leu Ala
180 185 190
Val Ala Ala Arg Lys Lys Leu Glu Gly Glu Leu Glu Glu Leu Lys Ala
195 200 205
Gln Met Ala Ser Ala Gly Gln Gly Lys Glu Glu Ala Val Lys Gln Leu
210 215 220
Arg Lys Met Gln Ala Gln Met Lys Glu Leu Trp Arg Glu Val Glu Glu
225 230 235 240
Thr Arg Thr Ser Arg Glu Glu Ile Phe Ser Gln Asn Arg Glu Ser Glu
245 250 255
Lys Arg Leu Lys Gly Leu Glu Ala Glu Val Leu Arg Leu Gln Glu Glu
260 265 270
Leu Ala Ala Ser Asp Arg Ala Arg Arg Gln Ala Gln Gln Asp Arg Asp
275 280 285
Glu Met Ala Asp Glu Val Ala Asn Gly Asn Leu Ser Lys Ala Ala Ile
290 295 300
Leu Glu Glu Lys Arg Gln Leu Glu Gly Arg Leu Gly Gln Leu Glu Glu
305 310 315 320
Glu Leu Glu Glu Glu Gln Thr Xaa Ser Glu Leu Leu Asn Asp Arg Tyr
325 330 335
Arg Lys Leu Leu Leu Gln Val Glu Ser Leu Thr Thr Glu Leu Ser Ala
340 345 350
Glu Arg Ser Phe Ser Ala Lys Ala Glu Ser Gly Arg Gln Gln Leu Glu

```
        355                 360                 365
Arg Gln Ile Gln Glu Leu Arg Gly Arg Leu Gly Glu Glu Asp Ala Gly
    370                 375                 380
Ala Arg Ala Arg His Lys Met Thr Ile Ala Ala Leu Glu Ser Lys Leu
385                 390                 395                 400
Ala Gln Ala Glu Glu Gln Leu Glu Gln Glu Thr Arg Glu Arg Ile Leu
                405                 410                 415
Ser Gly Lys Leu Val Pro Lys Ser Lys Lys Arg Phe Lys Glu Val Val
            420                 425                 430
Leu Gln Val Glu Glu Glu Arg Arg Val Ala Asp Gln Leu Arg Asp Gln
        435                 440                 445
Leu Glu Lys Gly Asn Leu Arg Val Lys Gln Leu Lys Arg Gln Leu Glu
    450                 455                 460
Glu Ala Glu Glu Glu Ala Ser Arg
465                 470
```

<210> 1967
<211> 401
<212> DNA
<213> Homo sapiens

<400> 1967
aaatttgaat cctggaaagc tgatctcgat aagtcgtttg tcgagctgtt tgcggcgttg
60
ccgacgcgcc taatttggat cgtgcagtaa gagcttctcc attcctcggc gccaaaggga
120
tgcatcacat ctcgcggcca gtcagctccc ctgggcttgc actcgtcgga gatgctggcc
180
ttgcaccaga tcctctgtgg ggcgtcgggt gtggctgggc attccagtcg gcagcttggt
240
tagtggactg taccggatct catttggctg accggaccgc cttagatagg gcgcttcgca
300
gttatcatcg ataccaccgg cattctcttg ggtggcatga acgcctcatc tctagatatg
360
caaacggccg gggttttcat gcgctcgaga agctgatgct g
401

<210> 1968
<211> 94
<212> PRT
<213> Homo sapiens

<400> 1968
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Met His His Ile Ser Arg Pro Val Ser Ser Pro Gly Leu Ala Leu Val
 1               5                  10                  15
Gly Asp Ala Gly Leu Ala Pro Asp Pro Leu Trp Gly Val Gly Cys Gly
            20                  25                  30
Trp Ala Phe Gln Ser Ala Ala Trp Leu Val Asp Cys Thr Gly Ser His
        35                  40                  45
Leu Ala Asp Arg Thr Ala Leu Asp Arg Ala Leu Arg Ser Tyr His Arg
    50                  55                  60
Tyr His Arg His Ser Leu Gly Trp His Glu Arg Leu Ile Ser Arg Tyr
65                  70                  75                  80
Ala Asn Gly Arg Gly Phe His Ala Leu Glu Lys Leu Met Leu
```

85 90

<210> 1969
<211> 464
<212> DNA
<213> Homo sapiens

<400> 1969
nncatcgacg cgcactggac tcatctgggt gacggcccac agatggacac tctgcgcgag
60
gaggtcgccg ttcaccgcgt cacggatgct gtcaccctgc tcggtcacgt cgccaacacc
120
caggtcatgg cgacccagcg tgatctcaaa ccgtcagtat tcgtcaacct ctcctcctcg
180
gaaggacttc ctgtatcaat gatggaggtt gcttccctcg gtatccccat tatcgcgact
240
ggcgtcggcg gagtaggaga aatcgtctcg tctgacaacg ggcatctatt gcctgccgag
300
ttcaccgaca cccaggcatc tgacgcgtta gtgcagctgg cacgtctgtc tgaggacgag
360
taccagcagg tgtgtcaggc ctcccgccag gtgtgggaag aaaagttccg cgcctctgtc
420
gtctaccccg aattctgtcg cgagtgctgg ggcgacgctg atca
464

<210> 1970
<211> 154
<212> PRT
<213> Homo sapiens

<400> 1970
Xaa Ile Asp Ala His Trp Thr His Leu Gly Asp Gly Pro Gln Met Asp
1 5 10 15
Thr Leu Arg Glu Glu Val Ala Val His Arg Val Thr Asp Ala Val Thr
20 25 30
Leu Leu Gly His Val Ala Asn Thr Gln Val Met Ala Thr Gln Arg Asp
35 40 45
Leu Lys Pro Ser Val Phe Val Asn Leu Ser Ser Ser Glu Gly Leu Pro
50 55 60
Val Ser Met Met Glu Val Ala Ser Leu Gly Ile Pro Ile Ile Ala Thr
65 70 75 80
Gly Val Gly Gly Val Gly Glu Ile Val Ser Ser Asp Asn Gly His Leu
85 90 95
Leu Pro Ala Glu Phe Thr Asp Thr Gln Ala Ser Asp Ala Leu Val Gln
100 105 110
Leu Ala Arg Leu Ser Glu Asp Glu Tyr Gln Gln Val Cys Gln Ala Ser
115 120 125
Arg Gln Val Trp Glu Glu Lys Phe Arg Ala Ser Val Val Tyr Pro Glu
130 135 140
Phe Cys Arg Glu Cys Trp Gly Asp Ala Asp
145 150

<210> 1971
<211> 520

<212> DNA
<213> Homo sapiens

<400> 1971
accggttgta ggtgtacaaa cactgctgac atcagccagc tcctgagtgt caggagagac
60
acagaagtac tcaggttgtt tgtgtgttga ccgagagaac agctcagatt gaggaacgag
120
acagacgacg acaaaaacaa ttagagcatc agttgataca atacaaatgg aatataatgc
180
atctaacatt tcaaattcaa gacatgattc tgatgaaatc agtggtaaaa tgaatacata
240
tatgaattct acgacttcta agaaggatac tggtgtgcaa acagatgact taaatatagg
300
aatattcacc aatgcagaat cacattgtgg atcattaatg gagagggaca tcacaaattg
360
ttcatctcct gagatttcgg cagaacttat tggacagttt agcaccaaga aaaacaagca
420
agaactaact caggataaag gagccagctt agaaaaagaa aacaatcggt gtaatgacca
480
gtgtaatcag ttcacaagaa ttgagaaaca aacaaaacag
520

<210> 1972
<211> 118
<212> PRT
<213> Homo sapiens

<400> 1972
Met Glu Tyr Asn Ala Ser Asn Ile Ser Asn Ser Arg His Asp Ser Asp
1 5 10 15
Glu Ile Ser Gly Lys Met Asn Thr Tyr Met Asn Ser Thr Thr Ser Lys
20 25 30
Lys Asp Thr Gly Val Gln Thr Asp Asp Leu Asn Ile Gly Ile Phe Thr
35 40 45
Asn Ala Glu Ser His Cys Gly Ser Leu Met Glu Arg Asp Ile Thr Asn
50 55 60
Cys Ser Ser Pro Glu Ile Ser Ala Glu Leu Ile Gly Gln Phe Ser Thr
65 70 75 80
Lys Lys Asn Lys Gln Glu Leu Thr Gln Asp Lys Gly Ala Ser Leu Glu
85 90 95
Lys Glu Asn Asn Arg Cys Asn Asp Gln Cys Asn Gln Phe Thr Arg Ile
100 105 110
Glu Lys Gln Thr Lys Gln
115

<210> 1973
<211> 331
<212> DNA
<213> Homo sapiens

<400> 1973
acgcgtacct atgcccagcg catggcggat cagttgaccg cggcactagg cagctactta
60

tccgcaggtc aaaagaaatc ggacggcctc ggatccttct tcgtggccac tacccttgaa
120
gagctacaag cgatgaacag cgatactcgc ttcaccacga gcgtgggaat cgacctatcc
180
cccgctcgat ctttctccgc ttgggcgctg cgcggaacga ctttttctgc gccgtcgatg
240
acaaaggctt cccgctcgag ctcggccgca ccaagcgcac cgcgtcgctg tggcaaaagc
300
tggcgctcgc cgccagtgaa atcgtgtgca c
331

<210> 1974
<211> 103
<212> PRT
<213> Homo sapiens

<400> 1974
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Glu Glu Leu Gln Ala Met Asn Ser Asp Thr Arg Phe Thr Thr Ser Val
        35   40   45
Gly Ile Asp Leu Ser Pro Ala Arg Ser Phe Ser Ala Trp Ala Leu Arg
    50   55   60
Gly Thr Thr Phe Ser Ala Pro Ser Met Thr Lys Ala Ser Arg Ser Ser
65   70   75   80
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Pro Pro Val Lys Ser Cys Ala
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<210> 1975
<211> 370
<212> DNA
<213> Homo sapiens

<400> 1975
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370

<210> 1976

<211> 121
<212> PRT
<213> Homo sapiens

<400> 1976
Met Arg Val Arg Ser Ser Ser Ile Ala Arg Val Ala Asp His Ala Val
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20 25 30
Arg Leu Arg Gly Gly Leu His Gln Ser Arg Asn Leu Gly Asp Arg Val
35 40 45
Val Gly Val Gly Leu Cys Leu Arg Arg Asp Val Ala Arg Ser Leu Arg
50 55 60
Gln Arg Ile Ala Asn Leu Leu Leu Thr Ala Arg Arg Val Gly Thr Arg
65 70 75 80
Leu Leu Pro Arg Leu Ala Gln Leu Gly Ala His Cys Thr Gln Arg Ile
85 90 95
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100 105 110
Gln Leu His Glu Arg Leu Ala Arg Arg
115 120

<210> 1977
<211> 551
<212> DNA
<213> Homo sapiens

<400> 1977
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420
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551

<210> 1978
<211> 101
<212> PRT
<213> Homo sapiens

<400> 1978
Met His Pro Trp His Pro Thr Ser Ser Gly Ile Cys Leu Leu Val Ser
1 5 10 15
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20 25 30
Pro Leu Pro Ala Val Ser Pro Thr Ser Phe Ile Pro Pro Val Thr Arg
35 40 45
Glu Val Gln Ile Phe Gln Pro Gly His Cys Leu Pro Ser Arg Leu Ala
50 55 60
Pro Pro Val His Leu Leu Cys Ser Ser Leu Cys Asn Ser Leu Ala Ala
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Cys Leu Leu Ser Pro Leu Thr Gln Leu Leu Thr Cys Pro Thr Pro Ala
85 90 95
Gln Pro Thr Ser Ser
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<210> 1979
<211> 5530
<212> DNA
<213> Homo sapiens

<400> 1979
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120
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240
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300
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360
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480
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4200

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5100
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5400
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5530

<210> 1980
<211> 929
<212> PRT
<213> Homo sapiens

<400> 1980
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Gln Pro Pro Thr Ala Ala Ala Ala Ala Gln Pro Arg Arg Arg Gln Gly
        35                  40                  45
Glu Glu Val Gln Glu Arg Ala Glu Pro Pro Gly His Pro His Pro Leu
    50                  55                  60
Ala Gln Arg Arg Arg Ser Lys Gly Leu Val Gln Asn Ile Asp Gln Leu
65                  70                  75                  80
Tyr Ser Gly Gly Gly Lys Val Gly Tyr Leu Val Tyr Ala Gly Gly Arg
                85                  90                  95
Arg Phe Leu Leu Asp Leu Glu Arg Asp Gly Ser Val Gly Ile Ala Gly
            100                 105                 110
Phe Val Pro Ala Gly Gly Gly Thr Ser Ala Pro Trp Arg His Arg Ser
        115                 120                 125
His Cys Phe Tyr Arg Gly Thr Val Asp Ala Ser Pro Arg Ser Leu Ala
    130                 135                 140
Val Phe Asp Leu Cys Gly Gly Leu Asp Gly Phe Phe Ala Val Lys His
145                 150                 155                 160
Ala Arg Tyr Thr Leu Lys Pro Leu Leu Arg Gly Pro Trp Ala Glu Glu
                165                 170                 175
Glu Lys Gly Arg Val Tyr Gly Asp Gly Ser Ala Arg Ile Leu His Val
            180                 185                 190
Tyr Thr Arg Arg Ala Ser Ala Ser Arg Pro Cys Arg Arg Ala Pro Ala
        195                 200                 205
Ala Lys Pro Pro Arg Pro His Arg Arg Pro Thr Ser Met Leu Arg Arg
    210                 215                 220
Thr Ala Thr Arg Ala Asp Ala Gln His Ala Ser Gln Leu Leu Asp Gln
225                 230                 235                 240
Ser Ala Leu Ser Pro Ala Gly Gly Ser Gly Pro Gln Thr Trp Trp Arg
                245                 250                 255
Arg Arg Arg Arg Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu Leu
            260                 265                 270
Val Ala Asp Ala Ser Met Ala Arg Leu Tyr Gly Arg Gly Leu Gln His
        275                 280                 285
Tyr Leu Leu Thr Leu Ala Ser Ile Ala Asn Arg Leu Tyr Ser His Ala
    290                 295                 300
Ser Ile Glu Asn His Ile Arg Leu Ala Val Val Lys Val Val Val Leu
305                 310                 315                 320
Gly Asp Lys Asp Lys Ser Leu Glu Val Ser Lys Asn Ala Ala Thr Thr
                325                 330                 335
Leu Lys Asn Phe Cys Lys Trp Gln His Gln His Asn Gln Leu Gly Asp
            340                 345                 350
Asp His Glu Glu His Tyr Asp Ala Ala Ile Leu Phe Thr Arg Glu Asp
        355                 360                 365
Leu Cys Gly His His Ser Cys Asp Thr Leu Gly Met Ala Asp Val Gly
    370                 375                 380
Thr Ile Cys Ser Pro Glu Arg Ser Cys Ala Val Ile Glu Asp Asp Gly
385                 390                 395                 400
Leu His Ala Ala Phe Thr Val Ala His Glu Ile Gly His Leu Leu Gly
                405                 410                 415
Leu Ser His Asp Asp Ser Lys Phe Cys Glu Glu Thr Phe Gly Ser Thr
            420                 425                 430
Glu Asp Lys Arg Leu Met Ser Ser Ile Leu Thr Ser Ile Asp Ala Ser
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        435                 440                 445
Lys Pro Trp Ser Lys Cys Thr Ser Ala Thr Ile Thr Glu Phe Leu Asp
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Asp Gly His Gly Asn Cys Leu Leu Asp Leu Pro Arg Lys Gln Ile Leu
465                 470                 475                 480
Gly Pro Glu Glu Leu Pro Gly Gln Thr Tyr Asp Ala Thr Gln Gln Cys
                485                 490                 495
Asn Leu Thr Phe Gly Pro Glu Tyr Ser Val Cys Pro Gly Met Asp Val
            500                 505                 510
Cys Ala Arg Leu Trp Cys Ala Val Val Arg Gln Gly Gln Met Val Cys
        515                 520                 525
Leu Thr Lys Lys Leu Pro Ala Val Glu Gly Thr Pro Cys Gly Lys Gly
    530                 535                 540
Arg Ile Cys Leu Gln Gly Lys Cys Val Asp Lys Thr Lys Lys Lys Tyr
545                 550                 555                 560
Tyr Ser Thr Ser Ser His Gly Asn Trp Gly Ser Trp Gly Ser Trp Gly
                565                 570                 575
Gln Cys Ser Arg Ser Cys Gly Gly Gly Val Gln Phe Ala Tyr Arg His
            580                 585                 590
Cys Asn Asn Pro Ala Pro Arg Asn Asn Gly Arg Tyr Cys Thr Gly Lys
        595                 600                 605
Arg Ala Ile Tyr His Ser Cys Ser Leu Met Pro Cys Pro Pro Asn Gly
    610                 615                 620
Lys Ser Phe Arg His Glu Gln Cys Glu Ala Lys Asn Gly Tyr Gln Ser
625                 630                 635                 640
Asp Ala Lys Gly Val Lys Thr Phe Val Glu Trp Val Pro Lys Tyr Ala
                645                 650                 655
Gly Val Leu Pro Ala Asp Val Cys Lys Leu Thr Cys Arg Ala Lys Gly
            660                 665                 670
Thr Gly Tyr Tyr Val Val Phe Ser Pro Lys Val Thr Asp Gly Thr Glu
        675                 680                 685
Cys Arg Pro Tyr Ser Asn Ser Val Cys Val Arg Gly Lys Cys Val Arg
    690                 695                 700
Thr Gly Cys Asp Gly Ile Ile Gly Ser Lys Leu Gln Tyr Asp Lys Cys
705                 710                 715                 720
Gly Val Cys Gly Gly Asp Asn Ser Ser Cys Thr Lys Ile Val Gly Thr
                725                 730                 735
Phe Asn Lys Lys Ser Lys Gly Tyr Thr Asp Val Val Arg Ile Pro Glu
            740                 745                 750
Gly Ala Thr His Ile Lys Val Arg Gln Phe Lys Ala Lys Asp Gln Thr
        755                 760                 765
Arg Phe Thr Ala Tyr Leu Ala Leu Lys Lys Lys Asn Gly Glu Tyr Leu
    770                 775                 780
Ile Asn Gly Lys Tyr Met Ile Ser Thr Ser Glu Thr Ile Ile Asp Ile
785                 790                 795                 800
Asn Gly Thr Val Met Asn Tyr Ser Gly Trp Ser His Arg Asp Asp Phe
                805                 810                 815
Leu His Gly Met Gly Tyr Ser Ala Thr Lys Glu Ile Leu Ile Val Gln
            820                 825                 830
Ile Leu Ala Thr Asp Pro Thr Lys Pro Leu Asp Val Arg Tyr Ser Phe
        835                 840                 845
Phe Val Pro Lys Lys Ser Thr Pro Lys Val Asn Ser Val Thr Ser His
    850                 855                 860
Gly Ser Asn Lys Val Gly Ser His Thr Ser Gln Pro Gln Trp Val Thr
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865                 870                 875                 880
Gly Pro Trp Leu Ala Cys Ser Arg Thr Cys Asp Thr Gly Trp His Thr
                885                 890                 895
Arg Thr Val Gln Cys Gln Asp Gly Asn Arg Lys Leu Ala Lys Gly Cys
            900                 905                 910
Pro Leu Ser Gln Arg Pro Ser Ala Phe Lys Gln Cys Leu Leu Lys Lys
        915                 920                 925
Cys
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<210> 1981
<211> 327
<212> DNA
<213> Homo sapiens

<400> 1981
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120
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180
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300
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327

<210> 1982
<211> 107
<212> PRT
<213> Homo sapiens

<400> 1982
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Met Val Tyr Arg Pro Phe Leu Val Pro Ser Ala Met Gly Asp Pro Gly
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Ser Val Gly Ala Ala Thr Leu Asn Glu Ser Met Cys Ala Ser Arg Leu
            20                  25                  30
Gly Val Asn Pro Arg Gly Val Asp Asn Arg Thr Ser Met Ala Val Phe
        35                  40                  45
Ser Pro Pro Lys Ala Ala Gly Gly Gly Arg Cys Pro Gly Pro Cys Arg
    50                  55                  60
Ile Met Ala Trp Pro Gly Gln Arg Ala Ser Ser Ser Gly Arg Gly Arg
65                  70                  75                  80
Gly Pro Ala Leu Ser Glu Trp Ala Ser Cys Leu Asn Gly Ser Lys Val
                85                  90                  95
Arg Ala Gly Ser Pro Gly Ser Glu Ala Asp Ala
            100                 105
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<210> 1983
<211> 383
<212> DNA
<213> Homo sapiens

<400> 1983
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120
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240
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383

<210> 1984
<211> 127
<212> PRT
<213> Homo sapiens

<400> 1984
Phe Asn Asn Met Val His Glu Leu Arg Glu Gln Gln His Ile Lys Asp
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20 25 30
Ala Gln Pro Glu Glu Arg Asn Val Pro Lys Arg Asp Ala Ser Val Phe
35 40 45
Phe Ile Asp Ile Ile Gly Ser Thr Lys Leu Ser Leu Glu Tyr Asp Ser
50 55 60
Tyr Thr Val Val Asp Leu Leu Asn Arg Phe Tyr Thr Ile Val Val Glu
65 70 75 80
Glu Val Asn Arg Ala Gly Gly Val Val Asn Lys Phe Ala Gly Asp Ala
85 90 95
Val Leu Ala Ile Phe Asn Val Pro His Asp His Pro Asp Pro Ala Gly
100 105 110
Ala Ser Leu Tyr Cys Ala Arg Val Val Met Asn Arg Phe Asp His
115 120 125

<210> 1985
<211> 381
<212> DNA
<213> Homo sapiens

<400> 1985
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240

cagaaccgaa gaaatatttt gcatgcgaaa ctcaattgag ccttcagtac ggccaaccaa
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ccacgccagc attttgaggt a
381

<210> 1986
<211> 124
<212> PRT
<213> Homo sapiens

<400> 1986
Met Leu Ala Trp Glu Lys Arg Ala Leu Ser Phe Thr Lys Ala His Glu
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Asn Arg Leu Leu Arg Gln Gly Pro Leu Val Gly Arg Thr Glu Gly Ser
20 25 30
Ile Glu Phe Arg Met Gln Asn Ile Ser Ser Val Leu Val Gln Met Gly
35 40 45
Leu Asp Arg Ile Lys Gly Tyr Lys Ala Cys Glu Pro Met Trp Gly Pro
50 55 60
Gly Gly Arg Pro Thr Thr Phe Ala Arg Pro Phe Ala Asp Thr Arg Val
65 70 75 80
Phe Glu Ser Asp Glu Thr Ala Gln Thr Ala Asp Glu Gln Thr Leu Ile
85 90 95
Arg Arg Ala Asn Lys Leu Gln Leu Lys Arg Phe Asp Gln Val Pro Asp
100 105 110
Gly Ile Ala Lys Pro Gln Gln Val Pro Ile Thr Ser
115 120

<210> 1987
<211> 419
<212> DNA
<213> Homo sapiens

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Leu Arg Gly Gln Leu Arg Glu Tyr Gln His Ile Gly Leu Asp Trp Leu
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Val Thr Met Tyr Glu Lys Lys Leu Asn Gly Ile Leu Ala Asp Glu Met
        435                 440                 445
Gly Leu Gly Lys Thr Ile Gln Thr Ile Ser Leu Leu Ala His Leu Ala
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Cys Glu Lys Gly Asn Trp Gly Pro His Leu Ile Ile Val Pro Thr Ser
465                 470                 475                 480
Val Met Leu Asn Trp Glu Met Glu Leu Lys Arg Trp Cys Pro Ser Phe
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Lys Ile Leu Thr Tyr Tyr Gly Ala Gln Lys Glu Arg Lys Leu Lys Arg
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Gln Gly Trp Thr Lys Pro Asn Ala Phe His Val Cys Ile Thr Ser Tyr
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Lys Leu Val Leu Gln Asp His Gln Ala Phe Arg Arg Lys Asn Trp Arg
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Tyr Leu Ile Leu Asp Glu Ala Gln Asn Ile Lys Asn Phe Lys Ser Gln
545                 550                 555                 560
Arg Trp Gln Ser Leu Leu Asn Phe Asn Ser Gln Arg Arg Leu Leu Leu
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Thr Gly Thr Pro Leu Gln Asn Ser Leu Met Glu Leu Trp Ser Leu Met
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His Phe Leu Met Pro His Val Phe Gln Ser His Arg Glu Phe Lys Glu
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Trp Phe Ser Asn Pro Leu Thr Gly Met Ile Glu Gly Ser Gln Glu Tyr
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Glu His Val Ile Arg Cys Arg Leu Ser Lys Arg Gln Arg Cys Leu Tyr
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Asp Asp Phe Met Ala Gln Thr Thr Thr Lys Glu Thr Leu Ala Thr Gly
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His Phe Met Ser Val Ile Asn Ile Leu Met Gln Leu Arg Lys Val Cys
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Asn His Pro Asn Leu Phe Asp Pro Arg Pro Val Thr Ser Pro Phe Ile
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Thr Pro Gly Ile Cys Phe Ser Thr Ala Ser Leu Val Leu Arg Ala Thr
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Asn Pro Arg Ala Pro Leu Gly Pro Val Pro Val Arg Pro Pro Pro Gly
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Pro Glu Leu Ser Ala Gln Pro Thr Pro Gly Pro Val Pro Gln Val Leu
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Ser Gly Thr Ser Arg Pro Pro Thr Pro Thr Leu Ser Leu Lys Pro Thr
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Pro Leu Thr Phe Gln Ile Gln Gly Asn Lys Leu Thr Leu Thr Gly Ala
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Gln Val Arg Gln Leu Ala Val Gly Gln Pro Arg Pro Leu Gln Met Pro
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Ala Pro Arg Asp Gly Leu Thr Pro Val Pro Pro Leu Ala Pro Ala Pro
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Arg Pro Pro Ser Ser Gly Leu Pro Ala Val Leu Asn Pro Arg Pro Thr
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Leu Thr Pro Gly Arg Leu Pro Thr Pro Thr Leu Gly Thr Ala Arg Ala
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Pro Met Pro Thr Pro Thr Leu Val Arg Pro Leu Leu Lys Leu Val His
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Ser Pro Ser Pro Glu Val Ser Ala Ser Ala Pro Gly Ala Ala Pro Leu
                1125                1130                1135
Thr Ile Ser Ser Pro Leu His Val Pro Ser Ser Leu Pro Gly Pro Ala
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Pro Thr Thr Leu Pro Ala Pro Ala Ser Ala Pro Leu Thr Ile Pro Ile
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Ser Ala Pro Leu Thr Val Ser Ala Ser Gly Pro Ala Leu Leu Thr Ser
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Val Thr Pro Pro Leu Ala Pro Val Val Pro Ala Ala Pro Gly Pro Pro
            1220                1225                1230
Ser Leu Ala Pro Ser Gly Ala Ser Pro Ser Ala Ser Ala Leu Thr Leu
        1235                1240                1245
Gly Leu Ala Thr Ala Pro Ser Leu Ser Ser Ser Gln Thr Pro Gly His
    1250                1255                1260
Pro Leu Leu Leu Ala Pro Thr Ser Ser His Val Pro Gly Leu Asn Ser
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Thr Val Ala Pro Ala Cys Ser Pro Val Leu Val Pro Ala Ser Ala Leu
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Ala Ser Pro Phe Pro Ser Ala Pro Asn Pro Ala Pro Ala Gln Ala Ser
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Leu Leu Ala Pro Ala Ser Ser Ala Ser Gln Ala Leu Ala Thr Pro Leu
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Ala Pro Met Ala Ala Pro Gln Thr Ala Ile Leu Ala Pro Ser Pro Ala
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Pro Pro Leu Ala Pro Leu Pro Val Leu Ala Pro Ser Pro Gly Ala Ala
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Pro Val Leu Ala Ser Ser Gln Thr Pro Val Pro Val Met Ala Pro Ser
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Thr Pro Val Leu Ala Pro Ser Ser Thr Gln Thr Met Leu Pro Ala Pro
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Val Pro Ser Pro Leu Pro Ser Pro Ala Ser Thr Gln Thr Leu Ala Leu
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Ala Pro Ala Leu Ala Pro Thr Leu Gly Gly Ser Ser Pro Ser Gln Thr
1425                1430                1435                1440
Leu Ser Leu Gly Thr Gly Asn Pro Gln Gly Pro Phe Pro Thr Gln Thr
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Leu Ser Leu Thr Pro Ala Ser Ser Leu Val Pro Thr Pro Ala Gln Thr
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Leu Ser Leu Ala Pro Gly Pro Pro Leu Gly Pro Thr Gln Thr Leu Ser
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Pro Ala His Thr Leu Thr Leu Ala Pro Ala Ser Ser Ser Ala Ser Leu
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Pro Thr Leu Gly Pro Ala Ala Ala Gln Thr Leu Ala Leu Ala Pro Ala
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Ser Thr Gln Ser Pro Ala Ser Gln Ala Ser Ser Leu Val Val Ser Ala
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Ser Lys Asp Glu Pro Asp Thr Leu Thr Leu Arg Ser Gly Pro Pro Ser
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Lys Arg Lys Arg Gln Arg Ser Glu Arg Leu Glu Arg Ile Phe Gln Leu
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Ser Glu Ala His Gly Ala Leu Ala Pro Val Tyr Gly Thr Glu Val Leu
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Asp Phe Cys Thr Leu Pro Gln Pro Val Ala Ser Pro Ile Gly Pro Arg
1665 1670 1675 1680
Ser Pro Gly Pro Ser His Pro Thr Phe Trp Thr Tyr Thr Glu Ala Ala
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His Arg Ala Val Leu Phe Pro Gln Gln Arg Leu Asp Gln Leu Ser Glu
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Ile Ile Glu Arg Phe Ile Phe Val Met Pro Pro Val Glu Ala Pro Pro
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Pro Ser Leu His Ala Cys His Pro Pro Pro Trp Leu Ala Pro Arg Gln
1730 1735 1740
Ala Ala Phe Gln Glu Gln Leu Ala Ser Glu Leu Trp Pro Arg Ala Arg
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Pro Leu His Arg Ile Val Cys Asn Met Arg Thr Gln Phe Pro Asp Leu
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Arg Leu Ile Gln Tyr Asp Cys Gly Lys Leu Gln Thr Leu Ala Val Leu
1780 1785 1790
Leu Arg Gln Leu Lys Ala Glu Gly His Arg Val Leu Ile Phe Thr Gln
1795 1800 1805
Met Thr Arg Met Leu Asp Val Leu Glu Gln Phe Leu Thr Tyr His Gly
1810 1815 1820
His Leu Tyr Leu Arg Leu Asp Gly Ser Thr Arg Val Glu Gln Arg Gln
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Ala Leu Met Glu Arg Phe Asn Ala Asp Lys Arg Ile Phe Cys Phe Ile
1845 1850 1855
Leu Ser Thr Arg Ser Gly Gly Val Gly Val Asn Leu Thr Gly Ala Asp
1860 1865 1870
Thr Val Val Phe Tyr Asp Ser Asp Trp Asn Pro Thr Met Asp Ala Gln
1875 1880 1885
Ala Gln Asp Arg Cys His Arg Ile Gly Gln Thr Arg Asp Val His Ile
1890 1895 1900
Tyr Arg Leu Ile Ser Glu Arg Thr Val Glu Glu Asn Ile Leu Lys Lys
1905 1910 1915 1920
Ala Asn Gln Lys Arg Met Leu Gly Asp Met Ala Ile Glu Gly Gly Asn
1925 1930 1935
Phe Thr Thr Ala Tyr Phe Lys Gln Gln Thr Ile Arg Glu Leu Phe Asp
1940 1945 1950
Met Pro Leu Glu Glu Pro Ser Ser Ser Ser Val Pro Ser Ala Pro Glu
1955 1960 1965
Glu Glu Glu Glu Thr Val Ala Ser Lys Gln Thr His Ile Leu Glu Gln
1970 1975 1980
Ala Leu Cys Arg Ala Glu Asp Glu Glu Asp Ile Arg Ala Ala Thr Gln
1985 1990 1995 2000
Ala Lys Ala Glu Gln Val Ala Glu Leu Ala Glu Phe Asn Glu Asn Asp
2005 2010 2015
Gly Phe Pro Ala Gly Glu Gly Glu Glu Ala Gly Arg Pro Gly Ala Glu

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2035 2040 2045
Gln Leu Thr Pro Ile Glu Arg Tyr Ala Met Lys Phe Leu Glu Ala Ser
2050 2055 2060
Leu Glu Glu Val Ser Arg Glu Glu Leu Lys Gln Ala Glu Glu Gln Val
2065 2070 2075 2080
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Ala Glu Thr Gln Gly Ala Asn His Thr Pro Val Ile Ser Ala His Gln
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Thr Arg Ser Thr Thr Thr Pro Pro Arg Cys Ser Pro Ala Arg Glu Arg
2165 2170 2175
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Ala Ala Ile Pro Ala Leu Val Pro Val Pro Val Ser Ala Pro Val Pro
2195 2200 2205
Ile Ser Ala Pro Asn Pro Ile Thr Ile Leu Pro Val His Ile Leu Pro
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Thr Pro Pro Pro Ala Cys Thr Pro Pro Pro Ala His Thr Pro Pro Pro
2245 2250 2255
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Pro Ser Val Pro Ile Ser Ala Ser Val Thr Asn Leu Pro Leu Gly Leu
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Thr Val Val Glu Glu Lys Glu Leu Val Arg Arg Arg Arg Gln Gln Arg
            2500                2505                2510
Gly Ala Ala Ser Thr Leu Val Pro Gly Val Ser Glu Thr Ser Ala Ser
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Pro Ile Gly Gly Pro Cys Glu Ala Ala Pro Ser Ser Ser Leu Pro Thr
2545                2550                2555                2560
Pro Pro Gln Gln Pro Phe Ile Ala Arg Arg His Ile Glu Leu Gly Val
                2565                2570                2575
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            2580                2585                2590
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Arg Ser Pro Ala Asp Ala Gly Arg Gly Val Asp Glu Ala Pro Ser Ser
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2625                2630                2635                2640
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Ser Pro Val Glu Lys Arg Arg Arg Gly Arg Pro Pro Lys Ala Arg Asp
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Pro Leu Leu Val Cys Pro Thr Ala Thr Val Ala Asn Thr Val Thr Thr
                2725                2730                2735
Val Thr Ile Ser Thr Ser Pro Pro Lys Arg Lys Arg Gly Arg Pro Pro
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Lys Asn Pro Pro Ser Pro Arg Pro Ser Gln Leu Pro Val Leu Asp Arg
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    2770                2775                2780
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Met Arg Gly Arg Lys Ser Gly Gly Ser Met Val Val Ala Val Ile Gln
            2820                2825                2830
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Pro Pro Val Val Ser Leu Thr Pro Lys Leu Arg Ser Thr Arg Leu Arg
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Pro Gln Gly Arg Ser Ile Ser Pro Pro Ser Gly Leu Pro Gln Pro His
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Leu Asn Ile Leu His Asp Glu Ala Val Arg Leu Leu Lys Ser Ser Arg
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His Leu Ile Leu Thr Val Lys Asp Val Gly Arg Leu Pro His Ala Arg
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Thr Thr Val Asp Glu Thr Lys Trp Ile Ala Ser Ser Arg Ile Arg Glu
195 200 205
Thr Met Ala Asn Ser Ala Gly Phe Leu Gly Asp Leu Thr Thr Glu Gly
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Ile Asn Lys Pro Gly Phe Tyr Lys Gly Pro Ala Gly Ser Gln Val Thr
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Val Arg Gly Thr Ile Ser Pro Gln Asp Leu Glu Arg Phe Asp His Leu
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Val Leu Arg Arg Glu Ile Glu Ser Met Lys Ala Arg Gln Pro Pro Gly
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Pro Gly Ala Gly Asp Thr Tyr Ser Met Val Ser Tyr Ser Asp Thr Gly
            340                 345                 350
Ser Ser Thr Gly Ser His Gly Thr Ser Thr Thr Val Ser Ser Ala Arg
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Gly Leu Ser Ser Phe Lys Pro Leu Pro Arg Pro Pro Pro Leu Ala Gln
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Leu Val Asn Gln His Pro Ile Gly Pro Phe Pro Arg Val Gln Ser Pro
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Pro His Leu Lys Ser Pro Ser Ala Glu Ala Thr Val Ala Gly Gly Cys
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Gln His Phe Val Met Val Glu Val His Arg Pro Asp Ser Glu Pro Asp
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Val Asn Glu Val Arg Ala Leu Pro Gln Thr Arg Thr Ala Ser Thr Leu
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Asp Ala Gly Glu Ala Glu Ala Ser Ala Pro Gly Arg Gly Arg Gln Ser
        595                 600                 605
Val Ser Thr Lys Ser Arg Ser Ser Lys Glu Leu Pro Arg Asn Glu Arg
    610                 615                 620
Pro Thr Asp Gly Ala Asn Lys Pro Pro Gly Leu Leu Glu Pro Thr Ser
625                 630                 635                 640
Thr Leu Val Arg Val Lys Lys Ser Ala Ala Thr Leu Gly Ile Ala Ile
                645                 650                 655
Glu Gly Gly Ala Asn Thr Arg Gln Pro Leu Pro Arg Ile Val Thr Ile
            660                 665                 670
Gln Arg Gly Gly Ser Ala His Asn Cys Gly Gln Leu Lys Val Gly His
        675                 680                 685
Val Ile Leu Glu Val Asn Gly Leu Thr Leu Arg Gly Lys Glu His Arg
```

690 695 700
Glu Ala Ala Arg Ile Ile Ala Glu Ala Phe Lys Thr Lys Asp Arg Asp
705 710 715 720
Tyr Ile Asp Phe Leu Val Thr Glu Phe Asn Val Met Leu
725 730

<210> 1993
<211> 957
<212> DNA
<213> Homo sapiens

<400> 1993
nngaaaacct acgggatgac acgtgccctc gatcacatcg acatcgccat cccagctggc
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cagtcggtcg ccgtcatggg gccgtccggg tcaggcaaga ccaccctgct gcactgcttg
120
tcggggatcc tctcgcctga ctccggcagt atcgaactgg ctctgccgga ccgcaccgtc
180
aacgtcgaaa acctctctaa cgaaggccga gcaaagctac gccgtcaatc ccttggtttc
240
gtcttccaac aaggaatgct cgtacccgag ctcactgctg tcgagaacac cgccctaccc
300
ctcatgctta acggcgtatc ccaaaccgat gcggtcaggt atgccaccca atggcttgaa
360
tcgatggggt taggcggcat ggaggatcgt cggattggtc agctctccgg gggccaagct
420
caacgcgtca ctattgcccg gtcccaggta atcgatccgt cgattgtctt cgctgacgaa
480
cccaccggag ccctcgactc agccaccgcc gtcgaagtca tggccattct gctttcggcg
540
acgaccgggc ggggacgcac cctcgtcgtc gtcacccatg acgaggacgt tgcccgccgc
600
tgccagcgca tccttcatct gcacgacggt cggatcgtct ctgaccacgt acgtcattcc
660
gatgggaggt ggtgatcatg actataacgc cccctatcga accgggaacc gccgatcaaa
720
ggatcccgtc cctccccgtc cccgagcccc tgggagctac gcccggacgt cttaccactg
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ctgcgatcct cagcatgacc ctccgtgcct cagccgctga ccactccacc tggcggttgc
840
cggtagttgc tttcgctgtc attgcaacca tcatcctcga cgtcactggc ggtgccgtca
900
tgatgtggca tctaccggga gacaactctg gcttctacaa gctgacctcg acaattg
957

<210> 1994
<211> 224
<212> PRT
<213> Homo sapiens

<400> 1994
Xaa Lys Thr Tyr Gly Met Thr Arg Ala Leu Asp His Ile Asp Ile Ala
1 5 10 15
Ile Pro Ala Gly Gln Ser Val Ala Val Met Gly Pro Ser Gly Ser Gly

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            20                  25                  30
Lys Thr Thr Leu Leu His Cys Leu Ser Gly Ile Leu Ser Pro Asp Ser
        35                  40                  45
Gly Ser Ile Glu Leu Ala Leu Pro Asp Arg Thr Val Asn Val Glu Asn
    50                  55                  60
Leu Ser Asn Glu Gly Arg Ala Lys Leu Arg Arg Gln Ser Leu Gly Phe
65                  70                  75                  80
Val Phe Gln Gln Gly Met Leu Val Pro Glu Leu Thr Ala Val Glu Asn
                85                  90                  95
Thr Ala Leu Pro Leu Met Leu Asn Gly Val Ser Gln Thr Asp Ala Val
            100                 105                 110
Arg Tyr Ala Thr Gln Trp Leu Glu Ser Met Gly Leu Gly Gly Met Glu
        115                 120                 125
Asp Arg Arg Ile Gly Gln Leu Ser Gly Gly Gln Ala Gln Arg Val Thr
    130                 135                 140
Ile Ala Arg Ser Gln Val Ile Asp Pro Ser Ile Val Phe Ala Asp Glu
145                 150                 155                 160
Pro Thr Gly Ala Leu Asp Ser Ala Thr Ala Val Glu Val Met Ala Ile
                165                 170                 175
Leu Leu Ser Ala Thr Thr Gly Arg Gly Arg Thr Leu Val Val Val Thr
            180                 185                 190
His Asp Glu Asp Val Ala Arg Arg Cys Gln Arg Ile Leu His Leu His
        195                 200                 205
Asp Gly Arg Ile Val Ser Asp His Val Arg His Ser Asp Gly Arg Trp
    210                 215                 220
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<210> 1995
<211> 285
<212> DNA
<213> Homo sapiens

<400> 1995
catcaccacc attatcaaca ccatcatcac caccattatc acctttatca ccaccatcat
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caccatcacc accatcatca ctaccaccat cacgcccatc atcatgtgat gactctcaat
120
actgtcctca tcatgtgtga cttggactgt ggaccagccc ctcgggctct gctctgctga
180
cctatattct ttgtctcttg ttcctgagaa gctgggagtt gagacccagt aaggtgttgt
240
acagacactt gtgaccccaa attccatgag acagaggacc tcccn
285

<210> 1996
<211> 59
<212> PRT
<213> Homo sapiens

<400> 1996
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His His His His Tyr Gln His His His His His His Tyr His Leu Tyr
 1               5                  10                  15
His His His His His His His His His His His Tyr His His His Ala
            20                  25                  30
His His His Val Met Thr Leu Asn Thr Val Leu Ile Met Cys Asp Leu
```

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        35                  40                  45
Asp Cys Gly Pro Ala Pro Arg Ala Leu Leu Cys
    50                  55

<210> 1997
<211> 313
<212> DNA
<213> Homo sapiens

<400> 1997
ccgctggtgg tggtgctgct gattggcatg gccatctata ccttccgcaa gaaagacctg
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ggcaagctgc acaagccggt cagcatcggc cggcgcgaga tgctggtggg gctggccatc
120
ggtggcggca tcggttttta cgacggcctg ttcgggccgg gtaccggcag tttcctgatg
180
ttcctgttcg tgcggttttt gcgttttgat ttcttgcatg cttctgccgc ggccaaggtt
240
gtcaacctgg ccaccaatgt ggcggcactg tgctttttca ttcccagcgg caatgtgctg
300
tatggctacg cgt
313

<210> 1998
<211> 104
<212> PRT
<213> Homo sapiens

<400> 1998
Pro Leu Val Val Val Leu Leu Ile Gly Met Ala Ile Tyr Thr Phe Arg
 1               5                  10                  15
Lys Lys Asp Leu Gly Lys Leu His Lys Pro Val Ser Ile Gly Arg Arg
            20                  25                  30
Glu Met Leu Val Gly Leu Ala Ile Gly Gly Gly Ile Gly Phe Tyr Asp
        35                  40                  45
Gly Leu Phe Gly Pro Gly Thr Gly Ser Phe Leu Met Phe Leu Phe Val
    50                  55                  60
Arg Phe Leu Arg Phe Asp Phe Leu His Ala Ser Ala Ala Ala Lys Val
65                  70                  75                  80
Val Asn Leu Ala Thr Asn Val Ala Ala Leu Cys Phe Phe Ile Pro Ser
                85                  90                  95
Gly Asn Val Leu Tyr Gly Tyr Ala
            100

<210> 1999
<211> 399
<212> DNA
<213> Homo sapiens

<400> 1999
ccgcggcgca agttggaatg gcaaaacatt ttcattcccg gcgagcaagg tagcttgagt
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tccactgcgc agagggcaga tgtgaagtac tccggtactg ttcattttac cggtgttggc
120
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ggaagaatgg atcttactct cgctgaccct gagattgtcg ttaacaatgg cgatgatcat
180
gtgattatgt ctgtgaagtc caagactatg gtcgggcagt tggttgacta tggccgtata
240
actttcgttg atatgaccgg ctctattacg cagggtcaaa acgatgcagc tcaggttgtg
300
gggaccaatg tcaagctgaa tagccaagcc gtcgatgcat tcgctggctt ctatcaagct
360
ggaaagccca tggatgacat cgattcgtcc ttaaagctt
399

<210> 2000
<211> 91
<212> PRT
<213> Homo sapiens

<400> 2000

Met	Asp	Leu	Thr	Leu	Ala	Asp	Pro	Glu	Ile	Val	Val	Asn	Asn	Gly	Asp
1				5				10					15		
Asp	His	Val	Ile	Met	Ser	Val	Lys	Ser	Lys	Thr	Met	Val	Gly	Gln	Leu
		20					25					30			
Val	Asp	Tyr	Gly	Arg	Ile	Thr	Phe	Val	Asp	Met	Thr	Gly	Ser	Ile	Thr
	35					40					45				
Gln	Gly	Gln	Asn	Asp	Ala	Ala	Gln	Val	Val	Gly	Thr	Asn	Val	Lys	Leu
50					55					60					
Asn	Ser	Gln	Ala	Val	Asp	Ala	Phe	Ala	Gly	Phe	Tyr	Gln	Ala	Gly	Lys
65				70					75						80
Pro	Met	Asp	Asp	Ile	Asp	Ser	Ser	Leu	Lys	Leu					
				85					90						

<210> 2001
<211> 1434
<212> DNA
<213> Homo sapiens

<400> 2001
nngaatgaag gacgtcataa tttgctgatc agcagtgcag ctgactggag gagggacaaa
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tttggcagga ccccactgca ctatgcagct gctaacggta gctaccagtg tgcagtaaca
120
ttggtgactg ctggggcagg tgtcaacgag gccgactgta aaggctgctc tcccctccac
180
tacgctgccg cttctgacac ttacaggnag agcggaaccc catacacctt ccagccatga
240
tgccgaagag ganncgagcc actgaaggag tcccgcagga aggaggcctt cttctgtctg
300
gagttcttac tggataacgg tgcagacccc tccctgcggg acaggcaggg ctacacagct
360
gtgcactatg cagccgccta tggcaacaga cagaacctcg aactgctctt agaaatgtcc
420
tttaactgcc tggaggatgt ggagagcacc attccagtca gccctttgca cttagctgcc
480
tacaacggtc actgtgaagc cttgaagacg ctggcggaga cgctggtgaa tctggacgta
540

agggaccaca agggccggac cgcactcttc ctggccacgg agcgcggctc tactgagtgt
600
gtggaggtgc ttacagccca cggcgcctct gccctcatca aggagcgcaa gcgcaagtgg
660
acacccctgc acgccgctgc tgcctctggc cacactgact ccctgcactt gctgatcgac
720
agtggggaac gagctgacat cacagatgtc atggatgcct atggacagac cccactgatg
780
ctggccatca tgaatggcca tgtggactgt gtacatctgc tgctagagaa aggatccaca
840
gctgatgctg ctgacctccg gggccgcact gccctccacc gcggggcagt gactggctgt
900
gaggactgcc tggctgccct gctggaccac gacgcatttg tgctgtgccg agactttaag
960
ggccgcacgc ccattcacct ggcctcagcc tgtggccaca ctgcagtact gcggaccctg
1020
ctgcaggctg ccctttccac agatcccctg gatgccgggg tggattacag cggatactcg
1080
cccatgcact gggcctccta cactggacat gaagattgtc tggagttgtt acttgaacac
1140
agcccgtttt cgtacctgga aggaaacccc ttcactcctt tgcactgtgc agtgattaat
1200
aaccaagaca gcaccacaga gatgctactg ggagctctgg gtgccaagat tgtgaacagc
1260
cgagatgcca aaggacggac ccccccttcac gccgctgcct tcgcggacaa tgtctctggg
1320
ctccggatgc tgctgcagca tcaagctgag gtgaacgcca ctgaccacac tggccgcact
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gcgctcatga cggcggctga gaacgggcag accgctgctg tggaatttct gctg
1434

<210> 2002
<211> 79
<212> PRT
<213> Homo sapiens

<400> 2002
Xaa Asn Glu Gly Arg His Asn Leu Leu Ile Ser Ser Ala Ala Asp Trp
1 5 10 15
Arg Arg Asp Lys Phe Gly Arg Thr Pro Leu His Tyr Ala Ala Ala Asn
20 25 30
Gly Ser Tyr Gln Cys Ala Val Thr Leu Val Thr Ala Gly Ala Gly Val
35 40 45
Asn Glu Ala Asp Cys Lys Gly Cys Ser Pro Leu His Tyr Ala Ala Ala
50 55 60
Ser Asp Thr Tyr Arg Xaa Ser Gly Thr Pro Tyr Thr Phe Gln Pro
65 70 75

<210> 2003
<211> 688
<212> DNA
<213> Homo sapiens

<400> 2003

ntcatgacta cggagacact gaagaaaatt cagattgata ggcagttttt cagcgatgtg
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attgcagata ccattaagga gttgcaagat tcggccactt acaacagtct cctgcaagct
120
ttgagcaaag agagggaaaa caaaatgcat ttctatgaca tcatttccag ggaggaaaaa
180
ggaagaaaac agataatatc acttcaaaaa cagctaatta atttcaaaaa ggaatggcaa
240
tttgaagtcc agagtcagaa tgagtatatt gctaacctca aggaccaact gcaagagatg
300
aaggcaaaat ccaacttgga gaatcgctac atgaaaacca ataccgagct gcagattgcc
360
cagacccaga aaaagtgtaa cagaacagag gaactcttgg tggaagagat tgagaaactc
420
aggatgaaaa ccgaagaaga ggcccggact catacagaga ttgaaatgtt ccttagaaag
480
gagcagcagg tgggtcccca cagcttttct atgctttgac ttttttttg tactctgctt
540
atactgagga aacaaaaaga atattttgaa ggaaaaccaa ccatcattct ttcagcctaa
600
tgaactttag ctcatgtttt ctttcagggt tatgcatctg aatagatatc ttatatagct
660
gtaatttgag agagtgcagg taaaattg
688

<210> 2004
<211> 172
<212> PRT
<213> Homo sapiens

<400> 2004
Xaa Met Thr Thr Glu Thr Leu Lys Lys Ile Gln Ile Asp Arg Gln Phe
 1   5   10   15
Phe Ser Asp Val Ile Ala Asp Thr Ile Lys Glu Leu Gln Asp Ser Ala
            20   25   30
Thr Tyr Asn Ser Leu Leu Gln Ala Leu Ser Lys Glu Arg Glu Asn Lys
        35   40   45
Met His Phe Tyr Asp Ile Ile Ser Arg Glu Glu Lys Gly Arg Lys Gln
    50   55   60
Ile Ile Ser Leu Gln Lys Gln Leu Ile Asn Phe Lys Lys Glu Trp Gln
65   70   75   80
Phe Glu Val Gln Ser Gln Asn Glu Tyr Ile Ala Asn Leu Lys Asp Gln
                85   90   95
Leu Gln Glu Met Lys Ala Lys Ser Asn Leu Glu Asn Arg Tyr Met Lys
            100   105   110
Thr Asn Thr Glu Leu Gln Ile Ala Gln Thr Gln Lys Lys Cys Asn Arg
        115   120   125
Thr Glu Glu Leu Leu Val Glu Glu Ile Glu Lys Leu Arg Met Lys Thr
    130   135   140
Glu Glu Glu Ala Arg Thr His Thr Glu Ile Glu Met Phe Leu Arg Lys
145   150   155   160
Glu Gln Gln Val Gly Pro His Ser Phe Ser Met Leu
                165   170

<210> 2005
<211> 354
<212> DNA
<213> Homo sapiens

<400> 2005
gctagcacca agccaaggtt atgtttcctt gcttgcatgt ggggtttctg gccagtcagc
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caagtgaact gattgacccc cagccctgtg gggaatttca gggggtatt gtcttggtca
120
tcggagtcag gggtggcctt tnagccaagg ctgcattaac ttttgggaaa agaaatggga
180
agcccgccgt gtcacagggt ctcctgaccg gctgggtagg gtttggcctt atcttacagc
240
cagtgctgtg tttgctcaga tggacgcaca tggaaaccag gctaggatca tcttcccaat
300
gtctactccc tgctttggtc tgtcctgaaa acaattgcaa agacattgtg gctg
354

<210> 2006
<211> 111
<212> PRT
<213> Homo sapiens

<400> 2006
Met Phe Pro Cys Leu His Val Gly Phe Leu Ala Ser Gln Pro Ser Glu
1 5 10 15
Leu Ile Asp Pro Gln Pro Cys Gly Glu Phe Gln Gly Gly Ile Val Leu
20 25 30
Val Ile Gly Val Arg Gly Gly Leu Xaa Ala Lys Ala Ala Leu Thr Phe
35 40 45
Gly Lys Arg Asn Gly Lys Pro Ala Val Ser Gln Gly Leu Leu Thr Gly
50 55 60
Trp Val Gly Phe Gly Leu Ile Leu Gln Pro Val Leu Cys Leu Leu Arg
65 70 75 80
Trp Thr His Met Glu Thr Arg Leu Gly Ser Ser Ser Gln Cys Leu Leu
85 90 95
Pro Ala Leu Val Cys Pro Glu Asn Asn Cys Lys Asp Ile Val Ala
100 105 110

<210> 2007
<211> 335
<212> DNA
<213> Homo sapiens

<400> 2007
nnacgcgtgc catgtgcatg tgtatatgca tgtatgtgcg tatgtgtgtg catgtgtgtg
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tgtatatgca tgtgtgtatg tgcatgtacg tgtnngtgca tatgcgtgtg catgcatgcg
120
tgtgcgtatg tgtgcatann catgtgcaca catgtacaca cgtgtacatg ttcatgcatg
180
tgcacgtgca tatgtgtaca cgtgtatgcg tgtacatgta tgagcatatg tacacgtgtg
240

gatgtgtgtg tatgcatgtg tgtgtgcaca gatatgcctt ttcctttcat acaggctggt
300
ttgagtattg ctggtaggca gggacaactt tccgt
335

<210> 2008
<211> 111
<212> PRT
<213> Homo sapiens

<400> 2008
Xaa Arg Val Pro Cys Ala Cys Val Tyr Ala Cys Met Cys Val Cys Val
1 5 10 15
Cys Met Cys Val Cys Ile Cys Met Cys Val Cys Ala Cys Thr Cys Xaa
20 25 30
Cys Ile Cys Val Cys Met His Ala Cys Ala Tyr Val Cys Ile Xaa Met
35 40 45
Cys Thr His Val His Thr Cys Thr Cys Ser Cys Met Cys Thr Cys Ile
50 55 60
Cys Val His Val Tyr Ala Cys Thr Cys Met Ser Ile Cys Thr Arg Val
65 70 75 80
Asp Val Cys Val Cys Met Cys Val Cys Thr Asp Met Pro Phe Pro Phe
85 90 95
Ile Gln Ala Gly Leu Ser Ile Ala Gly Arg Gln Gly Gln Leu Ser
100 105 110

<210> 2009
<211> 288
<212> DNA
<213> Homo sapiens

<400> 2009
gacatcaccc cgctgctggc caaccccaac ggtttctccg cagcgatcga ggaactggtg
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ctgcgttccc cacgcgacat cgacgtggtc gtcggcatgg aggctcgcgg cttcctcttc
120
gcagctccgg tcgccctggc catcggggca ggattcgtgc cggtgcgcaa gccggggaag
180
ctccccggcc aggtgtattc cgagaccttt gccatggagt acggggagga gaccctcacc
240
gtccaccagt acgccatcaa gccggggtcg cgcgtcatca tcgtcgac
288

<210> 2010
<211> 96
<212> PRT
<213> Homo sapiens

<400> 2010
Asp Ile Thr Pro Leu Leu Ala Asn Pro Asn Gly Phe Ser Ala Ala Ile
1 5 10 15
Glu Glu Leu Val Leu Arg Ser Pro Arg Asp Ile Asp Val Val Val Gly
20 25 30
Met Glu Ala Arg Gly Phe Leu Phe Ala Ala Pro Val Ala Leu Ala Ile

```
        35                  40                  45
Gly Ala Gly Phe Val Pro Val Arg Lys Pro Gly Lys Leu Pro Gly Gln
    50                  55                  60
Val Tyr Ser Glu Thr Phe Ala Met Glu Tyr Gly Glu Glu Thr Leu Thr
65                  70                  75                  80
Val His Gln Tyr Ala Ile Lys Pro Gly Ser Arg Val Ile Ile Val Asp
                85                  90                  95

<210> 2011
<211> 384
<212> DNA
<213> Homo sapiens

<400> 2011
ctcgagcagt ctctgcatgt taacaccccc gtacggcccg taaagcataa ccgtctccga
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cttgccgccg cctgcgtgct tcgctaggcg gccggtgaac ccacctgagg gccggatgta
120
gaagtcaacg gtggacgacg ggttggaggg tttgttgatt ggcgagtggg gaagcgagca
180
gattgtaaat tggtagaacg gggaacagag attagtcaca atgacgagaa cgacaacaga
240
atgttgattg ttatagccat ctctggagga gagggaaaaa gccaggtatc tagacagcga
300
aagcaaatgt gagccgaggg gacagtgccg tccttcgttc ctcggcaact cccacgaggc
360
accttccatt ctgtgggcag aatt
384

<210> 2012
<211> 123
<212> PRT
<213> Homo sapiens

<400> 2012
Met Glu Gly Ala Ser Trp Glu Leu Pro Arg Asn Glu Gly Arg His Cys
 1               5                  10                  15
Pro Leu Gly Ser His Leu Leu Ser Leu Ser Arg Tyr Leu Ala Phe Ser
            20                  25                  30
Leu Ser Ser Arg Asp Gly Tyr Asn Asn Gln His Ser Val Val Val Leu
        35                  40                  45
Val Ile Val Thr Asn Leu Cys Ser Pro Phe Tyr Gln Phe Thr Ile Cys
    50                  55                  60
Ser Leu Pro His Ser Pro Ile Asn Lys Pro Ser Asn Pro Ser Ser Thr
65                  70                  75                  80
Val Asp Phe Tyr Ile Arg Pro Ser Gly Gly Phe Thr Gly Arg Leu Ala
                85                  90                  95
Lys His Ala Gly Gly Gly Lys Ser Glu Thr Val Met Leu Tyr Gly Pro
            100                 105                 110
Tyr Gly Gly Val Asn Met Gln Arg Leu Leu Glu
        115                 120

<210> 2013
<211> 309
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<212> DNA
<213> Homo sapiens

<400> 2013
gcgtatcccc acggctacgg catgaccgcg cttatcggcc cggacctgtc caccgtcgaa
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gccttgctcg cccaggtcca cagcacacaa accccggtgt acctggccaa tatcaatgcc
120
gataaccaga cggttatcgc gggcagcgac ggggcaatga aagcagtcgc caatctggtc
180
cgcggcaacg gcgtcgccaa acgcttggcc gtcagcgtgc cgtcccattg tgcgctgctg
240
gaaaaacctg ccgaaacact ggcccaagcc ttcgctgaag tgacgctgaa aacgccgncn
300
nnncccncn
309

<210> 2014
<211> 103
<212> PRT
<213> Homo sapiens

<400> 2014
Ala Tyr Pro His Gly Tyr Gly Met Thr Ala Leu Ile Gly Pro Asp Leu
 1   5   10   15
Ser Thr Val Glu Ala Leu Leu Ala Gln Val His Ser Thr Gln Thr Pro
            20   25   30
Val Tyr Leu Ala Asn Ile Asn Ala Asp Asn Gln Thr Val Ile Ala Gly
        35   40   45
Ser Asp Gly Ala Met Lys Ala Val Ala Asn Leu Val Arg Gly Asn Gly
    50   55   60
Val Ala Lys Arg Leu Ala Val Ser Val Pro Ser His Cys Ala Leu Leu
65   70   75   80
Glu Lys Pro Ala Glu Thr Leu Ala Gln Ala Phe Ala Glu Val Thr Leu
                85   90   95
Lys Thr Pro Xaa Xaa Pro Xaa
            100

<210> 2015
<211> 329
<212> DNA
<213> Homo sapiens

<400> 2015
acgcgtgcca tgctcggtat ccgccgccac caccccgtct ttgggaccgg cgagttcacc
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gatctaggcg ggccggacat ggcagtgatg tccttcctac gtcacaacga gcacgaaacg
120
gtcctgtgcc tggctaatct ctccgatact gagcggacgg ttgcccttca ccttccacaa
180
ttcgcgggcg tggcgggctc ttctctcatc catggtcagg acgcgcaacc agtaaaagct
240
gacggaacac tgtccgtacc gttgtggcca tatggctatc gatggctgca gatgtccggt
300

gaggagaggt catgaccgct tgggaagac
329

<210> 2016
<211> 104
<212> PRT
<213> Homo sapiens

<400> 2016
Thr Arg Ala Met Leu Gly Ile Arg Arg His His Pro Val Phe Gly Thr
1 5 10 15
Gly Glu Phe Thr Asp Leu Gly Gly Pro Asp Met Ala Val Met Ser Phe
20 25 30
Leu Arg His Asn Glu His Glu Thr Val Leu Cys Leu Ala Asn Leu Ser
35 40 45
Asp Thr Glu Arg Thr Val Ala Leu His Leu Pro Gln Phe Ala Gly Val
50 55 60
Ala Gly Ser Ser Leu Ile His Gly Gln Asp Ala Gln Pro Val Lys Ala
65 70 75 80
Asp Gly Thr Leu Ser Val Pro Leu Trp Pro Tyr Gly Tyr Arg Trp Leu
85 90 95
Gln Met Ser Gly Glu Glu Arg Ser
100

<210> 2017
<211> 457
<212> DNA
<213> Homo sapiens

<400> 2017
accaaggtca gattcatggc ctcttttcct ccagcggcca gcaggaaacg cggggagccc
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ttgatcatct ccgacatcaa gaaaggcagc gtggcacaca ggacgggcac cctggagcca
120
ggcgacaagc tactggccat tgacaatatc cgcctggaca actgccccat ggaggacgcc
180
gtgcaaatcc tgcggcagtg cgaggacctg gtgaagctga agatccggaa ggacgaggac
240
aactctgatg agctggagac cacaggtgcc gtcagttaca cagtggagct gaagcgctac
300
gggggtcccc tgggcatcac catttcgggc acggaggaac cttttgaccc catttttcatc
360
tcaggcctcc ccaaacgtgg cctggctgag aggactggtg ccatccagtg ggggaaccgc
420
ttcggaccat aacaacgtta ttctcaggga cggacca
457

<210> 2018
<211> 143
<212> PRT
<213> Homo sapiens

<400> 2018
Thr Lys Val Arg Phe Met Ala Ser Phe Pro Pro Ala Ala Ser Arg Lys

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 1               5                  10                  15
Arg Gly Glu Pro Leu Ile Ile Ser Asp Ile Lys Lys Gly Ser Val Ala
            20                  25                  30
His Arg Thr Gly Thr Leu Glu Pro Gly Asp Lys Leu Leu Ala Ile Asp
        35                  40                  45
Asn Ile Arg Leu Asp Asn Cys Pro Met Glu Asp Ala Val Gln Ile Leu
    50                  55                  60
Arg Gln Cys Glu Asp Leu Val Lys Leu Lys Ile Arg Lys Asp Glu Asp
65                  70                  75                  80
Asn Ser Asp Glu Leu Glu Thr Thr Gly Ala Val Ser Tyr Thr Val Glu
                85                  90                  95
Leu Lys Arg Tyr Gly Gly Pro Leu Gly Ile Thr Ile Ser Gly Thr Glu
            100                 105                 110
Glu Pro Phe Asp Pro Ile Phe Ile Ser Gly Leu Pro Lys Arg Gly Leu
        115                 120                 125
Ala Glu Arg Thr Gly Ala Ile Gln Trp Gly Asn Arg Phe Gly Pro
    130                 135                 140
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<210> 2019
<211> 483
<212> DNA
<213> Homo sapiens

<400> 2019
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120
gactatctca acgtcatcag gggacatatc gacaccgatc ccggcctgac cgacgtcatc
180
cccattcagg gcatggcgag cgcgccgcat cttgatttcg caggcgaaat ccgcgcggcg
240
accagcttcc ccgtcttcca tgccgccaaa attcaggatg tcgccaccgc ccggcatgcg
300
attgccgccg gcaaggtcga catgatcggc atgacccgcg cccacatgac cgatccgcat
360
atcgtccgca agatcatgga aaaacaggag gaggacatcc gcccctgcgt cggcgccaat
420
tattgtcttg atcgcattta tcaaggcggc ctcgccttct gcattcacaa tgcggcaacc
480
ggc
483

<210> 2020
<211> 161
<212> PRT
<213> Homo sapiens

<400> 2020
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 1               5                  10                  15
Cys Leu Glu Asn Gly Thr Gly Lys Ala Glu Gly Ile Glu Ile Ser Arg
            20                  25                  30
Arg Leu Lys Glu Ser Gly Leu Ile Asp Tyr Leu Asn Val Ile Arg Gly
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        35                  40                  45
His Ile Asp Thr Asp Pro Gly Leu Thr Asp Val Ile Pro Ile Gln Gly
    50                  55                  60
Met Ala Ser Ala Pro His Leu Asp Phe Ala Gly Glu Ile Arg Ala Ala
65                  70                  75                  80
Thr Ser Phe Pro Val Phe His Ala Ala Lys Ile Gln Asp Val Ala Thr
                85                  90                  95
Ala Arg His Ala Ile Ala Ala Gly Lys Val Asp Met Ile Gly Met Thr
            100                 105                 110
Arg Ala His Met Thr Asp Pro His Ile Val Arg Lys Ile Met Glu Lys
        115                 120                 125
Gln Glu Glu Asp Ile Arg Pro Cys Val Gly Ala Asn Tyr Cys Leu Asp
    130                 135                 140
Arg Ile Tyr Gln Gly Gly Leu Ala Phe Cys Ile His Asn Ala Ala Thr
145                 150                 155                 160
Gly
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<210> 2021
<211> 797
<212> DNA
<213> Homo sapiens

<400> 2021
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120
ccctcctccc tcagtactcg cgagactacg aaaacacgtg ctgaaatgga cacccgctcc
180
gggagccagt gttccgtcac cccagaagcc atactcaata atgaaaagct ggtcttgccg
240
ccccgcatct ccagagtgaa cggctggtcg ttacccctgc actacttcca ggtggtgacc
300
tgggctgtct tcgtgggcct ttcctcggcc accttcggga tcttcattcc cttcctgcct
360
cacgcgtgga aatacatcgc ctatgtggta tccttttcat cgtggcatgg tctaagcggg
420
aggggttcct ggaggaccct gcgatggacc tggctgtggg gtctgggcca tggctgcccg
480
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540
tggcccctta tggttttggc cagccccggt taagggtcag gccaggccag cgttggctga
600
gggagttccg gagagggaat ctgtcaggag ggacagcagc cccctggcgt ggcgcaggac
660
ccgccctgct ggcagccttc cgctaaaatc cctgcgcagc attttgcaca tggccagccc
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780
gcgtttccat gccaagc
797

<210> 2022

<211> 135
<212> PRT
<213> Homo sapiens

<400> 2022
Met Asp Thr Arg Ser Gly Ser Gln Cys Ser Val Thr Pro Glu Ala Ile
1 5 10 15
Leu Asn Asn Glu Lys Leu Val Leu Pro Pro Arg Ile Ser Arg Val Asn
20 25 30
Gly Trp Ser Leu Pro Leu His Tyr Phe Gln Val Val Thr Trp Ala Val
35 40 45
Phe Val Gly Leu Ser Ser Ala Thr Phe Gly Ile Phe Ile Pro Phe Leu
50 55 60
Pro His Ala Trp Lys Tyr Ile Ala Tyr Val Val Ser Phe Ser Ser Trp
65 70 75 80
His Gly Leu Ser Gly Arg Gly Ser Trp Arg Thr Leu Arg Trp Thr Trp
85 90 95
Leu Trp Gly Leu Gly His Gly Cys Pro Val Ala Pro Val Thr Cys Pro
100 105 110
Gly Pro Asp Tyr Val Pro Arg Ala Cys Arg Trp Ala Gln Trp Pro Leu
115 120 125
Met Val Leu Ala Ser Pro Gly
130 135

<210> 2023
<211> 462
<212> DNA
<213> Homo sapiens

<400> 2023
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120
actgctccgc gcatcattac cgtccacatc ccagtggaca agatcggtga ggtcatcggc
180
cccaagggca agatgattaa ccagattcag gacgacactg gcgccaatat ctctattgag
240
gacgatggca cgattttcat cggggctgat aacggagatt cggccgagtc tgcccgttcg
300
atgatcaacg cgatcgctaa cccacagatg cccgaggtcg gtgagcgtta cctcggcacc
360
gtcgtcaaga cgacgagctt tggcgctttc gtctctctgc tgcccggcaa ggatggtctg
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462

<210> 2024
<211> 154
<212> PRT
<213> Homo sapiens

<400> 2024
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Ala Lys Glu Ala Arg Thr Ala Ile Leu Glu Val Met Asn Glu Ala Ile
            20                  25                  30
Asp Ser Pro Asp Glu Met Ala Pro Thr Ala Pro Arg Ile Ile Thr Val
        35                  40                  45
His Ile Pro Val Asp Lys Ile Gly Glu Val Ile Gly Pro Lys Gly Lys
    50                  55                  60
Met Ile Asn Gln Ile Gln Asp Asp Thr Gly Ala Asn Ile Ser Ile Glu
65                  70                  75                  80
Asp Asp Gly Thr Ile Phe Ile Gly Ala Asp Asn Gly Asp Ser Ala Glu
                85                  90                  95
Ser Ala Arg Ser Met Ile Asn Ala Ile Ala Asn Pro Gln Met Pro Glu
            100                 105                 110
Val Gly Glu Arg Tyr Leu Gly Thr Val Val Lys Thr Thr Ser Phe Gly
        115                 120                 125
Ala Phe Val Ser Leu Leu Pro Gly Lys Asp Gly Leu Leu His Ile Ser
    130                 135                 140
Lys Met Arg Asp Leu Asn Asp Gly Lys Arg
145                 150
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<210> 2025
<211> 872
<212> DNA
<213> Homo sapiens

<400> 2025
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120
agggaggtct gtacctcctc cctcatctca ttttacacaa ggcgacaggt cagaggccag
180
ggtgggacga gagcgaggga gcactgtctc tggcagcagc acttgccact ccacaatgtg
240
gagaccagaa cggcacccca gagagcacgg gggaaatggc tcatctttaa aacaatggca
300
gaagaaatcc agccaaggtc acttttcctg tgtgagcatg tttaaggcca gagagtggct
360
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420
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480
gcaccgcctc ctgtaactgc agctgaagct ggaaagagac cgcagagctc ttgagaggcg
540
cggaaaacca atggcgaaat attttgtcac agatgacctg caggttgttg tttacgcgct
600
gcgctccgca tttgttgact cgtaaatcac atcttgaaaa acagtcaaag aaattgcagt
660
cttcatctcc tgtgcagttt tgctcaagga tttccctcat tttaggttca aaaaaggcca
720
tgtccacatc aatagccacc actgtgaagt cgctccggat ggcaaagttt tccggcttga
780
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840

agctgagtgc gaggcccctg atggccctgg cc
872

<210> 2026
<211> 157
<212> PRT
<213> Homo sapiens

<400> 2026
Met Gly Asn His Phe Asp Arg Asp Cys Thr His Arg Leu His Leu Cys
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Asp Ile Lys Pro Glu Asn Phe Ala Ile Arg Ser Asp Phe Thr Val Val
20 25 30
Ala Ile Asp Val Asp Met Ala Phe Phe Glu Pro Lys Met Arg Glu Ile
35 40 45
Leu Glu Gln Asn Cys Thr Gly Asp Glu Asp Cys Asn Phe Phe Asp Cys
50 55 60
Phe Ser Arg Cys Asp Leu Arg Val Asn Lys Cys Gly Ala Gln Arg Val
65 70 75 80
Asn Asn Asn Leu Gln Val Ile Cys Asp Lys Ile Phe Arg His Trp Phe
85 90 95
Ser Ala Pro Leu Lys Ser Ser Ala Val Ser Phe Gln Leu Gln Leu Gln
100 105 110
Leu Gln Glu Ala Val Gln Glu Cys Ala Asp Pro Gly Val Pro Ser Gly
115 120 125
Asn Thr Arg Arg Ala Ala Ser Ser Val Phe Trp Lys Leu Arg Gln Leu
130 135 140
Leu Gln Ala Thr Leu Arg Glu Leu Gln Glu Ala Glu Lys
145 150 155

<210> 2027
<211> 721
<212> DNA
<213> Homo sapiens

<400> 2027
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120
agggttgtaa tgtcacttct gtctaattca ttacagaatt acagaatcaa atcatgttag
180
ccctagaaga aactgcagat cattttgttc aatcttctca ttatatagga aaggaaattt
240
gagggccagt gcaatggttt gccaaggtca cacaactagt tagtggaagg atccaggcat
300
tctaattcct ttctttcact aatacatttg gactgctcta cagaattact tctgtctgat
360
actatccact ttgaagagta gctagcatat agtagccatt tacttttggc tcaattaaaa
420
gcaaacattt ttgggacaaa atcaggcttt cctgattact tcttagataa cagagcccac
480
acagtattaa aacatgcagc ctttctttat gcaaaaagat tgaatatgga gccacttgaa
540

tcttaaactt cagtctgcag ctataaccaa tatcatcaga agttatacac aattggcaaa
600
agaatagctt attctgccca aatacttgtc cagtcactag gatcatttca ctttttgaa
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720
a
721

<210> 2028
<211> 114
<212> PRT
<213> Homo sapiens

<400> 2028
Met Asn Ser Arg Ser Gly Asn Thr Ser Leu Pro Lys Ala Asn Gly Ile
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Gln Lys Ser Glu Met Ile Leu Val Thr Gly Gln Val Phe Gly Gln Asn
            20   25   30
Lys Leu Phe Phe Cys Gln Leu Cys Ile Thr Ser Asp Asp Ile Gly Tyr
        35   40   45
Ser Cys Arg Leu Lys Phe Lys Ile Gln Val Ala Pro Tyr Ser Ile Phe
    50   55   60
Leu His Lys Glu Arg Leu His Val Leu Ile Leu Cys Gly Leu Cys Tyr
65   70   75   80
Leu Arg Ser Asn Gln Glu Ser Leu Ile Leu Ser Gln Lys Cys Leu Leu
                85   90   95
Leu Ile Glu Pro Lys Val Asn Gly Tyr Tyr Met Leu Ala Thr Leu Gln
            100   105   110
Ser Gly

<210> 2029
<211> 8028
<212> DNA
<213> Homo sapiens

<400> 2029
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120
gaggcggcgg tggtggctga gtccgtggtg gcagaggcga aggcgacagc tctaggggtt
180
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300
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420
gaagaggaag acagcctcaa gagccaagag ggggaaagtg tcacagaaga tatcagcttt
480

ctagagtctc caaatccaga aaacaaggac tatgaagagc caaagaaagt acggaaacca
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gctttgaccg ccattgaagg cacagcacat ggggagccct gccacttccc ttttcttttc
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660
gctacaacct atgactacaa agcagatgaa aagtggggct tttgtgaaac tgaagaagag
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960
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1080
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1320
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1380
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1980
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6480
aggaacacca tggtagactc tttttgtaaa tgtattttgt atttaatgaa atgcagtata
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aaggttggtg aagtgtaata taattgtgta aacaaatcct gttaatagag agatgtacag
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6660
tatgctgtaa tataccacaa ccaagcaccc tttccagaca gacttttttt aagctgaatg
6720
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6780
aatttgaatt tatctttcat tttaaactcc tgaaattcag atttttacaa gtccaatatt
6840
gccctaggga gaacatgaat ttgctaagaa atgttatctt ttaaatctct gatatctttg
6900
tcttgaagca gccttgatat gtagtaagcg tgattcactt tagcctgatt ataatattat
6960

ttatctaaag tttgtttatg cattgccttg tcccaggaat tttttaagag gacttgcaga
7020
gacacgtacc acacagtaac atttagacta aatatgctct gagtaaagga gaaatgaaaa
7080
aatattaaat caagagtgaa catgtacaca aagtgcaatt ggaagtgggc tacaaattta
7140
gcccccagct tcccagcagg caactcaaag aggtaactga ggtaaaatgt tccagctcag
7200
aagcattgga tcttggataa aaagcctaca tgatgcaaac tgtggcaact gagatgtcag
7260
atctcaagat ctcaaattgt acttgtggga gcacagtcag tgaccccaga tgaccttgac
7320
tgacctaaaa gttgtggggg aagtcggatg tcagagcctt aacaccagca ggtgaccatc
7380
caacctgggg caatgcctgc ctgttcacca cttagcctct ttctggcaag tcattagaat
7440
gtcctccatc ttcattggct gcaacttgat gagctacagc ctctttccta acttccttta
7500
tgatgctagt ttaggttggt tataccagct tggaagtatg cttagattaa gttacagcag
7560
atacacaaat tagatgcaag taaaaaaaat cagaatttct gtagtagaaa ctacgaaaaa
7620
taaaaaggaa agtttttact ttttgggtat ttttttacga ataagaaaaa gtgagcgtta
7680
atcagttcaa aaggaggtac tgctgtgtaa tgggctttgt acgttccttc tcatgtcact
7740
tacgtcacta cttcgccatc aaattgaaca agcttttaat tagatcctga aaattcacta
7800
tgctagtagt ttattggtag tattatattt tgagtagaac tctgattttc cctagaggcc
7860
aaattctttt tatctgggtt aatttctttt aaacataaca atgttaatgc tgaattgtat
7920
attaaatccc atttctaaaa accacacaat tttttctcat gtaagttgag tggaatgtgg
7980
ttagttaact gaatttggaa tgttcatata aataatttgt tgctgctc
8028

<210> 2030
<211> 794
<212> PRT
<213> Homo sapiens

<400> 2030
Met Arg Val Arg Ile Gly Leu Thr Leu Leu Leu Cys Ala Val Leu Leu
1 5 10 15
Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp Glu Ser
20 25 30
Leu Asp Ser Lys Thr Thr Leu Thr Ser Asp Glu Ser Val Lys Asp His
35 40 45
Thr Thr Ala Gly Arg Val Val Ala Gly Gln Ile Phe Leu Asp Ser Glu
50 55 60
Glu Ser Glu Leu Glu Ser Ser Ile Gln Glu Glu Glu Asp Ser Leu Lys
65 70 75 80
Ser Gln Glu Gly Glu Ser Val Thr Glu Asp Ile Ser Phe Leu Glu Ser

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                85                  90                  95
Pro Asn Pro Glu Asn Lys Asp Tyr Glu Glu Pro Lys Lys Val Arg Lys
            100                 105                 110
Pro Ala Leu Thr Ala Ile Glu Gly Thr Ala His Gly Glu Pro Cys His
        115                 120                 125
Phe Pro Phe Leu Phe Leu Asp Lys Glu Tyr Asp Glu Cys Thr Ser Asp
    130                 135                 140
Gly Arg Glu Asp Gly Arg Leu Trp Cys Ala Thr Thr Tyr Asp Tyr Lys
145                 150                 155                 160
Ala Asp Glu Lys Trp Gly Phe Cys Glu Thr Glu Glu Glu Ala Ala Lys
                165                 170                 175
Arg Arg Gln Met Gln Glu Ala Glu Met Met Tyr Gln Thr Gly Met Lys
            180                 185                 190
Ile Leu Asn Gly Ser Asn Lys Lys Ser Gln Lys Arg Glu Ala Tyr Arg
        195                 200                 205
Tyr Leu Gln Lys Ala Ala Ser Met Asn His Thr Lys Ala Leu Glu Arg
    210                 215                 220
Val Ser Tyr Ala Leu Leu Phe Gly Asp Tyr Leu Pro Gln Asn Ile Gln
225                 230                 235                 240
Ala Ala Arg Glu Met Phe Glu Lys Leu Thr Glu Glu Gly Ser Pro Lys
                245                 250                 255
Gly Gln Thr Ala Leu Gly Phe Leu Tyr Ala Ser Gly Leu Gly Val Asn
            260                 265                 270
Ser Ser Gln Ala Lys Ala Leu Val Tyr Tyr Thr Phe Gly Ala Leu Gly
        275                 280                 285
Gly Asn Leu Ile Ala His Met Val Leu Gly Tyr Arg Tyr Trp Ala Gly
    290                 295                 300
Ile Gly Val Leu Gln Ser Cys Glu Ser Ala Leu Thr His Tyr Arg Leu
305                 310                 315                 320
Val Ala Asn His Val Ala Ser Asp Ile Ser Leu Thr Gly Gly Ser Val
                325                 330                 335
Val Gln Arg Ile Arg Leu Pro Asp Glu Val Glu Asn Pro Gly Met Asn
            340                 345                 350
Ser Gly Met Leu Glu Glu Asp Leu Ile Gln Tyr Tyr Gln Phe Leu Ala
        355                 360                 365
Glu Lys Gly Asp Val Gln Ala Gln Val Gly Leu Gly Gln Leu His Leu
    370                 375                 380
His Gly Gly Arg Gly Val Glu Gln Asn His Gln Arg Ala Phe Asp Tyr
385                 390                 395                 400
Phe Asn Leu Ala Ala Asn Ala Gly Asn Ser His Ala Met Ala Phe Leu
                405                 410                 415
Gly Lys Met Tyr Ser Glu Gly Ser Asp Ile Val Pro Gln Ser Asn Glu
            420                 425                 430
Thr Ala Leu His Tyr Phe Lys Lys Ala Ala Asp Met Gly Asn Pro Val
        435                 440                 445
Gly Gln Ser Gly Leu Gly Met Ala Tyr Leu Tyr Gly Arg Gly Val Gln
    450                 455                 460
Val Asn Tyr Asp Leu Ala Leu Lys Tyr Phe Gln Lys Ala Ala Glu Gln
465                 470                 475                 480
Gly Trp Val Asp Gly Gln Leu Gln Leu Gly Ser Met Tyr Tyr Asn Gly
                485                 490                 495
Ile Gly Val Lys Arg Asp Tyr Lys Gln Ala Leu Lys Tyr Phe Asn Leu
            500                 505                 510
Ala Ser Gln Gly Gly His Ile Leu Ala Phe Tyr Asn Leu Ala Gln Met
```

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        515                 520                 525
His Ala Ser Gly Thr Gly Val Met Arg Ser Cys His Thr Ala Val Glu
    530                 535                 540
Leu Phe Lys Asn Val Cys Glu Arg Gly Arg Trp Ser Glu Arg Leu Met
545                 550                 555                 560
Thr Ala Tyr Asn Ser Tyr Lys Asp Gly Asp Tyr Asn Ala Ala Val Ile
                565                 570                 575
Gln Tyr Leu Leu Leu Ala Glu Gln Gly Tyr Glu Val Ala Gln Ser Asn
            580                 585                 590
Ala Ala Phe Ile Leu Asp Gln Arg Glu Ala Ser Ile Val Gly Glu Asn
        595                 600                 605
Glu Thr Tyr Pro Arg Ala Leu Leu His Trp Asn Arg Ala Ala Ser Gln
    610                 615                 620
Gly Tyr Thr Val Ala Arg Ile Lys Leu Gly Asp Tyr His Phe Tyr Gly
625                 630                 635                 640
Phe Gly Thr Asp Val Asp Tyr Glu Thr Ala Phe Ile His Tyr Arg Leu
                645                 650                 655
Ala Ser Glu Gln Gln His Ser Ala Gln Ala Met Phe Asn Leu Gly Tyr
            660                 665                 670
Met His Glu Lys Gly Leu Gly Ile Lys Gln Asp Ile His Leu Ala Lys
        675                 680                 685
Arg Phe Tyr Asp Met Ala Ala Glu Ala Ser Pro Asp Ala Gln Val Pro
    690                 695                 700
Val Phe Leu Ala Leu Cys Lys Leu Gly Val Val Tyr Phe Leu Gln Tyr
705                 710                 715                 720
Ile Arg Glu Thr Asn Ile Arg Asp Met Phe Thr Gln Leu Asp Met Asp
                725                 730                 735
Gln Leu Leu Gly Pro Glu Trp Asp Leu Tyr Leu Met Thr Ile Ile Ala
            740                 745                 750
Leu Leu Leu Gly Thr Val Ile Ala Tyr Arg Gln Arg Gln His Gln Asp
        755                 760                 765
Met Pro Ala Pro Arg Pro Pro Gly Pro Arg Pro Ala Pro Pro Gln Gln
    770                 775                 780
Glu Gly Pro Pro Glu Gln Gln Pro Pro Gln
785                 790
```

<210> 2031
<211> 662
<212> DNA
<213> Homo sapiens

<400> 2031
atcatcgaaa gcagcgcccg ccagcaggat tcgatttctc gccaactgac ccagcagttc
60
atcagccaat ggcaggcggc tcacccggcg gatcagatca ccgtgcgtga cgtggcgctg
120
aaccccgtgc cgcacctgga cacgcatctg ctcggcggct ggatgaaacc tgccgaacag
180
cgcagcgcga tcgaacaggc ttccctggac cgctccaatc aattgaccga cgaattgctc
240
gccgccgacg tgctggtgat ggctgcaccg atgtacaact tcgctatccc cagcaccctc
300
aaagcctggc tggaccacgt gttgcgtgcc ggtgtgacct tcaagtacac cgccaccggc
360

ccccagggat tgctgcacgg caagcgcgcg attgtgctga ccgctcgcgg cggcattcat
420
accggcgcca gctccgatca ccaggaaccg tacctgcgcc aggtcatggc ctttatcggg
480
attcatgacg tcacgttcat tcatgccgaa ggggtgaact tgagcggtga cttccaggaa
540
aaaggcctta accacgccaa ggcgttgctg gcgcaacttg tggcatgaac cgagtcaacg
600
gttaatcgtc acataatcgc cgggtgttta tatcgcttca cgcaaaccct tcaagtacgc
660
gt
662

<210> 2032
<211> 195
<212> PRT
<213> Homo sapiens

<400> 2032
Ile Ile Glu Ser Ser Ala Arg Gln Gln Asp Ser Ile Ser Arg Gln Leu
1 5 10 15
Thr Gln Gln Phe Ile Ser Gln Trp Gln Ala Ala His Pro Ala Asp Gln
20 25 30
Ile Thr Val Arg Asp Val Ala Leu Asn Pro Val Pro His Leu Asp Thr
35 40 45
His Leu Leu Gly Gly Trp Met Lys Pro Ala Glu Gln Arg Ser Ala Ile
50 55 60
Glu Gln Ala Ser Leu Asp Arg Ser Asn Gln Leu Thr Asp Glu Leu Leu
65 70 75 80
Ala Ala Asp Val Leu Val Met Ala Ala Pro Met Tyr Asn Phe Ala Ile
85 90 95
Pro Ser Thr Leu Lys Ala Trp Leu Asp His Val Leu Arg Ala Gly Val
100 105 110
Thr Phe Lys Tyr Thr Ala Thr Gly Pro Gln Gly Leu Leu His Gly Lys
115 120 125
Arg Ala Ile Val Leu Thr Ala Arg Gly Gly Ile His Thr Gly Ala Ser
130 135 140
Ser Asp His Gln Glu Pro Tyr Leu Arg Gln Val Met Ala Phe Ile Gly
145 150 155 160
Ile His Asp Val Thr Phe Ile His Ala Glu Gly Val Asn Leu Ser Gly
165 170 175
Asp Phe Gln Glu Lys Gly Leu Asn His Ala Lys Ala Leu Leu Ala Gln
180 185 190
Leu Val Ala
195

<210> 2033
<211> 380
<212> DNA
<213> Homo sapiens

<400> 2033
aaattttaaa acggtcatca tttaacaggc gaagctgtaa aacgcagtct tgaagaggga
60

atgaaaaaaa gtgatttgtt aaaaggatca cttcctatca aatcaatcaa cgctcatgga
120
caaaaagtca caatcaatac taaagaacct tatccagaat taaagtctga actcgcaagc
180
ccatttgctg ctatatacga cacaaaagct aaaaacaaag taactgatca acctgttggt
240
acgggtcctt atcaaattga cagttataaa cgttcgcaaa aaatcgtatt aaaacaattc
300
aaagactact ggcaaggtac gccaaaatta aaaagaatta atgtcactta tcatgaagat
360
ggtaatantc gtgttgatca
380

<210> 2034
<211> 106
<212> PRT
<213> Homo sapiens

<400> 2034
Met Lys Lys Ser Asp Leu Leu Lys Gly Ser Leu Pro Ile Lys Ser Ile
1 5 10 15
Asn Ala His Gly Gln Lys Val Thr Ile Asn Thr Lys Glu Pro Tyr Pro
20 25 30
Glu Leu Lys Ser Glu Leu Ala Ser Pro Phe Ala Ala Ile Tyr Asp Thr
35 40 45
Lys Ala Lys Asn Lys Val Thr Asp Gln Pro Val Gly Thr Gly Pro Tyr
50 55 60
Gln Ile Asp Ser Tyr Lys Arg Ser Gln Lys Ile Val Leu Lys Gln Phe
65 70 75 80
Lys Asp Tyr Trp Gln Gly Thr Pro Lys Leu Lys Arg Ile Asn Val Thr
85 90 95
Tyr His Glu Asp Gly Asn Xaa Arg Val Asp
100 105

<210> 2035
<211> 495
<212> DNA
<213> Homo sapiens

<400> 2035
ngaattcctt tactgcttgc aacacaggcc caagctactc gcagccatga tacttcctgt
60
cttcacttct ttcatgtatg tatgtatgta tgtatgtatg tatgtatgta tgtatgtatg
120
tatgctntaa tgttcccctt tcatctcgca tgtctccact tctgctgcta ttgctgttac
180
ttgtgtgttg gtgcacctaa tggtgtccca tatttctctg atgctgtgtt catttttctt
240
gattctttct actgtctggt cttcagtttg cataatccat attgttctct ctactagttc
300
actggtgctt ttgcctgcca gctctaattt actgttatcc cctttagtga aatttttttct
360
ttttttctct tctcattcca gttattatac agaactattc aacttcaaga tttgtggggt
420

tttgttttgt tttgttttga gaccccatct caaaaaaaaa aaaaaccagc tttctcctca
480
acttggggga acctt
495

<210> 2036
<211> 98
<212> PRT
<213> Homo sapiens

<400> 2036
Xaa Ile Pro Leu Leu Leu Ala Thr Gln Ala Gln Ala Thr Arg Ser His
1 5 10 15
Asp Thr Ser Cys Leu His Phe Phe His Val Cys Met Tyr Val Cys Met
20 25 30
Tyr Val Cys Met Tyr Val Cys Met Tyr Ala Xaa Met Phe Pro Phe His
35 40 45
Leu Ala Cys Leu His Phe Cys Cys Tyr Cys Cys Tyr Leu Cys Val Gly
50 55 60
Ala Pro Asn Gly Val Pro Tyr Phe Ser Asp Ala Val Phe Ile Phe Leu
65 70 75 80
Asp Ser Phe Tyr Cys Leu Val Phe Ser Leu His Asn Pro Tyr Cys Ser
85 90 95
Leu Tyr

<210> 2037
<211> 327
<212> DNA
<213> Homo sapiens

<400> 2037
acgcgtgaag ggaaggggga gaccccggca gaaatggaga aatgggggcg cacacagacg
60
ggaagagtga ggttggagtg cctttcccgc gctcatcttc cgtccccact ccacgcccag
120
caaatccaaa caccgcggcc tctggtggcc cgggcttcca tttcccctgg aggggcaagg
180
gcgtttcctc ttccgcccaa ccggggcgct gagcggcggg aacagcggcg ggggctttgt
240
ggtcccgggg ggtccgagtg tgtgtcaggg gctggggcgg gggatgggcg cggcccctgg
300
gtatccctca cggtcctggt tcatgag
327

<210> 2038
<211> 98
<212> PRT
<213> Homo sapiens

<400> 2038
Met Glu Lys Trp Gly Arg Thr Gln Thr Gly Arg Val Arg Leu Glu Cys
1 5 10 15
Leu Ser Arg Ala His Leu Pro Ser Pro Leu His Ala Gln Gln Ile Gln

```
            20                  25                  30
Thr Pro Arg Pro Leu Val Ala Arg Ala Ser Ile Ser Pro Gly Gly Ala
        35                  40                  45
Arg Ala Phe Pro Leu Pro Pro Asn Arg Gly Ala Glu Arg Arg Glu Gln
    50                  55                  60
Arg Arg Gly Leu Cys Gly Pro Gly Gly Ser Glu Cys Val Ser Gly Ala
65                  70                  75                  80
Gly Ala Gly Asp Gly Arg Gly Pro Trp Val Ser Leu Thr Val Leu Val
                85                  90                  95
His Glu
```

<210> 2039
<211> 307
<212> DNA
<213> Homo sapiens

<400> 2039
accggtgatc cactctgcga aagcggccgc gagcgaagcg ttcttggtct tcttcgagat
60
cgcgatgtat tgcccggaaa acagcggctt gatgccgtca ttgagaggct ctgggccaac
120
accggtacgg gcatatgcct gggcggcatt cttttggatg ttgcgaagaa aggacgcatt
180
cggcgtgccg aaagccaggg atccttcacc gtagaccttg gaccgatgga ggccccccggc
240
aatcgagtcc ttcgaaattc ccccttggca tacatgtcgg ccatcgtcgt cagccagagt
300
aacgcgt
307

<210> 2040
<211> 94
<212> PRT
<213> Homo sapiens

<400> 2040
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Met Ala Asp Met Tyr Ala Lys Gly Glu Phe Arg Arg Thr Arg Leu Pro
 1               5                  10                  15
Gly Ala Ser Ile Gly Pro Arg Ser Thr Val Lys Asp Pro Trp Leu Ser
            20                  25                  30
Ala Arg Arg Met Arg Pro Phe Phe Ala Thr Ser Lys Arg Met Pro Pro
        35                  40                  45
Arg His Met Pro Val Pro Val Leu Ala Gln Ser Leu Ser Met Thr Ala
    50                  55                  60
Ser Ser Arg Cys Phe Pro Gly Asn Thr Ser Arg Ser Arg Arg Arg Pro
65                  70                  75                  80
Arg Thr Leu Arg Ser Arg Pro Leu Ser Gln Ser Gly Ser Pro
                85                  90
```

<210> 2041
<211> 348
<212> DNA
<213> Homo sapiens

<400> 2041
nnccggcgat gcagggattc gcccgcgatg cgctcgaacc cggcgcgggg ggcgttcctc
60
gccagcttcc tgccgttcgc cagacgcatc gccgaggcgg gggtgcgcaa ttcgctcgcc
120
cagctggtcg ccaagctgac cctgcccggc atgcccgaca tctaccaggg ctgcgagatg
180
tgggacctca gcctggtcga ccgggacaat cgccgccccg tcgactacga gacacgcgac
240
gcggccctgg ccggctgggt cgcgaccccg ccggaggaac gcgccgcggc gctgcgcacc
300
ctgctgacgg attggcgcag cggcgcggtc aagctggccg tgacgcgt
348

<210> 2042
<211> 116
<212> PRT
<213> Homo sapiens

<400> 2042
Xaa Arg Arg Cys Arg Asp Ser Pro Ala Met Arg Ser Asn Pro Ala Arg
1 5 10 15
Gly Ala Phe Leu Ala Ser Phe Leu Pro Phe Ala Arg Arg Ile Ala Glu
20 25 30
Ala Gly Val Arg Asn Ser Leu Ala Gln Leu Val Ala Lys Leu Thr Leu
35 40 45
Pro Gly Met Pro Asp Ile Tyr Gln Gly Cys Glu Met Trp Asp Leu Ser
50 55 60
Leu Val Asp Arg Asp Asn Arg Arg Pro Val Asp Tyr Glu Thr Arg Asp
65 70 75 80
Ala Ala Leu Ala Gly Trp Val Ala Thr Pro Pro Glu Glu Arg Ala Ala
85 90 95
Ala Leu Arg Thr Leu Leu Thr Asp Trp Arg Ser Gly Ala Val Lys Leu
100 105 110
Ala Val Thr Arg
115

<210> 2043
<211> 712
<212> DNA
<213> Homo sapiens

<400> 2043
gatctgacgg tctcgactaa gcctgaccat tccgaggtca ccgacgccga ccttgccgtc
60
gaagattcgg tgcgcagagc cctgtctcga atgcgctccc gggatgccgt ccacggcgag
120
gaacgtgccg ataccgggga tggaccccgc cggtggatca ttgatccgat cgacggcact
180
gcgaattttc tgcgtggggt cccagtgtgg gccaccctca ttgccctcag cgtcgaggac
240
cagattgtcg catctgtggt ctctgctcct gccctcaagc gacgctggtg ggcagcccgt
300

ggctcaggag catggtcggg caaatccctg gcctcagcga caccgatcca cgtctcgaat
360
gtgcgcaatc ttgccgacgc attcttgtcc tactcttcgc tgcacggatg ggtcgagagc
420
ggacgagggc acgggttcgg tgaactcatg cggtcggtgt ggcggacccg agccttcggc
480
gatttctggt cttacatgat ggtggcagaa ggtgtcgtcg atgtggcatg cgagccggaa
540
ctcagcctgc acgacatggc cgccctcgac gctatcgtca ccgaggcggg cggtaagttc
600
accggtctcg atggcaaaga cggcccgtgg tctgggaatg ctctggcgtc gaatggtttc
660
cttcatgacc aggccctagc catggtccag cctcaggagt gagcaccgat cg
712

<210> 2044
<211> 233
<212> PRT
<213> Homo sapiens

<400> 2044
Asp Leu Thr Val Ser Thr Lys Pro Asp His Ser Glu Val Thr Asp Ala
1 5 10 15
Asp Leu Ala Val Glu Asp Ser Val Arg Arg Ala Leu Ser Arg Met Arg
20 25 30
Ser Arg Asp Ala Val His Gly Glu Glu Arg Ala Asp Thr Gly Asp Gly
35 40 45
Pro Arg Arg Trp Ile Ile Asp Pro Ile Asp Gly Thr Ala Asn Phe Leu
50 55 60
Arg Gly Val Pro Val Trp Ala Thr Leu Ile Ala Leu Ser Val Glu Asp
65 70 75 80
Gln Ile Val Ala Ser Val Val Ser Ala Pro Ala Leu Lys Arg Arg Trp
85 90 95
Trp Ala Ala Arg Gly Ser Gly Ala Trp Ser Gly Lys Ser Leu Ala Ser
100 105 110
Ala Thr Pro Ile His Val Ser Asn Val Arg Asn Leu Ala Asp Ala Phe
115 120 125
Leu Ser Tyr Ser Ser Leu His Gly Trp Val Glu Ser Gly Arg Gly His
130 135 140
Gly Phe Gly Glu Leu Met Arg Ser Val Trp Arg Thr Arg Ala Phe Gly
145 150 155 160
Asp Phe Trp Ser Tyr Met Met Val Ala Glu Gly Val Val Asp Val Ala
165 170 175
Cys Glu Pro Glu Leu Ser Leu His Asp Met Ala Ala Leu Asp Ala Ile
180 185 190
Val Thr Glu Ala Gly Gly Lys Phe Thr Gly Leu Asp Gly Lys Asp Gly
195 200 205
Pro Trp Ser Gly Asn Ala Leu Ala Ser Asn Gly Phe Leu His Asp Gln
210 215 220
Ala Leu Ala Met Val Gln Pro Gln Glu
225 230

<210> 2045
<211> 406

<212> DNA
<213> Homo sapiens

<400> 2045
nnttggacac cggcgactat gccgccaccg cacggatcaa tcgcggaccc agggcagggg
60
atgcgccgga tgggcgacgg tgatggaccg ggcgctggac ctgggcggtc gcttcgacga
120
cantacaggc tttggccgag gcgggttgga agaaaccggt caaccggtgg tttggccccg
180
catcaatgcc cagaaccaga agccttgcgc attcgtccca ggccgttcaa ggccgatggc
240
gagatcgtcg cgatgactgg cgacggtgtc aacgacgccc cctcgctcaa ggcggcccat
300
atcggtgtcg ccatggacaa acgcggcacc gacgtcgcgc gcgaggcttc cgccatggtc
360
ctgctcgagg atgattttgg atcgatcgtg cagtcggtcc ggctcg
406

<210> 2046
<211> 135
<212> PRT
<213> Homo sapiens

<400> 2046
Xaa Trp Thr Pro Ala Thr Met Pro Pro Pro His Gly Ser Ile Ala Asp
 1   5   10   15
Pro Gly Gln Gly Met Arg Arg Met Gly Asp Gly Asp Gly Pro Gly Ala
            20   25   30
Gly Pro Gly Arg Ser Leu Arg Arg Xaa Tyr Arg Leu Trp Pro Arg Arg
        35   40   45
Val Gly Arg Asn Arg Ser Thr Gly Gly Leu Ala Pro His Gln Cys Pro
    50   55   60
Glu Pro Glu Ala Leu Arg Ile Arg Pro Arg Pro Phe Lys Ala Asp Gly
65   70   75   80
Glu Ile Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Pro Ser Leu
                85   90   95
Lys Ala Ala His Ile Gly Val Ala Met Asp Lys Arg Gly Thr Asp Val
            100   105   110
Ala Arg Glu Ala Ser Ala Met Val Leu Leu Glu Asp Asp Phe Gly Ser
        115   120   125
Ile Val Gln Ser Val Arg Leu
    130   135

<210> 2047
<211> 796
<212> DNA
<213> Homo sapiens

<400> 2047
aagctttgga acgagacccc tgagctctgg gttcagcccc gaggaagccc agcaacagga
60
tgaggaattt gagaagaaga ttccaagtgt ggaagacagc cttggagagg gcagcaggga
120

tgctggccgg ccaggagaga gaggatccgg gggcttgttc agtcctagca ctgcccacgt
180
gccggatggg gcactcgggc agagagacca gagcagctgg caaaacagtg atgctagcca
240
ggaggtggga gggcatcagg agagacagca ggcaggggct cagggccctg gcagtgctga
300
cctggaagat ggggagatgg gaaagcgagg ctgggtcggt gagtttagcc tcagtgttgg
360
cccccagcga gaggcagcat ttagcccagg gcagcaggac tggagccggg acttctgcat
420
cgaggccagt gagaggagct atcagtttgg catcattggc aacgacagag tgagtggtgc
480
tggctttagc ccttctagca agatggaagg tggtcacttt gtgcctcctg ggaagaccac
540
agctggctcg gtggactgga ctgaccagct gggtctcagg aacttggaag tgtccagctg
600
tgtgggttct gggggctcga gcgaggccag ggagagtgcc gtgggacaga tgggctggtc
660
aggtggcctg agcttgagag acatgaacct gaccggctgt ttggaaagtg gagggtctga
720
agagccgggg ggaatcggaa ttggggagaa ggactggact tctgatgtta atgtgaagag
780
caaagatttg gctgag
796

<210> 2048
<211> 160
<212> PRT
<213> Homo sapiens

<400> 2048
Met Gly Lys Arg Gly Trp Val Gly Glu Phe Ser Leu Ser Val Gly Pro
1 5 10 15
Gln Arg Glu Ala Ala Phe Ser Pro Gly Gln Gln Asp Trp Ser Arg Asp
20 25 30
Phe Cys Ile Glu Ala Ser Glu Arg Ser Tyr Gln Phe Gly Ile Ile Gly
35 40 45
Asn Asp Arg Val Ser Gly Ala Gly Phe Ser Pro Ser Ser Lys Met Glu
50 55 60
Gly Gly His Phe Val Pro Pro Gly Lys Thr Thr Ala Gly Ser Val Asp
65 70 75 80
Trp Thr Asp Gln Leu Gly Leu Arg Asn Leu Glu Val Ser Ser Cys Val
85 90 95
Gly Ser Gly Gly Ser Ser Glu Ala Arg Glu Ser Ala Val Gly Gln Met
100 105 110
Gly Trp Ser Gly Gly Leu Ser Leu Arg Asp Met Asn Leu Thr Gly Cys
115 120 125
Leu Glu Ser Gly Gly Ser Glu Glu Pro Gly Gly Ile Gly Ile Gly Glu
130 135 140
Lys Asp Trp Thr Ser Asp Val Asn Val Lys Ser Lys Asp Leu Ala Glu
145 150 155 160

<210> 2049
<211> 516

<212> DNA
<213> Homo sapiens

<400> 2049
cgcgtcgctt acggtgcgct gaataccagc ctgctggcgc tggcggtcag cttcgcgtcg
60
ctgttcctcg ggatagtgtt cgggctgatg ccacgtctga tgtgcggggt gattgaactg
120
gccaacgctc ccccgccaat cgccctgggc ctgttagtag tcgccattag cggcccttca
180
gcctacggtg ccgcctgtgc ggtgatgttg gtcagttggg ctccgctggc cgcccattgt
240
gcttcgttgt tggcggaagc ccgcacgcag ccctatatcc gcatgttgcc ggtattgggc
300
gtcggccgat ggcgcacgct gacccactac ctgctgccgg cgctctctgc tcccctgctg
360
cgccacgcca tgttgcgtct gccgggcatt gcgctggcgc tggcggcctt gggttttttt
420
ggtcttgggc cgcagccacc cagtgcagaa tgggggctgg tgctggcgga aggcatgcct
480
tatctcgaac gggcgccctg gggagtcctg gcaccg
516

<210> 2050
<211> 172
<212> PRT
<213> Homo sapiens

<400> 2050
Arg Val Ala Tyr Gly Ala Leu Asn Thr Ser Leu Leu Ala Leu Ala Val
1 5 10 15
Ser Phe Ala Ser Leu Phe Leu Gly Ile Val Phe Gly Leu Met Pro Arg
20 25 30
Leu Met Cys Gly Val Ile Glu Leu Ala Asn Ala Pro Pro Pro Ile Ala
35 40 45
Leu Gly Leu Leu Val Val Ala Ile Ser Gly Pro Ser Ala Tyr Gly Ala
50 55 60
Ala Cys Ala Val Met Leu Val Ser Trp Ala Pro Leu Ala Ala His Cys
65 70 75 80
Ala Ser Leu Leu Ala Glu Ala Arg Thr Gln Pro Tyr Ile Arg Met Leu
85 90 95
Pro Val Leu Gly Val Gly Arg Trp Arg Thr Leu Thr His Tyr Leu Leu
100 105 110
Pro Ala Leu Ser Ala Pro Leu Leu Arg His Ala Met Leu Arg Leu Pro
115 120 125
Gly Ile Ala Leu Ala Leu Ala Ala Leu Gly Phe Phe Gly Leu Gly Pro
130 135 140
Gln Pro Pro Ser Ala Glu Trp Gly Leu Val Leu Ala Glu Gly Met Pro
145 150 155 160
Tyr Leu Glu Arg Ala Pro Trp Gly Val Leu Ala Pro
165 170

<210> 2051
<211> 411

<212> DNA
<213> Homo sapiens

<400> 2051
gagcaaaact atcgttctac cggcaatatt ctgaaaagtg ccaaccaact tatttcgaat
60
aatagtgatc gtctcggtaa gaatttatgg accgacggtg aaatggggga gccagtaggt
120
atttatgcag catttaatga attagatgag gcaaaatttg tggcgtctca aatccaaaat
180
tgggtagatg atggtgggga attagatgat tgtgctgttt tatatcgtag taatagccaa
240
tctcgtgtta ttgaagaagc cttgattcgt tgccaaattc cttatcgaat ttatggcggg
300
atgcgattct tcgaacgcca agaaattaaa gatgcgttgg catatttacg tttaattaat
360
aatcgtcaag atgatgccgc atttgagcgt gtgattaata cgcctacgcg t
411

<210> 2052
<211> 137
<212> PRT
<213> Homo sapiens

<400> 2052
Glu Gln Asn Tyr Arg Ser Thr Gly Asn Ile Leu Lys Ser Ala Asn Gln
 1   5   10   15
Leu Ile Ser Asn Asn Ser Asp Arg Leu Gly Lys Asn Leu Trp Thr Asp
            20   25   30
Gly Glu Met Gly Glu Pro Val Gly Ile Tyr Ala Ala Phe Asn Glu Leu
        35   40   45
Asp Glu Ala Lys Phe Val Ala Ser Gln Ile Gln Asn Trp Val Asp Asp
    50   55   60
Gly Gly Glu Leu Asp Asp Cys Ala Val Leu Tyr Arg Ser Asn Ser Gln
65   70   75   80
Ser Arg Val Ile Glu Glu Ala Leu Ile Arg Cys Gln Ile Pro Tyr Arg
                85   90   95
Ile Tyr Gly Gly Met Arg Phe Phe Glu Arg Gln Glu Ile Lys Asp Ala
            100   105   110
Leu Ala Tyr Leu Arg Leu Ile Asn Asn Arg Gln Asp Asp Ala Ala Phe
        115   120   125
Glu Arg Val Ile Asn Thr Pro Thr Arg
    130   135

<210> 2053
<211> 287
<212> DNA
<213> Homo sapiens

<400> 2053
nccatggaag ccttcaatct tgtaagagaa agtgaacagc tgttttccat atgccaaatc
60
ccgctcctct gctggatcct gtgtaccagt ctgaagcaag agatgcagaa aggaaaagac
120

ctggccctga cctgccagag cactacctct gtgtactcct ctttcgtctt taacctgttc
180
acacctgagg gtgccgaggg cccgactccg caaacccagc accagctgaa ggccctgtgc
240
tccctggctg cagagggtat gtggacagac acatttgagt tttgtga
287

<210> 2054
<211> 79
<212> PRT
<213> Homo sapiens

<400> 2054
Ile Cys Gln Ile Pro Leu Leu Cys Trp Ile Leu Cys Thr Ser Leu Lys
1 5 10 15
Gln Glu Met Gln Lys Gly Lys Asp Leu Ala Leu Thr Cys Gln Ser Thr
20 25 30
Thr Ser Val Tyr Ser Ser Phe Val Phe Asn Leu Phe Thr Pro Glu Gly
35 40 45
Ala Glu Gly Pro Thr Pro Gln Thr Gln His Gln Leu Lys Ala Leu Cys
50 55 60
Ser Leu Ala Ala Glu Gly Met Trp Thr Asp Thr Phe Glu Phe Cys
65 70 75

<210> 2055
<211> 298
<212> DNA
<213> Homo sapiens

<400> 2055
nnacgcgttg ttatgaacaa tgacggtgtc ctctaccccg atacctgcgt gggtactgat
60
tcccacacca ccatggaaaa tggtcttggc attctgggct ggggcgtcgg tggtattgaa
120
gccgaggctg ctatgcttgg ccagcccatc tccatgctta tcccccgtgt tgttggcttt
180
aaacttactg gccaaacaca gccgggtgtc accgctacag atgttgttct taccattact
240
gatatgcttc gccagcatgg tgtgggtgga aaattcgggg aattctatgg gggaagcg
298

<210> 2056
<211> 99
<212> PRT
<213> Homo sapiens

<400> 2056
Xaa Arg Val Val Met Asn Asn Asp Gly Val Leu Tyr Pro Asp Thr Cys
1 5 10 15
Val Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly Leu Gly Ile Leu
20 25 30
Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala Met Leu Gly Gln
35 40 45
Pro Ile Ser Met Leu Ile Pro Arg Val Val Gly Phe Lys Leu Thr Gly

```
    50                  55                  60
Gln Thr Gln Pro Gly Val Thr Ala Thr Asp Val Val Leu Thr Ile Thr
65                  70                  75                  80
Asp Met Leu Arg Gln His Gly Val Gly Gly Lys Phe Gly Glu Phe Tyr
                85                  90                  95
Gly Gly Ser
```

<210> 2057
<211> 569
<212> DNA
<213> Homo sapiens

<400> 2057
acgcgtcccg acagtaccga ctataacgga ggaaactatc aggaacggta taaaatttta
60
gcagaaattc gtaaggctct tgaagacgga gatcgccaaa aagccaaacg attagctgaa
120
caaaatctag ttggaccaaa caacgcccag tatggtcgtt atctagcctt tggtgatatc
180
ttcatggtct tcaataacca gaaaaagggg ctggatacag ttacagacta tcaccgtggt
240
ttggatatca cagaagccac tactacaact tcttacaccc aagatggaac gacctttaaa
300
agagaaacct tctcaagtta ccctgatgat gttactgtta ctcacttgac ccaaaaaggg
360
gacaaaaaac ttgattttac agtttggaat agcttaacag aagatttact tgctaacgga
420
gactactcag cggaatattc taactacaag agtggccatg ttacgacaga cccaaatggt
480
atcctactaa aaggtacagt caaagataat ggcctccagt tcgcatccta tctaggaatt
540
aaaacggacg gaaaagttac tgttcatga
569

<210> 2058
<211> 128
<212> PRT
<213> Homo sapiens

<400> 2058
```
Met Val Phe Asn Asn Gln Lys Lys Gly Leu Asp Thr Val Thr Asp Tyr
 1               5                  10                  15
His Arg Gly Leu Asp Ile Thr Glu Ala Thr Thr Thr Thr Ser Tyr Thr
            20                  25                  30
Gln Asp Gly Thr Thr Phe Lys Arg Glu Thr Phe Ser Ser Tyr Pro Asp
        35                  40                  45
Asp Val Thr Val Thr His Leu Thr Gln Lys Gly Asp Lys Lys Leu Asp
    50                  55                  60
Phe Thr Val Trp Asn Ser Leu Thr Glu Asp Leu Leu Ala Asn Gly Asp
65                  70                  75                  80
Tyr Ser Ala Glu Tyr Ser Asn Tyr Lys Ser Gly His Val Thr Thr Asp
                85                  90                  95
Pro Asn Gly Ile Leu Leu Lys Gly Thr Val Lys Asp Asn Gly Leu Gln
```

```
            100                 105                 110
Phe Ala Ser Tyr Leu Gly Ile Lys Thr Asp Gly Lys Val Thr Val His
        115                 120                 125

<210> 2059
<211> 644
<212> DNA
<213> Homo sapiens

<400> 2059
gaattcgtgc caccgtgcca atacttcgcc acgcaacaga gtgccgtcag cggattgggc
60
agcaatcgac ctgtaggact cagccatgat cgactgggca tcctcgtata gtcgcgatgc
120
cgcaaccgcc tgcgcttcca agcctgcagc gacgtaagag gccctctcac acactgaacc
180
gatcgctcca gacaacgtgg aagcgataac ctcgcgtcgc ttctgctgat tctgggccaa
240
gctcgacaag aagaaccgca gaggggcgac ggcctggtca gggagcgcac cttcagcgtt
300
cgtcttggtc tccgggacag caaaaagcgg ggaatcagcc aggccacgct ccgtcatgag
360
tcggccgagg tccgccggta cctctctcat ggcttccaca ggaacgcggt cacacaccac
420
cgcgatcgac gcgtgcctct cttgagcctc gttgaggaaa tcccacggca cagcgtcagc
480
gtagcgggct gctgaggtga caaagatcca cagatccgcg gcctggagca actgagccgc
540
cagatcacga ttgcgggtca ccacagagtc gatgtccggg gcatcgagga tggccaaacc
600
tcgcggaatc cttgactccg cgacgagctg caaactcgac gcgt
644

<210> 2060
<211> 130
<212> PRT
<213> Homo sapiens

<400> 2060
Met Arg Glu Val Pro Ala Asp Leu Gly Arg Leu Met Thr Glu Arg Gly
 1               5                  10                  15
Leu Ala Asp Ser Pro Leu Phe Ala Val Pro Glu Thr Lys Thr Asn Ala
            20                  25                  30
Glu Gly Ala Leu Pro Asp Gln Ala Val Ala Pro Leu Arg Phe Phe Leu
        35                  40                  45
Ser Ser Leu Ala Gln Asn Gln Gln Lys Arg Arg Glu Val Ile Ala Ser
    50                  55                  60
Thr Leu Ser Gly Ala Ile Gly Ser Val Cys Glu Arg Ala Ser Tyr Val
65                  70                  75                  80
Ala Ala Gly Leu Glu Ala Gln Ala Val Ala Ala Ser Arg Leu Tyr Glu
                85                  90                  95
Asp Ala Gln Ser Ile Met Ala Glu Ser Tyr Arg Ser Ile Ala Ala Gln
            100                 105                 110
Ser Ala Asp Gly Thr Leu Leu Arg Gly Glu Val Leu Ala Arg Trp His
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115 120 125
Glu Phe
130

<210> 2061
<211> 481
<212> DNA
<213> Homo sapiens

<400> 2061
gttaacctgg taaggagagc gacacaggaa ggtgcagggg ttgccatggt gtggccccag
60
atgctgtgat tacgcgccag ccccgtcaca ccgtacgggt ggtaggactg ggcaaagaag
120
acgccgccac ctggatgcac tgaggtgtgc acagccacgt ggagatgatg ctgggggctc
180
acggtgactc tcaggaggcc ctggcctggc ctatctggag ccttctctgt gaaatgaggc
240
tggtaacgcc cactagcagg gttgtagggg acatggatct gtggccacct cctcaagggt
300
tgccacacgc accaggtcct gactgggagt ccggccccca gggcctgtgg atggctggcc
360
tgggcccagc ctccgccccc aagggtgctg gcacctggca tgtgcccgac agttggggcc
420
ggctggtggg aaggtgtgtg tcaggtggcg gagcctcggt gccaggatct cactcacgcg
480
t
481

<210> 2062
<211> 133
<212> PRT
<213> Homo sapiens

<400> 2062
Met Pro Gly Ala Ser Thr Leu Gly Gly Gly Gly Trp Ala Gln Ala Ser
1 5 10 15
His Pro Gln Ala Leu Gly Ala Gly Leu Pro Val Arg Thr Trp Cys Val
20 25 30
Trp Gln Pro Leu Arg Arg Trp Pro Gln Ile His Val Pro Tyr Asn Pro
35 40 45
Ala Ser Gly Arg Tyr Gln Pro His Phe Thr Glu Lys Ala Pro Asp Arg
50 55 60
Pro Gly Gln Gly Leu Leu Arg Val Thr Val Ser Pro Gln His His Leu
65 70 75 80
His Val Ala Val His Thr Ser Val His Pro Gly Gly Gly Val Phe Phe
85 90 95
Ala Gln Ser Tyr His Pro Tyr Gly Val Thr Gly Leu Ala Arg Asn His
100 105 110
Ser Ile Trp Gly His Thr Met Ala Thr Pro Ala Pro Ser Cys Val Ala
115 120 125
Leu Leu Thr Arg Leu
130

<210> 2063
<211> 419
<212> DNA
<213> Homo sapiens

<400> 2063
gccggcgccg tcgagcgcgt gcctttcaat atcgaggccc aagacatggt gctgctcatc
60
gcggacacca atgccccgca catgctttcc gacggccaat acgcctcccg ccggggcatc
120
atcgacgccg tccaatctgc cgccggttgc tccatccgcg agatctcgaa tgcggtggac
180
tttgccgcca ccgtcaatcc cgccgaggcg gaactctatc gccgccgcgt gcaccacgtg
240
gtggaagaaa ccaaccggac cctagatgcc gctaccgcgc tggcatcttc cgatctagat
300
acattccggc ggcttatgcg cgagagccac atctccctgc gcgaccttta tgaggtcacc
360
actccggagc tcgactccgt ttttaccgcg gccggcgagc tgggcgctcg catgannnn
419

<210> 2064
<211> 139
<212> PRT
<213> Homo sapiens

<400> 2064
Ala Gly Ala Val Glu Arg Val Pro Phe Asn Ile Glu Ala Gln Asp Met
 1   5   10   15
Val Leu Leu Ile Ala Asp Thr Asn Ala Pro His Met Leu Ser Asp Gly
            20   25   30
Gln Tyr Ala Ser Arg Arg Gly Ile Ile Asp Ala Val Gln Ser Ala Ala
        35   40   45
Gly Cys Ser Ile Arg Glu Ile Ser Asn Ala Val Asp Phe Ala Ala Thr
    50   55   60
Val Asn Pro Ala Glu Ala Glu Leu Tyr Arg Arg Arg Val His His Val
65   70   75   80
Val Glu Glu Thr Asn Arg Thr Leu Asp Ala Ala Thr Ala Leu Ala Ser
                85   90   95
Ser Asp Leu Asp Thr Phe Arg Arg Leu Met Arg Glu Ser His Ile Ser
            100   105   110
Leu Arg Asp Leu Tyr Glu Val Thr Thr Pro Glu Leu Asp Ser Val Phe
        115   120   125
Thr Ala Ala Gly Glu Leu Gly Ala Arg Met Xaa
    130   135

<210> 2065
<211> 598
<212> DNA
<213> Homo sapiens

<400> 2065
gccggcgcta tggcctctct gctcgccgac gccgccgatg cccttcccgg cgcaaaggtg
60

cgcgcgaccg ttactggatc ggcgggattg ggaaccgcag aggcattggg ccttactttc
120
attcaggagg tcatagctga gacggccgcc gtccaacgtt ggaatcccga cgccgacgtg
180
cttctcgaac tcggtggtga ggatgccaag atcacctacc ttaagccggt ccccgaacag
240
cgcatgaatg gttcgtgtgc tggtggcacc ggtgccttca tcgaccagat ggctaccctg
300
ctgcacaccg acactcccgg cctcaatgac ctcgcatccc gagccaagac catccatccg
360
atcgcctcgc gctgtggtgt ttttgccaag tccgaccttc agcccctcat taacgaggga
420
gcccgccacg aggatctggc tgcctcggtc ctgcaggctg tcgccactca gtgcattgcc
480
ggcctggcat gtggtcgccc gattcgaggt aaggtcatct tccttggcgg tccgcttcac
540
tttatgccaa gtttgcgaga cgctttctcg cgcgtcctcg acggtaaggt tgacgcgt
598

<210> 2066
<211> 199
<212> PRT
<213> Homo sapiens

<400> 2066
Ala Gly Ala Met Ala Ser Leu Leu Ala Asp Ala Ala Asp Ala Leu Pro
 1   5   10   15
Gly Ala Lys Val Arg Ala Thr Val Thr Gly Ser Ala Gly Leu Gly Thr
            20   25   30
Ala Glu Ala Leu Gly Leu Thr Phe Ile Gln Glu Val Ile Ala Glu Thr
        35   40   45
Ala Ala Val Gln Arg Trp Asn Pro Asp Ala Asp Val Leu Leu Glu Leu
    50   55   60
Gly Gly Glu Asp Ala Lys Ile Thr Tyr Leu Lys Pro Val Pro Glu Gln
65   70   75   80
Arg Met Asn Gly Ser Cys Ala Gly Gly Thr Gly Ala Phe Ile Asp Gln
                85   90   95
Met Ala Thr Leu Leu His Thr Asp Thr Pro Gly Leu Asn Asp Leu Ala
            100   105   110
Ser Arg Ala Lys Thr Ile His Pro Ile Ala Ser Arg Cys Gly Val Phe
        115   120   125
Ala Lys Ser Asp Leu Gln Pro Leu Ile Asn Glu Gly Ala Arg His Glu
    130   135   140
Asp Leu Ala Ala Ser Val Leu Gln Ala Val Ala Thr Gln Cys Ile Ala
145   150   155   160
Gly Leu Ala Cys Gly Arg Pro Ile Arg Gly Lys Val Ile Phe Leu Gly
                165   170   175
Gly Pro Leu His Phe Met Pro Ser Leu Arg Asp Ala Phe Ser Arg Val
            180   185   190
Leu Asp Gly Lys Val Asp Ala
        195

<210> 2067
<211> 366

<212> DNA
<213> Homo sapiens

<400> 2067
ttccagcaga tgctgcaaac ctggacccgc agcggcacgc tgcaggaggc cgtggccaac
60
aagatcgccg aatggctgga tgccgacctg caacagtggg acatttcccg cgatgcaccg
120
tacttcggtt tcgagatccc gggcgagcca ggcaagtatt tctacgtgtg gctggacgcg
180
ccgatcggct acatggccag tttcaagaac ctgtgcgacc gcacgccgga gctggacttc
240
gatgctttct gggccaagga ctccaccgcc gagctgtacc atttcatcgg caaggacatc
300
gtcaacttcc acgccctgtt ctggccggcg atgctcgaag gctcgggcta ccgtaaaccg
360
accggt
366

<210> 2068
<211> 122
<212> PRT
<213> Homo sapiens

<400> 2068
Phe Gln Gln Met Leu Gln Thr Trp Thr Arg Ser Gly Thr Leu Gln Glu
1 5 10 15
Ala Val Ala Asn Lys Ile Ala Glu Trp Leu Asp Ala Asp Leu Gln Gln
20 25 30
Trp Asp Ile Ser Arg Asp Ala Pro Tyr Phe Gly Phe Glu Ile Pro Gly
35 40 45
Glu Pro Gly Lys Tyr Phe Tyr Val Trp Leu Asp Ala Pro Ile Gly Tyr
50 55 60
Met Ala Ser Phe Lys Asn Leu Cys Asp Arg Thr Pro Glu Leu Asp Phe
65 70 75 80
Asp Ala Phe Trp Ala Lys Asp Ser Thr Ala Glu Leu Tyr His Phe Ile
85 90 95
Gly Lys Asp Ile Val Asn Phe His Ala Leu Phe Trp Pro Ala Met Leu
100 105 110
Glu Gly Ser Gly Tyr Arg Lys Pro Thr Gly
115 120

<210> 2069
<211> 280
<212> DNA
<213> Homo sapiens

<400> 2069
cctagagagg atggtggaga ctgtgcgtgt gcagggtgtt ccggaacctt ccctgggatg
60
catggggcct cgccgcaggc catctctcca gacctgggct caccctgccc ctgtgctgtt
120
gcctttggct ggaattccac cccagccttc ttgcctcaag aacgcccttc ccccttcaga
180

tctcatgggc acaggccccg tcttcctaaa cggggtcaga gcccccagta atcatgacaa
240
agaccctctc ctcgatcaag ctttggtcaa gctcctaccc
280

<210> 2070
<211> 90
<212> PRT
<213> Homo sapiens

<400> 2070
Met Val Glu Thr Val Arg Val Gln Gly Val Pro Glu Pro Ser Leu Gly
 1   5   10   15
Cys Met Gly Pro Arg Arg Arg Pro Ser Leu Gln Thr Trp Ala His Pro
            20   25   30
Ala Pro Val Leu Leu Pro Leu Ala Gly Ile Pro Pro Gln Pro Ser Cys
        35   40   45
Leu Lys Asn Ala Leu Pro Pro Ser Asp Leu Met Gly Thr Gly Pro Val
    50   55   60
Phe Leu Asn Gly Val Arg Ala Pro Ser Asn His Asp Lys Asp Pro Leu
65   70   75   80
Leu Asp Gln Ala Leu Val Lys Leu Leu Pro
                85   90

<210> 2071
<211> 399
<212> DNA
<213> Homo sapiens

<400> 2071
acgcgtgtcc agcagactta gaaagcaggt tcctcttgtc atacagcacg ttaacatagc
60
tgacgaggcc tgggtgtctt catcagtact gtgatgactc tttcaccttt gacttcagat
120
gctggcgctt tttacttttt gtgccaaact ctacacatga aacacttttg gaataactac
180
agacatgact ttctttatct ggggaaaagg agggcattaa accagattag gggctgggag
240
gggaggttgt caggggatga gctgctcctg aggaagaggc agagatcaag cttcactcag
300
cagctggatt ctcacctagt ttatagactg aaatcctgca aggtggttac aacagtgaac
360
aatatgttca tacataaaga ctctaccctc aggtgatca
399

<210> 2072
<211> 100
<212> PRT
<213> Homo sapiens

<400> 2072
Met Thr Leu Ser Pro Leu Thr Ser Asp Ala Gly Ala Phe Tyr Phe Leu
 1   5   10   15
Cys Gln Thr Leu His Met Lys His Phe Trp Asn Asn Tyr Arg His Asp

```
            20                  25                  30
Phe Leu Tyr Leu Gly Lys Arg Arg Ala Leu Asn Gln Ile Arg Gly Trp
        35                  40                  45
Glu Gly Arg Leu Ser Gly Asp Glu Leu Leu Leu Arg Lys Arg Gln Arg
    50                  55                  60
Ser Ser Phe Thr Gln Gln Leu Asp Ser His Leu Val Tyr Arg Leu Lys
65                  70                  75                  80
Ser Cys Lys Val Val Thr Thr Val Asn Asn Met Phe Ile His Lys Asp
                85                  90                  95
Ser Thr Leu Arg
            100
```

<210> 2073
<211> 339
<212> DNA
<213> Homo sapiens

<400> 2073
ggatccactt ctgtgccttt ccagcttcta gaggctgcct gcgttccttg gctcgtggcc
60
ccttcctcca ccttcaagcc agcagcggag gcctgagtcc ttctcatgcc atctctctgt
120
tctctctcct gcctcctcct ccacactgaa ggacccctgt gatcacactg gccccccccac
180
cggatgaccc aggataatcc atctccctgt ttgaaggtcg gctgattagc aaccttcatt
240
ccatctgcct ccttcattcc ccctggccat gtaatgggat tcacagcttc tggggattag
300
gacatggaca tcttgtggcg ggggcataat tctgtcgac
339

<210> 2074
<211> 85
<212> PRT
<213> Homo sapiens

<400> 2074
```
Met Lys Glu Ala Asp Gly Met Lys Val Ala Asn Gln Pro Thr Phe Lys
 1               5                  10                  15
Gln Gly Asp Gly Leu Ser Trp Val Ile Arg Trp Gly Gly Gln Cys Asp
            20                  25                  30
His Arg Gly Pro Ser Val Trp Arg Arg Arg Gln Glu Arg Glu Gln Arg
        35                  40                  45
Asp Gly Met Arg Arg Thr Gln Ala Ser Ala Ala Gly Leu Lys Val Glu
    50                  55                  60
Glu Gly Ala Thr Ser Gln Gly Thr Gln Ala Ala Ser Arg Ser Trp Lys
65                  70                  75                  80
Gly Thr Glu Val Asp
                85
```

<210> 2075
<211> 481
<212> DNA
<213> Homo sapiens

<400> 2075
ntggccaggt tgacctcaaa ggtgtacatt gttttatgtg gcgacaatgg actgtcagaa
60
accaaggagc tctcctgtcc agagaagtcc ctgtttgaaa ggaattccag acacaccttt
120
atcctgagcg ctcctgccca actgggcctg ctgaggaaga tccgcctctg gcacgacagc
180
cgtgggcctt ccccaggctg gttcatcagc cacgtgatgg tgaaggagct gcacacggga
240
cagggctggt tcttccctgc ccagtgctgg ctgtctgccg gcaggcatga tggtcgcgtg
300
gagcgggagc tcacctgtct gcaaggggga ctcggcttct ggaagctttt ctattgcaag
360
ttcacagagt acctggagga tttccatgtc tggctgtcgg tgtacagcag gccctcctcc
420
agccgctacc tgcacacgcc gcgccccacc gtgtccttct ccctgctgtg cgtctacgcg
480
t
481

<210> 2076
<211> 160
<212> PRT
<213> Homo sapiens

<400> 2076
Xaa Ala Arg Leu Thr Ser Lys Val Tyr Ile Val Leu Cys Gly Asp Asn
 1   5   10   15
Gly Leu Ser Glu Thr Lys Glu Leu Ser Cys Pro Glu Lys Ser Leu Phe
            20   25   30
Glu Arg Asn Ser Arg His Thr Phe Ile Leu Ser Ala Pro Ala Gln Leu
        35   40   45
Gly Leu Leu Arg Lys Ile Arg Leu Trp His Asp Ser Arg Gly Pro Ser
    50   55   60
Pro Gly Trp Phe Ile Ser His Val Met Val Lys Glu Leu His Thr Gly
65   70   75   80
Gln Gly Trp Phe Phe Pro Ala Gln Cys Trp Leu Ser Ala Gly Arg His
                85   90   95
Asp Gly Arg Val Glu Arg Glu Leu Thr Cys Leu Gln Gly Gly Leu Gly
            100   105   110
Phe Trp Lys Leu Phe Tyr Cys Lys Phe Thr Glu Tyr Leu Glu Asp Phe
        115   120   125
His Val Trp Leu Ser Val Tyr Ser Arg Pro Ser Ser Ser Arg Tyr Leu
    130   135   140
His Thr Pro Arg Pro Thr Val Ser Phe Ser Leu Leu Cys Val Tyr Ala
145   150   155   160

<210> 2077
<211> 1410
<212> DNA
<213> Homo sapiens

<400> 2077

ncagagtgtt ttgagctatc tggtatccca aatgatgtga atactttcag aaaccaatgg
60
caaattgaac ccaactgttt gcgaattcgg cacgagtaaa gatcttttt ttttttttgt
120
ttttttttt ttttttttt ttttgctttc taaagtggct ttaatatcac acaagcggct
180
ctttggtcta cagtgagaga aaacagaggg agccaggaaa ggctccccgc tggcctctgg
240
agtccaggag ccttaggaag gctgaaacaa gccctgacca gcaggcttag ttgtcctgag
300
aagagccagt gaggccacct ggtccagttc accaggtttc ccagggaagc acaggcatct
360
ctgggtcccc gagcacagtg ccagggaaga caccccaat ccccatctga acaggccgag
420
ggcagcatgg gaaaggctca gactgcaggt tcatcccgca ggatggtaag gacacgtgct
480
cctccctcgc aagagcaggc ttgtgcacag cccggcacag ggccagccag ggcggccct
540
gcggctgtgc agcgcttacc agggggagga gttcagccat caggaccttt tccaagtgga
600
tctgctggtc cagcacagcc actcgcagct tgagggccgc cagggtctgc agctcctggg
660
tgctggagta gacaagcagc tgggnnggct ccatgcaggc tccgctctac ccccacagga
720
cggcgaggct ccgggggcc tnnccccaca gacatggtct tggtggctgt tccgccaccg
780
ctgcacgcag ctcctgcagc ctgtgcagac actggcccac catggcctgc agcccctcca
840
gcgtgagcag gcagcggtac tcctgcatcc agtccatggg ggctgctgag agctcctccc
900
tcatgcgcag tctcagcagc gagcaggcct tccgcaggcg ccccgcctcc gcctccacct
960
ccacagcact gagcctgggc tggggcccgc ctgaagctgt ctgcatgttc tggaggaact
1020
gggttttggc agcggcggca tccgtggaat cactggtctg tgtggaactg agctgggccc
1080
acaggctcga gttctgggaa gctgctttcc tgaatgccgc aggcagccgc agcaggtgcc
1140
ccttctcctt gagtgtgaag gcttctgggg cctgaggagc agcggatggg gccatttgct
1200
ggtccctgag gcccgcccca ggcctggggg ttcgggctcc catcccaaca cgggtcccat
1260
cccccactga cagcagccgg cgctcagggt ggcccttggc aggcaccgtg gtctggcgga
1320
ggcccttggt gggtctcgtg tctgaagcat ggccaccagc ttggcctggg gaatgcggtg
1380
gggcggaggc tgtcgtgcca gaagaggtga
1410

<210> 2078
<211> 106
<212> PRT
<213> Homo sapiens

<400> 2078
Gly His Leu Val Gln Phe Thr Arg Phe Pro Arg Glu Ala Gln Ala Ser
1 5 10 15
Leu Gly Pro Arg Ala Gln Cys Gln Gly Arg His Pro Gln Ser Pro Ser
20 25 30
Glu Gln Ala Glu Gly Ser Met Gly Lys Ala Gln Thr Ala Gly Ser Ser
35 40 45
Arg Arg Met Val Arg Thr Arg Ala Pro Pro Ser Gln Glu Gln Ala Cys
50 55 60
Ala Gln Pro Gly Thr Gly Pro Ala Arg Ala Ala Pro Ala Ala Val Gln
65 70 75 80
Arg Leu Pro Gly Gly Gly Val Gln Pro Ser Gly Pro Phe Pro Ser Gly
85 90 95
Ser Ala Gly Pro Ala Gln Pro Leu Ala Ala
100 105

<210> 2079
<211> 565
<212> DNA
<213> Homo sapiens

<400> 2079
atttacctcg caaccgaccc tgatcgtgaa ggtgaaagca tcagctggca catccagcag
60
gtactggcgg tcaaatccta caaacgcatt accttcaacg agatcactct caagcgcgtt
120
gaagaggcac tggccaatcc tcgacaaatc gatctgaaca gagttgcctc acaggaatgc
180
cggcgtgtgc ttgaccgctt ggtggggtac ctggtgaccc aagagttgcg gcgcctgatg
240
ggcaaaccta cttccgctgg ccgcgttcaa tcacccgccg tgtttcttgt ggtcttgcgc
300
gaacgcgaga tccgcaactt tcaggtgatc aatcactttg gcgtgcgtct gttctttgcc
360
gatgtaagtc ggggcaccac ttggtatgcc gagtggcaac cggtaccgga tttcgcaagc
420
aagcacttcc cctatgttca ggatagcaac ctggctcagc acgtcgccgg cactcgaaat
480
gtggtcgtgg agtcctgcga ggatcgcaag gccgagcgtc atcctcctgc accattcatc
540
tcatccactc ttcaacaggc cgcca
565

<210> 2080
<211> 188
<212> PRT
<213> Homo sapiens

<400> 2080
Ile Tyr Leu Ala Thr Asp Pro Asp Arg Glu Gly Glu Ser Ile Ser Trp
1 5 10 15
His Ile Gln Gln Val Leu Ala Val Lys Ser Tyr Lys Arg Ile Thr Phe
20 25 30
Asn Glu Ile Thr Leu Lys Arg Val Glu Glu Ala Leu Ala Asn Pro Arg

```
        35                  40                  45
Gln Ile Asp Leu Asn Arg Val Ala Ser Gln Glu Cys Arg Arg Val Leu
    50                  55                  60
Asp Arg Leu Val Gly Tyr Leu Val Thr Gln Glu Leu Arg Arg Leu Met
65                  70                  75                  80
Gly Lys Pro Thr Ser Ala Gly Arg Val Gln Ser Pro Ala Val Phe Leu
                85                  90                  95
Val Val Leu Arg Glu Arg Glu Ile Arg Asn Phe Gln Val Ile Asn His
            100                 105                 110
Phe Gly Val Arg Leu Phe Phe Ala Asp Val Ser Arg Gly Thr Thr Trp
        115                 120                 125
Tyr Ala Glu Trp Gln Pro Val Pro Asp Phe Ala Ser Lys His Phe Pro
    130                 135                 140
Tyr Val Gln Asp Ser Asn Leu Ala Gln His Val Ala Gly Thr Arg Asn
145                 150                 155                 160
Val Val Val Glu Ser Cys Glu Asp Arg Lys Ala Glu Arg His Pro Pro
                165                 170                 175
Ala Pro Phe Ile Ser Ser Thr Leu Gln Gln Ala Ala
            180                 185
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<210> 2081
<211> 319
<212> DNA
<213> Homo sapiens

<400> 2081
aagcttatgg aaaaacgggg atacggagag gagtatataa atcgctataa aatgatgaca
60
aggttccatc atcaacgggt tccactagta attttggtgt gtggaactgc ctgtactgga
120
aaatcaacaa tcgctacaca acttgctcag aggctcaatt tgcctaatgt tttgcagacg
180
gacatggtgt atgagctgct gcggacatca acagatgcgc cacttacttc agttcctgtg
240
tgggctcgcg attttaattc acctgaagag cttatcactg aattctgcag agaatgcaga
300
gttgtacgca agggtttgg
319

<210> 2082
<211> 106
<212> PRT
<213> Homo sapiens

<400> 2082

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Lys Leu Met Glu Lys Arg Gly Tyr Gly Glu Glu Tyr Ile Asn Arg Tyr
 1               5                  10                  15
Lys Met Met Thr Arg Phe His His Gln Arg Val Pro Leu Val Ile Leu
            20                  25                  30
Val Cys Gly Thr Ala Cys Thr Gly Lys Ser Thr Ile Ala Thr Gln Leu
        35                  40                  45
Ala Gln Arg Leu Asn Leu Pro Asn Val Leu Gln Thr Asp Met Val Tyr
    50                  55                  60
Glu Leu Leu Arg Thr Ser Thr Asp Ala Pro Leu Thr Ser Val Pro Val
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65 70 75 80
Trp Ala Arg Asp Phe Asn Ser Pro Glu Glu Leu Ile Thr Glu Phe Cys
85 90 95
Arg Glu Cys Arg Val Val Arg Lys Gly Leu
100 105

<210> 2083
<211> 382
<212> DNA
<213> Homo sapiens

<400> 2083
nngcctgatt gcgacatggc cgtcgagtgc gctgtaacac gcaagcagct atataccatc
60
atacctactg ttgaatgcaa ctgtggccac gttttctgct ttggctgtgg tttggatgga
120
caccagccgg tcatttgtgc tgttgtccgc ttgtggctga aaaaatgtgc ggatgacagt
180
gagacgtcca actggatcgg cgctaatacc aaggaatgcc ccaaatgctg ttcgacgatt
240
gaaaagaatg gcggatgtaa tcatatgacg tgtcgcaagt gcaaatacga attttgttgg
300
atttgctcgg gcccatggtc ggagcacgga aacaactatt acaactgcaa tcggtacgat
360
gaaaaggcag gagatgaagg tn
382

<210> 2084
<211> 127
<212> PRT
<213> Homo sapiens

<400> 2084
Xaa Pro Asp Cys Asp Met Ala Val Glu Cys Ala Val Thr Arg Lys Gln
1 5 10 15
Leu Tyr Thr Ile Ile Pro Thr Val Glu Cys Asn Cys Gly His Val Phe
20 25 30
Cys Phe Gly Cys Gly Leu Asp Gly His Gln Pro Val Ile Cys Ala Val
35 40 45
Val Arg Leu Trp Leu Lys Lys Cys Ala Asp Asp Ser Glu Thr Ser Asn
50 55 60
Trp Ile Gly Ala Asn Thr Lys Glu Cys Pro Lys Cys Cys Ser Thr Ile
65 70 75 80
Glu Lys Asn Gly Gly Cys Asn His Met Thr Cys Arg Lys Cys Lys Tyr
85 90 95
Glu Phe Cys Trp Ile Cys Ser Gly Pro Trp Ser Glu His Gly Asn Asn
100 105 110
Tyr Tyr Asn Cys Asn Arg Tyr Asp Glu Lys Ala Gly Asp Glu Gly
115 120 125

<210> 2085
<211> 478
<212> DNA
<213> Homo sapiens

<400> 2085
nnggatccca aagaccgcga tattgccatg gtgttccaaa actatgccct ctacccgcac
60
atgactgtcg ccgacaacat gggttttgcc ctcaaactgg cgaaagtgga taagaaagaa
120
atccggcgtc gcgtggagga agccgccgaa ctcctcgacc tcaccgacta tctggaccgc
180
aaacccaagg cactctccgg tggccagcgg cagcgcgtcg ccatggggcg cgctattgtt
240
cgttcccccc gcgtcttctt gatggacgag cctctttcta acctggatgc gcgtctgcgt
300
gtccgcaccc gcgcccagat tgcggaactg cagcgccgcc tgggcaccac caccgtttat
360
gtcacccatg accaggtgga ggctatgacg atgggggatc gtgtggctgt tctctgtgcc
420
gggaaactgc agcaggtgga tactccacgt aatcttttcg accaccccgc taacgcgt
478

<210> 2086
<211> 159
<212> PRT
<213> Homo sapiens

<400> 2086
Xaa Asp Pro Lys Asp Arg Asp Ile Ala Met Val Phe Gln Asn Tyr Ala
 1   5   10   15
Leu Tyr Pro His Met Thr Val Ala Asp Asn Met Gly Phe Ala Leu Lys
            20   25   30
Leu Ala Lys Val Asp Lys Lys Glu Ile Arg Arg Arg Val Glu Glu Ala
        35   40   45
Ala Glu Leu Leu Asp Leu Thr Asp Tyr Leu Asp Arg Lys Pro Lys Ala
    50   55   60
Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala Ile Val
65   70   75   80
Arg Ser Pro Arg Val Phe Leu Met Asp Glu Pro Leu Ser Asn Leu Asp
                85   90   95
Ala Arg Leu Arg Val Arg Thr Arg Ala Gln Ile Ala Glu Leu Gln Arg
            100   105   110
Arg Leu Gly Thr Thr Thr Val Tyr Val Thr His Asp Gln Val Glu Ala
        115   120   125
Met Thr Met Gly Asp Arg Val Ala Val Leu Cys Ala Gly Lys Leu Gln
    130   135   140
Gln Val Asp Thr Pro Arg Asn Leu Phe Asp His Pro Ala Asn Ala
145   150   155

<210> 2087
<211> 731
<212> DNA
<213> Homo sapiens

<400> 2087
gataattctc tacacggcat gagctgggga cgtacccccc ttgccaacgt cacctcacgg
60

tcgtaccgtg gtgattagca gctagccgag gcgctagccg ccatataaga ttcccaaatt
120
aaaagaaaaa gcattgcgtc ggccaagaat tgctgtcgct gctgcaacgg ctactgcgct
180
ggtcggatca atcgcagcaa tcacccccctc ccccaggcag aagctaactc caataggcca
240
cgctcggtag ctcaagccgc tatcgccacg gatggaaagg ggataatcaa caaggactgc
300
cgtgatgcag tcatcaacga tgcaaagctg cgtgccgcga ttgccggtgc gttggttaag
360
gctggattta gttccgccga cgcggtggct ctagcgccgc gtattgccag agaaatggca
420
aaagagggcg tcctcctcat caaccaccac aagctaaagg ctctcatcgg agcccaggtg
480
ggtctgctca ctgatgcgaa gatccagcgt gctgccgctg cagtggacct cggcatcaaa
540
gccactctag ctgcgacaat cattcccaac gcgctgcatt cagcggcatt caaggatgcg
600
gtggtcgcaa atcttgtcgc cgccggtctg acaagaagtt ggcaaaggct acggctgtcg
660
ccattgccgc aactgcgctc aatcccgctc tcgggccgat cgcaaagact gaggccatta
720
aggctgagat c
731

<210> 2088
<211> 105
<212> PRT
<213> Homo sapiens

<400> 2088
Met Ala Lys Glu Gly Val Leu Leu Ile Asn His His Lys Leu Lys Ala
 1   5   10   15
Leu Ile Gly Ala Gln Val Gly Leu Leu Thr Asp Ala Lys Ile Gln Arg
            20   25   30
Ala Ala Ala Ala Val Asp Leu Gly Ile Lys Ala Thr Leu Ala Ala Thr
        35   40   45
Ile Ile Pro Asn Ala Leu His Ser Ala Ala Phe Lys Asp Ala Val Val
    50   55   60
Ala Asn Leu Val Ala Ala Gly Leu Thr Arg Ser Trp Gln Arg Leu Arg
65   70   75   80
Leu Ser Pro Leu Pro Gln Leu Arg Ser Ile Pro Leu Ser Gly Arg Ser
                85   90   95
Gln Arg Leu Arg Pro Leu Arg Leu Arg
            100   105

<210> 2089
<211> 315
<212> DNA
<213> Homo sapiens

<400> 2089
accggtgtgg accaggctca gctgcgcgac gccatgtttt cctaccttcc ccaccacaag
60

ctcggggaat tcgacatcga tctgttgctg gaccatcgcg attcccgtca gcccatcatc
120
ttcgacaccg accacttcga ggggtacgag cgcccccgcc tcgtgctgca cgaagtcacc
180
gatcaacttg gccaagcgtt ccttgtattg gaaggcccag agccggctct cggctgggaa
240
tcgttggtgg cgtctctcac gagtcttgtc gactctatgg ggatccgtct gaccggcatt
300
accgattcga tcccg
315

<210> 2090
<211> 105
<212> PRT
<213> Homo sapiens

<400> 2090
Thr Gly Val Asp Gln Ala Gln Leu Arg Asp Ala Met Phe Ser Tyr Leu
1 5 10 15
Pro His His Lys Leu Gly Glu Phe Asp Ile Asp Leu Leu Leu Asp His
20 25 30
Arg Asp Ser Arg Gln Pro Ile Ile Phe Asp Thr Asp His Phe Glu Gly
35 40 45
Tyr Glu Arg Pro Arg Leu Val Leu His Glu Val Thr Asp Gln Leu Gly
50 55 60
Gln Ala Phe Leu Val Leu Glu Gly Pro Glu Pro Ala Leu Gly Trp Glu
65 70 75 80
Ser Leu Val Ala Ser Leu Thr Ser Leu Val Asp Ser Met Gly Ile Arg
85 90 95
Leu Thr Gly Ile Thr Asp Ser Ile Pro
100 105

<210> 2091
<211> 322
<212> DNA
<213> Homo sapiens

<400> 2091
actcttgtcc attgtctctg tctctgcgtt tttctctctg tctctctgtg tctctgtctc
60
tgtgtccctg tccagttctg tnnctgtgtg tgcgcgcatc tctctctgtg tctctgtnng
120
agtctctgtc tcttttgtct ctgtctctct ctgtgtctct gcccattttg gtctctgctt
180
tctttcctct gtgtgtctct ccatttctgt ctctcttcct ctgtctctct ccatttctgt
240
ctctgctctt tttctctctg tgtgtctctt ttgtctctct gtttctctgc gtgtctctgt
300
ccatttctgt cccttcacgc gt
322

<210> 2092
<211> 107
<212> PRT

<213> Homo sapiens

<400> 2092
Thr Leu Val His Cys Leu Cys Leu Cys Val Phe Leu Ser Val Ser Leu
1 5 10 15
Cys Leu Cys Leu Cys Val Pro Val Gln Phe Cys Xaa Cys Val Cys Ala
20 25 30
His Leu Ser Leu Cys Leu Cys Xaa Ser Leu Cys Leu Phe Cys Leu Cys
35 40 45
Leu Ser Leu Cys Leu Cys Pro Phe Trp Ser Leu Leu Ser Phe Leu Cys
50 55 60
Val Ser Leu His Phe Cys Leu Ser Ser Ser Val Ser Leu His Phe Cys
65 70 75 80
Leu Cys Ser Phe Ser Leu Cys Val Ser Leu Leu Ser Leu Cys Phe Ser
85 90 95
Ala Cys Leu Cys Pro Phe Leu Ser Leu His Ala
100 105

<210> 2093
<211> 324
<212> DNA
<213> Homo sapiens

<400> 2093
gccggcgtca tgcaaacgat caaggtggcg caatttcgcc tctgccatag tcgaaaaatg
60
tttgtggtgg cctacccgcg agagacccag gagatggtgc tcgatgcgca taaccgcgcc
120
tttgcgttct ttggcggcgt accgcagcgg gttatctacg acaaccttaa aaccgcagtg
180
gatgcgatct tggtcggcaa ggatcgaatc ttcaaccggc gcttcctggc gttggctaat
240
cattacctgt ttgaacctgt agcctgtacg cctgctgctg gctgggagaa gggccaagtt
300
gagaatcaag ttcgcaacat acgc
324

<210> 2094
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2094
Ala Gly Val Met Gln Thr Ile Lys Val Ala Gln Phe Arg Leu Cys His
1 5 10 15
Ser Arg Lys Met Phe Val Val Ala Tyr Pro Arg Glu Thr Gln Glu Met
20 25 30
Val Leu Asp Ala His Asn Arg Ala Phe Ala Phe Phe Gly Gly Val Pro
35 40 45
Gln Arg Val Ile Tyr Asp Asn Leu Lys Thr Ala Val Asp Ala Ile Leu
50 55 60
Val Gly Lys Asp Arg Ile Phe Asn Arg Arg Phe Leu Ala Leu Ala Asn
65 70 75 80
His Tyr Leu Phe Glu Pro Val Ala Cys Thr Pro Ala Ala Gly Trp Glu

85 90 95
Lys Gly Gln Val Glu Asn Gln Val Arg Asn Ile Arg
100 105

<210> 2095
<211> 402
<212> DNA
<213> Homo sapiens

<400> 2095
cccgtcacag accaggaaga agcagacaat atgatcgctt ctttcgacac ttatgttcgc
60
accctgcccc ccgccgccaa tcttctgctt aaacaattcc atattgtgga tgttgcccgg
120
cgcgtggtgg gcgtgggttc agtgggcacc cactccctgg tactgctact gtccggcccc
180
aatgatgaac ctcttgtgct gcaagtgaaa gaagccctcc ccagtgtcct caccacccat
240
gggaaactgc cggatgcttt ttcggaactg tccgctgggg actcctccgg gctcctcccc
300
gataatcttg ataagcatat taaagccggc aatggctacc gggtggtggc gtgccagcag
360
attctgcagg cccactcgga tccgctgctg gggtggacgc gt
402

<210> 2096
<211> 134
<212> PRT
<213> Homo sapiens

<400> 2096
Pro Val Thr Asp Gln Glu Glu Ala Asp Asn Met Ile Ala Ser Phe Asp
1 5 10 15
Thr Tyr Val Arg Thr Leu Pro Pro Ala Ala Asn Leu Leu Leu Lys Gln
20 25 30
Phe His Ile Val Asp Val Ala Arg Arg Val Val Gly Val Gly Ser Val
35 40 45
Gly Thr His Ser Leu Val Leu Leu Leu Ser Gly Pro Asn Asp Glu Pro
50 55 60
Leu Val Leu Gln Val Lys Glu Ala Leu Pro Ser Val Leu Thr Thr His
65 70 75 80
Gly Lys Leu Pro Asp Ala Phe Ser Glu Leu Ser Ala Gly Asp Ser Ser
85 90 95
Gly Leu Leu Pro Asp Asn Leu Asp Lys His Ile Lys Ala Gly Asn Gly
100 105 110
Tyr Arg Val Val Ala Cys Gln Gln Ile Leu Gln Ala His Ser Asp Pro
115 120 125
Leu Leu Gly Trp Thr Arg
130

<210> 2097
<211> 641
<212> DNA
<213> Homo sapiens

<400> 2097
ncgtttctca cccgccctcc agcctcatca gcagctgtgg gctcaggccc ccctcccgag
60
gcggagcagg cgtggccgca gagcagcggg gaggaggagc tgcagctcca gctggccctg
120
gccatgagca aggaggaggc cgaccaggta ctgggcgtgc agctggggct gtctgtccgc
180
cacccgcctc cacgcctcac ttcaggctcc ctcccagcca ggcgtgggcc tggccctcac
240
tgtcgctgct ccacatgctg tcactcgtct cctccccagt cctgcctcat cctcacnccg
300
ccgtccctct gcgtgtcact ctctgcctgt cctcactggt tcagggaccc ccagcctctc
360
tttattcggc tctatctgac cctggctctg cctctgactc tgcctctggc ccctcccgtc
420
atgcccctca cactctctct cccccagccc ccgtcctgcg gccccgagga cgacgcccag
480
ctccagctgg cccttagttt gagccgagaa gagcatgata aggtcagagc agcctccctg
540
tccctgcccc tgccaggggc tcccctcaga ccagccccgt cgccccttcc taagtcaccc
600
cccaccatcc tgctgggccc gaagcccaca ggctcacgcg t
641

<210> 2098
<211> 213
<212> PRT
<213> Homo sapiens

<400> 2098
Xaa Phe Leu Thr Arg Pro Pro Ala Ser Ser Ala Ala Val Gly Ser Gly
 1   5   10   15
Pro Pro Pro Glu Ala Glu Gln Ala Trp Pro Gln Ser Ser Gly Glu Glu
            20   25   30
Glu Leu Gln Leu Gln Leu Ala Leu Ala Met Ser Lys Glu Glu Ala Asp
        35   40   45
Gln Val Leu Gly Val Gln Leu Gly Leu Ser Val Arg His Pro Pro Pro
    50   55   60
Arg Leu Thr Ser Gly Ser Leu Pro Ala Arg Arg Gly Pro Gly Pro His
65   70   75   80
Cys Arg Cys Ser Thr Cys Cys His Ser Ser Pro Pro Gln Ser Cys Leu
                85   90   95
Ile Leu Thr Pro Pro Ser Leu Cys Val Ser Leu Ser Ala Cys Pro His
            100   105   110
Trp Phe Arg Asp Pro Gln Pro Leu Phe Ile Arg Leu Tyr Leu Thr Leu
        115   120   125
Ala Leu Pro Leu Thr Leu Pro Leu Ala Pro Pro Val Met Pro Leu Thr
    130   135   140
Leu Ser Leu Pro Gln Pro Pro Ser Cys Gly Pro Glu Asp Asp Ala Gln
145   150   155   160
Leu Gln Leu Ala Leu Ser Leu Ser Arg Glu Glu His Asp Lys Val Arg
                165   170   175
Ala Ala Ser Leu Ser Leu Pro Leu Pro Gly Ala Pro Leu Arg Pro Ala

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            180                 185                 190
Pro Ser Pro Leu Pro Lys Ser Pro Pro Thr Ile Leu Leu Gly Pro Lys
        195                 200                 205
Pro Thr Gly Ser Arg
    210

<210> 2099
<211> 347
<212> DNA
<213> Homo sapiens

<400> 2099
acgcgtgtgc cctgtcccct gccagacatg gacagcacct gcccacaggg gtgctcagtg
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gaggcagtgc ccagggctgc tgtgcccatg cgtgtaccct gtcctctgcc agacgcggac
120
agcacctgcc cacggggtgc tcagtggagg cagtgcccag ggctgctgtg cccacgtgtg
180
tgccctcaga catccctccc cagacacttg ctgcatgacc caggaggtgg caggcagtgg
240
cagtattctg ttcaggtgag ctcagaggtg gcaggtgcct ggctgcggcc ctgcctcact
300
ccgacagcct ctgcctccag tccactggct catcccacat ggcctga
347

<210> 2100
<211> 106
<212> PRT
<213> Homo sapiens

<400> 2100
Met Asp Ser Thr Cys Pro Gln Gly Cys Ser Val Glu Ala Val Pro Arg
 1               5                  10                  15
Ala Ala Val Pro Met Arg Val Pro Cys Pro Leu Pro Asp Ala Asp Ser
            20                  25                  30
Thr Cys Pro Arg Gly Ala Gln Trp Arg Gln Cys Pro Gly Leu Leu Cys
        35                  40                  45
Pro Arg Val Cys Pro Gln Thr Ser Leu Pro Arg His Leu Leu His Asp
    50                  55                  60
Pro Gly Gly Gly Arg Gln Trp Gln Tyr Ser Val Gln Val Ser Ser Glu
65                  70                  75                  80
Val Ala Gly Ala Trp Leu Arg Pro Cys Leu Thr Pro Thr Ala Ser Ala
                85                  90                  95
Ser Ser Pro Leu Ala His Pro Thr Trp Pro
            100                 105

<210> 2101
<211> 549
<212> DNA
<213> Homo sapiens

<400> 2101
ctctctccga ccgcgttgac ggtccagccg gtccgcacgc cgtcatcgga atcggcatca
60
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acgtttcgat ggggcgtgac gaattgcccc tgccgacggc gacctctctg gctctgtgtg
120
ggttgaacca cgacaagaat gagttgctgg ccagccttct catccacctt gacgagctat
180
taacagtgtg gttggagacc ggaacggtgc gggatcagta tgtggcccgc tgtgacacca
240
ttggtactcc ggtccgtctg accttcgacc cagaaatcgt gggtggtggt gaggggggca
300
ttgagggcat cggtgtcgac gttgacgttg atggcgctat cgtggtggaa acttctgacg
360
ggcgtcgcag tttcaacgct gctgacgttc atcatttgcg aaccaggtga gttccgctac
420
ggcgtcctga gcgttcccac catctagact gctgactatg acgacccaca ttttggccct
480
tggtggtggc ggtttctcga tgtcgaaccg cggtgagcct accgctctcg accgtcacat
540
ccctgacct
549

<210> 2102
<211> 113
<212> PRT
<213> Homo sapiens

<400> 2102
Met Gly Arg Asp Glu Leu Pro Leu Pro Thr Ala Thr Ser Leu Ala Leu
 1   5   10   15
Cys Gly Leu Asn His Asp Lys Asn Glu Leu Leu Ala Ser Leu Leu Ile
            20   25   30
His Leu Asp Glu Leu Leu Thr Val Trp Leu Glu Thr Gly Thr Val Arg
        35   40   45
Asp Gln Tyr Val Ala Arg Cys Asp Thr Ile Gly Thr Pro Val Arg Leu
    50   55   60
Thr Phe Asp Pro Glu Ile Val Gly Gly Gly Glu Gly Ala Ile Glu Gly
65   70   75   80
Ile Gly Val Asp Val Asp Val Asp Gly Ala Ile Val Val Glu Thr Ser
                85   90   95
Asp Gly Arg Arg Ser Phe Asn Ala Ala Asp Val His His Leu Arg Thr
            100   105   110
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<210> 2103
<211> 459
<212> DNA
<213> Homo sapiens

<400> 2103
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atgattatgg cggcagtgcg acagatcccc gcccaccatg agttactcgc ttcaggggtt
120
tgggaggggg acgcatatcg gtacgaccag gttggtatgg aaatcaaagg gaatgacgtc
180

ggtatcgtcg gatgcggagc ggtcgggtgc cgggttgcgg ctgtgatggc ggccatgggt
240
gcgaccgtgc gtgtcttcga cccgtgggcc actcctgatt cttttccagc tggcgtgatg
300
gcatgtgatg atctcgatga ggttctgagg ctcagccgca tcctcactct ccacgctcgt
360
gccaacgagg acaaccgtca catgattggc gttgaacaat tagctgagat gcctgatggc
420
tccgtcctcg tcaactgtgc ccgtggctcg ctggtcgac
459

<210> 2104
<211> 153
<212> PRT
<213> Homo sapiens

<400> 2104
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His Thr Ile Ala Met Ile Met Ala Ala Val Arg Gln Ile Pro Ala His
20 25 30
His Glu Leu Leu Ala Ser Gly Val Trp Glu Gly Asp Ala Tyr Arg Tyr
35 40 45
Asp Gln Val Gly Met Glu Ile Lys Gly Asn Asp Val Gly Ile Val Gly
50 55 60
Cys Gly Ala Val Gly Cys Arg Val Ala Ala Val Met Ala Ala Met Gly
65 70 75 80
Ala Thr Val Arg Val Phe Asp Pro Trp Ala Thr Pro Asp Ser Phe Pro
85 90 95
Ala Gly Val Met Ala Cys Asp Asp Leu Asp Glu Val Leu Arg Leu Ser
100 105 110
Arg Ile Leu Thr Leu His Ala Arg Ala Asn Glu Asp Asn Arg His Met
115 120 125
Ile Gly Val Glu Gln Leu Ala Glu Met Pro Asp Gly Ser Val Leu Val
130 135 140
Asn Cys Ala Arg Gly Ser Leu Val Asp
145 150

<210> 2105
<211> 4057
<212> DNA
<213> Homo sapiens

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120
cccctatatg gctccagtcg gttttggggg gggcagctaa gtgggggagg gggaacacaa
180
aagtttgggc aaaacattaa cctgacaaag cttgattccg gaaaaaaatc cctcaagagc
240
gcaaggccag cttagccaac tggcagctga gtggaaaggt tcagtcctct cgggcagctc
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cggtggcacc tagaggggag agggtgcagg ctttgaagcc agaaagacat ggatgcaagt
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420
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600
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660
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720
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1320
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1380
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1800
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1860
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1920

ctttatatca attatacatt taatataatt taatttaaaa taatttaaag attcttagga
1980
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2340
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2700
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3540

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3660
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3900
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4057

<210> 2106
<211> 240
<212> PRT
<213> Homo sapiens

<400> 2106
Ser Asn Gln Ser Val Phe Leu Leu Phe Ser Asp Leu Leu Pro Gln Leu
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Glu Ala Pro Ser Ser Leu Thr Pro Ser Ser Glu Leu Ser Ser Pro Gly
20 25 30
Gln Ser Glu Leu Thr Asn Met Asp Leu Ala Ala Leu Phe Ser Asp Thr
35 40 45
Pro Ala Asn Ala Ser Gly Ser Ala Gly Gly Ser Asp Glu Ala Leu Asn
50 55 60
Ser Gly Ile Leu Thr Ile Asp Val Thr Ser Val Ser Ser Ser Leu Gly
65 70 75 80
Gly Asn Leu Pro Ala Asn Asn Ser Ser Leu Gly Pro Met Glu Pro Leu
85 90 95
Val Leu Val Ala His Ser Asp Ile Pro Pro Ser Leu Asp Ser Pro Leu
100 105 110
Val Leu Gly Thr Ala Ala Thr Val Leu Gln Gln Gly Ser Phe Ser Val
115 120 125
Asp Asp Val Gln Thr Val Ser Ala Gly Ala Leu Gly Cys Leu Val Ala
130 135 140
Leu Pro Met Lys Asn Leu Ser Asp Asp Pro Leu Ala Leu Thr Ser Asn
145 150 155 160
Ser Asn Leu Ala Ala His Ile Thr Thr Pro Thr Ser Ser Ser Thr Pro
165 170 175
Arg Glu Asn Ala Ser Val Pro Glu Leu Leu Ala Pro Ile Lys Val Glu
180 185 190
Pro Asp Ser Pro Ser Arg Pro Gly Ala Val Gly Gln Gln Glu Gly Ser
195 200 205
His Gly Leu Pro Gln Ser Thr Leu Pro Ser Pro Ala Glu Gln His Gly
210 215 220
Ala Gln Asp Thr Glu Leu Ser Ala Gly Thr Gly Asn Phe Tyr Leu Val

225 230 235 240

<210> 2107
<211> 305
<212> DNA
<213> Homo sapiens

<400> 2107
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agtcctggct tggctctcgt tccagatctt aatgattctt tgagtccagt ctcaggggag
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gcctcaggcc tggtgtctga aaacaccccc agacctgatg acagcagagc tatcgctcca
180
gcctcctctc aaatcaccag ttcttgttct ggtgaacccc tggacctgga ttccaaggat
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300
ccncn
305

<210> 2108
<211> 92
<212> PRT
<213> Homo sapiens

<400> 2108
Met Ala Gln Val Pro Met Leu Asn Leu Leu Pro Ser Pro Gly Leu Ala
1 5 10 15
Leu Val Pro Asp Leu Asn Asp Ser Leu Ser Pro Val Ser Gly Glu Ala
20 25 30
Ser Gly Leu Val Ser Glu Asn Thr Pro Arg Pro Asp Asp Ser Arg Ala
35 40 45
Ile Ala Pro Ala Ser Leu Gln Ile Thr Ser Ser Cys Ser Gly Glu Pro
50 55 60
Leu Asp Leu Asp Ser Lys Asp Val Ser Arg Pro Asp Ser Gln Gly Arg
65 70 75 80
Leu Cys Pro Ala Ser Asn Pro Ile Leu Ala Xaa Pro
85 90

<210> 2109
<211> 700
<212> DNA
<213> Homo sapiens

<400> 2109
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120
taccaagcgt ccagtgaggc tcccccagcg aaacggagga acgaaacttc atttctccca
180
gccaagaaaa ctagtgttaa agaaactcag aggactttta aggggaacgc acaaaaaatg
240

ttttctccaa agaagcattc ggttagcaca agtgatagaa accaggagga gagacagtgc
300
attaagactt catcactgtt taaaaacaac cctgacattc cagaactcca cagacctgtg
360
gtaaagcagg tgcaagaaaa agtgtttact tcagctgctt ttcatgagct gggcctccac
420
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480
aagcaaagta ttcctgtgtt gctggaaggc agagatgctc tcgtgagatc ccagacgggc
540
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600
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660
aggctccctt ttgggacaag ttttaagcac atgctttcat
700

<210> 2110
<211> 233
<212> PRT
<213> Homo sapiens

<400> 2110
Xaa Ala Ser Pro Thr Gln Thr Met Ala Ala Ala Asp Gly Ser Leu Phe
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Asp Asn Pro Arg Thr Phe Ser Arg Arg Pro Pro Ala Gln Ala Ser Arg
            20   25   30
Gln Ala Lys Ala Thr Lys Arg Lys Tyr Gln Ala Ser Ser Glu Ala Pro
        35   40   45
Pro Ala Lys Arg Arg Asn Glu Thr Ser Phe Leu Pro Ala Lys Lys Thr
    50   55   60
Ser Val Lys Glu Thr Gln Arg Thr Phe Lys Gly Asn Ala Gln Lys Met
65   70   75   80
Phe Ser Pro Lys Lys His Ser Val Ser Thr Ser Asp Arg Asn Gln Glu
                85   90   95
Glu Arg Gln Cys Ile Lys Thr Ser Ser Leu Phe Lys Asn Asn Pro Asp
            100   105   110
Ile Pro Glu Leu His Arg Pro Val Val Lys Gln Val Gln Glu Lys Val
        115   120   125
Phe Thr Ser Ala Ala Phe His Glu Leu Gly Leu His Pro His Leu Ile
    130   135   140
Ser Thr Ile Asn Thr Val Leu Lys Met Ser Ser Met Thr Ser Val Gln
145   150   155   160
Lys Gln Ser Ile Pro Val Leu Leu Glu Gly Arg Asp Ala Leu Val Arg
                165   170   175
Ser Gln Thr Gly Ser Gly Lys Ile Leu Ala Tyr Cys Ile Pro Val Val
            180   185   190
Gln Ser Leu Gln Ala Met Glu Ser Lys Ile Gln Arg Ser Asp Gly Pro
        195   200   205
Tyr Ala Leu Val Leu Val Pro Thr Arg Glu Val Ser Arg Leu Pro Phe
    210   215   220
Gly Thr Ser Phe Lys His Met Leu Ser
225   230

<210> 2111
<211> 339
<212> DNA
<213> Homo sapiens

<400> 2111
acgcgttgtg ccggcccgga cccgatcatc gctgcccagc gtttcggtgc ggtttccgat
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caaatggaaa tcacccgcaa ggctctgaaa aagcacggtc gcggcaacaa gctggcaatt
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gccgagctgg tggccctggc tgagctgttc atgccaatca agctggtgcc gaagcaattt
180
gaaggcctgg ttgagcgtgt gcgcagtgct cttgagcgtc tgcgtgccca agagcgcgca
240
atcatgcagc tctgcgtacg tgatgcacgc atgccgcgtg ccgacttcct gcgccagttt
300
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339

<210> 2112
<211> 113
<212> PRT
<213> Homo sapiens

<400> 2112
Thr Arg Cys Ala Gly Pro Asp Pro Ile Ile Ala Ala Gln Arg Phe Gly
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Ala Val Ser Asp Gln Met Glu Ile Thr Arg Lys Ala Leu Lys Lys His
20 25 30
Gly Arg Gly Asn Lys Leu Ala Ile Ala Glu Leu Val Ala Leu Ala Glu
35 40 45
Leu Phe Met Pro Ile Lys Leu Val Pro Lys Gln Phe Glu Gly Leu Val
50 55 60
Glu Arg Val Arg Ser Ala Leu Glu Arg Leu Arg Ala Gln Glu Arg Ala
65 70 75 80
Ile Met Gln Leu Cys Val Arg Asp Ala Arg Met Pro Arg Ala Asp Phe
85 90 95
Leu Arg Gln Phe Pro Gly Asn Glu Val Asp Glu Ser Trp Thr Asp Ala
100 105 110
Leu

<210> 2113
<211> 2329
<212> DNA
<213> Homo sapiens

<400> 2113
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atcacagtaa tctggggcgt gtccccagaa gacaatggca acccactaaa tcccaagagt
120
aaagggaagt tgacattaga tagcagtttt aacatcgcca gcccagcttc ccaggcctgg
180

attttgcact tctgtcaaaa actgagaaac caaacattct tttaccagac tgatgaacag
240
gacttcacca gctgcttcat tgagacattc aaacagtgga tggaaaacca ggactgtgat
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360
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420
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1380
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2160
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2220
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2329

<210> 2114
<211> 758
<212> PRT
<213> Homo sapiens

<400> 2114
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Leu His Met Pro Ile Thr Val Ile Trp Gly Val Ser Pro Glu Asp Asn
            20   25   30
Gly Asn Pro Leu Asn Pro Lys Ser Lys Gly Lys Leu Thr Leu Asp Ser
        35   40   45
Ser Phe Asn Ile Ala Ser Pro Ala Ser Gln Ala Trp Ile Leu His Phe
    50   55   60
Cys Gln Lys Leu Arg Asn Gln Thr Phe Phe Tyr Gln Thr Asp Glu Gln
65   70   75   80
Asp Phe Thr Ser Cys Phe Ile Glu Thr Phe Lys Gln Trp Met Glu Asn
                85   90   95
Gln Asp Cys Asp Glu Pro Ala Leu Tyr Pro Cys Cys Ser His Trp Ser
            100   105   110
Phe Pro Tyr Lys Gln Glu Ile Phe Glu Leu Cys Ile Lys Arg Ala Ile
        115   120   125
Met Glu Leu Glu Arg Ser Thr Gly Tyr His Leu Asp Ser Lys Thr Pro
    130   135   140
Gly Pro Arg Phe Asp Ile Asn Asp Thr Ile Arg Ala Val Val Leu Glu
145   150   155   160
Phe Gln Ser Thr Tyr Leu Phe Thr Leu Ala Tyr Glu Lys Met His Gln
                165   170   175
Phe Tyr Lys Glu Val Asp Ser Trp Ile Ser Ser Glu Leu Ser Ser Ala
            180   185   190
Pro Glu Gly Leu Ser Asn Gly Trp Phe Val Ser Asn Leu Glu Phe Tyr
        195   200   205
Asp Leu Gln Asp Ser Leu Ser Asp Gly Thr Leu Ile Ala Met Gly Leu
    210   215   220
Ser Val Ala Val Ala Phe Ser Val Met Leu Leu Thr Thr Trp Asn Ile

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225                 230                 235                 240
Ile Ile Ser Leu Tyr Ala Ile Ile Ser Ile Ala Gly Thr Ile Phe Val
                245                 250                 255
Thr Val Gly Ser Leu Val Leu Leu Gly Trp Glu Leu Asn Val Leu Glu
            260                 265                 270
Ser Val Thr Ile Ser Val Ala Val Gly Leu Ser Val Asp Phe Ala Val
        275                 280                 285
His Tyr Gly Val Ala Tyr Arg Leu Ala Pro Asp Pro Asp Arg Glu Gly
    290                 295                 300
Lys Val Ile Phe Ser Leu Ser Arg Val Gly Ser Ala Met Ala Met Ala
305                 310                 315                 320
Ala Leu Thr Thr Phe Val Ala Gly Ala Met Met Ile Pro Ser Thr Val
                325                 330                 335
Leu Ala Tyr Thr Gln Leu Gly Thr Phe Met Met Leu Ile Met Cys Ile
            340                 345                 350
Ser Trp Ala Phe Ala Thr Phe Phe Phe Gln Cys Met Cys Arg Cys Leu
        355                 360                 365
Gly Pro Gln Gly Thr Cys Gly Gln Ile Pro Leu Pro Lys Lys Leu Gln
    370                 375                 380
Cys Ser Ala Phe Ser His Ala Leu Ser Thr Ser Pro Ser Asp Lys Gly
385                 390                 395                 400
Gln Ser Lys Thr His Thr Ile Asn Ala Tyr His Leu Asp Pro Arg Gly
                405                 410                 415
Pro Lys Ser Glu Leu Glu His Glu Phe Tyr Glu Leu Glu Pro Leu Ala
            420                 425                 430
Ser His Ser Cys Thr Ala Pro Glu Lys Thr Thr Tyr Glu Glu Thr His
        435                 440                 445
Ile Cys Ser Glu Phe Phe Asn Ser Gln Ala Lys Asn Leu Gly Met Pro
    450                 455                 460
Val His Ala Ala Tyr Asn Ser Glu Leu Ser Lys Ser Thr Glu Ser Asp
465                 470                 475                 480
Thr Gly Ser Ala Leu Leu Gln Pro Pro Leu Glu Gln His Thr Val Cys
                485                 490                 495
His Phe Phe Ser Leu Asn Gln Arg Cys Ser Cys Pro Asp Ala Tyr Lys
            500                 505                 510
His Leu Asn Tyr Gly Pro His Ser Cys Gln Gln Met Gly Asp Cys Leu
        515                 520                 525
Cys His Gln Cys Ser Pro Thr Thr Ser Ser Phe Val Gln Ile Gln Asn
    530                 535                 540
Gly Val Ala Pro Leu Lys Ala Thr His Gln Ala Val Glu Gly Phe Val
545                 550                 555                 560
His Pro Ile Thr His Ile His His Cys Pro Cys Leu Gln Gly Arg Val
                565                 570                 575
Lys Pro Ala Gly Met Gln Asn Ser Leu Pro Arg Asn Phe Phe Leu His
            580                 585                 590
Pro Val Gln His Ile Gln Ala Gln Glu Lys Ile Gly Lys Thr Asn Val
        595                 600                 605
His Ser Leu Gln Arg Ser Ile Glu Glu His Leu Pro Lys Met Ala Glu
    610                 615                 620
Pro Ser Ser Phe Val Cys Arg Ser Thr Gly Ser Leu Leu Lys Thr Cys
625                 630                 635                 640
Cys Asp Pro Glu Asn Lys Gln Arg Glu Leu Cys Lys Asn Arg Asp Val
                645                 650                 655
Ser Asn Leu Glu Ser Ser Gly Gly Thr Glu Asn Lys Ala Gly Gly Lys
```

660 665 670
Val Glu Leu Ser Leu Ser Gln Thr Asp Ala Ser Val Asn Ser Glu His
675 680 685
Phe Asn Gln Asn Glu Pro Lys Val Leu Phe Asn His Leu Met Gly Glu
690 695 700
Ala Gly Cys Arg Ser Cys Pro Asn Asn Ser Gln Ser Cys Gly Arg Ile
705 710 715 720
Val Arg Val Lys Cys Asn Ser Val Asp Cys Gln Met Pro Asn Met Glu
725 730 735
Ala Asn Val Pro Ala Val Leu Thr His Ser Glu Leu Ser Gly Glu Ser
740 745 750
Leu Leu Ile Lys Thr Leu
755

<210> 2115
<211> 461
<212> DNA
<213> Homo sapiens

<400> 2115
acgcgtctct ggcctgggag cgggctcccc cgacacgcca ccttccctgc cagatggtgc
60
ttctgggtat tccagaatct ggaatggggg atgcctatcc ccctcctgag cccacctgct
120
ggtcttgggt ccttggagcc caccaagtcc acaaccacct gctctgaata gaaagctgac
180
attgaaccga acagccgcgt cggaggggga tatctgtgga gagctgtgac tgggagccgg
240
tgtgtgcctt tctgtggtca tttctcgagt cctctgccgg ctgctgccag gtgaaggcat
300
ctccatgccc agccggtggg cagctggggc gggtggacct ccagcttctg cccgacgggg
360
ttcagatgac cgagatccta cgggattgcc aatgtgtggg gacgggggggc tttcaggggc
420
gggaaaacat gtccccatcc gtgggaagtg gagccacgtg g
461

<210> 2116
<211> 146
<212> PRT
<213> Homo sapiens

<400> 2116
Met Gly Thr Cys Phe Pro Ala Pro Glu Ser Pro Pro Ser Pro His Ile
1 5 10 15
Gly Asn Pro Val Gly Ser Arg Ser Ser Glu Pro Arg Arg Ala Glu Ala
20 25 30
Gly Gly Pro Pro Ala Pro Ala Ala His Arg Leu Gly Met Glu Met Pro
35 40 45
Ser Pro Gly Ser Ser Arg Gln Arg Thr Arg Glu Met Thr Thr Glu Arg
50 55 60
His Thr Pro Ala Pro Ser His Ser Ser Pro Gln Ile Ser Pro Ser Asp
65 70 75 80
Ala Ala Val Arg Phe Asn Val Ser Phe Leu Phe Arg Ala Gly Gly Cys

```
                85                  90                  95
Gly Leu Gly Gly Leu Gln Gly Pro Lys Thr Ser Arg Trp Ala Gln Glu
            100                 105                 110
Gly Asp Arg His Pro Pro Phe Gln Ile Leu Glu Tyr Pro Glu Ala Pro
        115                 120                 125
Ser Gly Arg Glu Gly Gly Val Ser Gly Glu Pro Ala Pro Arg Pro Glu
    130                 135                 140
Thr Arg
145
```

<210> 2117
<211> 360
<212> DNA
<213> Homo sapiens

<400> 2117
nnacgcgttg gggagacgac ggtgaccttc ccagcaagct catcgcagga tgaaacaatc
60
cgcgccagcg ttaagacctt ctcgcgggct gtcaccgccg atctggagaa gtgtggaccg
120
atcaggtgac actcgcggta gactgaatag atgcctgagt ctgaagacac tgtgtggctg
180
acccaagagg ccttcgataa gctcacccag gagctggagt acctcaaagg cgaaggccgc
240
accgtcattg ccaacaagat tgccgacgcc cgttcggaag gcgacctttc tgagaacggc
300
ggctaccatg ccgcccgtga ggagcagggg caggccgagg cccgcatccg tcaactcgag
360

<210> 2118
<211> 70
<212> PRT
<213> Homo sapiens

<400> 2118
```
Met Pro Glu Ser Glu Asp Thr Val Trp Leu Thr Gln Glu Ala Phe Asp
 1               5                  10                  15
Lys Leu Thr Gln Glu Leu Glu Tyr Leu Lys Gly Glu Gly Arg Thr Val
            20                  25                  30
Ile Ala Asn Lys Ile Ala Asp Ala Arg Ser Glu Gly Asp Leu Ser Glu
        35                  40                  45
Asn Gly Gly Tyr His Ala Ala Arg Glu Glu Gln Gly Gln Ala Glu Ala
    50                  55                  60
Arg Ile Arg Gln Leu Glu
65                  70
```

<210> 2119
<211> 465
<212> DNA
<213> Homo sapiens

<400> 2119
nacgcgtgaa gggcgcgtgt cggcctctca ctggcgcagc ctgcactgcc gctgccgcct
60

cgccccgccc ttgccttggc gttgtctctg gcactgtggc ggactgacca cggcccgggc
120
atgggctgca agggagacgc gagcggagtt tgctataaaa tgggagttct ggttgtactc
180
actgttctgt ggctgttctc ctcagtaaag gccgactcaa aagccattac aacctctctt
240
acaacaaaat ggttttccac tccattgttg ttagaagcca gtgagttttt agcagaagac
300
agtcaagaga aattttggaa ttttgtagaa gccagtcaaa atattggatc atcagatcat
360
gacggtaccg attattccta ctatcatgca atattggagg ctgcatttca gtttctgtca
420
cccctccagc agaatttgtt taaattttgt ctgtcccttc acgcg
465

<210> 2120
<211> 115
<212> PRT
<213> Homo sapiens

<400> 2120
Met Gly Cys Lys Gly Asp Ala Ser Gly Val Cys Tyr Lys Met Gly Val
1 5 10 15
Leu Val Val Leu Thr Val Leu Trp Leu Phe Ser Ser Val Lys Ala Asp
20 25 30
Ser Lys Ala Ile Thr Thr Ser Leu Thr Thr Lys Trp Phe Ser Thr Pro
35 40 45
Leu Leu Leu Glu Ala Ser Glu Phe Leu Ala Glu Asp Ser Gln Glu Lys
50 55 60
Phe Trp Asn Phe Val Glu Ala Ser Gln Asn Ile Gly Ser Ser Asp His
65 70 75 80
Asp Gly Thr Asp Tyr Ser Tyr Tyr His Ala Ile Leu Glu Ala Ala Phe
85 90 95
Gln Phe Leu Ser Pro Leu Gln Gln Asn Leu Phe Lys Phe Cys Leu Ser
100 105 110
Leu His Ala
115

<210> 2121
<211> 336
<212> DNA
<213> Homo sapiens

<400> 2121
ccggacaagg tcaatggaat gaaaacctcc cggccgacag acaatagtat aaatgttaca
60
tgtggtcctc cttatgaaac taatggccct aaaacctttt acattttggt agtcagaagt
120
ggaggttctt ttgttacaaa atacaacaag acaaactgtc agttttatgt agataatctc
180
tactattcaa ctgactatga gtttctggtc tcttttcaca atggagtgta cgagggagat
240
tcagttataa gaaatgagtc aacaaatttt aatgctaaag ccctgattat attcctggtg
300

tttctgatta ttgtgacatc aatagccttg cttgtt
336

<210> 2122
<211> 112
<212> PRT
<213> Homo sapiens

<400> 2122
Pro Asp Lys Val Asn Gly Met Lys Thr Ser Arg Pro Thr Asp Asn Ser
1 5 10 15
Ile Asn Val Thr Cys Gly Pro Pro Tyr Glu Thr Asn Gly Pro Lys Thr
20 25 30
Phe Tyr Ile Leu Val Val Arg Ser Gly Gly Ser Phe Val Thr Lys Tyr
35 40 45
Asn Lys Thr Asn Cys Gln Phe Tyr Val Asp Asn Leu Tyr Tyr Ser Thr
50 55 60
Asp Tyr Glu Phe Leu Val Ser Phe His Asn Gly Val Tyr Glu Gly Asp
65 70 75 80
Ser Val Ile Arg Asn Glu Ser Thr Asn Phe Asn Ala Lys Ala Leu Ile
85 90 95
Ile Phe Leu Val Phe Leu Ile Ile Val Thr Ser Ile Ala Leu Leu Val
100 105 110

<210> 2123
<211> 426
<212> DNA
<213> Homo sapiens

<400> 2123
aactgggccg agttcggcaa cctgcacccg ttcgccccgg ccgagcaaag cgctggttat
60
cagcaactga ccgacgaact ggaagcgatg ctctgcgccg ccacaggtta tgacgcgatc
120
tccctgcagc cgaacgctgg ctcccagggc gagtacgccg gtctgctggc gatccgcgct
180
taccaccaga gccgtggcga tgagcgtcgc gacatctgcc tgattccgtc ctctgcccac
240
ggcaccaacc cggcaaccgc caacatggcc ggcatgcgcg tggtcgtgac cgcttgcgac
300
gcccgcggca acgtcgacat cgaagacctg cgcgccaagg ctatcgagca ccgcgaacac
360
ctcgcggcgc tgatgatcac ctacccgtcg acccacggcg tgttcgaaga aggcatccgc
420
gagatc
426

<210> 2124
<211> 142
<212> PRT
<213> Homo sapiens

<400> 2124
Asn Trp Ala Glu Phe Gly Asn Leu His Pro Phe Ala Pro Ala Glu Gln

```
 1               5                  10                  15
Ser Ala Gly Tyr Gln Gln Leu Thr Asp Glu Leu Glu Ala Met Leu Cys
            20                  25                  30
Ala Ala Thr Gly Tyr Asp Ala Ile Ser Leu Gln Pro Asn Ala Gly Ser
        35                  40                  45
Gln Gly Glu Tyr Ala Gly Leu Leu Ala Ile Arg Ala Tyr His Gln Ser
    50                  55                  60
Arg Gly Asp Glu Arg Arg Asp Ile Cys Leu Ile Pro Ser Ser Ala His
65                  70                  75                  80
Gly Thr Asn Pro Ala Thr Ala Asn Met Ala Gly Met Arg Val Val Val
                85                  90                  95
Thr Ala Cys Asp Ala Arg Gly Asn Val Asp Ile Glu Asp Leu Arg Ala
            100                 105                 110
Lys Ala Ile Glu His Arg Glu His Leu Ala Ala Leu Met Ile Thr Tyr
        115                 120                 125
Pro Ser Thr His Gly Val Phe Glu Glu Gly Ile Arg Glu Ile
    130                 135                 140
```

<210> 2125
<211> 285
<212> DNA
<213> Homo sapiens

<400> 2125
ngtatggcat ctgctgcttc aagttttgtg gtgacaccaa atgtcacttc taacacaacc
60
acagtcaagc ccaatatggt tatgttacct attcaaaaca caagaggttc aagattggtt
120
ctaaaggcgg ctgaagacgc ggcaccaccg gctgtcaccg ttgaagcggc caaggaagag
180
aagccgaagc caccaccaat tggacctaag agaggagcca aggtgagaat tcttaggaag
240
gagtcatact ggttcaaagg agtgggatca gttgtgactg ttgat
285

<210> 2126
<211> 95
<212> PRT
<213> Homo sapiens

<400> 2126

```
Xaa Met Ala Ser Ala Ala Ser Ser Phe Val Val Thr Pro Asn Val Thr
 1               5                  10                  15
Ser Asn Thr Thr Thr Val Lys Pro Asn Met Val Met Leu Pro Ile Gln
            20                  25                  30
Asn Thr Arg Gly Ser Arg Leu Val Leu Lys Ala Ala Glu Asp Ala Ala
        35                  40                  45
Pro Pro Ala Val Thr Val Glu Ala Ala Lys Glu Glu Lys Pro Lys Pro
    50                  55                  60
Pro Pro Ile Gly Pro Lys Arg Gly Ala Lys Val Arg Ile Leu Arg Lys
65                  70                  75                  80
Glu Ser Tyr Trp Phe Lys Gly Val Gly Ser Val Val Thr Val Asp
                85                  90                  95
```

<210> 2127
<211> 454
<212> DNA
<213> Homo sapiens

<400> 2127
atggcagcca agatgcttgc attgttcgct ctcctagctc tttgtgcaag cgccactagt
60
gcgacgcata ttccagggca cttgtcacca gtcatgccat tgggtaccat gaacccatgc
120
atgcagtact gcatgatgca acaggggctt gccagcttga tggcgtgtcc gtccctgatg
180
ctgcagcaac tgttggcctt accgcttcag acgatgccag tgatgatgcc acagatgatg
240
acgcctaaca tgatgtcacc attgatgatg ccgagcatga tgtcaccaat ggtcttgccg
300
agcatgatgt cgcaaatgat gatgccacaa tgtcactgcg acgccgtctc gcagattatg
360
ctgcaacagc agttaccatt catgttcaac ccaatggcca tgacgattcc acccatgttc
420
ttacagcaac cctttgttgg tgctgcattc taga
454

<210> 2128
<211> 150
<212> PRT
<213> Homo sapiens

<400> 2128
Met Ala Ala Lys Met Leu Ala Leu Phe Ala Leu Leu Ala Leu Cys Ala
 1   5   10   15
Ser Ala Thr Ser Ala Thr His Ile Pro Gly His Leu Ser Pro Val Met
            20   25   30
Pro Leu Gly Thr Met Asn Pro Cys Met Gln Tyr Cys Met Met Gln Gln
        35   40   45
Gly Leu Ala Ser Leu Met Ala Cys Pro Ser Leu Met Leu Gln Gln Leu
    50   55   60
Leu Ala Leu Pro Leu Gln Thr Met Pro Val Met Met Pro Gln Met Met
65   70   75   80
Thr Pro Asn Met Met Ser Pro Leu Met Met Pro Ser Met Met Ser Pro
                85   90   95
Met Val Leu Pro Ser Met Met Ser Gln Met Met Met Pro Gln Cys His
            100   105   110
Cys Asp Ala Val Ser Gln Ile Met Leu Gln Gln Gln Leu Pro Phe Met
        115   120   125
Phe Asn Pro Met Ala Met Thr Ile Pro Pro Met Phe Leu Gln Gln Pro
    130   135   140
Phe Val Gly Ala Ala Phe
145   150

<210> 2129
<211> 354
<212> DNA
<213> Homo sapiens

<400> 2129
acgcgtgact tggtgaacaa acccatatcc atcacccccc tcggtgttga tacggaaata
60
ctcacgccct ttgacaagcg gcgtgatgcg aacggcggtg acggggtggt gcgcatcggg
120
actatcaagg ctctccactc caaatatggg atcggtgaac tcatccgtgc cttcagtcgg
180
gtccatgatg aacggcctaa taccgtcctt cgtatctggg gcggcggccc agacgagaat
240
cccctcaagg tcttggctcg ccgtcttgtc ccggacggtt cggtggagtt tcgcggtgcc
300
attgatcatt ctgaggtcag aaatgccttg ggtagtttgg acatctttgc cgcc
354

<210> 2130
<211> 118
<212> PRT
<213> Homo sapiens

<400> 2130
Thr Arg Asp Leu Val Asn Lys Pro Ile Ser Ile Thr Pro Phe Gly Val
1 5 10 15
Asp Thr Glu Ile Leu Thr Pro Phe Asp Lys Arg Arg Asp Ala Asn Gly
20 25 30
Gly Asp Gly Val Val Arg Ile Gly Thr Ile Lys Ala Leu His Ser Lys
35 40 45
Tyr Gly Ile Gly Glu Leu Ile Arg Ala Phe Ser Arg Val His Asp Glu
50 55 60
Arg Pro Asn Thr Val Leu Arg Ile Trp Gly Gly Gly Pro Asp Glu Asn
65 70 75 80
Pro Leu Lys Val Leu Ala Arg Arg Leu Val Pro Asp Gly Ser Val Glu
85 90 95
Phe Arg Gly Ala Ile Asp His Ser Glu Val Arg Asn Ala Leu Gly Ser
100 105 110
Leu Asp Ile Phe Ala Ala
115

<210> 2131
<211> 324
<212> DNA
<213> Homo sapiens

<400> 2131
gcatcgcggc cattggttat gtgtgcctat tccattggtt atgtggaagg ttgggatcag
60
ccagacagtc attatgatgg tttgttacag ctgggcgagt ggggctttcg aatcaatgac
120
ctgatgaaga cggtagaggg cgcggcaggg tgcattgagt attatgaaat gctcaacgaa
180
caacgccccg acttgtctta tgacatagac ggtattgttt ataaagttga tcagattgac
240
ctgcaagaag agcttggttt tattgctcgt gcgccacgct gggcaattgc tcgaaaattt
300

cctgctcaag aagaagttac gcgt
324

<210> 2132
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2132
Ala Ser Arg Pro Leu Val Met Cys Ala Tyr Ser Ile Gly Tyr Val Glu
1 5 10 15
Gly Trp Asp Gln Pro Asp Ser His Tyr Asp Gly Leu Leu Gln Leu Gly
20 25 30
Glu Trp Gly Phe Arg Ile Asn Asp Leu Met Lys Thr Val Glu Gly Ala
35 40 45
Ala Gly Cys Ile Glu Tyr Tyr Glu Met Leu Asn Glu Gln Arg Pro Asp
50 55 60
Leu Ser Tyr Asp Ile Asp Gly Ile Val Tyr Lys Val Asp Gln Ile Asp
65 70 75 80
Leu Gln Glu Glu Leu Gly Phe Ile Ala Arg Ala Pro Arg Trp Ala Ile
85 90 95
Ala Arg Lys Phe Pro Ala Gln Glu Glu Val Thr Arg
100 105

<210> 2133
<211> 292
<212> DNA
<213> Homo sapiens

<400> 2133
ggtacctgca atatggtatt gcatgacatg aataaatttt tccttactct gaactcacta
60
gtggctgtct ttagaggacc cggcgaactt ttcctgcttt ttcccacttg ctccatcaca
120
tacatcacat caccaacacc catcacatac atacacagtc atgaacggcc atcaggccac
180
accagattac atcgctgtgg atccaaccct gcattttcct gcccctcctt tactgcgagt
240
gtcacctcta cccggaaagg tcttcaacct ccaagtttcc cagtaattta tt
292

<210> 2134
<211> 93
<212> PRT
<213> Homo sapiens

<400> 2134
Met Val Leu His Asp Met Asn Lys Phe Phe Leu Thr Leu Asn Ser Leu
1 5 10 15
Val Ala Val Phe Arg Gly Pro Gly Glu Leu Phe Leu Leu Phe Pro Thr
20 25 30
Cys Ser Ile Thr Tyr Ile Thr Ser Pro Thr Pro Ile Thr Tyr Ile His
35 40 45
Ser His Glu Arg Pro Ser Gly His Thr Arg Leu His Arg Cys Gly Ser

```
    50                  55                  60
Asn Pro Ala Phe Ser Cys Pro Ser Phe Thr Ala Ser Val Thr Ser Thr
65                  70                  75                  80
Arg Lys Gly Leu Gln Pro Pro Ser Phe Pro Val Ile Tyr
                85                  90
```

<210> 2135
<211> 439
<212> DNA
<213> Homo sapiens

<400> 2135
acgcgttcca ttggtgtgtc gaatttcaag accgagcatc tggacgccat cgaggggggcc
60
actccgagcg tcgaccaaat cgagatgcat ccctcgttca accaggcgac cttccgcgca
120
gagctggccg agcgcggcat taacccggag gcctggagcc cgctgggcca gtcgaaggac
180
ctcgacaatc ccgtcctcac cgatatttcc aaggcgactg gaaagacgcc tgcccaggtg
240
gtcattcgct ggcacctgca gatcggcaac gtggtattcc ccaagtcggt gacaccatca
300
cgaattgccg agaactttga tgtgttcgat ttcgagctgt ctgacgagca gatcgccgca
360
attgatggcc tggatcacgg caacaggctc ggtggtgacc cttctaccgc cgacttctga
420
ttctgcaaca ataaccggt
439

<210> 2136
<211> 139
<212> PRT
<213> Homo sapiens

<400> 2136
```
Thr Arg Ser Ile Gly Val Ser Asn Phe Lys Thr Glu His Leu Asp Ala
 1               5                  10                  15
Ile Glu Gly Ala Thr Pro Ser Val Asp Gln Ile Glu Met His Pro Ser
            20                  25                  30
Phe Asn Gln Ala Thr Phe Arg Ala Glu Leu Ala Glu Arg Gly Ile Asn
        35                  40                  45
Pro Glu Ala Trp Ser Pro Leu Gly Gln Ser Lys Asp Leu Asp Asn Pro
    50                  55                  60
Val Leu Thr Asp Ile Ser Lys Ala Thr Gly Lys Thr Pro Ala Gln Val
65                  70                  75                  80
Val Ile Arg Trp His Leu Gln Ile Gly Asn Val Val Phe Pro Lys Ser
                85                  90                  95
Val Thr Pro Ser Arg Ile Ala Glu Asn Phe Asp Val Phe Asp Phe Glu
            100                 105                 110
Leu Ser Asp Glu Gln Ile Ala Ala Ile Asp Gly Leu Asp His Gly Asn
        115                 120                 125
Arg Leu Gly Gly Asp Pro Ser Thr Ala Asp Phe
    130                 135
```

<210> 2137
<211> 330
<212> DNA
<213> Homo sapiens

<400> 2137
nnccttttgcc ttggctgata ccctcaccac ctgggaacat cccccagaca ccctcttaac
60
tccgggacag agatggctgg cggagcctgg ggccgcctgg cctgttactt ggagttcctg
120
aagaaggagg agctgaagga gttccagctt ctgctcgcca ataaagcgca ctccaggagc
180
tcttccggtg agacacccgc tcagccagag aagacgagtg gcatggaggt ggcctcgtac
240
ctggtggctc agtatgggga gcagcgggcc tgggacctag ccctccatac ctgggagcag
300
atggggctga ggtcactgtg cgcccaagcc
330

<210> 2138
<211> 86
<212> PRT
<213> Homo sapiens

<400> 2138
Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu
 1   5   10   15
Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala
            20   25   30
His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr
        35   40   45
Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln
    50   55   60
Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg
65   70   75   80
Ser Leu Cys Ala Gln Ala
                85

<210> 2139
<211> 433
<212> DNA
<213> Homo sapiens

<400> 2139
gagcagttga gcgcccagaa caccgggatc aacagcaacc tgtcggacat ggccggccag
60
gtgaacaagc tggcgagtac catcgcccag tacaacgatc agatttccaa agtcaccacc
120
gccgccggtg ccccgaacga cctgctggac cagcgcagcg aggcggtgcg ccagttgtcc
180
gagctggtcg ggacccaggt ggtccagcgc ggttcgagtt atgacgtcta tatcggcagc
240
ggtcagcgcc tggtgatggg caacagcacc aacaccctgt ccgcagtgcc gagcaaggac
300

gacccgagcc agtcggcctt gcagctggat cgcggcacca gcaccgtcga tatcacctcc
360
acggtgaccg gtggcgagat cggtggtctg ctgcgctatc gcagcgatgt gctcgacccg
420
tcgatcaacg cgt
433

<210> 2140
<211> 144
<212> PRT
<213> Homo sapiens

<400> 2140
Glu Gln Leu Ser Ala Gln Asn Thr Gly Ile Asn Ser Asn Leu Ser Asp
1 5 10 15
Met Ala Gly Gln Val Asn Lys Leu Ala Ser Thr Ile Ala Gln Tyr Asn
20 25 30
Asp Gln Ile Ser Lys Val Thr Thr Ala Ala Gly Ala Pro Asn Asp Leu
35 40 45
Leu Asp Gln Arg Ser Glu Ala Val Arg Gln Leu Ser Glu Leu Val Gly
50 55 60
Thr Gln Val Val Gln Arg Gly Ser Ser Tyr Asp Val Tyr Ile Gly Ser
65 70 75 80
Gly Gln Arg Leu Val Met Gly Asn Ser Thr Asn Thr Leu Ser Ala Val
85 90 95
Pro Ser Lys Asp Asp Pro Ser Gln Ser Ala Leu Gln Leu Asp Arg Gly
100 105 110
Thr Ser Thr Val Asp Ile Thr Ser Thr Val Thr Gly Gly Glu Ile Gly
115 120 125
Gly Leu Leu Arg Tyr Arg Ser Asp Val Leu Asp Pro Ser Ile Asn Ala
130 135 140

<210> 2141
<211> 426
<212> DNA
<213> Homo sapiens

<400> 2141
nnatatccat gcagcgatcc tcatcaattt gctgtgttat taggctttgg tgcgacggct
60
gtttatcctt atctttcttt ccgcttgatc aatgatatgg tggataaagg cgaagtgtta
120
ggtgacccaa ttgcttgtca tgttaaatat cgtaaaggta ttaacaaagg cttgatgaaa
180
atcctgtcta aaatgggtat ttcaacgatt gcctcttatc gtggtgcgca attgtttgaa
240
gcggttggct tggatactaa agtggtcgac ctttgtttca aaggcgttgc aagtcgtatc
300
aaaggtgctc gttttgaaga tttccagcgt gatcaagcaa cgattgccaa taatgcttgg
360
aagttacgta aacctattca acagggcggt tatcttaaat acgtacatga ctctgagtat
420
cacgcg
426

<210> 2142
<211> 142
<212> PRT
<213> Homo sapiens

<400> 2142
Xaa Tyr Pro Cys Ser Asp Pro His Gln Phe Ala Val Leu Leu Gly Phe
1 5 10 15
Gly Ala Thr Ala Val Tyr Pro Tyr Leu Ser Phe Arg Leu Ile Asn Asp
20 25 30
Met Val Asp Lys Gly Glu Val Leu Gly Asp Pro Ile Ala Cys His Val
35 40 45
Lys Tyr Arg Lys Gly Ile Asn Lys Gly Leu Met Lys Ile Leu Ser Lys
50 55 60
Met Gly Ile Ser Thr Ile Ala Ser Tyr Arg Gly Ala Gln Leu Phe Glu
65 70 75 80
Ala Val Gly Leu Asp Thr Lys Val Val Asp Leu Cys Phe Lys Gly Val
85 90 95
Ala Ser Arg Ile Lys Gly Ala Arg Phe Glu Asp Phe Gln Arg Asp Gln
100 105 110
Ala Thr Ile Ala Asn Asn Ala Trp Lys Leu Arg Lys Pro Ile Gln Gln
115 120 125
Gly Gly Tyr Leu Lys Tyr Val His Asp Ser Glu Tyr His Ala
130 135 140

<210> 2143
<211> 1008
<212> DNA
<213> Homo sapiens

<400> 2143
gccggcttga caagcatgtt caccggtgac gctgtcgtga tcgtcgaggt gagccaattg
60
tgtcatattg tacgcagtat gtcttttcaa cgattcttgg cgggggtggc agccatcttg
120
cttctcctgc ctactgcgtg cgctgatgat gcgcaggcgc ccgttgtcga taacctcggg
180
acggtcctca gcccctccaa ctccctcatt cgcgagccgg cgaattcgtc agtcaacggg
240
acgctcaaga gcacatatga gtacctccgg ctcatcgacg gtcacgatct acccgacgac
300
gatggctacg ctcatgatca tctggtcgcg gctttgcgcc cgtatttggt gaatggtgga
360
gacagtcggc aggcccacgt cacccaactc atggcggcgt catccctgaa aaccctcaac
420
gcgttgtccg acaaggagag atcagaggtc gacaaacgta cccgcctgcc gaagggctgc
480
atcacgagaa agacggtgat gacggatctg cccatcgcga cgatgaggcg ggagatcggc
540
ctgtccaacg acgggttgtg cctcacaccg tggaaggtca agacgacttc ttccgaggag
600
gctcggtggg cgatgcaggc gctggccagt gccgacctat tcagcaatgc taaggacgcc
660

gagaaatggg ggtgggagtc gatctcggac gggtatttgc gccatctcga gacctacagt
720
ggcccgagta cgactatcgc gatggccttg tcggcggcga ataccgtctc tacattgtct
780
cgttcccagt tgcaacgcat cggcgacagt ctcgcggatg cgccatatcc gaggaaggac
840
cttggtccgg cgctcattcg caatggaaag ccggtcaagg acaagtgcag tatcgaatcg
900
gcgtacctgt tgaggtattc cgggaattgg gcgtggtgac atgacggttt cttggcaagg
960
tgtgaccaag acattcccct cgggcgattc cgcgcgtggg gggtgcac
1008

<210> 2144
<211> 307
<212> PRT
<213> Homo sapiens

<400> 2144
Met Phe Thr Gly Asp Ala Val Val Ile Val Glu Val Ser Gln Leu Cys
1 5 10 15
His Ile Val Arg Ser Met Ser Phe Gln Arg Phe Leu Ala Gly Val Ala
20 25 30
Ala Ile Leu Leu Leu Leu Pro Thr Ala Cys Ala Asp Asp Ala Gln Ala
35 40 45
Pro Val Val Asp Asn Leu Gly Thr Val Leu Ser Pro Ser Asn Ser Leu
50 55 60
Ile Arg Glu Pro Ala Asn Ser Ser Val Asn Gly Thr Leu Lys Ser Thr
65 70 75 80
Tyr Glu Tyr Leu Arg Leu Ile Asp Gly His Asp Leu Pro Asp Asp Asp
85 90 95
Gly Tyr Ala His Asp His Leu Val Ala Ala Leu Arg Pro Tyr Leu Val
100 105 110
Asn Gly Gly Asp Ser Arg Gln Ala His Val Thr Gln Leu Met Ala Ala
115 120 125
Ser Ser Leu Lys Thr Leu Asn Ala Leu Ser Asp Lys Glu Arg Ser Glu
130 135 140
Val Asp Lys Arg Thr Arg Leu Pro Lys Gly Cys Ile Thr Arg Lys Thr
145 150 155 160
Val Met Thr Asp Leu Pro Ile Ala Thr Met Arg Arg Glu Ile Gly Leu
165 170 175
Ser Asn Asp Gly Leu Cys Leu Thr Pro Trp Lys Val Lys Thr Thr Ser
180 185 190
Ser Glu Glu Ala Arg Trp Ala Met Gln Ala Leu Ala Ser Ala Asp Leu
195 200 205
Phe Ser Asn Ala Lys Asp Ala Glu Lys Trp Gly Trp Glu Ser Ile Ser
210 215 220
Asp Gly Tyr Leu Arg His Leu Glu Thr Tyr Ser Gly Pro Ser Thr Thr
225 230 235 240
Ile Ala Met Ala Leu Ser Ala Ala Asn Thr Val Ser Thr Leu Ser Arg
245 250 255
Ser Gln Leu Gln Arg Ile Gly Asp Ser Leu Ala Asp Ala Pro Tyr Pro
260 265 270
Arg Lys Asp Leu Gly Pro Ala Leu Ile Arg Asn Gly Lys Pro Val Lys

```
        275                 280                 285
Asp Lys Cys Ser Ile Glu Ser Ala Tyr Leu Leu Arg Tyr Ser Gly Asn
    290                 295                 300
Trp Ala Trp
305
```

<210> 2145
<211> 389
<212> DNA
<213> Homo sapiens

<400> 2145
tctagaatcg tgtataacat tctacacaat aagctaagcc tactcttgta gagtgcgatc
60
atgacaaccc ttgaacaatc attatctcaa attcccgcat tttcgattat tcatgaacat
120
ttatttagct cggcccagcc ttctgctgaa caactaaaat tgattaaaga gtttggttgt
180
agcacagtca ttaaccttgc tttaactaat gcttcaaatc atcttgagaa tgaagaccgt
240
atttgtttag accttggttt aaattatatt catattccaa ttgattggga gatgccttct
300
gctgagcagt gcttattagt tttagatttg attgatcatt tagtgcaaaa tgaaattgtt
360
tggatacatt gcgccaaaaa taaacgcgt
389

<210> 2146
<211> 109
<212> PRT
<213> Homo sapiens

<400> 2146

```
Met Thr Thr Leu Glu Gln Ser Leu Ser Gln Ile Pro Ala Phe Ser Ile
 1               5                  10                  15
Ile His Glu His Leu Phe Ser Ser Ala Gln Pro Ser Ala Glu Gln Leu
            20                  25                  30
Lys Leu Ile Lys Glu Phe Gly Cys Ser Thr Val Ile Asn Leu Ala Leu
        35                  40                  45
Thr Asn Ala Ser Asn His Leu Glu Asn Glu Asp Arg Ile Cys Leu Asp
    50                  55                  60
Leu Gly Leu Asn Tyr Ile His Ile Pro Ile Asp Trp Glu Met Pro Ser
65                  70                  75                  80
Ala Glu Gln Cys Leu Leu Val Leu Asp Leu Ile Asp His Leu Val Gln
                85                  90                  95
Asn Glu Ile Val Trp Ile His Cys Ala Lys Asn Lys Arg
            100                 105
```

<210> 2147
<211> 235
<212> DNA
<213> Homo sapiens

<400> 2147

ctccctgcgg gctgcgtctc cgaggacatg tgcagtcctg acccctgttt caatggtggg
60
acttgcctcg tcacctggaa tgacttccac tgtacctgcc ctgccaattt cacggggcct
120
acatgtgccc agcagctgtg gtgtcccggc cagccctgtc tcccacctgc cacgtgtgtg
180
gcggaggcca cgttccgcga gggtcccccc gccgcgttca gcgggcacaa cgcgt
235

<210> 2148
<211> 78
<212> PRT
<213> Homo sapiens

<400> 2148
Leu Pro Ala Gly Cys Val Ser Glu Asp Met Cys Ser Pro Asp Pro Cys
1 5 10 15
Phe Asn Gly Gly Thr Cys Leu Val Thr Trp Asn Asp Phe His Cys Thr
20 25 30
Cys Pro Ala Asn Phe Thr Gly Pro Thr Cys Ala Gln Gln Leu Trp Cys
35 40 45
Pro Gly Gln Pro Cys Leu Pro Pro Ala Thr Cys Val Ala Glu Ala Thr
50 55 60
Phe Arg Glu Gly Pro Pro Ala Ala Phe Ser Gly His Asn Ala
65 70 75

<210> 2149
<211> 1474
<212> DNA
<213> Homo sapiens

<400> 2149
ntactgccac cattggaact tttgatgttg atggggaaga gttgcaacac ctccagggtt
60
gtcctgctga tggtggctgc gaatgatttg ccttgacaat agctgaaaaa ccaccatctg
120
caacacgtgg gagtaagact tctcctgctc tttgccagtg gtctgaggtg atgaaccacc
180
ctggcttggt gtgctgtgtc cagcaaacta caggggtgcc gctggtagtt atggtgaaac
240
cagacacttt tcttatccac gagattaaga ctcttcctgc taaagcgaag atccaagaca
300
tggttgctat taggcacacg gcctgcaatg agcagcagcg gacaacaatg attctgctgt
360
gtgaggatgg cagcctgcgc atttacatgg ccaacgtgga gaacacctcc tactggctgc
420
agccatccct gcagcccagc agtgtcatca gcatcatgaa gcctgttcga aagcgcaaaa
480
cagctacaat cacaacccng cacgtctagc caggtgactt tccccattga ctttttgaa
540
cacaaccagc agctgacaga tgtggagttt ggtggtaacg acctcctaca ggtctataat
600
gcacaacaga taaaacaccg gctgaattcc actggcatgt atgtggccaa caccaagccc
660

ggaggcttca ccattgagat tagtaacaac aatagcacta tggtgatgac aggcatgcgg
720
atccagattg ggactcaagc aatagaacgg gccccgtcat atatcgagat cttcggcaga
780
actatgcagc tcaacctgag tcgctcacgc tggtttgact tccccttcac cagagaagaa
840
gccctgcagg ctgataagaa gctgaacctc ttcattgggg cctcggtgga tccagcaggt
900
gtcaccatga tagatgctgt aaaaatttat ggcaagacta aggagcagtt tggctggcct
960
gatgagcccc cagaagaatt cccttctgcc tctgtcagca acatctgccc ttcaaatctg
1020
aaccagagca acggcactgg agatagcgac tcagctgccc ccactacgac cagtggaact
1080
gtcctggaga ggctggttgt gagttcttta gaagccctgg aaagctgctt tgccgttggc
1140
ccaatcatcg agaaggagag aaacaagaat gctgctcagg agctggccac tttgctgttg
1200
tccctgccag cacctgccag tgtccagcag cagtccaaga gccttctggc cagcctgcac
1260
accagccgct cggcctacca cagccacaag gtaactgttc tctcagggaa aggaaattgc
1320
agtgctgaca gggaatcaaa taagttagct cttcattgta aagcaacagc acagcaaagt
1380
aaggtagagg gaggatagca ttcagattag acctacattt tacagagttt ctcctgagaa
1440
attctcaagt gccactcaaa actgagggta agcc
1474

<210> 2150
<211> 312
<212> PRT
<213> Homo sapiens

<400> 2150
Ser Leu Phe Glu Ser Ala Lys Gln Leu Gln Ser Gln Pro Xaa Thr Ser
1 5 10 15
Ser Gln Val Thr Phe Pro Ile Asp Phe Phe Glu His Asn Gln Gln Leu
20 25 30
Thr Asp Val Glu Phe Gly Gly Asn Asp Leu Leu Gln Val Tyr Asn Ala
35 40 45
Gln Gln Ile Lys His Arg Leu Asn Ser Thr Gly Met Tyr Val Ala Asn
50 55 60
Thr Lys Pro Gly Gly Phe Thr Ile Glu Ile Ser Asn Asn Asn Ser Thr
65 70 75 80
Met Val Met Thr Gly Met Arg Ile Gln Ile Gly Thr Gln Ala Ile Glu
85 90 95
Arg Ala Pro Ser Tyr Ile Glu Ile Phe Gly Arg Thr Met Gln Leu Asn
100 105 110
Leu Ser Arg Ser Arg Trp Phe Asp Phe Pro Phe Thr Arg Glu Glu Ala
115 120 125
Leu Gln Ala Asp Lys Lys Leu Asn Leu Phe Ile Gly Ala Ser Val Asp
130 135 140
Pro Ala Gly Val Thr Met Ile Asp Ala Val Lys Ile Tyr Gly Lys Thr

```
145                 150                 155                 160
Lys Glu Gln Phe Gly Trp Pro Asp Glu Pro Pro Glu Glu Phe Pro Ser
                165                 170                 175
Ala Ser Val Ser Asn Ile Cys Pro Ser Asn Leu Asn Gln Ser Asn Gly
            180                 185                 190
Thr Gly Asp Ser Asp Ser Ala Ala Pro Thr Thr Thr Ser Gly Thr Val
        195                 200                 205
Leu Glu Arg Leu Val Val Ser Ser Leu Glu Ala Leu Glu Ser Cys Phe
    210                 215                 220
Ala Val Gly Pro Ile Ile Glu Lys Glu Arg Asn Lys Asn Ala Ala Gln
225                 230                 235                 240
Glu Leu Ala Thr Leu Leu Leu Ser Leu Pro Ala Pro Ala Ser Val Gln
                245                 250                 255
Gln Gln Ser Lys Ser Leu Leu Ala Ser Leu His Thr Ser Arg Ser Ala
            260                 265                 270
Tyr His Ser His Lys Val Thr Val Leu Ser Gly Lys Gly Asn Cys Ser
        275                 280                 285
Ala Asp Arg Glu Ser Asn Lys Leu Ala Leu His Cys Lys Ala Thr Ala
    290                 295                 300
Gln Gln Ser Lys Val Glu Gly Gly
305                 310
```

<210> 2151
<211> 511
<212> DNA
<213> Homo sapiens

<400> 2151
gccggcgttt acctgtgggg cccggtcggg cgcggcaaga cctggctgat ggatcaattc
60
caccaaagcc tgnncgggtg ccggcgcngg cggcagcact ttcatcactt catgggctgg
120
gtgcatcagc gctcctttca gttgaccggg atcgccgatc cattgcgggc gctggctcgt
180
gagctggcgg ccgaggtgcg ggtgctgtgt ttcgatgagc tgttcgtcaa tgacatcggt
240
gacgcgatca ttctcgggcg cctgtttcag gtgatgttcg acgcaggcgt ggtggtggtc
300
tgcacctcca atctgccgcc ggatcagctg tatgccgacg gcttcaaccg cgaccgcttc
360
ctgccggcga tcaccgcgat caaacagcac atgcaagtgg tcgcggtgaa tggcgcggaa
420
gatcatcgct tgcatcccgg cgccatcgag cagcgttact gggtcgctct gccggagcag
480
ggtagcgcgt tgagccaggt gttcgacgcg t
511

<210> 2152
<211> 170
<212> PRT
<213> Homo sapiens

<400> 2152
Ala Gly Val Tyr Leu Trp Gly Pro Val Gly Arg Gly Lys Thr Trp Leu

```
 1               5                  10                  15
Met Asp Gln Phe His Gln Ser Leu Xaa Gly Cys Arg Arg Xaa Arg Gln
            20                  25                  30
His Phe His His Phe Met Gly Trp Val His Gln Arg Ser Phe Gln Leu
        35                  40                  45
Thr Gly Ile Ala Asp Pro Leu Arg Ala Leu Ala Arg Glu Leu Ala Ala
    50                  55                  60
Glu Val Arg Val Leu Cys Phe Asp Glu Leu Phe Val Asn Asp Ile Gly
65                  70                  75                  80
Asp Ala Ile Ile Leu Gly Arg Leu Phe Gln Val Met Phe Asp Ala Gly
                85                  90                  95
Val Val Val Val Cys Thr Ser Asn Leu Pro Pro Asp Gln Leu Tyr Ala
            100                 105                 110
Asp Gly Phe Asn Arg Asp Arg Phe Leu Pro Ala Ile Thr Ala Ile Lys
        115                 120                 125
Gln His Met Gln Val Val Ala Val Asn Gly Ala Glu Asp His Arg Leu
    130                 135                 140
His Pro Gly Ala Ile Glu Gln Arg Tyr Trp Val Ala Leu Pro Glu Gln
145                 150                 155                 160
Gly Ser Ala Leu Ser Gln Val Phe Asp Ala
                165                 170
```

<210> 2153
<211> 528
<212> DNA
<213> Homo sapiens

<400> 2153
nnaccggtgc caaagagctg gggatcaacc tgccgaacac cgccggtacg cagcaggtgt
60
tcagtacgtg cacggcgatt ggcggcggca attgggacca ctccgcgctg atcaagggcc
120
tggagcatat ggccaacttt tcgattcgcg atcaataagc cacaccgctc ccacctttga
180
tggcattcca agtctgaaat tgatccatct ctaataacaa aaatccccgg gagcccgctt
240
atgtcggtcg atccgcaaca cctgcttcgc gagctgtttg ccacagccat cgatgccgcc
300
cacccccggc atgtccttga accttatctg cccgctgacc gcacaggccg tgtgattgtg
360
attgggcccg gcaaaaccgc acccgccatg gccctcgtcg tcgagaacgg ctggcaaggc
420
gaagtcaccg gcctggtggt cacccgctac ggccacggcg cgccgtgcaa aaaaatcgaa
480
gtggtcgagg ccgctcaccc ggtgccggat gccgccggcc tggcggtg
528

<210> 2154
<211> 96
<212> PRT
<213> Homo sapiens

<400> 2154
Met Ser Val Asp Pro Gln His Leu Leu Arg Glu Leu Phe Ala Thr Ala

```
 1               5                  10                  15
Ile Asp Ala Ala His Pro Arg His Val Leu Glu Pro Tyr Leu Pro Ala
            20                  25                  30
Asp Arg Thr Gly Arg Val Ile Val Ile Gly Pro Gly Lys Thr Ala Pro
        35                  40                  45
Ala Met Ala Leu Val Val Glu Asn Gly Trp Gln Gly Glu Val Thr Gly
    50                  55                  60
Leu Val Val Thr Arg Tyr Gly His Gly Ala Pro Cys Lys Lys Ile Glu
65                  70                  75                  80
Val Val Glu Ala Ala His Pro Val Pro Asp Ala Ala Gly Leu Ala Val
                85                  90                  95
```

<210> 2155
<211> 297
<212> DNA
<213> Homo sapiens

<400> 2155
gtgcaccgcc acggcacacc cgccatgccg cgccgctatt tcgaggccct gctgcaggag
60
ttcggccccg actgcgaggt gctcaccgtc accgattcag agggcaaccc cctcagttcg
120
gtgctcagtt tctacttccg tgatgaagtg ctgccctact atgcgggcga cgccgtcgcg
180
gcgcgcgaac tggcggccaa tgacttcaaa tactgggagc tgatgcgacg cgcctgtgcg
240
cgcggcctca aggtgtttga ctacggccgc agcaagcagg gcacgggctc ctacgcn
297

<210> 2156
<211> 91
<212> PRT
<213> Homo sapiens

<400> 2156
```
Met Pro Arg Arg Tyr Phe Glu Ala Leu Leu Gln Glu Phe Gly Pro Asp
 1               5                  10                  15
Cys Glu Val Leu Thr Val Thr Asp Ser Glu Gly Asn Pro Leu Ser Ser
            20                  25                  30
Val Leu Ser Phe Tyr Phe Arg Asp Glu Val Leu Pro Tyr Tyr Ala Gly
        35                  40                  45
Asp Ala Val Ala Ala Arg Glu Leu Ala Ala Asn Asp Phe Lys Tyr Trp
    50                  55                  60
Glu Leu Met Arg Arg Ala Cys Ala Arg Gly Leu Lys Val Phe Asp Tyr
65                  70                  75                  80
Gly Arg Ser Lys Gln Gly Thr Gly Ser Tyr Ala
                85                  90
```

<210> 2157
<211> 711
<212> DNA
<213> Homo sapiens

<400> 2157

naccgagata acgaggtcgt catcatctcc actgggtccc aaggtgagcc actttcggcc
60
ctagcaagga tcgccaaccg agagcaccga gacatcgagg tgggggaggg agataccgtt
120
ttgctggcat cctctctcat cccgggtaat gagaatgccg tctatcgagt gattaatggc
180
ctgacgaagc ttggcgccgc cgtggtacat aagggcaacg ctttggtcca cgtttccggc
240
catgccgcag ccggagagct gctgtacgcg tataacatcg tgcggccacg cgctgtgatg
300
ccgattcatg gtgaggtgcg tcatcttgtc gctaatgccg atctggccaa agcaaccggt
360
gtcgatgaga acaacgtggt gcttgtcgag gacggcgggg ttattgacct tgttgacgga
420
gtaccgcgag ttgttggcaa ggtcgatgcc tcgtacatcc ttgttgacgg atctggggtg
480
ggggagctta ccgaggacac gctcactgat cgccgtatcc tcggtgagga gggattcttg
540
tcagtcgtca ccgtggtcga cacccgctcg gcgtcagtgg tgtctcgccc ggcgatccag
600
gcgcgtggtt ttgccgaggg cgactcggtc ttcgcggaga tcaccgacca gatcgtcacc
660
gagctagaga aggcgatggc cggtggtatg gacgataccc accggttgca a
711

<210> 2158
<211> 237
<212> PRT
<213> Homo sapiens

<400> 2158
Xaa Arg Asp Asn Glu Val Val Ile Ile Ser Thr Gly Ser Gln Gly Glu
1 5 10 15
Pro Leu Ser Ala Leu Ala Arg Ile Ala Asn Arg Glu His Arg Asp Ile
20 25 30
Glu Val Gly Glu Gly Asp Thr Val Leu Leu Ala Ser Ser Leu Ile Pro
35 40 45
Gly Asn Glu Asn Ala Val Tyr Arg Val Ile Asn Gly Leu Thr Lys Leu
50 55 60
Gly Ala Ala Val Val His Lys Gly Asn Ala Leu Val His Val Ser Gly
65 70 75 80
His Ala Ala Ala Gly Glu Leu Leu Tyr Ala Tyr Asn Ile Val Arg Pro
85 90 95
Arg Ala Val Met Pro Ile His Gly Glu Val Arg His Leu Val Ala Asn
100 105 110
Ala Asp Leu Ala Lys Ala Thr Gly Val Asp Glu Asn Asn Val Val Leu
115 120 125
Val Glu Asp Gly Gly Val Ile Asp Leu Val Asp Gly Val Pro Arg Val
130 135 140
Val Gly Lys Val Asp Ala Ser Tyr Ile Leu Val Asp Gly Ser Gly Val
145 150 155 160
Gly Glu Leu Thr Glu Asp Thr Leu Thr Asp Arg Arg Ile Leu Gly Glu
165 170 175
Glu Gly Phe Leu Ser Val Val Thr Val Val Asp Thr Arg Ser Ala Ser

```
            180                 185                 190
Val Val Ser Arg Pro Ala Ile Gln Ala Arg Gly Phe Ala Glu Gly Asp
        195                 200                 205
Ser Val Phe Ala Glu Ile Thr Asp Gln Ile Val Thr Glu Leu Glu Lys
    210                 215                 220
Ala Met Ala Gly Gly Met Asp Asp Thr His Arg Leu Gln
225                 230                 235

<210> 2159
<211> 322
<212> DNA
<213> Homo sapiens

<400> 2159
tcgcgagcac actccagcct ctggagagac gacaacgcgt gaaggggcac cagcttgcgg
60
ggcagcagct ccaggggcgg cctgggaggg ctttgtgcag aagaagcctg tttccttcta
120
cctgtttgga aaagttgtct ctgcagatgg tgggtgagag ttcgctgcca gggccactgt
180
cttccctgcc ctgcggacac ttcttcccca ccttcctaaa gctgtgggag acctggagcc
240
gtggagcatc aatggctctt tgactcagga atcttaaaaa atcacaccct ggggctacca
300
tgggggcctt ctggttctcc tt
322

<210> 2160
<211> 100
<212> PRT
<213> Homo sapiens

<400> 2160
Met Val Ala Pro Gly Cys Asp Phe Leu Arg Phe Leu Ser Gln Arg Ala
 1               5                  10                  15
Ile Asp Ala Pro Arg Leu Gln Val Ser His Ser Phe Arg Lys Val Gly
            20                  25                  30
Lys Lys Cys Pro Gln Gly Arg Glu Asp Ser Gly Pro Gly Ser Glu Leu
        35                  40                  45
Ser Pro Thr Ile Cys Arg Asp Asn Phe Ser Lys Gln Val Glu Gly Asn
    50                  55                  60
Arg Leu Leu Leu His Lys Ala Leu Pro Gly Arg Pro Trp Ser Cys Cys
65                  70                  75                  80
Pro Ala Ser Trp Cys Pro Phe Thr Arg Cys Arg Leu Ser Arg Gly Trp
                85                  90                  95
Ser Val Leu Ala
            100

<210> 2161
<211> 1070
<212> DNA
<213> Homo sapiens

<400> 2161
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tcttagggga agggaaggct tatctgaaga gtagacctct ggttttgaat gagggagaca
60
gtggggatat gaggggagga aacctcaaaa agaatatgta tccatcacta tgaaaggtta
120
ggctatacag gggaagcctc caaagggaaa tctggaaaaa tgttctgaga gggacattaa
180
ggatgtactc agaaattaag aaaacatatt aggacttgcc aaaagtgaga gaagcaactg
240
aggagactta tatgcaaaaa tcgcaaagaa ggagagaaca aaagatggag gttggatgct
300
aaatagggaa agagaacgcg tgaatgaggt agggggcaga acatgcagtg cagaaaaaca
360
acagatatgg aagggcatta aagagggcta aatgggaata ttaggaaatg agagttggga
420
atttgtcaga gttgtgtatt aacaaggaga gggtaaggta agaaggtggc aaagtaagag
480
ccagggcata aggttttgct gtccaggaag ctttgttgga aaaatgttag aagtaatggg
540
tttggtcagt atggtgagag gtgagagagg ctaaatggga tgggcataaa gggcaggcca
600
gtggcaagaa tcctatgaaa gtgtaggcag atctgagagc acagacaaat acagtggaga
660
atgtggcaca gggcagaggg cagtgggctg agcagcgagt gcccatgggg aggggagtat
720
ccagaagaac ccattgagtc cctaagaatg acacacaggt gacagctgaa agaaggaggg
780
acacagaaga tatagcagca tgattctctg gggcaaaatg aggaagaaag gaatggaaga
840
agaaagtgaa gggttcctgc tgatgtgagg ggatgactgg aggaaaggca ggtattgact
900
ggggggtaaa ggaaccattc ttggatcaag gttatgatgg aataagaagg aagagagagc
960
tggctagctg agtaaaggac catcgtataa aacagacaaa agttaagact agatggagtg
1020
gcaactaggc agatcagatg tatttttaaa aggggaaact gctaagatct
1070

<210> 2162
<211> 145
<212> PRT
<213> Homo sapiens

<400> 2162

Met	Val	Leu	Tyr	Ser	Ala	Ser	Gln	Leu	Ser	Leu	Pro	Ser	Tyr	Ser	Ile
1				5				10						15	
Ile	Thr	Leu	Ile	Gln	Glu	Trp	Phe	Leu	Tyr	Pro	Pro	Val	Asn	Thr	Cys
			20					25					30		
Leu	Ser	Ser	Ser	His	Pro	Leu	Thr	Ser	Ala	Gly	Thr	Leu	His	Phe	Leu
		35					40					45			
Leu	Pro	Phe	Leu	Ser	Ser	Ser	Phe	Cys	Pro	Arg	Glu	Ser	Cys	Cys	Tyr
	50					55					60				
Ile	Phe	Cys	Val	Pro	Pro	Ser	Phe	Ser	Cys	His	Leu	Cys	Val	Ile	Leu
65					70					75					80
Arg	Asp	Ser	Met	Gly	Ser	Ser	Gly	Tyr	Ser	Pro	Pro	His	Gly	His	Ser

```
                85                  90                  95
Leu Leu Ser Pro Leu Pro Ser Ala Leu Cys His Ile Leu His Cys Ile
            100                 105                 110
Cys Leu Cys Ser Gln Ile Cys Leu His Phe His Arg Ile Leu Ala Thr
        115                 120                 125
Gly Leu Pro Phe Met Pro Ile Pro Phe Ser Leu Ser His Leu Ser Pro
    130                 135                 140
Tyr
145
```

<210> 2163
<211> 657
<212> DNA
<213> Homo sapiens

<400> 2163
tatttaaatc tttataaaaa aggtaggagg atcaggactt cgacccccttt aaaacgcggc
60
ggcctccctc caatccacct ccacttccta cacccacccc gctctccccc ccccccctttt
120
tggttccggg ttggaaggtt gggtgaaatg ggaaccgaat accaatttca cccgggaacc
180
agtaatgccc atgataaccg ccaagttggg accgaagttg ggatccataa gtacgggcgg
240
ccagtggggt ggaattgggt taagcccccct cccagccttt ctccgaccgc gtgctccgtc
300
agacatgcca agaggctctc tctccaggag agccacctgt gaaacccacc cggcatgctc
360
ctcccaccac tgtgcacaga cgagtgcctg ggctccagag agggagggag ctgaaggcct
420
cagacaggag tccgtcccgt ccagtcccat catcccaaga aacatccggc ccgactccct
480
gcagctccat ggctcaacaa ggtgcggatg cctgctggac ctggctgctt tccatccaac
540
tttgatccct tccccaagag gaagagtgct acctagggac aagtgtggtg cgcacaggca
600
tgcagcctgg tctcttgctc aggcggcttg cgcagattcc tagaggaatc tgcagcg
657

<210> 2164
<211> 152
<212> PRT
<213> Homo sapiens

<400> 2164
```
Met Pro Met Ile Thr Ala Lys Leu Gly Pro Lys Leu Gly Ser Ile Ser
 1               5                  10                  15
Thr Gly Gly Gln Trp Gly Gly Ile Gly Leu Ser Pro Leu Pro Ala Phe
            20                  25                  30
Leu Arg Pro Arg Ala Pro Ser Asp Met Pro Arg Gly Ser Leu Ser Arg
        35                  40                  45
Arg Ala Thr Cys Glu Thr His Pro Ala Cys Ser Ser His His Cys Ala
    50                  55                  60
Gln Thr Ser Ala Trp Ala Pro Glu Arg Glu Gly Ala Glu Gly Leu Arg
```

65 70 75 80
Gln Glu Ser Val Pro Ser Ser Pro Ile Ile Pro Arg Asn Ile Arg Pro
85 90 95
Asp Ser Leu Gln Leu His Gly Ser Thr Arg Cys Gly Cys Leu Leu Asp
100 105 110
Leu Ala Ala Phe His Pro Thr Leu Ile Pro Ser Pro Arg Gly Arg Val
115 120 125
Leu Pro Arg Asp Lys Cys Gly Ala His Arg His Ala Ala Trp Ser Leu
130 135 140
Ala Gln Ala Ala Cys Ala Asp Ser
145 150

<210> 2165
<211> 962
<212> DNA
<213> Homo sapiens

<400> 2165
nctttctcat cgacagcgac gcacaaccgg cgacatcacc ggtgacggtt caaggtggca
60
gcccgagggc ccgccgtgaa cttattgtgt cgtcttatgg aagaaaagtc actcggaagt
120
accgtaaatc accccagcgc ctcatccccc gaatctgttc gccatctgct gtcgcccctg
180
cgcttaaggc atcaccccac tagactgacc gaagtctcgc cgagggaggc tagggaggct
240
taggtggcca ggaatgacat cgggacgacg tctacgcgtc gaataggcag cggacgtacg
300
tcgagtaccg gccgtacggt ggtgtcttct gaccgcacac gcagagctat cgctaaaaga
360
ttgatggccc gcacctcagc tatgacgacg gccactctag aggaaatggg tcgtcgacac
420
tcctggttcc gtgatctgtc agccgaagaa agatcgtgga tctcgatcgt ggctcgctca
480
ggtattgacg gcttcgtcca gtggtttgct gacgatgacg ccgagcccta ctcccccacc
540
gacgtcttcg acgtggcgcc ccggtccatg acccgcaaga tctccttgca ccagacagtc
600
gagctcgtcc gcaccacgat tgacgtcgtt gaggcacaaa ttgagaccga aatgccacgc
660
ggtgatcgcc aagtgctgcg cactgccatc gttcactact cccgcgaggt ggccttcgcc
720
gccgccgagg tttacgcgcg agccgccgaa cgtcgcggta cctgggatga acgtctggaa
780
tccctcgtcg ttgatgccgt cgtgcgagcc gacgccgatg aacagctcat ctcgcgagct
840
tctactctcg gctggcgccc gggcatcaac ctctgcgtcg ttgtcgggcg ggccccgacg
900
accgagcatg aactccacgt gctgcgacgt gatggagaac gcatgcagat gacggtgcta
960
gc
962

<210> 2166

<211> 239
<212> PRT
<213> Homo sapiens

<400> 2166
Val Ala Arg Asn Asp Ile Gly Thr Thr Ser Thr Arg Arg Ile Gly Ser
1 5 10 15
Gly Arg Thr Ser Ser Thr Gly Arg Thr Val Val Ser Ser Asp Arg Thr
20 25 30
Arg Arg Ala Ile Ala Lys Arg Leu Met Ala Arg Thr Ser Ala Met Thr
35 40 45
Thr Ala Thr Leu Glu Glu Met Gly Arg Arg His Ser Trp Phe Arg Asp
50 55 60
Leu Ser Ala Glu Glu Arg Ser Trp Ile Ser Ile Val Ala Arg Ser Gly
65 70 75 80
Ile Asp Gly Phe Val Gln Trp Phe Ala Asp Asp Asp Ala Glu Pro Tyr
85 90 95
Ser Pro Thr Asp Val Phe Asp Val Ala Pro Arg Ser Met Thr Arg Lys
100 105 110
Ile Ser Leu His Gln Thr Val Glu Leu Val Arg Thr Thr Ile Asp Val
115 120 125
Val Glu Ala Gln Ile Glu Thr Glu Met Pro Arg Gly Asp Arg Gln Val
130 135 140
Leu Arg Thr Ala Ile Val His Tyr Ser Arg Glu Val Ala Phe Ala Ala
145 150 155 160
Ala Glu Val Tyr Ala Arg Ala Ala Glu Arg Arg Gly Thr Trp Asp Glu
165 170 175
Arg Leu Glu Ser Leu Val Val Asp Ala Val Val Arg Ala Asp Ala Asp
180 185 190
Glu Gln Leu Ile Ser Arg Ala Ser Thr Leu Gly Trp Arg Pro Gly Ile
195 200 205
Asn Leu Cys Val Val Val Gly Arg Ala Pro Thr Thr Glu His Glu Leu
210 215 220
His Val Leu Arg Arg Asp Gly Glu Arg Met Gln Met Thr Val Leu
225 230 235

<210> 2167
<211> 325
<212> DNA
<213> Homo sapiens

<400> 2167
accggtgcag tttgtgaggg gttggtgacg cccgatcggg aggttcacgc cgtcacggcg
60
catccacatt atcccgactg gaagatctcg ccaggttacg gacagtggtc gcgtagcgaa
120
cagatcgaca gtgtgactgt gacgcgagtc agacacttcg tcccgcggcg tcccacggcg
180
attcttcgag cggtgtctga ggtgacgttc gggttgcgtc tctgcgccgt ccgttggcga
240
agcaccgcgg cgattgtggc tgtgtcgccg gccttgctct cgacgcggtc gcgcgggtcg
300
tgcgctgatc tcccacagca taccc
325

<210> 2168
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2168
Thr Gly Ala Val Cys Glu Gly Leu Val Thr Pro Asp Arg Glu Val His
1 5 10 15
Ala Val Thr Ala His Pro His Tyr Pro Asp Trp Lys Ile Ser Pro Gly
20 25 30
Tyr Gly Gln Trp Ser Arg Ser Glu Gln Ile Asp Ser Val Thr Val Thr
35 40 45
Arg Val Arg His Phe Val Pro Arg Arg Pro Thr Ala Ile Leu Arg Ala
50 55 60
Val Ser Glu Val Thr Phe Gly Leu Arg Leu Cys Ala Val Arg Trp Arg
65 70 75 80
Ser Thr Ala Ala Ile Val Ala Val Ser Pro Ala Leu Leu Ser Thr Arg
85 90 95
Ser Arg Gly Ser Cys Ala Asp Leu Pro Gln His Thr
100 105

<210> 2169
<211> 309
<212> DNA
<213> Homo sapiens

<400> 2169
gaggacgcct acgtgctcat cacccagggc aagatctcgg cgatcgccga cgtcctgccg
60
atcctggaga aggtcgtcaa ggccggcaag ccgctgctcg tcatcgccga ggacatcgac
120
ggggaggccc tgtccaccct cgtcgtcaat aagatccgcg gtaccttcag ctcggtggca
180
gtcaaggcgc ccggcttcgg tgaccgccgc aaggcaatgc tgcaggacat cgccaccctc
240
accggtggtc aggtcgtcgc tcccgaggtt gggctcaagc tcgaccaggt gggcctcgag
300
gttcagggc
309

<210> 2170
<211> 103
<212> PRT
<213> Homo sapiens

<400> 2170
Glu Asp Ala Tyr Val Leu Ile Thr Gln Gly Lys Ile Ser Ala Ile Ala
1 5 10 15
Asp Val Leu Pro Ile Leu Glu Lys Val Val Lys Ala Gly Lys Pro Leu
20 25 30
Leu Val Ile Ala Glu Asp Ile Asp Gly Glu Ala Leu Ser Thr Leu Val
35 40 45
Val Asn Lys Ile Arg Gly Thr Phe Ser Ser Val Ala Val Lys Ala Pro

```
    50                  55                  60
Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln Asp Ile Ala Thr Leu
65                  70                  75                  80
Thr Gly Gly Gln Val Val Ala Pro Glu Val Gly Leu Lys Leu Asp Gln
                85                  90                  95
Val Gly Leu Glu Val Gln Gly
            100
```

<210> 2171
<211> 518
<212> DNA
<213> Homo sapiens

<400> 2171
cgcgtaatgt gtattaaggt ccttggtggc tcgcatcgcc gttatgcagc aatcggtgat
60
atcatcaaag tttcagtgaa ggaagcaatt cctcgcggaa aaattaaaaa aggtaatgtt
120
cattcagctg tggtagtgcg taccagaaaa ggtgtacgtc gtcccgatgg ttctgttatt
180
cgttttgatc gcaacgcagc ggttatcttg aatgcaaaca accagccagt cggtacacgt
240
atctttggcc ctgtaacccg tgagcttcga aatgaaaatt tcatgaagat tgtttcactg
300
gcgccagaag tactgtaagg aaccgaaaat ggcagcaaaa ataaaacgtg acgatgaagt
360
aattgttatt gccggtaaag ataaaggtaa aactgggaaa gtttctcaag ttttaactaa
420
cggtaaagta attattgaag gtgtaaatgt tcaaaagaaa caccaaaaac caaaccctca
480
agcgggcgtg gaaggcggaa tcattgaaca gaatgcat
518

<210> 2172
<211> 105
<212> PRT
<213> Homo sapiens

<400> 2172
```
Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr Ala
 1               5                  10                  15
Ala Ile Gly Asp Ile Ile Lys Val Ser Val Lys Glu Ala Ile Pro Arg
            20                  25                  30
Gly Lys Ile Lys Lys Gly Asn Val His Ser Ala Val Val Val Arg Thr
        35                  40                  45
Arg Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp Arg
    50                  55                  60
Asn Ala Ala Val Ile Leu Asn Ala Asn Asn Gln Pro Val Gly Thr Arg
65                  70                  75                  80
Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Asn Glu Asn Phe Met Lys
                85                  90                  95
Ile Val Ser Leu Ala Pro Glu Val Leu
            100                 105
```

<210> 2173
<211> 475
<212> DNA
<213> Homo sapiens

<400> 2173
nntggggaag aaatgccggt gcatgcactt tgtgcagcat taggtgcagg ggtgatgcag
60
cgggcgcgtg ccttttgcgg cggggtttcg agcattcatc tggtgcatgc attttcgcat
120
gcatttcttg tatcctcgtc atgcgtttct ccccatgcac acacattatc gcctttgcac
180
ccgcagggac gcatggaata cctcgtgaaa tggaagggat ggtcgcagaa gtacagcaca
240
tgggaaccgg aggaaaacat cctggatgct cgcttgctcg cagcctttga ggaaagggaa
300
agagagatgg agctctatgg ccccaaaaag cgtggaccca agcccaaaac cttcctcctc
360
aaagcgcagg ccaaggcaaa ggccaaaact tacgagtttc gaagtgactc agccaggggc
420
atccggatcc cctaccctgg ccgctcgccc caggacctgg cctccacttc ccggg
475

<210> 2174
<211> 158
<212> PRT
<213> Homo sapiens

<400> 2174
Xaa Gly Glu Glu Met Pro Val His Ala Leu Cys Ala Ala Leu Gly Ala
1 5 10 15
Gly Val Met Gln Arg Ala Arg Ala Phe Cys Gly Gly Val Ser Ser Ile
20 25 30
His Leu Val His Ala Phe Ser His Ala Phe Leu Val Ser Ser Ser Cys
35 40 45
Val Ser Pro His Ala His Thr Leu Ser Pro Leu His Pro Gln Gly Arg
50 55 60
Met Glu Tyr Leu Val Lys Trp Lys Gly Trp Ser Gln Lys Tyr Ser Thr
65 70 75 80
Trp Glu Pro Glu Glu Asn Ile Leu Asp Ala Arg Leu Leu Ala Ala Phe
85 90 95
Glu Glu Arg Glu Arg Glu Met Glu Leu Tyr Gly Pro Lys Lys Arg Gly
100 105 110
Pro Lys Pro Lys Thr Phe Leu Leu Lys Ala Gln Ala Lys Ala Lys Ala
115 120 125
Lys Thr Tyr Glu Phe Arg Ser Asp Ser Ala Arg Gly Ile Arg Ile Pro
130 135 140
Tyr Pro Gly Arg Ser Pro Gln Asp Leu Ala Ser Thr Ser Arg
145 150 155

<210> 2175
<211> 462
<212> DNA
<213> Homo sapiens

<400> 2175
cgcgacaccc tctttggtgg gcgccttcct tctccgaatt cgcgaaccct ccagactctg
60
gcccaggagg ttgtcgagcg tggagccgat atcggcattg ccactgatgg tgacgcagac
120
cgcctcggta tcattgatga ccaggggcat ttcttgcatc ccaaccagat cctcgtattg
180
ctgtacacct accttctgga ggacaaggga tggcaggtgc cctgcgtgcg taacctcgcg
240
acgacccacc tgcttgaccg tgtcgccgag gcccacgggc agacctgtta cgaggtaccg
300
gtcggattta agtgggtgtc gtccaagatg gccgagacca acgccgtcat cggtggtgag
360
tcctccggtg gtttgaccgt ccaggggcat attgcaggca aggatggtgt ctatgctggc
420
accctgctgg tggaaatgat cgccaagcgg ggtaagaagc tt
462

<210> 2176
<211> 154
<212> PRT
<213> Homo sapiens

<400> 2176
Arg Asp Thr Leu Phe Gly Gly Arg Leu Pro Ser Pro Asn Ser Arg Thr
1 5 10 15
Leu Gln Thr Leu Ala Gln Glu Val Val Glu Arg Gly Ala Asp Ile Gly
20 25 30
Ile Ala Thr Asp Gly Asp Ala Asp Arg Leu Gly Ile Ile Asp Asp Gln
35 40 45
Gly His Phe Leu His Pro Asn Gln Ile Leu Val Leu Leu Tyr Thr Tyr
50 55 60
Leu Leu Glu Asp Lys Gly Trp Gln Val Pro Cys Val Arg Asn Leu Ala
65 70 75 80
Thr Thr His Leu Leu Asp Arg Val Ala Glu Ala His Gly Gln Thr Cys
85 90 95
Tyr Glu Val Pro Val Gly Phe Lys Trp Val Ser Ser Lys Met Ala Glu
100 105 110
Thr Asn Ala Val Ile Gly Gly Glu Ser Ser Gly Gly Leu Thr Val Gln
115 120 125
Gly His Ile Ala Gly Lys Asp Gly Val Tyr Ala Gly Thr Leu Leu Val
130 135 140
Glu Met Ile Ala Lys Arg Gly Lys Lys Leu
145 150

<210> 2177
<211> 478
<212> DNA
<213> Homo sapiens

<400> 2177
ctcgagaatc atgacggcga cgacgtgact atctccaccc gtgtgcctcg tgacggcggg
60

accttggact cgattgtcgg cgtgctggcc ggggcatcct ggtatcagcg ggagatccac
120
gacttttttg gtgtgaggtt tgtcggccct ggggcagatg atcgtgccct ccttgtccac
180
gatgcaccga aaccgcccct gcgcaaggaa gctgtgttgg cgcagcgagc tgacaccgtg
240
tggccgggtg cggctgacca ggctggctcg aagtccgcga gtcgacgtct gccggtcggc
300
gttcctgacc ctgagacgtg gcggcgtatc aaagacggcg aggatattcc ggatgccgag
360
gtcatcgcgg ccatgtctgg ccggcgcccg cgatcagctg cccgtcgaat ggcaagcacg
420
gcgtcaggca ggcaggcatg agacattcga ctatcaacct tgacgtcgac gcgtgcac
478

<210> 2178
<211> 146
<212> PRT
<213> Homo sapiens

<400> 2178
Leu Glu Asn His Asp Gly Asp Asp Val Thr Ile Ser Thr Arg Val Pro
1 5 10 15
Arg Asp Gly Gly Thr Leu Asp Ser Ile Val Gly Val Leu Ala Gly Ala
20 25 30
Ser Trp Tyr Gln Arg Glu Ile His Asp Phe Phe Gly Val Arg Phe Val
35 40 45
Gly Pro Gly Ala Asp Asp Arg Ala Leu Leu Val His Asp Ala Pro Lys
50 55 60
Pro Pro Leu Arg Lys Glu Ala Val Leu Ala Gln Arg Ala Asp Thr Val
65 70 75 80
Trp Pro Gly Ala Ala Asp Gln Ala Gly Ser Lys Ser Ala Ser Arg Arg
85 90 95
Leu Pro Val Gly Val Pro Asp Pro Glu Thr Trp Arg Arg Ile Lys Asp
100 105 110
Gly Glu Asp Ile Pro Asp Ala Glu Val Ile Ala Ala Met Ser Gly Arg
115 120 125
Arg Pro Arg Ser Ala Ala Arg Arg Met Ala Ser Thr Ala Ser Gly Arg
130 135 140
Gln Ala
145

<210> 2179
<211> 296
<212> DNA
<213> Homo sapiens

<400> 2179
gtgcacttcc gagtggacgt cgagcgtcgc attaacgggg ccggcgcggt gggcgcacac
60
aagacgtcga tgctgcagga tctggacngc gaccgcgcga tggagatcga cccgctcgtc
120
tccgtcgttc aggagatggg acgcctggcc aacgtgccga cgcccacgct cgatgtcgtg
180

ctcccactga tcaagcaacg tgaattcatg acgaagccgg atgccgtggc ggccgcgcag
240
gaacgtctgg ctaaagcggc ataaaccagc cgccgaaacc agcggcataa cgcggn
296

<210> 2180
<211> 87
<212> PRT
<213> Homo sapiens

<400> 2180
Val His Phe Arg Val Asp Val Glu Arg Arg Ile Asn Gly Ala Gly Ala
1 5 10 15
Val Gly Ala His Lys Thr Ser Met Leu Gln Asp Leu Asp Xaa Asp Arg
20 25 30
Ala Met Glu Ile Asp Pro Leu Val Ser Val Val Gln Glu Met Gly Arg
35 40 45
Leu Ala Asn Val Pro Thr Pro Thr Leu Asp Val Val Leu Pro Leu Ile
50 55 60
Lys Gln Arg Glu Phe Met Thr Lys Pro Asp Ala Val Ala Ala Ala Gln
65 70 75 80
Glu Arg Leu Ala Lys Ala Ala
85

<210> 2181
<211> 387
<212> DNA
<213> Homo sapiens

<400> 2181
ngcgcgccgg gatggatcat agtctggctc gatgcatcac gtgcgcgcat gcgcgcgctg
60
tcgattcccg acggcatgat cgcggcactc gaccgtaccg gcaaggcgca aacgcacctc
120
acgctggcat cgccggaagc gggtgtcgtc agcgaactga acgtgcgcga cggtgcgatg
180
gtcgcgccgg ggcagacgct cgcgaagatt tcgggcctct cgaagctctg gctgatcgtc
240
gagattccgg aagcgctcgc gctcgatgcg cgtccgggca tgaccgtcga cgcgacgttc
300
tcgggcgatc cgacgcagca tttcaccggg cgtatccgcg agatcctgcc gggcatcacc
360
accagtagcc gcacgcttca ggcgcgc
387

<210> 2182
<211> 129
<212> PRT
<213> Homo sapiens

<400> 2182
Xaa Ala Pro Gly Trp Ile Ile Val Trp Leu Asp Ala Ser Arg Ala Arg
1 5 10 15
Met Arg Ala Leu Ser Ile Pro Asp Gly Met Ile Ala Ala Leu Asp Arg

```
            20                  25                  30
Thr Gly Lys Ala Gln Thr His Leu Thr Leu Ala Ser Pro Glu Ala Gly
        35                  40                  45
Val Val Ser Glu Leu Asn Val Arg Asp Gly Ala Met Val Ala Pro Gly
    50                  55                  60
Gln Thr Leu Ala Lys Ile Ser Gly Leu Ser Lys Leu Trp Leu Ile Val
65                  70                  75                  80
Glu Ile Pro Glu Ala Leu Ala Leu Asp Ala Arg Pro Gly Met Thr Val
                85                  90                  95
Asp Ala Thr Phe Ser Gly Asp Pro Thr Gln His Phe Thr Gly Arg Ile
            100                 105                 110
Arg Glu Ile Leu Pro Gly Ile Thr Thr Ser Ser Arg Thr Leu Gln Ala
        115                 120                 125
Arg
```

<210> 2183
<211> 310
<212> DNA
<213> Homo sapiens

<400> 2183
aagcttgaaa aacaaatttg tgcacagtct gataacccaa aaatgactga tggattggct
60
ctgcattttc caagcaggga ggggtcgggc atggagaatg aaacattctg agaaaagact
120
taaatgtgga aacttttggt tcaagagggt attctaggag atacaagaaa tatctcctgg
180
gggcatccaa agggaataac actgtaatct tgagtgatgt atggttccat tgcccgagga
240
atagggatga aaaccataaa ctcctttggg tgggtattaa cttatcantc aaagttacca
300
tanataatgg
310

<210> 2184
<211> 100
<212> PRT
<213> Homo sapiens

<400> 2184
```
Met Val Thr Leu Xaa Asp Lys Leu Ile Pro Thr Gln Arg Ser Leu Trp
 1               5                  10                  15
Phe Ser Ser Leu Phe Leu Gly Gln Trp Asn His Thr Ser Leu Lys Ile
            20                  25                  30
Thr Val Leu Phe Pro Leu Asp Ala Pro Arg Arg Tyr Phe Leu Tyr Leu
        35                  40                  45
Leu Glu Tyr Pro Leu Glu Pro Lys Val Ser Thr Phe Lys Ser Phe Leu
    50                  55                  60
Arg Met Phe His Ser Pro Cys Pro Thr Pro Pro Cys Leu Glu Asn Ala
65                  70                  75                  80
Glu Pro Ile His Gln Ser Phe Leu Gly Tyr Gln Thr Val His Lys Phe
                85                  90                  95
Val Phe Gln Ala
```

100

<210> 2185
<211> 723
<212> DNA
<213> Homo sapiens

<400> 2185
ngaatatcca tgcagcagct cgtcgacaat tttgacggtg ccatccctga cgatcttgac
60
tctcttgtga ccctgcccgg agtcggtcgt aagaccgcca atgttgtttt aggtaatgcc
120
ttcggcatcc ccggaatcac cccggacacc cacgtcatgc gggtatctcg acgtctgggc
180
tggaccgatg cgactacccc cgccaaggtg gaaaccgacc tggctgagct ttttgacccg
240
tctgaatggg tgatgttgtg tcaccgcctc atctggcacg ggcggcggcg ctgtcactcg
300
cggcgtcctg cctgcggggt atgcccggtt gccgagtggt gcccgtcctt cggggaaggc
360
ccaacggatc ccgaggaggc cgccacgtta gtccgggagc cgcgtcgatg aggggatga
420
acgttttcgg cgcggtgatg gccgccttga tgtttgctgg ctgcgggga gatgcgggca
480
tagctcatca gcgtgaaaat gccggaatac cggggtgctc gcatttgccg tcggggccga
540
ttgcgaaaag ttccgggccg gccacagagg gccggcccat gcccgatcac ggcttgcaat
600
gccttggtga ggggccgacg atctccatgt ctcgggcgac atcgaggggc gtgaccgtcg
660
tgacgatctg ggcgtcgtgg tgtcgaccat gtcgtagtga ggctccgctc attgcgaacg
720
cgt
723

<210> 2186
<211> 136
<212> PRT
<213> Homo sapiens

<400> 2186
Xaa Ile Ser Met Gln Gln Leu Val Asp Asn Phe Asp Gly Ala Ile Pro
1 5 10 15
Asp Asp Leu Asp Ser Leu Val Thr Leu Pro Gly Val Gly Arg Lys Thr
20 25 30
Ala Asn Val Val Leu Gly Asn Ala Phe Gly Ile Pro Gly Ile Thr Pro
35 40 45
Asp Thr His Val Met Arg Val Ser Arg Arg Leu Gly Trp Thr Asp Ala
50 55 60
Thr Thr Pro Ala Lys Val Glu Thr Asp Leu Ala Glu Leu Phe Asp Pro
65 70 75 80
Ser Glu Trp Val Met Leu Cys His Arg Leu Ile Trp His Gly Arg Arg
85 90 95
Arg Cys His Ser Arg Arg Pro Ala Cys Gly Val Cys Pro Val Ala Glu

```
            100                 105                 110
Trp Cys Pro Ser Phe Gly Glu Gly Pro Thr Asp Pro Glu Glu Ala Ala
        115                 120                 125
Thr Leu Val Arg Glu Pro Arg Arg
    130                 135

<210> 2187
<211> 342
<212> DNA
<213> Homo sapiens

<400> 2187
nnacgcgtga aggatgcgcc ccggtcgacc ggccatccgt cttgcctcgc aggcatccag
60
cccgccatat gctgcaaccg caacaccgct ttgccgtcgc atggcatctc cactccggat
120
cgcatcgatc cacgagggct atcggcgcga aagaagttgc cggggcaaaa tcccggcgag
180
gaaagcccga tggagtggaa gacgctgctc aacgacaccc gcttcggagg ggtcgccagc
240
ctcgatggga cgcgcggacg gtcggagttc cagaaggacc acgaccggat catcttctcc
300
gaagccttcc gcaagctggg ccgcaagacc caggtgcacc cg
342

<210> 2188
<211> 51
<212> PRT
<213> Homo sapiens

<400> 2188
Met Glu Trp Lys Thr Leu Leu Asn Asp Thr Arg Phe Gly Gly Val Ala
 1               5                  10                  15
Ser Leu Asp Gly Thr Arg Gly Arg Ser Glu Phe Gln Lys Asp His Asp
            20                  25                  30
Arg Ile Ile Phe Ser Glu Ala Phe Arg Lys Leu Gly Arg Lys Thr Gln
        35                  40                  45
Val His Pro
    50

<210> 2189
<211> 1412
<212> DNA
<213> Homo sapiens

<400> 2189
ntcgcttcat ggtgcgcaat tacgacaacg ccaagtctca gaatgccgag gcttacaccg
60
cgttcttcca cgcgatgcta gatgccgggg tcaacctgcc gccatcgtgc tttgaggcct
120
ggttcctctc ggacgctcac gacgacgaag ctttcgaggt ttccgcgcc gccctgccga
180
gggctgccca ggcggctgcc caggtgatca gtgcctgaca ccgggctgac ttcgcaggtc
240
```

atcgaggcaa tctgtgcctg gttcgacgcc aacggacgcg atctgccgtg gcgccgaccc
300
ggcacctccg cgtggggcgt gcttgttagc gaggtcatga gccaacagac cccgatgtcc
360
cgggtgatcg ggccgtggca cgagtggatg aaccgctggc ccacccctga tgatttggcg
420
gaggaggact ctggggaagc ggttgccgcg tgggggcgcc tgggttaccc gcgtcgggcc
480
ttacgcctgc attcctgtgc cgtcacgatc gccaccgagc acgacggggg tgtgcccaac
540
agtgacgacg agctcgtcgc cctcccgggt attggcgact acaccgcgag cgcagtcgtc
600
tcttttgcgt ttggcggccg cgccacagtg cttgacacca atgtacgtcg cctcatcgct
660
agagcagagt ctgggatcgc aaactgtcca acctcggtga cgagggctga gcgggtagtc
720
gccgacgcgt tggttcccga cgaagacgtc cgagcggcca agtgggcggt ggcgtcgatg
780
gaattggggg cactggtatg cacggcgcgg tctccgcagt gtgaggtctg cccgatccgg
840
gatggctgca ggtgggtgat cgacggtagg ccggacaatg ccccggcccg tcgaggacag
900
ccatggaagg gcacggatcg ccagtgccgc ggcgtgatta tggacgtggt gcgcaacagc
960
cctcacgggg tgaaggtcca gatggctctt tccgcctggc ccgagctcga tcaggcatca
1020
aggtgcctgg aatccttact cgatgacggt ttagtgcacc gacgaggtaa ccttattagc
1080
ctgtgacctg agaaattctt ggccccgacc acccaaacag accgagtcca gcagtgatgc
1140
cgctgggtta tccttagagg cggtcctcaa attggatcag ccaaaccacg tcaccgatca
1200
agacaccatg agcacaacac ccaaacagcc gcgcacggcg acagctgccc gacgccgaca
1260
cattgtcgac catctgcgtt ctttggggca ctcggagtcc atcggagatc tttaccaact
1320
gttcggtgtc tctacatcga cgattcgccg cgatgtcgat gccctctcgg atgaatccaa
1380
gatctggaag atttccgggg gagacgtcat ga
1412

<210> 2190
<211> 292
<212> PRT
<213> Homo sapiens

<400> 2190
Ser Val Pro Asp Thr Gly Leu Thr Ser Gln Val Ile Glu Ala Ile Cys
1 5 10 15
Ala Trp Phe Asp Ala Asn Gly Arg Asp Leu Pro Trp Arg Arg Pro Gly
20 25 30
Thr Ser Ala Trp Gly Val Leu Val Ser Glu Val Met Ser Gln Gln Thr
35 40 45
Pro Met Ser Arg Val Ile Gly Pro Trp His Glu Trp Met Asn Arg Trp

```
    50                  55                  60
Pro Thr Pro Asp Asp Leu Ala Glu Glu Asp Ser Gly Glu Ala Val Ala
65                  70                  75                  80
Ala Trp Gly Arg Leu Gly Tyr Pro Arg Arg Ala Leu Arg Leu His Ser
                85                  90                  95
Cys Ala Val Thr Ile Ala Thr Glu His Asp Gly Gly Val Pro Asn Ser
            100                 105                 110
Asp Asp Glu Leu Val Ala Leu Pro Gly Ile Gly Asp Tyr Thr Ala Ser
        115                 120                 125
Ala Val Val Ser Phe Ala Phe Gly Gly Arg Ala Thr Val Leu Asp Thr
    130                 135                 140
Asn Val Arg Arg Leu Ile Ala Arg Ala Glu Ser Gly Ile Ala Asn Cys
145                 150                 155                 160
Pro Thr Ser Val Thr Arg Ala Glu Arg Val Val Ala Asp Ala Leu Val
                165                 170                 175
Pro Asp Glu Asp Val Arg Ala Ala Lys Trp Ala Val Ala Ser Met Glu
            180                 185                 190
Leu Gly Ala Leu Val Cys Thr Ala Arg Ser Pro Gln Cys Glu Val Cys
        195                 200                 205
Pro Ile Arg Asp Gly Cys Arg Trp Val Ile Asp Gly Arg Pro Asp Asn
    210                 215                 220
Ala Pro Ala Arg Arg Gly Gln Pro Trp Lys Gly Thr Asp Arg Gln Cys
225                 230                 235                 240
Arg Gly Val Ile Met Asp Val Val Arg Asn Ser Pro His Gly Val Lys
                245                 250                 255
Val Gln Met Ala Leu Ser Ala Trp Pro Glu Leu Asp Gln Ala Ser Arg
            260                 265                 270
Cys Leu Glu Ser Leu Leu Asp Asp Gly Leu Val His Arg Arg Gly Asn
        275                 280                 285
Leu Ile Ser Leu
    290
```

<210> 2191
<211> 502
<212> DNA
<213> Homo sapiens

<400> 2191
nnacgcgtcg agaatctcta ctcctgcccg aacaacgtcc ggcttcgtca ggctcacgat
60
gactcccttg acgacgacac catttccggg ggtagcccac attggtgctg cctcatggac
120
tacattgaat cccgttcaat cctgaacggc gttcaggacg tctccagtct cggaaggacc
180
agagtattgc tgaatctagc cgacatgacc gaacgcggcc tgaggggga gtccattacc
240
cgcgaggagg ccctcgagat tcttcgcagc agtgatgatg agctcatgtc aatcatcgcc
300
gccgccggaa aagtgcgtcg ccacttttc gataaccggg ttcgcctcaa ctacctggtc
360
aacctcaagt ccggcctgtg tcccgaagac tgctcctatt gctcgcagcg tctgggatcg
420
cgtgccgaga tcacgaaata ctcctgggcc gatccgcaga aggtacacga cgccgtcgag
480

gctgggattg ccggtggtgc ac
502

<210> 2192
<211> 104
<212> PRT
<213> Homo sapiens

<400> 2192
Leu Asn Leu Ala Asp Met Thr Glu Arg Gly Leu Arg Gly Glu Ser Ile
1 5 10 15
Thr Arg Glu Glu Ala Leu Glu Ile Leu Arg Ser Ser Asp Asp Glu Leu
20 25 30
Met Ser Ile Ile Ala Ala Ala Gly Lys Val Arg Arg His Phe Phe Asp
35 40 45
Asn Arg Val Arg Leu Asn Tyr Leu Val Asn Leu Lys Ser Gly Leu Cys
50 55 60
Pro Glu Asp Cys Ser Tyr Cys Ser Gln Arg Leu Gly Ser Arg Ala Glu
65 70 75 80
Ile Thr Lys Tyr Ser Trp Ala Asp Pro Gln Lys Val His Asp Ala Val
85 90 95
Glu Ala Gly Ile Ala Gly Gly Ala
100

<210> 2193
<211> 321
<212> DNA
<213> Homo sapiens

<400> 2193
ccatggggaa tgcagagcac ggacagtcac acagactgtc ctctctggcc ttctggaccc
60
aacatactcc tcttgccaac tgggtattac tggaccttac tgggccttac tggacccaac
120
atactcctct tgccaactgg ggatttaaaa attttaaaag ccccttttatc tccctccaca
180
agtcatgtac tgccaacagg gacacactgt tttctttgga aaccctgctg tgtgcccaga
240
cagaggtccc actgccctgg gacagctccc ttgcctanag gggaaggagg gtgtgtgtgc
300
tgtgtgtgtt taggttgggg a
321

<210> 2194
<211> 106
<212> PRT
<213> Homo sapiens

<400> 2194
Met Gly Asn Ala Glu His Gly Gln Ser His Arg Leu Ser Ser Leu Ala
1 5 10 15
Phe Trp Thr Gln His Thr Pro Leu Ala Asn Trp Val Leu Leu Asp Leu
20 25 30
Thr Gly Pro Tyr Trp Thr Gln His Thr Pro Leu Ala Asn Trp Gly Phe

```
        35                  40                  45
Lys Asn Phe Lys Ser Pro Phe Ile Ser Leu His Lys Ser Cys Thr Ala
    50                  55                  60
Asn Arg Asp Thr Leu Phe Ser Leu Glu Thr Leu Leu Cys Ala Gln Thr
65                  70                  75                  80
Glu Val Pro Leu Pro Trp Asp Ser Ser Leu Ala Xaa Arg Gly Arg Arg
                85                  90                  95
Val Cys Val Leu Cys Val Phe Arg Leu Gly
            100                 105
```

<210> 2195
<211> 504
<212> DNA
<213> Homo sapiens

<400> 2195
nacgcgtctc cctacatcaa tgcccaccgc gattgcacct ttgttgtcat gctccctggc
60
gacggtgtgg cacaccccaa ctttggcaat atcgtccacg acctggtgct gttgcacagc
120
ctgggtgtgc gtctggtact ggtccacggt tcgcgcccgc agatcgacag ccgccttgag
180
gcacgaggcc tggtgccgta ttaccacaag ggcatgcgtg tcaccgatgc atcaacgctc
240
gaatgcgtga tcgatgctgt cgggcaactg cgcattgcga ttgaagcgcg cttgtcgatg
300
gacatggcgt cttcgccaat gcagggttcg cgtctgcgcg tagccagcgg caacctggtc
360
actgcgcggc cgatcggcgt gctcgacggt gtggattttc accataccgg cgaagtgcgc
420
cgggtggacc gcaagggcat caaccgcctg ctcgatgagc gctcgattgt gctgctgtcg
480
cccttgggtt actcgcccac cggt
504

<210> 2196
<211> 168
<212> PRT
<213> Homo sapiens

<400> 2196

```
Xaa Ala Ser Pro Tyr Ile Asn Ala His Arg Asp Cys Thr Phe Val Val
 1               5                  10                  15
Met Leu Pro Gly Asp Gly Val Ala His Pro Asn Phe Gly Asn Ile Val
            20                  25                  30
His Asp Leu Val Leu Leu His Ser Leu Gly Val Arg Leu Val Leu Val
        35                  40                  45
His Gly Ser Arg Pro Gln Ile Asp Ser Arg Leu Glu Ala Arg Gly Leu
    50                  55                  60
Val Pro Tyr Tyr His Lys Gly Met Arg Val Thr Asp Ala Ser Thr Leu
65                  70                  75                  80
Glu Cys Val Ile Asp Ala Val Gly Gln Leu Arg Ile Ala Ile Glu Ala
                85                  90                  95
Arg Leu Ser Met Asp Met Ala Ser Ser Pro Met Gln Gly Ser Arg Leu
```

```
            100                 105                 110
Arg Val Ala Ser Gly Asn Leu Val Thr Ala Arg Pro Ile Gly Val Leu
        115                 120                 125
Asp Gly Val Asp Phe His His Thr Gly Glu Val Arg Arg Val Asp Arg
    130                 135                 140
Lys Gly Ile Asn Arg Leu Leu Asp Glu Arg Ser Ile Val Leu Leu Ser
145                 150                 155                 160
Pro Leu Gly Tyr Ser Pro Thr Gly
                165
```

<210> 2197
<211> 351
<212> DNA
<213> Homo sapiens

<400> 2197
acaagtccgt cgacgattcg ctttccggag gcgggcccag gaatggtaat gaaacccgag
60
ttatggggcc ctgcgctcga cgagattgcc gcgggaaaac gtgccggagg ggctgaacag
120
ttagattccg cagtgcagca catccacggt gctactcacg ataaactgtc cggtgctgtt
180
ccgaaacgct acgatggtcg ggatgtcttg gcaggcgagg acccgaatgc accgttgctg
240
cttgtgccta gcccggctgg tgcagtgttt agtcaaaata aggcacaagc ctggtccaat
300
gaagaccaca ttgttttttgc ctgtgggcgc tatgaaggta ttgatcaacg c
351

<210> 2198
<211> 117
<212> PRT
<213> Homo sapiens

<400> 2198
```
Thr Ser Pro Ser Thr Ile Arg Phe Pro Glu Ala Gly Pro Gly Met Val
 1               5                  10                  15
Met Lys Pro Glu Leu Trp Gly Pro Ala Leu Asp Glu Ile Ala Ala Gly
            20                  25                  30
Lys Arg Ala Gly Gly Ala Glu Gln Leu Asp Ser Ala Val Gln His Ile
        35                  40                  45
His Gly Ala Thr His Asp Lys Leu Ser Gly Ala Val Pro Lys Arg Tyr
    50                  55                  60
Asp Gly Arg Asp Val Leu Ala Gly Glu Asp Pro Asn Ala Pro Leu Leu
65                  70                  75                  80
Leu Val Pro Ser Pro Ala Gly Ala Val Phe Ser Gln Asn Lys Ala Gln
                85                  90                  95
Ala Trp Ser Asn Glu Asp His Ile Val Phe Ala Cys Gly Arg Tyr Glu
            100                 105                 110
Gly Ile Asp Gln Arg
        115
```

<210> 2199
<211> 457

<212> DNA
<213> Homo sapiens

<400> 2199
agacgccggc cgccaagatc tgcatcccta ggccacgcta agaccctggg gaagagcgca
60
ggagcccggg agaagggctg gaaggagggg actggacgtg cggagaattc ccccctaaaa
120
ggcagaagcc cccgccccca ccctccgagc tccgttcggg cagagcgcct gcctgcctgc
180
cgttgctggg ggcgcccacc tcgcccagcc atgccaggcc cggccaccga cgcggggaag
240
atccctttct gcgacgccaa ggaagaaatc cgtgccgggc tcgaaagctc tgagggcggc
300
ggcggcccgg agaggccagg cgcgcgcggg cagcggcaga acatcgtctg gaggaatgtc
360
gtcctgatga gcttgctcca cttgggggcc gtgtactccc tggtgctcat ccccaaagcc
420
aagccactca ctctgctctg gggtaagtcc cgccggc
457

<210> 2200
<211> 152
<212> PRT
<213> Homo sapiens

<400> 2200
Arg Arg Arg Pro Pro Arg Ser Ala Ser Leu Gly His Ala Lys Thr Leu
 1   5   10   15
Gly Lys Ser Ala Gly Ala Arg Glu Lys Gly Trp Lys Glu Gly Thr Gly
            20   25   30
Arg Ala Glu Asn Ser Pro Leu Lys Gly Arg Ser Pro Arg Pro His Pro
        35   40   45
Pro Ser Ser Val Arg Ala Glu Arg Leu Pro Ala Cys Arg Cys Trp Gly
    50   55   60
Arg Pro Pro Arg Pro Ala Met Pro Gly Pro Ala Thr Asp Ala Gly Lys
65   70   75   80
Ile Pro Phe Cys Asp Ala Lys Glu Glu Ile Arg Ala Gly Leu Glu Ser
                85   90   95
Ser Glu Gly Gly Gly Gly Pro Glu Arg Pro Gly Ala Arg Gly Gln Arg
            100   105   110
Gln Asn Ile Val Trp Arg Asn Val Val Leu Met Ser Leu Leu His Leu
        115   120   125
Gly Ala Val Tyr Ser Leu Val Leu Ile Pro Lys Ala Lys Pro Leu Thr
    130   135   140
Leu Leu Trp Gly Lys Ser Arg Arg
145   150

<210> 2201
<211> 336
<212> DNA
<213> Homo sapiens

<400> 2201

agtactgcga tggacagcta tgtcgtggat ggtggtcgca aattacatgt ttgtggtaac
60
aaccctgatt gcgatggtta tgaagtcgaa gaaggcgaat tcaagatcaa gggttatgat
120
ggtccgacta tcccatgcga taaatgtgat ggtgagatgc agcttaaaac gggtcgtttt
180
ggtccatatt tcgcatgtac tagctgtgac aatactcgta aggtactcaa gagtggtcaa
240
cctgctccgc cacgtgtaga cccaatcaaa atggagcatc tacgttcaac gaagcatgat
300
gatttcttcg tcttacgtga gggcgctgct ggttta
336

<210> 2202
<211> 112
<212> PRT
<213> Homo sapiens

<400> 2202
Ser Thr Ala Met Asp Ser Tyr Val Val Asp Gly Gly Arg Lys Leu His
1 5 10 15
Val Cys Gly Asn Asn Pro Asp Cys Asp Gly Tyr Glu Val Glu Glu Gly
20 25 30
Glu Phe Lys Ile Lys Gly Tyr Asp Gly Pro Thr Ile Pro Cys Asp Lys
35 40 45
Cys Asp Gly Glu Met Gln Leu Lys Thr Gly Arg Phe Gly Pro Tyr Phe
50 55 60
Ala Cys Thr Ser Cys Asp Asn Thr Arg Lys Val Leu Lys Ser Gly Gln
65 70 75 80
Pro Ala Pro Pro Arg Val Asp Pro Ile Lys Met Glu His Leu Arg Ser
85 90 95
Thr Lys His Asp Asp Phe Phe Val Leu Arg Glu Gly Ala Ala Gly Leu
100 105 110

<210> 2203
<211> 273
<212> DNA
<213> Homo sapiens

<400> 2203
ctcgagagat gcagtcccag ccggggtggg aagctgtgca gacagccccg gatctgggac
60
gtgatggaaa actcaacaga ctggttcaga tcttggcccg gagcccagag gcaccgggga
120
cccccagggc tgtttctccc tggccacacc agtaccccac ttccaaatgc cctgtaggtg
180
accaccaggc cacacaggcc cgtctgaggg gccacaggct gtgcaccatg ggacgcaggc
240
ctgtccctgc ctccctccga tgtcctgatg gtg
273

<210> 2204
<211> 88
<212> PRT

<213> Homo sapiens

<400> 2204
Met Gln Ser Gln Pro Gly Trp Glu Ala Val Gln Thr Ala Pro Asp Leu
1 5 10 15
Gly Arg Asp Gly Lys Leu Asn Arg Leu Val Gln Ile Leu Ala Arg Ser
20 25 30
Pro Glu Ala Pro Gly Thr Pro Arg Ala Val Ser Pro Trp Pro His Gln
35 40 45
Tyr Pro Thr Ser Lys Cys Pro Val Gly Asp His Gln Ala Thr Gln Ala
50 55 60
Arg Leu Arg Gly His Arg Leu Cys Thr Met Gly Arg Arg Pro Val Pro
65 70 75 80
Ala Ser Leu Arg Cys Pro Asp Gly
85

<210> 2205
<211> 387
<212> DNA
<213> Homo sapiens

<400> 2205
gnnnnnggng nnnnactggt gtgcatggtt aaaatcctgc aagctactgg gttgccacag
60
catctgtccc actttgtgtt ctgcaaatac agcttctggg atcaacagga gccggtgatt
120
gtcgctcctg aagtggacac ctcctcctct tccgtcagca aggagccgca ctgcatggtt
180
gtctttgatc attgcaatga gttttctgtt aacatcaccg aagactttat cgagcatctt
240
tccgaaggag cattggcaat tgaagtatat ggacataaaa taaacgatcc ccggaaaaac
300
cccgccctgt gggatttggg aatcatccaa gcaaagacac gtagtcttcg ggacagatgg
360
agtgaagtgc ccaggaaatt ggaattc
387

<210> 2206
<211> 129
<212> PRT
<213> Homo sapiens

<400> 2206
Xaa Xaa Gly Xaa Xaa Leu Val Cys Met Val Lys Ile Leu Gln Ala Thr
1 5 10 15
Gly Leu Pro Gln His Leu Ser His Phe Val Phe Cys Lys Tyr Ser Phe
20 25 30
Trp Asp Gln Gln Glu Pro Val Ile Val Ala Pro Glu Val Asp Thr Ser
35 40 45
Ser Ser Ser Val Ser Lys Glu Pro His Cys Met Val Val Phe Asp His
50 55 60
Cys Asn Glu Phe Ser Val Asn Ile Thr Glu Asp Phe Ile Glu His Leu
65 70 75 80
Ser Glu Gly Ala Leu Ala Ile Glu Val Tyr Gly His Lys Ile Asn Asp

```
                85                  90                  95
Pro Arg Lys Asn Pro Ala Leu Trp Asp Leu Gly Ile Ile Gln Ala Lys
            100                 105                 110
Thr Arg Ser Leu Arg Asp Arg Trp Ser Glu Val Pro Arg Lys Leu Glu
        115                 120                 125
Phe
```

<210> 2207
<211> 667
<212> DNA
<213> Homo sapiens

<400> 2207
atctccaacc ccgagaccct ctccaataca gccggcttcg agggctacat cgacctgggc
60
cgcgagctct ccagcctgca ctcactgctc tgggaggccg tcagccagct ggagcagagc
120
atagtatcca aactgggacc cctgcctcgg atcctgaggg acgtccacac agcactgagc
180
accccaggta gcgggcagct cccagggacc aatgacctgg cctccacacc gggctctggc
240
agcagcagca tctcagctgg gctgcagaag atggtgattg agaacgatct ttccggtctg
300
atagatttca cccggttacc gtctccaacc cccgaaaaca aggacttgtt ttttgtcaca
360
aggtcctccg gggtccagcc ctcacctgcc cgcagctcga gttactcgga agccaacgag
420
cctgatcttc agatggccaa cggtggcaag agcctctcca tggtggacct ccaggacgcc
480
cgcacgctgg atggggaggc aggctccccg gcgggccccg acgtcctccc cacagatggg
540
caggccgctg cagctcagct ggtggccggg tggccggccc gggcaacccc agtgaacctg
600
gcagggctgg ccacggtgcg gcgggcaggc cagacaccaa ccacaccagg cacctccgag
660
ggcgcgc
667

<210> 2208
<211> 222
<212> PRT
<213> Homo sapiens

<400> 2208
```
Ile Ser Asn Pro Glu Thr Leu Ser Asn Thr Ala Gly Phe Glu Gly Tyr
 1               5                  10                  15
Ile Asp Leu Gly Arg Glu Leu Ser Ser Leu His Ser Leu Leu Trp Glu
            20                  25                  30
Ala Val Ser Gln Leu Glu Gln Ser Ile Val Ser Lys Leu Gly Pro Leu
        35                  40                  45
Pro Arg Ile Leu Arg Asp Val His Thr Ala Leu Ser Thr Pro Gly Ser
    50                  55                  60
Gly Gln Leu Pro Gly Thr Asn Asp Leu Ala Ser Thr Pro Gly Ser Gly
```

65 70 75 80
Ser Ser Ser Ile Ser Ala Gly Leu Gln Lys Met Val Ile Glu Asn Asp
85 90 95
Leu Ser Gly Leu Ile Asp Phe Thr Arg Leu Pro Ser Pro Thr Pro Glu
100 105 110
Asn Lys Asp Leu Phe Phe Val Thr Arg Ser Ser Gly Val Gln Pro Ser
115 120 125
Pro Ala Arg Ser Ser Ser Tyr Ser Glu Ala Asn Glu Pro Asp Leu Gln
130 135 140
Met Ala Asn Gly Gly Lys Ser Leu Ser Met Val Asp Leu Gln Asp Ala
145 150 155 160
Arg Thr Leu Asp Gly Glu Ala Gly Ser Pro Ala Gly Pro Asp Val Leu
165 170 175
Pro Thr Asp Gly Gln Ala Ala Ala Ala Gln Leu Val Ala Gly Trp Pro
180 185 190
Ala Arg Ala Thr Pro Val Asn Leu Ala Gly Leu Ala Thr Val Arg Arg
195 200 205
Ala Gly Gln Thr Pro Thr Thr Pro Gly Thr Ser Glu Gly Ala
210 215 220

<210> 2209
<211> 353
<212> DNA
<213> Homo sapiens

<400> 2209
ngggaagttg gtactagcct cccaaagcca ctctcctgag tgacattgag agcatcctat
60
agagaaggcc atgagagaga tagcactggg acagatggtg tcagcagagg ggactccaga
120
ccacagcaga agtgaccaag ctgtagcttc cttagatggc cccaagggtg ggaggcttca
180
cacagcagag cctgggtctg gaggcacctt ggggatgttt ttccccatta ggcccctgag
240
ctctatggaa gcacttaact gcctgttccc cgcttattct gtgtttaaac caaggaaaca
300
acatgcctgg ggtctgaaat cctggattca aatcctgact gtgttgtgtg ctt
353

<210> 2210
<211> 94
<212> PRT
<213> Homo sapiens

<400> 2210
Met Arg Glu Ile Ala Leu Gly Gln Met Val Ser Ala Glu Gly Thr Pro
1 5 10 15
Asp His Ser Arg Ser Asp Gln Ala Val Ala Ser Leu Asp Gly Pro Lys
20 25 30
Gly Gly Arg Leu His Thr Ala Glu Pro Gly Ser Gly Gly Thr Leu Gly
35 40 45
Met Phe Phe Pro Ile Arg Pro Leu Ser Ser Met Glu Ala Leu Asn Cys
50 55 60
Leu Phe Pro Ala Tyr Ser Val Phe Lys Pro Arg Lys Gln His Ala Trp

65 70 75 80
Gly Leu Lys Ser Trp Ile Gln Ile Leu Thr Val Leu Cys Ala
85 90

<210> 2211
<211> 493
<212> DNA
<213> Homo sapiens

<400> 2211
ctgaccacat ctccgacgat cctagacctc tgttctgcat ctcggacacc accgactgct
60
cactgtaccc tgggactgca cagagggaaa cgattaccaa acccagagac ggggaccgga
120
aggaaggagg ggaaggggat ggatccatgt actttggggt tggagaaatg ggggacagca
180
agtctcctca acccaaatac agccccccctg ggaggctcct gccccgtctc tgtggatagt
240
gagcccagct gcaagggcgg cctgccaggg acaaacccac caaaaggaaa gatgttgtag
300
aaccaaagag aggctccctg aaagaggcgt ctcccggggc ctccaagccc gggagcgccc
360
ggcggacagg gggcagtggc caagtctgtg cggaccctga ccgcctcaga gaacgagagc
420
atgcgcaaag tcatgcccat caccaagtcc agcagaggcg ccggctggag gcgaccagag
480
ctgtcatccc ggg
493

<210> 2212
<211> 126
<212> PRT
<213> Homo sapiens

<400> 2212
Met Gly Met Thr Leu Arg Met Leu Ser Phe Ser Glu Ala Val Arg Val
1 5 10 15
Arg Thr Asp Leu Ala Thr Ala Pro Cys Pro Pro Gly Ala Pro Gly Leu
20 25 30
Gly Gly Pro Gly Arg Arg Leu Phe Gln Gly Ala Ser Leu Trp Phe Tyr
35 40 45
Asn Ile Phe Pro Phe Gly Gly Phe Val Pro Gly Arg Pro Pro Leu Gln
50 55 60
Leu Gly Ser Leu Ser Thr Glu Thr Gly Gln Glu Pro Pro Arg Gly Ala
65 70 75 80
Val Phe Gly Leu Arg Arg Leu Ala Val Pro His Phe Ser Asn Pro Lys
85 90 95
Val His Gly Ser Ile Pro Phe Pro Ser Phe Leu Pro Val Pro Val Ser
100 105 110
Gly Phe Gly Asn Arg Phe Pro Leu Cys Ser Pro Arg Val Gln
115 120 125

<210> 2213
<211> 327

<212> DNA
<213> Homo sapiens

<400> 2213
acgcgtccga ccggcagttc cggcagctgc gggaaagctg cgatgcgctc gccgagcatt
60
gccggtgctt cgacacactg ggttatatcg ccctcaaagc acaggtctac gaaggttctg
120
acggaaggcc cggccaatcc gatcgcggcc tcggcgctgc gcatcatccg ggcgcgcgtg
180
tcgcagctct ggggcacgtc gctgctccgc aacggacggg cggaacagag tgtggtggag
240
atcgcccggt tggtcgacgc gatcacgtca cgggacgagg aagccgccca gcgtgcactg
300
ctcgaccaca atcgcagcgc gttggaa
327

<210> 2214
<211> 95
<212> PRT
<213> Homo sapiens

<400> 2214
Met Arg Ser Pro Ser Ile Ala Gly Ala Ser Thr His Trp Val Ile Ser
 1   5   10   15
Pro Ser Lys His Arg Ser Thr Lys Val Leu Thr Glu Gly Pro Ala Asn
            20   25   30
Pro Ile Ala Ala Ser Ala Leu Arg Ile Ile Arg Ala Arg Val Ser Gln
        35   40   45
Leu Trp Gly Thr Ser Leu Leu Arg Asn Gly Arg Ala Glu Gln Ser Val
    50   55   60
Val Glu Ile Ala Arg Leu Val Asp Ala Ile Thr Ser Arg Asp Glu Glu
65   70   75   80
Ala Ala Gln Arg Ala Leu Leu Asp His Asn Arg Ser Ala Leu Glu
                85   90   95

<210> 2215
<211> 430
<212> DNA
<213> Homo sapiens

<400> 2215
ctggggatca tgccctacat cactgcgtcg atcatcctgc agctgctgac agtcgtgatc
60
ccgaagctgg aaacccttaa gaaggagggc gcgtccggtc agaacaagat cacccagtac
120
acccgttacc tcactctcgt gcttggcctg ttgcaggcaa cggccttcgt cacgcttgcc
180
acctccggcc gtctattcac cnntgcagct ntgccagtcg tctactccac ctcggtcttc
240
gaagtcgtcg tcatgatcct gactatgacg gccggtacga ccatcgtcat gtggatgggt
300
gagctcatca ccgaccgcgg tatcggcaac ggtatgtcga tcatgatttt cactcagatt
360

gcggcgcgtt tccctgactc gctgtggtct atcaaggtcg ctcgaaatgg cgccggtcag
420
gctcacgcgt
430

<210> 2216
<211> 143
<212> PRT
<213> Homo sapiens

<400> 2216
Leu Gly Ile Met Pro Tyr Ile Thr Ala Ser Ile Ile Leu Gln Leu Leu
1 5 10 15
Thr Val Val Ile Pro Lys Leu Glu Thr Leu Lys Lys Glu Gly Ala Ser
20 25 30
Gly Gln Asn Lys Ile Thr Gln Tyr Thr Arg Tyr Leu Thr Leu Val Leu
35 40 45
Gly Leu Leu Gln Ala Thr Ala Phe Val Thr Leu Ala Thr Ser Gly Arg
50 55 60
Leu Phe Thr Xaa Ala Ala Xaa Pro Val Val Tyr Ser Thr Ser Val Phe
65 70 75 80
Glu Val Val Val Met Ile Leu Thr Met Thr Ala Gly Thr Thr Ile Val
85 90 95
Met Trp Met Gly Glu Leu Ile Thr Asp Arg Gly Ile Gly Asn Gly Met
100 105 110
Ser Ile Met Ile Phe Thr Gln Ile Ala Ala Arg Phe Pro Asp Ser Leu
115 120 125
Trp Ser Ile Lys Val Ala Arg Asn Gly Ala Gly Gln Ala His Ala
130 135 140

<210> 2217
<211> 444
<212> DNA
<213> Homo sapiens

<400> 2217
accagggccg cttcgaagga cctctctcca gctatcgtga cgacgacggc gaagcgggct
60
atgacgtggc tcgatgacga cgtgggcgcc gacctgttga atcaggctga ttccatggac
120
catgccctgg aggccaccgt cccaggtcgg gtcaccacgc cggacgccca agtcatccag
180
acctgtgccg tgttgcgtga ccttgctcgc gtggcagtca gccagctggg ccgaaatgac
240
gaggactcta gggaaccagt cgatgcggag agagtacagg ctcaagcgnc gatgcgggag
300
gttttcgaga ccgccgaacg catggtgggg ctggccgccg ccgacgtggt gtgggtctct
360
gagtctgaga agggataccg cagcattcac gtcgctccgc tgagtgttgg cggcttgcta
420
cgagagaatg tctttgctca gtcc
444

<210> 2218

<211> 148
<212> PRT
<213> Homo sapiens

<400> 2218
Thr Arg Ala Ala Ser Lys Asp Leu Ser Pro Ala Ile Val Thr Thr Thr
1 5 10 15
Ala Lys Arg Ala Met Thr Trp Leu Asp Asp Asp Val Gly Ala Asp Leu
20 25 30
Leu Asn Gln Ala Asp Ser Met Asp His Ala Leu Glu Ala Thr Val Pro
35 40 45
Gly Arg Val Thr Thr Pro Asp Ala Gln Val Ile Gln Thr Cys Ala Val
50 55 60
Leu Arg Asp Leu Ala Arg Val Ala Val Ser Gln Leu Gly Arg Asn Asp
65 70 75 80
Glu Asp Ser Arg Glu Pro Val Asp Ala Glu Arg Val Gln Ala Gln Ala
85 90 95
Xaa Met Arg Glu Val Phe Glu Thr Ala Glu Arg Met Val Gly Leu Ala
100 105 110
Ala Ala Asp Val Val Trp Val Ser Glu Ser Glu Lys Gly Tyr Arg Ser
115 120 125
Ile His Val Ala Pro Leu Ser Val Gly Gly Leu Leu Arg Glu Asn Val
130 135 140
Phe Ala Gln Ser
145

<210> 2219
<211> 688
<212> DNA
<213> Homo sapiens

<400> 2219
acgcgtaccg tcgttggcat gagcgtcctg ccactggaaa tttggctgtc attcagctac
60
ggcattacga atatggcgtg gatgtggcta tggttcgacg agcccggaaa ccgttgggag
120
tggtcgatcc ttttccccgc tgggtggctg accagcgctt tggtcagtca ggggttcggt
180
ggaatgttcc atagtgtgca gattgcgcgt catgtcagca gttaccacgg catcatggtc
240
gctttcgcgc tcgttgggta cggatggctt gcgatgcaca acttgcgtca ccctgatgag
300
cgctattcga ttcgctcggc cttgataatc ggcatcggca tccagttcac ctgggaggca
360
gtgctgatga tctcgggtat caggccgttg acatggcgcc cgcttgttat cgattctctc
420
atcgagacga atctcggcgc tccgttcatg ttgctcattg tgaaagcttg gcgcgcgcca
480
cccgaaggaa ttcctggctc taccagtccg cgcccgaccg cccgtggcac agcgcgagtc
540
tatatgaggg atgatcttgt ttctcgacgc cttctacagc gtccttgaga gcctctgcga
600
gcgaagggcg cgggtgtagg tctccccggg gctcgttgtg gtccctcctc tgcgtgacgc
660

agagccgtgt gatgaggcga agtcatga
688

<210> 2220
<211> 189
<212> PRT
<213> Homo sapiens

<400> 2220
Met Ser Val Leu Pro Leu Glu Ile Trp Leu Ser Phe Ser Tyr Gly Ile
1 5 10 15
Thr Asn Met Ala Trp Met Trp Leu Trp Phe Asp Glu Pro Gly Asn Arg
20 25 30
Trp Glu Trp Ser Ile Leu Phe Pro Ala Gly Trp Leu Thr Ser Ala Leu
35 40 45
Val Ser Gln Gly Phe Gly Gly Met Phe His Ser Val Gln Ile Ala Arg
50 55 60
His Val Ser Ser Tyr His Gly Ile Met Val Ala Phe Ala Leu Val Gly
65 70 75 80
Tyr Gly Trp Leu Ala Met His Asn Leu Arg His Pro Asp Glu Arg Tyr
85 90 95
Ser Ile Arg Ser Ala Leu Ile Ile Gly Ile Gly Ile Gln Phe Thr Trp
100 105 110
Glu Ala Val Leu Met Ile Ser Gly Ile Arg Pro Leu Thr Trp Arg Pro
115 120 125
Leu Val Ile Asp Ser Leu Ile Glu Thr Asn Leu Gly Ala Pro Phe Met
130 135 140
Leu Leu Ile Val Lys Ala Trp Arg Ala Pro Pro Glu Gly Ile Pro Gly
145 150 155 160
Ser Thr Ser Pro Arg Pro Thr Ala Arg Gly Thr Ala Arg Val Tyr Met
165 170 175
Arg Asp Asp Leu Val Ser Arg Arg Leu Leu Gln Arg Pro
180 185

<210> 2221
<211> 530
<212> DNA
<213> Homo sapiens

<400> 2221
actagtgtag ctgcaatata tactcgggat ttactacagt taagccttat ccttccaccc
60
aaagaagagc aaaccgccat cgctaacgtc ctttccgaca tggacaccga actcgacgcc
120
ctacaacaac gcctcagtaa aaccaaaacc atcaagcaag gcatgatgca agaactactc
180
acagggaaaa cgaggttggt atgagccaca aggtgaattt agtgcatgag ctggataagc
240
gtattatctc ggtaaatacg ttattgtcac agcctgagct tgctattccg gcttatcagc
300
ggccttataa atggtcacaa gagaacctaa atgcgctgat gagtgattta cgaatttatc
360
gtaacaaatc ggcttatcgg ctggggacgg tggtttttca ttatcataat gaacccgtag
420

acaacgagaa tacccacaag ctggatattg tagacggtca gcaacgtacc ttaaccttgt
480
tgctgctagt caaagccatt ttagaagaac ggttgtctgc gttaacgcgt
530

<210> 2222
<211> 67
<212> PRT
<213> Homo sapiens

<400> 2222
Thr Ser Val Ala Ala Ile Tyr Thr Arg Asp Leu Leu Gln Leu Ser Leu
 1   5   10   15
Ile Leu Pro Pro Lys Glu Glu Gln Thr Ala Ile Ala Asn Val Leu Ser
            20   25   30
Asp Met Asp Thr Glu Leu Asp Ala Leu Gln Gln Arg Leu Ser Lys Thr
        35   40   45
Lys Thr Ile Lys Gln Gly Met Met Gln Glu Leu Leu Thr Gly Lys Thr
    50   55   60
Arg Leu Val
65

<210> 2223
<211> 482
<212> DNA
<213> Homo sapiens

<400> 2223
cggccgccgc ggtagtgagc cctgcgtcgg tggcgtaatg gaaaatgctg cgctggttgg
60
acaggcgcga gacattgttg tggacgatgc cgctgtcgat cggtggcacg ccggtgaaga
120
tgcatttatc caacggccgg gacagggccg gcagttcaca gtccagtttg taaagcgctg
180
cgcgtcctgc gctgatatag gcctggagat gccccatggc gtgtcgggca acctcgtagt
240
tcaggccgtc gagcaccaca aggatgacgt tgtgcttcat aaggggagac gctccgcaac
300
gataggcttg actcatttca cttgaggaac ggggtcaaaa ctgtgggcgc gggcaagccc
360
gctcccacac aagcccgtgc ccacattgga tctccaatgt gggctacagc cttactgcat
420
attgatgatg acttcttcct gccacttctg cggcagtgcc ttggaggtct tttcccacgc
480
gt
482

<210> 2224
<211> 105
<212> PRT
<213> Homo sapiens

<400> 2224
Met Ser Gln Ala Tyr Arg Cys Gly Ala Ser Pro Leu Met Lys His Asn

```
 1               5                  10                  15
Val Ile Leu Val Val Leu Asp Gly Leu Asn Tyr Glu Val Ala Arg His
            20                  25                  30
Ala Met Gly His Leu Gln Ala Tyr Ile Ser Ala Gly Arg Ala Ala Leu
        35                  40                  45
Tyr Lys Leu Asp Cys Glu Leu Pro Ala Leu Ser Arg Pro Leu Asp Lys
    50                  55                  60
Cys Ile Phe Thr Gly Val Pro Pro Ile Asp Ser Gly Ile Val His Asn
65                  70                  75                  80
Asn Val Ser Arg Leu Ser Asn Gln Arg Ser Ile Phe His Tyr Ala Thr
                85                  90                  95
Asp Ala Gly Leu Thr Thr Ala Ala Ala
            100                 105
```

<210> 2225
<211> 753
<212> DNA
<213> Homo sapiens

<400> 2225
nacgcgtctg atccacacgg gccactgacg tggcgttatg acagggagcg ggccggtgcc
60
ggcgtcatcc tcgatctcat gggtcacgga gaggatctcg tccagtatct actcaaaggg
120
cgattcactg aggtgtccgc cgtgtccgag acgttcatcc gtcagcgtcc caagccactc
180
aaggagggca tcggccacac aggttgggtc gtctcggacg agctcgggcc ggtgggcaac
240
gaggattatt gcgctgtcat cgcccgtatg gaaaacggag tgatgtgcac cctggagtcc
300
agtcgggtca gtgttgggcc gcgcgcggag tacatcgtcg agatctatgg aaccgacgga
360
tcaatccggt ggaacttcga ggatctcaac catttgcagg tctgtctggg gcgaaacaat
420
cgtgccctgc agggatatgt caactgcatg gccggaccag acttcccgga gttcatgcgt
480
ttccaaccgg gagccggaac atccatgggc tttgacgaca tgaaggtcgt tgaggctgcg
540
aaattcgtcc gaggggtctt ggatgggcag caatatggcc catctgtcgc cgatggttgg
600
gcctcagcgg aggtcaacga tgcgatcgtt gcctcctgcg ggggaccatg cctggcatga
660
cgtgaagccg gtttcgggga gaaccacgtt cgataagtga ccgcgtcatc gcgtgtctgt
720
gaccaggcct ggcggcacaa ccaggtcgcc ggc
753

<210> 2226
<211> 219
<212> PRT
<213> Homo sapiens

<400> 2226
Xaa Ala Ser Asp Pro His Gly Pro Leu Thr Trp Arg Tyr Asp Arg Glu

```
 1               5                  10                  15
Arg Ala Gly Ala Gly Val Ile Leu Asp Leu Met Gly His Gly Glu Asp
            20                  25                  30
Leu Val Gln Tyr Leu Leu Lys Gly Arg Phe Thr Glu Val Ser Ala Val
        35                  40                  45
Ser Glu Thr Phe Ile Arg Gln Arg Pro Lys Pro Leu Lys Glu Gly Ile
    50                  55                  60
Gly His Thr Gly Trp Val Val Ser Asp Glu Leu Gly Pro Val Gly Asn
65                  70                  75                  80
Glu Asp Tyr Cys Ala Val Ile Ala Arg Met Glu Asn Gly Val Met Cys
                85                  90                  95
Thr Leu Glu Ser Ser Arg Val Ser Val Gly Pro Arg Ala Glu Tyr Ile
            100                 105                 110
Val Glu Ile Tyr Gly Thr Asp Gly Ser Ile Arg Trp Asn Phe Glu Asp
        115                 120                 125
Leu Asn His Leu Gln Val Cys Leu Gly Arg Asn Asn Arg Ala Leu Gln
    130                 135                 140
Gly Tyr Val Asn Cys Met Ala Gly Pro Asp Phe Pro Glu Phe Met Arg
145                 150                 155                 160
Phe Gln Pro Gly Ala Gly Thr Ser Met Gly Phe Asp Asp Met Lys Val
                165                 170                 175
Val Glu Ala Ala Lys Phe Val Arg Gly Val Leu Asp Gly Gln Gln Tyr
            180                 185                 190
Gly Pro Ser Val Ala Asp Gly Trp Ala Ser Ala Glu Val Asn Asp Ala
        195                 200                 205
Ile Val Ala Ser Cys Gly Gly Pro Cys Leu Ala
    210                 215
```

<210> 2227
<211> 324
<212> DNA
<213> Homo sapiens

<400> 2227
ggatccgaaa cgttgggagc ataaagcagc atggcgcacc tactgaagac ggtggtggct
60
ggctgttcat gtcctttcct tagcaacttg gggtcctcta aggttctacc tgggaagaga
120
gactttgtac gaacgcttcg tactcaccag gcactgtggt gtaaatcccc ggtaaagcca
180
ggaattccat ataagcagtt gacagttggg gtccccaagg agattttcca aaacgagaag
240
cgagttgcat tgtctcctgc gggggtccag gccctggtca agcagggctt caatgttgtc
300
gtggaatcag gcgcaggcga agct
324

<210> 2228
<211> 98
<212> PRT
<213> Homo sapiens

<400> 2228
Met Ala His Leu Leu Lys Thr Val Val Ala Gly Cys Ser Cys Pro Phe

```
 1               5                  10                  15
Leu Ser Asn Leu Gly Ser Ser Lys Val Leu Pro Gly Lys Arg Asp Phe
            20                  25                  30
Val Arg Thr Leu Arg Thr His Gln Ala Leu Trp Cys Lys Ser Pro Val
        35                  40                  45
Lys Pro Gly Ile Pro Tyr Lys Gln Leu Thr Val Gly Val Pro Lys Glu
    50                  55                  60
Ile Phe Gln Asn Glu Lys Arg Val Ala Leu Ser Pro Ala Gly Val Gln
65                  70                  75                  80
Ala Leu Val Lys Gln Gly Phe Asn Val Val Val Glu Ser Gly Ala Gly
                85                  90                  95
Glu Ala
```

<210> 2229
<211> 320
<212> DNA
<213> Homo sapiens

<400> 2229
acgcgtgaag gggccctgtg acgaggtcat ttctgtccat gggggggtcca gatggtgagg
60
cccacagaga gggaacgggc gggggggaggg gaggagagaa gacagactca ggcagaaccc
120
tagctcagcc ccttcctgcg tgcctggccc tgggaggatg ccatccccag tcccctcttc
180
tgggccctgc tctggggact cggcacagat ggatccagtg catcctcagc cccctgagaa
240
gctgtgctgc catcagctcc ttctctgggt acagggcacg ggaagcggct gcccagcagg
300
cctcggtccc gccaagctgt
320

<210> 2230
<211> 94
<212> PRT
<213> Homo sapiens

<400> 2230
```
Met Gly Gly Pro Asp Gly Glu Ala His Arg Glu Gly Thr Gly Gly Gly
 1               5                  10                  15
Arg Gly Gly Glu Lys Thr Asp Ser Gly Arg Thr Leu Ala Gln Pro Leu
            20                  25                  30
Pro Ala Cys Leu Ala Leu Gly Gly Cys His Pro Gln Ser Pro Leu Leu
        35                  40                  45
Gly Pro Ala Leu Gly Thr Arg His Arg Trp Ile Gln Cys Ile Leu Ser
    50                  55                  60
Pro Leu Arg Ser Cys Ala Ala Ile Ser Ser Phe Ser Gly Tyr Arg Ala
65                  70                  75                  80
Arg Glu Ala Ala Ala Gln Gln Ala Ser Val Pro Pro Ser Cys
                85                  90
```

<210> 2231
<211> 671

<212> DNA
<213> Homo sapiens

<400> 2231
gggctgtcta ccacgggctt cgggacttgg ggcagcttcc tgagctctct gagctgcagt
60
tccttcaacc acaaaatgag gagagtgcag gacctcagag gcttactgtg aggatggaga
120
aaagcccagt tcaatgcccc actgggaaat gcttcccatt aattgtggaa ttgtcgtgcc
180
catttactgt cggggtgaca gggggggtgg gggtcagagt agagacagga gaaggaagtg
240
agcatttgtg ggatacccac cacgtgccag ggactgaacc ctatctggat ctcctgcagc
300
cctcccaatg gcactgtgaa gccagtgttg ttttacagat gaggaaactg agatttgtgg
360
ctataacaga taaacagatg accctgaatg gggcaggtca tgtcatctgc catagataca
420
tgcatagaac aatgcaaacc agtcagtccc ctctgagtca gaccaggctg accatcaggg
480
acatgcagac actggcaggg ctggggttgt tccccatcgg tgatagcctg gtgcccccat
540
ggcccctgat gcccacggct gtctggaagg ctgggtcact gctgagaaga caaggagaca
600
ttttctctca ccagctttct tttttctatt ccttcttaga cacctgagct gcggtgatca
660
cagctcttaa g
671

<210> 2232
<211> 177
<212> PRT
<213> Homo sapiens

<400> 2232
Met Glu Lys Ser Pro Val Gln Cys Pro Thr Gly Lys Cys Phe Pro Leu
 1   5   10   15
Ile Val Glu Leu Ser Cys Pro Phe Thr Val Gly Val Thr Gly Gly Val
            20   25   30
Gly Val Arg Val Glu Thr Gly Glu Gly Ser Glu His Leu Trp Asp Thr
        35   40   45
His His Val Pro Gly Thr Glu Pro Tyr Leu Asp Leu Leu Gln Pro Ser
    50   55   60
Gln Trp His Cys Glu Ala Ser Val Val Leu Gln Met Arg Lys Leu Arg
65   70   75   80
Phe Val Ala Ile Thr Asp Lys Gln Met Thr Leu Asn Gly Ala Gly His
                85   90   95
Val Ile Cys His Arg Tyr Met His Arg Thr Met Gln Thr Ser Gln Ser
            100   105   110
Pro Leu Ser Gln Thr Arg Leu Thr Ile Arg Asp Met Gln Thr Leu Ala
        115   120   125
Gly Leu Gly Leu Phe Pro Ile Gly Asp Ser Leu Val Pro Pro Trp Pro
    130   135   140
Leu Met Pro Thr Ala Val Trp Lys Ala Gly Ser Leu Leu Arg Arg Gln

145 150 155 160
Gly Asp Ile Phe Ser His Gln Leu Ser Phe Phe Tyr Ser Phe Leu Asp
165 170 175
Thr

<210> 2233
<211> 6199
<212> DNA
<213> Homo sapiens

<400> 2233
acgcgtgatg atcgggaatg tgaaaatcag ctggttctgc tgcttggttt caacaccttt
60
gatttcatta aagtgttgcg gcagcacagg atgatgattt tatactgtac cttgctggcc
120
agtgcacaaa gtgaagctga aaaggaaagg attatgggaa agatggaagc tgacccagag
180
ctatccaagt tcctctacca gcttcatgaa accgagaagg aggatctgat ccgagaggaa
240
aggtcccgga gagagcgagt gcgtcagtct cgaatggaca cagatctgga aaccatggat
300
ctcgaccagg gtggagaggc actggctcca cggcaggttc tggacttgga ggacctggtt
360
tttacccaag ggagccactt tatggccaat aaacgctgtc agcttcctga tggatcctcc
420
cgtcgccagc gtaagggcta tgaagaggtg catgtgcctg ctttgaagcc caagcccttt
480
ggctcagaag aacaattgct cccggtggaa aagctgccaa agtatgccca ggctgggttt
540
gagggcttca aaacgctgaa ccggatccag agtaagctct accgtgctgc ccttgagacg
600
gatgagaatc tgctgctgtg tgctcctact ggtgctggga agaccaacgt ggccctgatg
660
tgcatgctcc gagagattgg gaaacacata aacatggacg gcacaatcaa tgtggatgac
720
ttcaagatta tctacatagc tcccatgcgc tccctggtcc aggagatggt gggcagcttt
780
ggaaagcgcc tggccacata tggcatcact gttgctgagc tgactgggga tcaccagcta
840
tgcaaggagg aaatcagtgc cacacagatt atcgtctgca cccctgagaa gtgggacatc
900
atcacacgca agggcgggga gcgcacctac acccagctgg tgcgactcat tgtcttggat
960
gagatccatc ttctacatga tgacagaggt cctgtcttag aagctttggt ggccagggcc
1020
atccgaaaca ttgagatgac ccaagaagat gtccgactca ttggtctcag tgctaccctc
1080
cccaactatg aagatgtggc caccttttctg cgagtcgacc ctgctaaggg cctcttctac
1140
tttgataaca gcttccgccc cgtgcctctg gaacaaacat atgtgggcat cacagagaaa
1200
aaagctatca aacgtttcca gatcatgaat gaaatagtct atgagaaaat catggaacat
1260

gctggaaaaa atcaggtgct cgtgtttgtc cattctcgca aagaaactgg gaagacagca
1320
agggcaatcc gtgacatgtg tctggagaag gacactttgg gtctgtttct tcgcgagggt
1380
tctgcctcca ctgaagtcct tcgtacagaa gcagagcagt gcaagaactt ggagctgaag
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1500
ctcgtggagg atctttttgc tgataaacat attcaggttt tagtttccac cgcaactcta
1560
gcttggggtg tgaatctccc tgcacataca gtcatcatca aaggcaccca ggtgtacagt
1620
ccagagaagg ggcgttggac agaactggga gcactggaca ttctgcagat gctgggacgt
1680
gccggaagac cccagtatga caccaagggt gaaggcatac tcatcacatc tcatggggag
1740
ctacagtact acctgtccct cctcaatcaa caacttccta ttgaaagcca gatggtttca
1800
aagcttcctg acatgctcaa tgcagaaatc gtgctaggaa atgtccagaa tgccaaggat
1860
gcggtgaact ggctgggcta tgcctacctc tatatccgaa tgctgcgatc cccaaccctc
1920
tatggcatct ctcatgatga cctcaaggga gatcccctgc tggaccagcg ccgactagat
1980
ctggttcata cagctgccct gatgctggac aagaacaatc tggtcaagta cgacaagaag
2040
acgggcaact tccaggtgac agaactgggc cgtatagcca gccactacta catcaccaat
2100
gatacagtgc agacttacaa ccagctgctg aagcccaccc tgagtgagat tgagcttttc
2160
agggtcttct cattgtcctc tgagttcaag aacatcacag tgagagagga ggagaagctg
2220
gagctgcaga agttgctgga gagggtgcct atccctgtaa aggagagcat tgaggaaccc
2280
agtgctaaga tcaacgttct tctgcaagcc ttcatctcac agctgaaatt ggagggcttt
2340
gcactgatgg ctgacatggt gtatgtcaca cagtcggctg gccggttgat gcgagcgata
2400
tttgaaattg tcctgaaccg aggttgggca cagcttacag acaagaccct gaacctctgc
2460
aagatgatcg acaaacgcat gtggcagtcc atgtgtcctc tgcgccagtt ccggaaactc
2520
cctgaggaag tagtgaagaa gattgagaag aagaatttcc cctttgagcg tctgtacgac
2580
ctgaatcata atgagattgg ggagcttatc cgcatgccaa agatggggaa gaccatccac
2640
aaatatgtcc atctgtttcc caagttggag ttgtcagtgc acctgcagcc tatcacacgc
2700
tccaccctga aggtggagct gaccatcacg ccagacttcc agtgggatga aaaggtgcat
2760
ggttcatccg aggctttttg gattctggtg gaggatgtgg acagcgaggt gattctgcac
2820
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2880

gtgcctgtct ttgaaccgct gccccctcag tacttcatcc gagtggtgtc tgaccgctgg
2940
ctctcttgtg agacccagct gcctgtctcc ttccggcacc tgatcttgcc ggagaagtac
3000
ccccctccaa ccgaactttt ggacctgcag cccttgcccg tgtctgctct gagaaacagt
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gcctttgaga gtctttacca agataaattt cctttcttca atcccatcca gacccaggtg
3120
tttaacactg tatacaacag tgacgacaac gtgtttgtgg gggcccccac gggcagcggg
3180
aagactattt gtgcagagtt tgccatcctg cgaatgctgc tgcagagctc ggaggggcgc
3240
tgtgtgtaca tcacccccat ggaggccctg gcagagcagg tatacatgga ctggtacgag
3300
aagttccagg acaggctcaa caagaaggtg gtactcctga caggcgagac cagcacagac
3360
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3420
tcccggcgat ggaagcagcg caagaacgtg cagaacatca acctcttcgt ggtggatgag
3480
gtccacctta tcgggggcga gaatgggcct gtcttagaag tgatctgctc ccgaatgcgc
3540
tacatctcct cccagattga gcggcccatt cgcattgtgg cactcagctc ttcgctctcc
3600
aatgccaagg atgtggccca ctggctgggc tgcagtgcca cctccacctt caacttccat
3660
cccaatgtgc gtcccgtccc cttggagctg cacatccagg gcttcaacat cagccataca
3720
caaacccgcc tgctctccat ggccaagcct gtgtaccatg ctatcaccaa gcactcgccc
3780
aagaagcctg tcattgtctt tgtgccgtct cgcaagcaga cccgcctcac tgccattgac
3840
atcctcacca cctgtgcagc agacatccaa cggcagaggt tcttgcactg caccgagaag
3900
gatctgattc cgtacctgga gaagctaagt gacagcacgc tcaaggaaac gctgctaaat
3960
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4020
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4140
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4200
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4260
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4320
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4440
atctcccatc gtcacttgtc ggaccacttg tcagagctgg tggagcagac cctgagtgac
4500

ctggagcagt ccaagtgcat cagcatcgag gacgagatgg acgtggcgcc tctgaaccta
4560
ggcatgatcg ccgcctacta ttacatcaac tacaccacca ttgagctctt cagcatgtcc
4620
ctcaatgcca agaccaaggt gcgagggctt atcgagatca tctccaatgc agcagagtat
4680
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4740
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4800
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4860
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5640
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5700
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5760
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5820
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5880
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5940
ggtgtgctgt cccctgtagc ctcgtgagtc agcccagagg agggtacatg cgactgtggc
6000
ctggcctcag tggtacccac acatcagcac taccacaaga accaacactg agcctcggaa
6060
gctagatcac aggttagggg tttctctaga tgggggttct gaaatttgca gtgtctgctc
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6180
taaacaggtt ttctaatcc
6199

<210> 2234
<211> 1701
<212> PRT
<213> Homo sapiens

<400> 2234
Arg Arg Gln Arg Lys Gly Tyr Glu Glu Val His Val Pro Ala Leu Lys
1 5 10 15
Pro Lys Pro Phe Gly Ser Glu Glu Gln Leu Leu Pro Val Glu Lys Leu
20 25 30
Pro Lys Tyr Ala Gln Ala Gly Phe Glu Gly Phe Lys Thr Leu Asn Arg
35 40 45
Ile Gln Ser Lys Leu Tyr Arg Ala Ala Leu Glu Thr Asp Glu Asn Leu
50 55 60
Leu Leu Cys Ala Pro Thr Gly Ala Gly Lys Thr Asn Val Ala Leu Met
65 70 75 80
Cys Met Leu Arg Glu Ile Gly Lys His Ile Asn Met Asp Gly Thr Ile
85 90 95
Asn Val Asp Asp Phe Lys Ile Ile Tyr Ile Ala Pro Met Arg Ser Leu
100 105 110
Val Gln Glu Met Val Gly Ser Phe Gly Lys Arg Leu Ala Thr Tyr Gly
115 120 125
Ile Thr Val Ala Glu Leu Thr Gly Asp His Gln Leu Cys Lys Glu Glu
130 135 140
Ile Ser Ala Thr Gln Ile Ile Val Cys Thr Pro Glu Lys Trp Asp Ile
145 150 155 160
Ile Thr Arg Lys Gly Gly Glu Arg Thr Tyr Thr Gln Leu Val Arg Leu
165 170 175
Ile Val Leu Asp Glu Ile His Leu Leu His Asp Asp Arg Gly Pro Val
180 185 190
Leu Glu Ala Leu Val Ala Arg Ala Ile Arg Asn Ile Glu Met Thr Gln
195 200 205
Glu Asp Val Arg Leu Ile Gly Leu Ser Ala Thr Leu Pro Asn Tyr Glu
210 215 220
Asp Val Ala Thr Phe Leu Arg Val Asp Pro Ala Lys Gly Leu Phe Tyr
225 230 235 240
Phe Asp Asn Ser Phe Arg Pro Val Pro Leu Glu Gln Thr Tyr Val Gly
245 250 255
Ile Thr Glu Lys Lys Ala Ile Lys Arg Phe Gln Ile Met Asn Glu Ile
260 265 270
Val Tyr Glu Lys Ile Met Glu His Ala Gly Lys Asn Gln Val Leu Val
275 280 285
Phe Val His Ser Arg Lys Glu Thr Gly Lys Thr Ala Arg Ala Ile Arg
290 295 300
Asp Met Cys Leu Glu Lys Asp Thr Leu Gly Leu Phe Leu Arg Glu Gly
305 310 315 320
Ser Ala Ser Thr Glu Val Leu Arg Thr Glu Ala Glu Gln Cys Lys Asn
325 330 335
Leu Glu Leu Lys Asp Leu Leu Pro Tyr Gly Phe Ala Ile His His Ala

```
            340                 345                 350
Gly Met Thr Arg Val Asp Arg Thr Leu Val Glu Asp Leu Phe Ala Asp
        355                 360                 365
Lys His Ile Gln Val Leu Val Ser Thr Ala Thr Leu Ala Trp Gly Val
    370                 375                 380
Asn Leu Pro Ala His Thr Val Ile Ile Lys Gly Thr Gln Val Tyr Ser
385                 390                 395                 400
Pro Glu Lys Gly Arg Trp Thr Glu Leu Gly Ala Leu Asp Ile Leu Gln
                405                 410                 415
Met Leu Gly Arg Ala Gly Arg Pro Gln Tyr Asp Thr Lys Gly Glu Gly
            420                 425                 430
Ile Leu Ile Thr Ser His Gly Glu Leu Gln Tyr Tyr Leu Ser Leu Leu
        435                 440                 445
Asn Gln Gln Leu Pro Ile Glu Ser Gln Met Val Ser Lys Leu Pro Asp
    450                 455                 460
Met Leu Asn Ala Glu Ile Val Leu Gly Asn Val Gln Asn Ala Lys Asp
465                 470                 475                 480
Ala Val Asn Trp Leu Gly Tyr Ala Tyr Leu Tyr Ile Arg Met Leu Arg
                485                 490                 495
Ser Pro Thr Leu Tyr Gly Ile Ser His Asp Asp Leu Lys Gly Asp Pro
            500                 505                 510
Leu Leu Asp Gln Arg Arg Leu Asp Leu Val His Thr Ala Ala Leu Met
        515                 520                 525
Leu Asp Lys Asn Asn Leu Val Lys Tyr Asp Lys Lys Thr Gly Asn Phe
    530                 535                 540
Gln Val Thr Glu Leu Gly Arg Ile Ala Ser His Tyr Tyr Ile Thr Asn
545                 550                 555                 560
Asp Thr Val Gln Thr Tyr Asn Gln Leu Leu Lys Pro Thr Leu Ser Glu
                565                 570                 575
Ile Glu Leu Phe Arg Val Phe Ser Leu Ser Ser Glu Phe Lys Asn Ile
            580                 585                 590
Thr Val Arg Glu Glu Glu Lys Leu Glu Leu Gln Lys Leu Leu Glu Arg
        595                 600                 605
Val Pro Ile Pro Val Lys Glu Ser Ile Glu Glu Pro Ser Ala Lys Ile
    610                 615                 620
Asn Val Leu Leu Gln Ala Phe Ile Ser Gln Leu Lys Leu Glu Gly Phe
625                 630                 635                 640
Ala Leu Met Ala Asp Met Val Tyr Val Thr Gln Ser Ala Gly Arg Leu
                645                 650                 655
Met Arg Ala Ile Phe Glu Ile Val Leu Asn Arg Gly Trp Ala Gln Leu
            660                 665                 670
Thr Asp Lys Thr Leu Asn Leu Cys Lys Met Ile Asp Lys Arg Met Trp
        675                 680                 685
Gln Ser Met Cys Pro Leu Arg Gln Phe Arg Lys Leu Pro Glu Glu Val
    690                 695                 700
Val Lys Lys Ile Glu Lys Lys Asn Phe Pro Phe Glu Arg Leu Tyr Asp
705                 710                 715                 720
Leu Asn His Asn Glu Ile Gly Glu Leu Ile Arg Met Pro Lys Met Gly
                725                 730                 735
Lys Thr Ile His Lys Tyr Val His Leu Phe Pro Lys Leu Glu Leu Ser
            740                 745                 750
Val His Leu Gln Pro Ile Thr Arg Ser Thr Leu Lys Val Glu Leu Thr
        755                 760                 765
Ile Thr Pro Asp Phe Gln Trp Asp Glu Lys Val His Gly Ser Ser Glu
```

```
    770                 775                 780
Ala Phe Trp Ile Leu Val Glu Asp Val Asp Ser Glu Val Ile Leu His
785                 790                 795                 800
His Glu Tyr Phe Leu Leu Lys Ala Lys Tyr Ala Gln Asp Glu His Leu
                805                 810                 815
Ile Thr Phe Phe Val Pro Val Phe Glu Pro Leu Pro Pro Gln Tyr Phe
            820                 825                 830
Ile Arg Val Val Ser Asp Arg Trp Leu Ser Cys Glu Thr Gln Leu Pro
        835                 840                 845
Val Ser Phe Arg His Leu Ile Leu Pro Glu Lys Tyr Pro Pro Pro Thr
    850                 855                 860
Glu Leu Leu Asp Leu Gln Pro Leu Pro Val Ser Ala Leu Arg Asn Ser
865                 870                 875                 880
Ala Phe Glu Ser Leu Tyr Gln Asp Lys Phe Pro Phe Phe Asn Pro Ile
                885                 890                 895
Gln Thr Gln Val Phe Asn Thr Val Tyr Asn Ser Asp Asp Asn Val Phe
            900                 905                 910
Val Gly Ala Pro Thr Gly Ser Gly Lys Thr Ile Cys Ala Glu Phe Ala
        915                 920                 925
Ile Leu Arg Met Leu Leu Gln Ser Ser Glu Gly Arg Cys Val Tyr Ile
    930                 935                 940
Thr Pro Met Glu Ala Leu Ala Glu Gln Val Tyr Met Asp Trp Tyr Glu
945                 950                 955                 960
Lys Phe Gln Asp Arg Leu Asn Lys Lys Val Val Leu Leu Thr Gly Glu
                965                 970                 975
Thr Ser Thr Asp Leu Lys Leu Leu Gly Lys Gly Asn Ile Ile Ile Ser
            980                 985                 990
Thr Pro Glu Lys Trp Asp Ile Leu Ser Arg Arg Trp Lys Gln Arg Lys
        995                 1000                1005
Asn Val Gln Asn Ile Asn Leu Phe Val Val Asp Glu Val His Leu Ile
    1010                1015                1020
Gly Gly Glu Asn Gly Pro Val Leu Glu Val Ile Cys Ser Arg Met Arg
1025                1030                1035                1040
Tyr Ile Ser Ser Gln Ile Glu Arg Pro Ile Arg Ile Val Ala Leu Ser
                1045                1050                1055
Ser Ser Leu Ser Asn Ala Lys Asp Val Ala His Trp Leu Gly Cys Ser
            1060                1065                1070
Ala Thr Ser Thr Phe Asn Phe His Pro Asn Val Arg Pro Val Pro Leu
        1075                1080                1085
Glu Leu His Ile Gln Gly Phe Asn Ile Ser His Thr Gln Thr Arg Leu
    1090                1095                1100
Leu Ser Met Ala Lys Pro Val Tyr His Ala Ile Thr Lys His Ser Pro
1105                1110                1115                1120
Lys Lys Pro Val Ile Val Phe Val Pro Ser Arg Lys Gln Thr Arg Leu
                1125                1130                1135
Thr Ala Ile Asp Ile Leu Thr Thr Cys Ala Ala Asp Ile Gln Arg Gln
            1140                1145                1150
Arg Phe Leu His Cys Thr Glu Lys Asp Leu Ile Pro Tyr Leu Glu Lys
        1155                1160                1165
Leu Ser Asp Ser Thr Leu Lys Glu Thr Leu Leu Asn Gly Val Gly Tyr
    1170                1175                1180
Leu His Glu Gly Leu Ser Pro Met Glu Arg Arg Leu Val Glu Gln Leu
1185                1190                1195                1200
Phe Ser Ser Gly Ala Ile Gln Val Val Val Ala Ser Arg Ser Leu Cys
```

```
                1205                1210                1215
Trp Gly Met Asn Val Ala Ala His Leu Val Ile Ile Met Asp Thr Gln
            1220                1225                1230
Tyr Tyr Asn Gly Lys Ile His Ala Tyr Val Asp Tyr Pro Ile Tyr Asp
        1235                1240                1245
Val Leu Gln Met Val Gly His Ala Asn Arg Pro Leu Gln Asp Asp Glu
    1250                1255                1260
Gly Arg Cys Val Ile Met Cys Gln Gly Ser Lys Lys Asp Phe Phe Lys
1265                1270                1275                1280
Lys Phe Leu Tyr Glu Pro Leu Pro Val Glu Ser His Leu Asp His Cys
                1285                1290                1295
Met His Asp His Phe Asn Ala Glu Ile Val Thr Lys Thr Ile Glu Asn
            1300                1305                1310
Lys Gln Asp Ala Val Asp Tyr Leu Thr Trp Thr Phe Leu Tyr Arg Arg
        1315                1320                1325
Met Thr Gln Asn Pro Asn Tyr Tyr Asn Leu Gln Gly Ile Ser His Arg
    1330                1335                1340
His Leu Ser Asp His Leu Ser Glu Leu Val Glu Gln Thr Leu Ser Asp
1345                1350                1355                1360
Leu Glu Gln Ser Lys Cys Ile Ser Ile Glu Asp Glu Met Asp Val Ala
                1365                1370                1375
Pro Leu Asn Leu Gly Met Ile Ala Ala Tyr Tyr Tyr Ile Asn Tyr Thr
            1380                1385                1390
Thr Ile Glu Leu Phe Ser Met Ser Leu Asn Ala Lys Thr Lys Val Arg
        1395                1400                1405
Gly Leu Ile Glu Ile Ile Ser Asn Ala Ala Glu Tyr Glu Asn Ile Pro
    1410                1415                1420
Ile Arg His His Glu Asp Asn Leu Leu Arg Gln Leu Ala Gln Lys Val
1425                1430                1435                1440
Pro His Lys Leu Asn Asn Pro Lys Phe Asn Asp Pro His Val Lys Thr
                1445                1450                1455
Asn Leu Leu Leu Gln Ala His Leu Ser Arg Met Gln Leu Ser Ala Glu
            1460                1465                1470
Leu Gln Ser Asp Thr Glu Glu Ile Leu Ser Lys Ala Ile Arg Leu Ile
        1475                1480                1485
Gln Ala Cys Val Asp Val Leu Ser Ser Asn Gly Trp Leu Ser Pro Ala
    1490                1495                1500
Leu Ala Ala Met Glu Leu Ala Gln Met Val Thr Gln Ala Met Trp Ser
1505                1510                1515                1520
Lys Asp Ser Tyr Leu Lys Gln Leu Pro His Phe Thr Ser Glu His Ile
                1525                1530                1535
Lys Arg Cys Thr Asp Lys Gly Val Glu Ser Val Phe Asp Ile Met Glu
            1540                1545                1550
Met Glu Asp Glu Glu Arg Asn Ala Leu Leu Gln Leu Thr Asp Ser Gln
        1555                1560                1565
Ile Ala Asp Val Ala Arg Phe Cys Asn Arg Tyr Pro Asn Ile Glu Leu
    1570                1575                1580
Ser Tyr Glu Val Val Asp Lys Asp Ser Ile Arg Ser Gly Gly Pro Val
1585                1590                1595                1600
Val Val Leu Val Gln Leu Glu Arg Glu Glu Glu Val Thr Gly Pro Val
                1605                1610                1615
Ile Ala Pro Leu Phe Pro Gln Lys Arg Glu Glu Gly Trp Trp Val Val
            1620                1625                1630
Ile Gly Asp Ala Lys Ser Asn Ser Leu Ile Ser Ile Lys Arg Leu Thr
```

```
        1635                1640                1645
Leu Gln Gln Lys Ala Lys Val Lys Leu Asp Phe Val Ala Pro Ala Thr
    1650                1655                1660
Gly Ala His Asn Tyr Thr Leu Tyr Phe Met Ser Asp Ala Tyr Met Gly
1665                1670                1675                1680
Cys Asp Gln Glu Tyr Lys Phe Ser Val Asp Val Lys Glu Ala Glu Thr
                1685                1690                1695
Asp Ser Asp Ser Asp
            1700
```

<210> 2235
<211> 586
<212> DNA
<213> Homo sapiens

<400> 2235
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tcagtgcttg cacattctcc actggcagaa tgactcccga cgtggctcgg gctccccgga
120
agacacccct cgaagcagtg gtgcctctag catcttcgac ctgaggaacc tggcagctga
180
ctcattgttg ccctctctgc tagagcgggc ggccccagaa gatgtggacc ggcgcaatga
240
agcccttcga cggcagcacc ggcccccggc cctgcttccc ctctacccgg cacctgacga
300
ggatgaagcc ggggaacgct gtagccgcct agagccaccc ccgcgagcac tttggacaaa
360
ggatcttggt caagtgtctg tcgctcaagt tcgagattga aattgagccc atctttggga
420
tcttggctct gtatgatgtg cggaagaaaa agaagatctc ggaaaacttc tacttcgacc
480
tgaactcgga ctccatgaag gggctgcttc gggctcatgg cacccaccct gccatctcca
540
ccctggcccg ctctgccatc ttctctgtga cctacccctc acgcgt
586

<210> 2236
<211> 123
<212> PRT
<213> Homo sapiens

<400> 2236
```
Met Ser Pro Lys Gln Pro Leu His Gly Val Arg Val Gln Val Glu Val
 1               5                  10                  15
Glu Val Phe Arg Asp Leu Leu Phe Leu Pro His Ile Ile Gln Ser Gln
            20                  25                  30
Asp Pro Lys Asp Gly Leu Asn Phe Asn Leu Glu Leu Glu Arg Gln Thr
        35                  40                  45
Leu Asp Gln Asp Pro Leu Ser Lys Val Leu Ala Gly Val Ala Leu Gly
    50                  55                  60
Gly Tyr Ser Val Pro Arg Leu His Pro Arg Gln Val Pro Gly Arg Gly
65                  70                  75                  80
Glu Ala Gly Pro Gly Ala Gly Ala Ala Val Glu Gly Leu His Cys Ala
```

```
                85                  90                  95
Gly Pro His Leu Leu Gly Pro Pro Ala Leu Ala Glu Arg Ala Thr Met
            100                 105                 110
Ser Gln Leu Pro Gly Ser Ser Gly Arg Arg Cys
        115                 120
```

<210> 2237
<211> 421
<212> DNA
<213> Homo sapiens

<400> 2237
cctaggaagg cacacctgtg tcccactgca gccaagagga agcaccccaa acactcctct
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tggggcgcag gagtgctggc cagcttgggg atagtccctg gaagtggtcg ggagcactga
120
gggaggagct gaggtccaag ccctcctcca gtgcatcacc ctggtcagga gtggggcagt
180
gtggagccag gggctcttca gccagcacct gctgcactat gggctccagc tgtgcaagac
240
cacccgtgag aaggagtctt gttgggagca gggtggggaa gcactgtggg agaggtgtcc
300
ttggctcggg tagcagggac cttgatgtat cttgaagcca gggggccgac tgaggcgctt
360
gtctgaaggc ctccatgaga gggagggggc tggagggggc tgttcccaat aatagctcta
420
t
421

<210> 2238
<211> 124
<212> PRT
<213> Homo sapiens

<400> 2238
```
Met Glu Ala Phe Arg Gln Ala Pro Gln Ser Ala Pro Trp Leu Gln Asp
 1               5                  10                  15
Thr Ser Arg Ser Leu Leu Pro Glu Pro Arg Thr Pro Leu Pro Gln Cys
            20                  25                  30
Phe Pro Thr Leu Leu Pro Thr Arg Leu Leu Leu Thr Gly Gly Leu Ala
        35                  40                  45
Gln Leu Glu Pro Ile Val Gln Gln Val Leu Ala Glu Glu Pro Leu Ala
    50                  55                  60
Pro His Cys Pro Thr Pro Asp Gln Gly Asp Ala Leu Glu Glu Gly Leu
65                  70                  75                  80
Asp Leu Ser Ser Ser Leu Ser Ala Pro Asp His Phe Gln Gly Leu Ser
                85                  90                  95
Pro Ser Trp Pro Ala Leu Leu Arg Pro Lys Arg Ser Val Trp Gly Ala
            100                 105                 110
Ser Ser Trp Leu Gln Trp Asp Thr Gly Val Pro Ser
        115                 120
```

<210> 2239
<211> 623

<212> DNA
<213> Homo sapiens

<400> 2239
gctagcagga ctcagaaatc tgctgttgag cacaaagcca aaaaatctct gtcccatcct
60
agccattcca ggcctgggcc catggtcacc ccacacaata aggctaagag tccaggtgtc
120
aggcagccag gcagcagctc tagctcagcc cctgggcagc ccagcacagg ggttgctcga
180
cccacagtta gttctggccc tgtgcctagg cgccagaatg gcagctccag ctcaggacct
240
gagcgatcaa tcagtgggtc caagaagcca accaatgact caaatccctc taggcggaca
300
gtcagtggta catgtggccc tggacaacct gcaagcagct caggtggccc tgggcgaccc
360
atcagtggtt cagttagttc tgcaagaccc ttgggcagct ctcgtggccc tggccggcct
420
gtgagcagtc cacatgaact tcgacgacca gtgagtggct tgggcccccc ggggcggtct
480
gtcagtggcc ctgggagatc cataagtggc ccaattccag ctggacggac tgtcagtaat
540
tcagtcccag gaagaccagt gagcagcttg ggacctgggc aaacagttag tagctcaggt
600
cccactataa agcctaagtg cac
623

<210> 2240
<211> 207
<212> PRT
<213> Homo sapiens

<400> 2240
Ala Ser Arg Thr Gln Lys Ser Ala Val Glu His Lys Ala Lys Lys Ser
1 5 10 15
Leu Ser His Pro Ser His Ser Arg Pro Gly Pro Met Val Thr Pro His
20 25 30
Asn Lys Ala Lys Ser Pro Gly Val Arg Gln Pro Gly Ser Ser Ser Ser
35 40 45
Ser Ala Pro Gly Gln Pro Ser Thr Gly Val Ala Arg Pro Thr Val Ser
50 55 60
Ser Gly Pro Val Pro Arg Arg Gln Asn Gly Ser Ser Ser Ser Gly Pro
65 70 75 80
Glu Arg Ser Ile Ser Gly Ser Lys Lys Pro Thr Asn Asp Ser Asn Pro
85 90 95
Ser Arg Arg Thr Val Ser Gly Thr Cys Gly Pro Gly Gln Pro Ala Ser
100 105 110
Ser Ser Gly Gly Pro Gly Arg Pro Ile Ser Gly Ser Val Ser Ser Ala
115 120 125
Arg Pro Leu Gly Ser Ser Arg Gly Pro Gly Arg Pro Val Ser Ser Pro
130 135 140
His Glu Leu Arg Arg Pro Val Ser Gly Leu Gly Pro Pro Gly Arg Ser
145 150 155 160
Val Ser Gly Pro Gly Arg Ser Ile Ser Gly Pro Ile Pro Ala Gly Arg

```
                165                 170                 175
Thr Val Ser Asn Ser Val Pro Gly Arg Pro Val Ser Ser Leu Gly Pro
            180                 185                 190
Gly Gln Thr Val Ser Ser Ser Gly Pro Thr Ile Lys Pro Lys Cys
        195                 200                 205
```

<210> 2241
<211> 656
<212> DNA
<213> Homo sapiens

<400> 2241
nnacgcgtga agggcagcag caacaccacg gagtgtgttc ccgtgcccac ctccgagcac
60
gtggccgaga tcgtgggcag gcaaggctgc aagattaagg ccttgagggc caagaccaac
120
acctacatta gaaccccggg aaggggcgag gaaccagtgt tcatggtgac agggcgacgg
180
gaggacgtgg ccacagcccg gcgggaaatc atctcagcag cggagcactt ctccatgatc
240
cgtgcctccc gcaacaagtc aggcgccgcc tttggtgtgg ctcctgctct gcccggccag
300
gtgaccatcc gtgtgcgggt gccctaccgc gtggtggggc tggtggtggg ccccaaaggg
360
gcaaccatca agcgcatcca gcagcaaacc aacacataca ttatcacacc aagccgtgac
420
cgcgaccccg tgttcgagat cacgggtgcc ccaggcaacg tggagcgtgc gcgcgaggag
480
atcgagacgc acatcgcggt gcgcactggc aagatcctcg agtacaacaa tgaaaacgac
540
ttcctggcgg ggagccccga cgcagcaatc gatagccgct actccgacgc ctggcgggtg
600
caccagcccg gctgcaagcc cctctccacc ttccggcaga acagcctggg ctgcag
656

<210> 2242
<211> 218
<212> PRT
<213> Homo sapiens

<400> 2242
```
Xaa Arg Val Lys Gly Ser Ser Asn Thr Thr Glu Cys Val Pro Val Pro
 1               5                  10                  15
Thr Ser Glu His Val Ala Glu Ile Val Gly Arg Gln Gly Cys Lys Ile
            20                  25                  30
Lys Ala Leu Arg Ala Lys Thr Asn Thr Tyr Ile Arg Thr Pro Gly Arg
        35                  40                  45
Gly Glu Glu Pro Val Phe Met Val Thr Gly Arg Arg Glu Asp Val Ala
    50                  55                  60
Thr Ala Arg Arg Glu Ile Ile Ser Ala Ala Glu His Phe Ser Met Ile
65                  70                  75                  80
Arg Ala Ser Arg Asn Lys Ser Gly Ala Ala Phe Gly Val Ala Pro Ala
                85                  90                  95
Leu Pro Gly Gln Val Thr Ile Arg Val Arg Val Pro Tyr Arg Val Val
```

```
            100                 105                 110
Gly Leu Val Val Gly Pro Lys Gly Ala Thr Ile Lys Arg Ile Gln Gln
        115                 120                 125
Gln Thr Asn Thr Tyr Ile Ile Thr Pro Ser Arg Asp Arg Asp Pro Val
    130                 135                 140
Phe Glu Ile Thr Gly Ala Pro Gly Asn Val Glu Arg Ala Arg Glu Glu
145                 150                 155                 160
Ile Glu Thr His Ile Ala Val Arg Thr Gly Lys Ile Leu Glu Tyr Asn
                165                 170                 175
Asn Glu Asn Asp Phe Leu Ala Gly Ser Pro Asp Ala Ala Ile Asp Ser
            180                 185                 190
Arg Tyr Ser Asp Ala Trp Arg Val His Gln Pro Gly Cys Lys Pro Leu
        195                 200                 205
Ser Thr Phe Arg Gln Asn Ser Leu Gly Cys
    210                 215
```

<210> 2243
<211> 384
<212> DNA
<213> Homo sapiens

<400> 2243
gaattcagca tttaaatgtc actcgttggc atgcaatttg ctgtcatgaa aacgactgtg
60
gattcatttc ctggtaagaa tcttctgact tattgagctg catgtcagaa gcaaaaagca
120
aaaaaaccaa atatgtacat aaaacagtgt tatcattcct taaaagagaa ggaaaataaa
180
tccctaaata atgtggactg gaacacagaa atccaaggct ggccgcacgg gtcctggctg
240
ggatggcatc cggggagctg ctgctgggga cgtgcttgcc ggcacaggtc aggggagccg
300
ggttctgcct cctccttgcc cactctcttt gcgccctccc tgtgctcgcc tgtcttgttt
360
tacctcccat cctgggccct tgga
384

<210> 2244
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2244
```
Met Gly Gly Lys Thr Arg Gln Ala Ser Thr Gly Arg Ala Gln Arg Glu
 1               5                  10                  15
Trp Ala Arg Arg Arg Gln Asn Pro Ala Pro Leu Thr Cys Ala Gly Lys
            20                  25                  30
His Val Pro Ser Ser Ser Ser Pro Asp Ala Ile Pro Ala Arg Thr Arg
        35                  40                  45
Ala Ala Ser Leu Gly Phe Leu Cys Ser Ser Pro His Tyr Leu Gly Ile
    50                  55                  60
Tyr Phe Pro Ser Leu Leu Arg Asn Asp Asn Thr Val Leu Cys Thr Tyr
65                  70                  75                  80
Leu Val Phe Leu Leu Phe Ala Ser Asp Met Gln Leu Asn Lys Ser Glu
```

```
                85                  90                  95
Asp Ser Tyr Gln Glu Met Asn Pro Gln Ser Phe Ser
            100                 105

<210> 2245
<211> 632
<212> DNA
<213> Homo sapiens

<400> 2245
acgcgtgcga ttaccgtcaa cgctggtgtg gtgagcgctg atctgcacga gcggacgtct
60
tcgagagaag aggtcggacg cgagaggctc aactatggtc acaccttggc ccacgctatt
120
gaggcccaca agcatttcac gtggcgtcat ggcgaggctg acgcggtggg catggtgttt
180
gcggccgaac tgtcgcaccg gtacctggga ctgtccgatg aggtcgttgc gcgcacccgc
240
actatcctgt ctgagatcgg attgcctgtt acctgtgacg agattaagtg ggcagatctg
300
cgcaagacga tgaacgtgga caagaaaacc agggtagacc cgcagaccgg gcgtcaagtg
360
ttgcggtttg tcggtattca caaacccggt caggtcgcca tgatcgtcga ccctgacgag
420
gccgctttag ccgagtgcta cgaccggtgt tccgcacggt aaaaacgttc ggaaatgaac
480
atgtggctgc gggtcagtcg gcattcaggc ctccgtgacg ccgtcgaccc caagtgatgt
540
gacgattcgg gaaatatctt gttgggcact cttgagcctc gcctgattcc ccatacccga
600
cttaagttca gtatcgacgg catgaatccg ga
632

<210> 2246
<211> 153
<212> PRT
<213> Homo sapiens

<400> 2246
Thr Arg Ala Ile Thr Val Lys Ala Gly Val Val Ser Ala Asp Leu His
 1               5                  10                  15
Glu Arg Thr Ser Ser Arg Glu Glu Val Gly Arg Glu Arg Leu Asn Tyr
            20                  25                  30
Gly His Thr Leu Ala His Ala Ile Glu Ala His Lys His Phe Thr Trp
        35                  40                  45
Arg His Gly Glu Ala Asp Ala Val Gly Met Val Phe Ala Ala Glu Leu
    50                  55                  60
Ser His Arg Tyr Leu Gly Leu Ser Asp Glu Val Val Ala Arg Thr Arg
65                  70                  75                  80
Thr Ile Leu Ser Glu Ile Gly Leu Pro Val Thr Cys Asp Glu Ile Lys
                85                  90                  95
Trp Ala Asp Leu Arg Lys Thr Met Asn Val Asp Lys Lys Thr Arg Val
            100                 105                 110
Asp Pro Gln Thr Gly Arg Gln Val Leu Arg Phe Val Gly Ile His Lys
```

```
        115                 120                 125
Pro Gly Gln Val Ala Met Ile Val Asp Pro Asp Glu Ala Ala Leu Ala
    130                 135                 140
Glu Cys Tyr Asp Arg Cys Ser Ala Arg
145                 150

<210> 2247
<211> 324
<212> DNA
<213> Homo sapiens

<400> 2247
gggcgttcgc ctccagggtt ctccccgaca ctggatgcca acctgcccag gggcagaagg
60
gaggttgggc gtggggagtg ccgggtacag tcagagttgc caggacagtt tggagcagtg
120
cctcttaatc ttggccgcac agcacctggg agctttaaat agacccccac gccctgggcg
180
cccccaccgc tgacccaccc gatctcagct ctgcctttcc cgcctctctg ctgggttgca
240
taagccagcg attcccaacc ccggctgtac ctggaagcta ccccaggagc ttctggagaa
300
tgtgccgtgt gagccatccc cctg
324

<210> 2248
<211> 105
<212> PRT
<213> Homo sapiens

<400> 2248
Met Ala His Thr Ala His Ser Pro Glu Ala Pro Gly Val Ala Ser Arg
 1               5                  10                  15
Tyr Ser Arg Gly Trp Glu Ser Leu Ala Tyr Ala Thr Gln Gln Arg Gly
            20                  25                  30
Gly Lys Gly Arg Ala Glu Ile Gly Trp Val Ser Gly Gly Gly Ala Gln
        35                  40                  45
Gly Val Gly Val Tyr Leu Lys Leu Pro Gly Ala Val Arg Pro Arg Leu
    50                  55                  60
Arg Gly Thr Ala Pro Asn Cys Pro Gly Asn Ser Asp Cys Thr Arg His
65                  70                  75                  80
Ser Pro Arg Pro Thr Ser Leu Leu Pro Leu Gly Arg Leu Ala Ser Ser
                85                  90                  95
Val Gly Glu Asn Pro Gly Gly Glu Arg
            100                 105

<210> 2249
<211> 394
<212> DNA
<213> Homo sapiens

<400> 2249
gaaaaccgga taacagggtg tatacaagcc tctgagttct gggagcaaca accagctcaa
60
```

cccgcaaggg aaagtgagaa agcaattaag ttgggaaccg cggggttttc ccattcccac
120
ggtggaaacc gcggccagtg aattgaaatc cgcttcctta aggcgaaatg ggcccttaaa
180
aggcaaggtc aaccgcccgc cagtgtgatg gaatttgcaa gaattcggtt tagcaccctc
240
ccggcttttc tcccgaccgc gtgcagggtg ggctgcgctg ggcctgggag gaactgggag
300
ctgggggctc atgtcctgta taaaggggct gcaggggcgc tgtctccccc cagaagactg
360
gccacatggg gacaggcctc ctgggggcag atct
394

<210> 2250
<211> 104
<212> PRT
<213> Homo sapiens

<400> 2250
Met Ser Pro Gln Leu Pro Val Pro Pro Arg Pro Ser Ala Ala His Pro
1 5 10 15
Ala Arg Gly Arg Glu Lys Ser Arg Glu Gly Ala Lys Pro Asn Ser Cys
20 25 30
Lys Phe His His Thr Gly Gly Arg Leu Thr Leu Pro Phe Lys Gly Pro
35 40 45
Phe Arg Leu Lys Glu Ala Asp Phe Asn Ser Leu Ala Ala Val Ser Thr
50 55 60
Val Gly Met Gly Lys Pro Arg Gly Ser Gln Leu Asn Cys Phe Leu Thr
65 70 75 80
Phe Pro Cys Gly Leu Ser Trp Leu Leu Leu Pro Glu Leu Arg Gly Leu
85 90 95
Tyr Thr Pro Cys Tyr Pro Val Phe
100

<210> 2251
<211> 654
<212> DNA
<213> Homo sapiens

<400> 2251
acgcgtactt attcgccacc atgattatga ccagtgtttc cagtccgttc agttgttgca
60
gtggaatagt caggttaaat ttaatgtgac cgtttatcgc aatctgccga ccactcgcga
120
ttcaatcatg acttcgtgat aaaagattga gtgtgaggtt ataacgccga agcggtaaaa
180
attttaattt ttgccgctga ggggttgacc aagcgaagcg cggtaggttt tctgcttagg
240
agtttaatca tgtttcagac ttttatttct cgccataatt caaacttttt ttctgataag
300
ctggttctca cttctgttac tccagcttct tcggcacctg ttttacagac acctaaagct
360
acatcgtcaa cgttatattt tgatagtttg acggttaatg ctggtaatgg tggttttctt
420

cattgcattc agatggatac atctgtcaac gccgctaatc aggttgtttc tgttggtgct
480
gatattgctt ttgatgccga ccctaaattt tttgcctgtt tggttcgctt tgagtcttct
540
tcggttccga ctaccctccc gactgcctat gatgtttatc ctttggatgg tcgccatgat
600
ggtggttatt ataccgtcaa ggactgtgtg actattgacg tccttcctcg tacg
654

<210> 2252
<211> 135
<212> PRT
<213> Homo sapiens

<400> 2252
Met Phe Gln Thr Phe Ile Ser Arg His Asn Ser Asn Phe Phe Ser Asp
1 5 10 15
Lys Leu Val Leu Thr Ser Val Thr Pro Ala Ser Ser Ala Pro Val Leu
20 25 30
Gln Thr Pro Lys Ala Thr Ser Ser Thr Leu Tyr Phe Asp Ser Leu Thr
35 40 45
Val Asn Ala Gly Asn Gly Gly Phe Leu His Cys Ile Gln Met Asp Thr
50 55 60
Ser Val Asn Ala Ala Asn Gln Val Val Ser Val Gly Ala Asp Ile Ala
65 70 75 80
Phe Asp Ala Asp Pro Lys Phe Phe Ala Cys Leu Val Arg Phe Glu Ser
85 90 95
Ser Ser Val Pro Thr Thr Leu Pro Thr Ala Tyr Asp Val Tyr Pro Leu
100 105 110
Asp Gly Arg His Asp Gly Gly Tyr Tyr Thr Val Lys Asp Cys Val Thr
115 120 125
Ile Asp Val Leu Pro Arg Thr
130 135

<210> 2253
<211> 327
<212> DNA
<213> Homo sapiens

<400> 2253
ggatcctgct gggcctcttt tacgtgatgt tgacccagcc gctggtgcgc attattcgcg
60
cactgagcac cagcaagcag gcccgcctgg attgcccacc gggtcacgaa aacgatgaaa
120
tcggcgtatt ggtcaacgtc gccaaccagc aattcgacaa tatggaaacc gaaatcgagc
180
agcgccgcca cgccgaggac cgcctcaccg aatacctggg ccaactggaa gatatcgtct
240
ccgcacgcac cctggagctc aaggccagca accaacgctt gagccaatcc aacgatgagc
300
tggaagcggc aaagttgacc gccttgg
327

<210> 2254

<211> 100
<212> PRT
<213> Homo sapiens

<400> 2254
Met Leu Thr Gln Pro Leu Val Arg Ile Ile Arg Ala Leu Ser Thr Ser
1 5 10 15
Lys Gln Ala Arg Leu Asp Cys Pro Pro Gly His Glu Asn Asp Glu Ile
20 25 30
Gly Val Leu Val Asn Val Ala Asn Gln Gln Phe Asp Asn Met Glu Thr
35 40 45
Glu Ile Glu Gln Arg Arg His Ala Glu Asp Arg Leu Thr Glu Tyr Leu
50 55 60
Gly Gln Leu Glu Asp Ile Val Ser Ala Arg Thr Leu Glu Leu Lys Ala
65 70 75 80
Ser Asn Gln Arg Leu Ser Gln Ser Asn Asp Glu Leu Glu Ala Ala Lys
85 90 95
Leu Thr Ala Leu
100

<210> 2255
<211> 357
<212> DNA
<213> Homo sapiens

<400> 2255
nngctagcac atgagaagtg tgaagtttat actttgcttg ggcgatcacg ccgttttcca
60
aatatggctc atgcaacttc tggccaaagg ggtcacattg agcgtgctgc tatcaatgct
120
cctgtacagg gcagtgcagc tgatgttgct atgtgtgcaa tgcttgagat agacaggaat
180
actcgtctta aggagcttgg ttggacgcta ctcttgcagg tgcatgatga agtgatactg
240
gaagggcctt cagagtctgc ggagtnggcc aagtccatag ttgttgagtg catgtctaag
300
cccttctatg gcaccaatat cctgagggtc gaccttgctg ttgatgcc a gtgtgca
357

<210> 2256
<211> 119
<212> PRT
<213> Homo sapiens

<400> 2256
Xaa Leu Ala His Glu Lys Cys Glu Val Tyr Thr Leu Leu Gly Arg Ser
1 5 10 15
Arg Arg Phe Pro Asn Met Ala His Ala Thr Ser Gly Gln Arg Gly His
20 25 30
Ile Glu Arg Ala Ala Ile Asn Ala Pro Val Gln Gly Ser Ala Ala Asp
35 40 45
Val Ala Met Cys Ala Met Leu Glu Ile Asp Arg Asn Thr Arg Leu Lys
50 55 60
Glu Leu Gly Trp Thr Leu Leu Leu Gln Val His Asp Glu Val Ile Leu

65 70 75 80
Glu Gly Pro Ser Glu Ser Ala Glu Xaa Ala Lys Ser Ile Val Val Glu
85 90 95
Cys Met Ser Lys Pro Phe Tyr Gly Thr Asn Ile Leu Arg Val Asp Leu
100 105 110
Ala Val Asp Ala Lys Cys Ala
115

<210> 2257
<211> 626
<212> DNA
<213> Homo sapiens

<400> 2257
nnaatgacaa aaaatatgaa ccaaaatagt gacagtggca gtacaaataa ctataaaagc
60
ctgaaaccta aattagaaaa tctgagttct ttaccaccag attctgacag aacatcagaa
120
gtatatctac atgaagaatt acagcaggac atgcaaaagt ttaagaatga ggtcaacaca
180
ttagaagaag agttcctggc tttgaagaaa gaaaatgttc aacttcataa agaggttgaa
240
gaagaaatgg agaagcacag aagtaatagc acagaattat caggaaccct aactgatggt
300
actactgttg gcaatgatga tgatggacta aatcagcaga ttcctaggaa ggaaaatgaa
360
gagcatgaca ggcctgcaga taaaacagct aatgaaaaga acaaggtcaa aaaccaaata
420
tatcctgagg ctgactttgc tgactcaatg gagccatctg aaatagcctc agaggattgt
480
gaattgtctc actctgttta tgagaatttt atgttgctga ttgaacaact tagaatggag
540
tataaaggta ggaccactgc ataaatgcaa ggccttttga tgtatcctgc agtaatgtgt
600
gtatacattg ctgagaactg acgcgt
626

<210> 2258
<211> 187
<212> PRT
<213> Homo sapiens

<400> 2258
Xaa Met Thr Lys Asn Met Asn Gln Asn Ser Asp Ser Gly Ser Thr Asn
1 5 10 15
Asn Tyr Lys Ser Leu Lys Pro Lys Leu Glu Asn Leu Ser Ser Leu Pro
20 25 30
Pro Asp Ser Asp Arg Thr Ser Glu Val Tyr Leu His Glu Glu Leu Gln
35 40 45
Gln Asp Met Gln Lys Phe Lys Asn Glu Val Asn Thr Leu Glu Glu Glu
50 55 60
Phe Leu Ala Leu Lys Lys Glu Asn Val Gln Leu His Lys Glu Val Glu
65 70 75 80
Glu Glu Met Glu Lys His Arg Ser Asn Ser Thr Glu Leu Ser Gly Thr

```
                85                  90                  95
Leu Thr Asp Gly Thr Thr Val Gly Asn Asp Asp Asp Gly Leu Asn Gln
            100                 105                 110
Gln Ile Pro Arg Lys Glu Asn Glu Glu His Asp Arg Pro Ala Asp Lys
        115                 120                 125
Thr Ala Asn Glu Lys Asn Lys Val Lys Asn Gln Ile Tyr Pro Glu Ala
    130                 135                 140
Asp Phe Ala Asp Ser Met Glu Pro Ser Glu Ile Ala Ser Glu Asp Cys
145                 150                 155                 160
Glu Leu Ser His Ser Val Tyr Glu Asn Phe Met Leu Leu Ile Glu Gln
                165                 170                 175
Leu Arg Met Glu Tyr Lys Gly Arg Thr Thr Ala
            180                 185

<210> 2259
<211> 425
<212> DNA
<213> Homo sapiens

<400> 2259
acgcgtcaca atgataaagc cattatattc atcaagaggt aaatcattct tgaaattttc
60
taaaggtaaa cacttacgtg taacacgttc atcaaagaat tcaggaacca catattctgg
120
acggtcatct acgactgtaa cacgacagcc aataaacaat agcaaatcag taatagctcg
180
gctaacatga cctgcaccta atacgagaac tgacggatca ttttctacag gttgtacgaa
240
acactccatt tcgcctacca tgcatagaga attcagcttt gctttatcta cagtaaatcc
300
ttcaatagga gttccgtata gaacccttcc atcttcagca taaatagtct tatccccttg
360
acgaggaccg gatagaacgg taaccattac ggtagcttca gtaacctgta gacgattttt
420
catga
425

<210> 2260
<211> 141
<212> PRT
<213> Homo sapiens

<400> 2260
Met Lys Asn Arg Leu Gln Val Thr Glu Ala Thr Val Met Val Thr Val
 1               5                  10                  15
Leu Ser Gly Pro Arg Gln Gly Asp Lys Thr Ile Tyr Ala Glu Asp Gly
            20                  25                  30
Arg Val Leu Tyr Gly Thr Pro Ile Glu Gly Phe Thr Val Asp Lys Ala
        35                  40                  45
Lys Leu Asn Ser Leu Cys Met Val Gly Glu Met Glu Cys Phe Val Gln
    50                  55                  60
Pro Val Glu Asn Asp Pro Ser Val Leu Val Leu Gly Ala Gly His Val
65                  70                  75                  80
Ser Arg Ala Ile Thr Asp Leu Leu Leu Phe Ile Gly Cys Arg Val Thr
```

```
                85                  90                  95
Val Val Asp Asp Arg Pro Glu Tyr Val Val Pro Glu Phe Phe Asp Glu
            100                 105                 110
Arg Val Thr Arg Lys Cys Leu Pro Leu Glu Asn Phe Lys Asn Asp Leu
        115                 120                 125
Pro Leu Asp Glu Tyr Asn Gly Phe Ile Ile Val Thr Arg
    130                 135                 140
```

<210> 2261
<211> 660
<212> DNA
<213> Homo sapiens

<400> 2261
ngctagctgc tgctcctgag gatcggccgc agaatattgc tgccgatctg tccgggttgc
60
ttgagcccaa gcgcgaggtc gatgtgtccg gcgaccgcgc gcgttgcggt gggagcatag
120
tgtcggtgca cgctgaccga gaggtccgtg cggagagtac tcccgatgat atttgcgggc
180
agctcgatgc cgtggccgcc atgatggccc ttgtctatgg gtcgaatgtg actattcccg
240
acgatgccgg gaggctcttc gacaagcttc actgaacggt gttcaattgg tcccaacggc
300
tgcccatgtg ggcagccgct ctatctcgtc atgggaagga acccgatgtc gtcacgcaat
360
ggtttccagg ccaccgacct ggctcttatc gcggtctttg cagccctcat tgctgtgcta
420
gccgtcatcc cgccgatgtt catggtgggg gcggtccctt ttgcccttca gatggttgcc
480
gtcatgctgg cgccgatggt gctgggaagt atccgtggcg gatgcgcggt aggcttgtat
540
atccttgtcg gcgcgctggg gctgcccgtc ttcagcggtg ggtctagcgg gattggcgtc
600
ctggtgggtc ccactggtgg gtatctatgg ggatggctga tcggcgcttt cgtggcgggt
660

<210> 2262
<211> 139
<212> PRT
<213> Homo sapiens

<400> 2262
```
Met Pro Gly Gly Ser Ser Thr Ser Phe Thr Glu Arg Cys Ser Ile Gly
 1               5                  10                  15
Pro Asn Gly Cys Pro Cys Gly Gln Pro Leu Tyr Leu Val Met Gly Arg
            20                  25                  30
Asn Pro Met Ser Ser Arg Asn Gly Phe Gln Ala Thr Asp Leu Ala Leu
        35                  40                  45
Ile Ala Val Phe Ala Ala Leu Ile Ala Val Leu Ala Val Ile Pro Pro
    50                  55                  60
Met Phe Met Val Gly Ala Val Pro Phe Ala Leu Gln Met Val Ala Val
65                  70                  75                  80
Met Leu Ala Pro Met Val Leu Gly Ser Ile Arg Gly Gly Cys Ala Val
```

```
                85                  90                  95
Gly Leu Tyr Ile Leu Val Gly Ala Leu Gly Leu Pro Val Phe Ser Gly
            100                 105                 110
Gly Ser Ser Gly Ile Gly Val Leu Val Gly Pro Thr Gly Gly Tyr Leu
        115                 120                 125
Trp Gly Trp Leu Ile Gly Ala Phe Val Ala Gly
    130                 135
```

<210> 2263
<211> 491
<212> DNA
<213> Homo sapiens

<400> 2263
nacgcgttcc cggtcgaccg aggcaaaggc aaaagtaagc agggtgcccg tagtccccgt
60
tcccaccgcg gtatggctgg gtcactgctg acagatggcg tccccctgct gatctttccg
120
gagggcaccc ggtctcgcac cggcgcaatg ggcaccttca aacctggggc tgccgcattg
180
gctatttcac gtggggttcc ggttatcccg attgctttag taggagcatg ggcggctatg
240
ccgtccgagc aagccaggtt accaaaagga cgtccattgg tccacgtggc tattggacac
300
cctatggacc ctgttcccgg cgagatcgcc caccaattct ccgaacggat tcgtcgccag
360
gtcattgagt tgcacgacca aaccgcccgc gcctacggca tgccaaccct tgacgaatac
420
ggacgccacc gcgcgctaag ccaggcctcc gagagcggcg acaccgcatc caccaaccac
480
tcgacgtgca c
491

<210> 2264
<211> 163
<212> PRT
<213> Homo sapiens

<400> 2264

```
Xaa Ala Phe Pro Val Asp Arg Gly Lys Gly Lys Ser Lys Gln Gly Ala
 1               5                  10                  15
Arg Ser Pro Arg Ser His Arg Gly Met Ala Gly Ser Leu Leu Thr Asp
            20                  25                  30
Gly Val Pro Leu Leu Ile Phe Pro Glu Gly Thr Arg Ser Arg Thr Gly
        35                  40                  45
Ala Met Gly Thr Phe Lys Pro Gly Ala Ala Ala Leu Ala Ile Ser Arg
    50                  55                  60
Gly Val Pro Val Ile Pro Ile Ala Leu Val Gly Ala Trp Ala Ala Met
65                  70                  75                  80
Pro Ser Glu Gln Ala Arg Leu Pro Lys Gly Arg Pro Leu Val His Val
                85                  90                  95
Ala Ile Gly His Pro Met Asp Pro Val Pro Gly Glu Ile Ala His Gln
            100                 105                 110
Phe Ser Glu Arg Ile Arg Arg Gln Val Ile Glu Leu His Asp Gln Thr
```

```
        115                 120                 125
Ala Arg Ala Tyr Gly Met Pro Thr Leu Asp Glu Tyr Gly Arg His Arg
    130                 135                 140
Ala Leu Ser Gln Ala Ser Glu Ser Gly Asp Thr Ala Ser Thr Asn His
145                 150                 155                 160
Ser Thr Cys
```

<210> 2265
<211> 328
<212> DNA
<213> Homo sapiens

<400> 2265
ccatgggaat aggccaacac ggatggatct actgtataac ttgcctgcca tcaggaaaga
60
gtcaacacgg cagacacatg ctggcagaaa ccctgctgga gttgcccctg agcattgatg
120
cataccaccc gagaggagga gagggtggtg ggagaaatca gatcagagtt caaaatgcac
180
cggaagggct cggaaatgta agactgcacc ttgcaggaac tgtcaatgcc actaccaata
240
tcactcactt acgtcaagca cttgagagca gctgcgaaca caattctctg actcctaacc
300
tttagcacgt gactgggacc actggaca
328

<210> 2266
<211> 100
<212> PRT
<213> Homo sapiens

<400> 2266
```
Met Gly Ile Gly Gln His Gly Trp Ile Tyr Cys Ile Thr Cys Leu Pro
 1               5                  10                  15
Ser Gly Lys Ser Gln His Gly Arg His Met Leu Ala Glu Thr Leu Leu
            20                  25                  30
Glu Leu Pro Leu Ser Ile Asp Ala Tyr His Pro Arg Gly Gly Glu Gly
        35                  40                  45
Gly Gly Arg Asn Gln Ile Arg Val Gln Asn Ala Pro Glu Gly Leu Gly
    50                  55                  60
Asn Val Arg Leu His Leu Ala Gly Thr Val Asn Ala Thr Thr Asn Ile
65                  70                  75                  80
Thr His Leu Arg Gln Ala Leu Glu Ser Ser Cys Glu His Asn Ser Leu
                85                  90                  95
Thr Pro Asn Leu
            100
```

<210> 2267
<211> 370
<212> DNA
<213> Homo sapiens

<400> 2267

agatctatgc aggtagcgct ggtctccggg gggtaagttg tccactccct gtcagatggc
60
agaccatgga gggctaatgc aggctgggaa ggctaggcag agttcccaga aacaggtcac
120
cgagggagcc accactgaat tgcactctcg ctggggagtt aagccatatc cccctaagac
180
agcagtgacc ggagtggcca atctgtacag ggacaggctc aaggccacag caactcaggg
240
gacagagatg gtgaagcagg catgtcctaa agcctccctt cttaaccctg accttgaagg
300
acaggaaaca agtcatttac gtatgttgta ggcctagagc aagggattgc agagatgggc
360
gtcaacgcgt
370

<210> 2268
<211> 91
<212> PRT
<213> Homo sapiens

<400> 2268
Met Ala Asp His Gly Gly Leu Met Gln Ala Gly Lys Ala Arg Gln Ser
1 5 10 15
Ser Gln Lys Gln Val Thr Glu Gly Ala Thr Thr Glu Leu His Ser Arg
20 25 30
Trp Gly Val Lys Pro Tyr Pro Pro Lys Thr Ala Val Thr Gly Val Ala
35 40 45
Asn Leu Tyr Arg Asp Arg Leu Lys Ala Thr Ala Thr Gln Gly Thr Glu
50 55 60
Met Val Lys Gln Ala Cys Pro Lys Ala Ser Leu Leu Asn Pro Asp Leu
65 70 75 80
Glu Gly Gln Glu Thr Ser His Leu Arg Met Leu
85 90

<210> 2269
<211> 507
<212> DNA
<213> Homo sapiens

<400> 2269
ctctccgacc gcgtcaaccc cggcaatatc cgcaagttcg acgaccagat cgaatcgatt
60
tgtaaggctg ccaccgagca cggtacgagc atccgaatcg gcgtgaatgc tgggtctctc
120
gacaaacgtc tgcttgacaa atacggagcc ccgaccgccg aggctatggt ggagtcggca
180
ctgtgggagg ccagcctctt tgagcaatac ggattccggg atttcaaaat ctcggtgaag
240
caccacgacc cggtcgtcat gatccgtgcc tatgaacagc tcgccgccaa atgcgattat
300
ccccttcatt tgggcgttac tgaggctggt ccggccttcc aaggcaccat caagtcggcg
360
gtggccttcg ggcatctcct tgccgagggt atcggcgata ccatacgcgt ctccttgtcg
420

gctgatccgg tcgaggaagt caaggtgggt atcaagatcc tggagtcgct caacctacgt
480
cctcgaggtc tagagatcgt ctcctgc
507

<210> 2270
<211> 169
<212> PRT
<213> Homo sapiens

<400> 2270
Leu Ser Asp Arg Val Asn Pro Gly Asn Ile Arg Lys Phe Asp Asp Gln
1 5 10 15
Ile Glu Ser Ile Cys Lys Ala Ala Thr Glu His Gly Thr Ser Ile Arg
20 25 30
Ile Gly Val Asn Ala Gly Ser Leu Asp Lys Arg Leu Leu Asp Lys Tyr
35 40 45
Gly Ala Pro Thr Ala Glu Ala Met Val Glu Ser Ala Leu Trp Glu Ala
50 55 60
Ser Leu Phe Glu Gln Tyr Gly Phe Arg Asp Phe Lys Ile Ser Val Lys
65 70 75 80
His His Asp Pro Val Val Met Ile Arg Ala Tyr Glu Gln Leu Ala Ala
85 90 95
Lys Cys Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Ala
100 105 110
Phe Gln Gly Thr Ile Lys Ser Ala Val Ala Phe Gly His Leu Leu Ala
115 120 125
Glu Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val
130 135 140
Glu Glu Val Lys Val Gly Ile Lys Ile Leu Glu Ser Leu Asn Leu Arg
145 150 155 160
Pro Arg Gly Leu Glu Ile Val Ser Cys
165

<210> 2271
<211> 573
<212> DNA
<213> Homo sapiens

<400> 2271
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240
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300
cgggcgctca aggccaaggc cacgcgtacc gggcgtgtat cggcgcggat tctcgacgac
360
atgctcgctg gggtcatcct gatcgacacc gccggtgcgg ccgtgggcaa atgcaacggg
420

ctgacggtgc tggaagtcgg cgattcggcg ttcggcgtgc cggcgcggat ttccgccacg
480
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573

<210> 2272
<211> 191
<212> PRT
<213> Homo sapiens

<400> 2272
Xaa Ala Asp Pro Asp Phe Gln Glu Met Leu Arg Ala Leu Val Asp Phe
1 5 10 15
Asp Glu Asp Ile Pro Met Val Asp Glu Ser Leu Glu Gln Phe Ala Gln
20 25 30
Leu Leu Lys Thr Arg Thr Ser Glu Glu Gly Met Ala Pro Leu Thr Ser
35 40 45
Asp Ala Val Ala Arg Leu Ala Thr Tyr Ser Ala Arg Leu Ala Asp His
50 55 60
Gln Gly Arg Val Ser Ala Arg Ile Gly Asp Leu Phe Gln Leu Val Ser
65 70 75 80
Glu Ala Asp Phe Ile Arg His Leu Ala Gly Asp Glu Met Thr Asp Ala
85 90 95
Gly His Ile Glu Arg Ala Leu Lys Ala Lys Ala Thr Arg Thr Gly Arg
100 105 110
Val Ser Ala Arg Ile Leu Asp Asp Met Leu Ala Gly Val Ile Leu Ile
115 120 125
Asp Thr Ala Gly Ala Ala Val Gly Lys Cys Asn Gly Leu Thr Val Leu
130 135 140
Glu Val Gly Asp Ser Ala Phe Gly Val Pro Ala Arg Ile Ser Ala Thr
145 150 155 160
Val Tyr Pro Gly Gly Ser Gly Ile Val Asp Ile Glu Arg Glu Val Asn
165 170 175
Leu Gly Gln Pro Ile His Ser Lys Gly Val Met Ile Leu Thr Gly
180 185 190

<210> 2273
<211> 4355
<212> DNA
<213> Homo sapiens

<400> 2273
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120
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240
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300

aacctgaaga aggggaacat cgtgaagggc atgagagagc tccgggaggt gctgcggact
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420
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480
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960
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2160
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4200
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4320
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4355

<210> 2274
<211> 158
<212> PRT
<213> Homo sapiens

<400> 2274
Ser Phe Gln His Ala Ser Gly Phe Leu Gly Glu His Ser Pro Gly Gly
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Gln Arg Ser Cys Arg Gly Gly Leu Ser Leu Glu Arg Leu Pro Asn Ser
20 25 30
Ile Ala Ser Arg Phe Arg Leu Thr Glu Arg Glu Glu Glu Val Ile Thr
35 40 45
Cys Phe Glu Arg Ala Ser Trp Ile Ala Gln Val Phe Leu Gln Glu Leu
50 55 60
Glu Lys Thr Thr Asn Asn Ser Thr Ser Arg His Leu Lys Gly Cys His
65 70 75 80
Pro Leu Asp Tyr Glu Leu Thr Tyr Phe Leu Glu Ala Ala Leu Gln Ser
85 90 95
Ala Tyr Val Lys Asn Leu Lys Lys Gly Asn Ile Val Lys Gly Met Arg
100 105 110
Glu Leu Arg Glu Val Leu Arg Thr Val Glu Thr Lys Ala Thr Gln Asn
115 120 125
Phe Lys Val Met Ala Ala Lys His Leu Ala Gly Val Leu Leu His Ser
130 135 140
Leu Ser Gly Val Leu Leu Glu Pro Pro Val Pro Pro Ser Ala

145 150 155

<210> 2275
<211> 608
<212> DNA
<213> Homo sapiens

<400> 2275
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ccctgcatct gtcatcactt atgaaaccca aacagagaga tctagagcac aaacaataca
120
aaggagaaca ggagacctca aaaggaagaa ccaggctgtg ccccaacctt ttttccaaac
180
caaagttctg gcttcactac acccactgct atgacacctc ctgttctaac cacagccgaa
240
acttcagtca agcccagtgt ctctgcattc actcattccc caccagaaaa cacaactggg
300
atttcaagca caatcagttt tcattcaaga actcttaatc tgacagatgt gattgaagaa
360
ctagcccaag caagtactca gactttgaag agcacaattg cttctgaaac aactttgtcc
420
agcaaatcac accagagtac cacaactagg aaagcaatca ttagacactc aaccatacca
480
ccattcttga gcagcagtgc tactctaata ccagttccca tctcccctcc ctttactcag
540
agagcagtta ctgacaacgt ggcgactccc atttccgggc ttatgacaaa tacagtggtc
600
aagctgcg
608

<210> 2276
<211> 167
<212> PRT
<213> Homo sapiens

<400> 2276
Ser Thr Asn Asn Thr Lys Glu Asn Arg Arg Pro Gln Lys Glu Glu Pro
1 5 10 15
Gly Cys Ala Pro Thr Phe Phe Pro Asn Gln Ser Ser Gly Phe Thr Thr
20 25 30
Pro Thr Ala Met Thr Pro Pro Val Leu Thr Thr Ala Glu Thr Ser Val
35 40 45
Lys Pro Ser Val Ser Ala Phe Thr His Ser Pro Pro Glu Asn Thr Thr
50 55 60
Gly Ile Ser Ser Thr Ile Ser Phe His Ser Arg Thr Leu Asn Leu Thr
65 70 75 80
Asp Val Ile Glu Glu Leu Ala Gln Ala Ser Thr Gln Thr Leu Lys Ser
85 90 95
Thr Ile Ala Ser Glu Thr Thr Leu Ser Ser Lys Ser His Gln Ser Thr
100 105 110
Thr Thr Arg Lys Ala Ile Ile Arg His Ser Thr Ile Pro Pro Phe Leu
115 120 125
Ser Ser Ser Ala Thr Leu Ile Pro Val Pro Ile Ser Pro Pro Phe Thr

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    130                 135                 140
Gln Arg Ala Val Thr Asp Asn Val Ala Thr Pro Ile Ser Gly Leu Met
145                 150                 155                 160
Thr Asn Thr Val Val Lys Leu
                165
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<210> 2277
<211> 640
<212> DNA
<213> Homo sapiens

<400> 2277
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120
gacagggaca ctgagggatg aaagccccca cgctctggcc tgccctgctc agtcagggcc
180
gctggcatgg gccgttcttc ccctgggact gcacagcctg gacccnccac caagtcctgt
240
tgcccaccct ggctcagctc tcctccagcc gcatgcctgc cttcctccct cctttcccca
300
tacccagtcc tgccatctcc cagctgcaag gtccatgcca ccccacagga agagcctcag
360
cggctgtcct cagaccccac cctgtctgcc ccgaccctgc cgcctcacca aattctaagc
420
acaccatgac ccggcctgcc ctggtgtgct gcccatggcc cggcgtgacc cagtgtgctg
480
cccatggccc agcgtcccag tgtgctgccc acggcccagc ctgaccgacc cggtgtgctg
540
cccgcggccc ggcctgaccc agtgtgctgc tctgggaagg aagcctggtg ggaacagtgc
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640

<210> 2278
<211> 95
<212> PRT
<213> Homo sapiens

<400> 2278
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Gly Arg Ser Ser Pro Gly Thr Ala Gln Pro Gly Pro Xaa Thr Lys Ser
            20                  25                  30
Cys Cys Pro Pro Trp Leu Ser Ser Pro Pro Ala Ala Cys Leu Pro Ser
        35                  40                  45
Ser Leu Leu Ser Pro Tyr Pro Val Leu Pro Ser Pro Ser Cys Lys Val
    50                  55                  60
His Ala Thr Pro Gln Glu Glu Pro Gln Arg Leu Ser Ser Asp Pro Thr
65                  70                  75                  80
Leu Ser Ala Pro Thr Leu Pro Pro His Gln Ile Leu Ser Thr Pro
                85                  90                  95
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<210> 2279
<211> 331
<212> DNA
<213> Homo sapiens

<400> 2279
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tagtgcgttt gtgggccaca gttcacaagg atgggccctg cctccgggtc agaagaaccc
120
ttccggacca gggggatgca caggggccaa gagaatgcat ggaatcagag ggcactggcc
180
ccactcactc cccatcatcg cctgcagtgt tgttttcatt cctgcactgt gcctttgttt
240
cctttcttgg tacctcattt actcctgcct gcatctcctc cctttcccac ggctcacctc
300
tctcttggag ttctggggca gtgccaatcg g
331

<210> 2280
<211> 91
<212> PRT
<213> Homo sapiens

<400> 2280
Met Ile Val Arg Leu Trp Ala Thr Val His Lys Asp Gly Pro Cys Leu
 1   5   10   15
Arg Val Arg Arg Thr Leu Pro Asp Gln Gly Asp Ala Gln Gly Pro Arg
            20   25   30
Glu Cys Met Glu Ser Glu Gly Thr Gly Pro Thr His Ser Pro Ser Ser
        35   40   45
Pro Ala Val Leu Phe Ser Phe Leu His Cys Ala Phe Val Ser Phe Leu
    50   55   60
Gly Thr Ser Phe Thr Pro Ala Cys Ile Ser Ser Leu Ser His Gly Ser
65   70   75   80
Pro Leu Ser Trp Ser Ser Gly Ala Val Pro Ile
                85   90

<210> 2281
<211> 409
<212> DNA
<213> Homo sapiens

<400> 2281
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ttcaactaat gaaggtcaag aaacaaatca gtgggaacaa gaaaaatcat acctaggtga
120
gatgacaaat tcaagcattg ccacagaaaa ttttcctgct gtcagttctc ccacccaact
180
gataatgaag ccaggctctg aatgggatgg ctctacccca agtgaggact cccgaggtac
240
ctttgtgcca gatattttac atggcaactt tcaagagggt gggcagctgg cctctgccgc
300

gcctgacttg tggatagatg ctaagaagcc cttcagtttg aaagcagatg gtgagaatcc
360
tgatatcctg acgcactgcg aacatgacta cggggagacg acaacgcgt
409

<210> 2282
<211> 96
<212> PRT
<213> Homo sapiens

<400> 2282
Met Thr Asn Ser Ser Ile Ala Thr Glu Asn Phe Pro Ala Val Ser Ser
1 5 10 15
Pro Thr Gln Leu Ile Met Lys Pro Gly Ser Glu Trp Asp Gly Ser Thr
20 25 30
Pro Ser Glu Asp Ser Arg Gly Thr Phe Val Pro Asp Ile Leu His Gly
35 40 45
Asn Phe Gln Glu Gly Gly Gln Leu Ala Ser Ala Ala Pro Asp Leu Trp
50 55 60
Ile Asp Ala Lys Lys Pro Phe Ser Leu Lys Ala Asp Gly Glu Asn Pro
65 70 75 80
Asp Ile Leu Thr His Cys Glu His Asp Tyr Gly Glu Thr Thr Thr Arg
85 90 95

<210> 2283
<211> 404
<212> DNA
<213> Homo sapiens

<400> 2283
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caatggaccc gacgagcttg tgaacatctt cttgtcgtct tttttcttgt aggagcggta
120
ccgacaattt ctagtaaatt ccgacgaaag tttattgtaa aatactctgc aacctctttt
180
ctgctctgcc atctgggtgg gggttgcaac tttccacatc actgtcgagt gcttcgtaac
240
cgtcttcaac cctgtcatcg ttcttctcag ttgcaccaag cttttggacg tgcggtgata
300
cgacttccag ctaaagcgca ggcgtcccat gccacttcct ctccgaagat gcgtaaagtt
360
cgcaccagga agcaaggcgc ggtcgagcga tcttccgcgc catg
404

<210> 2284
<211> 122
<212> PRT
<213> Homo sapiens

<400> 2284
Met Asp Leu Arg Ser Gln Arg Arg Gln Trp Thr Arg Arg Ala Cys Glu
1 5 10 15
His Leu Leu Val Val Phe Phe Leu Val Gly Ala Val Pro Thr Ile Ser

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            20                  25                  30
Ser Lys Phe Arg Arg Lys Phe Ile Val Lys Tyr Ser Ala Thr Ser Phe
        35                  40                  45
Leu Leu Cys His Leu Gly Gly Gly Cys Asn Phe Pro His His Cys Arg
    50                  55                  60
Val Leu Arg Asn Arg Leu Gln Pro Cys His Arg Ser Ser Gln Leu His
65                  70                  75                  80
Gln Ala Phe Gly Arg Ala Val Ile Arg Leu Pro Ala Lys Ala Gln Ala
                85                  90                  95
Ser His Ala Thr Ser Ser Pro Lys Met Arg Lys Val Arg Thr Arg Lys
            100                 105                 110
Gln Gly Ala Val Glu Arg Ser Ser Ala Pro
        115                 120
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<210> 2285
<211> 6505
<212> DNA
<213> Homo sapiens

<400> 2285
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120
accgagggcc gggcggcact ggacatcgtg cacccggttc gagtcgacgc ggggggctcc
180
ttcctgtcct acgagctgtg gccccgcgca ctgcgcaagc gggatgtatc tgtgcgccga
240
gacgcgcccg ccttctacga gctacaatac cgcgggcgcg agctgcgctt caacctgacc
300
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360
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420
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480
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540
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600
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660
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720
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780
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900
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960
tgcaagtggc agaaaagcat caacatgaag ggggatgccc atcccctgca ccatgacact
1020

gccatcctgc tcaccagaaa ggacctgtgt gcagccatga accggccctg tgagaccctg
1080
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1260
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1320
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1680
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1740
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1800
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1860
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1980
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<210> 2286
<211> 1784
<212> PRT
<213> Homo sapiens

<400> 2286
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35 40 45
Ile Val His Pro Val Arg Val Asp Ala Gly Gly Ser Phe Leu Ser Tyr
50 55 60
Glu Leu Trp Pro Arg Ala Leu Arg Lys Arg Asp Val Ser Val Arg Arg
65 70 75 80
Asp Ala Pro Ala Phe Tyr Glu Leu Gln Tyr Arg Gly Arg Glu Leu Arg
85 90 95
Phe Asn Leu Thr Ala Asn Gln His Leu Leu Ala Pro Gly Phe Val Ser
100 105 110
Glu Thr Arg Arg Arg Gly Gly Leu Gly Arg Ala His Ile Arg Ala His
115 120 125
Thr Pro Ala Cys His Leu Leu Gl, Glu Val Gln Asp Pro Glu Leu Glu
130 135 140
Gly Gly Leu Ala Ala Ile Ser Ala Cys Asp Gly Leu Lys Gly Val Phe
145 150 155 160
Gln Leu Ser Asn Glu Asp Tyr Phe Ile Glu Pro Leu Asp Ser Ala Pro
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Ala Arg Pro Gly His Ala Gln Pro His Val Val Tyr Lys Arg Gln Ala
180 185 190
Pro Glu Arg Leu Ala Gln Arg Gly Asp Ser Ser Ala Pro Ser Thr Cys

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Ala Ala Ala Val Ala Ala Ala Thr Ala Arg Arg Leu His Gln Arg Ser
225                 230                 235                 240
Val Ser Lys Glu Lys Trp Val Glu Thr Leu Val Val Ala Asp Ala Lys
                245                 250                 255
Met Val Glu Tyr His Gly Gln Pro Gln Val Glu Ser Tyr Val Leu Thr
            260                 265                 270
Ile Met Asn Met Val Ala Gly Leu Phe His Asp Pro Ser Ile Gly Asn
        275                 280                 285
Pro Ile His Ile Thr Ile Val Arg Leu Val Leu Leu Glu Asp Glu Glu
    290                 295                 300
Glu Asp Leu Lys Ile Thr His His Ala Asp Asn Thr Leu Lys Ser Phe
305                 310                 315                 320
Cys Lys Trp Gln Lys Ser Ile Asn Met Lys Gly Asp Ala His Pro Leu
                325                 330                 335
His His Asp Thr Ala Ile Leu Leu Thr Arg Lys Asp Leu Cys Ala Ala
            340                 345                 350
Met Asn Arg Pro Cys Glu Thr Leu Gly Leu Ser His Val Ala Gly Met
        355                 360                 365
Cys Gln Pro His Arg Ser Cys Ser Ile Asn Glu Asp Thr Gly Leu Pro
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Leu Ala Phe Thr Val Ala His Glu Leu Gly His Ser Phe Gly Ile Gln
385                 390                 395                 400
His Asp Gly Ser Gly Asn Asp Cys Glu Pro Val Gly Lys Arg Pro Phe
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            420                 425                 430
Arg Cys Ser Arg Gln Tyr Ile Thr Arg Phe Leu Asp Arg Gly Trp Gly
        435                 440                 445
Leu Cys Leu Asp Asp Pro Pro Ala Lys Asp Ile Ile Asp Phe Pro Ser
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Val Pro Pro Gly Val Leu Tyr Asp Val Ser His Gln Cys Arg Leu Gln
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Tyr Gly Ala Tyr Ser Ala Phe Cys Glu Asp Met Asp Asn Val Cys His
                485                 490                 495
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Ala Val Asp Gly Thr Arg Cys Gly Glu Asn Lys Trp Cys Leu Ser Gly
        515                 520                 525
Glu Cys Val Pro Val Gly Phe Arg Pro Glu Ala Val Asp Gly Gly Trp
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Ser Gly Trp Ser Ala Trp Ser Ile Cys Ser Arg Ser Cys Gly Met Gly
545                 550                 555                 560
Val Gln Ser Ala Glu Arg Gln Cys Thr Gln Pro Thr Pro Lys Tyr Lys
                565                 570                 575
Gly Arg Tyr Cys Val Gly Glu Arg Lys Arg Phe Arg Leu Cys Asn Leu
            580                 585                 590
Gln Ala Cys Pro Ala Gly Arg Pro Ser Phe Arg His Val Gln Cys Ser
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His Phe Asp Ala Met Leu Tyr Lys Gly Gln Leu His Thr Trp Val Pro
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Val Val Asn Asp Val Asn Pro Cys Glu Leu His Cys Arg Pro Ala Asn
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690 695 700
Gly Thr Phe Xaa Arg Arg Pro Arg Val Xaa Gly Tyr Val Asp Val Gly
705 710 715 720
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Ala Ala Asn Phe Leu Ala Leu Arg Ser Glu Asp Pro Glu Lys Tyr Phe
740 745 750
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755 760 765
Gly Thr Thr Phe Thr Tyr Ala Arg Arg Gly Asn Trp Glu Asn Leu Thr
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785 790 795 800
Arg Gly Pro Gly Gly Gly Ser Arg Gly Gly Val Pro Arg Pro Ser Thr
805 810 815
Leu His Gly Arg Ser Arg Pro Gly Gly Val Ser Pro Gly Ser Val Thr
820 825 830
Glu Pro Gly Ser Glu Pro Gly Pro Pro Ala Ala Ala Ser Thr Ser Val
835 840 845
Ser Pro Ser Leu Lys Trp Pro Asn Leu Val Ala Ala Val His Arg Gly
850 855 860
Gly Trp Gly Gln Ala Pro Leu Gly Leu Gly Gly Trp Arg Arg His Leu
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Val Leu Met Gly Pro Arg Leu Pro Thr Gln Leu Leu Phe Gln Glu Ser
885 890 895
Asn Pro Gly Val His Tyr Glu Tyr Thr Ile His Arg Glu Ala Gly Gly
900 905 910
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915 920 925
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930 935 940
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945 950 955 960
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965 970 975
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980 985 990
Cys Gly Pro Gly Gly Leu Ser Arg Arg Ala Val Leu Cys Ile Arg Ser
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Val Pro Cys Asp Glu Ala Gln Gln Pro Ala Ser Glu Val Thr Cys Ser
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Leu Pro Leu Cys Arg Trp Pro Leu Gly Thr Leu Gly Pro Glu Gly Ser
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Gly Ser Gly Ser Ser Ser His Glu Leu Phe Asn Glu Ala Asp Phe Ile
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Pro His His Leu Ala Pro Arg Pro Ser Pro Ala Ser Ser Pro Lys Pro
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Gly Thr Met Gly Asn Ala Ile Glu Glu Glu Ala Pro Glu Leu Asp Leu
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Pro Gly Pro Val Phe Val Asp Asp Phe Tyr Tyr Asp Tyr Asn Phe Ile
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Asp Leu Ala Gly Thr Gly Asp Arg Thr Pro Pro Pro His Ser His Pro
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Gly Lys Asp Ser Gln Ser Gln Leu Pro Pro Pro Trp Arg Asp Arg Thr
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Gly Gly Thr Val Ala Trp Glu Pro Ala Leu Glu Gly Gly Leu Gly Pro
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Val Asp Ser Glu Leu Trp Pro Thr Val Gly Val Ala Ser Leu Leu Pro
            1380                1385                1390
Pro Pro Ile Ala Pro Leu Pro Glu Met Lys Val Arg Asp Ser Ser Leu
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Glu Pro Gly Thr Pro Ser Phe Pro Ala Pro Gly Pro Gly Ser Trp Asp
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Gly Leu Gly His Met Pro Glu Pro Ala Leu Asn Pro Gly Pro Lys Gly
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Ser Ser Gly Arg Asp Glu Asp Cys Ala Pro Ala Gly Arg Pro Gln Pro
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Ala Arg Arg Cys His Leu Arg Pro Cys Ala Thr Trp His Ser Gly Asn
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Trp Ser Lys Cys Ser Arg Ser Cys Gly Gly Gly Ser Ser Val Arg Asp
    1570                1575                1580
Val Gln Cys Val Asp Thr Arg Asp Leu Arg Pro Leu Arg Pro Phe His
1585                1590                1595                1600
Cys Gln Pro Gly Pro Ala Lys Pro Pro Ala His Arg Pro Cys Gly Ala
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Gln Pro Cys Leu Ser Trp Tyr Thr Ser Ser Trp Arg Glu Cys Ser Glu
            1620                1625                1630
Ala Cys Gly Gly Gly Glu Gln Gln Arg Leu Val Thr Cys Pro Glu Pro
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Gly Leu Cys Glu Glu Ala Leu Arg Pro Asn Thr Thr Arg Pro Cys Asn
    1650                1655                1660
Thr His Pro Cys Thr Gln Trp Val Val Gly Pro Trp Gly Gln Cys Ser
1665                1670                1675                1680
Ala Pro Cys Gly Gly Gly Val Gln Arg Arg Leu Val Lys Cys Val Asn
                1685                1690                1695
Thr Gln Thr Gly Leu Pro Glu Glu Asp Ser Asp Gln Cys Gly His Glu
            1700                1705                1710
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        1715                1720                1725
Val Glu Pro Pro Arg Cys Glu Arg Asp Arg Leu Ser Phe Gly Phe Cys
    1730                1735                1740
Glu Thr Leu Arg Leu Leu Gly Arg Cys Gln Leu Pro Thr Ile Arg Thr
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<212> PRT
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Ile Phe Leu Tyr Gly Pro Cys Ser Ser Gln Pro Leu Ile Leu Glu Leu
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Gly Thr Gly Ser Ala Thr Ser Met Leu Leu Ser Cys Cys Ser Pro Ala
50 55 60
Trp Asn Val Pro Tyr Leu Ala Asn Ser Tyr Cys Ser Ser Val Thr Leu
65 70 75 80
Leu Asp Thr Phe Leu Pro Leu Ser Leu Val Arg Cys Ser Pro Leu Gly
85 90 95
Ser His Gly Pro Leu Cys Val Pro Val Val Ala Gln Gln Lys Pro Pro
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<210> 2289
<211> 381
<212> DNA
<213> Homo sapiens

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<210> 2290
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<212> PRT
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Ile Asp Tyr Thr Gly Gly Leu Lys His Gln Ile Leu Gln Ser His Gly
35 40 45
Gln Asp Ala Glu Leu Ser Gly Thr Leu Ser Leu Val Leu Thr Gln Gly
50 55 60
Cys Lys Arg Ile Xaa Arg Gly Tyr Trp Phe Lys Asn Trp Pro Pro Thr
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Arg Ile His Phe
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<211> 573
<212> DNA
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573

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<211> 140
<212> PRT
<213> Homo sapiens

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Lys Ala Val Gly Ser Asp Arg Arg Ala Glu Asp Leu Gly Pro Gln Glu
35 40 45
Leu Arg Glu Ala Ser Ala Ala Phe Phe Ala Gly Gly His Asp Val Ile
50 55 60
Val Ala Arg Arg His Tyr Thr Asp Glu Gly Thr Thr Thr Ala Asp Val
65 70 75 80
Ala Gly Ser Ala Ser Leu Thr Val Asn Glu His Arg Ala Phe Met Ala
85 90 95
Leu Thr Val Asp Ser Met Ala Gln Leu His Arg His Asn Glu His Val
100 105 110
Arg Tyr Val Val Val Phe Gln Asn Trp Leu Lys Pro Ala Gly Ala Ser
115 120 125
Ile Asp His Leu His Lys Gln Val Val Ala Ile Asp
130 135 140

<210> 2293
<211> 358
<212> DNA
<213> Homo sapiens

<400> 2293
acgcgtgaag gaatggaagc tgctctcgtc ggtgcacaca agactggcgg gtgcccattg
60
gtgaacactg tcgctaagaa ctggttgaac cggctcaaca cgccggatat gaaacccact
120
gaggagatca agcggcagtt ccaaggtctg cattggttgg gacgtaagta tgggctcaac
180
cacggagagt tctatcttga cgacgagcag tgggccacgc tcatggccgg gtcctctttc
240
gaggcgaatc cgcgcattaa gagcaacttt gattccgagg gcgctgttgt ggatccggat
300
tccgattcac ttgctggggc tgatcgagat gcccgaggtg cttcggatgc atgccttc
358

<210> 2294
<211> 115
<212> PRT
<213> Homo sapiens

<400> 2294
Met Glu Ala Ala Leu Val Gly Ala His Lys Thr Gly Gly Cys Pro Leu

```
 1               5                  10                  15
Val Asn Thr Val Ala Lys Asn Trp Leu Asn Arg Leu Asn Thr Pro Asp
            20                  25                  30
Met Lys Pro Thr Glu Glu Ile Lys Arg Gln Phe Gln Gly Leu His Trp
        35                  40                  45
Leu Gly Arg Lys Tyr Gly Leu Asn His Gly Glu Phe Tyr Leu Asp Asp
    50                  55                  60
Glu Gln Trp Ala Thr Leu Met Ala Gly Ser Ser Phe Glu Ala Asn Pro
65                  70                  75                  80
Arg Ile Lys Ser Asn Phe Asp Ser Glu Gly Ala Val Val Asp Pro Asp
                85                  90                  95
Ser Asp Ser Leu Ala Gly Ala Asp Arg Asp Ala Arg Gly Ala Ser Asp
            100                 105                 110
Ala Cys Leu
        115
```

<210> 2295
<211> 546
<212> DNA
<213> Homo sapiens

<400> 2295
ggcaccgatc cgagtggtgg tgccgggatt aggncggatc tanaaacatt ctccgccctt
60
ggggcgtatg gctgctcggt cattaccgca ctggtagcgc aaaatacgcg cggcgtgcag
120
tcggtgtatc gtatcgaacc ggattttgtc ggtgcacaac tggactctgt gttcagcgat
180
gtccgcattg attccaccaa aatcggcatg ctggcagagg cggatatcgt ggaagcggtc
240
gcggagcgcc tcaaacatta tcgcgttaaa aacgtggtac ttgatacggt gatgctggcg
300
aaaagtggcg atccgctgct atctcctgct gctgtcgaaa ctctgcgaaa acaccttctg
360
ccacacgtcg cgctgatcac gccaaatttg ccggaggcgg cggcgctgct ggatgcgcct
420
catgcccgta ccgagcacga gatgaaagag caggggcgcg cacttctggc gcttggctgc
480
gaggcagtgc tgatgaaagg cggccatctt gacgatcctg agagcccgga ctggctcttc
540
acgcgt
546

<210> 2296
<211> 182
<212> PRT
<213> Homo sapiens

<400> 2296
```
Gly Thr Asp Pro Ser Gly Gly Ala Gly Ile Arg Xaa Asp Leu Xaa Thr
 1               5                  10                  15
Phe Ser Ala Leu Gly Ala Tyr Gly Cys Ser Val Ile Thr Ala Leu Val
            20                  25                  30
Ala Gln Asn Thr Arg Gly Val Gln Ser Val Tyr Arg Ile Glu Pro Asp
```

```
        35                  40                  45
Phe Val Gly Ala Gln Leu Asp Ser Val Phe Ser Asp Val Arg Ile Asp
    50                  55                  60
Ser Thr Lys Ile Gly Met Leu Ala Glu Ala Asp Ile Val Glu Ala Val
65                  70                  75                  80
Ala Glu Arg Leu Lys His Tyr Arg Val Lys Asn Val Val Leu Asp Thr
                85                  90                  95
Val Met Leu Ala Lys Ser Gly Asp Pro Leu Leu Ser Pro Ala Ala Val
            100                 105                 110
Glu Thr Leu Arg Lys His Leu Leu Pro His Val Ala Leu Ile Thr Pro
        115                 120                 125
Asn Leu Pro Glu Ala Ala Ala Leu Leu Asp Ala Pro His Ala Arg Thr
    130                 135                 140
Glu His Glu Met Lys Glu Gln Gly Arg Ala Leu Leu Ala Leu Gly Cys
145                 150                 155                 160
Glu Ala Val Leu Met Lys Gly Gly His Leu Asp Asp Pro Glu Ser Pro
                165                 170                 175
Asp Trp Leu Phe Thr Arg
            180
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<210> 2297
<211> 414
<212> DNA
<213> Homo sapiens

<400> 2297
gggaattccg ggcccttccc cccaagcccg ggtaattttt tgtattttta aaaaaaaagg
60
gaattttccc acgttggggg ggggggggttc ggacttttttc ccccaaaaac ccccccccccc
120
caccccccca aaggccgaaa agcagggcca aaacccccgg gacccccccc gggggggggca
180
aaaggaaaaa ccccttttttt ttttttttttt ttttatacac atgagggtct ctggttaata
240
aatgttgaga tgtagggtta ggtgagatta aacaggttct ttttttcatg atttctcgga
300
gtctttatga tgctccacac cagtacttct caaagctgac tgtgtataca aaacactggg
360
gatctgaccc acatgtaaag tctgatttct ttggtctggg gcaggcctga aatn
414

<210> 2298
<211> 67
<212> PRT
<213> Homo sapiens

<400> 2298
Lys Lys Arg Glu Phe Ser His Val Gly Gly Gly Gly Phe Gly Leu Phe
 1   5   10   15
Pro Pro Lys Thr Pro Pro Pro His Pro Pro Lys Gly Arg Lys Ala Gly
            20   25   30
Pro Lys Pro Pro Gly Pro Pro Pro Gly Gly Ala Lys Gly Lys Thr Pro
        35   40   45
Phe Phe Phe Phe Phe Phe Tyr Thr His Glu Gly Leu Trp Leu Ile Asn

50 55 60
Val Glu Met
65

<210> 2299
<211> 987
<212> DNA
<213> Homo sapiens

<400> 2299
ngagatgtct aagttatttt ttttttcccg gaaggcaaat ggctggcgtg gaagcacaac
60
ccgctttcac tcttcgaatt tgtgcttagc tcttttcttg taccctgcga ctcgtgacca
120
acatgctgtg atgtgtgccg agggaggaat tggtcagcta cacaacctgg atcttaccac
180
agtttggata tgactgaggc tctccaatgg gccagatatc actggcgacg gctgatcaga
240
ggtgcaacca gggatgatga ttcagggcca tacaactatt cctcgttgct cgcctgtggg
300
cgcaagtcct ctcagatccc taaactgtca ggaaggcacc ggattgttgt tccccacatc
360
cagcccttca aggatgagta tgagaagttc tccggagcct atgtgaacaa tcgaatacga
420
acaacaaagt acacacttct gaattttgtg ccaagaaatt tatttgaaca atttcacaga
480
gctgccaatt tatatttcct gttcctagtt gtcctgaact gggtaccttt ggtagaagcc
540
ttccaaaagg aaatcaccat gttgcctctg gtggtggtcc ttacaattat cgcaattaaa
600
gatggcctgg aagattatcg gaaatacaaa attgacaaac agatcaataa tttaataact
660
aaagtttata gtaggaaaga gaaaaaatac attgaccgat gctggaaaga cgttactgtt
720
ggggacttta ttcgcctctc ctgcaacgag gtcatccctg cagacatggt actactcttt
780
tccactgatc cagatggaat ctgtcacatt gagacttctg gtcttgatgg agagagcaat
840
ttaaaacaga ggcaggtggt tcggggatat gcagaacagg actctgaagt tgatcctgag
900
aagttttcca gtaggataga atgtgaaagc ccaaacaatg acctcagcag attccgaggc
960
ttcctagaac attccaacaa agaacgc
987

<210> 2300
<211> 266
<212> PRT
<213> Homo sapiens

<400> 2300
Met Thr Glu Ala Leu Gln Trp Ala Arg Tyr His Trp Arg Arg Leu Ile
1 5 10 15
Arg Gly Ala Thr Arg Asp Asp Asp Ser Gly Pro Tyr Asn Tyr Ser Ser

```
            20                  25                  30
Leu Leu Ala Cys Gly Arg Lys Ser Ser Gln Ile Pro Lys Leu Ser Gly
        35                  40                  45
Arg His Arg Ile Val Val Pro His Ile Gln Pro Phe Lys Asp Glu Tyr
    50                  55                  60
Glu Lys Phe Ser Gly Ala Tyr Val Asn Asn Arg Ile Arg Thr Thr Lys
65                  70                  75                  80
Tyr Thr Leu Leu Asn Phe Val Pro Arg Asn Leu Phe Glu Gln Phe His
                85                  90                  95
Arg Ala Ala Asn Leu Tyr Phe Leu Phe Leu Val Val Leu Asn Trp Val
            100                 105                 110
Pro Leu Val Glu Ala Phe Gln Lys Glu Ile Thr Met Leu Pro Leu Val
        115                 120                 125
Val Val Leu Thr Ile Ile Ala Ile Lys Asp Gly Leu Glu Asp Tyr Arg
    130                 135                 140
Lys Tyr Lys Ile Asp Lys Gln Ile Asn Asn Leu Ile Thr Lys Val Tyr
145                 150                 155                 160
Ser Arg Lys Glu Lys Lys Tyr Ile Asp Arg Cys Trp Lys Asp Val Thr
                165                 170                 175
Val Gly Asp Phe Ile Arg Leu Ser Cys Asn Glu Val Ile Pro Ala Asp
            180                 185                 190
Met Val Leu Leu Phe Ser Thr Asp Pro Asp Gly Ile Cys His Ile Glu
        195                 200                 205
Thr Ser Gly Leu Asp Gly Glu Ser Asn Leu Lys Gln Arg Gln Val Val
    210                 215                 220
Arg Gly Tyr Ala Glu Gln Asp Ser Glu Val Asp Pro Glu Lys Phe Ser
225                 230                 235                 240
Ser Arg Ile Glu Cys Glu Ser Pro Asn Asn Asp Leu Ser Arg Phe Arg
                245                 250                 255
Gly Phe Leu Glu His Ser Asn Lys Glu Arg
            260                 265
```

<210> 2301
<211> 390
<212> DNA
<213> Homo sapiens

<400> 2301
tatcccaagc gcttcaaatt tgatgccgat gagttctact tgaaatcgtc cgaggaaatg
60
nncgccacct cttccgcgna tttccctgaa gcctgcgata acactatgga aatcgctgag
120
nncgttgcca cgttgaattc aacacaaacg caanactaca tgcccgattt ccccacccg
180
gaggggggaga atgaggaatc ctggttcgtc aaagaagttg aacgcggttt gcactaccga
240
ttccccgagg gcattcccga tgacgtacgc aagcaggcag attatgaagt agggattatt
300
acccagatgg gattccccgg ctacttcttg gtggtcgcgg attttatcaa ctgggcgaag
360
aataacggaa ttcgagtggg ccccgggcgt
390

<210> 2302

<211> 130
<212> PRT
<213> Homo sapiens

<400> 2302
Tyr Pro Lys Arg Phe Lys Phe Asp Ala Asp Glu Phe Tyr Leu Lys Ser
1 5 10 15
Ser Glu Glu Met Xaa Ala Thr Ser Ser Ala Xaa Phe Pro Glu Ala Cys
20 25 30
Asp Asn Thr Met Glu Ile Ala Glu Xaa Val Ala Thr Leu Asn Ser Thr
35 40 45
Gln Thr Gln Xaa Tyr Met Pro Asp Phe Pro Thr Pro Glu Gly Glu Asn
50 55 60
Glu Glu Ser Trp Phe Val Lys Glu Val Glu Arg Gly Leu His Tyr Arg
65 70 75 80
Phe Pro Glu Gly Ile Pro Asp Asp Val Arg Lys Gln Ala Asp Tyr Glu
85 90 95
Val Gly Ile Ile Thr Gln Met Gly Phe Pro Gly Tyr Phe Leu Val Val
100 105 110
Ala Asp Phe Ile Asn Trp Ala Lys Asn Asn Gly Ile Arg Val Gly Pro
115 120 125
Gly Arg
130

<210> 2303
<211> 638
<212> DNA
<213> Homo sapiens

<400> 2303
nnggatccag gctgcccctg tgtgtctcct tcagtcttcg ttagctgcct gctgctgtct
60
gcacctgtgt ttggctacct gggcgaccga catagccgca aggctaccat gagcttcggt
120
atcttgctgt ggtcaggagc tggcctctct agctccttca tctccccccg gtattcttgg
180
ctcttcttcc tgtcccgggg catcgagggc actggctcgg ccagctactc caccatcgcg
240
cccaccgtcc tgggcgacct cttcgtgagg gaccagcgca cccgcgtgct ggctgtcttc
300
tacatcttta tccccgttgg aagtggtctg ggctacgtgc tggggtcggc tgtgacgatg
360
ctgactggga actggcgctg ggccctccga gtcatgccct gcctggaggc cgtggccttg
420
atcctgctta tcctgctggt tccagaccca ccccggggag ctgccgagac acaggggggag
480
ggggccgtgg gaggcttcag aagcagctgg tgtgaggacg tcagatacct ggggaaaaac
540
tggagttttg tgtggtcgac cctcggagtg accgccatgg cctttgtgac tggagccctg
600
gggttctggg cccccaagtt tctgctcgag gcacgcgt
638

<210> 2304

<211> 212
<212> PRT
<213> Homo sapiens

<400> 2304
Xaa Asp Pro Gly Cys Pro Cys Val Ser Pro Ser Val Phe Val Ser Cys
1 5 10 15
Leu Leu Leu Ser Ala Pro Val Phe Gly Tyr Leu Gly Asp Arg His Ser
20 25 30
Arg Lys Ala Thr Met Ser Phe Gly Ile Leu Leu Trp Ser Gly Ala Gly
35 40 45
Leu Ser Ser Ser Phe Ile Ser Pro Arg Tyr Ser Trp Leu Phe Phe Leu
50 55 60
Ser Arg Gly Ile Glu Gly Thr Gly Ser Ala Ser Tyr Ser Thr Ile Ala
65 70 75 80
Pro Thr Val Leu Gly Asp Leu Phe Val Arg Asp Gln Arg Thr Arg Val
85 90 95
Leu Ala Val Phe Tyr Ile Phe Ile Pro Val Gly Ser Gly Leu Gly Tyr
100 105 110
Val Leu Gly Ser Ala Val Thr Met Leu Thr Gly Asn Trp Arg Trp Ala
115 120 125
Leu Arg Val Met Pro Cys Leu Glu Ala Val Ala Leu Ile Leu Leu Ile
130 135 140
Leu Leu Val Pro Asp Pro Pro Arg Gly Ala Ala Glu Thr Gln Gly Glu
145 150 155 160
Gly Ala Val Gly Gly Phe Arg Ser Ser Trp Cys Glu Asp Val Arg Tyr
165 170 175
Leu Gly Lys Asn Trp Ser Phe Val Trp Ser Thr Leu Gly Val Thr Ala
180 185 190
Met Ala Phe Val Thr Gly Ala Leu Gly Phe Trp Ala Pro Lys Phe Leu
195 200 205
Leu Glu Ala Arg
210

<210> 2305
<211> 340
<212> DNA
<213> Homo sapiens

<400> 2305
gcccccgcct ctatcttccg gcatcgtcac agtcgcatcg tgacggtact ggctggagtc
60
tcggaccagc acactttgac cgtcgtggtc gcctcgtgac atggggtaac gcgaacctcg
120
tcgctcctgt tcttgacctc ttccgtgccc ccattgacaa cgatcgggca agttcactgg
180
cccgcaacgc tattggtgac gcagcactcg cagctggtct cgaccgactc gtccacacca
240
cggcgtcggt gcgcgacgag ggcgatgagt tggtcgtcgt tactcgcagc gctgctgccg
300
ccgcacgcaa ttccatgacg acaacgtgga gttggcgcgc
340

<210> 2306

<211> 101
<212> PRT
<213> Homo sapiens

<400> 2306
Met Glu Leu Arg Ala Ala Ala Ala Ala Leu Arg Val Thr Thr Thr Asn
1 5 10 15
Ser Ser Pro Ser Ser Arg Thr Asp Ala Val Val Trp Thr Ser Arg Ser
20 25 30
Arg Pro Ala Ala Ser Ala Ala Ser Pro Ile Ala Leu Arg Ala Ser Glu
35 40 45
Leu Ala Arg Ser Leu Ser Met Gly Ala Arg Lys Arg Ser Arg Thr Gly
50 55 60
Ala Thr Arg Phe Ala Leu Pro His Val Thr Arg Arg Pro Arg Arg Ser
65 70 75 80
Lys Cys Ala Gly Pro Arg Leu Gln Pro Val Pro Ser Arg Cys Asp Cys
85 90 95
Asp Asp Ala Gly Arg
100

<210> 2307
<211> 360
<212> DNA
<213> Homo sapiens

<400> 2307
ngcttctcag ctgaaggggg agataaagct ctacataaga tgggtccagg tgggggcaaa
60
gccaaggcac tgggtggggc tggcagtggg agcaagggct cagcaggtgg cggaagcaag
120
cgacggctga gcagcgaaga cagctccctg gagccagacc tggccgagat gagcctggat
180
gacagcagcc tggccctggg cgcagaggcc aggaccttcg ggggattccc tgagagccct
240
ccaccctgtc ctctccacgg tggctcccga ggcccttcca ctttccttcc tgagccccca
300
gatacttatg aagaagatgg tgatgagagt ggcaatgggc ttcccaaaac caaagaggca
360

<210> 2308
<211> 120
<212> PRT
<213> Homo sapiens

<400> 2308
Xaa Phe Ser Ala Glu Gly Gly Asp Lys Ala Leu His Lys Met Gly Pro
1 5 10 15
Gly Gly Gly Lys Ala Lys Ala Leu Gly Gly Ala Gly Ser Gly Ser Lys
20 25 30
Gly Ser Ala Gly Gly Gly Ser Lys Arg Arg Leu Ser Ser Glu Asp Ser
35 40 45
Ser Leu Glu Pro Asp Leu Ala Glu Met Ser Leu Asp Asp Ser Ser Leu
50 55 60
Ala Leu Gly Ala Glu Ala Arg Thr Phe Gly Gly Phe Pro Glu Ser Pro

65 70 75 80
Pro Pro Cys Pro Leu His Gly Gly Ser Arg Gly Pro Ser Thr Phe Leu
85 90 95
Pro Glu Pro Pro Asp Thr Tyr Glu Glu Asp Gly Asp Glu Ser Gly Asn
100 105 110
Gly Leu Pro Lys Thr Lys Glu Ala
115 120

<210> 2309
<211> 395
<212> DNA
<213> Homo sapiens

<400> 2309
ggatccctac aaatggggcc ctgctctgag cacattccca tgagggctgc ctgccctgtg
60
cactctctgc cctgggccgc ggggcctgac tgggttccca cctcctccta cccactgggg
120
tcttttccag caggcacagg gattcctcat gggggaggca gagcccaccc gtctgtcctc
180
ggtgacggcc tgagctgtgc acggcctccc ctgccctcct gttctcaggc cccccagggt
240
ccatccagcc ccagcgtgtg gcgttctggc tcttccctgg agtctcctcc cagaccacgc
300
gactccactc acactgtgcc tagcggactg tgtggttgat gcagccggct cacttgagtg
360
tgttgtgtta tgcccacaac aggcttgccg tcacc
395

<210> 2310
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2310
Met Gly Pro Cys Ser Glu His Ile Pro Met Arg Ala Ala Cys Pro Val
1 5 10 15
His Ser Leu Pro Trp Ala Ala Gly Pro Asp Trp Val Pro Thr Ser Ser
20 25 30
Tyr Pro Leu Gly Ser Phe Pro Ala Gly Thr Gly Ile Pro His Gly Gly
35 40 45
Gly Arg Ala His Pro Ser Val Leu Gly Asp Gly Leu Ser Cys Ala Arg
50 55 60
Pro Pro Leu Pro Ser Cys Ser Gln Ala Pro Gln Gly Pro Ser Ser Pro
65 70 75 80
Ser Val Trp Arg Ser Gly Ser Ser Leu Glu Ser Pro Pro Arg Pro Arg
85 90 95
Asp Ser Thr His Thr Val Pro Ser Gly Leu Cys Gly
100 105

<210> 2311
<211> 378
<212> DNA
<213> Homo sapiens

<400> 2311
gtgcacgccg agatgctgcc gcaagacaag cagcgtgtcg tcggcgagtt gaagcgccag
60
ggcttctcag tgatcaaggt cggcgatggc atcaatgatt gcgacgctct cgccgcggcg
120
gatgtcggca gtcccatggg cggcagcgcg gacgtggctc tcgaaacggc cgatgctgcc
180
gtccttcacg gacgggtggg ggacgtcttc gcgatgatcg ccctatcgaa gcgaaccatg
240
gccaacattc gacagaacat cgcgatcgcg atcgggctaa aggcggtgtt ccttgtaacg
300
accgtcgtcg gcatcacggg gctttggcct gcaatcctcg ccgatacggg gaccacggag
360
cttgtgacca tgaacgcg
378

<210> 2312
<211> 126
<212> PRT
<213> Homo sapiens

<400> 2312
Val His Ala Glu Met Leu Pro Gln Asp Lys Gln Arg Val Val Gly Glu
 1   5   10   15
Leu Lys Arg Gln Gly Phe Ser Val Ile Lys Val Gly Asp Gly Ile Asn
            20   25   30
Asp Cys Asp Ala Leu Ala Ala Ala Asp Val Gly Ser Pro Met Gly Gly
        35   40   45
Ser Ala Asp Val Ala Leu Glu Thr Ala Asp Ala Ala Val Leu His Gly
    50   55   60
Arg Val Gly Asp Val Phe Ala Met Ile Ala Leu Ser Lys Arg Thr Met
65   70   75   80
Ala Asn Ile Arg Gln Asn Ile Ala Ile Ala Ile Gly Leu Lys Ala Val
                85   90   95
Phe Leu Val Thr Thr Val Val Gly Ile Thr Gly Leu Trp Pro Ala Ile
            100   105   110
Leu Ala Asp Thr Gly Thr Thr Glu Leu Val Thr Met Asn Ala
        115   120   125

<210> 2313
<211> 669
<212> DNA
<213> Homo sapiens

<400> 2313
ctagtggcat ggtctcgctg gtctttagtg gagcataccg acacatcggt gactcaaacg
60
atccgaatca tggctcgtcc tggttggcct ggaaccatta acgtacgcct cacccatcgc
120
ttaagcgacg ccggtctagc tgtcgaagtc accgcgcgca atgtcggtac gacagcgggg
180
ccgcttggat acgcagcaca cccctatctc tgtctgggtg gcaccatcga cgactggaca
240

gtcgacgccc cgtttacctc gtggttacag gtcgatgatc ggctgctacc aatgcagatg
300
cgcgagatgg acagcatcca cgcgctgaac ggtctcacgg gcggacagcg caccttcgat
360
accgcttaca ccgtgaaagg aggacggaac cgtcggatcg cccgcatggc gtatccgggt
420
ctcaacggtg aaacgagcca cgaattgtgg ggcgacgccg cgatgagctg ggtgcaagtc
480
tacactccag acgaccgcca cagtctggcc atcgagccaa tgacctgcgg cccagatgca
540
tttaatgagg gcccgaccca cggtgacgtc attcgactgg agcccggtaa tgacgtcaca
600
ctgcactggg gcatcgccta acccgcggaa gctcgaaagg acaaggacgg gaaggcagga
660
ttcacgcgt
669

<210> 2314
<211> 206
<212> PRT
<213> Homo sapiens

<400> 2314
Leu Val Ala Trp Ser Arg Trp Ser Leu Val Glu His Thr Asp Thr Ser
1 5 10 15
Val Thr Gln Thr Ile Arg Ile Met Ala Arg Pro Gly Trp Pro Gly Thr
20 25 30
Ile Asn Val Arg Leu Thr His Arg Leu Ser Asp Ala Gly Leu Ala Val
35 40 45
Glu Val Thr Ala Arg Asn Val Gly Thr Thr Ala Gly Pro Leu Gly Tyr
50 55 60
Ala Ala His Pro Tyr Leu Cys Leu Gly Gly Thr Ile Asp Asp Trp Thr
65 70 75 80
Val Asp Ala Pro Phe Thr Ser Trp Leu Gln Val Asp Asp Arg Leu Leu
85 90 95
Pro Met Gln Met Arg Glu Met Asp Ser Ile His Ala Leu Asn Gly Leu
100 105 110
Thr Gly Gly Gln Arg Thr Phe Asp Thr Ala Tyr Thr Val Lys Gly Gly
115 120 125
Arg Asn Arg Arg Ile Ala Arg Met Ala Tyr Pro Gly Leu Asn Gly Glu
130 135 140
Thr Ser His Glu Leu Trp Gly Asp Ala Ala Met Ser Trp Val Gln Val
145 150 155 160
Tyr Thr Pro Asp Asp Arg His Ser Leu Ala Ile Glu Pro Met Thr Cys
165 170 175
Gly Pro Asp Ala Phe Asn Glu Gly Pro Thr His Gly Asp Val Ile Arg
180 185 190
Leu Glu Pro Gly Asn Asp Val Thr Leu His Trp Gly Ile Ala
195 200 205

<210> 2315
<211> 546
<212> DNA
<213> Homo sapiens

<400> 2315
nacgcgtccc tcatcgatac cgagcccggg atgggaaaac gggtgtatcg cgttgaggcc
60
acccaaggcc gaccaattcg catcgataag gcggtcgctt atcacacttc tcgcggcgtg
120
ccggtacatg aactgtttga ccgagtgcgc cgcagcttag accgagtgcg tgaacagggg
180
cacaacgtct actacgacga acagcgtgca tggcttgacg attactgggc aacggctgat
240
gttgaggtcg agggtgcccc gaccggtatt cagcaggctg tcaggtggaa ccttttccag
300
attgctcagg catcagcccg tgcagatcaa cttggcattc cggcaaaggg tgtaaccggg
360
tcaggctatg aaggccacta cttttgggac actgaggttt atgtcatccc gatgttgacc
420
tacactcatc caagaatcgc tgagaatgcg ctgagattcc gggtgaatac ccttccgcaa
480
gctcgacgcc gggctaagga attgtctgaa cgaggcgccc ttttcccgtg gcgaacaatc
540
accggt
546

<210> 2316
<211> 182
<212> PRT
<213> Homo sapiens

<400> 2316
Xaa Ala Ser Leu Ile Asp Thr Glu Pro Gly Met Gly Lys Arg Val Tyr
 1   5   10   15
Arg Val Glu Ala Thr Gln Gly Arg Pro Ile Arg Ile Asp Lys Ala Val
            20   25   30
Ala Tyr His Thr Ser Arg Gly Val Pro Val His Glu Leu Phe Asp Arg
        35   40   45
Val Arg Arg Ser Leu Asp Arg Val Arg Glu Gln Gly His Asn Val Tyr
    50   55   60
Tyr Asp Glu Gln Arg Ala Trp Leu Asp Asp Tyr Trp Ala Thr Ala Asp
65   70   75   80
Val Glu Val Glu Gly Ala Pro Thr Gly Ile Gln Gln Ala Val Arg Trp
                85   90   95
Asn Leu Phe Gln Ile Ala Gln Ala Ser Ala Arg Ala Asp Gln Leu Gly
            100   105   110
Ile Pro Ala Lys Gly Val Thr Gly Ser Gly Tyr Glu Gly His Tyr Phe
        115   120   125
Trp Asp Thr Glu Val Tyr Val Ile Pro Met Leu Thr Tyr Thr His Pro
    130   135   140
Arg Ile Ala Glu Asn Ala Leu Arg Phe Arg Val Asn Thr Leu Pro Gln
145   150   155   160
Ala Arg Arg Arg Ala Lys Glu Leu Ser Glu Arg Gly Ala Leu Phe Pro
                165   170   175
Trp Arg Thr Ile Thr Gly
            180

<210> 2317
<211> 496
<212> DNA
<213> Homo sapiens

<400> 2317
gccggcgggc tcgggaacgg tcactgacct gcagcaggca atggcggtcg cggtttaatc
60
agggttctgc acggagtttt ggatagtccg tccagtcgcc actggcaagg cgcgaccagg
120
cagctgctga cgctgctgtg atgccgagga gatcggagac gattcgtggg tgcatctgcc
180
gggtcagttc gatcagcgcg gtcgttcgag cgcttcctga acgcagcccc tgctggcgca
240
gacgtcggct gagtgggcct ggtgtgagat gcaaccccgg attcctgcca ggaaagagcc
300
atccctcggg tcggtgtctc gatgtgtcag cgagctcggc gatcgcattc ccgaggacct
360
cgggcagttc gattggctcg gctccgatgg tgagcttccc cggtcgtgat gtcacgtcga
420
cctgctcacg ggtgagcgcg acgatgcgag tgaggtggag gccgtagagg agcacgagca
480
acccagcggc acgcgt
496

<210> 2318
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2318
Met Pro Arg Arg Ser Glu Thr Ile Arg Gly Cys Ile Cys Arg Val Ser
1 5 10 15
Ser Ile Ser Ala Val Val Arg Ala Leu Pro Glu Arg Ser Pro Cys Trp
20 25 30
Arg Arg Arg Arg Leu Ser Gly Pro Gly Val Arg Cys Asn Pro Gly Phe
35 40 45
Leu Pro Gly Lys Ser His Pro Ser Gly Arg Cys Leu Asp Val Ser Ala
50 55 60
Ser Ser Ala Ile Ala Phe Pro Arg Thr Ser Gly Ser Ser Ile Gly Ser
65 70 75 80
Ala Pro Met Val Ser Phe Pro Gly Arg Asp Val Thr Ser Thr Cys Ser
85 90 95
Arg Val Ser Ala Thr Met Arg Val Arg Trp Arg Pro
100 105

<210> 2319
<211> 1748
<212> DNA
<213> Homo sapiens

<400> 2319
ntgatcaagt ctcggtctct ggattatacc tttgttcctc gaacttggat ctttcctgct
60

gaatatactc aattccaaaa ttatgtgaaa gaattgaaga aaaaacggaa gcagaaaact
120
tttatagtga aaccagctaa tggtgcaatg ggtcatggga tttctttgat aagaaatggt
180
gacaaacttc catctcagga tcatttgatt gttcaagaat acattgaaaa gcctttccta
240
atggaaggtt acaagtttga cttacgaatt tatattctgg ttacatcgtg tgatccacta
300
aaaatatttc tctaccatga tgggcttgtg cgaatgggta cagagaagta cattccacct
360
aatgagtcca atttgaccca gttatacatg catctgacaa actactccgt gaacaagcat
420
aatgagcatt ttgaacggga tgaaactgag aacaaaggca gcaaacgttc catcaaatgg
480
tttacagaat tccttcaagc aaatcaacat gatgttgcta agttttggag tgatatttca
540
gaattggtgg taaagaccct gattgtagca gaacctcatg tcctgcatgc ctatcgaatg
600
tgtagacctg gtcaacctcc aggaagcgaa agtgtctgct ttgaagtcct gggatttgat
660
attttgttgg atagaaaact aaagccatgg cttctggaga ttaaccgagc cccaagcttt
720
ggaactgatc agaaaataga ctatgatgta aaaaggggag tgctgctaaa tgcgttgaag
780
ctactaaaca taaggaccag tgacaaaaga agaaacttgg ccaaacaaaa agctgaggct
840
caaaggaggc tctatggtca aaattcaatt aaaaggctct taccaggctc ctcagactgg
900
gaacagcaga gacaccagtt ggagaggcgg aaagaagagt tgaaagagag actcgctcaa
960
gtacgaaagc agatctcacg agaagaacat gaaaatcgac atatggggaa ttatagacga
1020
atttatcctc ctgaagataa agcattactt gaaaagtatg aaaatttgtt agctgttgcc
1080
tttcagacct tcctttcagg aagagcagct tcattccagc gagagttgaa taatcctttg
1140
aaaaggatga aggaagaaga tattttggat cttctggagc aatgtgaaat tgatgatgaa
1200
aagttgatgg gaaaaactac caagactcga ggaccaaagc ctctgtgttc tatgcctgag
1260
agtactgaga taatgaaaag accaaagtac tgcagcagtg acagcagtta tgatagtagc
1320
agcagctctt cagaatctga cgaaaatgaa aaagaagagt accaaaataa gaaaagagaa
1380
aagcaagtta catataatct taaaccctcc aaccactaca aattaattca acaacccagc
1440
tccataagac gttcagtcag ctgccctcgg tccatctctg ctcaatcacc ttccagtggg
1500
gacacccgcc cattttctgc tcaacaaatg atatctgtgt cacggccaac ttctgcatct
1560
cggtcacatt ccttaaaccc gggccttcct cctacatgag gcatctgcct cacagtaatg
1620
atgcctgctc taccaactct caagtgagtg agtctttgcg gcaactgaaa acaaaagaac
1680

aagaagatga tctaacaagt cagaccttat ttgttctcaa agacatgaag atccggtttc
1740
caggaaag
1748

<210> 2320
<211> 532
<212> PRT
<213> Homo sapiens

<400> 2320
Xaa Ile Lys Ser Arg Ser Leu Asp Tyr Thr Phe Val Pro Arg Thr Trp
 1   5   10   15
Ile Phe Pro Ala Glu Tyr Thr Gln Phe Gln Asn Tyr Val Lys Glu Leu
            20   25   30
Lys Lys Lys Arg Lys Gln Lys Thr Phe Ile Val Lys Pro Ala Asn Gly
        35   40   45
Ala Met Gly His Gly Ile Ser Leu Ile Arg Asn Gly Asp Lys Leu Pro
    50   55   60
Ser Gln Asp His Leu Ile Val Gln Glu Tyr Ile Glu Lys Pro Phe Leu
65   70   75   80
Met Glu Gly Tyr Lys Phe Asp Leu Arg Ile Tyr Ile Leu Val Thr Ser
                85   90   95
Cys Asp Pro Leu Lys Ile Phe Leu Tyr His Asp Gly Leu Val Arg Met
            100   105   110
Gly Thr Glu Lys Tyr Ile Pro Pro Asn Glu Ser Asn Leu Thr Gln Leu
        115   120   125
Tyr Met His Leu Thr Asn Tyr Ser Val Asn Lys His Asn Glu His Phe
    130   135   140
Glu Arg Asp Glu Thr Glu Asn Lys Gly Ser Lys Arg Ser Ile Lys Trp
145   150   155   160
Phe Thr Glu Phe Leu Gln Ala Asn Gln His Asp Val Ala Lys Phe Trp
                165   170   175
Ser Asp Ile Ser Glu Leu Val Val Lys Thr Leu Ile Val Ala Glu Pro
            180   185   190
His Val Leu His Ala Tyr Arg Met Cys Arg Pro Gly Gln Pro Pro Gly
        195   200   205
Ser Glu Ser Val Cys Phe Glu Val Leu Gly Phe Asp Ile Leu Leu Asp
    210   215   220
Arg Lys Leu Lys Pro Trp Leu Leu Glu Ile Asn Arg Ala Pro Ser Phe
225   230   235   240
Gly Thr Asp Gln Lys Ile Asp Tyr Asp Val Lys Arg Gly Val Leu Leu
                245   250   255
Asn Ala Leu Lys Leu Leu Asn Ile Arg Thr Ser Asp Lys Arg Arg Asn
            260   265   270
Leu Ala Lys Gln Lys Ala Glu Ala Gln Arg Arg Leu Tyr Gly Gln Asn
        275   280   285
Ser Ile Lys Arg Leu Leu Pro Gly Ser Ser Asp Trp Glu Gln Gln Arg
    290   295   300
His Gln Leu Glu Arg Arg Lys Glu Glu Leu Lys Glu Arg Leu Ala Gln
305   310   315   320
Val Arg Lys Gln Ile Ser Arg Glu Glu His Glu Asn Arg His Met Gly
                325   330   335
Asn Tyr Arg Arg Ile Tyr Pro Pro Glu Asp Lys Ala Leu Leu Glu Lys

```
            340                 345                 350
Tyr Glu Asn Leu Leu Ala Val Ala Phe Gln Thr Phe Leu Ser Gly Arg
        355                 360                 365
Ala Ala Ser Phe Gln Arg Glu Leu Asn Asn Pro Leu Lys Arg Met Lys
    370                 375                 380
Glu Glu Asp Ile Leu Asp Leu Leu Glu Gln Cys Glu Ile Asp Asp Glu
385                 390                 395                 400
Lys Leu Met Gly Lys Thr Thr Lys Thr Arg Gly Pro Lys Pro Leu Cys
                405                 410                 415
Ser Met Pro Glu Ser Thr Glu Ile Met Lys Arg Pro Lys Tyr Cys Ser
            420                 425                 430
Ser Asp Ser Ser Tyr Asp Ser Ser Ser Ser Ser Ser Glu Ser Asp Glu
        435                 440                 445
Asn Glu Lys Glu Glu Tyr Gln Asn Lys Lys Arg Glu Lys Gln Val Thr
    450                 455                 460
Tyr Asn Leu Lys Pro Ser Asn His Tyr Lys Leu Ile Gln Gln Pro Ser
465                 470                 475                 480
Ser Ile Arg Arg Ser Val Ser Cys Pro Arg Ser Ile Ser Ala Gln Ser
                485                 490                 495
Pro Ser Ser Gly Asp Thr Arg Pro Phe Ser Ala Gln Gln Met Ile Ser
            500                 505                 510
Val Ser Arg Pro Thr Ser Ala Ser Arg Ser His Ser Leu Asn Pro Gly
        515                 520                 525
Leu Pro Pro Thr
    530
```

<210> 2321
<211> 433
<212> DNA
<213> Homo sapiens

<400> 2321
caattgtgtg gacgtgtcta tgtgtgtttc taattctata ctatcttgaa aatggttcag
60
cgttctagaa atacagccac ataatttttt ttgttttgaa aaactgctca gcaaatgcat
120
acaggtcata atggcaggta acagaccatt tattgaagtg ctgaaacaaa tagaaaacaa
180
agtccaggac accatcacag agcagtactt cccttgtgag atactctcag ctaagtaaga
240
attgagtgag acaacaataa aacaaatacc cataggcttt tcaaacagta acaacccgct
300
cagggttagc agcatttcta gaccttgatg gtaaaatgat gttctcaacc tttgctttca
360
gacactggat cactgcttaa gtagccttta tcttttcccc ctaatttttg ttgaagatgc
420
cagaggtgga gtg
433

<210> 2322
<211> 105
<212> PRT
<213> Homo sapiens

<400> 2322
Met Leu Leu Thr Leu Ser Gly Leu Leu Leu Phe Glu Lys Pro Met Gly
1 5 10 15
Ile Cys Phe Ile Val Val Ser Leu Asn Ser Tyr Leu Ala Glu Ser Ile
20 25 30
Ser Gln Gly Lys Tyr Cys Ser Val Met Val Ser Trp Thr Leu Phe Ser
35 40 45
Ile Cys Phe Ser Thr Ser Ile Asn Gly Leu Leu Pro Ala Ile Met Thr
50 55 60
Cys Met His Leu Leu Ser Ser Phe Ser Lys Gln Lys Lys Leu Cys Gly
65 70 75 80
Cys Ile Ser Arg Thr Leu Asn His Phe Gln Asp Ser Ile Glu Leu Glu
85 90 95
Thr His Ile Asp Thr Ser Thr Gln Leu
100 105

<210> 2323
<211> 532
<212> DNA
<213> Homo sapiens

<400> 2323
acgcgtcaaa actggcaaag ctggcggctt agggggaggg gcaagtggac ttggaggccc
60
tcctccactg tgcacccccc tggaaaaaaa gcggaggggg catcaagtaa aagtttcttg
120
ccaggcagag ccagctcggc ggcccccccgc acatagctgg ggttagcagg ggttgcttct
180
ctgccgggca cagcgntctc caggagccag ccggggagag ctgagccaag gccgaaggag
240
ccgcctgcgg gcttagccgc cccctcccgc ccgttggccc cagagcggac gctgggacgc
300
ccggggtctg gcagctctgc gcccggctag gagcgggcgg gcgagcatta gcctgcgtcc
360
tggagaaggg gcgcagcgcc gcagttgagg ccgaagcagc ccctcgcggg cgtaggatac
420
ctgtcagtga gcgcccggat tgcacggccc ccgggtagtg cctgccggcg aggggcggga
480
gctcgggtga cttggccatc cccatccccg gcccaggccc ggagggcggc cg
532

<210> 2324
<211> 51
<212> PRT
<213> Homo sapiens

<400> 2324
Thr Arg Gln Asn Trp Gln Ser Trp Arg Leu Arg Gly Arg Gly Lys Trp
1 5 10 15
Thr Trp Arg Pro Ser Ser Thr Val His Pro Leu Gly Lys Lys Ala Glu
20 25 30
Gly Ala Ser Ser Lys Ser Phe Leu Pro Gly Arg Ala Ser Ser Ala Ala
35 40 45
Pro Arg Thr

50

<210> 2325
<211> 459
<212> DNA
<213> Homo sapiens

<400> 2325
nnacgcgtgc aggaccgcat gagcgccatc tgggagagag gagtggttgg aggaaagatg
60
gatgagaacc gttttgtggc cgttaccagt tccaacgcag ctaagcttct gaacctgtat
120
ccccgcaagg gccgcattat tcccggagcc gatgctgatg tggtggtgtg ggacccagaa
180
gccacaaaga ccatctcagc cagcacgcag gtccagggag gagacttcaa cctgtatgag
240
aacatgcgct gccacggcgt gccactggtc accatcagcc gggggcgcgt cgtgtatgag
300
aacggcgtct tcatgtgcgc cgagggcacc ggcaagttct gtcccctgag gtccttccca
360
gacactgtct acaagaagct ggtccagaga gagaagactt taaaggttag aggagtggcc
420
cgcactccct acctgggggа tgtcgctgtt gtcgtgcac
459

<210> 2326
<211> 153
<212> PRT
<213> Homo sapiens

<400> 2326
Xaa Arg Val Gln Asp Arg Met Ser Ala Ile Trp Glu Arg Gly Val Val
1 5 10 15
Gly Gly Lys Met Asp Glu Asn Arg Phe Val Ala Val Thr Ser Ser Asn
20 25 30
Ala Ala Lys Leu Leu Asn Leu Tyr Pro Arg Lys Gly Arg Ile Ile Pro
35 40 45
Gly Ala Asp Ala Asp Val Val Val Trp Asp Pro Glu Ala Thr Lys Thr
50 55 60
Ile Ser Ala Ser Thr Gln Val Gln Gly Gly Asp Phe Asn Leu Tyr Glu
65 70 75 80
Asn Met Arg Cys His Gly Val Pro Leu Val Thr Ile Ser Arg Gly Arg
85 90 95
Val Val Tyr Glu Asn Gly Val Phe Met Cys Ala Glu Gly Thr Gly Lys
100 105 110
Phe Cys Pro Leu Arg Ser Phe Pro Asp Thr Val Tyr Lys Lys Leu Val
115 120 125
Gln Arg Glu Lys Thr Leu Lys Val Arg Gly Val Ala Arg Thr Pro Tyr
130 135 140
Leu Gly Asp Val Ala Val Val Val His
145 150

<210> 2327
<211> 599

<212> DNA
<213> Homo sapiens

<400> 2327
gaattccaga agatcaagta ttcctacgat gccctggaga agaagcagtt tctccccgtg
60
gcctttcctg tgggaaacgc cttctcatac tatcagagca acagaggctt ccaggaagac
120
tcagagatcc gagcagctga gaagaaattt gggagcaaca aggccgagat ggtggtgcct
180
gacttctcgg agcttttcaa ggagagagcc acagcccccc tctttgtatt tcaggtgttc
240
tgtgtggggc tctggtgcct ggatgagtac tggtactaca gcgtctttac gctatccatg
300
ctggtggcgt tcgaggcctc gctggtgcag cagcagatgc ggaacatgtc ggagatccgg
360
aagatgggca acaagcccca catgatccag gtctaccgaa gccgcaagtg gaggcccatt
420
gccagtgatg agatcgtacc aggggacatc gtctccatcg gtgaggccgg gttccgctca
480
gtcccagtgg gagccccagc ctcagggcct ctggccaacc ctcctgcctc tgccctgcag
540
gccgctcccc acaggagaac ctggtgccat gtgacgtgct tctgctgcga ggccgctgc
599

<210> 2328
<211> 199
<212> PRT
<213> Homo sapiens

<400> 2328
Glu Phe Gln Lys Ile Lys Tyr Ser Tyr Asp Ala Leu Glu Lys Lys Gln
 1   5   10   15
Phe Leu Pro Val Ala Phe Pro Val Gly Asn Ala Phe Ser Tyr Tyr Gln
            20   25   30
Ser Asn Arg Gly Phe Gln Glu Asp Ser Glu Ile Arg Ala Ala Glu Lys
        35   40   45
Lys Phe Gly Ser Asn Lys Ala Glu Met Val Val Pro Asp Phe Ser Glu
    50   55   60
Leu Phe Lys Glu Arg Ala Thr Ala Pro Phe Phe Val Phe Gln Val Phe
65   70   75   80
Cys Val Gly Leu Trp Cys Leu Asp Glu Tyr Trp Tyr Tyr Ser Val Phe
                85   90   95
Thr Leu Ser Met Leu Val Ala Phe Glu Ala Ser Leu Val Gln Gln Gln
            100   105   110
Met Arg Asn Met Ser Glu Ile Arg Lys Met Gly Asn Lys Pro His Met
        115   120   125
Ile Gln Val Tyr Arg Ser Arg Lys Trp Arg Pro Ile Ala Ser Asp Glu
    130   135   140
Ile Val Pro Gly Asp Ile Val Ser Ile Gly Glu Ala Gly Phe Arg Ser
145   150   155   160
Val Pro Val Gly Ala Pro Ala Ser Gly Pro Leu Ala Asn Pro Pro Ala
                165   170   175
Ser Ala Leu Gln Ala Ala Pro His Arg Arg Thr Trp Cys His Val Thr

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            180                 185                 190
Cys Phe Cys Cys Glu Ala Ala
        195
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<210> 2329
<211> 392
<212> DNA
<213> Homo sapiens

<400> 2329
acgcgttcca tgaatgctgg tgcggctgcc gcgattgcta tgtacgcctg gacgacgcag
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tggtgtccaa agccacgcac tagctgatcg gggagaaccg tcaccctcta ggctcgtgtc
120
atgagcacgc aacccactga ggaaccactc cgactagttg tggcattcaa tccagtgcct
180
agtgcctccc gggttgctca tcatcatgcg acgagatttc gcctggcggt gcaggccttc
240
attgtcgtcg tcattggtgg tttgttgtgg gcgttgacgg ccgacgcctt ccagttatcg
300
acggtgatgt ggatgctcgg ggcatgggtg gtgctattcc tcgtgctttt cgtcatccag
360
aatctgcggc tgcacgccgc tcgcaaggat cc
392

<210> 2330
<211> 90
<212> PRT
<213> Homo sapiens

<400> 2330
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Met Ser Thr Gln Pro Thr Glu Glu Pro Leu Arg Leu Val Val Ala Phe
 1               5                  10                  15
Asn Pro Val Pro Ser Ala Ser Arg Val Ala His His His Ala Thr Arg
            20                  25                  30
Phe Arg Leu Ala Val Gln Ala Phe Ile Val Val Val Ile Gly Gly Leu
        35                  40                  45
Leu Trp Ala Leu Thr Ala Asp Ala Phe Gln Leu Ser Thr Val Met Trp
    50                  55                  60
Met Leu Gly Ala Trp Val Val Leu Phe Leu Val Leu Phe Val Ile Gln
65                  70                  75                  80
Asn Leu Arg Leu His Ala Ala Arg Lys Asp
                85                  90
```

<210> 2331
<211> 2813
<212> DNA
<213> Homo sapiens

<400> 2331
nnggagcaag agagttatta aaagtgggtg gaagacttcc tggtgcagga ggctcactcc
60
gatttaaggt gcccgagtcc acgctgatgg actgccgtag acaactgaaa gacagtaagc
120

aaattttatc tattacaaag aactttaaag ttgagaatat tggacctctt cctataactg
180
tttcgtctct gaaaattaat gggtataact gccaaggtta tggattcgag gtgctggatt
240
gggattcagt ttcccctgga cccaaacaca tcccgcgata tcagcattgt gttcactcca
300
gactttacct cctcctgggt aattcgggac ctaagtcttg taaccgcagc ggacctagaa
360
tttcgcttca ctctcaatgt gactctccct catcacctgt tgcccttgtg tgcagacgtg
420
gttccaggac ccagctggga ggagtcattt tggaggctca cggtcttctt tgtcagtttg
480
tccctgttgg gtgtgatttt aatagccttc caacaagcac agtacattct catggaattc
540
atgaaaacaa gacagaggca aaatgctagc tcctcttcac agcaaaacaa tggtcctatg
600
gatgtaatca gcccccattc ttacaaaagc aattgcaaga actttctcga tacatatggc
660
ccctctgata aaggcagggg gaagaactgc cttccagtga acactcccca aagcaggatc
720
cagaatgctg caaagaggag cccagccacc tatggtcatt ctcagaagaa gcacaaatgc
780
tcagtgtatt acagtaaaca caaaaccagc acagctgcgg ccagcagcac cagcacgact
840
actgaggaaa aacagacttc acccctgggc agctcactgc ctgctgctaa agaggacatt
900
tgcactgatg ccatgcgtga gaactggatc agcctcagat atgcaagtgg cataaatgtc
960
aacctgcaga agaatttaac ccttcccaaa aacttactga ataaagaaga aaacacactg
1020
aaaaacacaa ttgttttcag taatccttct tcagaatgta gtatgaagga gggaatacag
1080
acatgtatgt ttcctaagga aactgacatt aaaacttcag agaacacagc tgagttcaag
1140
gaacgggagc tctgtccact gaagacctcc aagaaactac ctgaaaacca tttaccaaga
1200
aactcacctc agtaccacca gccagacttg ccagaaattt ccaggaaaaa taatgggaat
1260
aaccagcaag tacctgtcaa gaatgaagta gatcattgtg aaaatttgaa gaaggtggac
1320
acaaagcctt cttcagaaaa gaagattcac aaaacatcta gagaagacat gttttctgag
1380
aaacaggaca tacctttcgt agagcaagaa gatccttata ggaagaaaaa gcttcaggag
1440
aaaagagaag gaaatttaca aaatttaaat tggagtaaaa gtcgaacatg tagaaagaac
1500
aagaaaaggg gtgttgctcc agtctcaagg cctcctgaac agagtgatct aaagcttgtg
1560
tgcagtgact ttgagaggtc tgagctgagc agtgacatca atgtaagaag ctggtgtata
1620
caggaaagca ctagggaggt ttgtaaagca gatgccgaaa ttgcaagcag tttacctgct
1680
gcccagagag aggcaggtta ctaccagaag cctgagaaga aatgtgtgga caagttctgc
1740

tccgattcca gctctgactg tgggagctcc tctggcagcg tgcgtgccag ccggggcagc
1800
tgggggagct ggagcagcac cagcagctcc gacggggata agaagcccat ggtggacgcc
1860
cagcacttcc tgccggccgg agacagtgtt tcacaaaatg attttccttc tgaagctccc
1920
atctccttga atctttctca taacatctgc aatcccatga ccgtgaatag tctcccacaa
1980
tacgcagagc cttcctgtcc cagccttcct gccgggccca caggtgttga agaagataaa
2040
ggtctttact cacctggaga cctgtggccc actccgccag tgtgtgtgac aagcagctta
2100
aactgcaccc tggagaacgg cgtgccttgt gtgattcagg agtcggcccc ggttcataat
2160
agtttcattg attggagtgc aacatgcgaa ggccagtttt ccagcgcata ctgtccattg
2220
gaattgaacg attacaatgc ctttccagaa gaaaacatga actatgccaa tggcttcccc
2280
tgtcctgcag atgttcagac agactttatt gatcacaact ctcagtctac ctggaacacc
2340
ccacccaaca tgcctgctgc ctggggacat gccagtttca tcagctctcc gccctacctc
2400
acaagcaccc gaagcttgtc tccaatgtct ggacttttg gttccatctg ggccccgcaa
2460
agcgatgtgt atgaaaattg ctgccccatc aaccccacca cggaacattc gacccacatg
2520
gaaaaccaag cggtcgtgtg caaggaatac tacccggggt tcaacccgtt tcgcgcctat
2580
atgaacctgg acatatggac taccacagcg aataggaatg caaatttccc actgtctaga
2640
gactcgagtt actgtgggaa tgtgtgaaaa taattggatt tttaaacaat gtgaataaag
2700
aggcttgtgt tttgattact agtgtaaact ggttattgag atagattatg acattggtgg
2760
atattttggc acttttatat gaaaataaat tttttaatga aaaaaaaaaa aaa
2813

<210> 2332
<211> 789
<212> PRT
<213> Homo sapiens

<400> 2332
Pro Asp Phe Thr Ser Ser Trp Val Ile Arg Asp Leu Ser Leu Val Thr
1 5 10 15
Ala Ala Asp Leu Glu Phe Arg Phe Thr Leu Asn Val Thr Leu Pro His
20 25 30
His Leu Leu Pro Leu Cys Ala Asp Val Val Pro Gly Pro Ser Trp Glu
35 40 45
Glu Ser Phe Trp Arg Leu Thr Val Phe Phe Val Ser Leu Ser Leu Leu
50 55 60
Gly Val Ile Leu Ile Ala Phe Gln Gln Ala Gln Tyr Ile Leu Met Glu
65 70 75 80
Phe Met Lys Thr Arg Gln Arg Gln Asn Ala Ser Ser Ser Ser Gln Gln

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                85                  90                  95
Asn Asn Gly Pro Met Asp Val Ile Ser Pro His Ser Tyr Lys Ser Asn
            100                 105                 110
Cys Lys Asn Phe Leu Asp Thr Tyr Gly Pro Ser Asp Lys Gly Arg Gly
        115                 120                 125
Lys Asn Cys Leu Pro Val Asn Thr Pro Gln Ser Arg Ile Gln Asn Ala
    130                 135                 140
Ala Lys Arg Ser Pro Ala Thr Tyr Gly His Ser Gln Lys Lys His Lys
145                 150                 155                 160
Cys Ser Val Tyr Tyr Ser Lys His Lys Thr Ser Thr Ala Ala Ala Ser
                165                 170                 175
Ser Thr Ser Thr Thr Thr Glu Glu Lys Gln Thr Ser Pro Leu Gly Ser
            180                 185                 190
Ser Leu Pro Ala Ala Lys Glu Asp Ile Cys Thr Asp Ala Met Arg Glu
        195                 200                 205
Asn Trp Ile Ser Leu Arg Tyr Ala Ser Gly Ile Asn Val Asn Leu Gln
    210                 215                 220
Lys Asn Leu Thr Leu Pro Lys Asn Leu Leu Asn Lys Glu Glu Asn Thr
225                 230                 235                 240
Leu Lys Asn Thr Ile Val Phe Ser Asn Pro Ser Ser Glu Cys Ser Met
                245                 250                 255
Lys Glu Gly Ile Gln Thr Cys Met Phe Pro Lys Glu Thr Asp Ile Lys
            260                 265                 270
Thr Ser Glu Asn Thr Ala Glu Phe Lys Glu Arg Glu Leu Cys Pro Leu
        275                 280                 285
Lys Thr Ser Lys Lys Leu Pro Glu Asn His Leu Pro Arg Asn Ser Pro
    290                 295                 300
Gln Tyr His Gln Pro Asp Leu Pro Glu Ile Ser Arg Lys Asn Asn Gly
305                 310                 315                 320
Asn Asn Gln Gln Val Pro Val Lys Asn Glu Val Asp His Cys Glu Asn
                325                 330                 335
Leu Lys Lys Val Asp Thr Lys Pro Ser Ser Glu Lys Lys Ile His Lys
            340                 345                 350
Thr Ser Arg Glu Asp Met Phe Ser Glu Lys Gln Asp Ile Pro Phe Val
        355                 360                 365
Glu Gln Glu Asp Pro Tyr Arg Lys Lys Lys Leu Gln Glu Lys Arg Glu
    370                 375                 380
Gly Asn Leu Gln Asn Leu Asn Trp Ser Lys Ser Arg Thr Cys Arg Lys
385                 390                 395                 400
Asn Lys Lys Arg Gly Val Ala Pro Val Ser Arg Pro Pro Glu Gln Ser
                405                 410                 415
Asp Leu Lys Leu Val Cys Ser Asp Phe Glu Arg Ser Glu Leu Ser Ser
            420                 425                 430
Asp Ile Asn Val Arg Ser Trp Cys Ile Gln Glu Ser Thr Arg Glu Val
        435                 440                 445
Cys Lys Ala Asp Ala Glu Ile Ala Ser Ser Leu Pro Ala Ala Gln Arg
    450                 455                 460
Glu Ala Gly Tyr Tyr Gln Lys Pro Glu Lys Lys Cys Val Asp Lys Phe
465                 470                 475                 480
Cys Ser Asp Ser Ser Ser Asp Cys Gly Ser Ser Ser Gly Ser Val Arg
                485                 490                 495
Ala Ser Arg Gly Ser Trp Gly Ser Trp Ser Ser Thr Ser Ser Ser Asp
            500                 505                 510
Gly Asp Lys Lys Pro Met Val Asp Ala Gln His Phe Leu Pro Ala Gly
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        515                 520                 525
Asp Ser Val Ser Gln Asn Asp Phe Pro Ser Glu Ala Pro Ile Ser Leu
    530                 535                 540
Asn Leu Ser His Asn Ile Cys Asn Pro Met Thr Val Asn Ser Leu Pro
545                 550                 555                 560
Gln Tyr Ala Glu Pro Ser Cys Pro Ser Leu Pro Ala Gly Pro Thr Gly
                565                 570                 575
Val Glu Glu Asp Lys Gly Leu Tyr Ser Pro Gly Asp Leu Trp Pro Thr
            580                 585                 590
Pro Pro Val Cys Val Thr Ser Ser Leu Asn Cys Thr Leu Glu Asn Gly
        595                 600                 605
Val Pro Cys Val Ile Gln Glu Ser Ala Pro Val His Asn Ser Phe Ile
    610                 615                 620
Asp Trp Ser Ala Thr Cys Glu Gly Gln Phe Ser Ser Ala Tyr Cys Pro
625                 630                 635                 640
Leu Glu Leu Asn Asp Tyr Asn Ala Phe Pro Glu Glu Asn Met Asn Tyr
                645                 650                 655
Ala Asn Gly Phe Pro Cys Pro Ala Asp Val Gln Thr Asp Phe Ile Asp
            660                 665                 670
His Asn Ser Gln Ser Thr Trp Asn Thr Pro Pro Asn Met Pro Ala Ala
        675                 680                 685
Trp Gly His Ala Ser Phe Ile Ser Ser Pro Pro Tyr Leu Thr Ser Thr
    690                 695                 700
Arg Ser Leu Ser Pro Met Ser Gly Leu Phe Gly Ser Ile Trp Ala Pro
705                 710                 715                 720
Gln Ser Asp Val Tyr Glu Asn Cys Cys Pro Ile Asn Pro Thr Thr Glu
                725                 730                 735
His Ser Thr His Met Glu Asn Gln Ala Val Val Cys Lys Glu Tyr Tyr
            740                 745                 750
Pro Gly Phe Asn Pro Phe Arg Ala Tyr Met Asn Leu Asp Ile Trp Thr
        755                 760                 765
Thr Thr Ala Asn Arg Asn Ala Asn Phe Pro Leu Ser Arg Asp Ser Ser
    770                 775                 780
Tyr Cys Gly Asn Val
785

<210> 2333
<211> 501
<212> DNA
<213> Homo sapiens

<400> 2333
cgtatgattg gtgtgggaca aatactattc aacaagagta cctaaatcat tgtttaaggc
60
gaagtaataa atatgaatgg ggtgtatcat ataatgaaca acgaatatcc atatagtgca
120
gacgaagttc ttcacaaagc aaaatcatat ttgtcagcag atgaatatga gtatgtttta
180
aaaagctatc atattgctta tgaagcacat aaaggtcagt tccgaaaaaa cggattacca
240
tacattatgc atcctataca agttgcaggt attttaacag aaatgcgatt agacggaccg
300
acgattgtcg caggtttttt gcatgatgta attgaagata caccgtatac atttgaagat
360
```

gtaaaagaaa tgttcaatga agaagttgct cgaattgttg atggtgtgac gaagcttaaa
420
aaaataaaat accgctcaaa agaagaacaa caagctgaaa atcatcgcaa gttatttatt
480
gcgattgcca aagatgtacg c
501

<210> 2334
<211> 143
<212> PRT
<213> Homo sapiens

<400> 2334
Met Asn Gly Val Tyr His Ile Met Asn Asn Glu Tyr Pro Tyr Ser Ala
1 5 10 15
Asp Glu Val Leu His Lys Ala Lys Ser Tyr Leu Ser Ala Asp Glu Tyr
20 25 30
Glu Tyr Val Leu Lys Ser Tyr His Ile Ala Tyr Glu Ala His Lys Gly
35 40 45
Gln Phe Arg Lys Asn Gly Leu Pro Tyr Ile Met His Pro Ile Gln Val
50 55 60
Ala Gly Ile Leu Thr Glu Met Arg Leu Asp Gly Pro Thr Ile Val Ala
65 70 75 80
Gly Phe Leu His Asp Val Ile Glu Asp Thr Pro Tyr Thr Phe Glu Asp
85 90 95
Val Lys Glu Met Phe Asn Glu Glu Val Ala Arg Ile Val Asp Gly Val
100 105 110
Thr Lys Leu Lys Lys Ile Lys Tyr Arg Ser Lys Glu Glu Gln Gln Ala
115 120 125
Glu Asn His Arg Lys Leu Phe Ile Ala Ile Ala Lys Asp Val Arg
130 135 140

<210> 2335
<211> 387
<212> DNA
<213> Homo sapiens

<400> 2335
ggatcctgag cgtggggact tctttgcact ccacagaacc ctcacttgta cctctacttt
60
tctctgcaga tggaccacac agcattcccc tgtggctgct gcagggaggg ctgtgagaac
120
cccatgggcc gtgtggaatt taatcaggca agagttcaga cccatttcat ccacacactc
180
acccgcctgc agttggaaca ggaggctgag agctttaggg agctggaggc ccctgcccag
240
ggcagcccac ccagccctgg tgaggaggcc ctggtcccta ctttcccact ggccaagccc
300
cccatgaaca atgagctggg agacaacagc tgcagcagcg acatgactga ttcttccaca
360
gcatcttcat cagcatcggg cactagt
387

<210> 2336

<211> 106
<212> PRT
<213> Homo sapiens

<400> 2336
Met Asp His Thr Ala Phe Pro Cys Gly Cys Cys Arg Glu Gly Cys Glu
1 5 10 15
Asn Pro Met Gly Arg Val Glu Phe Asn Gln Ala Arg Val Gln Thr His
20 25 30
Phe Ile His Thr Leu Thr Arg Leu Gln Leu Glu Gln Glu Ala Glu Ser
35 40 45
Phe Arg Glu Leu Glu Ala Pro Ala Gln Gly Ser Pro Pro Ser Pro Gly
50 55 60
Glu Glu Ala Leu Val Pro Thr Phe Pro Leu Ala Lys Pro Pro Met Asn
65 70 75 80
Asn Glu Leu Gly Asp Asn Ser Cys Ser Ser Asp Met Thr Asp Ser Ser
85 90 95
Thr Ala Ser Ser Ser Ala Ser Gly Thr Ser
100 105

<210> 2337
<211> 359
<212> DNA
<213> Homo sapiens

<400> 2337
ngagaagagg aggagtcatc ggcaggggcc ggcatctcca ggcctcgcca agccgctggg
60
accatgtgca gctcaagaat ggcctccggc ccatcggcct cggggcaggg gaagggcagc
120
ttctctgcac cagcttccct gctgggctcc agggcccaca ggctgaggcc gggggcccag
180
gggtcaatgc caggcaccct gctattgagg aacctatcca ggaggaagga ctcgggcaga
240
cctgcgggat cctcgtcctc ccacgggtcc tcatggcaga agcagaagga gctggagtcg
300
ctgaggtccg tgggcaggcg ggctgggccc aacgtggggt caccgacctc ctcaaagct
359

<210> 2338
<211> 98
<212> PRT
<213> Homo sapiens

<400> 2338
Met Cys Ser Ser Arg Met Ala Ser Gly Pro Ser Ala Ser Gly Gln Gly
1 5 10 15
Lys Gly Ser Phe Ser Ala Pro Ala Ser Leu Leu Gly Ser Arg Ala His
20 25 30
Arg Leu Arg Pro Gly Ala Gln Gly Ser Met Pro Gly Thr Leu Leu Leu
35 40 45
Arg Asn Leu Ser Arg Arg Lys Asp Ser Gly Arg Pro Ala Gly Ser Ser
50 55 60
Ser Ser His Gly Ser Ser Trp Gln Lys Gln Lys Glu Leu Glu Ser Leu

65 70 75 80
Arg Ser Val Gly Arg Arg Ala Gly Pro Asn Val Gly Ser Pro Thr Ser
85 90 95
Ser Lys

<210> 2339
<211> 439
<212> DNA
<213> Homo sapiens

<400> 2339
acgcgtggcg tcagtccagg cagacttggg aggtcgccta caccgtcaac tcggttgcga
60
ccctgtcctc caccttcgtc gtcgcagtcg tcagtgtcct gtggtttgtg ccctccgggc
120
actggtcccg gtagggcttg taatgctggg gcgctcggcg cgatgtgcca gttccttggt
180
gagttactcc tctacactgg tgtgaacaag accggagaat tccccccccat attctcgttt
240
cccgctcgtc ccgcacgtca ttgggactgg cttttacgcg gtagtggttg ccgtactctg
300
gttgctctgc ggcacggtcg gcaggggggat catgtcatga gtccgacggt gagcgagcgg
360
cgtcttagcg cgccaatgcg acgtggcatc gtggcactgt gcgtggcgat ggccttcgtg
420
ttgtcggggt gcggtgctg
439

<210> 2340
<211> 92
<212> PRT
<213> Homo sapiens

<400> 2340
Met Cys Gln Phe Leu Gly Glu Leu Leu Leu Tyr Thr Gly Val Asn Lys
1 5 10 15
Thr Gly Glu Phe Pro Pro Ile Phe Ser Phe Pro Ala Arg Pro Ala Arg
20 25 30
His Trp Asp Trp Leu Leu Arg Gly Ser Gly Cys Arg Thr Leu Val Ala
35 40 45
Leu Arg His Gly Arg Gln Gly Asp His Val Met Ser Pro Thr Val Ser
50 55 60
Glu Arg Arg Leu Ser Ala Pro Met Arg Arg Gly Ile Val Ala Leu Cys
65 70 75 80
Val Ala Met Ala Phe Val Leu Ser Gly Cys Gly Ala
85 90

<210> 2341
<211> 411
<212> DNA
<213> Homo sapiens

<400> 2341

gccaaacctc ccctccatcc tgcccaagat ggatcttgct gagcctccct ggcatatgcc
60
tctgcaggag gagccagagg aggtcacgga ggaggaggag gaaagggaag aagaggagag
120
ggagaaggaa gcagaggagg aggaggaaga ggaagagctg ctcctgtgag cgggtcccca
180
ggagccaccg cacaggccca tgccccttca cctagcacca gcagcagcac cagcagccag
240
agtcctgggg ccacccggca caggcaggag gattctggag accaggccac atcaggcnat
300
ggaagtggag agcagtgtga aacccacctt gtcagtgccc tcagtcaccc caagtacagt
360
ggccccgggg gttcagaact atagccagga gtctgggggc actgagtggc n
411

<210> 2342
<211> 113
<212> PRT
<213> Homo sapiens

<400> 2342
Ala Ser Leu Ala Tyr Ala Ser Ala Gly Gly Ala Arg Gly Gly His Gly
 1   5   10   15
Gly Gly Gly Gly Lys Gly Arg Arg Gly Glu Gly Glu Gly Ser Arg Gly
            20   25   30
Gly Gly Gly Arg Gly Arg Ala Ala Pro Val Ser Gly Ser Pro Gly Ala
        35   40   45
Thr Ala Gln Ala His Ala Pro Ser Pro Ser Thr Ser Ser Ser Thr Ser
    50   55   60
Ser Gln Ser Pro Gly Ala Thr Arg His Arg Gln Glu Asp Ser Gly Asp
65   70   75   80
Gln Ala Thr Ser Gly Xaa Gly Ser Gly Glu Gln Cys Glu Thr His Leu
                85   90   95
Val Ser Ala Leu Ser His Pro Lys Tyr Ser Gly Pro Gly Gly Ser Glu
            100   105   110
Leu

<210> 2343
<211> 522
<212> DNA
<213> Homo sapiens

<400> 2343
ggcccgcaga agatgctgat gccttcacag tttcccaacc agggccagca gggattctct
60
ggaggccagg gaccctacca agccatgtcc caggacatgg gcaataccca agacatgttc
120
agccctgatc agagctcaat gcccatgagc aacgtgggca ccacccggct cagccacatg
180
cctctgcccc ctgcgtccaa tcctcctggg accgtgcatt cagccccaaa ccgggggcta
240
ggcaggcggc cttcggacct caccatcagt attaatcaga tgggctcacc gggcatgggg
300

cacttgaagt cgcccaccct tagccaggtg cactcacccc tggtcacctc gccctctgcc
360
aacctcaagt caccccagac tccctcacag atggtgccct tgccttctgc caacccgcca
420
ggacctctca agtcgcccca ggtcctcggc tcctccctca gtgtccgttc acccactggc
480
tcgcccagca ggctcaagtc tccttccatg gcggtgcctt ct
522

<210> 2344
<211> 174
<212> PRT
<213> Homo sapiens

<400> 2344
Gly Pro Gln Lys Met Leu Met Pro Ser Gln Phe Pro Asn Gln Gly Gln
1 5 10 15
Gln Gly Phe Ser Gly Gly Gln Gly Pro Tyr Gln Ala Met Ser Gln Asp
20 25 30
Met Gly Asn Thr Gln Asp Met Phe Ser Pro Asp Gln Ser Ser Met Pro
35 40 45
Met Ser Asn Val Gly Thr Thr Arg Leu Ser His Met Pro Leu Pro Pro
50 55 60
Ala Ser Asn Pro Pro Gly Thr Val His Ser Ala Pro Asn Arg Gly Leu
65 70 75 80
Gly Arg Arg Pro Ser Asp Leu Thr Ile Ser Ile Asn Gln Met Gly Ser
85 90 95
Pro Gly Met Gly His Leu Lys Ser Pro Thr Leu Ser Gln Val His Ser
100 105 110
Pro Leu Val Thr Ser Pro Ser Ala Asn Leu Lys Ser Pro Gln Thr Pro
115 120 125
Ser Gln Met Val Pro Leu Pro Ser Ala Asn Pro Pro Gly Pro Leu Lys
130 135 140
Ser Pro Gln Val Leu Gly Ser Ser Leu Ser Val Arg Ser Pro Thr Gly
145 150 155 160
Ser Pro Ser Arg Leu Lys Ser Pro Ser Met Ala Val Pro Ser
165 170

<210> 2345
<211> 561
<212> DNA
<213> Homo sapiens

<400> 2345
nagatctccg tcttgatctt gagcaccgag gcactggggg gggaggacag cagccgcggg
60
ggcctccacc agcccgcgtc caggccgcct gggctcgacg cgctggacag gcgccggcgg
120
ctggcgctgc cgccctttg ccgtttccgc cttttcttgc gcttctggtg cttgctggag
180
gcctgcgcgc ccgcctcgcc tgcgctgtcc gagtccttgg cgctgtcgga cgtgagtgac
240
tcgcagttct gcagccgcag gtccgactcg ctctccacca tagctattaa tgccaagaat
300

gcaaatgaaa agaatatcat ctgggtgaat taccttctta gcaatcctga gtacaaggac
360
acacccatgg acatcgcaca gctcccccat ctgccggaga aaacttccga atcctcggag
420
acatccgact ctgagtcaga ctctaaagac acctcaggta ttacagagga caacgagaac
480
tccaagnntc cgacgagaag gggaaccagt ccgagaacag cgaagacccg gagcccgacc
540
ggaagaagtc gggcaacgcg t
561

<210> 2346
<211> 187
<212> PRT
<213> Homo sapiens

<400> 2346
Xaa Ile Ser Val Leu Ile Leu Ser Thr Glu Ala Leu Gly Gly Glu Asp
1 5 10 15
Ser Ser Arg Gly Gly Leu His Gln Pro Ala Ser Arg Pro Pro Gly Leu
20 25 30
Asp Ala Leu Asp Arg Arg Arg Arg Leu Ala Leu Pro Pro Phe Cys Arg
35 40 45
Phe Arg Leu Phe Leu Arg Phe Trp Cys Leu Leu Glu Ala Cys Ala Pro
50 55 60
Ala Ser Pro Ala Leu Ser Glu Ser Leu Ala Leu Ser Asp Val Ser Asp
65 70 75 80
Ser Gln Phe Cys Ser Arg Arg Ser Asp Ser Leu Ser Thr Ile Ala Ile
85 90 95
Asn Ala Lys Asn Ala Asn Glu Lys Asn Ile Ile Trp Val Asn Tyr Leu
100 105 110
Leu Ser Asn Pro Glu Tyr Lys Asp Thr Pro Met Asp Ile Ala Gln Leu
115 120 125
Pro His Leu Pro Glu Lys Thr Ser Glu Ser Ser Glu Thr Ser Asp Ser
130 135 140
Glu Ser Asp Ser Lys Asp Thr Ser Gly Ile Thr Glu Asp Asn Glu Asn
145 150 155 160
Ser Lys Xaa Pro Thr Arg Arg Gly Thr Ser Pro Arg Thr Ala Lys Thr
165 170 175
Arg Ser Pro Thr Gly Arg Ser Arg Ala Thr Arg
180 185

<210> 2347
<211> 375
<212> DNA
<213> Homo sapiens

<400> 2347
atcagcgaag aacacggcag gaccctggaa gacgccgccg gtgaattgaa gcgtggtatc
60
gagaacgtcg agtacgcctg cgccgcgccg gaagtactga agggtgaata cagccgtaac
120
gtcggtccga acatcgacgc ctggtccgat ttccagccgc tgggcgtggt ggcggggatc
180

acgccattca acttcccggc gatggtgccc ctgtggatgt atccgttggc gatcgtttgc
240
ggtaactgct ttatcctcaa gccgtccgag cgtgatccga gctcgacctt gctgatcgcc
300
cagctgttgc aggaagccgg tttgcccaaa ggtgtgctga acgtggtgca tggtgacaag
360
accgcggtgg acgcg
375

<210> 2348
<211> 125
<212> PRT
<213> Homo sapiens

<400> 2348
Ile Ser Glu Glu His Gly Arg Thr Leu Glu Asp Ala Ala Gly Glu Leu
1 5 10 15
Lys Arg Gly Ile Glu Asn Val Glu Tyr Ala Cys Ala Ala Pro Glu Val
20 25 30
Leu Lys Gly Glu Tyr Ser Arg Asn Val Gly Pro Asn Ile Asp Ala Trp
35 40 45
Ser Asp Phe Gln Pro Leu Gly Val Val Ala Gly Ile Thr Pro Phe Asn
50 55 60
Phe Pro Ala Met Val Pro Leu Trp Met Tyr Pro Leu Ala Ile Val Cys
65 70 75 80
Gly Asn Cys Phe Ile Leu Lys Pro Ser Glu Arg Asp Pro Ser Ser Thr
85 90 95
Leu Leu Ile Ala Gln Leu Leu Gln Glu Ala Gly Leu Pro Lys Gly Val
100 105 110
Leu Asn Val Val His Gly Asp Lys Thr Ala Val Asp Ala
115 120 125

<210> 2349
<211> 417
<212> DNA
<213> Homo sapiens

<400> 2349
nnnaaaaaaa aaaaaaaaaa aaaaacacaa tatttaatgg acgcggttta ttcagcaggt
60
gctgacaaag tttttggtgt cccaggagat tttaatctag ccttttttaga tgatattatt
120
gcacataatc atattaaatg gattggtaat acaaatgaac ttaatgcaag ttatgccgct
180
gacggatatg cacgtattaa tggcatcggt gcaatggtaa caacatttgg agtgggtgaa
240
ttaagtgctg tcaacggaat cgctggatct tatgctgagc gtgtaccagt tattgccatc
300
actggggcac ctactcgagc tgtagaacaa gaaggcaaat acgttcacca ttcccttggc
360
gaaggaactt ttgatgatta tagaaaaatg tttgagccta ttacaacagc gcaagct
417

<210> 2350

<211> 139
<212> PRT
<213> Homo sapiens

<400> 2350
Xaa Lys Lys Lys Lys Lys Lys Lys Thr Gln Tyr Leu Met Asp Ala Val
1 5 10 15
Tyr Ser Ala Gly Ala Asp Lys Val Phe Gly Val Pro Gly Asp Phe Asn
20 25 30
Leu Ala Phe Leu Asp Asp Ile Ile Ala His Asn His Ile Lys Trp Ile
35 40 45
Gly Asn Thr Asn Glu Leu Asn Ala Ser Tyr Ala Ala Asp Gly Tyr Ala
50 55 60
Arg Ile Asn Gly Ile Gly Ala Met Val Thr Thr Phe Gly Val Gly Glu
65 70 75 80
Leu Ser Ala Val Asn Gly Ile Ala Gly Ser Tyr Ala Glu Arg Val Pro
85 90 95
Val Ile Ala Ile Thr Gly Ala Pro Thr Arg Ala Val Glu Gln Glu Gly
100 105 110
Lys Tyr Val His His Ser Leu Gly Glu Gly Thr Phe Asp Asp Tyr Arg
115 120 125
Lys Met Phe Glu Pro Ile Thr Thr Ala Gln Ala
130 135

<210> 2351
<211> 696
<212> DNA
<213> Homo sapiens

<400> 2351
nacgcgttgc cgcgcgataa ctctggtgag ggtcttgctg gggccctgct ggcccttgtt
60
ggctccgccc agctgtgcga ccgttcctgg atcaccgacc agtatgaccg gttcgtgcgt
120
ggcaatactg tgctcgctca gccgaatgat gccggcatga ttcgtattga cgacaacctc
180
ggcatcgcgc tgtccttgga cgctaacgga cgccagacca cccttaaccc gtatcttggc
240
gcccagctgg ctctttgcga ggcttaccgg aatgtggctg tctctggcgc aactccggtg
300
gctgtcactg attgcctcaa ttatggctcc ccgtacgatc ccgatgtcat gtggcaattc
360
gacgagacca tccttggtct ggttgacggc tgccgcgagc ttggcgtgcc ggttacgggc
420
ggtaacgttt ccctgcacaa ccgcactgga gatgagtcga ttcggcctac tccgctcgtt
480
ggtgtgctcg gcgttattga tgacgtgcat cgtcgcatcc cgtcggcctt cgcacacgac
540
ggcgacgctg tcttgctgct aggaacgacg aagtgcgagt tcggcggatc ggtctatgag
600
gacgtcatcc acgctggcca cctaggcggt atgcccccga tgcccgacct gaatgccgag
660
aaggccctgg ccgcggtgat ggtggaagcg tcgaag
696

<210> 2352
<211> 232
<212> PRT
<213> Homo sapiens

<400> 2352
Xaa Ala Leu Pro Arg Asp Asn Ser Gly Glu Gly Leu Ala Gly Ala Leu
1 5 10 15
Leu Ala Leu Val Gly Ser Ala Gln Leu Cys Asp Arg Ser Trp Ile Thr
20 25 30
Asp Gln Tyr Asp Arg Phe Val Arg Gly Asn Thr Val Leu Ala Gln Pro
35 40 45
Asn Asp Ala Gly Met Ile Arg Ile Asp Asp Asn Leu Gly Ile Ala Leu
50 55 60
Ser Leu Asp Ala Asn Gly Arg Gln Thr Thr Leu Asn Pro Tyr Leu Gly
65 70 75 80
Ala Gln Leu Ala Leu Cys Glu Ala Tyr Arg Asn Val Ala Val Ser Gly
85 90 95
Ala Thr Pro Val Ala Val Thr Asp Cys Leu Asn Tyr Gly Ser Pro Tyr
100 105 110
Asp Pro Asp Val Met Trp Gln Phe Asp Glu Thr Ile Leu Gly Leu Val
115 120 125
Asp Gly Cys Arg Glu Leu Gly Val Pro Val Thr Gly Gly Asn Val Ser
130 135 140
Leu His Asn Arg Thr Gly Asp Glu Ser Ile Arg Pro Thr Pro Leu Val
145 150 155 160
Gly Val Leu Gly Val Ile Asp Asp Val His Arg Arg Ile Pro Ser Ala
165 170 175
Phe Ala His Asp Gly Asp Ala Val Leu Leu Leu Gly Thr Thr Lys Cys
180 185 190
Glu Phe Gly Gly Ser Val Tyr Glu Asp Val Ile His Ala Gly His Leu
195 200 205
Gly Gly Met Pro Pro Met Pro Asp Leu Asn Ala Glu Lys Ala Leu Ala
210 215 220
Ala Val Met Val Glu Ala Ser Lys
225 230

<210> 2353
<211> 422
<212> DNA
<213> Homo sapiens

<400> 2353
nnagcaatct cagaagaatt gctggctgag ttttcaaact atggtgtcaa agtagtaccg
60
atttcaggtg atgtttcaga ctttgcagat gccaagcgta tggtagatca agcgattaca
120
gaactcggtt ctgttgatgt cttggtcaac aatgctggga tcactcaaga tacgcttatg
180
ctcaagatga ccgaagaaga ctttgaaaaa gtgattaaga tcaacttgac aggtgccttc
240
aacatgacgc aagcagtctt gaaacagatg atcaaggcac gtgaaggtgc gattatcaac
300

atgtctagtg tggtcggttt gatgggaaat atcggacaag ccaactatgc agcttctaaa
360
gcaggcttga ttggttttac caagtcagtt gcacgtgaag ttgccaatcg caacgtacgc
420
gt
422

<210> 2354
<211> 140
<212> PRT
<213> Homo sapiens

<400> 2354
Xaa Ala Ile Ser Glu Glu Leu Leu Ala Glu Phe Ser Asn Tyr Gly Val
 1   5   10   15
Lys Val Val Pro Ile Ser Gly Asp Val Ser Asp Phe Ala Asp Ala Lys
            20   25   30
Arg Met Val Asp Gln Ala Ile Thr Glu Leu Gly Ser Val Asp Val Leu
        35   40   45
Val Asn Asn Ala Gly Ile Thr Gln Asp Thr Leu Met Leu Lys Met Thr
    50   55   60
Glu Glu Asp Phe Glu Lys Val Ile Lys Ile Asn Leu Thr Gly Ala Phe
65   70   75   80
Asn Met Thr Gln Ala Val Leu Lys Gln Met Ile Lys Ala Arg Glu Gly
                85   90   95
Ala Ile Ile Asn Met Ser Ser Val Val Gly Leu Met Gly Asn Ile Gly
            100   105   110
Gln Ala Asn Tyr Ala Ala Ser Lys Ala Gly Leu Ile Gly Phe Thr Lys
        115   120   125
Ser Val Ala Arg Glu Val Ala Asn Arg Asn Val Arg
    130   135   140

<210> 2355
<211> 5191
<212> DNA
<213> Homo sapiens

<400> 2355
cttgccaagt ttgacggtga agtgatctgt gaacctccca acaacaaact ggacaaattc
60
agcggaaccc tctactggaa ggaaaataag ttccctctga gcaaccagaa catgctgctg
120
cggggctgtg tgctgcgaaa caccgagtgg tgcttcgggc tggtcatctt tgcaggtcct
180
gacactaagc tgatgcaaaa cagcggcaga acaaagttca aaagaacgag tatcgatcgc
240
ctaatgaata ccctggtgct ctggattttt ggattcctgg tttgcatggg ggtgatcctg
300
gccattggca atgccatctg ggagcacgag gtggggatgc gtttccaggt ctacctgccg
360
tgggatgagg cagtggacag tgccttcttc tctggcttcc tctccttctg gtcctacatc
420
atcatcctca acaccgttgt gcccatttca ctctatgtca gtgtggaggt catccgtctg
480

ggccacagct acttcatcaa ctgggataag aagatgttct gcatgaagaa gcggacgcct
540
gcagaagccc gcaccaccac cctaaacgag gagctgggcc aggtggagta catcttctcc
600
gacaagacgg gcaccctcac ccagaacatc atggttttca acaagtgctc catcaatggc
660
cacagctatg gtgatgtgtt tgacgtcctg ggacacaaag ctgaattggg agagaggcct
720
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<210> 2356
<211> 1000
<212> PRT
<213> Homo sapiens

<400> 2356
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Leu Asp Lys Phe Ser Gly Thr Leu Tyr Trp Lys Glu Asn Lys Phe Pro
20 25 30
Leu Ser Asn Gln Asn Met Leu Leu Arg Gly Cys Val Leu Arg Asn Thr
35 40 45
Glu Trp Cys Phe Gly Leu Val Ile Phe Ala Gly Pro Asp Thr Lys Leu
50 55 60
Met Gln Asn Ser Gly Arg Thr Lys Phe Lys Arg Thr Ser Ile Asp Arg
65 70 75 80
Leu Met Asn Thr Leu Val Leu Trp Ile Phe Gly Phe Leu Val Cys Met
85 90 95
Gly Val Ile Leu Ala Ile Gly Asn Ala Ile Trp Glu His Glu Val Gly
100 105 110
Met Arg Phe Gln Val Tyr Leu Pro Trp Asp Glu Ala Val Asp Ser Ala
115 120 125
Phe Phe Ser Gly Phe Leu Ser Phe Trp Ser Tyr Ile Ile Ile Leu Asn
130 135 140
Thr Val Val Pro Ile Ser Leu Tyr Val Ser Val Glu Val Ile Arg Leu
145 150 155 160
Gly His Ser Tyr Phe Ile Asn Trp Asp Lys Lys Met Phe Cys Met Lys
165 170 175
Lys Arg Thr Pro Ala Glu Ala Arg Thr Thr Thr Leu Asn Glu Glu Leu
180 185 190
Gly Gln Val Glu Tyr Ile Phe Ser Asp Lys Thr Gly Thr Leu Thr Gln
195 200 205
Asn Ile Met Val Phe Asn Lys Cys Ser Ile Asn Gly His Ser Tyr Gly
210 215 220
Asp Val Phe Asp Val Leu Gly His Lys Ala Glu Leu Gly Glu Arg Pro
225 230 235 240
Glu Pro Val Asp Phe Ser Phe Asn Pro Leu Ala Asp Lys Lys Phe Leu
245 250 255
Phe Trp Asp Pro Ser Leu Leu Glu Ala Val Lys Ile Gly Asp Pro His
260 265 270
Thr His Glu Phe Phe Arg Leu Leu Ser Leu Cys His Thr Val Met Ser
275 280 285
Glu Glu Lys Asn Glu Gly Glu Leu Tyr Tyr Lys Ala Gln Ser Pro Asp
290 295 300
Glu Gly Ala Leu Val Thr Ala Ala Arg Asn Phe Gly Phe Val Phe Arg
305 310 315 320
Ser Arg Thr Pro Lys Thr Ile Thr Val His Glu Met Gly Thr Ala Ile
325 330 335
Thr Tyr Gln Leu Leu Ala Ile Leu Asp Phe Asn Asn Ile Arg Lys Arg
340 345 350
Met Ser Val Ile Val Arg Asn Pro Glu Gly Lys Ile Arg Leu Tyr Cys
355 360 365
Lys Gly Ala Asp Thr Ile Leu Leu Asp Arg Leu His His Ser Thr Gln
370 375 380
Glu Leu Leu Asn Thr Thr Met Asp His Leu Asn Glu Tyr Ala Gly Glu
385 390 395 400
Gly Leu Arg Thr Leu Val Leu Ala Tyr Lys Asp Leu Asp Glu Glu Tyr
405 410 415
Tyr Glu Glu Trp Ala Glu Arg Arg Leu Gln Ala Ser Leu Ala Gln Asp

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            420                 425                 430
Ser Arg Glu Asp Arg Leu Ala Ser Ile Tyr Glu Glu Val Glu Asn Asn
        435                 440                 445
Met Met Leu Leu Gly Ala Thr Ala Ile Glu Asp Lys Leu Gln Gln Gly
    450                 455                 460
Val Pro Glu Thr Ile Ala Leu Leu Thr Leu Ala Asn Ile Lys Ile Trp
465                 470                 475                 480
Val Leu Thr Gly Asp Lys Gln Glu Thr Ala Val Asn Ile Gly Tyr Ser
                485                 490                 495
Cys Lys Met Leu Thr Asp Asp Met Thr Glu Val Phe Ile Val Thr Gly
            500                 505                 510
His Thr Val Leu Glu Val Arg Glu Glu Xaa Gln Glu Ser Pro Gly Glu
        515                 520                 525
Asp Asp Gly Leu Ile Xaa Arg Ser Val Gly Asn Gly Phe Thr Tyr Gln
    530                 535                 540
Asp Lys Leu Ser Ser Ser Lys Leu Thr Ser Val Leu Glu Ala Val Ala
545                 550                 555                 560
Gly Glu Tyr Ala Leu Val Ile Asn Gly His Ser Leu Ala His Ala Leu
                565                 570                 575
Glu Ala Asp Met Glu Leu Glu Phe Leu Glu Thr Ala Cys Ala Cys Lys
            580                 585                 590
Ala Val Ile Cys Cys Arg Val Thr Pro Leu Gln Lys Ala Gln Val Val
        595                 600                 605
Glu Leu Val Lys Lys Tyr Lys Lys Ala Val Thr Leu Ala Ile Gly Asp
    610                 615                 620
Gly Ala Asn Asp Val Ser Met Ile Lys Thr Ala His Ile Gly Val Gly
625                 630                 635                 640
Ile Ser Gly Gln Glu Gly Ile Gln Ala Val Leu Ala Ser Asp Tyr Ser
                645                 650                 655
Phe Ser Gln Phe Lys Phe Leu Gln Arg Leu Leu Leu Val His Gly Arg
            660                 665                 670
Trp Ser Tyr Leu Arg Met Cys Lys Phe Leu Cys Tyr Phe Phe Tyr Lys
        675                 680                 685
Asn Phe Ala Phe Thr Met Val His Phe Trp Phe Gly Phe Phe Cys Gly
    690                 695                 700
Phe Ser Ala Gln Thr Val Tyr Asp Gln Tyr Phe Ile Thr Leu Tyr Asn
705                 710                 715                 720
Ile Val Tyr Thr Ser Leu Pro Val Leu Ala Met Gly Val Phe Asp Gln
                725                 730                 735
Asp Val Pro Glu Gln Arg Ser Met Glu Tyr Pro Lys Leu Tyr Glu Pro
            740                 745                 750
Gly Gln Leu Asn Leu Leu Phe Asn Lys Arg Glu Phe Phe Ile Cys Ile
        755                 760                 765
Ala Gln Gly Ile Tyr Thr Ser Val Leu Met Phe Phe Ile Pro Tyr Gly
    770                 775                 780
Val Phe Ala Asp Ala Thr Arg Asp Asp Gly Thr Gln Leu Ala Asp Tyr
785                 790                 795                 800
Gln Ser Phe Ala Val Thr Val Ala Thr Ser Leu Val Ile Val Val Ser
                805                 810                 815
Val Gln Ile Gly Leu Asp Thr Gly Tyr Trp Thr Ala Ile Asn His Phe
            820                 825                 830
Phe Ile Trp Gly Ser Leu Ala Val Tyr Phe Ala Ile Leu Phe Ala Met
        835                 840                 845
His Ser Asn Gly Leu Phe Asp Met Phe Pro Asn Gln Phe Arg Phe Val
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    850                 855                 860
Gly Asn Ala Gln Asn Thr Leu Ala Gln Pro Thr Val Trp Leu Thr Ile
865                 870                 875                 880
Val Leu Thr Thr Val Val Cys Ile Met Pro Val Val Ala Phe Arg Phe
                885                 890                 895
Leu Arg Leu Asn Leu Lys Pro Asp Leu Ser Asp Thr Val Arg Tyr Thr
            900                 905                 910
Gln Leu Val Arg Lys Lys Gln Lys Ala Gln His Arg Cys Met Arg Arg
        915                 920                 925
Val Gly Arg Thr Gly Ser Arg Arg Ser Gly Tyr Ala Phe Ser His Gln
    930                 935                 940
Glu Gly Phe Gly Glu Leu Ile Met Ser Gly Lys Asn Met Arg Leu Ser
945                 950                 955                 960
Ser Leu Ala Leu Ser Ser Phe Thr Thr Arg Ser Ser Ser Ser Trp Ile
                965                 970                 975
Glu Ser Leu Arg Arg Lys Lys Ser Asp Ser Ala Ser Ser Pro Ser Gly
            980                 985                 990
Gly Ala Asp Lys Pro Leu Lys Gly
        995                 1000
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<210> 2357
<211> 408
<212> DNA
<213> Homo sapiens

<400> 2357
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ggtgcgccaa acggtgaaga cgaggtttcc cgcaagctca tcaccgtgtg gggtgctgag
180
ccacaaaacc cactcctgcc agccgacacc aatgaaaccg gcggcacgaa agtcatcacc
240
gccttgttcg ccggcctggt gtattacgac gccgacggca aaacccataa tgatgtggcc
300
aaatccattg acttcgatgg cgaccgcacc tacacggtga cgctgcggaa aaccagattc
360
gccgacggta ctgaggtgaa ggcccataat tttgtgaaag ctgccgca
408

<210> 2358
<211> 98
<212> PRT
<213> Homo sapiens

<400> 2358
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Tyr Gly Gly Ala Pro Asn Gly Glu Asp Glu Val Ser Arg Lys Leu Ile
 1               5                  10                  15
Thr Val Trp Gly Ala Glu Pro Gln Asn Pro Leu Leu Pro Ala Asp Thr
            20                  25                  30
Asn Glu Thr Gly Gly Thr Lys Val Ile Thr Ala Leu Phe Ala Gly Leu
        35                  40                  45
Val Tyr Tyr Asp Ala Asp Gly Lys Thr His Asn Asp Val Ala Lys Ser
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    50                  55                  60
Ile Asp Phe Asp Gly Asp Arg Thr Tyr Thr Val Thr Leu Arg Lys Thr
65                  70                  75                  80
Arg Phe Ala Asp Gly Thr Glu Val Lys Ala His Asn Phe Val Lys Ala
                85                  90                  95
Ala Ala
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<210> 2359
<211> 324
<212> DNA
<213> Homo sapiens

<400> 2359
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gttgagcaga cgtgtcgtga gtacggcgaa gaacttgggc ttgtaattga gtttcagcaa
120
accaatcacg aagggcaaat gattgaatgg attcaccacg cccgtagaag gattgcgggg
180
attgtgatca atccaggagc atggacccat acatcggcag ccatccacga tgcgttgatt
240
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300
aggcattttt cctacgtgtc acgc
324

<210> 2360
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2360
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Asn Leu Asn Met Leu Gly Leu Arg Glu Pro Glu Val Tyr Gly Ser Glu
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Thr Leu Ala Asp Val Glu Gln Thr Cys Arg Glu Tyr Gly Glu Glu Leu
            20                  25                  30
Gly Leu Val Ile Glu Phe Gln Gln Thr Asn His Glu Gly Gln Met Ile
        35                  40                  45
Glu Trp Ile His His Ala Arg Arg Arg Ile Ala Gly Ile Val Ile Asn
    50                  55                  60
Pro Gly Ala Trp Thr His Thr Ser Ala Ala Ile His Asp Ala Leu Ile
65                  70                  75                  80
Ala Ala Glu Val Pro Val Ile Glu Val His Ile Ser Asn Val His Arg
                85                  90                  95
Arg Glu Asp Phe Arg His Phe Ser Tyr Val Ser Arg
            100                 105
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<210> 2361
<211> 398
<212> DNA
<213> Homo sapiens

<400> 2361

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120
gatcaacaca gaccagctgg tcaaggggga cctccatccc tgccctgtcc tcacggagct
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gtagggagag tcccaaaggc aggtggtggg gctggggcct ccaacagctg ggtcctctca
240
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300
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360
tgcagctcca cacccgggaa acaccacatg ctcgcttt
398

<210> 2362
<211> 98
<212> PRT
<213> Homo sapiens

<400> 2362
Met Pro Leu Pro Ser Arg Ser Thr Gln Thr Ser Trp Ser Arg Gly Thr
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Ser Ile Pro Ala Leu Ser Ser Arg Ser Cys Arg Glu Ser Pro Lys Gly
20 25 30
Arg Trp Trp Gly Trp Gly Leu Gln Gln Leu Gly Pro Leu Ile Ser Leu
35 40 45
Lys Ala Gln Gln His Thr Val Ser Gln Val Cys Gln Val Pro Gln His
50 55 60
Gly His Pro Ala Leu Thr Ala Pro Pro Arg Leu Pro Ala Cys His His
65 70 75 80
Leu His Lys His Met Leu Gln Leu His Thr Arg Glu Thr Pro His Ala
85 90 95
Arg Phe

<210> 2363
<211> 833
<212> DNA
<213> Homo sapiens

<400> 2363
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cagcacaagg ggaggtccca agaaccagaa cttacatcac tgcctccgag ttcagaggtt
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300
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360

ggcccctgct gtggtgctag gtccccagat gagagatcac ggtcatgaag atcagccccc
420
aaggcagccc cttccnttcc agcctgggct ctggcgtgtt ctaggtgctc acttccatgg
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720
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833

<210> 2364
<211> 135
<212> PRT
<213> Homo sapiens

<400> 2364
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Lys His His Gln Gln His Lys Gly Arg Ser Gln Glu Pro Glu Leu Thr
20 25 30
Ser Leu Pro Pro Ser Ser Glu Val Ser Phe Pro Thr Phe Ser Glu Leu
35 40 45
Ser Val Ser Met Ala Ser Ser Ala Thr Ser Ala Thr Ser Pro Asp Val
50 55 60
Leu Ala Ser Val Ser Ile Ala Ser Ser Trp Arg Ser Ser Ala Arg Cys
65 70 75 80
Ser Lys Pro Thr Ala Xaa Arg Ser Lys Arg Asp Cys Val Thr Thr Gln
85 90 95
Lys Val Ala Gln Gly Leu Ala Ala Val Pro Ser Gly Ser Leu Cys Ala
100 105 110
Gln Pro Pro Ser Ala Gly Phe Pro Gly Pro Cys Cys Gly Ala Arg Ser
115 120 125
Pro Asp Glu Arg Ser Arg Ser
130 135

<210> 2365
<211> 429
<212> DNA
<213> Homo sapiens

<400> 2365
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ctccgtcagt tcgcccaaca acctctgaac gaagtcaaga ttctccggca ctggagccaa
120
ggtgcttgcc ctggcatgaa cgccccaggg gaggtcgacg ccgtcgggat tctcacaccg
180

atggtgatgg gactcggttt ccaaccacgg ttccatgtga cccagacagt tctggttggc
240
cccgagctcg atgcctcgtc cgcgacacag accatcgagc cacctcatgt cctccgccgt
300
cacggggctg cggtcggccc acacctcctc ctcaccgcgg taggcaaatc ccgcttcacc
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420
ggaacgcgt
429

<210> 2366
<211> 132
<212> PRT
<213> Homo sapiens

<400> 2366
Met Ala Arg Cys Gly Leu Asn His Leu Glu Leu Tyr Gly Glu Ala Gly
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Phe Ala Tyr Arg Gly Glu Glu Glu Val Trp Ala Asp Arg Ser Pro Val
            20   25   30
Thr Ala Glu Asp Met Arg Trp Leu Asp Gly Leu Cys Arg Gly Arg Gly
        35   40   45
Ile Glu Leu Gly Ala Asn Gln Asn Cys Leu Gly His Met Glu Pro Trp
    50   55   60
Leu Glu Thr Glu Ser His His His Arg Cys Glu Asn Pro Asp Gly Val
65   70   75   80
Asp Leu Pro Trp Gly Val His Ala Arg Ala Ser Thr Leu Ala Pro Val
                85   90   95
Pro Glu Asn Leu Asp Phe Val Gln Arg Leu Leu Gly Glu Leu Thr Glu
            100   105   110
Thr Val Ser Ser Lys Phe Leu Asn Val Gly Leu Asp Glu Pro Trp Glu
        115   120   125
Leu Gly Thr Gly
    130

<210> 2367
<211> 474
<212> DNA
<213> Homo sapiens

<400> 2367
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gggggtcacg agctcaccga cgcgcgcgcg ttcgcctcgt ggggcgtcga tttcgtcaaa
120
tacgatcggt gctccggtga ctccgcgcac gacgaccagg tcgcctcgtt caccgcgatg
180
cgtgacgcaa tccgatccac cggacgcccc atggtgtaca gcatcaaccc caacagcgaa
240
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300
accaacgaca tctcgccggt gtggaccact cggccggccg gtgccgatgc gacaccggca
360

tcggggtatc aggggatccg cgacatcatc gacgccgtgg ccccgatcgg cgcacgggtt
420
gcgacggcag cttcgtcgac atggacatgc tcgtcgtcgg tgtcggcaac gcgt
474

<210> 2368
<211> 158
<212> PRT
<213> Homo sapiens

<400> 2368
Xaa Ala Arg Glu Lys Thr Cys Ala Gln Phe Gly Gly Thr Tyr Pro Gly
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Ser Ala Gly Ser Gly Gly His Glu Leu Thr Asp Ala Arg Ala Phe Ala
            20   25   30
Ser Trp Gly Val Asp Phe Val Lys Tyr Asp Arg Cys Ser Gly Asp Ser
        35   40   45
Ala His Asp Asp Gln Val Ala Ser Phe Thr Ala Met Arg Asp Ala Ile
    50   55   60
Arg Ser Thr Gly Arg Pro Met Val Tyr Ser Ile Asn Pro Asn Ser Glu
65   70   75   80
Ser Pro Asp Arg Ser Gly Ala Gln Phe Asp Trp Gly Gly Val Ala Thr
                85   90   95
Met Thr Arg Thr Thr Asn Asp Ile Ser Pro Val Trp Thr Thr Arg Pro
            100   105   110
Ala Gly Ala Asp Ala Thr Pro Ala Ser Gly Tyr Gln Gly Ile Arg Asp
        115   120   125
Ile Ile Asp Ala Val Ala Pro Ile Gly Ala Arg Val Ala Thr Ala Ala
    130   135   140
Ser Ser Thr Trp Thr Cys Ser Ser Ser Val Ser Ala Thr Arg
145   150   155

<210> 2369
<211> 408
<212> DNA
<213> Homo sapiens

<400> 2369
ctgaatggca ggcaggcaga ggccaccaga gccagccccc cgagaagccc tgctgagcca
60
aaggggagcg ccctgggacc taacccagag ccccatctca ccttcccccg ttctttcaaa
120
gtgcctcccc caaccccagt caggacttcg tccatcccag ttcaggaagc acaagaggct
180
cccgaaagga agaggggggcc accaagaagg ctcccagccg actcccactg cctcccagct
240
tccacatccg ccccgcctcc caggtctacc cagacagggc ccccgagcnc agactgccct
300
ggggagctca aggccacagc accagccagc ccaaggcttg gccagtccca gtcccaagca
360
gatgaacgag ctgggactcc gcctccagcc cctcccctgc cccctcct
408

<210> 2370

<211> 136
<212> PRT
<213> Homo sapiens

<400> 2370
Leu Asn Gly Arg Gln Ala Glu Ala Thr Arg Ala Ser Pro Pro Arg Ser
1 5 10 15
Pro Ala Glu Pro Lys Gly Ser Ala Leu Gly Pro Asn Pro Glu Pro His
20 25 30
Leu Thr Phe Pro Arg Ser Phe Lys Val Pro Pro Pro Thr Pro Val Arg
35 40 45
Thr Ser Ser Ile Pro Val Gln Glu Ala Gln Glu Ala Pro Glu Arg Lys
50 55 60
Arg Gly Pro Pro Arg Arg Leu Pro Ala Asp Ser His Cys Leu Pro Ala
65 70 75 80
Ser Thr Ser Ala Pro Pro Pro Arg Ser Thr Gln Thr Gly Pro Pro Ser
85 90 95
Xaa Asp Cys Pro Gly Glu Leu Lys Ala Thr Ala Pro Ala Ser Pro Arg
100 105 110
Leu Gly Gln Ser Gln Ser Gln Ala Asp Glu Arg Ala Gly Thr Pro Pro
115 120 125
Pro Ala Pro Pro Leu Pro Pro Pro
130 135

<210> 2371
<211> 327
<212> DNA
<213> Homo sapiens

<400> 2371
gaattcggtg tgcgatgcga gcctgcagcc tgggagcaga gacaaggagc aaaggcggtg
60
agagggttgc cagggcaccc agttacagct ggagctgcag gggacccatc cctcgagaga
120
ggcaggcact agtcatgagg caagagatgc ctcagaagag gatgctggcc gcagggcaca
180
gcagagaggg agatagcccg gggcactcct caggaccggg cctcagggga cagcaaacaa
240
gattcctgat agacgcgccc aggtcatgcc ttttcagtgg tgtgagccag gttctggcgt
300
caggcgggcc aaggttttca tgcagcn
327

<210> 2372
<211> 104
<212> PRT
<213> Homo sapiens

<400> 2372
Met Arg Ala Cys Ser Leu Gly Ala Glu Thr Arg Ser Lys Gly Gly Glu
1 5 10 15
Arg Val Ala Arg Ala Pro Ser Tyr Ser Trp Ser Cys Arg Gly Pro Ile
20 25 30
Pro Arg Glu Arg Gln Ala Leu Val Met Arg Gln Glu Met Pro Gln Lys

```
        35                  40                  45
Arg Met Leu Ala Ala Gly His Ser Arg Glu Gly Asp Ser Pro Gly His
    50                  55                  60
Ser Ser Gly Pro Gly Leu Arg Gly Gln Gln Thr Arg Phe Leu Ile Asp
65                  70                  75                  80
Ala Pro Arg Ser Cys Leu Phe Ser Gly Val Ser Gln Val Leu Ala Ser
                85                  90                  95
Gly Gly Pro Arg Phe Ser Cys Ser
            100
```

<210> 2373
<211> 591
<212> DNA
<213> Homo sapiens

<400> 2373
gaattctgac attcaggaag tcaattgcag aaggtttaac caagttgatt ctgttttacc
60
aaatcctgtc tattctgaaa agcggccaat gccagactca tctcatgatg tgaaagttct
120
cacttcaaag acatcagctg ttgagatgac ccaggcagta ttgaatactc agctttcatc
180
agaaaatgtt accaaagttg agcaaaattc accagcagtt tgtgaaacaa tttctgttcc
240
caagtccatg tccactgagg aatataaatc aaaaattcaa aatgaaaata tgctacttct
300
cgctttgctt tcacaggcac gtaagactca gaagacagta ttaaaagatg ctaatcaaac
360
tattcaggat tctaaaccag acagttgtga aatgaatcca aatacccaaa tgactggtaa
420
ccaactgaat ttgaagaaca tggaaactcc aagtacttct aatgtaagtg gcagggtttt
480
ggacaactcc ttttgcagtg gacaagaatc ctcaacaaaa ggaatgcctg ctaaaagtga
540
cagtagctgt tccatggaag tgctagcaac ctgtctttcc ctgtggaaaa a
591

<210> 2374
<211> 167
<212> PRT
<213> Homo sapiens

<400> 2374
```
Met Pro Asp Ser Ser His Asp Val Lys Val Leu Thr Ser Lys Thr Ser
 1               5                  10                  15
Ala Val Glu Met Thr Gln Ala Val Leu Asn Thr Gln Leu Ser Ser Glu
            20                  25                  30
Asn Val Thr Lys Val Glu Gln Asn Ser Pro Ala Val Cys Glu Thr Ile
        35                  40                  45
Ser Val Pro Lys Ser Met Ser Thr Glu Glu Tyr Lys Ser Lys Ile Gln
    50                  55                  60
Asn Glu Asn Met Leu Leu Leu Ala Leu Leu Ser Gln Ala Arg Lys Thr
65                  70                  75                  80
Gln Lys Thr Val Leu Lys Asp Ala Asn Gln Thr Ile Gln Asp Ser Lys
```

```
                85                  90                  95
Pro Asp Ser Cys Glu Met Asn Pro Asn Thr Gln Met Thr Gly Asn Gln
            100                 105                 110
Leu Asn Leu Lys Asn Met Glu Thr Pro Ser Thr Ser Asn Val Ser Gly
        115                 120                 125
Arg Val Leu Asp Asn Ser Phe Cys Ser Gly Gln Glu Ser Ser Thr Lys
    130                 135                 140
Gly Met Pro Ala Lys Ser Asp Ser Ser Cys Ser Met Glu Val Leu Ala
145                 150                 155                 160
Thr Cys Leu Ser Leu Trp Lys
                165
```

<210> 2375
<211> 535
<212> DNA
<213> Homo sapiens

<400> 2375
ntggccatgt cgttgctcag cagcggcacc ctggacagtt accttgagcg tcacaaacaa
60
ctggacgcga tgcgcatgct gcacttcttc gccctcgacg aagaaaaccc cgccagcatc
120
tataactgcc tgcgcgccgc gcggggcaat gcccacgcgg tacgcgggcg gatcaccgcc
180
gacatgtggg aaaacctcaa cgccacctgg ctggaaatgc gcagcatcgc cgccgggggc
240
ctggcccggc atggcatcag ccacttctgt gactgggtca agcagcgttc gcacctgttc
300
cgcggggcaa cctcgggcac catcatgcgc aacgacgctt accggtttat tcgcctgggc
360
acgtttgtcg agcgcgcgga caacaccctg cgcctgctgg atgcgcgcta cgaaatgttt
420
ggtgaggagt cggaagaggt cagcgacctg tcggcacgcg ggtattacca gtggagcgcc
480
ctgctgcggg ccttgtcgtc attcgaggcg tataccgaac tgtaccccaa cgcgt
535

<210> 2376
<211> 178
<212> PRT
<213> Homo sapiens

<400> 2376
```
Xaa Ala Met Ser Leu Leu Ser Ser Gly Thr Leu Asp Ser Tyr Leu Glu
 1               5                  10                  15
Arg His Lys Gln Leu Asp Ala Met Arg Met Leu His Phe Phe Ala Leu
            20                  25                  30
Asp Glu Glu Asn Pro Ala Ser Ile Tyr Asn Cys Leu Arg Ala Ala Arg
        35                  40                  45
Gly Asn Ala His Ala Val Arg Gly Arg Ile Thr Ala Asp Met Trp Glu
    50                  55                  60
Asn Leu Asn Ala Thr Trp Leu Glu Met Arg Ser Ile Ala Ala Gly Gly
65                  70                  75                  80
Leu Ala Arg His Gly Ile Ser His Phe Cys Asp Trp Val Lys Gln Arg
```

```
                85                  90                  95
Ser His Leu Phe Arg Gly Ala Thr Ser Gly Thr Ile Met Arg Asn Asp
            100                 105                 110
Ala Tyr Arg Phe Ile Arg Leu Gly Thr Phe Val Glu Arg Ala Asp Asn
        115                 120                 125
Thr Leu Arg Leu Leu Asp Ala Arg Tyr Glu Met Phe Gly Glu Glu Ser
    130                 135                 140
Glu Glu Val Ser Asp Leu Ser Ala Arg Gly Tyr Tyr Gln Trp Ser Ala
145                 150                 155                 160
Leu Leu Arg Ala Leu Ser Ser Phe Glu Ala Tyr Thr Glu Leu Tyr Pro
                165                 170                 175
Asn Ala
```

<210> 2377
<211> 622
<212> DNA
<213> Homo sapiens

<400> 2377
acgcgtgaag ggttgaggct tcagaagtgg tagggaagaa cagaagctcc cttctgaggg
60
agcacccagg agatgaaagg aaccaatcct gggtggtcct gcaccaggct tatcaacccc
120
tgacagacaa atggaaaact tctgtgatgg tgggacatga aaaaatattt cacccttctg
180
ataaaatgga accagcagat agaagtagga atttttctgt taggtgaaat gtttttaaaa
240
atatgtatac aggaaaaagc ataaaacagt attgactggc aaacatagaa ctggaatgta
300
aatataatgt tctttgccct gaatgattta agtggcatga taaaactcat gccacagact
360
gggtaagaca aggaatctaa tccactctaa aaagaagaaa agcatagtaa aattctcctt
420
agagttagaa ttattaatag ttcctatcta ctatttaatt taatcatagt taatgatgag
480
aatttcttaa atttaaagct tctgatgatg ctaaatgtgc atttctcatg attccttaaa
540
acaatttttg taaattctat tcctaggacc ttctgctttc agaaaaatta atgtcttgta
600
ttcttcgtat tggaggagat ct
622

<210> 2378
<211> 109
<212> PRT
<213> Homo sapiens

<400> 2378
```
Met Ser Phe Ile Met Pro Leu Lys Ser Phe Arg Ala Lys Asn Ile Ile
 1               5                  10                  15
Phe Thr Phe Gln Phe Tyr Val Cys Gln Ser Ile Leu Phe Tyr Ala Phe
            20                  25                  30
Ser Cys Ile His Ile Phe Lys Asn Ile Ser Pro Asn Arg Lys Ile Pro
```

```
        35                  40                  45
Thr Ser Ile Cys Trp Phe His Phe Ile Arg Arg Val Lys Tyr Phe Phe
    50                  55                  60
Met Ser His His His Arg Ser Phe Pro Phe Val Cys Gln Gly Leu Ile
65                  70                  75                  80
Ser Leu Val Gln Asp His Pro Gly Leu Val Pro Phe Ile Ser Trp Val
                85                  90                  95
Leu Pro Gln Lys Gly Ala Ser Val Leu Pro Tyr His Phe
            100                 105
```

<210> 2379
<211> 342
<212> DNA
<213> Homo sapiens

<400> 2379
tcatgacctg gagacttcgg aaactcaaca agactgcagg gcacccaggg gcaccagccc
60
cggtcaccgc agaggatcag tgcactttgc catctggcag atcaactcat ggcacaactg
120
ggaaacataa cattcacgct tgtgaaccga gacgccatac cccagcggtg ccgagagcaa
180
cagtgctgtg caggtctggg cagatgaggg cctccaggac acgaggactc actcgctcac
240
cctgcccact gggcagctgc tcgccactcc cctcctggag ggcaggacgg acaccacaca
300
cacacacaag cagggaagct gtgcagcagt ggggagaaag ca
342

<210> 2380
<211> 113
<212> PRT
<213> Homo sapiens

<400> 2380
```
Met Thr Trp Arg Leu Arg Lys Leu Asn Lys Thr Ala Gly His Pro Gly
 1               5                  10                  15
Ala Pro Ala Pro Val Thr Ala Glu Asp Gln Cys Thr Leu Pro Ser Gly
            20                  25                  30
Arg Ser Thr His Gly Thr Thr Gly Lys His Asn Ile His Ala Cys Glu
        35                  40                  45
Pro Arg Arg His Thr Pro Ala Val Pro Arg Ala Thr Val Leu Cys Arg
    50                  55                  60
Ser Gly Gln Met Arg Ala Ser Arg Thr Arg Gly Leu Thr Arg Ser Pro
65                  70                  75                  80
Cys Pro Leu Gly Ser Cys Ser Pro Leu Pro Ser Trp Arg Ala Gly Arg
                85                  90                  95
Thr Pro His Thr His Thr Ser Arg Glu Ala Val Gln Gln Trp Gly Glu
            100                 105                 110
Ser
```

<210> 2381
<211> 434

<212> DNA
<213> Homo sapiens

<400> 2381
gtgcaccctg gccatatgga cgccagcgac gtcggcgtct tgcgtgacgt ggaaccgatc
60
ggcccaagta gagagatgga ttttgaatgg tgacgatgta cccgccgcag caagtggatg
120
ccgtcctctt tgacatggac ggaaccctgc tcaacaccct gccggcctgg tgcgtggcat
180
ctgagcatct gtggggcact tctctggctg acgctgacag cgccaaggtt gacgggggca
240
ccgtcgacga cgtcgttgag ctgtatctgc gagaccaccc tcaggcagat ccccaggcca
300
ccatcgagcg tttcatggac atccttgacg ccaacctggc tggccacacc gagccgatgc
360
ccggagctga ccgcctcgtg aagaggctgt caggtcatgt acccatcgct gtggtgtcga
420
attccccgac gcgt
434

<210> 2382
<211> 116
<212> PRT
<213> Homo sapiens

<400> 2382
Met Val Thr Met Tyr Pro Pro Gln Gln Val Asp Ala Val Leu Phe Asp
 1   5   10   15
Met Asp Gly Thr Leu Leu Asn Thr Leu Pro Ala Trp Cys Val Ala Ser
            20   25   30
Glu His Leu Trp Gly Thr Ser Leu Ala Asp Ala Asp Ser Ala Lys Val
        35   40   45
Asp Gly Gly Thr Val Asp Asp Val Val Glu Leu Tyr Leu Arg Asp His
    50   55   60
Pro Gln Ala Asp Pro Gln Ala Thr Ile Glu Arg Phe Met Asp Ile Leu
65   70   75   80
Asp Ala Asn Leu Ala Gly His Thr Glu Pro Met Pro Gly Ala Asp Arg
                85   90   95
Leu Val Lys Arg Leu Ser Gly His Val Pro Ile Ala Val Val Ser Asn
            100   105   110
Ser Pro Thr Arg
        115

<210> 2383
<211> 393
<212> DNA
<213> Homo sapiens

<400> 2383
acgcgtgcgt tcagatgagc gccggacgaa actcctcggt cgcttcggca ggcatggatt
60
catgtcggca cgggcctttg aacaggatcg ccgtcgcgtg gctatccgcc gcgggtgggg
120

cagaaaacgc ccactctccc ttccccaggc gccggccgtc gagtcgtcta cgcaacgcac
180
gtctacatag gtgacttttt catacccccа ctttcgtact cggatgggct cggcgtgctc
240
gatgtcggca cgaaaaatta aatgcactga atgcgggttg tcgcacagga tgcatctcgt
300
ctttcttgat gccacccacc ttgttacata ttctgccatg caaaacacct tgtgattttt
360
ggcggagtgc aacatggtat gtgtatgcca ctg
393

<210> 2384
<211> 125
<212> PRT
<213> Homo sapiens

<400> 2384
Met Leu His Ser Ala Lys Asn His Lys Val Phe Cys Met Ala Glu Tyr
1 5 10 15
Val Thr Arg Trp Val Ala Ser Arg Lys Thr Arg Cys Ile Leu Cys Asp
20 25 30
Asn Pro His Ser Val His Leu Ile Phe Arg Ala Asp Ile Glu His Ala
35 40 45
Glu Pro Ile Arg Val Arg Lys Trp Gly Tyr Glu Lys Val Thr Tyr Val
50 55 60
Asp Val Arg Cys Val Asp Asp Ser Thr Ala Gly Ala Trp Gly Arg Glu
65 70 75 80
Ser Gly Arg Phe Leu Pro His Pro Arg Arg Ile Ala Thr Arg Arg Arg
85 90 95
Ser Cys Ser Lys Ala Arg Ala Asp Met Asn Pro Cys Leu Pro Lys Arg
100 105 110
Pro Arg Ser Phe Val Arg Arg Ser Ser Glu Arg Thr Arg
115 120 125

<210> 2385
<211> 347
<212> DNA
<213> Homo sapiens

<400> 2385
acgcgttccc aaagtaggat ggctgggata gagggaaagg acatctttca ggcttgttat
60
gcactgtgct gtggactctt gttgtggggt cctaggtctg cccagcattt tggggttcac
120
cccgtgaccc tctacgggtt tccatgcccc cagcaccacg tccatcatca tttctggggt
180
cccctcacct cagagagcct gcttcctatg actgcgtggg ccagctggag aaggacgacc
240
caagacccct caagtttctg tgtcctgacc ccaagcatag gcctgagtgc tcctggggcc
300
caagggcctt tacgcactac tctctggggc ccactgtctg cactctt
347

<210> 2386

<211> 109
<212> PRT
<213> Homo sapiens

<400> 2386
Met Ala Gly Ile Glu Gly Lys Asp Ile Phe Gln Ala Cys Tyr Ala Leu
1 5 10 15
Cys Cys Gly Leu Leu Leu Trp Gly Pro Arg Ser Ala Gln His Phe Gly
20 25 30
Val His Pro Val Thr Leu Tyr Gly Phe Pro Cys Pro Gln His His Val
35 40 45
His His His Phe Trp Gly Pro Leu Thr Ser Glu Ser Leu Leu Pro Met
50 55 60
Thr Ala Trp Ala Ser Trp Arg Arg Thr Thr Gln Asp Pro Ser Ser Phe
65 70 75 80
Cys Val Leu Thr Pro Ser Ile Gly Leu Ser Ala Pro Gly Ala Gln Gly
85 90 95
Pro Leu Arg Thr Thr Leu Trp Gly Pro Leu Ser Ala Leu
100 105

<210> 2387
<211> 715
<212> DNA
<213> Homo sapiens

<400> 2387
ncggccgcac ttcaccttac ggaggggaga taatgagatc aattagaggc gccgtcaccg
60
cgccggagac agctgccgcc gcatagtaat cacccgcggg ctgggtgcgc gggggctccc
120
cgctacctgc gcgcctgctg ctcccaccac gcggcaccga cccgggcgcg cccccggccc
180
ctgtccgcag cccacagcca caccgcgcac cctacaccct ccttgcgcct ctgctgggga
240
gctcaccccc tccactcgca cagtgcgctg cggcccgggg tgtgggaggt cccgggactt
300
gggttgtgag tgcctgtgtg ggggtagggg caggtgtccg cttgtgcgca tatgggcatg
360
agtgtacatg gcgtgtgcct ggagatgggc gagtgcaggc tggaatgtgc cggcgtggca
420
cgtgtgtggg cccaaataga tgcgtgtgtg atcacatgtt gtgttcgtgt ttgcacctcg
480
tgtgcctgtg tgtccgtatt tgagtgctta caggaatgtg ggtggtgagt acccgtatgt
540
gggtgcatct gcacttgtgc gtgtgtgtgt gtaggcgcgt gtgtgtgcgt gtgtgtgtta
600
ngggatacgt gtagatgtgc attagtgtga ctgtgtgtgc tcatgtgcct gtgcacgtgt
660
gtttgaggtt tgtgtgcatg ggtagcgtct gtgagagcca tgtgtatatc tgcag
715

<210> 2388
<211> 58
<212> PRT

<213> Homo sapiens

<400> 2388
Met Gly Met Ser Val His Gly Val Cys Leu Glu Met Gly Glu Cys Arg
1 5 10 15
Leu Glu Cys Ala Gly Val Ala Arg Val Trp Ala Gln Ile Asp Ala Cys
20 25 30
Val Ile Thr Cys Cys Val Arg Val Cys Thr Ser Cys Ala Cys Val Ser
35 40 45
Val Phe Glu Cys Leu Gln Glu Cys Gly Trp
50 55

<210> 2389
<211> 336
<212> DNA
<213> Homo sapiens

<400> 2389
ntcaccctgc cgccggaagg ttgctcgtac cgcatggcca tcgtcaccat gaagaagtcg
60
tatccgggcc acgccaagcg cgtcatgttg ggtgtctggt cgtttttgcg acagttcatg
120
tataccaagt tcgttatcgt caccgacgac gatatcaacg cccgcgactg gaacgacgtg
180
atctgggcca tcaccacgcg catggacccc aagcgcgaca cggtgatgat cgataacacg
240
ccgatcgact acctcgactt cgcctcgccg gtgtccggcc tgggttcgaa gatggggctc
300
gatcccacgc acaaatggcc cggccacacc acccgn
336

<210> 2390
<211> 112
<212> PRT
<213> Homo sapiens

<400> 2390
Xaa Thr Leu Pro Pro Glu Gly Cys Ser Tyr Arg Met Ala Ile Val Thr
1 5 10 15
Met Lys Lys Ser Tyr Pro Gly His Ala Lys Arg Val Met Leu Gly Val
20 25 30
Trp Ser Phe Leu Arg Gln Phe Met Tyr Thr Lys Phe Val Ile Val Thr
35 40 45
Asp Asp Asp Ile Asn Ala Arg Asp Trp Asn Asp Val Ile Trp Ala Ile
50 55 60
Thr Thr Arg Met Asp Pro Lys Arg Asp Thr Val Met Ile Asp Asn Thr
65 70 75 80
Pro Ile Asp Tyr Leu Asp Phe Ala Ser Pro Val Ser Gly Leu Gly Ser
85 90 95
Lys Met Gly Leu Asp Pro Thr His Lys Trp Pro Gly His Thr Thr Arg
100 105 110

<210> 2391
<211> 388

<212> DNA
<213> Homo sapiens

<400> 2391
gtcgactaac ctgcgtacag ccgccaccct acgtttagtc gcgaagcgtg tcggctccat
60
gttcattccg gagctacacc atgaataaag tactacctga tccacccatc gatcccgcaa
120
aagaccgcgt cgctttcaac cgcgccatcg accattacct gcctacccag ggcttccact
180
gcgtcaacga agacctgagt ttcgaagacg ccctgctcta caccgccagc ctgctcgaca
240
gtgcctctgc cacggcgctg gattgcggtg agctgctgca aagccctgaa cgggcgaaga
300
tcctggccgt gtggcatttg ctggaaattg caaaaaccac cgtagatcgc ttccccatcg
360
agtgcctgac cgcaccaaag ccctgcct
388

<210> 2392
<211> 102
<212> PRT
<213> Homo sapiens

<400> 2392
Met Asn Lys Val Leu Pro Asp Pro Pro Ile Asp Pro Ala Lys Asp Arg
 1   5   10   15
Val Ala Phe Asn Arg Ala Ile Asp His Tyr Leu Pro Thr Gln Gly Phe
            20   25   30
His Cys Val Asn Glu Asp Leu Ser Phe Glu Asp Ala Leu Leu Tyr Thr
        35   40   45
Ala Ser Leu Leu Asp Ser Ala Ser Ala Thr Ala Leu Asp Cys Gly Glu
    50   55   60
Leu Leu Gln Ser Pro Glu Arg Ala Lys Ile Leu Ala Val Trp His Leu
65   70   75   80
Leu Glu Ile Ala Lys Thr Thr Val Asp Arg Phe Pro Ile Glu Cys Leu
                85   90   95
Thr Ala Pro Lys Pro Cys
            100

<210> 2393
<211> 411
<212> DNA
<213> Homo sapiens

<400> 2393
aacctgtcta ccgaggacca ggccgagcag gtagagattg tgaagcgctc tgagtccggc
60
atggtcaccg accccatcac tgcgcgcccg gatatgacca tcggggaagt agacgcgctg
120
tgcgcccgct tccgcatctc cggcctgccg gtggtagacg aggacggcac cctgatgggc
180
atttgcacca cccgcgatat gcgcttcgag cctgactttg accgcaaggt cagcgaggtc
240

atgacggcta tgccgcttgt tgttgcgcgc gagggtgtat ctaagaagga agccctcgaa
300
ctgctctcgg ccaataaggt ggaaaagctg cccatcgtcg atgcggataa taagctcacc
360
ggcctgatta ccgtcaagga ctttgtcaag accgagcagt accccaacgc g
411

<210> 2394
<211> 137
<212> PRT
<213> Homo sapiens

<400> 2394
Asn Leu Ser Thr Glu Asp Gln Ala Glu Gln Val Glu Ile Val Lys Arg
 1   5   10   15
Ser Glu Ser Gly Met Val Thr Asp Pro Ile Thr Ala Arg Pro Asp Met
            20   25   30
Thr Ile Gly Glu Val Asp Ala Leu Cys Ala Arg Phe Arg Ile Ser Gly
        35   40   45
Leu Pro Val Val Asp Glu Asp Gly Thr Leu Met Gly Ile Cys Thr Thr
    50   55   60
Arg Asp Met Arg Phe Glu Pro Asp Phe Asp Arg Lys Val Ser Glu Val
65   70   75   80
Met Thr Ala Met Pro Leu Val Val Ala Arg Glu Gly Val Ser Lys Lys
                85   90   95
Glu Ala Leu Glu Leu Leu Ser Ala Asn Lys Val Glu Lys Leu Pro Ile
            100   105   110
Val Asp Ala Asp Asn Lys Leu Thr Gly Leu Ile Thr Val Lys Asp Phe
        115   120   125
Val Lys Thr Glu Gln Tyr Pro Asn Ala
    130   135

<210> 2395
<211> 362
<212> DNA
<213> Homo sapiens

<400> 2395
aagctttcag aggagtttgc taaagtgtta aggatttgca tattttcaac tttagtcata
60
tctaagtgcc ccaataaaac agcgcggcgc attgggggct ggctttcatc aacaactaac
120
ttagcaatat taatctgacc ttttcctggt gattgggcat ttagtaataa tgcggggcca
180
atatcatcat actttccaaa tatttttgat ttt.:agaca tcaactgaag ttgtgaccat
240
ttactgtctt tgtcttgatg gcaatctaaa caaacatctc ttgtattaag ttgttcactt
300
acccaaggat taggcactct aaaggcatga tcgcgtcgat catcgactcc catgtaacgc
360
gt
362

<210> 2396

<211> 117
<212> PRT
<213> Homo sapiens

<400> 2396
Met Gly Val Asp Asp Arg Arg Asp His Ala Phe Arg Val Pro Asn Pro
1 5 10 15
Trp Val Ser Glu Gln Leu Asn Thr Arg Asp Val Cys Leu Asp Cys His
20 25 30
Gln Asp Lys Asp Ser Lys Trp Ser Gln Leu Gln Leu Met Ser Lys Lys
35 40 45
Ser Lys Ile Phe Gly Lys Tyr Asp Asp Ile Gly Pro Ala Leu Leu Leu
50 55 60
Asn Ala Gln Ser Pro Gly Lys Gly Gln Ile Asn Ile Ala Lys Leu Val
65 70 75 80
Val Asp Glu Ser Gln Pro Pro Met Arg Arg Ala Val Leu Leu Gly His
85 90 95
Leu Asp Met Thr Lys Val Glu Asn Met Gln Ile Leu Asn Thr Leu Ala
100 105 110
Asn Ser Ser Glu Ser
115

<210> 2397
<211> 449
<212> DNA
<213> Homo sapiens

<400> 2397
nacagcacac tccgcctcct ccgacgatca tagctttcac gtcggacatg atcccccgcc
60
tagtgtacta ctggtccttc tccgtccctc cctacgggga ccacacttcc tacaccatgg
120
aagggtacat caacaacact ctctccatct tcaaagtcgc agacttcaaa aacaaaagca
180
agggaaaccc gtactctgac ctgggtaacc ataccacatg caggtatcgt gatttccgat
240
acccacctgg acacccccag gagtataaac acaacatcta ctattggcat gtgattgcag
300
ccaagctggc ttttatcatt gtcatggagc acgtcatcta ctctgtgaaa tttttcattt
360
catatgcaat tcccgatgta tcaaagcgca caaagagcaa gatccagaga gaaaaatacc
420
taacccaaaa gcttcttcat gagaatcac
449

<210> 2398
<211> 76
<212> PRT
<213> Homo sapiens

<400> 2398
Cys Thr Thr Gly Pro Ser Pro Ser Leu Pro Thr Gly Thr Thr Leu Pro
1 5 10 15
Thr Pro Trp Lys Gly Thr Ser Thr Thr Leu Ser Pro Ser Ser Lys Ser

```
            20                  25                  30
Gln Thr Ser Lys Thr Lys Ala Arg Glu Thr Arg Thr Leu Thr Trp Val
        35                  40                  45
Thr Ile Pro His Ala Gly Ile Val Ile Ser Asp Thr His Leu Asp Thr
    50                  55                  60
Pro Arg Ser Ile Asn Thr Thr Ser Thr Ile Gly Met
65                  70                  75
```

<210> 2399
<211> 344
<212> DNA
<213> Homo sapiens

<400> 2399
acgcgtcatg cttcacgaaa cgggtcacgc gcttcattac caagcagctg gcaaacacaa
60
cttgtatttc gagcgggttg cgccagtcga gatcatggag ttcgtggcct actgcttgca
120
gtttctgacg atcgagcgcc tggccatgtc aggggaactt tcgggtaaag aacaggaact
180
agtcaaaccc tttgctggtc cggccaggct tggaggggtt cgaaaaccta caacgccaca
240
aaacggttcc agcactgggt ttataaacag cctaaaatcc cgacaagtaa agaactcgat
300
accgtatggc ttgagatgcg acacacgctc ggggtggatt ggtc
344

<210> 2400
<211> 112
<212> PRT
<213> Homo sapiens

<400> 2400
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Met Leu His Glu Thr Gly His Ala Leu His Tyr Gln Ala Ala Gly Lys
 1               5                  10                  15
His Asn Leu Tyr Phe Glu Arg Val Ala Pro Val Glu Ile Met Glu Phe
            20                  25                  30
Val Ala Tyr Cys Leu Gln Phe Leu Thr Ile Glu Arg Leu Ala Met Ser
        35                  40                  45
Gly Glu Leu Ser Gly Lys Glu Gln Glu Leu Val Lys Pro Phe Ala Gly
    50                  55                  60
Pro Ala Arg Leu Gly Gly Val Arg Lys Pro Thr Thr Pro Gln Asn Gly
65                  70                  75                  80
Ser Ser Thr Gly Phe Ile Asn Ser Leu Lys Ser Arg Gln Val Lys Asn
                85                  90                  95
Ser Ile Pro Tyr Gly Leu Arg Cys Asp Thr Arg Ser Gly Trp Ile Gly
            100                 105                 110
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<210> 2401
<211> 479
<212> DNA
<213> Homo sapiens

<400> 2401

nntaccgagg taaaactcga tagcctcggt gtcaccgacc agatgcgctc tgggcgctgc
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120
gactttgagt tttcctttac ctacctgcag tacttcgaca aactagagcg cgccaacttc
180
gcgctcaacc aactgctgga tctcaccgaa gacggcaccg actgggatga ccgcgacgtg
240
gctacttccc tcgagctcac aggcgacgac ggcggctggt ggtcattttt caccaacctc
300
gtggacaagt acggcgcagt cccggccgag gtcatgcctg aggtgcactc gtccggccac
360
accgaccaga tgaatcgcga tatcgccacc atcatccgcc gcgccgcgca ccgtgcggtg
420
gaaggcgagg gggatcgcgg gggcatcgtc aagcaagccc gccccgatat ccaacgcgt
479

<210> 2402
<211> 159
<212> PRT
<213> Homo sapiens

<400> 2402
Xaa Thr Glu Val Lys Leu Asp Ser Leu Gly Val Thr Asp Gln Met Arg
1 5 10 15
Ser Gly Arg Cys Trp Met Phe Ala Ala Leu Asn Val Phe Arg His Arg
20 25 30
Ala Ala Lys Glu Leu Asn Ile Asp Asp Phe Glu Phe Ser Phe Thr Tyr
35 40 45
Leu Gln Tyr Phe Asp Lys Leu Glu Arg Ala Asn Phe Ala Leu Asn Gln
50 55 60
Leu Leu Asp Leu Thr Glu Asp Gly Thr Asp Trp Asp Asp Arg Asp Val
65 70 75 80
Ala Thr Ser Leu Glu Leu Thr Gly Asp Asp Gly Gly Trp Trp Ser Phe
85 90 95
Phe Thr Asn Leu Val Asp Lys Tyr Gly Ala Val Pro Ala Glu Val Met
100 105 110
Pro Glu Val His Ser Ser Gly His Thr Asp Gln Met Asn Arg Asp Ile
115 120 125
Ala Thr Ile Ile Arg Arg Ala Ala His Arg Ala Val Glu Gly Glu Gly
130 135 140
Asp Arg Gly Gly Ile Val Lys Gln Ala Arg Pro Asp Ile Gln Arg
145 150 155

<210> 2403
<211> 387
<212> DNA
<213> Homo sapiens

<400> 2403
ntcatgaacg gcgataaccc gctggactcg tctgcggttc acccggaagc ctacccgctg
60
gtgcagcgta ttgccgccga gaccggccgt gatatccgtt cgctgatcgg tgacgccgcg
120

ttcctcaagc gcctggaccc gaagaagtac accgacgaaa ccttcggtgt gccgaccatc
180
accgacatcc tgcaagagct ggaaaaacct ggccgcgacc cgcgtcccga gttcaagacc
240
gccgagttcc aggacggtgt tgaagacctc aaggacctgc agccgggcat gatcctcgaa
300
ggcgtggtca ccaacgtgac caactttggc gcctttgtgg atatcggcgt gcatcaggac
360
ggtttggtgc acatctctgc actttcg
387

<210> 2404
<211> 129
<212> PRT
<213> Homo sapiens

<400> 2404
Xaa Met Asn Gly Asp Asn Pro Leu Asp Ser Ser Ala Val His Pro Glu
 1   5   10   15
Ala Tyr Pro Leu Val Gln Arg Ile Ala Ala Glu Thr Gly Arg Asp Ile
            20   25   30
Arg Ser Leu Ile Gly Asp Ala Ala Phe Leu Lys Arg Leu Asp Pro Lys
        35   40   45
Lys Tyr Thr Asp Glu Thr Phe Gly Val Pro Thr Ile Thr Asp Ile Leu
    50   55   60
Gln Glu Leu Glu Lys Pro Gly Arg Asp Pro Arg Pro Glu Phe Lys Thr
65   70   75   80
Ala Glu Phe Gln Asp Gly Val Glu Asp Leu Lys Asp Leu Gln Pro Gly
                85   90   95
Met Ile Leu Glu Gly Val Val Thr Asn Val Thr Asn Phe Gly Ala Phe
            100   105   110
Val Asp Ile Gly Val His Gln Asp Gly Leu Val His Ile Ser Ala Leu
        115   120   125
Ser

<210> 2405
<211> 859
<212> DNA
<213> Homo sapiens

<400> 2405
ttgcaagtaa catcaaaagt catctacaga agcaaaagac aaaaaggccc ctccacctgc
60
aaattaaatg gaataatttg ctttatgaga agctcaccat tggggtcatt cttatttttt
120
ctcactccac atttcactac aaaccaagga aagctccctc atggaccgac atctggtgag
180
ccttcatctc tcccctggca atgcctggcc acctgacacc tggcctccct cctctttcca
240
gcaatcctgg taccaacgaa tggctcacca ccacccaccc caatgcccag accgcagacc
300
tgcattcctc ccatctcaca gccccaaatc caaaccgtta ttcattctac ctcccatcct
360

actcctcacg aatttcttcc accgtagact ctggttaatt ggactgactg aagcccaggg
420
gtcagtttct gtcctaagag cgctccaggt ggctgcaccc tgtgcccaga gccaggcccc
480
ctgctatagg ctcgctgcac tccccctgca ggtgctgggg acaccgcaac cctcctcctg
540
gggacaccta cttgcctttg caggccctcg ggggtcactt ctcccaggaa gccgcctctg
600
ggtgaggtaa tatccctcta tcacagcatt ggccacacca cattgcaaac gctgctgggg
660
tccactgtct tcaccaatta caccatgagc tccacagact ccaggaccat ggcttctacc
720
tctcagttcc cagtgctagc tatggggccc agcacacagg gaacagcagt tcaattaccc
780
agttcactga agggcagacc tgggatcata cagggagcaa ggaagcttga gccccttcag
840
gagaagggga agaacgcgt
859

<210> 2406
<211> 149
<212> PRT
<213> Homo sapiens

<400> 2406
Met Asp Arg His Leu Val Ser Leu His Leu Ser Pro Gly Asn Ala Trp
 1   5   10   15
Pro Pro Asp Thr Trp Pro Pro Ser Ser Phe Gln Gln Ser Trp Tyr Gln
            20   25   30
Arg Met Ala His His His Pro Pro Gln Cys Pro Asp Arg Arg Pro Ala
        35   40   45
Phe Leu Pro Ser His Ser Pro Lys Ser Lys Pro Leu Phe Ile Leu Pro
    50   55   60
Pro Ile Leu Leu Leu Thr Asn Phe Phe His Arg Arg Leu Trp Leu Ile
65   70   75   80
Gly Leu Thr Glu Ala Gln Gly Ser Val Ser Val Leu Arg Ala Leu Gln
                85   90   95
Val Ala Ala Pro Cys Ala Gln Ser Gln Ala Pro Cys Tyr Arg Leu Ala
            100   105   110
Ala Leu Pro Leu Gln Val Leu Gly Thr Pro Gln Pro Ser Ser Trp Gly
        115   120   125
His Leu Leu Ala Phe Ala Gly Pro Arg Gly Ser Leu Leu Pro Gly Ser
    130   135   140
Arg Leu Trp Val Arg
145

<210> 2407
<211> 303
<212> DNA
<213> Homo sapiens

<400> 2407
nacgcgtggt ttatcttcag catggtgatc gcgattggtt tagccgttat ggctgcggtc
60

gtattcatcg agcaaggcca gcgacgtatc ccggtgcagt acgccaagcg gatggtgggg
120
cgccgaatgt ttggtggctc gacgacgtac attccgctca aggtaaacca atctggcgtt
180
atcccggtca tctttgcctc gtcgatcctg taccttccgg tgctctacgc aactttccgg
240
ccgcagacgt ccgcggcaaa gtggatcggt cactacttca cgcgcggtga ccatccggtg
300
tac
303

<210> 2408
<211> 101
<212> PRT
<213> Homo sapiens

<400> 2408
Xaa Ala Trp Phe Ile Phe Ser Met Val Ile Ala Ile Gly Leu Ala Val
 1   5   10   15
Met Ala Ala Val Val Phe Ile Glu Gln Gly Gln Arg Arg Ile Pro Val
            20   25   30
Gln Tyr Ala Lys Arg Met Val Gly Arg Arg Met Phe Gly Gly Ser Thr
        35   40   45
Thr Tyr Ile Pro Leu Lys Val Asn Gln Ser Gly Val Ile Pro Val Ile
    50   55   60
Phe Ala Ser Ser Ile Leu Tyr Leu Pro Val Leu Tyr Ala Thr Phe Arg
65   70   75   80
Pro Gln Thr Ser Ala Ala Lys Trp Ile Gly His Tyr Phe Thr Arg Gly
                85   90   95
Asp His Pro Val Tyr
            100

<210> 2409
<211> 322
<212> DNA
<213> Homo sapiens

<400> 2409
ccatggtttc aagcccccat tgtgtcagcc cagagagcaa ctggagaccc tctgacacca
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cctcccggcc caacaggagg ggaagccgaa attcagattg tggaaactgc ctacaatttt
120
cttccggcca aatgaccctc cctaggctac caagaccctg gcctaagggg agccgaggtc
180
tcggcccgac tgcagacgcc cgcaccctga ctccagatgc ctccgaggca tccaggtggg
240
ccctgagggg cctgctgtgg ctttgttctt gttggctggg ctgggggtct gacctggtga
300
gggacatgag tgtcagtgtg gg
322

<210> 2410
<211> 106
<212> PRT

<213> Homo sapiens

<400> 2410
Met Val Ser Ser Pro His Cys Val Ser Pro Glu Ser Asn Trp Arg Pro
1 5 10 15
Ser Asp Thr Thr Ser Arg Pro Asn Arg Arg Gly Ser Arg Asn Ser Asp
20 25 30
Cys Gly Asn Cys Leu Gln Phe Ser Ser Gly Gln Met Thr Leu Pro Arg
35 40 45
Leu Pro Arg Pro Trp Pro Lys Gly Ser Arg Gly Leu Gly Pro Thr Ala
50 55 60
Asp Ala Arg Thr Leu Thr Pro Asp Ala Ser Glu Ala Ser Arg Trp Ala
65 70 75 80
Leu Arg Gly Leu Leu Trp Leu Cys Ser Cys Trp Leu Gly Trp Gly Ser
85 90 95
Asp Leu Val Arg Asp Met Ser Val Ser Val
100 105

<210> 2411
<211> 371
<212> DNA
<213> Homo sapiens

<400> 2411
ccatgggctg ggtgctggag acacgagatc aggcaggccc tgcccctggg gctcattcta
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gggtctgcgg cagacaggga gacagaggga gctgtgagag ccctgaggct gagtggcttt
120
ctggggaagc accatcccta gggacctccg cgttcggtca gtggccgctg ctgtcggtgt
180
gcagagcaga ggctggggcg agagtggtca gcaggcctgc tggtggcagc ttgtgcagga
240
agggaggatg gaggttggct tgtggctggc aagagggtgg catgcacgtc gctgaaaggc
300
aggcctgggc ccgaggcctg ggtgtgggga cgcctgagga gactgtacag tgtggagtcg
360
gggggctgc g
371

<210> 2412
<211> 123
<212> PRT
<213> Homo sapiens

<400> 2412
Met Gly Trp Val Leu Glu Thr Arg Asp Gln Ala Gly Pro Ala Pro Gly
1 5 10 15
Ala His Ser Arg Val Cys Gly Arg Gln Gly Asp Arg Gly Ser Cys Glu
20 25 30
Ser Pro Glu Ala Glu Trp Leu Ser Gly Glu Ala Pro Ser Leu Gly Thr
35 40 45
Ser Ala Phe Gly Gln Trp Pro Leu Leu Ser Val Cys Arg Ala Glu Ala
50 55 60
Gly Ala Arg Val Val Ser Arg Pro Ala Gly Gly Ser Leu Cys Arg Lys

```
65                  70                  75                  80
Gly Gly Trp Arg Leu Ala Cys Gly Trp Gln Glu Gly Gly Met His Val
                85                  90                  95
Ala Glu Arg Gln Ala Trp Ala Arg Gly Leu Gly Val Gly Thr Pro Glu
            100                 105                 110
Glu Thr Val Gln Cys Gly Val Gly Gly Ala Ala
        115                 120
```

<210> 2413
<211> 784
<212> DNA
<213> Homo sapiens

<400> 2413
cccgggagag ttgggcgggg caggggtgtt catggcatac tcgggattgt gtcatttggt
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gtggctggat ttagggtgca tataaaggca gtgaggctgg agaagtattc taggtctgct
120
taggctcact gaggaattgg ggttcttcct gaagagcatg gagcccttgg aggacctcca
180
cagcaggcag agagacggca gcctcctggg atctgattgc ccagccccac ttacacaggt
240
ggctgaggtg agctcttccc atggagtgca tccttcctga tcagcctgag gagagcaggg
300
ccccaccatc ctgcacctgg tgcagaaaaa ccctgtgaag ctgcactaca gaaagacacc
360
accaggtggc aggcctggag attgcatgga ggccccgccc cccccaacca attctttgat
420
aatagcacag tgttgaagag agggggccat aaaagactga atccctgttc atgccaggct
480
ggctctgccc aacatatatg agactgcaag ttctgccact gtgggctgtg tacccacaag
540
ccacaggtcc ctctgaacct gtgaatcagg tcttgggagc tattcgagca ggctggattt
600
tctcctctgc ctcgggggac ctgagagtaa gttacagact tcatgaccct tcaccccaaa
660
acacttgagt atgtatcacc taagaacaag ggcattctcc tgtagaacca caatgcaatt
720
tgcaagttca ggaaatttaa ctgatacaat actattatct aattacggag agaagacaac
780
gcgt
784

<210> 2414
<211> 137
<212> PRT
<213> Homo sapiens

<400> 2414
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Met Lys Ser Val Thr Tyr Ser Gln Val Pro Arg Gly Arg Gly Glu Asn
 1               5                  10                  15
Pro Ala Cys Ser Asn Ser Ser Gln Asp Leu Ile His Arg Phe Arg Gly
            20                  25                  30
Thr Cys Gly Leu Trp Val His Ser Pro Gln Trp Gln Asn Leu Gln Ser
```

```
        35                  40                  45
His Ile Cys Trp Ala Glu Pro Ala Trp His Glu Gln Gly Phe Ser Leu
    50                  55                  60
Leu Trp Pro Pro Leu Phe Asn Thr Val Leu Leu Ser Lys Asn Trp Leu
65                  70                  75                  80
Gly Gly Ala Gly Pro Pro Cys Asn Leu Gln Ala Cys His Leu Val Val
                85                  90                  95
Ser Phe Cys Ser Ala Ala Ser Gln Gly Phe Ser Ala Pro Gly Ala Gly
            100                 105                 110
Trp Trp Gly Pro Ala Leu Leu Arg Leu Ile Arg Lys Asp Ala Leu His
        115                 120                 125
Gly Lys Ser Ser Pro Gln Pro Pro Val
    130                 135
```

<210> 2415
<211> 2164
<212> DNA
<213> Homo sapiens

<400> 2415
ctcgtgccag cgtcctcgcg ggtctgaatg gaagggtcga ggtcgtcgtc ggcggcgagc
60
agatcctgaa gccagaactc caccccggcg cccgcgccat gcggcgggag aggtgcggcg
120
ccccccaccc gcgtcgccgc catggaggtg ctgcggcgct cttcggtctt cgctgcggag
180
atcatggacg cctttgatcg ctggcccaca gacaaggagc tggtggccca ggctaaagca
240
ctaggccggg agtacgtgca cgcgcggctt ttgcgcgccg gcctctcctg gagcgctcca
300
gagcgtgcct cgcctgcccc tggaggacgc ctggctgagg tgtgcgcggt gctgctgcgc
360
ctgggcgatg agctggagat gatccggccc agcgtctacc gcaacgtggc gcgtcagctg
420
cacatctccc tgcagtctga gcctgtggtg accgatgcgt tcctggccgt ggctggccac
480
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600
ctgggggagt tcgtgcgcaa gaccctggca acctggctgc ggagacgcgg cggatggact
660
gatgtcctca agtgtgtggt cagcacagac cctggcctcc gctcccactg gctggtggct
720
gcactctgca gcttcggccg cttcctgaag gctgccttct tcgtgctgct gccagagaga
780
tgagctgccc acctggcagt ggccgcagcc tggccctctg ggcccaacgc aggaggccct
840
cagcacccga acacatcttc ctcctcccca cccgagcctg gagcactcta acctcggaga
900
ccccctaagc cccgttcctc cgcagaccca ggccctccgg aagggtgagt ggggaggggc
960
tttcctgagc ctggagctgg gctttggggc agcctgcgac cctccccgct tgtgtccctt
1020

ctcctgtgat ctctgtgttt tccctttttct ttctggggcc aggaagtcag ggtcaactcc
1080
caggcctcag gtgaaggggc ccagaacacc tgctctcacc tgagccccag gtgaaggggc
1140
ccgggaacac ctgctctcac ctgagcccca ggtgaagggg cccgggaaca cctgctctca
1200
cctgagcccc tggtgaaggg gcccggaaca cctgctctca cctgagcccc aggtgaaggg
1260
gcccggaaca cctgctctca cctgagcccc aggtgaaggg gcccggaaca cttgctctca
1320
cctgagcccc aggtgaaggg gcccgggaac acctctcacc tgaacccggg ggtcccatcc
1380
caggaagaag ggccatctca ggacatgagt cctcaggggc cctgcacatt caatctgaag
1440
gtgaccctgg cctggctgaa gctggaagag ctgtggggac tcagcctgta aacagagcgt
1500
aaggttcaca tgctggttgc ttaatccgtt tctggaggaa gagtatgaca cccacttgtg
1560
atggggtcct tgtgcggtgg ggaccggggc cggcgggctc caggccagca cacctaaccc
1620
atggatgtgg aacctacggc cgagaaggaa tgttgcatga gtcggatccc agtccattgt
1680
cagtggaggg tgagggtgac cccatctgct atttttgtgc tcatcctcat acaaccattt
1740
ggggatgtgc ctattagggc tccgtaagaa ctcagatgcc tgggaagccc agcccctcag
1800
gtgcccccac acacagcctt cccttgacgc ctacatttct aggcacatgt gaggcatctt
1860
tcctggagcc ccgagccagc cctgtccctc cccagtgcag catggcactc aggagataca
1920
ggctggacat ggggcagtcg ttctggggag gcctggccta gcagccaccc acctgagccc
1980
tcccggccag gcttcgtgct ggggtgggcc atgtgccagg acaggagggt cccggcggaa
2040
agccagcccc ggactcatcg tgacattgag atcccactgg agggtagggg tggtaataaa
2100
cttctccaaa cgataaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
2160
aaaa
2164

<210> 2416
<211> 213
<212> PRT
<213> Homo sapiens

<400> 2416
Met Glu Val Leu Arg Arg Ser Ser Val Phe Ala Ala Glu Ile Met Asp
 1   5   10   15
Ala Phe Asp Arg Trp Pro Thr Asp Lys Glu Leu Val Ala Gln Ala Lys
            20   25   30
Ala Leu Gly Arg Glu Tyr Val His Ala Arg Leu Leu Arg Ala Gly Leu
        35   40   45
Ser Trp Ser Ala Pro Glu Arg Ala Ser Pro Ala Pro Gly Gly Arg Leu

```
    50                  55                  60
Ala Glu Val Cys Ala Val Leu Leu Arg Leu Gly Asp Glu Leu Glu Met
65                  70                  75                  80
Ile Arg Pro Ser Val Tyr Arg Asn Val Ala Arg Gln Leu His Ile Ser
                85                  90                  95
Leu Gln Ser Glu Pro Val Val Thr Asp Ala Phe Leu Ala Val Ala Gly
            100                 105                 110
His Ile Phe Ser Ala Gly Ile Thr Trp Gly Lys Val Val Ser Leu Tyr
        115                 120                 125
Ala Val Ala Ala Gly Leu Ala Val Asp Cys Val Arg Gln Ala Gln Pro
    130                 135                 140
Ala Met Val His Ala Leu Val Asp Cys Leu Gly Glu Phe Val Arg Lys
145                 150                 155                 160
Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly Trp Thr Asp Val Leu
                165                 170                 175
Lys Cys Val Val Ser Thr Asp Pro Gly Leu Arg Ser His Trp Leu Val
            180                 185                 190
Ala Ala Leu Cys Ser Phe Gly Arg Phe Leu Lys Ala Ala Phe Phe Val
        195                 200                 205
Leu Leu Pro Glu Arg
    210
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<210> 2417
<211> 615
<212> DNA
<213> Homo sapiens

<400> 2417
nnagatcttt ggaatgggca gaactactaa atacagttaa tgcaccaaca agggtaagta
60
aagctgattt gattttcata ttgatacctc aatagttaag tgaaggacta gttattgctc
120
cagttgttag ttttcacact ttaaaaaagg ctttcaatta taaaatcttt ctccattatt
180
acgtttttttc acaactgtga tccacgccac agttgcaaat aatcaacata gaaaaattaa
240
ataacataat tgatgaaaag ttagtttttc acaaaaatac gaaaaatttc atcacctaga
300
gaggaaaatg ttatgacaac ctatttcgat aaaattgaaa aaatctcctt tgagggagaa
360
aaatccacaa atccttttgc tttcaaacat tatgatgcta atcaagtaat tttaggtaaa
420
actatggctg aacatttacg cttaacggtg tgttattggc ataccttttg ctggaatggg
480
aatgatatgt ttgggctagg ttctttggaa cgaagttggc agaaaaattc aaatttgctt
540
gctggcgcag aacaaaaagc cgatattgct tttgagtttt tgaataagtt aggcgtgcct
600
tattattgtt ttcat
615

<210> 2418
<211> 101
<212> PRT

<213> Homo sapiens

<400> 2418
Met Thr Thr Tyr Phe Asp Lys Ile Glu Lys Ile Ser Phe Glu Gly Glu
1 5 10 15
Lys Ser Thr Asn Pro Phe Ala Phe Lys His Tyr Asp Ala Asn Gln Val
20 25 30
Ile Leu Gly Lys Thr Met Ala Glu His Leu Arg Leu Thr Val Cys Tyr
35 40 45
Trp His Thr Phe Cys Trp Asn Gly Asn Asp Met Phe Gly Leu Gly Ser
50 55 60
Leu Glu Arg Ser Trp Gln Lys Asn Ser Asn Leu Leu Ala Gly Ala Glu
65 70 75 80
Gln Lys Ala Asp Ile Ala Phe Glu Phe Leu Asn Lys Leu Gly Val Pro
85 90 95
Tyr Tyr Cys Phe His
100

<210> 2419
<211> 318
<212> DNA
<213> Homo sapiens

<400> 2419
aaattttcag aagtcctggt gttgcgcggt caaacaggga ccgaggaggg acgaccgcct
60
ccccgtgacg ctgcttcttc ttcctgcctg cagctgaggg gtctgttttg tgtcgcttcc
120
gctccttcct cacgtacaca gggggcagct tagcctctgg gatgggagtg gcttcataca
180
tgagacacat gcccgagtcg aggtagatgt cgctgtcgtc ctgcggcggg gtgggtgggg
240
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aggcatcccc tcacgcgt
318

<210> 2420
<211> 98
<212> PRT
<213> Homo sapiens

<400> 2420
Met Glu Tyr Val Tyr Glu Asp Val Asp Gly Gln Thr Glu Val Met Pro
1 5 10 15
Phe Trp Thr Pro Pro Thr Pro Pro Gln Asp Asp Ser Asp Ile Tyr Leu
20 25 30
Asp Ser Gly Met Cys Leu Met Tyr Glu Ala Thr Pro Ile Pro Glu Ala
35 40 45
Lys Leu Pro Pro Val Tyr Val Arg Lys Glu Arg Lys Arg His Lys Thr
50 55 60
Asp Pro Ser Ala Ala Gly Arg Lys Lys Lys Gln Arg His Gly Glu Ala
65 70 75 80
Val Val Pro Pro Arg Ser Leu Phe Asp Arg Ala Thr Pro Gly Leu Leu

85 90 95
Lys Ile

<210> 2421
<211> 420
<212> DNA
<213> Homo sapiens

<400> 2421
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120
ctgtcgcaag tctgagtagg gattatcatg acggatacaa cttcagcccc gcgttacgcg
180
ctgcgtgggc tacagcttat tggctggcgt gacatgcaac acgcgctgga tttcctgttc
240
gcggacgggc agatgaaatc gggcacgctg gtggccatca acgcagaaaa gatgctggcg
300
gttgaagata atgcggaagt gaaaagcctg attgaagccg cggagtttaa atacccggcc
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ggtattagcg tagtgcgttc aattcgtaaa aagttccccc acgctggagt gtgctcgcga
420

<210> 2422
<211> 91
<212> PRT
<213> Homo sapiens

<400> 2422
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20 25 30
Asp Gly Gln Met Lys Ser Gly Thr Leu Val Ala Ile Asn Ala Glu Lys
35 40 45
Met Leu Ala Val Glu Asp Asn Ala Glu Val Lys Ser Leu Ile Glu Ala
50 55 60
Ala Glu Phe Lys Tyr Pro Ala Gly Ile Ser Val Val Arg Ser Ile Arg
65 70 75 80
Lys Lys Phe Pro His Ala Gly Val Cys Ser Arg
85 90

<210> 2423
<211> 371
<212> DNA
<213> Homo sapiens

<400> 2423
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gagctcaacg ccaagcacaa gaagatattg gaaggtcttc tacggcatcc tgagaataga
120

gaatgcgcag actgcaagtc aaagggtcct cgatgggcaa gtgtgaatct aggtatcttt
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atatgcatga catgttctgg cattcataga agcctggggg tgcacatatc taaggtaaga
240
tctgccaccc tggatacatg gctgccagag caagttgcat ttattcaatc aatgggaaac
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360
gagaatttga t
371

<210> 2424
<211> 112
<212> PRT
<213> Homo sapiens

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Met Asn Glu Lys Ala Ser Val Ser Lys Glu Leu Asn Ala Lys His Lys
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Lys Ile Leu Glu Gly Leu Leu Arg His Pro Glu Asn Arg Glu Cys Ala
            20   25   30
Asp Cys Lys Ser Lys Gly Pro Arg Trp Ala Ser Val Asn Leu Gly Ile
        35   40   45
Phe Ile Cys Met Thr Cys Ser Gly Ile His Arg Ser Leu Gly Val His
    50   55   60
Ile Ser Lys Val Arg Ser Ala Thr Leu Asp Thr Trp Leu Pro Glu Gln
65   70   75   80
Val Ala Phe Ile Gln Ser Met Gly Asn Glu Lys Ala Asn Ser Tyr Trp
                85   90   95
Glu Ala Glu Leu Pro Pro Asn Tyr Asp Arg Val Gly Ile Glu Asn Leu
            100   105   110

<210> 2425
<211> 411
<212> DNA
<213> Homo sapiens

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180
cgctgcaagg aagccggcat gaacgactgc ctgttcaagc ccatcagcct gaccaccctc
240
aaccagaaac tcgccgacgt cacgccgcgc ccgcgtccga gccaggccgc cttcagcctc
300
gacggcctgc acgccctgac cgggggcgag ccgctgctga tgcgtcgctt gatcgacgag
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411

<210> 2426

<211> 137
<212> PRT
<213> Homo sapiens

<400> 2426
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Asp Cys Asn Met Pro Val Leu Asn Gly Tyr Glu Met Thr Arg Arg Leu
20 25 30
Arg Glu His Glu Ala Xaa Ala Met Thr Ser Arg Pro Ala Arg Gly Phe
35 40 45
Gly Phe Thr Ala His Ala Gln Pro Glu Glu Arg Pro Arg Cys Lys Glu
50 55 60
Ala Gly Met Asn Asp Cys Leu Phe Lys Pro Ile Ser Leu Thr Thr Leu
65 70 75 80
Asn Gln Lys Leu Ala Asp Val Thr Pro Arg Pro Arg Pro Ser Gln Ala
85 90 95
Ala Phe Ser Leu Asp Gly Leu His Ala Leu Thr Gly Gly Glu Pro Leu
100 105 110
Leu Met Arg Arg Leu Ile Asp Glu Leu Leu Ser Ser Cys Gln Ala Ala
115 120 125
Arg Glu Ala Leu Leu Gly Leu Pro Ile
130 135

<210> 2427
<211> 293
<212> DNA
<213> Homo sapiens

<400> 2427
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tggagcgtaa aatgttgcag agcccagcta gaagccagga ggagcagaca ccctgctgat
120
ggagcccaac aagaaagatg ttgtgtccct cctggtgagc gctgtcccag tgcacccgat
180
aatggcgaag aaaatgtgcc tctttcagga aaagtatagg aaatgagaga agactgtgac
240
aactcatgac ctgcatcctt aatatccagt gacttcatct ccccttcacg cgt
293

<210> 2428
<211> 72
<212> PRT
<213> Homo sapiens

<400> 2428
His Asn Lys Gly Leu Gly Ile Leu Val Pro Cys Ala Ile Xaa Ala Ala
1 5 10 15
Phe Leu Leu Ile Trp Ser Val Lys Cys Cys Arg Ala Gln Leu Glu Ala
20 25 30
Arg Arg Ser Arg His Pro Ala Asp Gly Ala Gln Gln Glu Arg Cys Cys
35 40 45
Val Pro Pro Gly Glu Arg Cys Pro Ser Ala Pro Asp Asn Gly Glu Glu

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    50                  55                  60
Asn Val Pro Leu Ser Gly Lys Val
65                  70

<210> 2429
<211> 428
<212> DNA
<213> Homo sapiens

<400> 2429
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atcgccgaga tggcggggct acaggctgct cagtcgatcc gggaatcctt gaacaaggct
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gatgtcctgc tcaatggggt agagacgtcg accggtccgc agccgggtgc gcttgctttg
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ctggaacagg ccgtacatga gctggatggc actggggatg ctgatcctcg cgccgctgag
240
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gcggctattc agcggctgtt gagggcgcgc accaccaccc tcgacgatct cctcgactcc
420
actgcggc
428

<210> 2430
<211> 142
<212> PRT
<213> Homo sapiens

<400> 2430
Ser Arg Arg Val Gly Glu Val Asp Ala Val Asp Pro Lys Pro His Glu
 1               5                  10                  15
Asp Asp Asp Leu Ile Ala Glu Met Ala Gly Leu Gln Ala Ala Gln Ser
            20                  25                  30
Ile Arg Glu Ser Leu Asn Lys Ala Asp Val Leu Leu Asn Gly Val Glu
        35                  40                  45
Thr Ser Thr Gly Pro Gln Pro Gly Ala Leu Ala Leu Leu Glu Gln Ala
    50                  55                  60
Val His Glu Leu Asp Gly Thr Gly Asp Ala Asp Pro Arg Ala Ala Glu
65                  70                  75                  80
Leu Ala Glu Arg Ala Arg Gln Met Ser Tyr Asp Leu Thr Asp Leu Ala
                85                  90                  95
Ala Ser Val Ala Gly His Ala Ala Arg Ala Glu Ala Asp Pro Gln Arg
            100                 105                 110
Leu Glu Glu Leu Gly Gly Arg Leu Ala Ala Ile Gln Arg Leu Leu Arg
        115                 120                 125
Ala Arg Thr Thr Thr Leu Asp Asp Leu Leu Asp Ser Thr Ala
    130                 135                 140

<210> 2431
<211> 409
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<212> DNA
<213> Homo sapiens

<400> 2431
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120
aatggcgagg taacaatttc tggggcaaaa aatgccgcat taccaatcct atttgctact
180
ttattatctg agggtgatat caatttaagc aatgtaccgc ttttaaaaga tattgccacc
240
actatcgagt tgttaaaaga gctgggtgct actgctactc agactcaaca ctgcgtgcat
300
attaatgcga aagaagttaa gaactatact gcttcttatg aattagtgag aagtatgcgt
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409

<210> 2432
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2432
Met Gly Gln Phe Ile Ile Gln Gly Gly Cys Gln Leu Asn Gly Glu Val
 1   5   10   15
Thr Ile Ser Gly Ala Lys Asn Ala Ala Leu Pro Ile Leu Phe Ala Thr
            20   25   30
Leu Leu Ser Glu Gly Asp Ile Asn Leu Ser Asn Val Pro Leu Leu Lys
        35   40   45
Asp Ile Ala Thr Thr Ile Glu Leu Leu Lys Glu Leu Gly Ala Thr Ala
    50   55   60
Thr Gln Thr Gln His Cys Val His Ile Asn Ala Lys Glu Val Lys Asn
65   70   75   80
Tyr Thr Ala Ser Tyr Glu Leu Val Arg Ser Met Arg Ala Ser Ile Leu
                85   90   95
Ala Leu Gly Pro Leu Val Ala Arg Phe Gly Glu Ala
            100   105

<210> 2433
<211> 655
<212> DNA
<213> Homo sapiens

<400> 2433
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120
gctctatgat gctcacgtaa caatgaaatc acggaatctc tctctcagaa catttccccg
180
ttgtgaagca gcacgtgact ataatctttt cccaggttta cccctgaagt tcaagtgcaa
240

tgcccctgca cagcacagag caggggacga taggaggcgt gccttctcca gctgaaccac
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cgggccagcc gggcgggcag tgggggttgg ggggagggtt gacccattgg tgctgccacg
360
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420
atctggggac atcagggaaa gcagcaaggg tctggctgat tgtgcaaaaa gaacttttc
480
tgtgactgcc gtgttccaaa cacacccttt gcttttacaa aaacccaaac tgggaggttt
540
agcaaaaggc acagtttcag agcataataa agacagagca gaatgggaga ggaggttaat
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655

<210> 2434
<211> 137
<212> PRT
<213> Homo sapiens

<400> 2434
Met Ala His Leu Ile Asn Leu Leu Ser His Ser Ala Leu Ser Leu Leu
1 5 10 15
Cys Ser Glu Thr Val Pro Phe Ala Lys Pro Pro Ser Leu Gly Phe Cys
20 25 30
Lys Ser Lys Gly Cys Val Trp Asn Thr Ala Val Thr Glu Lys Val Leu
35 40 45
Phe Ala Gln Ser Ala Arg Pro Leu Leu Leu Ser Leu Met Ser Pro Asp
50 55 60
Trp Ala Phe Ile Val Pro Cys Thr Glu Ala Ser Leu Ser Pro Arg Ser
65 70 75 80
Cys Leu Phe Gly Arg Gly Ser Thr Asn Gly Ser Thr Leu Pro Pro Thr
85 90 95
Pro Thr Ala Arg Pro Ala Gly Pro Val Val Gln Leu Glu Lys Ala Arg
100 105 110
Leu Leu Ser Ser Pro Ala Leu Cys Cys Ala Gly Ala Leu His Leu Asn
115 120 125
Phe Arg Gly Lys Pro Gly Lys Arg Leu
130 135

<210> 2435
<211> 401
<212> DNA
<213> Homo sapiens

<400> 2435
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120
gcagatattg accaagcggt ccagggtgcg atgggcgcca agatgcgcaa tatcggcgag
180
gcctgcaccg cagctaaccg cttcttggtc cacgagtctg ttgctgagga gttctctgag
240

aaactcgttg cggagtttga gaagctcaat ctgggcaatg gtatggacga aggtattacc
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tgcggacctc tcgtcgagtc caaggctttg gagagcattg cggcattggt ggacgatgct
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401

<210> 2436
<211> 133
<212> PRT
<213> Homo sapiens

<400> 2436
Lys Leu Ser Phe Thr Gly Ser Thr Pro Val Gly Arg Thr Leu Leu Lys
1 5 10 15
Xaa Ala Ala Asp Asn Val Leu Arg Thr Ser Met Glu Leu Gly Xaa Asn
20 25 30
Ala Pro Phe Ile Val Phe Glu Asp Ala Asp Ile Asp Gln Ala Val Gln
35 40 45
Gly Ala Met Gly Ala Lys Met Arg Asn Ile Gly Glu Ala Cys Thr Ala
50 55 60
Ala Asn Arg Phe Leu Val His Glu Ser Val Ala Glu Glu Phe Ser Glu
65 70 75 80
Lys Leu Val Ala Glu Phe Glu Lys Leu Asn Leu Gly Asn Gly Met Asp
85 90 95
Glu Gly Ile Thr Cys Gly Pro Leu Val Glu Ser Lys Ala Leu Glu Ser
100 105 110
Ile Ala Ala Leu Val Asp Asp Ala Ala Glu Lys Gly Ala Thr Ile Ser
115 120 125
Thr Gly Gly Lys Arg
130

<210> 2437
<211> 449
<212> DNA
<213> Homo sapiens

<400> 2437
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atggtatgta tttttcaagc tagacgttca taatggtaga acatgaggag gaaaactgcc
180
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300
tgcctatgta cggatttggt ccaatgcctc agcctgacct cagggacctt cgggggtctg
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449

<210> 2438
<211> 99
<212> PRT
<213> Homo sapiens

<400> 2438
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Cys Asp Thr Val Thr Gly Pro Cys Ser Gly Leu Asp Ser Cys Ile Arg
20 25 30
Val Leu Asp Gly Asn Arg Trp His Ser Lys Gly Gly Ala Gln Phe Arg
35 40 45
Glu Met Pro Met Tyr Gly Phe Gly Pro Met Pro Gln Pro Asp Leu Arg
50 55 60
Asp Leu Arg Gly Ser Ala Pro Arg Pro Pro Leu His Ile Cys Asp Pro
65 70 75 80
Thr His Phe His Pro Ser Ala Thr Phe Lys Phe Gln Ser Phe His Phe
85 90 95
Ile Ala Val

<210> 2439
<211> 4425
<212> DNA
<213> Homo sapiens

<400> 2439
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240
aagcggaggg acagcaatgc tgccccttg ttggaaatcc tcactgacca gtgcctcacc
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420
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2280
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4425

<210> 2440
<211> 1306
<212> PRT
<213> Homo sapiens

<400> 2440
Pro Ser Ala Ser Asp Gln Ser Thr Trp Tyr Leu Asp Glu Ser Thr Leu
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Thr Asp Asn Ile Lys Lys Thr Leu His Lys Phe Cys Gly Pro Ser Pro
20 25 30
Val Val Phe Ser Asp Val Asn Ser Met Tyr Leu Ser Ser Thr Glu Pro
35 40 45
Pro Ala Ala Ala Glu Trp Ala Cys Leu Leu Arg Pro Leu Arg Gly Arg
50 55 60
Glu Pro Glu Gly Val Trp Asn Leu Leu Ser Ile Val Arg Glu Met Phe
65 70 75 80
Lys Arg Arg Asp Ser Asn Ala Ala Pro Leu Leu Glu Ile Leu Thr Asp
85 90 95
Gln Cys Leu Thr Tyr Glu Gln Ile Thr Gly Trp Trp Tyr Ser Val Arg
100 105 110
Thr Ser Ala Ser His Ser Ser Ala Ser Gly His Thr Gly Arg Ser Asn
115 120 125
Gly Gln Ser Glu Val Ala Ala His Ala Cys Ala Ser Met Cys Asp Glu
130 135 140
Met Val Thr Leu Trp Arg Leu Ala Val Leu Asp Pro Ala Leu Ser Pro
145 150 155 160
Gln Arg Arg Arg Glu Leu Cys Thr Gln Leu Arg Gln Trp Gln Leu Lys
165 170 175
Val Ile Glu Asn Val Lys Arg Gly Gln His Lys Lys Thr Leu Glu Arg
180 185 190
Leu Phe Pro Gly Phe Arg Pro Ala Val Glu Ala Cys Tyr Phe Asn Trp
195 200 205
Glu Glu Ala Tyr Pro Leu Pro Gly Val Thr Tyr Ser Gly Thr Asp Arg
210 215 220
Lys Leu Ala Leu Cys Trp Ala Arg Ala Leu Pro Ser Arg Pro Gly Ala
225 230 235 240
Ser Arg Ser Gly Gly Leu Glu Glu Ser Arg Asp Arg Pro Arg Pro Leu
245 250 255
Pro Thr Glu Pro Ala Val Arg Pro Lys Glu Pro Gly Thr Lys Arg Lys

```
            260                 265                 270
Gly Leu Gly Glu Gly Val Pro Ser Ser Gln Arg Gly Pro Arg Arg Leu
        275                 280                 285
Ser Ala Glu Gly Gly Asp Lys Ala Leu His Lys Met Gly Pro Gly Gly
    290                 295                 300
Gly Lys Ala Lys Ala Leu Gly Gly Ala Gly Ser Gly Ser Lys Gly Ser
305                 310                 315                 320
Ala Gly Gly Gly Ser Lys Arg Arg Leu Ser Ser Glu Asp Ser Ser Leu
                325                 330                 335
Glu Pro Asp Leu Ala Glu Met Ser Leu Asp Asp Ser Ser Leu Ala Leu
            340                 345                 350
Gly Ala Glu Ala Ser Thr Phe Gly Gly Phe Pro Glu Ser Pro Pro Pro
        355                 360                 365
Cys Pro Leu His Gly Gly Ser Arg Gly Pro Ser Thr Phe Leu Pro Glu
    370                 375                 380
Pro Pro Asp Thr Tyr Glu Glu Asp Gly Gly Val Tyr Phe Ser Glu Gly
385                 390                 395                 400
Pro Glu Pro Pro Thr Ala Ser Val Gly Pro Pro Gly Leu Leu Pro Gly
                405                 410                 415
Asp Val Cys Thr Gln Asp Asp Leu Pro Ser Thr Asp Glu Ser Gly Asn
            420                 425                 430
Gly Leu Pro Lys Thr Lys Glu Ala Ala Pro Ala Val Gly Glu Glu Asp
        435                 440                 445
Asp Asp Tyr Gln Ala Tyr Tyr Leu Asn Ala Gln Asp Gly Ala Gly Gly
    450                 455                 460
Glu Glu Glu Lys Ala Glu Gly Gly Ala Gly Glu Glu His Asp Leu Phe
465                 470                 475                 480
Ala Gly Leu Lys Pro Leu Glu Gln Glu Ser Arg Met Glu Val Leu Phe
                485                 490                 495
Ala Cys Ala Glu Ala Leu His Ala His Gly Tyr Ser Ser Glu Ala Ser
            500                 505                 510
Arg Leu Thr Val Glu Leu Ala Gln Asp Leu Leu Ala Asn Pro Pro Asp
        515                 520                 525
Leu Lys Gly Lys Lys Asn Lys Val Ser Thr Ser Arg Gln Thr Trp Val
    530                 535                 540
Ala Thr Asn Thr Leu Ser Lys Ala Ala Phe Leu Leu Thr Val Leu Ser
545                 550                 555                 560
Glu Arg Pro Glu Arg His Asn Leu Ala Phe Arg Val Gly Met Phe Ala
                565                 570                 575
Leu Glu Leu Gln Arg Pro Pro Ala Ser Thr Lys Ala Leu Glu Val Lys
            580                 585                 590
Leu Ala Tyr Gln Glu Ser Glu Val Ala Ala Leu Leu Lys Lys Ile Pro
        595                 600                 605
Leu Gly Pro Ser Glu Met Ser Thr Met Arg Cys Arg Ala Glu Glu Leu
    610                 615                 620
Arg Glu Gly Thr Leu Cys Asp Tyr Arg Pro Val Leu Pro Leu Met Leu
625                 630                 635                 640
Ala Ser Phe Ile Phe Asp Val Leu Cys Ala Pro Val Val Ser Pro Thr
                645                 650                 655
Gly Ser Arg Pro Pro Ser Arg Asn Trp Asn Ser Glu Thr Pro Gly Asp
            660                 665                 670
Glu Glu Leu Gly Phe Glu Ala Ala Val Ala Ala Leu Gly Met Lys Thr
        675                 680                 685
Thr Val Ser Glu Ala Glu His Pro Leu Leu Cys Glu Gly Thr Arg Arg
```

690 695 700
Glu Lys Gly Asp Leu Ala Leu Ala Leu Met Ile Thr Tyr Lys Asp Asp
705 710 715 720
Gln Ala Lys Leu Lys Lys Ile Leu Asp Lys Leu Leu Asp Arg Glu Ser
725 730 735
Gln Thr His Lys Pro Gln Thr Leu Ser Ser Phe Tyr Ser Ser Ser Arg
740 745 750
Pro Thr Thr Ala Ser Gln Arg Ser Pro Ser Lys His Gly Gly Pro Ser
755 760 765
Ala Pro Gly Ala Leu Gln Pro Leu Thr Ser Gly Ser Ala Gly Pro Ala
770 775 780
Gln Pro Gly Ser Val Ala Gly Ala Gly Pro Gly Pro Thr Glu Gly Phe
785 790 795 800
Thr Glu Lys Asn Val Pro Glu Ser Ser Pro His Ser Pro Cys Glu Gly
805 810 815
Leu Pro Ser Glu Ala Ala Leu Thr Pro Arg Pro Glu Gly Lys Val Pro
820 825 830
Ser Arg Leu Ala Leu Gly Ser Arg Gly Gly Tyr Asn Gly Arg Gly Trp
835 840 845
Gly Ser Ser Gly Arg Pro Lys Lys Lys His Thr Gly Met Ala Ser Ile
850 855 860
Asp Ser Ser Ala Pro Glu Thr Thr Ser Asp Ser Ser Pro Thr Leu Ser
865 870 875 880
Arg Arg Pro Leu Arg Gly Gly Trp Ala Pro Thr Ser Trp Gly Arg Gly
885 890 895
Gln Asp Ser Asp Ser Ile Ser Ser Ser Ser Ser Asp Ser Leu Gly Ser
900 905 910
Ser Ser Ser Ser Gly Ser Arg Arg Ala Ser Ala Ser Gly Gly Ala Arg
915 920 925
Ala Lys Thr Val Glu Val Gly Arg Tyr Lys Gly Arg Arg Pro Glu Ser
930 935 940
His Ala Pro His Val Pro Asn Gln Pro Ser Glu Ala Ala Ala His Phe
945 950 955 960
Tyr Phe Glu Leu Ala Lys Thr Val Leu Ile Lys Ala Gly Gly Asn Ser
965 970 975
Ser Thr Ser Ile Phe Thr His Pro Ser Ser Ser Gly Gly His Gln Gly
980 985 990
Pro His Arg Asn Leu His Leu Cys Ala Phe Glu Ile Gly Leu Tyr Ala
995 1000 1005
Leu Gly Leu His Asn Phe Val Ser Pro Asn Trp Leu Ser Arg Thr Tyr
1010 1015 1020
Ser Ser His Val Ser Trp Ile Thr Gly Gln Ala Met Glu Ile Gly Ser
1025 1030 1035 1040
Ala Ala Leu Thr Ile Leu Val Glu Cys Trp Asp Gly His Leu Thr Pro
1045 1050 1055
Pro Glu Val Ala Ser Leu Ala Asp Arg Ala Ser Arg Ala Arg Asp Ser
1060 1065 1070
Asn Met Val Arg Ala Ala Ala Glu Leu Ala Leu Ser Cys Leu Pro His
1075 1080 1085
Ala His Ala Leu Asn Pro Asn Glu Ile Gln Arg Ala Leu Val Gln Cys
1090 1095 1100
Lys Glu Gln Asp Asn Leu Met Leu Glu Lys Ala Cys Met Ala Val Glu
1105 1110 1115 1120
Glu Ala Ala Lys Gly Gly Gly Val Tyr Pro Glu Val Leu Phe Glu Val

```
                1125                1130                1135
Ala His Gln Trp Phe Trp Leu Tyr Glu Gln Thr Ala Gly Gly Ser Ser
            1140                1145                1150
Thr Ala Arg Glu Gly Ala Thr Ser Cys Ser Ala Ser Gly Ile Arg Ala
        1155                1160                1165
Gly Gly Glu Ala Gly Arg Gly Met Pro Glu Gly Arg Gly Gly Pro Gly
    1170                1175                1180
Thr Glu Pro Val Thr Val Ala Ala Ala Ala Val Thr Ala Ala Ala Thr
1185                1190                1195                1200
Val Val Pro Val Ile Ser Val Gly Ser Ser Leu Tyr Pro Gly Pro Gly
                1205                1210                1215
Leu Gly His Gly His Ser Pro Gly Leu His Pro Tyr Thr Ala Leu Gln
            1220                1225                1230
Pro His Leu Pro Cys Ser Pro Gln Tyr Leu Thr His Pro Ala His Pro
        1235                1240                1245
Ala His Pro Met Pro His Met Pro Arg Pro Ala Val Phe Pro Val Pro
    1250                1255                1260
Ser Ser Ala Tyr Pro Gln Val Arg Pro Val Phe Cys Trp Gly Val Arg
1265                1270                1275                1280
His Gly Lys Ile Leu Gly Ile His Arg Gly Leu Glu Trp Val Leu Trp
                1285                1290                1295
Glu Tyr Asn Trp Ser Val Gly Glu Ser Trp
            1300                1305
```

<210> 2441
<211> 2244
<212> DNA
<213> Homo sapiens

<400> 2441

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nacgcgtgtg tgtctgcatg catccatgtg tctgtacatg tatgtctcca tgtgtggtgt
60
ggaggacaca gaaggatgga gggaaaggca ccactcacag aggcggcgct ggagaatttt
120
ccatttgtta ttttgggttt ggtgaacatg cactttgcgt catgcaaatc aggtttctaa
180
acattaacaa ccggagagaa atgacatttt ggggccgccg gtgactcttg cgtgcctctg
240
ctgccccctg gtggcagccc cgagtcactt ccagcagggc ccccccaccc caagggccca
300
gcctcgggca ggaagggtac aaagcccccg ccgtggttct gccacgaggt ctcctggaaa
360
tgaggggaac agcacagcga cgtccttgcg tcctaaatgc atcccctggt ggccgttttt
420
cgccacacag gcttggcaaa atctctgcgt cactgagcag cattttaacc tcttgaatga
480
gatgcctccg acctttttgga tcctctttct gcacctctca ggggacaggt cccgtctgta
540
cggcgctgcc tacgagaaac ccaagttcat tactgcagcc aaaggaaagg tgcaggcggt
600
gggaggctcc tgcaaggtga tgcgtctggc cataagtccc actgccttct cccacctgct
660
ggcctgtgcc cagcagttcc ggaagcagac ccaggcccag gtgtacagtg aggacatggc
720
```

cctgaacata ggctcggaac cagaaggcct gcaggtggaa gagaaggagc gccctgtgca
780
gaggctcagt agcgtcctgg ggcccctgga ggagcttctg cagccgctat tccccctgct
840
cagcctctcc aaggccagag tgcagacacc tgcggttgtt gccgattcag ggaagtcgaa
900
gggcaaagac aaggagagga aaacgtccac aggacaacac agcacagtcc agcctgaggt
960
tgccgataag atagtcctgg tcacagacag acatctcctg gagctgccac tggaaggtct
1020
ctctgtgttc gatgaaggga caatttcctc tgtgtcacga gaattttctc ttcaaatgct
1080
gtggaatcgc ctccataaag aagagacaga aggtggcgtg aaaaaggagg gaagaagcag
1140
agaccccaaa aagagaagcc tagcgaagaa gggcaggaag ggcagcatcc cccggaccat
1200
ccccccctgac tgcatcatag tcgactcaga caacttcaag ttcgtcgtgg acccatacga
1260
ggaggcccag ggcccagaaa tgctaactcc tgtctccatc acccaagaca ttttggaaag
1320
attccaagac acattcacgt cgcgatgggc gggacatctg ggaagcaagc actttcccag
1380
ccaggcccag tgggagcagg ccctgggcag ctgcagcggt ttcttcttct atggaatgga
1440
gagcttcctg tcccatatat tagtggagag attggtcgcc atgaacttgc aagagtgcca
1500
ggtggcagtc ctgctggacc tggcacggtc ctaccagagc ttgaagaggc acatggagag
1560
cgtggagcac aggagatctg ttggccgttg ggaagccaat tggagaaacg gtgcgtctcc
1620
ttcagaagat gagtggcgac gaggcggtga accaaggcga ggcttctcag accttgaagg
1680
acaagctgct gctgctccaa agctccgagc tccttcccac cacgctcaac ttggtcctgt
1740
atgggctgcc gcaccaagcc atcgggtagt gcaggcctgg acctgcctcc catcagctgc
1800
tggggcccca gcacttgcct ctgcccttgg ctctgcccct ctgccaaccc atccccacct
1860
cccggctccc atccccagct cccagctcgc tctccccttc ctgggcctct ccccagccct
1920
tggtgcagcc tcagccaggg accctccccc agcgacttcc cgcaaggcag ccgcctggac
1980
ctcgagctct gcctgcctgt gtgcgccatg gggtctgcgt cggggctgga gctgcgtctc
2040
ttcccggggc caggacaagg gcggcctccc cttggcggcg ctggtgctga gttgcttaga
2100
ccagaagact attcagaccg tgagcctgtt tttgatttga gtgttccact aaacaaacaa
2160
caaaagccca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
2220
aaaaaaaaaa aaaaaaaaaa aaaa
2244

<210> 2442

<211> 168
<212> PRT
<213> Homo sapiens

<400> 2442
Met Gly Cys Arg Thr Lys Pro Ser Gly Ser Ala Gly Leu Asp Leu Pro
1 5 10 15
Pro Ile Ser Cys Trp Gly Pro Ser Thr Cys Leu Cys Pro Trp Leu Cys
20 25 30
Pro Ser Ala Asn Pro Ser Pro Pro Pro Gly Ser His Pro Gln Leu Pro
35 40 45
Ala Arg Ser Pro Leu Pro Gly Pro Leu Pro Ser Pro Trp Cys Ser Leu
50 55 60
Ser Gln Gly Pro Ser Pro Ser Asp Phe Pro Gln Gly Ser Arg Leu Asp
65 70 75 80
Leu Glu Leu Cys Leu Pro Val Cys Ala Met Gly Ser Ala Ser Gly Leu
85 90 95
Glu Leu Arg Leu Phe Pro Gly Pro Gly Gln Gly Arg Pro Pro Leu Gly
100 105 110
Gly Ala Gly Ala Glu Leu Leu Arg Pro Glu Asp Tyr Ser Asp Arg Glu
115 120 125
Pro Val Phe Asp Leu Ser Val Pro Leu Asn Lys Gln Gln Lys Pro Lys
130 135 140
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
145 150 155 160
Lys Lys Lys Lys Lys Lys Lys Lys
165

<210> 2443
<211> 361
<212> DNA
<213> Homo sapiens

<400> 2443
nccgtgcgcg ctatcttgcg tcgtacgccg tccagggaag atgaaaaaat gctacaaacg
60
gccgatggac gattgcgcat tgatatcgaa tccatgcgca cctttgtaga gggcaaagaa
120
gtccatttga cgaaaaacga atttttaatt gtgcagactt tgtttacgca ccccaataag
180
atctatacgc gcgatgaaat tatcgaagtc accttcggaa tggattatga ggcctttgac
240
cgtgccattg atacccatat caaaaacatt cgccagaaga ttgaagcgga tccgaaaaac
300
cccgtctata tccgcacggt ttatggtgtc gggtatctgc ccggaggctt tgatgaagct
360
t
361

<210> 2444
<211> 120
<212> PRT
<213> Homo sapiens

<400> 2444
Xaa Val Arg Ala Ile Leu Arg Arg Thr Pro Ser Arg Glu Asp Glu Lys
1 5 10 15
Met Leu Gln Thr Ala Asp Gly Arg Leu Arg Ile Asp Ile Glu Ser Met
20 25 30
Arg Thr Phe Val Glu Gly Lys Glu Val His Leu Thr Lys Asn Glu Phe
35 40 45
Leu Ile Val Gln Thr Leu Phe Thr His Pro Asn Lys Ile Tyr Thr Arg
50 55 60
Asp Glu Ile Ile Glu Val Thr Phe Gly Met Asp Tyr Glu Ala Phe Asp
65 70 75 80
Arg Ala Ile Asp Thr His Ile Lys Asn Ile Arg Gln Lys Ile Glu Ala
85 90 95
Asp Pro Lys Asn Pro Val Tyr Ile Arg Thr Val Tyr Gly Val Gly Tyr
100 105 110
Leu Pro Gly Gly Phe Asp Glu Ala
115 120

<210> 2445
<211> 403
<212> DNA
<213> Homo sapiens

<400> 2445
agatctgttg aatgaagcag gtgccactta gacattcact tcactgactc caaccacaac
60
ctccccttca tttgatatcc tgctcttggc agaaggatgg agaaagagca tcgcacaaag
120
aggaagcatg tttatcctgt tcagattact gcttctgcca ggctgctgct gctgttgggt
180
tctgcacatt tgctctttat taagcaaatg tcagagctgg gtgctggcaa gggaatcccc
240
tgtatttaca caggtaaacc tgagagccag agggccccaa accatcctgg ctgcgaggga
300
caagctatta gagttaataa cagtgcactg gcattccttc aaaatcctaa tggaagcata
360
aataaaaaga ggaaagtccc ctttacccaa gaacctgaaa aan
403

<210> 2446
<211> 102
<212> PRT
<213> Homo sapiens

<400> 2446
Met Glu Lys Glu His Arg Thr Lys Arg Lys His Val Tyr Pro Val Gln
1 5 10 15
Ile Thr Ala Ser Ala Arg Leu Leu Leu Leu Leu Gly Ser Ala His Leu
20 25 30
Leu Phe Ile Lys Gln Met Ser Glu Leu Gly Ala Gly Lys Gly Ile Pro
35 40 45
Cys Ile Tyr Thr Gly Lys Pro Glu Ser Gln Arg Ala Pro Asn His Pro
50 55 60
Gly Cys Glu Gly Gln Ala Ile Arg Val Asn Asn Ser Ala Leu Ala Phe

65 70 75 80
Leu Gln Asn Pro Asn Gly Ser Ile Asn Lys Lys Arg Lys Val Pro Phe
85 90 95
Thr Gln Glu Pro Glu Lys
100

<210> 2447
<211> 744
<212> DNA
<213> Homo sapiens

<400> 2447
nacgcgtcga ggtttgccag tcacgggttg cgggtggggc aggtactact caccgtcaat
60
gacctggtgc ggcccacttc gtaccgcaat gcctggtcaa ccctcgacac tttgctgggg
120
ttgggcgtcg tgccgatcgt caacgagaac gacacggtcg ccaccggaga aattcggttt
180
ggcgataatg atcggcttgc tgccctggta gccgagctgg tgcgcgctca agccctcatt
240
ctgctctctg acgttgacgc cttgtacacc gcccatccgg attcaccgga tgctcgtcgc
300
gtggaggttg tggaggacat cgatgcattg gatgtcgata cccataaagc tggttcgggg
360
gtgggaaccg gcggcatgac cacgaaactt gaagccgccc gaatggccac ctgtgccggg
420
gtaccggtgg tactcgcagc ggcggtggat gccccggacg ttctggctgg tgcccccgtg
480
gtcacctact tccgcccgct ggcgacgcga cggccccgac ggttgctgtg gttggccgac
540
gctgccaccc cgcagggaca gatcgtcatc gacgacggag ctgtcgaagc tttgacacag
600
cgtcattcct cgttgttggc ggtgggtgtg actcgggtac acggggattt ccaagcaggc
660
gacccagtga cgatcctggc ctccgacggt cgagttgttg gtcgcggtat cgcccagttc
720
tcccatgatg aggtgcgcgt catg
744

<210> 2448
<211> 248
<212> PRT
<213> Homo sapiens

<400> 2448
Xaa Ala Ser Arg Phe Ala Ser His Gly Leu Arg Val Gly Gln Val Leu
1 5 10 15
Leu Thr Val Asn Asp Leu Val Arg Pro Thr Ser Tyr Arg Asn Ala Trp
20 25 30
Ser Thr Leu Asp Thr Leu Leu Gly Leu Gly Val Val Pro Ile Val Asn
35 40 45
Glu Asn Asp Thr Val Ala Thr Gly Glu Ile Arg Phe Gly Asp Asn Asp
50 55 60
Arg Leu Ala Ala Leu Val Ala Glu Leu Val Arg Ala Gln Ala Leu Ile

```
65                  70                  75                  80
Leu Leu Ser Asp Val Asp Ala Leu Tyr Thr Ala His Pro Asp Ser Pro
                85                  90                  95
Asp Ala Arg Arg Val Glu Val Val Glu Asp Ile Asp Ala Leu Asp Val
            100                 105                 110
Asp Thr His Lys Ala Gly Ser Gly Val Gly Thr Gly Gly Met Thr Thr
        115                 120                 125
Lys Leu Glu Ala Ala Arg Met Ala Thr Cys Ala Gly Val Pro Val Val
    130                 135                 140
Leu Ala Ala Ala Val Asp Ala Pro Asp Val Leu Ala Gly Ala Pro Val
145                 150                 155                 160
Gly Thr Tyr Phe Arg Pro Leu Ala Thr Arg Arg Pro Arg Arg Leu Leu
                165                 170                 175
Trp Leu Ala Asp Ala Ala Thr Pro Gln Gly Gln Ile Val Ile Asp Asp
            180                 185                 190
Gly Ala Val Glu Ala Leu Thr Gln Arg His Ser Ser Leu Leu Ala Val
        195                 200                 205
Gly Val Thr Arg Val His Gly Asp Phe Gln Ala Gly Asp Pro Val Thr
    210                 215                 220
Ile Leu Ala Ser Asp Gly Arg Val Val Gly Arg Gly Ile Ala Gln Phe
225                 230                 235                 240
Ser His Asp Glu Val Arg Val Met
                245
```

<210> 2449
<211> 296
<212> DNA
<213> Homo sapiens

<400> 2449
gtgcactttg ttacagccct ggaacatgaa cacatgccgt catcaactcc ccaaaatctc
60
ctactgctct cccctcctcc ctgggccctg tcctatcccc agaggccaga caggccttcc
120
tcgcatgcaa gagtctccct cgccctgccg gacagtggcc tccatctacc tgcctgtctt
180
gctggactcc agaacactcc agtcctttcc cccttggggg ttgggggggg ccccccctttt
240
ttttcccccc ctttccctct tcattccaca ggaggccagc ctcaacatcc ccnccc
296

<210> 2450
<211> 90
<212> PRT
<213> Homo sapiens

<400> 2450
```
Met Asn Thr Cys Arg His Gln Leu Pro Lys Ile Ser Tyr Cys Ser Pro
 1               5                  10                  15
Leu Leu Pro Gly Pro Cys Pro Ile Pro Arg Gly Gln Thr Gly Leu Pro
            20                  25                  30
Arg Met Gln Glu Ser Pro Ser Pro Cys Arg Thr Val Ala Ser Ile Tyr
        35                  40                  45
Leu Pro Val Leu Leu Asp Ser Arg Thr Leu Gln Ser Phe Pro Pro Trp
```

```
    50                  55                  60
Gly Leu Gly Gly Ala Pro Pro Phe Phe Pro Pro Leu Ser Leu Phe Ile
65                  70                  75                  80
Pro Gln Glu Ala Ser Leu Asn Ile Pro Xaa
                85                  90
```

<210> 2451
<211> 589
<212> DNA
<213> Homo sapiens

<400> 2451
nacgcgtgac tggattgctc aacgggtgag gaatcgagcg gttacgatgt cgggccgatc
60
tgcaacgatg atcttgtgag cgatgtattg accggtgtgt gggccgatct tgtgggccag
120
gagaaggctg tcggggtcct gcgtcgtgcc gccgaatcgc agccggggcg ctcgtcccat
180acgcatggct cattacgggt ccgcctggat caggtcggtc gaatgctgcg 240
aaggcctttg cagcggcgct acagtgcgtc gaccatggat gcgggcagtg caatgcctgt
300
cgaaccngcc tgtcaggcgc ccatcctgac gtcaccctcg tgcgtactga ggcgctgtct
360
attggcgtcg attgaggtcg tgaaatgggt ttgttcgagc gggcgatgaa ttcgggtccc
420
cggggcgtcc ccagggttgt cgtcgtcgaa gatgccgacc gcatcactga acgcggagct
480
gacgccttgc ttaaagctat cgaggagcct gcgccgaaaa ccgtctggtt gctgtgtgcc
540
cctactccag aggacgtcat cgtcacgatc aggtcgagat gtcggcgcc
589

<210> 2452
<211> 121
<212> PRT
<213> Homo sapiens

<400> 2452
```
Leu Asp Cys Ser Thr Gly Glu Glu Ser Ser Gly Tyr Asp Val Gly Pro
 1               5                  10                  15
Ile Cys Asn Asp Asp Leu Val Ser Asp Val Leu Thr Gly Val Trp Ala
            20                  25                  30
Asp Leu Val Gly Gln Glu Lys Ala Val Gly Val Leu Arg Arg Ala Ala
        35                  40                  45
Glu Ser Gln Pro Gly Arg Ser Ser His Ala Met Ser His Ala Trp Leu
    50                  55                  60
Ile Thr Gly Pro Pro Gly Ser Gly Arg Ser Asn Ala Ala Lys Ala Phe
65                  70                  75                  80
Ala Ala Ala Leu Gln Cys Val Asp His Gly Cys Gly Gln Cys Asn Ala
                85                  90                  95
Cys Arg Thr Xaa Leu Ser Gly Ala His Pro Asp Val Thr Leu Val Arg
            100                 105                 110
Thr Glu Ala Leu Ser Ile Gly Val Asp
        115                 120
```

<210> 2453
<211> 695
<212> DNA
<213> Homo sapiens

<400> 2453
nnacgcgtca gccatctgtg agtgctcaca ctatacacac atccccgggc acactcaggg
60
agattcacac attcctacga gcacacatgt gcctgcatga gttattcccc atgtgaacac
120
acaggttggc acacgcacat gcccctgggt atgctcatgt ccattcatcc atcccagcct
180
gtgcacgtcc tctcactcct gtgttcacac ctatgcccaa atgaaccaag ggacacacat
240
gcacaccctt atgtggtgca cacacactcg tgcacacgga gccacaccag cacatgctca
300
gaggcatttg tgtgcgtggg catttgcagc atgactcaga acggagtatg gggtggcgcg
360
gcgtggctgg ggaggtccca tcagcccgcc tctgaaaccc tcccaacctg cccatcctgg
420
cccaggcact gtgtctccgg cttgggcttc agccccggac cccaggacac cccggacaaa
480
gaggagctgc tctcgtctga agcctgctac gaatgcagga tcaatggcct ctcccctcgg
540
gaccggccac gacgcagtgc ccacagggac caccaggtga catgggtgct gcactaggca
600
ggggtggcca gggaatgggt gagtgtggga aagaggctgt ggacccgact tagtcatgtc
660
agcccccga agaaggagca ccaggctcca gatct
695

<210> 2454
<211> 166
<212> PRT
<213> Homo sapiens

<400> 2454
Met Ser Tyr Ser Pro Cys Glu His Thr Gly Trp His Thr His Met Pro
1 5 10 15
Leu Gly Met Leu Met Ser Ile His Pro Ser Gln Pro Val His Val Leu
20 25 30
Ser Leu Leu Cys Ser His Leu Cys Pro Asn Glu Pro Arg Asp Thr His
35 40 45
Ala His Pro Tyr Val Val His Thr His Ser Cys Thr Arg Ser His Thr
50 55 60
Ser Thr Cys Ser Glu Ala Phe Val Cys Val Gly Ile Cys Ser Met Thr
65 70 75 80
Gln Asn Gly Val Trp Gly Gly Ala Ala Trp Leu Gly Arg Ser His Gln
85 90 95
Pro Ala Ser Glu Thr Leu Pro Thr Cys Pro Ser Trp Pro Arg His Cys
100 105 110
Val Ser Gly Leu Gly Phe Ser Pro Gly Pro Gln Asp Thr Pro Asp Lys
115 120 125
Glu Glu Leu Leu Ser Ser Glu Ala Cys Tyr Glu Cys Arg Ile Asn Gly

```
    130                 135                 140
Leu Ser Pro Arg Asp Arg Pro Arg Arg Ser Ala His Arg Asp His Gln
145                 150                 155                 160
Val Thr Trp Val Leu His
                165
```

<210> 2455
<211> 378
<212> DNA
<213> Homo sapiens

<400> 2455
acgcgtcggc agaagcgtca gctgaccgtc ggagccgatc tgtccccagg cgtcgtcagc
60
ggaaccgcgc agaaggaaat ccacgcgctg ccgatcatga aggcgctccc catgggcgtc
120
aaagaactcg ttctgggcga atcgaagtgg caggacgagt tgatcaacaa cttcatcgtc
180
gcgctgtttg caggcgtggt gttgctgttc gcggtgctgg tgctgctgta ccggcgcttg
240
ctgccgccgt tcatcaacgt gatgtcgctg gcggtggcac cgctgggcgg gttgatcggc
300
ctgtggctga ccaacacgcc gatctcgatg ccggtctata tcggcttgat catgctgctc
360
ggcatcgtcg ccaagaat
378

<210> 2456
<211> 126
<212> PRT
<213> Homo sapiens

<400> 2456
```
Thr Arg Arg Gln Lys Arg Gln Leu Thr Val Gly Ala Asp Leu Ser Pro
 1               5                  10                  15
Gly Val Val Ser Gly Thr Ala Gln Lys Glu Ile His Ala Leu Pro Ile
            20                  25                  30
Met Lys Ala Leu Pro Met Gly Val Lys Glu Leu Val Leu Gly Glu Ser
        35                  40                  45
Lys Trp Gln Asp Glu Leu Ile Asn Asn Phe Ile Val Ala Leu Phe Ala
    50                  55                  60
Gly Val Val Leu Leu Phe Ala Val Leu Val Leu Leu Tyr Arg Arg Leu
65                  70                  75                  80
Leu Pro Pro Phe Ile Asn Val Met Ser Leu Ala Val Ala Pro Leu Gly
                85                  90                  95
Gly Leu Ile Gly Leu Trp Leu Thr Asn Thr Pro Ile Ser Met Pro Val
            100                 105                 110
Tyr Ile Gly Leu Ile Met Leu Leu Gly Ile Val Ala Lys Asn
        115                 120                 125
```

<210> 2457
<211> 754
<212> DNA
<213> Homo sapiens

<400> 2457
cctaggaatt taccaccatc aaagacttac attaaccagc tatccatgaa ctcacctgag
60
atgagcgaat gtgacatctt gcacactctg cgatggtctt ctcggctccg gatcagctcc
120
tatgtcaact ggataaagga tcaccttatc aaacagggaa tgaaggctga gcatgctagc
180
tcgcttctag aactggcatc caccactaag tgtagctcag tgaaatatga tgttgaaata
240
gtagaggaat acttcgctcg acagatctca tccttctgta gtatcgactg tgccaccatc
300
ttgcagctgc atgaaattcc cagtctgcag tccatctaca cccttgatgc cgcgattcta
360
aaaggcccag gtctttttgg gatgagcatt tttctaagat ggctgctgag actgatcctc
420
ataagtcgtc tgagattacc aagaacctac ttccagccac gctgcaactc attgacacct
480
atgcatcgtt caccagagcc tatttgctgc aaaactttaa tgaagaggga acaactgaga
540
aaccttccaa ggagaaactg caaggctttg ctgctgtttt ggctattggc tctagcaggt
600
gcaaggcaaa tactctgggt ccgacactgg ttcagaattt gccatcgtca gtgcagactg
660
tgtgtgagtc ctggaacaac atcaatacca atgaatttcc caatattgga tcctggcgca
720
atgcctttgc caatgacacc atcccttcac gcgt
754

<210> 2458
<211> 236
<212> PRT
<213> Homo sapiens

<400> 2458
Met Asn Ser Pro Glu Met Ser Glu Cys Asp Ile Leu His Thr Leu Arg
1 5 10 15
Trp Ser Ser Arg Leu Arg Ile Ser Ser Tyr Val Asn Trp Ile Lys Asp
20 25 30
His Leu Ile Lys Gln Gly Met Lys Ala Glu His Ala Ser Ser Leu Leu
35 40 45
Glu Leu Ala Ser Thr Thr Lys Cys Ser Ser Val Lys Tyr Asp Val Glu
50 55 60
Ile Val Glu Glu Tyr Phe Ala Arg Gln Ile Ser Ser Phe Cys Ser Ile
65 70 75 80
Asp Cys Ala Thr Ile Leu Gln Leu His Glu Ile Pro Ser Leu Gln Ser
85 90 95
Ile Tyr Thr Leu Asp Ala Ala Ile Leu Lys Gly Pro Gly Leu Phe Gly
100 105 110
Met Ser Ile Phe Leu Arg Trp Leu Leu Arg Leu Ile Leu Ile Ser Arg
115 120 125
Leu Arg Leu Pro Arg Thr Tyr Phe Gln Pro Arg Cys Asn Ser Leu Thr
130 135 140
Pro Met His Arg Ser Pro Glu Pro Ile Cys Cys Lys Thr Leu Met Lys

```
145                 150                 155                 160
Arg Glu Gln Leu Arg Asn Leu Pro Arg Arg Asn Cys Lys Ala Leu Leu
                165                 170                 175
Leu Phe Trp Leu Leu Ala Leu Ala Gly Ala Arg Gln Ile Leu Trp Val
            180                 185                 190
Arg His Trp Phe Arg Ile Cys His Arg Gln Cys Arg Leu Cys Val Ser
        195                 200                 205
Pro Gly Thr Thr Ser Ile Pro Met Asn Phe Pro Ile Leu Asp Pro Gly
    210                 215                 220
Ala Met Pro Leu Pro Met Thr Pro Ser Leu His Ala
225                 230                 235
```

<210> 2459
<211> 382
<212> DNA
<213> Homo sapiens

<400> 2459
accggtgcac agatcgttct ggccgcgtgc actgccccgc tcaagcaaat cgctatcaac
60
gctggtcttg agggcggcgt cgtggctgag aaggtcgctg gtctgcccgc aggacagggc
120
ctcaacgcgg ccaatgacga gtatgtcgac atggtagagg ccggcatcat tgacccggcc
180
aaggtgaccc gttcggctct gcagaacgcc gcgtccatcg cggccctgtt cctcaccact
240
gaagccgtca tcgctgacaa gcccgagcct gttaaggctc ccgctggcgg cggtgatatg
300
gacggtatgg gtggcatggg cggcatgatg tgatcgtgta ttgccttcgc tgatttgagt
360
gggatgccac tttgccccag gc
382

<210> 2460
<211> 110
<212> PRT
<213> Homo sapiens

<400> 2460
```
Thr Gly Ala Gln Ile Val Leu Ala Ala Cys Thr Ala Pro Leu Lys Gln
 1               5                  10                  15
Ile Ala Ile Asn Ala Gly Leu Glu Gly Gly Val Val Ala Glu Lys Val
            20                  25                  30
Ala Gly Leu Pro Ala Gly Gln Gly Leu Asn Ala Ala Asn Asp Glu Tyr
        35                  40                  45
Val Asp Met Val Glu Ala Gly Ile Ile Asp Pro Ala Lys Val Thr Arg
    50                  55                  60
Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Ala Leu Phe Leu Thr Thr
65                  70                  75                  80
Glu Ala Val Ile Ala Asp Lys Pro Glu Pro Val Lys Ala Pro Ala Gly
                85                  90                  95
Gly Gly Asp Met Asp Gly Met Gly Gly Met Gly Gly Met Met
            100                 105                 110
```

<210> 2461
<211> 558
<212> DNA
<213> Homo sapiens

<400> 2461
tccggacaaa agggttcaat cgaagtatgg ttagcctttt ccaagtcgcc aggacggacc
60
tgcaatgctg tttgtcgtca tgctcggggg caagcaccca cgggctaaaa tcgaaattca
120
cgatgtggta ttcgcagtcg cggatacgct gcaacacacc tacacccaat tgcgcgacgg
180
ctggttcggc agccctaagg tgtgcatatc gatgcgtgga tggccgtcga tggcgtcgac
240
ggctggaaag tcgaactcag ccagatggcg ccgcctgccg acgcgcatca cctgtacttc
300
atcaacctcg gcggctacga ggccaacgct tttggcgagg cccatcatta cctgctggtg
360
gtcgcccggg acaaacagga agccaagcgc aaggggcagc ggcaaatgtt gcaacactgg
420
tcccaggccc acaccgatgg cgtaatggat atcgacgact gcttgccgat tgatctggtg
480
gacggtcgct atgttcacct ggtgcaaggc ccgcaccagc cgatcatcca gcacaacgac
540
tacatcatcc tgccgcga
558

<210> 2462
<211> 148
<212> PRT
<213> Homo sapiens

<400> 2462
Met Val Ser Leu Phe Gln Val Ala Arg Thr Asp Leu Gln Cys Cys Leu
 1   5   10   15
Ser Ser Cys Ser Gly Ala Ser Thr His Gly Leu Lys Ser Lys Phe Thr
            20   25   30
Met Trp Tyr Ser Gln Ser Arg Ile Arg Cys Asn Thr Pro Thr Pro Asn
        35   40   45
Cys Ala Thr Ala Gly Ser Ala Ala Leu Arg Cys Ala Tyr Arg Cys Val
    50   55   60
Asp Gly Arg Arg Trp Arg Arg Arg Leu Glu Ser Arg Thr Gln Pro Asp
65   70   75   80
Gly Ala Ala Cys Arg Arg Ala Ser Pro Val Leu His Gln Pro Arg Arg
                85   90   95
Leu Arg Gly Gln Arg Phe Trp Arg Gly Pro Ser Leu Pro Ala Gly Gly
            100   105   110
Arg Pro Gly Gln Thr Gly Ser Gln Ala Gln Gly Ala Ala Ala Asn Val
        115   120   125
Ala Thr Leu Val Pro Gly Pro His Arg Trp Arg Asn Gly Tyr Arg Arg
    130   135   140
Leu Leu Ala Asp
145

<210> 2463
<211> 333
<212> DNA
<213> Homo sapiens

<400> 2463
cccaggggt aagccatgag cctgttgagc caagtggccc gggcgccgtt gagcgccaag
60
ttcggcctgc tgattattct gttatacgtc gcgctggcgc tgtgngcgcc gctgctggcg
120
ccctatggcg aaacccaggt ggtgggtgaa ggcttcgcgc cgtggagcgg ccagtttttg
180
ctgggcaccg ataacctggg gcgcgacatg ttcagccgcc tgatgtacgg cgcgcgcaat
240
accttgggca ttgccttcct gacgacgacg ctggcgtttc tgctcggtgg tttgagcggt
300
ttggtcgcgg cgatcaaggg cggttgggtc gac
333

<210> 2464
<211> 106
<212> PRT
<213> Homo sapiens

<400> 2464
Met Ser Leu Leu Ser Gln Val Ala Arg Ala Pro Leu Ser Ala Lys Phe
1 5 10 15
Gly Leu Leu Ile Ile Leu Leu Tyr Val Ala Leu Ala Leu Xaa Ala Pro
20 25 30
Leu Leu Ala Pro Tyr Gly Glu Thr Gln Val Val Gly Glu Gly Phe Ala
35 40 45
Pro Trp Ser Gly Gln Phe Leu Leu Gly Thr Asp Asn Leu Gly Arg Asp
50 55 60
Met Phe Ser Arg Leu Met Tyr Gly Ala Arg Asn Thr Leu Gly Ile Ala
65 70 75 80
Phe Leu Thr Thr Thr Leu Ala Phe Leu Leu Gly Gly Leu Ser Gly Leu
85 90 95
Val Ala Ala Ile Lys Gly Gly Trp Val Asp
100 105

<210> 2465
<211> 434
<212> DNA
<213> Homo sapiens

<400> 2465
nntcatgagg acatttccct catatttggt ggtggtaaat ccctcctggg acacggggaa
60
atgaccagag gctggcggcc cacctggcag gaacagatgc cagctctgct gcagccatcg
120
ccccttgagc gggtggctct gtgcctcttt ctgcactgct ggtgggtggt gctgttggct
180
gggtgatgga taccggctgc cagagatggc tcaggtgcca gctgctgggc tatctcaggc
240

actggctgct gggctatctc gggtgccggc tgctgggcta tctcaggcgc tggctgctgc
300
tgggctgtct cgggtgctgg ctgttgggac gtctcctgtc ctggcactgg gctctcgggt
360
gctgggtgcc agctgctgcc taccttgcac tgggctctgg gcactcactg cactcgggct
420
tttccatctc cgac
434

<210> 2466
<211> 82
<212> PRT
<213> Homo sapiens

<400> 2466
Trp Ile Pro Ala Ala Arg Asp Gly Ser Gly Ala Ser Cys Trp Ala Ile
1 5 10 15
Ser Gly Thr Gly Cys Trp Ala Ile Ser Gly Ala Gly Cys Trp Ala Ile
20 25 30
Ser Gly Ala Gly Cys Cys Trp Ala Val Ser Gly Ala Gly Cys Trp Asp
35 40 45
Val Ser Cys Pro Gly Thr Gly Leu Ser Gly Ala Gly Cys Gln Leu Leu
50 55 60
Pro Thr Leu His Trp Ala Leu Gly Thr His Cys Thr Arg Ala Phe Pro
65 70 75 80
Ser Pro

<210> 2467
<211> 306
<212> DNA
<213> Homo sapiens

<400> 2467
atggactcca ccggcaccgg agcaggggct aaggggaaga agggagcggc cgggcgcaag
60
gtcggcgggc caaggaagaa gtcggtgtcg aggtccgtga aggccggtct ccagttcccc
120
gtcggccgca tcgggcgcta cttgaagaag ggccgctacg cgcagcgtgt cggcaccggc
180
gcccccgtct acctcgccgc tgtcctcgaa tacctcgccg ctgaggttct ggagctcgcc
240
ggtaatgctg ccagggacaa caagaagact cgcattattc cgcgccacgt gcttctggcg
300
atccgg
306

<210> 2468
<211> 102
<212> PRT
<213> Homo sapiens

<400> 2468
Met Asp Ser Thr Gly Thr Gly Ala Gly Gly Lys Gly Lys Lys Gly Ala

```
 1               5                  10                  15
Ala Gly Arg Lys Val Gly Gly Pro Arg Lys Lys Ser Val Ser Arg Ser
            20                  25                  30
Val Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile Gly Arg Tyr Leu
        35                  40                  45
Lys Lys Gly Arg Tyr Ala Gln Arg Val Gly Thr Gly Ala Pro Val Tyr
    50                  55                  60
Leu Ala Ala Val Leu Glu Tyr Leu Ala Ala Glu Val Leu Glu Leu Ala
65                  70                  75                  80
Gly Asn Ala Ala Arg Asp Asn Lys Lys Thr Arg Ile Ile Pro Arg His
                85                  90                  95
Val Leu Leu Ala Ile Arg
            100
```

<210> 2469
<211> 489
<212> DNA
<213> Homo sapiens

<400> 2469
gccggcgtgg cacatggctt ccctgaagcc agcattgccc tggccaagga agctttgcag
60
aacagatgag atttcagctg ggacttgcag ccaagtggga tttggccttt tggggagaag
120
ggaaagggca ttcaaaggcc agggacagag tatggtcaaa ggcatggaga tgaggaagag
180
gggaccagag cagagggtca ggttggaaag cgagttgggg tcaatctgca aaggggctga
240
cgtgccaggt aaaaaacagg agcacagttt agttttgtcg gatcatttca ggtggaaggg
300
cagtgggaat gttggagaaa acacttttg gtgtcgttac attgaatctg ctcatctata
360
agaataaaac tttatttcat agagttattg tatggctcaa aataggtatg aagaattaag
420
aaaaagaatt ttagatttaa aatgaaaagg cacctacaaa agtagagtgg tagagttacc
480
aacgtggag
489

<210> 2470
<211> 115
<212> PRT
<213> Homo sapiens

<400> 2470
```
Met Ala Ser Leu Lys Pro Ala Leu Pro Trp Pro Arg Lys Leu Cys Arg
 1               5                  10                  15
Thr Asp Glu Ile Ser Ala Gly Thr Cys Ser Gln Val Gly Phe Gly Leu
            20                  25                  30
Leu Gly Arg Arg Glu Arg Ala Phe Lys Gly Gln Gly Gln Ser Met Val
        35                  40                  45
Lys Gly Met Glu Met Arg Lys Arg Gly Pro Glu Gln Arg Val Arg Leu
    50                  55                  60
Glu Ser Glu Leu Gly Ser Ile Cys Lys Gly Ala Asp Val Pro Gly Lys
```

```
65                  70                  75                  80
Lys Gln Glu His Ser Leu Val Leu Ser Asp His Phe Arg Trp Lys Gly
                85                  90                  95
Ser Gly Asn Val Gly Glu Asn Thr Phe Trp Cys Arg Tyr Ile Glu Ser
            100                 105                 110
Ala His Leu
        115
```

<210> 2471
<211> 779
<212> DNA
<213> Homo sapiens

<400> 2471
tggccatcct ccgtgacatg tacacttcca atatgccggt gtttgagccg ttcatagatc
60
ctcacatggt ggcccttgac ttctttcaca gtgaggacct ctgcttcatg aggctcataa
120
gaagaggagc taaggactat tttgtcatgg gggcgccaat ccactgcatc ttctactata
180
attctctcat ttcctgaggc aatatcagct ccaagatgtg tccaggagtt cttaggataa
240
gcactgtaaa gatgaacttt cccataaacc ccaattgttc ctgggtcaat atgaattcca
300
ttcatacggt cacaaaagac tccctctgag gctctaagga gaatcagaag cttttgttcc
360
ttttctaagg gattttctaa agtaccaact ttcagctccc cgcctgcaat gaccatgcat
420
gccacactca gaacattgct tctgtccaca gggaagtcta aggtccccat cacatacagc
480
cctttgaaga attggaaaat ctgtatccac aaggacagtt ctgttgggta aaatgagaac
540
gtcatcccca gggcctggaa tggtattgtt gtatcctccc cagccttctt caacaccttg
600
ccatgtttca gggagggacc attttaaagc tgattcaggg gcagaggtag aagctgaaat
660
agttgggggc ataccttcct tcacccggag aatgacttga acttggcctt cacctaaaac
720
cagataggtg agttgcctca gctggctatt gaagaaccag tcacagcctt ggttctggc
779

<210> 2472
<211> 181
<212> PRT
<213> Homo sapiens

<400> 2472

```
Met Thr Phe Ser Phe Tyr Pro Thr Glu Leu Ser Leu Trp Ile Gln Ile
 1               5                  10                  15
Phe Gln Phe Phe Lys Gly Leu Tyr Val Met Gly Thr Leu Asp Phe Pro
            20                  25                  30
Val Asp Arg Ser Asn Val Leu Ser Val Ala Cys Met Val Ile Ala Gly
        35                  40                  45
Gly Glu Leu Lys Val Gly Thr Leu Glu Asn Pro Leu Glu Lys Glu Gln
```

```
    50                  55                  60
Lys Leu Leu Ile Leu Leu Arg Ala Ser Glu Gly Val Phe Cys Asp Arg
65                  70                  75                  80
Met Asn Gly Ile His Ile Asp Pro Gly Thr Ile Gly Val Tyr Gly Lys
                85                  90                  95
Val His Leu Tyr Ser Ala Tyr Pro Lys Asn Ser Trp Thr His Leu Gly
            100                 105                 110
Ala Asp Ile Ala Ser Gly Asn Glu Arg Ile Ile Val Glu Asp Ala Val
        115                 120                 125
Asp Trp Arg Pro His Asp Lys Ile Val Leu Ser Ser Ser Ser Tyr Glu
    130                 135                 140
Pro His Glu Ala Glu Val Leu Thr Val Lys Glu Val Lys Gly His His
145                 150                 155                 160
Val Arg Ile Tyr Glu Arg Leu Lys His Arg His Ile Gly Ser Val His
                165                 170                 175
Val Thr Glu Asp Gly
            180
```

<210> 2473
<211> 698
<212> DNA
<213> Homo sapiens

<400> 2473
nngtgcacca agaaatggca gcctgacaag ctggtggtgg tatggactcg gcggaaccga
60
cgcatctgct ccaaggccca gctggcag ccgnnggcat ccagaaccca taccggggca
120
ccgtggtgtg gatggtacnc tgagaatgtg gacatctctg tgaccctcta cagggacccc
180
cacgtggacc agtatgaggc caaagagtgg acatttatta ttgaaaatga gtctaagggg
240
cagcggaagg tgctggccac ggccgaggtg gacctggccc gccatgccag ggcccgtgcc
300
ntgtccaagt ccncactgag gctgcggctg aagccaaagt cagtgaagac ggtgcaggct
360
gagctgagcc tcactctttc cggggtgctg ctgcgggagg gccgtgccac ggacgatgac
420
atgcagagtc tcgcaagcct catgagtgtg aagcctagtg atgtgggcaa cttggatgac
480
tttgctgaga gtgatgaaga tgaggctcat ggcccaggag ccccggaggc ccgggctcga
540
gtcccccagc caggtgggct cacagcctgc tgtggatcga gactgccaag acctggggag
600
ggagggttac ccgggccacc agccacttgc tgtgcccgcc ctgtgatggg aactcattac
660
tgcccaggca gtcccaacca acccagcagc ctcaattg
698

<210> 2474
<211> 232
<212> PRT
<213> Homo sapiens

<400> 2474
Xaa Cys Thr Lys Lys Trp Gln Pro Asp Lys Leu Val Val Val Trp Thr
1 5 10 15
Arg Arg Asn Arg Arg Ile Cys Ser Lys Ala His Ser Trp Gln Pro Xaa
20 25 30
Ala Ser Arg Thr His Thr Gly Ala Pro Trp Cys Gly Trp Tyr Xaa Glu
35 40 45
Asn Val Asp Ile Ser Val Thr Leu Tyr Arg Asp Pro His Val Asp Gln
50 55 60
Tyr Glu Ala Lys Glu Trp Thr Phe Ile Ile Glu Asn Glu Ser Lys Gly
65 70 75 80
Gln Arg Lys Val Leu Ala Thr Ala Glu Val Asp Leu Ala Arg His Ala
85 90 95
Arg Ala Arg Ala Xaa Ser Lys Ser Xaa Leu Arg Leu Arg Leu Lys Pro
100 105 110
Lys Ser Val Lys Thr Val Gln Ala Glu Leu Ser Leu Thr Leu Ser Gly
115 120 125
Val Leu Leu Arg Glu Gly Arg Ala Thr Asp Asp Asp Met Gln Ser Leu
130 135 140
Ala Ser Leu Met Ser Val Lys Pro Ser Asp Val Gly Asn Leu Asp Asp
145 150 155 160
Phe Ala Glu Ser Asp Glu Asp Glu Ala His Gly Pro Gly Ala Pro Glu
165 170 175
Ala Arg Ala Arg Val Pro Gln Pro Gly Gly Leu Thr Ala Cys Cys Gly
180 185 190
Ser Arg Leu Pro Arg Pro Gly Glu Gly Gly Leu Pro Gly Pro Pro Ala
195 200 205
Thr Cys Cys Ala Arg Pro Val Met Gly Thr His Tyr Cys Pro Gly Ser
210 215 220
Pro Asn Gln Pro Ser Ser Leu Asn
225 230

<210> 2475
<211> 1251
<212> DNA
<213> Homo sapiens

<400> 2475
ngcgcgcccg agatgcaggt gagcaagagg atgctggcgg ggggcgtgag gagcatgccc
60
agccccctcc tggcctgctg gcagcccatc ctcctgctgg tgctgggctc agtgctgtca
120
ggctcggcca cgggctgccc gccccgctgc gagtgctccg cccaggaccg cgctgtgctg
180
tgccaccgca agcgctttgt ggcagtcccc gagggcatcc ccaccgagac gcgcctgctg
240
gacctaggca agaaccgcat caaaacgctc aaccaggacg agttcgccag cttcccgcac
300
ctggaggagc tggagctcaa cgagaacatc gtgagcgccg tggagcccgg cgccttcaac
360
aacctcttca acctccggac gctgggtctc cgcagcaacc gcctgaagct catcccgcta
420
ggcgtcttca ctggcctcag caacctgacc aagctggaca tcagcgagaa caagatcgtt
480

atcctactgg actacatgtt tcaggacctg tacaacctca agtcactgga ggttggcgac
540
aatgacctcg tctacatctc tcaccgcgcc ttcagcggcc tcaacagcct ggagcagctg
600
acgctggaga aatgcaacct gacctccatc cccaccgagg cgctgtccca cctgcacggc
660
ctcatcgtcc tgaggctccg gcacctcaac atcaatgcca tccgggacta ctccttcaag
720
aggctgtacc gactcaaggt cttggagatc tcccactggc cctacttgga caccatgaca
780
cccaactgcc tctacggcct caacctgacg tccctgtcca tcacacactg caatctgacc
840
gctgtgccct acctggccgt ccgccaccta gtctatctcc gcttcctcaa cctctcctac
900
aaccccatca gcaccattga gggctccatg ttgcatgagc tgctccggct gcaggagatc
960
cagctggtgg gcgggcagct ggccgggtgg agccctgcct tccgcggcct caactacctg
1020
cgcgtgctca atgtctctgg caaccagctg accacactgg aggaatcagt cttccactcg
1080
gtgggcaacc tggagacact catcctggac tccaacccgc tggcctgcga ctgtcggctc
1140
ctgtgggtgt tccggcgccg tggcctacaa acttcaaccg gcagcagccc acgtgcgcca
1200
cgcccgagtt tgtccagggg caaggagttc aaggacttcc ctgatgtgct a
1251

<210> 2476
<211> 417
<212> PRT
<213> Homo sapiens

<400> 2476
Xaa Ala Pro Glu Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val
 1   5   10   15
Arg Ser Met Pro Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu
            20   25   30
Leu Val Leu Gly Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro
        35   40   45
Arg Cys Glu Cys Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys
    50   55   60
Arg Phe Val Ala Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu
65   70   75   80
Asp Leu Gly Lys Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala
                85   90   95
Ser Phe Pro His Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser
            100   105   110
Ala Val Glu Pro Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu
        115   120   125
Gly Leu Arg Ser Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr
    130   135   140
Gly Leu Ser Asn Leu Thr Lys Leu Asp Ile Ser Glu Asn Lys Ile Val
145   150   155   160
Ile Leu Leu Asp Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu

```
                165                 170                 175
Glu Val Gly Asp Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser
            180                 185                 190
Gly Leu Asn Ser Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr
        195                 200                 205
Ser Ile Pro Thr Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu
    210                 215                 220
Arg Leu Arg His Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys
225                 230                 235                 240
Arg Leu Tyr Arg Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu
                245                 250                 255
Asp Thr Met Thr Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu
            260                 265                 270
Ser Ile Thr His Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg
        275                 280                 285
His Leu Val Tyr Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser
    290                 295                 300
Thr Ile Glu Gly Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile
305                 310                 315                 320
Gln Leu Val Gly Gly Gln Leu Ala Gly Trp Ser Pro Ala Phe Arg Gly
                325                 330                 335
Leu Asn Tyr Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr
            340                 345                 350
Leu Glu Glu Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile
        355                 360                 365
Leu Asp Ser Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe
    370                 375                 380
Arg Arg Arg Gly Leu Gln Thr Ser Thr Gly Ser Ser Pro Arg Ala Pro
385                 390                 395                 400
Arg Pro Ser Leu Ser Arg Gly Lys Glu Phe Lys Asp Phe Pro Asp Val
                405                 410                 415
Leu
```

<210> 2477
<211> 548
<212> DNA
<213> Homo sapiens

<400> 2477
nagactgcga tcagacgcgc gtgcccagct gaaccaggtg cgtgagaagg ctgccttcag
60
gtggccgggg gctccctcca gctgtctctg gacggaggga cgggaagtgg ccagaagggg
120
aagtgtgagg agttcccgtc cagcctgtca tcagtctccc caggtcttga agcggcggcc
180
ctgctcctgg ccgtgaccat ggaccctctg gagaccccta tcaaggatgg catcctctac
240
cagcagcatg tcaagtttgg caagaagtgc tggcggaagg tgtgggctct gctgtatgca
300
ggaggcccat caggcgtggc acggctggag aactgggagg tccgggatgg tggcctggga
360
gcagcgggtg acaggtcggc ggggcctggc cggcgagggg agcgacgggt catccgcctg
420

gctgactgtg tgtccgtgct gccggctgac ggcgagagct gcccccggga caccggtgcc
480
ttcctgctca ccaccaccga gcgaagccat ctactggctg ctcagcaccg ccaggcctgg
540
atgggccc
548

<210> 2478<211> 113
<212> PRT
<213> Homo sapiens

<400> 2478
Leu Glu Thr Pro Ile Lys Asp Gly Ile Leu Tyr Gln Gln His Val Lys
1 5 10 15
Phe Gly Lys Lys Cys Trp Arg Lys Val Trp Ala Leu Leu Tyr Ala Gly
20 25 30
Gly Pro Ser Gly Val Ala Arg Leu Glu Asn Trp Glu Val Arg Asp Gly
35 40 45
Gly Leu Gly Ala Ala Gly Asp Arg Ser Ala Gly Pro Gly Arg Arg Gly
50 55 60
Glu Arg Arg Val Ile Arg Leu Ala Asp Cys Val Ser Val Leu Pro Ala
65 70 75 80
Asp Gly Glu Ser Cys Pro Arg Asp Thr Gly Ala Phe Leu Leu Thr Thr
85 90 95
Thr Glu Arg Ser His Leu Leu Ala Ala Gln His Arg Gln Ala Trp Met
100 105 110
Gly

<210> 2479
<211> 324
<212> DNA
<213> Homo sapiens

<400> 2479
gaattcatgg aggtctatga ggaggatgaa gaatatgcgt atgaaaaata tgaaacccat
60
ttcggcacga gctggatgga ggagaccgca ggcaccttct cactgaactg gtatcgcagc
120
aggtactgga atgacaatga agcagcagaa aggcttgcgt tgatgtgggc taaaaccttc
180
aaatatgcgt cgataaacgt ctcctggcag accgggatta gcaatagcga cgacgagggc
240
aatgaagatg aagacatgtt ctacgccggt atctccattc cgctgggagg cggggcgtac
300
tctaactcct ggtatcgtga atat
324

<210> 2480
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2480

```
Glu Phe Met Glu Val Tyr Glu Glu Asp Glu Glu Tyr Ala Tyr Glu Lys
 1               5                  10                  15
Tyr Glu Thr His Phe Gly Thr Ser Trp Met Glu Glu Thr Ala Gly Thr
            20                  25                  30
Phe Ser Leu Asn Trp Tyr Arg Ser Arg Tyr Trp Asn Asp Asn Glu Ala
        35                  40                  45
Ala Glu Arg Leu Ala Leu Met Trp Ala Lys Thr Phe Lys Tyr Ala Ser
    50                  55                  60
Ile Asn Val Ser Trp Gln Thr Gly Ile Ser Asn Ser Asp Asp Glu Gly
65                  70                  75                  80
Asn Glu Asp Glu Asp Met Phe Tyr Ala Gly Ile Ser Ile Pro Leu Gly
                85                  90                  95
Gly Gly Ala Tyr Ser Asn Ser Trp Tyr Arg Glu Tyr
            100                 105
```

<210> 2481
<211> 484
<212> DNA
<213> Homo sapiens

<400> 2481
gcgttcacta acgcttcaac aaactcttac aagcgtcttg ttcctggttt cgaagcacct
60
gttatgttgg cttactcagc tcgtaaccgt tctgcttcta tccgtatccc atacgttgca
120
agccctaaag gcaagcgtat tgaagctcgt ttccctgatc caaccgctaa cccataccta
180
gcattttcag ctatgttgat ggctggtatc gatggtatca aaaacaagat tcaccctggc
240
gatgcagcag acaaagattt gtacgacctt ccagctgaag aagcagccgc tatccctcaa
300
gttgctagca gcttagaaga agcgcttaag tgcctagatc aagaccgtga gttcttgact
360
caaggtggcg ttttctctga cgacatgatc gatgcttaca tcgctcttaa agcagaagaa
420
gcacagcgtg ttgcaatgac aacaacacca cttgagttcg aactttacta cagcctataa
480
gctt
484

<210> 2482
<211> 159
<212> PRT
<213> Homo sapiens

<400> 2482
```
Ala Phe Thr Asn Ala Ser Thr Asn Ser Tyr Lys Arg Leu Val Pro Gly
 1               5                  10                  15
Phe Glu Ala Pro Val Met Leu Ala Tyr Ser Ala Arg Asn Arg Ser Ala
            20                  25                  30
Ser Ile Arg Ile Pro Tyr Val Ala Ser Pro Lys Gly Lys Arg Ile Glu
        35                  40                  45
Ala Arg Phe Pro Asp Pro Thr Ala Asn Pro Tyr Leu Ala Phe Ser Ala
    50                  55                  60
```

Met Leu Met Ala Gly Ile Asp Gly Ile Lys Asn Lys Ile His Pro Gly
65 70 75 80
Asp Ala Ala Asp Lys Asp Leu Tyr Asp Leu Pro Ala Glu Glu Ala Ala
85 90 95
Ala Ile Pro Gln Val Ala Ser Ser Leu Glu Glu Ala Leu Lys Cys Leu
100 105 110
Asp Gln Asp Arg Glu Phe Leu Thr Gln Gly Gly Val Phe Ser Asp Asp
115 120 125
Met Ile Asp Ala Tyr Ile Ala Leu Lys Ala Glu Glu Ala Gln Arg Val
130 135 140
Ala Met Thr Thr Thr Pro Leu Glu Phe Glu Leu Tyr Tyr Ser Leu
145 150 155

<210> 2483
<211> 477
<212> DNA
<213> Homo sapiens

<400> 2483
acgcgtgtta gccaaatctt ggttcctccc gttctctcct tacccgagcc tgaggcccct
60
ctggagaaca ggcagcctct gaggaaacct ctgatccccg atcagccacc ccatcgcctg
120
cgtccccagc cgcttcctcc tggccttgtt ccccccttccc tgtgaaggag agaacagttt
180
cggctggccc tgagatgctg gcaggcctgc agtcagggca gtgggcgcct cccaccttga
240
aatggtcctt cgtggtgcag ttctgcttac ggggtagact ttgttgcctt ccacagagga
300
cagttagggt gggcaggaag gaagtctctg ccacaagtct gcattccagg ctgtttccag
360
aagtgggaat tctctcgtgc cctggagtct gggaatgcat ttttagtttc ccagcttcag
420
gtagaattga aattgagtga gccaacccac cacatccatc tggagccagg aactagt
477

<210> 2484
<211> 130
<212> PRT
<213> Homo sapiens

<400> 2484
Met His Ser Gln Thr Pro Gly His Glu Arg Ile Pro Thr Ser Gly Asn
1 5 10 15
Ser Leu Glu Cys Arg Leu Val Ala Glu Thr Ser Phe Leu Pro Thr Leu
20 25 30
Thr Val Leu Cys Gly Arg Gln Gln Ser Leu Pro Arg Lys Gln Asn Cys
35 40 45
Thr Thr Lys Asp His Phe Lys Val Gly Gly Ala His Cys Pro Asp Cys
50 55 60
Arg Pro Ala Ser Ile Ser Gly Pro Ala Glu Thr Val Leu Ser Phe Thr
65 70 75 80
Gly Lys Gly Glu Gln Gly Gln Glu Glu Ala Ala Gly Asp Ala Gly Asp
85 90 95

```
Gly Val Ala Asp Arg Gly Ser Glu Val Ser Ser Glu Ala Ala Cys Ser
            100                 105                 110
Pro Glu Gly Pro Gln Ala Arg Val Arg Arg Glu Arg Glu Glu Pro Arg
        115                 120                 125
Phe Gly
    130
```

<210> 2485
<211> 608
<212> DNA
<213> Homo sapiens

<400> 2485
accggtgagg cgaagtgcgg tggcaattac gcagcttcgc tgcgttccca gatcgatgcc
60
aagacccgcg actgcaacga ggtgctcttt gtcgatgcag ttgaacatcg ctggatcgag
120
gagctgggtg gtatgaactt catggccatc agcaaagacg gtcagctcgt caccccccgag
180
ctagctggca ccatcctgcg tggcgtgacc cgcaagtcca ttctggaagt tgcccccgac
240
ctcggtcttg aaccagtgga gcgcaagatc gatgttgacg agctccttga tggcgttcgc
300
tctggcgagt tcccggaagt cttcgcctgt ggtaccgccg cggttgtcac accgatcggc
360
tctttcctag atggagatac cgacgtgaag gtctctgagc ccaccggaaa gaccacgatg
420
gagatccgtc gccgtctgct ggatatccag ttcggacgcg ctgaggacac ccatggctgg
480
ttgaagcgag tctgctgacg gcgtcgacga ccattggggc cggccccaat gatgtgttca
540
cgatcgggct acgacggtgt cgatgacaat gtcttgcggc tggaaggttt gcccgacggt
600
gaacgcgt
608

<210> 2486
<211> 165
<212> PRT
<213> Homo sapiens

<400> 2486
```
Thr Gly Glu Ala Lys Cys Gly Gly Asn Tyr Ala Ala Ser Leu Arg Ser
 1               5                  10                  15
Gln Ile Asp Ala Lys Thr Arg Asp Cys Asn Glu Val Leu Phe Val Asp
            20                  25                  30
Ala Val Glu His Arg Trp Ile Glu Glu Leu Gly Gly Met Asn Phe Met
        35                  40                  45
Ala Ile Ser Lys Asp Gly Gln Leu Val Thr Pro Glu Leu Ala Gly Thr
    50                  55                  60
Ile Leu Arg Gly Val Thr Arg Lys Ser Ile Leu Glu Val Ala Pro Asp
65                  70                  75                  80
Leu Gly Leu Glu Pro Val Glu Arg Lys Ile Asp Val Asp Glu Leu Leu
                85                  90                  95
```

```
Asp Gly Val Arg Ser Gly Glu Phe Pro Glu Val Phe Ala Cys Gly Thr
            100                 105                 110
Ala Ala Val Val Thr Pro Ile Gly Ser Phe Leu Asp Gly Asp Thr Asp
        115                 120                 125
Val Lys Val Ser Glu Pro Thr Gly Lys Thr Thr Met Glu Ile Arg Arg
    130                 135                 140
Arg Leu Leu Asp Ile Gln Phe Gly Arg Ala Glu Asp Thr His Gly Trp
145                 150                 155                 160
Leu Lys Arg Val Cys
                165
```

<210> 2487
<211> 339
<212> DNA
<213> Homo sapiens

<400> 2487
nncccctcag gagagcagcc catggaaggt ccccccaag gggcccctga gagccctgac
60
agtctgcaaa gaaaccagaa agagctccag ggcctcctga cccaggtgca agccctggag
120
aaggaggccg caagcagtgt ggacgtgcag gccctgcgga ggctctttga ggccgtgccc
180
cagctgggag gggctgctcc tcaggctcct gctgcccacc aaaagcccga ggcctcagtg
240
gagcaggcct ttggggagct gacacgggtc agcacggaag ttgctcaact gaaggaacag
300
accttggtaa ggctgctgga cattgaagag gctgtgcac
339

<210> 2488
<211> 113
<212> PRT
<213> Homo sapiens

<400> 2488

```
Xaa Pro Ser Gly Glu Gln Pro Met Glu Gly Pro Pro Gln Gly Ala Pro
 1               5                  10                  15
Glu Ser Pro Asp Ser Leu Gln Arg Asn Gln Lys Glu Leu Gln Gly Leu
            20                  25                  30
Leu Thr Gln Val Gln Ala Leu Glu Lys Glu Ala Ala Ser Ser Val Asp
        35                  40                  45
Val Gln Ala Leu Arg Arg Leu Phe Glu Ala Val Pro Gln Leu Gly Gly
    50                  55                  60
Ala Ala Pro Gln Ala Pro Ala Ala His Gln Lys Pro Glu Ala Ser Val
65                  70                  75                  80
Glu Gln Ala Phe Gly Glu Leu Thr Arg Val Ser Thr Glu Val Ala Gln
                85                  90                  95
Leu Lys Glu Gln Thr Leu Val Arg Leu Leu Asp Ile Glu Glu Ala Val
            100                 105                 110
His
```

<210> 2489

<211> 594
<212> DNA
<213> Homo sapiens

<400> 2489
nacgcgttct tcggactggc gacgatgctg atttctatcc cgacgggggt gaagctattt
60
aactggctgg tcaccatcta tcacggccgg gtgcgtatca ccagccaggt tctttggacc
120
ctgggcttca tggtgacctt cgcgatcgga ggcatgaccg gcgtactgct ggccatcccg
180
ggtgctgact tcgtactgca caacagcctg ttcggaattg ctcacttcca caacgtgatc
240
atcggcggcg cagtattcgg ctacatcgca ggtttcagct tctacttccc gaaagcgttc
300
ggcttcaagc tgcacgaaag ctggggcaag gctgcattct ggttctggat ctcgggcttc
360
ttcgtcgcgt tcatgccgct ctatgcactg ggtttcatgg gcatgacccg ttgtttgaac
420
gccccccca cccctgagtg ggtcccgtac ctgtacgttg ccatggtcgg tgcactgatg
480
atcgctgtcg gtatcgcctg ccagttgatt cagctgtatg tcagcgtgcg tgatcgcaag
540
cagaacatgt gcgaatccgg cgacccatgg aatgcacaca ccctggaatg gtcg
594

<210> 2490
<211> 198
<212> PRT
<213> Homo sapiens

<400> 2490
Xaa Ala Phe Phe Gly Leu Ala Thr Met Leu Ile Ser Ile Pro Thr Gly
 1   5   10   15
Val Lys Leu Phe Asn Trp Leu Val Thr Ile Tyr His Gly Arg Val Arg
            20   25   30
Ile Thr Ser Gln Val Leu Trp Thr Leu Gly Phe Met Val Thr Phe Ala
        35   40   45
Ile Gly Gly Met Thr Gly Val Leu Leu Ala Ile Pro Gly Ala Asp Phe
    50   55   60
Val Leu His Asn Ser Leu Phe Gly Ile Ala His Phe His Asn Val Ile
65   70   75   80
Ile Gly Gly Ala Val Phe Gly Tyr Ile Ala Gly Phe Ser Phe Tyr Phe
                85   90   95
Pro Lys Ala Phe Gly Phe Lys Leu His Glu Ser Trp Gly Lys Ala Ala
            100   105   110
Phe Trp Phe Trp Ile Ser Gly Phe Phe Val Ala Phe Met Pro Leu Tyr
        115   120   125
Ala Leu Gly Phe Met Gly Met Thr Arg Cys Leu Asn Ala Pro Pro Thr
    130   135   140
Pro Glu Trp Val Pro Tyr Leu Tyr Val Ala Met Val Gly Ala Leu Met
145   150   155   160
Ile Ala Val Gly Ile Ala Cys Gln Leu Ile Gln Leu Tyr Val Ser Val
                165   170   175

```
Arg Asp Arg Lys Gln Asn Met Cys Glu Ser Gly Asp Pro Trp Asn Ala
            180                 185                 190
His Thr Leu Glu Trp Ser
        195
```

<210> 2491
<211> 592
<212> DNA
<213> Homo sapiens

<400> 2491
acgcgtcacg caactgtcaa acttgccaat ccgcttgacg atactcgccc ctacctacgc
60
actacgttgt tgcctggtct attccatgca gtaacgacga atatgtcgcg atctcaggat
120
gatcttgcag tgttcgaaag cggaactgta ttccgcgccg tcactccggc tgcggcaccg
180
cgtcccggtg tcgacgagcg cccctccgat gaagtccttg ccgagatcga cgccgccttg
240
ccagcccagc cgcgcatgct cgcggccgtg atctgtggca gctggctgcc cgatcgctgg
300
gatggagagt cggtcaaggc tgactggcga cacgctgtgc tggtcgccca gaaggctgct
360
gatgctcttg gcgtgaggct ggtgcgcaag gctgaccgtc aggctccatg gcatcccggt
420
cgttgtgcgg ctctcatcgt cgatgggaag gtcattggcc atgctggtga gttgcacccc
480
acagtagtgt cgaaggctgg tctgcctcag cgcacctgtg cggtcgagtt caatctagat
540
gctttggtag cctgcgctcc gagcggtggt gaggtcatgg ttatttcaag gt
592

<210> 2492
<211> 197
<212> PRT
<213> Homo sapiens

<400> 2492

```
Thr Arg His Ala Thr Val Lys Leu Ala Asn Pro Leu Asp Asp Thr Arg
 1               5                  10                  15
Pro Tyr Leu Arg Thr Thr Leu Leu Pro Gly Leu Phe His Ala Val Thr
            20                  25                  30
Thr Asn Met Ser Arg Ser Gln Asp Asp Leu Ala Val Phe Glu Ser Gly
        35                  40                  45
Thr Val Phe Arg Ala Val Thr Pro Ala Ala Ala Pro Arg Pro Gly Val
    50                  55                  60
Asp Glu Arg Pro Ser Asp Glu Val Leu Ala Glu Ile Asp Ala Ala Leu
65                  70                  75                  80
Pro Ala Gln Pro Arg Met Leu Ala Ala Val Ile Cys Gly Ser Trp Leu
                85                  90                  95
Pro Asp Arg Trp Asp Gly Glu Ser Val Lys Ala Asp Trp Arg His Ala
            100                 105                 110
Val Leu Val Ala Gln Lys Ala Ala Asp Ala Leu Gly Val Arg Leu Val
        115                 120                 125
```

```
Arg Lys Ala Asp Arg Gln Ala Pro Trp His Pro Gly Arg Cys Ala Ala
    130                 135                 140
Leu Ile Val Asp Gly Lys Val Ile Gly His Ala Gly Glu Leu His Pro
145                 150                 155                 160
Thr Val Val Ser Lys Ala Gly Leu Pro Gln Arg Thr Cys Ala Val Glu
                165                 170                 175
Phe Asn Leu Asp Ala Leu Val Ala Cys Ala Pro Ser Gly Gly Glu Val
            180                 185                 190
Met Val Ile Ser Arg
        195
```

<210> 2493
<211> 418
<212> DNA
<213> Homo sapiens

<400> 2493
acgcgtcagg ttgccggtga tcgtgccacc gtcacctcca tggtgccttc aggagcagac
60
ccccacacct atgagccgtc gctgcgtgac gttcggaccg tcgtgtattc gagagtcgcg
120
ctatcgaact acctcatgct cgaacctcat tcggtcatca agaccatcga ctcttcccta
180
cctacgggat ctatcaatgt ctccctggct gaggaagccc aaaagtacgg cgcacaagtg
240
atcccgctgg ttgaaaatgc caacctagac accgtgtggc tggggttgcg cgtcattggc
300
aagggcgcca ggcggggagc cgaccgctct tcctcggtct acctccagct gacgtcggtg
360
gaggggcctg gggacttcac tgcctatatc actgggacct ttggtcgacc tcagatct
418

<210> 2494
<211> 139
<212> PRT
<213> Homo sapiens

<400> 2494
```
Thr Arg Gln Val Ala Gly Asp Arg Ala Thr Val Thr Ser Met Val Pro
 1               5                  10                  15
Ser Gly Ala Asp Pro His Thr Tyr Glu Pro Ser Leu Arg Asp Val Arg
            20                  25                  30
Thr Val Val Tyr Ser Arg Val Ala Leu Ser Asn Tyr Leu Met Leu Glu
        35                  40                  45
Pro His Ser Val Ile Lys Thr Ile Asp Ser Ser Leu Pro Thr Gly Ser
    50                  55                  60
Ile Asn Val Ser Leu Ala Glu Glu Ala Gln Lys Tyr Gly Ala Gln Val
65                  70                  75                  80
Ile Pro Leu Val Glu Asn Ala Asn Leu Asp Thr Val Trp Leu Gly Leu
                85                  90                  95
Arg Val Ile Gly Lys Gly Ala Arg Arg Gly Ala Asp Arg Ser Ser Ser
            100                 105                 110
Val Tyr Leu Gln Leu Thr Ser Val Glu Gly Pro Gly Asp Phe Thr Ala
        115                 120                 125
```

Tyr Ile Thr Gly Thr Phe Gly Arg Pro Gln Ile
130 135

<210> 2495
<211> 1478
<212> DNA
<213> Homo sapiens

<400> 2495
nnggcctggc ccagttgcac cacgagcgct gcggacactc ggggcggcag tcggtctgtc
60
agtcctcccg ccaggtcccg cggcccgcac ctgccgcccg cacctgcagc tccgcacctg
120
cggccagtgc ctactgccct ctcttgccgc ccgcacctgc agccccgcac ctgccgcttg
180
cacctgcagc cccgcgctct acccggttca agcatggctg accaggcgcc cttcgacacg
240
gacgtcaaca ccctgacccg cttcgtcatg gaggagggca ggaaggcccg cggcacgggc
300
gagttgaccc agctgctcaa ctcgctctgc acagcagtca aagccatctc ttcggcggtg
360
cgcaaggcgg gcatcgcgca cctctatggc attgctggtt ctaccaacgt gacaggtgat
420
caagttaaga agctggacgt cctctccaac gacctggtta tgaacatgtt aaagtcatcc
480
tttgccacgt gtgttctcgt gtcagaagaa gataaacacg ccatcatagt ggaaccggag
540
aaaaggggta aatatgtggt ctgttttgat ccccttgatg gatcttccaa catcgattgc
600
cttgtgtccg ttggaaccat ttttggcatc tatagaaaga aatcaactga tgagccttct
660
gagaaggatg ctctgcaacc aggccggaac ctggtggcag ccggctacgc actgtatggc
720
agtgccacca tgctggtcct tgccatggac tgtggggtca actgcttcat gctggacccg
780
gccatcgggg agttcatttt ggtggacaag gatgtgaaga taaaaaagaa aggtaaaatc
840
tacagcctta acgagggcta cgccaaggac tttgaccctg ccgtcactga gtacatccag
900
aggaagaagt tccccccaga taattcagct ccttatgggg cccggtatgt gggctccatg
960
gtggctgatg ttcatcgcac tctggtctac ggagggatat ttctgtaccc cgctaacaag
1020
aagagcccca atggaaagct gagactgctg tacgaatgca accccatggc ctacgtcatg
1080
gagaaggctg ggggaatggc caccactggg aaggaggccg tgttagacgt cattcccaca
1140
gacattcacc agagggcgcc ggtgatcttg gggtcccccg acgacgtgct cgagttcctg
1200
aaggtgtatg agaagcactc tgcccagtga gcacctgccc tgcctgcatc cggagaattg
1260
cctctacctg gacctttttgt ctcacacagc agtaccctga cctgctgtgc accttacatt
1320

cctagagagc agaaataaaa agcatgacta tttccaccat caaatgctgt agaatgcttg
1380
gcactcccta accaaatgct gtctccataa tgccactggt gttaagatat attttgagtg
1440
gatggaggag aaataaactt attcctcctt aaaaaaaa
1478

<210> 2496
<211> 338
<212> PRT
<213> Homo sapiens

<400> 2496
Met Ala Asp Gln Ala Pro Phe Asp Thr Asp Val Asn Thr Leu Thr Arg
1 5 10 15
Phe Val Met Glu Glu Gly Arg Lys Ala Arg Gly Thr Gly Glu Leu Thr
20 25 30
Gln Leu Leu Asn Ser Leu Cys Thr Ala Val Lys Ala Ile Ser Ser Ala
35 40 45
Val Arg Lys Ala Gly Ile Ala His Leu Tyr Gly Ile Ala Gly Ser Thr
50 55 60
Asn Val Thr Gly Asp Gln Val Lys Lys Leu Asp Val Leu Ser Asn Asp
65 70 75 80
Leu Val Met Asn Met Leu Lys Ser Ser Phe Ala Thr Cys Val Leu Val
85 90 95
Ser Glu Glu Asp Lys His Ala Ile Ile Val Glu Pro Glu Lys Arg Gly
100 105 110
Lys Tyr Val Val Cys Phe Asp Pro Leu Asp Gly Ser Ser Asn Ile Asp
115 120 125
Cys Leu Val Ser Val Gly Thr Ile Phe Gly Ile Tyr Arg Lys Lys Ser
130 135 140
Thr Asp Glu Pro Ser Glu Lys Asp Ala Leu Gln Pro Gly Arg Asn Leu
145 150 155 160
Val Ala Ala Gly Tyr Ala Leu Tyr Gly Ser Ala Thr Met Leu Val Leu
165 170 175
Ala Met Asp Cys Gly Val Asn Cys Phe Met Leu Asp Pro Ala Ile Gly
180 185 190
Glu Phe Ile Leu Val Asp Lys Asp Val Lys Ile Lys Lys Lys Gly Lys
195 200 205
Ile Tyr Ser Leu Asn Glu Gly Tyr Ala Lys Asp Phe Asp Pro Ala Val
210 215 220
Thr Glu Tyr Ile Gln Arg Lys Lys Phe Pro Pro Asp Asn Ser Ala Pro
225 230 235 240
Tyr Gly Ala Arg Tyr Val Gly Ser Met Val Ala Asp Val His Arg Thr
245 250 255
Leu Val Tyr Gly Gly Ile Phe Leu Tyr Pro Ala Asn Lys Lys Ser Pro
260 265 270
Asn Gly Lys Leu Arg Leu Leu Tyr Glu Cys Asn Pro Met Ala Tyr Val
275 280 285
Met Glu Lys Ala Gly Gly Met Ala Thr Thr Gly Lys Glu Ala Val Leu 290
295 300
Asp Val Ile Pro Thr Asp Ile His Gln Arg Ala Pro Val Ile Leu Gly
305 310 315 320
Ser Pro Asp Asp Val Leu Glu Phe Leu Lys Val Tyr Glu Lys His Ser

325 330 335
Ala Gln

<210> 2497
<211> 399
<212> DNA
<213> Homo sapiens

<400> 2497
acgcgtgtct tggccggtga aacccttccc gcagcaggtt cagtacgtcg caccggcgag
60
cttggctacc tgccacagga tccccgcgac ccagacatgg aaatgatcgc gagggcaagg
120
atcctgtcag cgcgtggcct ggaccacata ctggaacgga tgcgcaccct ggagtatcag
180
atggcgaacg gttccgagga cgaccgtgcc gttgcgatgg acaaatacgc gaaggctgaa
240
gaccgtctcg tcgcggccgg tggctatggc gcctctgcag aggcagcccg aatcgcgtcg
300
aacttggggc ttgacgaccg cgtcctttcc cagccgttga aaaacctctc gggtggtcag
360
cgtcgtcgcg tcgagctggc gcgcatcctc ttttccgga
399

<210> 2498
<211> 133
<212> PRT
<213> Homo sapiens

<400> 2498
Thr Arg Val Leu Ala Gly Glu Thr Leu Pro Ala Ala Gly Ser Val Arg
1 5 10 15
Arg Thr Gly Glu Leu Gly Tyr Leu Pro Gln Asp Pro Arg Asp Pro Asp
20 25 30
Met Glu Met Ile Ala Arg Ala Arg Ile Leu Ser Ala Arg Gly Leu Asp
35 40 45
His Ile Leu Glu Arg Met Arg Thr Leu Glu Tyr Gln Met Ala Asn Gly
50 55 60
Ser Glu Asp Asp Arg Ala Val Ala Met Asp Lys Tyr Ala Lys Ala Glu
65 70 75 80
Asp Arg Leu Val Ala Ala Gly Gly Tyr Gly Ala Ser Ala Glu Ala Ala
85 90 95
Arg Ile Ala Ser Asn Leu Gly Leu Asp Asp Arg Val Leu Ser Gln Pro
100 105 110
Leu Lys Asn Leu Ser Gly Gly Gln Arg Arg Arg Val Glu Leu Ala Arg
115 120 125
Ile Leu Phe Ser Gly
130

<210> 2499
<211> 348
<212> DNA
<213> Homo sapiens

<400> 2499
nggccgggcg aagacccgtt ctatatggcc taccacgaca ccgagtgggg cgtgccggaa
60
tatgacgacc gcgcattgta cgagaagctc attctcgacg gattccaggc cggcctgtcg
120
tggatcacca tcctgcgcaa gcgcgacaac tttcgcaaag ccttcgacga tttccagccc
180
gagaagatag cgcgttacaa tgagaagaag gttcacgcgc tgatgaacga tgccggcatc
240
gtgcgcaacc gcgccaagat cgaaggcacg atcgccagcg cgaaggcgta tctcgacatc
300
atggaaaaag gcccgggctt ctccaggctg ctgtgggact tcgtcgac
348

<210> 2500
<211> 116
<212> PRT
<213> Homo sapiens

<400> 2500
Xaa Pro Gly Glu Asp Pro Phe Tyr Met Ala Tyr His Asp Thr Glu Trp
 1   5   10   15
Gly Val Pro Glu Tyr Asp Asp Arg Ala Leu Tyr Glu Lys Leu Ile Leu
            20   25   30
Asp Gly Phe Gln Ala Gly Leu Ser Trp Ile Thr Ile Leu Arg Lys Arg
        35   40   45
Asp Asn Phe Arg Lys Ala Phe Asp Asp Phe Gln Pro Glu Lys Ile Ala
    50   55   60
Arg Tyr Asn Glu Lys Lys Val His Ala Leu Met Asn Asp Ala Gly Ile
65   70   75   80
Val Arg Asn Arg Ala Lys Ile Glu Gly Thr Ile Ala Ser Ala Lys Ala
                85   90   95
Tyr Leu Asp Ile Met Glu Lys Gly Pro Gly Phe Ser Arg Leu Leu Trp
            100   105   110
Asp Phe Val Asp
        115

<210> 2501
<211> 569
<212> DNA
<213> Homo sapiens

<400> 2501
gaattcgatt catttgtggc aaatgcttac aatttgatga ttgtaaccca tcaaatcaca
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taatgcccat taagccactc catacacttc tttaaatagg aaaatatatg taaagtacgt
120
acttagcaca gggcctgacc tatagtaatg gtcaagaatg atagcggggg tgaggtatgg
180
ctttcaagag tcaaacaatt ttactggtgc atcatttcca tttattcttt ctcttttgca
240
taataaaacc actcttaaga ttctaccttg gttagttaga gacaacagtt ctctggaaag
300

tagattctat agcttcaact ccctgaagag atgtgtgcta atttacatca aaaaaatcct
360
taagggtata aaatatgcca agaactgtca acatcacaga ttaccactgg tagcttctgg
420
tatattgtta agtttccact taatttttaa gggacactag agaattagta tgactcacct
480
acactaagtt tatatactgt atttaacagt gtaattttca aatatgacag gaataaccca
540
gatgtgaaat gctgaatcat taatcacag
569

<210> 2502
<211> 100
<212> PRT
<213> Homo sapiens

<400> 2502
Met Ile Ala Gly Val Arg Tyr Gly Phe Gln Glu Ser Asn Asn Phe Thr
1 5 10 15
Gly Ala Ser Phe Pro Phe Ile Leu Ser Leu Leu His Asn Lys Thr Thr
20 25 30
Leu Lys Ile Leu Pro Trp Leu Val Arg Asp Asn Ser Ser Leu Glu Ser
35 40 45
Arg Phe Tyr Ser Phe Asn Ser Leu Lys Arg Cys Val Leu Ile Tyr Ile
50 55 60
Lys Lys Ile Leu Lys Gly Ile Lys Tyr Ala Lys Asn Cys Gln His His
65 70 75 80
Arg Leu Pro Leu Val Ala Ser Gly Ile Leu Leu Ser Phe His Leu Ile
85 90 95
Phe Lys Gly His
100

<210> 2503
<211> 419
<212> DNA
<213> Homo sapiens

<400> 2503
gccacgccag ccatctaccc tttcctcgac tcgccaaata agtattcact gaacatgtac
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aaggccttgc tacctcagca gtcctacagc ttggcccagc cgctgtattc tccagtctgc
120
accaatgggg agcgctttct ctacctgccg ccacctcact acgtcggtcc ccacatccca
180
tcgtccttgg catcacccat gaggctctcg acaccttcgg cctccccagc catcccgcct
240
ctcgtccatt gcgcagacaa aagcctcccg tggaagatgg gcgtcagccc tgggaatcct
300
gttgattccc acgcctatcc tcacatccag aacagtaagc agcccagggt tccctctgcc
360
aaggcggtca ccagtggcct gccgggggac acagctctcc tgttgccccc ctcacgcgt
419

<210> 2504

<211> 121
<212> PRT
<213> Homo sapiens

<400> 2504
Met Tyr Lys Ala Leu Leu Pro Gln Gln Ser Tyr Ser Leu Ala Gln Pro
1 5 10 15
Leu Tyr Ser Pro Val Cys Thr Asn Gly Glu Arg Phe Leu Tyr Leu Pro
20 25 30
Pro Pro His Tyr Val Gly Pro His Ile Pro Ser Ser Leu Ala Ser Pro
35 40 45
Met Arg Leu Ser Thr Pro Ser Ala Ser Pro Ala Ile Pro Pro Leu Val
50 55 60
His Cys Ala Asp Lys Ser Leu Pro Trp Lys Met Gly Val Ser Pro Gly
65 70 75 80
Asn Pro Val Asp Ser His Ala Tyr Pro His Ile Gln Asn Ser Lys Gln
85 90 95
Pro Arg Val Pro Ser Ala Lys Ala Val Thr Ser Gly Leu Pro Gly Asp
100 105 110
Thr Ala Leu Leu Leu Pro Pro Ser Arg
115 120

<210> 2505
<211> 540
<212> DNA
<213> Homo sapiens

<400> 2505
tccggagcca atccgactca ggccctcgtc tggagccagg tgctgttgag catggggttg
60
ccgctcgtgt tggtgccgtt ggctcggttc accggcgatc ggcgtctgat gggccaatgg
120
acgaatgggc gtgtcatggc cgccatcgcg tggatcgtcg tggcagcagt ctcggctctc
180
aacgtggttc tcgtcgtcga gacggtcatg ggtgcatgat ccttgagggc agttttctgg
240
cgacaatcgt gaaaatgagt gacaaactca agcgggtgac gacgccgaac cccgcaccga
300
cctctgccca cgagctagcc aacgatttgg ccactgcatt tcgcgggtac cctgctggag
360
tggcgatcct cacgacgatg ggagcggctg ggcccgaggg cttgacggtc tcctccctgg
420
cgtcggtgtc agtcgtcccg gctgttgtgt cggtgtcgtt gggtaatggt tcgacgaccc
480
tggccaccct gacggaggag tcccgcgtca tcgtccacat gcttgatgca gatcgcgcgc
540

<210> 2506
<211> 72
<212> PRT
<213> Homo sapiens

<400> 2506
Ser Gly Ala Asn Pro Thr Gln Ala Leu Val Trp Ser Gln Val Leu Leu

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 1               5                  10                  15
Ser Met Gly Leu Pro Leu Val Leu Val Pro Leu Ala Arg Phe Thr Gly
            20                  25                  30
Asp Arg Arg Leu Met Gly Gln Trp Thr Asn Gly Arg Val Met Ala Ala
        35                  40                  45
Ile Ala Trp Ile Val Val Ala Ala Val Ser Ala Leu Asn Val Val Leu
    50                  55                  60
Val Val Glu Thr Val Met Gly Ala
65                  70
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<210> 2507
<211> 922
<212> DNA
<213> Homo sapiens

<400> 2507
nacgcgtgaa gggcagagga gagagaccag tgaaggggga ggaggcggcc aaaaggagac
60
agcttcatgc ccccaggaca taaatagccc ggctgctgca ggtacctgaa ggagttcagg
120
acggagcagt gccccctgtt ttcacagcac aagtgcgcgc agcaccggcc gttcacctgc
180
ttccactggc acttcctcaa ccagcggcgc cgcaggcccc tccgcaggcg cgacggcacc
240
ttcaactaca gccccgacgt gtactgctcc aagtacaacg aagccaccgg cgtgtgcccc
300
gacggcgacg agtgtcccta cctgcaccgg acgacggggg acacagaacg caagtaccac
360
ctgcgttact acaaaacagg aacctgcatc cacgagacag acgcacgtgg ccactgcgtg
420
aagaatgggc tgcactgtgc cttcgcgcac gggccccatg acctccgctc ccctgtctac
480
gacatcaggg agcttcaggc catggaggcc ttgcagaatg gccagaccac ggtagagggg
540
agcatagagg gccagtcggc tggggctgcg agccatgcca tgatagaaaa gatcctcagc
600
gaggagcctc ggtggcaaga gactgcttat gtgctgggga actataagac ggagccttgc
660
aagaagcccc cgcggctgtg ccgccaaggc tatgcctgtc cctactacca caacagcaag
720
gaccggcggc ggagcccccg gaagcacaaa tacaggtcgt ctccatgtcc aaacgtcaag
780
cacggggatg agtggggaga ccctggcaag tgtgagaacg gagacgcctg ccagtactgc
840
cacacccgca ccgagcagca gttccacccc gagatctaca agtccaccaa gtgcaacgga
900
agggggggg gggtgaggga gg
922

<210> 2508
<211> 278
<212> PRT
<213> Homo sapiens

<400> 2508
Pro Gly Cys Cys Arg Tyr Leu Lys Glu Phe Arg Thr Glu Gln Cys Pro
1 5 10 15
Leu Phe Ser Gln His Lys Cys Ala Gln His Arg Pro Phe Thr Cys Phe
20 25 30
His Trp His Phe Leu Asn Gln Arg Arg Arg Arg Pro Leu Arg Arg Arg
35 40 45
Asp Gly Thr Phe Asn Tyr Ser Pro Asp Val Tyr Cys Ser Lys Tyr Asn
50 55 60
Glu Ala Thr Gly Val Cys Pro Asp Gly Asp Glu Cys Pro Tyr Leu His
65 70 75 80
Arg Thr Thr Gly Asp Thr Glu Arg Lys Tyr His Leu Arg Tyr Tyr Lys
85 90 95
Thr Gly Thr Cys Ile His Glu Thr Asp Ala Arg Gly His Cys Val Lys
100 105 110
Asn Gly Leu His Cys Ala Phe Ala His Gly Pro His Asp Leu Arg Ser
115 120 125
Pro Val Tyr Asp Ile Arg Glu Leu Gln Ala Met Glu Ala Leu Gln Asn
130 135 140
Gly Gln Thr Thr Val Glu Gly Ser Ile Glu Gly Gln Ser Ala Gly Ala
145 150 155 160
Ala Ser His Ala Met Ile Glu Lys Ile Leu Ser Glu Glu Pro Arg Trp
165 170 175
Gln Glu Thr Ala Tyr Val Leu Gly Asn Tyr Lys Thr Glu Pro Cys Lys
180 185 190
Lys Pro Pro Arg Leu Cys Arg Gln Gly Tyr Ala Cys Pro Tyr Tyr His
195 200 205
Asn Ser Lys Asp Arg Arg Arg Ser Pro Arg Lys His Lys Tyr Arg Ser
210 215 220
Ser Pro Cys Pro Asn Val Lys His Gly Asp Glu Trp Gly Asp Pro Gly
225 230 235 240
Lys Cys Glu Asn Gly Asp Ala Cys Gln Tyr Cys His Thr Arg Thr Glu
245 250 255
Gln Gln Phe His Pro Glu Ile Tyr Lys Ser Thr Lys Cys Asn Gly Arg
260 265 270
Gly Gly Gly Val Arg Glu
275

<210> 2509
<211> 348
<212> DNA
<213> Homo sapiens

<400> 2509
gccggccttg acctgggccg ggcgatggct ccacggcaag gtccaatact ccgtgcgctt
60
gtggcgctgg acttcgtcga tgcccgcgag gttttgctgc ccgcgaccat tggactggac
120
gttcatgaac gggtggagcc cggcaaaacc gaaactcaac caatccttgg ggatgctgga
180
cggcaggttg ccgagggcaa acacgttgac cacgttcgca ccgacaccac cgaccacggc
240
caccgctccc agcggaatct cgtagactta gcgccagggt tggtaaggcg tgtagcggtc
300

gtaacgacgg gtgacctcga actcggggct tcaaagtctt ctgctgtg
348

<210> 2510
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2510
Met Ala Pro Arg Gln Gly Pro Ile Leu Arg Ala Leu Val Ala Leu Asp
 1   5   10   15
Phe Val Asp Ala Arg Glu Val Leu Leu Pro Ala Thr Ile Gly Leu Asp
            20   25   30
Val His Glu Arg Val Glu Pro Gly Lys Thr Glu Thr Gln Pro Ile Leu
        35   40   45
Gly Asp Ala Gly Arg Gln Val Ala Glu Gly Lys His Val Asp His Val
    50   55   60
Arg Thr Asp Thr Thr Asp His Gly His Arg Ser Gln Arg Asn Leu Val
65   70   75   80
Asp Leu Ala Pro Gly Leu Val Arg Arg Val Ala Val Val Thr Thr Gly
                85   90   95
Asp Leu Glu Leu Gly Ala Ser Lys Ser Ser Ala Val
            100   105

<210> 2511
<211> 663
<212> DNA
<213> Homo sapiens

<400> 2511
nnacgcgtgt gggaccatat caggggagcc cgatggttct caggtaaggg ccggggtggt
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tccctgacta ggctgctgtc gttggctccc gtcgtcaacg agcaagatct gcaagtgctc
120
cctgtcatcg cacacgtcgg ttatccgcag gccgccgacg agtattacca gttgctttta
180
gcattacgcc caggacgcgt tgctggcctg gcggagatcg tcgtcaacgg tcaacctttt
240
accgtcactg acgccactga ggatgaacta gctctcactg cttgggctcg tatcctcctc
300
gagggaactc ccatcgccat ggatggatcg tggcagctgc atcgccgtcg agcggccccc
360
gagccagttc ggttcgctaa gcgcttcggt ggtgagcaat cgaacacctc gatcatggtg
420
ggcgacgcca tcatcatcaa aatgttccgc cgcctggagc ccggcgacaa ccttgacatc
480
accgtgcata gcgccctcaa cgatgccggg atctcatcgg tggccacatt gtacggcttt
540
atgtccggac agatccccgc tgaggaacac atcccggtcg atctagctat gatcattgag
600
aggttgccac agccccggga tggctgggaa ctcatcactg ccaaggcagt cgatctcgtc
660
gac
663

<210> 2512
<211> 221
<212> PRT
<213> Homo sapiens

<400> 2512
Xaa Arg Val Trp Asp His Ile Arg Gly Ala Arg Trp Phe Ser Gly Lys
1 5 10 15
Gly Arg Gly Gly Ser Leu Thr Arg Leu Leu Ser Leu Ala Pro Val Val
20 25 30
Asn Glu Gln Asp Leu Gln Val Leu Pro Val Ile Ala His Val Gly Tyr
35 40 45
Pro Gln Ala Ala Asp Glu Tyr Tyr Gln Leu Leu Leu Ala Leu Arg Pro
50 55 60
Gly Arg Val Ala Gly Leu Ala Glu Ile Val Val Asn Gly Gln Pro Phe
65 70 75 80
Thr Val Thr Asp Ala Thr Glu Asp Glu Leu Ala Leu Thr Ala Trp Ala
85 90 95
Arg Ile Leu Leu Glu Gly Thr Pro Ile Ala Met Asp Gly Ser Trp Gln
100 105 110
Leu His Arg Arg Arg Ala Ala Pro Glu Pro Val Arg Phe Ala Lys Arg
115 120 125
Phe Gly Gly Glu Gln Ser Asn Thr Ser Ile Met Val Gly Asp Ala Ile
130 135 140
Ile Ile Lys Met Phe Arg Arg Leu Glu Pro Gly Asp Asn Leu Asp Ile
145 150 155 160
Thr Val His Ser Ala Leu Asn Asp Ala Gly Ile Ser Ser Val Ala Thr
165 170 175
Leu Tyr Gly Phe Met Ser Gly Gln Ile Pro Ala Glu Glu His Ile Pro
180 185 190
Val Asp Leu Ala Met Ile Ile Glu Arg Leu Pro Gln Pro Arg Asp Gly
195 200 205
Trp Glu Leu Ile Thr Ala Lys Ala Val Asp Leu Val Asp
210 215 220

<210> 2513
<211> 368
<212> DNA
<213> Homo sapiens

<400> 2513
ctggctggaa tgatcacctt tacctgcaac ctggctgaga atgtgtccag caaagttcgt
60
cagcttgacc tggccaagaa ccgcctctat caggccattc agagagctga tgacatcttg
120
gacctgaagt tctgcatgga tggagttcag actgctttga ggagtgaaga ttatgagcag
180
gctgcagcac atattcatcg ctacttgtgc ctggacaagt cggtcattga gctcagccga
240
cagggcaaag agggtcagca tccgaaactg gagcatgatt gatgccaacc tgaaattgct
300
gcaggaagct gagcaacgtc tcaaagccat tgtggcagag aagtttgcca ttgccaccaa
360

ggaaggtg
368

<210> 2514
<211> 93
<212> PRT
<213> Homo sapiens

<400> 2514
Leu Ala Gly Met Ile Thr Phe Thr Cys Asn Leu Ala Glu Asn Val Ser
1 5 10 15
Ser Lys Val Arg Gln Leu Asp Leu Ala Lys Asn Arg Leu Tyr Gln Ala
20 25 30
Ile Gln Arg Ala Asp Asp Ile Leu Asp Leu Lys Phe Cys Met Asp Gly
35 40 45
Val Gln Thr Ala Leu Arg Ser Glu Asp Tyr Glu Gln Ala Ala Ala His
50 55 60
Ile His Arg Tyr Leu Cys Leu Asp Lys Ser Val Ile Glu Leu Ser Arg
65 70 75 80
Gln Gly Lys Glu Gly Gln His Pro Lys Leu Glu His Asp
85 90

<210> 2515
<211> 351
<212> DNA
<213> Homo sapiens

<400> 2515
agatcttaag ggccccagga atttgttttg ttttcctttt taactcccca ggtaattatg
60
gctcatcctg gaccagaccc ttcctacccc tccaactccc caacaactgg gcaattggaa
120
tatcagtcca tccctaaaag ccaaccaggc tctcccgagg gaggcaggaa atccctgctc
180
cctccatccc ccaccgggaa tgctgcaggg ggcttgaggg aggcgacaca gtggggagct
240
ctgggtgcag gtgggcagac aatgggccaa cacacccccc cagccccgct ccagtatcag
300
cattccagac ccacccacct gggcccttgg tcaccgggag acctcacgcg t
351

<210> 2516
<211> 98
<212> PRT
<213> Homo sapiens

<400> 2516
Met Ala His Pro Gly Pro Asp Pro Ser Tyr Pro Ser Asn Ser Pro Thr
1 5 10 15
Thr Gly Gln Leu Glu Tyr Gln Ser Ile Pro Lys Ser Gln Pro Gly Ser
20 25 30
Pro Glu Gly Gly Arg Lys Ser Leu Leu Pro Pro Ser Pro Thr Gly Asn
35 40 45
Ala Ala Gly Gly Leu Arg Glu Ala Thr Gln Trp Gly Ala Leu Gly Ala

```
    50                  55                  60
Gly Gly Gln Thr Met Gly Gln His Thr Pro Ser Ala Pro Leu Gln Tyr
65                  70                  75                  80
Gln His Ser Arg Pro Thr His Leu Gly Pro Trp Ser Pro Gly Asp Leu
                85                  90                  95
Thr Arg
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<210> 2517
<211> 356
<212> DNA
<213> Homo sapiens

<400> 2517
acgcgtggaa agacagtgac tgtgagtgtg tacgcatggg agcagaaggg gaggacaaac
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ggaggtggcc agtgagtcag gaggcggggg ggggggctag ggcttcccca ggggtcagga
120
cctgtcacca accaaacccc atgggcctat tcagcagccc caacttggct ggtctggccg
180
aggccacaca ttccctgggg actgagctcc aaggtgctgg gtccctgagc aggaagcggc
240
cagtgttgag tgggcagtgt ctcactccag ccccctccttc ccaggccagt tcttctcatc
300
tccctcagtc tttcccaagc aggccctcat ctacagggca gacctgactg gctagc
356

<210> 2518
<211> 103
<212> PRT
<213> Homo sapiens

<400> 2518
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Met Gly Ala Glu Gly Glu Asp Lys Arg Arg Trp Pro Val Ser Gln Glu
 1               5                  10                  15
Ala Gly Gly Gly Ala Arg Ala Ser Pro Gly Val Arg Thr Cys His Gln
            20                  25                  30
Pro Asn Pro Met Gly Leu Phe Ser Ser Pro Asn Leu Ala Gly Leu Ala
        35                  40                  45
Glu Ala Thr His Ser Leu Gly Thr Glu Leu Gln Gly Ala Gly Ser Leu
    50                  55                  60
Ser Arg Lys Arg Pro Val Leu Ser Gly Gln Cys Leu Thr Pro Ala Pro
65                  70                  75                  80
Pro Ser Gln Ala Ser Ser Ser His Leu Pro Gln Ser Phe Pro Ser Arg
                85                  90                  95
Pro Ser Ser Thr Gly Gln Thr
            100
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<210> 2519
<211> 830
<212> DNA
<213> Homo sapiens

<400> 2519

accggtcagt ctgcgcggca gcaccgcacc ccggagccgc agctcttcct cccgcttgcc
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cgacagccct ggtgccaagc cctgtctgag ccccaccagg aggaagcgcg tgctggctgc
120
tctccatctg ctctgggact ctggcctgct gcttcctctg cctgccactc cccaaccccg
180
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300
acacctcctt gcaggactca tggctaccgt gggctcgcac caccagcctc cccatgcgtt
360
ttcctgcctc tgcttttgct caatctgctc aatgacagaa acgcgacaac agagggcact
420
ttctccaaac ccagctctcc ctcgaggctc ccatcctgct gctcacgctg aggccactct
480
accctgccct ccgcagctca caggcagacc tggagcccag tgactacagg gttggcctcc
540
tcatcttgcc accactcaca atgcccagca gtgttaaaat ccggcaggat gcacccgctt
600
gggaagcagt ccccaaagca gaatcgtcac cacatctgaa tagtttctgc catcccactg
660
acaggccagc atctaaaaga gatgtgcgct gagcgtccgt tatgtggtgg cgtcgctgtg
720
gtttcttaac cagaacgcaa aatcctgtga ccaggattat caccggctcg tttcatacat
780
gagacggggg aagccaaagt aaccactcag gccacagcag aaaaacgcgt
830

<210> 2520
<211> 107
<212> PRT
<213> Homo sapiens

<400> 2520
Met Ser Pro Ala Arg Arg Cys Leu Gly Leu Gly Pro Glu Asn Phe Gly
1 5 10 15
Glu Glu Val Gly Leu Leu Cys Asn Cys Leu Val Pro Phe Lys Val Ile
20 25 30
Leu Pro Cys Trp Gly Arg Cys Ser Ser Ser Phe Gln Arg Arg Lys Arg
35 40 45
Gly Trp Gly Val Ala Gly Arg Gly Ser Ser Arg Pro Glu Ser Gln Ser
50 55 60
Arg Trp Arg Ala Ala Ser Thr Arg Phe Leu Leu Val Gly Leu Arg Gln
65 70 75 80
Gly Leu Ala Pro Gly Leu Ser Gly Lys Arg Glu Glu Glu Leu Arg Leu
85 90 95
Arg Gly Ala Val Leu Pro Arg Arg Leu Thr Gly
100 105

<210> 2521
<211> 4291
<212> DNA
<213> Homo sapiens

<400> 2521
ctctctctct ttcgggcgga gtcgcccacc actgccagcc cagcgctggg gggacctgct
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ccaggctgta gccgcaggac cccaccaccc cccatggctc ccctggcctt ggtgggggtc
120
acactcctcc tggcggctcc cccatgctcc ggggcagcca ccccaacccc ctccctgccg
180
cctcccccgg ccaatgacag cgacaccagc acaggggget gccaggggtc ctaccgctgc
240
cagccggggg tgctgctgcc cgtgtgggag cccgacgacc cgtcgctggg tgacaaggcg
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gcacgggcag tggtgtactt tgtggccatg gtctacatgt ttctgggagt gtccatcatc
360
gccgaccgtt tcatggcggc catcgaggtc atcacgtcaa aagagaagga gatcaccatc
420
accaaggcca acggtgagac cagcgtgggc accgttcgca tctggaatga gacggtgtcc
480
aacctcacgc tcatggccct gggctcctcc gcacctgaga tcctgctgtc agtcatcgaa
540
gtctgcggcc acaacttcca ggcgggtgag ctgggcccag gcaccatcgt gggcagcgct
600
gccttcaaca tgtttgtggt catcgccgtg tgcatctacg tcatcccagc cggcgagagc
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720
gtctggcttt atctcatcct tgctgttttt tcccccggtg tggtccaggt gtgggaggcg
780
ctgctgaccc tggtcttctt cccggtgtgc gtggtattcg cctggatggc cgacaagcgg
840
ctgctcttct acaagtacgt gtacaagcgc taccgcaccg acccacgcag cggcatcatc
900
ataggcgccg agggcgaccc cccgaagagc atcgagctgg acggcacgtt cgtgggcgcc
960
gaggccccag gtgagctggg cggcctgggc ccgggccccg ccgaggcgcg cgagctggac
1020
gccagccgcc gcgaggtcat ccagatcctc aaggacctca agcagaagca cccggacaag
1080
gatctggagc agctggtggg catcgccaac tactacgcgc tgctgcacca gcagaagagc
1140
cgcgccttct accgcatcca ggccacgcgg ctgatgaccg gcgccgggaa cgtgctgcgc
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1260
gacgacggcg ccagccgcat cttcttcgag cctagcctct accactgcct ggagaactgc
1320
ggctccgtgc tgctgtccgt cacgtgccag ggcggcgagg gcaacagcac cttctacgtg
1380
gactaccgca ctgaggacgg ctctgccaag gcgggctccg actacgagta cagcgagggc
1440
acgctggtgt tcaaaccagg cgagacgcag aaggagctgc gcatcggcat catcgacgac
1500
gacatcttcg aggaggacga gcatttcttc gtgcggctgc tgaacctgcg cgtgggcgac
1560

gcgcagggca tgttcgagcc ggacggcggc gggcggccca aggggcggct ggtggcgccg
1620
ctgctggcca ccgtcaccat cctggacgac gaccacgcag gcatcttctc cttccaggac
1680
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1740
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1980
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2100
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2160
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2880
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3120
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3180

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3240
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3720
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4291

<210> 2522
<211> 952
<212> PRT
<213> Homo sapiens

<400> 2522
Leu Ser Leu Phe Arg Ala Glu Ser Pro Thr Thr Ala Ser Pro Ala Leu
1 5 10 15
Gly Gly Pro Ala Pro Gly Cys Ser Arg Arg Thr Pro Pro Pro Pro Met
20 25 30
Ala Pro Leu Ala Leu Val Gly Val Thr Leu Leu Leu Ala Ala Pro Pro
35 40 45
Cys Ser Gly Ala Ala Thr Pro Thr Pro Ser Leu Pro Pro Pro Pro Ala
50 55 60
Asn Asp Ser Asp Thr Ser Thr Gly Gly Cys Gln Gly Ser Tyr Arg Cys

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65                  70                  75                  80
Gln Pro Gly Val Leu Leu Pro Val Trp Glu Pro Asp Asp Pro Ser Leu
                85                  90                  95
Gly Asp Lys Ala Ala Arg Ala Val Val Tyr Phe Val Ala Met Val Tyr
            100                 105                 110
Met Phe Leu Gly Val Ser Ile Ile Ala Asp Arg Phe Met Ala Ala Ile
        115                 120                 125
Glu Val Ile Thr Ser Lys Glu Lys Glu Ile Thr Ile Thr Lys Ala Asn
    130                 135                 140
Gly Glu Thr Ser Val Gly Thr Val Arg Ile Trp Asn Glu Thr Val Ser
145                 150                 155                 160
Asn Leu Thr Leu Met Ala Leu Gly Ser Ser Ala Pro Glu Ile Leu Leu
                165                 170                 175
Ser Val Ile Glu Val Cys Gly His Asn Phe Gln Ala Gly Glu Leu Gly
            180                 185                 190
Pro Gly Thr Ile Val Gly Ser Ala Ala Phe Asn Met Phe Val Val Ile
        195                 200                 205
Ala Val Cys Ile Tyr Val Ile Pro Ala Gly Glu Ser Arg Lys Ile Lys
    210                 215                 220
His Leu Arg Val Phe Phe Val Thr Ala Ser Trp Ser Ile Phe Ala Tyr
225                 230                 235                 240
Val Trp Leu Tyr Leu Ile Leu Ala Val Phe Ser Pro Gly Val Val Gln
                245                 250                 255
Val Trp Glu Ala Leu Leu Thr Leu Val Phe Phe Pro Val Cys Val Val
            260                 265                 270
Phe Ala Trp Met Ala Asp Lys Arg Leu Leu Phe Tyr Lys Tyr Val Tyr
        275                 280                 285
Lys Arg Tyr Arg Thr Asp Pro Arg Ser Gly Ile Ile Ile Gly Ala Glu
    290                 295                 300
Gly Asp Pro Pro Lys Ser Ile Glu Leu Asp Gly Thr Phe Val Gly Ala
305                 310                 315                 320
Glu Ala Pro Gly Glu Leu Gly Gly Leu Gly Pro Gly Pro Ala Glu Ala
                325                 330                 335
Arg Glu Leu Asp Ala Ser Arg Arg Glu Val Ile Gln Ile Leu Lys Asp
            340                 345                 350
Leu Lys Gln Lys His Pro Asp Lys Asp Leu Glu Gln Leu Val Gly Ile
        355                 360                 365
Ala Asn Tyr Tyr Ala Leu Leu His Gln Gln Lys Ser Arg Ala Phe Tyr
    370                 375                 380
Arg Ile Gln Ala Thr Arg Leu Met Thr Gly Ala Gly Asn Val Leu Arg
385                 390                 395                 400
Arg His Ala Ala Asp Ala Ser Arg Arg Ala Ala Pro Ala Glu Gly Ala
                405                 410                 415
Gly Glu Asp Glu Asp Asp Gly Ala Ser Arg Ile Phe Phe Glu Pro Ser
            420                 425                 430
Leu Tyr His Cys Leu Glu Asn Cys Gly Ser Val Leu Leu Ser Val Thr
        435                 440                 445
Cys Gln Gly Gly Glu Gly Asn Ser Thr Phe Tyr Val Asp Tyr Arg Thr
    450                 455                 460
Glu Asp Gly Ser Ala Lys Ala Gly Ser Asp Tyr Glu Tyr Ser Glu Gly
465                 470                 475                 480
Thr Leu Val Phe Lys Pro Gly Glu Thr Gln Lys Glu Leu Arg Ile Gly
                485                 490                 495
Ile Ile Asp Asp Asp Ile Phe Glu Glu Asp Glu His Phe Phe Val Arg
```

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                500                 505                 510
Leu Leu Asn Leu Arg Val Gly Asp Ala Gln Gly Met Phe Glu Pro Asp
        515                 520                 525
Gly Gly Gly Arg Pro Lys Gly Arg Leu Val Ala Pro Leu Leu Ala Thr
    530                 535                 540
Val Thr Ile Leu Asp Asp Asp His Ala Gly Ile Phe Ser Phe Gln Asp
545                 550                 555                 560
Arg Leu Leu His Val Ser Glu Cys Met Gly Thr Val Asp Val Arg Val
                565                 570                 575
Val Arg Ser Ser Gly Ala Arg Gly Thr Val Arg Leu Pro Tyr Arg Thr
            580                 585                 590
Val Asp Gly Thr Ala Arg Gly Gly Gly Val His Tyr Glu Asp Ala Cys
        595                 600                 605
Gly Glu Leu Glu Phe Gly Asp Asp Glu Thr Met Lys Thr Leu Gln Val
    610                 615                 620
Lys Ile Val Asp Asp Glu Glu Tyr Glu Lys Lys Asp Asn Phe Phe Ile
625                 630                 635                 640
Glu Leu Gly Gln Pro Gln Trp Leu Lys Arg Gly Ile Ser Ala Leu Leu
                645                 650                 655
Leu Asn Gln Gly Asp Gly Asp Arg Lys Leu Thr Ala Glu Glu Glu Glu
            660                 665                 670
Ala Arg Arg Ile Ala Glu Met Gly Lys Pro Val Leu Gly Glu Asn Cys
        675                 680                 685
Arg Leu Glu Val Ile Ile Glu Glu Ser Tyr Asp Phe Lys Asn Thr Val
    690                 695                 700
Asp Lys Leu Ile Lys Lys Thr Asn Leu Ala Leu Val Ile Gly Thr His
705                 710                 715                 720
Ser Trp Arg Glu Gln Phe Leu Glu Ala Ile Thr Val Ser Ala Gly Asp
                725                 730                 735
Glu Glu Glu Glu Glu Asp Gly Ser Arg Glu Glu Arg Leu Pro Ser Cys
            740                 745                 750
Phe Asp Tyr Val Met His Phe Leu Thr Val Phe Trp Lys Val Leu Phe
        755                 760                 765
Ala Cys Val Pro Pro Thr Glu Tyr Cys His Gly Trp Ala Cys Phe Gly
    770                 775                 780
Val Ser Ile Leu Val Ile Gly Leu Leu Thr Ala Leu Ile Gly Asp Leu
785                 790                 795                 800
Ala Ser His Phe Gly Cys Thr Val Gly Leu Lys Asp Ser Val Asn Ala
                805                 810                 815
Val Val Phe Val Ala Leu Gly Thr Ser Ile Pro Asp Thr Phe Ala Ser
            820                 825                 830
Lys Val Ala Ala Leu Gln Asp Gln Cys Ala Asp Ala Ser Ile Gly Asn
        835                 840                 845
Val Thr Gly Ser Asn Ala Val Asn Val Phe Leu Gly Leu Gly Val Ala
    850                 855                 860
Trp Ser Val Ala Ala Val Tyr Trp Ala Val Gln Gly Arg Pro Phe Glu
865                 870                 875                 880
Val Arg Thr Gly Thr Leu Ala Phe Ser Val Thr Leu Phe Thr Val Phe
                885                 890                 895
Ala Phe Val Gly Ile Ala Val Leu Leu Tyr Arg Arg Arg Pro His Ile
            900                 905                 910
Gly Gly Glu Leu Gly Gly Pro Arg Gly Pro Lys Leu Ala Thr Thr Ala
        915                 920                 925
Leu Phe Leu Gly Leu Trp Leu Leu Tyr Ile Leu Phe Ala Ser Leu Glu
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    930                 935                 940
Ala Tyr Cys His Ile Arg Gly Phe
945                 950

<210> 2523
<211> 392
<212> DNA
<213> Homo sapiens

<400> 2523
nnnattacct acgttcgcac cctgtcagga ttcgcctaca ccgcatttgt cgtggatgtc
60
ttcagccgaa aaattgttgg tgttgctaca cgctcgacga tgcgtaccga tgcgctgccc
120
atggaggctt tggagcatgc gttaacgact gcagggcgaa ttcatggaaa ccagttaatt
180
caccatagcg atcggggcag ccagtacgtg tcactgaagt attccaccgc gttagcggaa
240
tccggaatcc gtccgagtgt gggaacagtc ggcgattctt atgacaatgc tctagccgaa
300
acagtcaacg gtctctacaa ggcggaactg attcatgccc aaggtccgtg gacgtcggtc
360
ggagaagtcg aattggccac cttgcggnnn nn
392

<210> 2524
<211> 130
<212> PRT
<213> Homo sapiens

<400> 2524
Xaa Ile Thr Tyr Val Arg Thr Leu Ser Gly Phe Ala Tyr Thr Ala Phe
 1               5                  10                  15
Val Val Asp Val Phe Ser Arg Lys Ile Val Gly Val Ala Thr Arg Ser
            20                  25                  30
Thr Met Arg Thr Asp Ala Leu Pro Met Glu Ala Leu Glu His Ala Leu
        35                  40                  45
Thr Thr Ala Gly Arg Ile His Gly Asn Gln Leu Ile His His Ser Asp
    50                  55                  60
Arg Gly Ser Gln Tyr Val Ser Leu Lys Tyr Ser Thr Ala Leu Ala Glu
65                  70                  75                  80
Ser Gly Ile Arg Pro Ser Val Gly Thr Val Gly Asp Ser Tyr Asp Asn
                85                  90                  95
Ala Leu Ala Glu Thr Val Asn Gly Leu Tyr Lys Ala Glu Leu Ile His
            100                 105                 110
Ala Gln Gly Pro Trp Thr Ser Val Gly Glu Val Glu Leu Ala Thr Leu
        115                 120                 125
Arg Xaa
    130

<210> 2525
<211> 378
<212> DNA
<213> Homo sapiens
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<400> 2525
acgcgttctc gggcgagggc atcgcagatt tcgaatgcac ggtgatggcg gtgtgccgca
60
tccccttga atacgtggtg ctgtcaccgc cgcgggaatc aagaaccgca cgttgcgcaa
120
atcgctgcgc tacgcaccaa cgtggtcggc aagatgttgg tcagcggcga gccccgcnaa
180
tgattcatat ctccgatatc agcacgacag gggcgtcatt ccgctctgca catcggcttg
240
gaagtcagcg gtgcgcccgc acgcctgcga tttcgggtga agacgcgcga ctaccattca
300
gaactggtgg ccgcaacact cattcgcagc gagaagcccg ccgatttgcc caacacctat
360
caatacggcg tggaattc
378

<210> 2526
<211> 111
<212> PRT
<213> Homo sapiens

<400> 2526
Met Ala Val Cys Arg Ile Pro Phe Glu Tyr Val Val Leu Ser Pro Pro
1 5 10 15
Arg Glu Ser Arg Thr Ala Arg Cys Ala Asn Arg Cys Ala Thr His Gln
20 25 30
Arg Gly Arg Gln Asp Val Gly Gln Arg Arg Ala Pro Xaa Met Ile His
35 40 45
Ile Ser Asp Ile Ser Thr Thr Gly Ala Ser Phe Arg Ser Ala His Arg
50 55 60
Leu Gly Ser Gln Arg Cys Ala Arg Thr Pro Ala Ile Ser Gly Glu Asp
65 70 75 80
Ala Arg Leu Pro Phe Arg Thr Gly Gly Arg Asn Thr His Ser Gln Arg
85 90 95
Glu Ala Arg Arg Phe Ala Gln His Leu Ser Ile Arg Arg Gly Ile
100 105 110

<210> 2527
<211> 305
<212> DNA
<213> Homo sapiens

<400> 2527
ntggtcacct tccgaatggg acggcggccc aaacccgaga tcatggccag caaagagcag
60
cagatccaga gagacgacct tggagccagt ccccagagca gcagccagcc agaccacggc
120
cgcctctccc ccccagaagc tcccgacagg cccaccatct ccacggcctc cgagacctca
180
gtgtacgtga cctggattcc ccgtgggaat ggtgggttcc caatccagtc cttccgtgtg
240
gagtacaaga agctaaagaa agtgggagac tggattctgg ccaccagcgc catcccccca
300

cgcgt
305

<210> 2528
<211> 101
<212> PRT
<213> Homo sapiens

<400> 2528
Xaa Val Thr Phe Arg Met Gly Arg Arg Pro Lys Pro Glu Ile Met Ala
1 5 10 15
Ser Lys Glu Gln Gln Ile Gln Arg Asp Asp Leu Gly Ala Ser Pro Gln
20 25 30
Ser Ser Ser Gln Pro Asp His Gly Arg Leu Ser Pro Pro Glu Ala Pro
35 40 45
Asp Arg Pro Thr Ile Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr
50 55 60
Trp Ile Pro Arg Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val
65 70 75 80
Glu Tyr Lys Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser
85 90 95
Ala Ile Pro Pro Arg
100

<210> 2529
<211> 387
<212> DNA
<213> Homo sapiens

<400> 2529
acgcgtctcc ccgtggtggg tcccgatccc ccggccggct ctgccactga agcctctccc
60
tgtgtcctcc gtgccccccg agtggcctgc tagcccgctc tcccacacag tctccttgat
120
gtgaagtgtc acccggcttg ctgcggcgtg tctccgccgt aacacgtgta taccggctca
180
gccatggcgg cggctgctgg gaaggctcct gcgtatggct ttgccatccg ggacccgggc
240
tttgctctgc aggggtgggc ttctgagcag aggaaggcca gaggtaacca ggtccatgca
300
cgtttgtgtc tttccacaat gtcgggcttt tatggatgct tttagtctca gtcacaaaag
360
ccatgagctc cacaggttcc tgaggga
387

<210> 2530
<211> 121
<212> PRT
<213> Homo sapiens

<400> 2530
Met Ala Phe Val Thr Glu Thr Lys Ser Ile His Lys Ser Pro Thr Leu
1 5 10 15
Trp Lys Asp Thr Asn Val His Gly Pro Gly Tyr Leu Trp Pro Ser Ser

```
            20                  25                  30
Ala Gln Lys Pro Thr Pro Ala Glu Gln Ser Pro Gly Pro Gly Trp Gln
        35                  40                  45
Ser His Thr Gln Glu Pro Ser Gln Gln Pro Pro Pro Trp Leu Ser Arg
    50                  55                  60
Tyr Thr Arg Val Thr Ala Glu Thr Arg Arg Ser Lys Pro Gly Asp Thr
65                  70                  75                  80
Ser His Gln Gly Asp Cys Val Gly Glu Arg Ala Ser Arg Pro Leu Gly
                85                  90                  95
Gly His Gly Gly His Arg Glu Arg Leu Gln Trp Gln Ser Arg Pro Gly
            100                 105                 110
Asp Arg Asp Pro Pro Arg Gly Asp Ala
        115                 120
```

<210> 2531
<211> 396
<212> DNA
<213> Homo sapiens

<400> 2531
tctagagata caaaaagtac tctatacact gagagacatc tggataaata caaaggttga
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gctttccaac cagctgaaga tgacaagact aaaccccaag tcgctgcagc tctgtgtcat
120
ctcatcagca gccctggaga tgacaaagat agtgctgagg gggaacagac cttcgtcatc
180
agttaaagat atgctagctt ttctttttct tccagacatt cctgaatcca gagaactttc
240
ctgtaatgcg tcaaatcctt taggtctcaa ttctttccct agagagacaa ggagcacagt
300
tcgttcccaa ggcccccat gcttggcgag ggcgtctctg ctttccaggc agggtcctgc
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tgcctccacc cacgtgcagg gaaaggaagg acgcgt
396

<210> 2532
<211> 105
<212> PRT
<213> Homo sapiens

<400> 2532
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Met Thr Arg Leu Asn Pro Lys Ser Leu Gln Leu Cys Val Ile Ser Ser
 1               5                  10                  15
Ala Ala Leu Glu Met Thr Lys Ile Val Leu Arg Gly Asn Arg Pro Ser
            20                  25                  30
Ser Ser Val Lys Asp Met Leu Ala Phe Leu Phe Leu Pro Asp Ile Pro
        35                  40                  45
Glu Ser Arg Glu Leu Ser Cys Asn Ala Ser Asn Pro Leu Gly Leu Asn
    50                  55                  60
Ser Phe Pro Arg Glu Thr Arg Ser Thr Val Arg Ser Gln Gly Pro Pro
65                  70                  75                  80
Cys Leu Ala Arg Ala Ser Leu Leu Ser Arg Gln Gly Pro Ala Ala Ser
                85                  90                  95
Thr His Val Gln Gly Lys Glu Gly Arg
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100 105

<210> 2533
<211> 495
<212> DNA
<213> Homo sapiens

<400> 2533
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gctgtggcan cccccatgga cgtgatcaag tcgagactgc aggcagacgg gcagggccag
120
aggcgctacc ggggtctcct gcactgtatg gtgaccagcg ttcgagagga gggacccegg
180
gtccttttca aggggctggt actcaattgc tgccgcgcct tccctgtcaa catggtggtc
240
ttcgtcgcct atgaggcagt gctgaggctc gcccggggtc tgctcacata gccggtcccc
300
acgcccagcg gcccacccac cagcagctgc tggaggtcgt agtggctgga ggaggcaagg
360
ggtagtgtgg ctgggttcgg gaccccacag ggccattgcc caggagaatg aggagcctcc
420
ctgcagtgtt gtcggccgag gcctgagctc gccctgccca gctactgacc tcaggtcgag
480
gggcccgcca gccat
495

<210> 2534
<211> 96
<212> PRT
<213> Homo sapiens

<400> 2534
Xaa Arg Pro Asp Val Pro Gly Val Leu Val Ala Gly Gly Cys Ala Gly
1 5 10 15
Val Leu Ala Trp Ala Val Ala Xaa Pro Met Asp Val Ile Lys Ser Arg
20 25 30
Leu Gln Ala Asp Gly Gln Gly Gln Arg Arg Tyr Arg Gly Leu Leu His
35 40 45
Cys Met Val Thr Ser Val Arg Glu Glu Gly Pro Arg Val Leu Phe Lys
50 55 60
Gly Leu Val Leu Asn Cys Cys Arg Ala Phe Pro Val Asn Met Val Val
65 70 75 80
Phe Val Ala Tyr Glu Ala Val Leu Arg Leu Ala Arg Gly Leu Leu Thr
85 90 95

<210> 2535
<211> 1904
<212> DNA
<213> Homo sapiens

<400> 2535
ncggcccggg aacgtggctg gttggaggag gtagatcacc ctttctgcgg gggacgattt
60

cgtcggtggt aggctgctac catgaggttg aatcagaaca ccttgctgct ggggaagaag
120
gtggtccttg taccctacac ctcggagcat gtgcccagca ggtaccacga gtggatgaaa
180
tcagaggagc tgcagcgttt gacagcctcg gagccgctga ccctggagca ggagtatgcc
240
atgcagtgca gctggcagga agatgcagac aagtgtacct tcattgtgct ggatgccgag
300
aagtggcagg cccagccagg cgccaccgaa gagagctgca tggtgggaga cgtgaacctc
360
ttcctcacag atctagaaga ccccaccttg ggggagatcg aggtcatgat tgcagagccc
420
agctgcaggg gtaagggcct tggcactgag gccgttctcg cgatgctgtc ttacggagtg
480
accacgctag gtctgaccaa gtttgaggct aaaattgggc aaggaaatga accaagcatc
540
cggatgttcc agaaacttca ctttgagcag gtggctacga gcagtgtttt tcaggaggtg
600
accctcagac tgacagtgag tgagtccgag catcagtggc ttctggagca gaccagccac
660
gtggaagaga agccttacag agatgggtcg gcagagccct gctgatggct gggccttgtg
720
ggcagccact ctgtgtgagc agggtgttgg gcccatacac ttcaaagacc agagccctgc
780
actgggagag tgctcctggc ccaggctggg aatcaccttt cgaggccctt cagactctgg
840
cggggcttgc tgtggcctcc ctccagctag tggtgtggct gagcagactc cagggccagg
900
gccagttccc ttctcccctc ccggccaaac ccagacccag actctaggaa gctggaatgg
960
agggcaggga tccatgggag atgtcgggat gaaggtggga gctggaggtg caggggacc
1020
tggaacatgg atgggagtgg acaggccttt ctccttagag gccagaggtg ctgccctggc
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1140
agctaccacg agccccagcc tcacagtgtc cactcaaggg cagcttggtc ctcttgtcct
1200
gcagaggcag gctggtgtga ccctgggaac ttgacccggg aacaacaggt ggtccagagt
1260
gagtgtggcc tggcccctca acctagtgtc cgtcctcctc tctcctggag ccagtcttga
1320
gtttaaaggc attagtgtta gatacagctc cttgtggctg gaaaacaccc ctctgctgat
1380
aaagctcagg gggcactgag gaagcagagg ccccttgggg gtgccctcct gaagagagcg
1440
tcaggccatc agctctgtcc ctctggtgct cccacgtctg ttcctcaccc tccatctctg
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1560
ggctacctgg caccctatgg cttacaaagt agagttggcc cagtttcctt ccacctgagg
1620
ggagcactct gactcctaac agtcttcctt gccctgccat catctggggt ggctggctgt
1680

caagaaaggc cgggcatgct ttctaaacac agccacagga ggcttgtagg gcatcttcca
1740
ggtggggaaa cagtcttaga taagtaaggt gacttgccta aggcctccca gcacccttga
1800
tcttggagtc tcacagcaga ctgcatgtga acaactggaa ccgaaaacat gcctcagtat
1860
aaaacaaaca ttataaaacg aaaaaaaaaa aaaaaaaaag tact
1904

<210> 2536
<211> 207
<212> PRT
<213> Homo sapiens

<400> 2536
Met Arg Leu Asn Gln Asn Thr Leu Leu Leu Gly Lys Lys Val Val Leu
1 5 10 15
Val Pro Tyr Thr Ser Glu His Val Pro Ser Arg Tyr His Glu Trp Met
20 25 30
Lys Ser Glu Glu Leu Gln Arg Leu Thr Ala Ser Glu Pro Leu Thr Leu
35 40 45
Glu Gln Glu Tyr Ala Met Gln Cys Ser Trp Gln Glu Asp Ala Asp Lys
50 55 60
Cys Thr Phe Ile Val Leu Asp Ala Glu Lys Trp Gln Ala Gln Pro Gly
65 70 75 80
Ala Thr Glu Glu Ser Cys Met Val Gly Asp Val Asn Leu Phe Leu Thr
85 90 95
Asp Leu Glu Asp Pro Thr Leu Gly Glu Ile Glu Val Met Ile Ala Glu
100 105 110
Pro Ser Cys Arg Gly Lys Gly Leu Gly Thr Glu Ala Val Leu Ala Met
115 120 125
Leu Ser Tyr Gly Val Thr Thr Leu Gly Leu Thr Lys Phe Glu Ala Lys
130 135 140
Ile Gly Gln Gly Asn Glu Pro Ser Ile Arg Met Phe Gln Lys Leu His
145 150 155 160
Phe Glu Gln Val Ala Thr Ser Ser Val Phe Gln Glu Val Thr Leu Arg
165 170 175
Leu Thr Val Ser Glu Ser Glu His Gln Trp Leu Leu Glu Gln Thr Ser
180 185 190
His Val Glu Glu Lys Pro Tyr Arg Asp Gly Ser Ala Glu Pro Cys
195 200 205

<210> 2537
<211> 509
<212> DNA
<213> Homo sapiens

<400> 2537
acgcgttctc gtaaggacaa gcttgacgcc gaggtgcatg ccggtgaagg caccccggg
60
gatgtcatcg tgctgcggtt ttccggagcc atggcgaagc gtcctgcctc agttatcctt
120
ccgctgctac tgtcggactc ccccgtcatt gcgtggtggc ccttctccgg ccctgacaac
180

ctcgcctcgg accccatcgg agcccttgcg gaccgccgca tcaccgactc ggcagctgac
240
aaagatccgt gcaaagccct catacgccgt gcggctcacc taaccgaggg tgactccgac
300
ctgtgttggg ctcgcaccac cagctggaga gccctagctg cagcagcttt ggatcaacat
360
ccagcgaccg tcaagttcgc tcgggtagag tcagccgccg gtaatgcgcc ggcgatgctg
420
ctggcagcct ggctaggatt gcgtctcggc gtcccggtcg agcgggtgac aaccgacgcg
480
cccggcatct ccgcgatcgt catgtcgac
509

<210> 2538
<211> 169
<212> PRT
<213> Homo sapiens

<400> 2538
Thr Arg Ser Arg Lys Asp Lys Leu Asp Ala Glu Val His Ala Gly Glu
1 5 10 15
Gly Thr Pro Gly Asp Val Ile Val Leu Arg Phe Ser Gly Ala Met Ala
20 25 30
Lys Arg Pro Ala Ser Val Ile Leu Pro Leu Leu Leu Ser Asp Ser Pro
35 40 45
Val Ile Ala Trp Trp Pro Phe Ser Gly Pro Asp Asn Leu Ala Ser Asp
50 55 60
Pro Ile Gly Ala Leu Ala Asp Arg Arg Ile Thr Asp Ser Ala Ala Asp
65 70 75 80
Lys Asp Pro Cys Lys Ala Leu Ile Arg Arg Ala Ala His Leu Thr Glu
85 90 95
Gly Asp Ser Asp Leu Cys Trp Ala Arg Thr Thr Ser Trp Arg Ala Leu
100 105 110
Ala Ala Ala Ala Leu Asp Gln His Pro Ala Thr Val Lys Phe Ala Arg
115 120 125
Val Glu Ser Ala Ala Gly Asn Ala Pro Ala Met Leu Leu Ala Ala Trp
130 135 140
Leu Gly Leu Arg Leu Gly Val Pro Val Glu Arg Val Thr Thr Asp Ala
145 150 155 160
Pro Gly Ile Ser Ala Ile Val Met Ser
165

<210> 2539
<211> 453
<212> DNA
<213> Homo sapiens

<400> 2539
aagcttctac tgccgcgagc acgtcgtcca ccgtcgaggt catggttcta gtttgccgcg
60
tcgcggcatg acccgaggat agtgacgtgg gacaatggct acgtgcgttt tctcaacgag
120
cagccgaact acgacctgac gtatgacgac gtcttcatgg caccaaaccg ttcctcggtg
180

gggtcccgca tgaacgtcga cctcacgtca acagacgggc taggcactcc tctgcccctc
240
gtagtggcca atatgaccgc aatttccgga cgtcgcatgg cagagaccat cgccaggcgc
300
ggaggcattg ctgttctgcc ccaagatatc ccggcggatt tcgtcgcccg gtccattcgg
360
cgcgtcaaag atgcgcatac tcgattcgac accccagtca ccgtcaaccc gacaacgact
420
gtcggtgagg ccatgaactt gctcaacaag cgc
453

<210> 2540
<211> 134
<212> PRT
<213> Homo sapiens

<400> 2540
Phe Ala Ala Ser Arg His Asp Pro Arg Ile Val Thr Trp Asp Asn Gly
 1   5   10   15
Tyr Val Arg Phe Leu Asn Glu Gln Pro Asn Tyr Asp Leu Thr Tyr Asp
            20   25   30
Asp Val Phe Met Ala Pro Asn Arg Ser Ser Val Gly Ser Arg Met Asn
        35   40   45
Val Asp Leu Thr Ser Thr Asp Gly Leu Gly Thr Pro Leu Pro Leu Val
    50   55   60
Val Ala Asn Met Thr Ala Ile Ser Gly Arg Arg Met Ala Glu Thr Ile
65   70   75   80
Ala Arg Arg Gly Gly Ile Ala Val Leu Pro Gln Asp Ile Pro Ala Asp
                85   90   95
Phe Val Ala Arg Ser Ile Arg Arg Val Lys Asp Ala His Thr Arg Phe
            100   105   110
Asp Thr Pro Val Thr Val Asn Pro Thr Thr Thr Val Gly Glu Ala Met
        115   120   125
Asn Leu Leu Asn Lys Arg
    130

<210> 2541
<211> 564
<212> DNA
<213> Homo sapiens

<400> 2541
accggtctcc cacggagttc tgtttcctca ggtactgcac tgtatacaac tctaaatgca
60
ccctgcatgg aacccattgc agggcacacg cagtctacat gtatcccagg ttttatgctc
120
acagagcctg caatactccg tgtctggaat acgttatttg ctgcacacct cccagaggaa
180
catgtaacgt ctgtgtaaca tgctatcctg cacacatctg aaagaatctg tgtacacaac
240
actattatgc tgtgcacaca tttcctcata ttctgtgtag agagcacctc attttgtact
300
caaatattcg gcttccataa caagttacat tgctcacatc ttaaaatatt cattacacgt
360

gaaaccaccg catggtaccg acatccttct ggaatgtccc gcacagaggc tgatatatgt
420
gcacagttct cactgttctg cgtgcccagc ccctcacact ggacgcccac ctcacactct
480
tctgccaagg gagactttgg ttctcccctt ccctgtgctg gctgtgcggg ccacagtcct
540
ctgcacgcca gcagcatgac gcgt
564

<210> 2542
<211> 106
<212> PRT
<213> Homo sapiens

<400> 2542
Met Leu Cys Thr His Phe Leu Ile Phe Cys Val Glu Ser Thr Ser Phe
1 5 10 15
Cys Thr Gln Ile Phe Gly Phe His Asn Lys Leu His Cys Ser His Leu
20 25 30
Lys Ile Phe Ile Thr Arg Glu Thr Thr Ala Trp Tyr Arg His Pro Ser
35 40 45
Gly Met Ser Arg Thr Glu Ala Asp Ile Cys Ala Gln Phe Ser Leu Phe
50 55 60
Cys Val Pro Ser Pro Ser His Trp Thr Pro Thr Ser His Ser Ser Ala
65 70 75 80
Lys Gly Asp Phe Gly Ser Pro Leu Pro Cys Ala Gly Cys Ala Gly His
85 90 95
Ser Pro Leu His Ala Ser Ser Met Thr Arg
100 105

<210> 2543
<211> 387
<212> DNA
<213> Homo sapiens

<400> 2543
cgcctgaagg gggcggggaa aatggaatgg gggggaaggg cgcgggtggg gacatgctgg
60
aacgtgccca tgctttctgc accacactgg atgactgaag gggaaggaac gagcgtctta
120
ccgctcctga tgagattttt gtttttgcct aacaaagaaa tgtgtatgaa tgcacgtctg
180
tttgcagggg cagggaggag gagggtcctt ggaatagctg ccgacaacag ctggaactcc
240
tgtctgggtc ccccagctgg gctagagagg gcagtgatca tctgtccact ggacaggaag
300
gtttgcaaag ggctgtttgc ttactgggtc ccaattttta gccttctgaa gcccctgtcc
360
aatggggccc agcaggcagc agtgctg
387

<210> 2544
<211> 122
<212> PRT

<213> Homo sapiens

<400> 2544
Met Glu Trp Gly Gly Arg Ala Arg Val Gly Thr Cys Trp Asn Val Pro
1 5 10 15
Met Leu Ser Ala Pro His Trp Met Thr Glu Gly Glu Gly Thr Ser Val
20 25 30
Leu Pro Leu Leu Met Arg Phe Leu Phe Leu Pro Asn Lys Glu Met Cys
35 40 45
Met Asn Ala Arg Leu Phe Ala Gly Ala Gly Arg Arg Arg Val Leu Gly
50 55 60
Ile Ala Ala Asp Asn Ser Trp Asn Ser Cys Leu Gly Pro Pro Ala Gly
65 70 75 80
Leu Glu Arg Ala Val Ile Ile Cys Pro Leu Asp Arg Lys Val Cys Lys
85 90 95
Gly Leu Phe Ala Tyr Trp Val Pro Ile Phe Ser Leu Leu Lys Pro Leu
100 105 110
Ser Asn Gly Ala Gln Gln Ala Ala Val Leu
115 120

<210> 2545
<211> 336
<212> DNA
<213> Homo sapiens

<400> 2545
gcgattattt tcgtgctgcc cggacttatc atggtcggct ggtggtcagg tttcccgtac
60
tggaccaccc tcgctatctg tctagtcggc ggcatcctcg gcgttatgta ctcgattccg
120
ctgcgtcggg ccctcgtgac aggctcggat cttccctacc cggagggcgt cgcaggagct
180
gaggtgctca aagtaggcga ttccgctggt gccgccgagg ctaacaaggt gggtctgcga
240
gtcatcatcg tcggttctgt ggtctctgca gcgtacgccc tgttgtcgga tcttaagctt
300
gtgaagtcgg cgctgaccaa gcctttcaag acgggc
336

<210> 2546
<211> 112
<212> PRT
<213> Homo sapiens

<400> 2546
Ala Ile Ile Phe Val Leu Pro Gly Leu Ile Met Val Gly Trp Trp Ser
1 5 10 15
Gly Phe Pro Tyr Trp Thr Thr Leu Ala Ile Cys Leu Val Gly Gly Ile
20 25 30
Leu Gly Val Met Tyr Ser Ile Pro Leu Arg Arg Ala Leu Val Thr Gly
35 40 45
Ser Asp Leu Pro Tyr Pro Glu Gly Val Ala Gly Ala Glu Val Leu Lys
50 55 60
Val Gly Asp Ser Ala Gly Ala Ala Glu Ala Asn Lys Val Gly Leu Arg

65 70 75 80
Val Ile Ile Val Gly Ser Val Val Ser Ala Ala Tyr Ala Leu Leu Ser
85 90 95
Asp Leu Lys Leu Val Lys Ser Ala Leu Thr Lys Pro Phe Lys Thr Gly
100 105 110

<210> 2547
<211> 556
<212> DNA
<213> Homo sapiens

<400> 2547
acgcgtgcac acacacacac gcaggcgtac acgctcacaa gtgcacacac acatatgagt
60
ttcccacaca tctcaccata tcactttctc tttacttttt aaagacaggg cacttgccct
120
tatggccaat aatattatgc ccaagctaca acattccgag tcaatcacaa aggttataaa
180
cttcatttga actgaagacc acctgtaagc acgcagctca aatgttctca cctagaaatt
240
caagttgtgt ttggaaagtg gacttaacgg tcaaagaaaa aggcctggcc aacttcagag
300
agggacaccc agccctgcta cgttgcgtgt cattatgtgg tgctgtgcta tccatagaga
360
aagaggagat gaaaaagatt ctacaaagag agatcaaact gcaagaaagc acaaagattt
420
catcaccaca atatgaaggc ctccttggta taaatgactt ttttaggtcc caataagaaa
480
taccatctat tctatctgga attattttat tagcttcaaa ttttattcta agattcatac
540
tatcagatca tctaga
556

<210> 2548
<211> 106
<212> PRT
<213> Homo sapiens

<400> 2548
Met Asn Leu Arg Ile Lys Phe Glu Ala Asn Lys Ile Ile Pro Asp Arg
1 5 10 15
Ile Asp Gly Ile Ser Tyr Trp Asp Leu Lys Lys Ser Phe Ile Pro Arg
20 25 30
Arg Pro Ser Tyr Cys Gly Asp Glu Ile Phe Val Leu Ser Cys Ser Leu
35 40 45
Ile Ser Leu Cys Arg Ile Phe Phe Ile Ser Ser Phe Ser Met Asp Ser
50 55 60
Thr Ala Pro His Asn Asp Thr Gln Arg Ser Arg Ala Gly Cys Pro Ser
65 70 75 80
Leu Lys Leu Ala Arg Pro Phe Ser Leu Thr Val Lys Ser Thr Phe Gln
85 90 95
Thr Gln Leu Glu Phe Leu Gly Glu Asn Ile
100 105

<210> 2549
<211> 435
<212> DNA
<213> Homo sapiens

<400> 2549
nnccagcctc tctccgaccg cgtacgtatt gaatttgata aagaagccaa cacggttgtt
60
atcgatgata atggtgtcgg catgtctcgt gaagaagcca ttacaaactt aggtacgatt
120
gctaaatcgg gcacctcttc tttcttagag caattgagtg gcgatcagaa aaaagacagc
180
caacttattg gtcaattcgg tgtaggcttt tactctgctt tcatcgttgc tgataaagta
240
acagtagaaa cacgtcgcgc aggtgcgacg gaaaatgaag cggttcgctg ggtatctgat
300
ggttctggtg aatttactat tgagacgatc gataaagcga ctcgtggtac acgcattact
360
ttgcatctga aagcagatga aaaagatttc gcagacaact tccgtctacg ttcattagta
420
acaaaatatt ctgat
435

<210> 2550
<211> 145
<212> PRT
<213> Homo sapiens

<400> 2550
Xaa Gln Pro Leu Ser Asp Arg Val Arg Ile Glu Phe Asp Lys Glu Ala
 1   5   10   15
Asn Thr Val Val Ile Asp Asp Asn Gly Val Gly Met Ser Arg Glu Glu
            20   25   30
Ala Ile Thr Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Ser Ser Phe
        35   40   45
Leu Glu Gln Leu Ser Gly Asp Gln Lys Lys Asp Ser Gln Leu Ile Gly
    50   55   60
Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Ile Val Ala Asp Lys Val
65   70   75   80
Thr Val Glu Thr Arg Arg Ala Gly Ala Thr Glu Asn Glu Ala Val Arg
                85   90   95
Trp Val Ser Asp Gly Ser Gly Glu Phe Thr Ile Glu Thr Ile Asp Lys
            100   105   110
Ala Thr Arg Gly Thr Arg Ile Thr Leu His Leu Lys Ala Asp Glu Lys
        115   120   125
Asp Phe Ala Asp Asn Phe Arg Leu Arg Ser Leu Val Thr Lys Tyr Ser
    130   135   140
Asp
145

<210> 2551
<211> 403
<212> DNA
<213> Homo sapiens

<400> 2551
nngccggcca gcctcacatc agtctctccg ccccggggaa ggctcagcac tttaaatcga
60
ggactccact tctggggacg cctggttcgt tcgcccacca ggcctaggct acgctccatg
120
ctcccccagc aatctctgtc tacacctcct gcggcgcctt gccctcctcc gacccctttc
180
cagccannaa gtcccccccac cccttcagag aagcagcctc aaattccaga agtggaggct
240
ccagcctccc cgcgaggtac cagcccccaca gtcttctggg agccattgtg gccagggacg
300
gcctctggac tgccaggctg ggttggggac cagggaacat cggtctactc aggtgtgagg
360
gggcaggtct ggcctgcccc aaagttggct ccatcctgga can
403

<210> 2552
<211> 134
<212> PRT
<213> Homo sapiens

<400> 2552
Xaa Pro Ala Ser Leu Thr Ser Val Ser Pro Pro Arg Gly Arg Leu Ser
 1   5   10   15
Thr Leu Asn Arg Gly Leu His Phe Trp Gly Arg Leu Val Arg Ser Pro
            20   25   30
Thr Arg Pro Arg Leu Arg Ser Met Leu Pro Gln Gln Ser Leu Ser Thr
        35   40   45
Pro Pro Ala Ala Pro Cys Pro Pro Pro Thr Pro Phe Gln Pro Xaa Ser
    50   55   60
Pro Pro Thr Pro Ser Glu Lys Gln Pro Gln Ile Pro Glu Val Glu Ala
65   70   75   80
Pro Ala Ser Pro Arg Gly Thr Ser Pro Thr Val Phe Trp Glu Pro Leu
                85   90   95
Trp Pro Gly Thr Ala Ser Gly Leu Pro Gly Trp Val Gly Asp Gln Gly
            100   105   110
Thr Ser Val Tyr Ser Gly Val Arg Gly Gln Val Trp Pro Ala Pro Lys
        115   120   125
Leu Ala Pro Ser Trp Thr
    130

<210> 2553
<211> 380
<212> DNA
<213> Homo sapiens

<400> 2553
actagtgtcc ctataagaaa aggaaaggac caagacacag gaaagatgaa gcagagattg
60
gagagataca gcatgggcca aggagcactg ggagccagca gcagctggaa gaggcaggag
120
gcatcctccc tagaccgcac aggatgctac tgggtgagcc tgctgtcctg gaaaaggcgt
180

gaagtctgcc tgagtgggca ggggcttctg cgcagcaccc agcaaggcca aggtggaagg
240
gaccctcctg gcccctgtcc tggctccacc ctcagctgct ggcaggtggg tcaccaggcc
300
tctgcccaaa gaaactcctg caggcagctc tggacccccc gtcttacaca ccttctcact
360
gagcctgcca gcatcccagn
380

<210> 2554
<211> 111
<212> PRT
<213> Homo sapiens

<400> 2554
Met Lys Gln Arg Leu Glu Arg Tyr Ser Met Gly Gln Gly Ala Leu Gly
1 5 10 15
Ala Ser Ser Ser Trp Lys Arg Gln Glu Ala Ser Ser Leu Asp Arg Thr
20 25 30
Gly Cys Tyr Trp Val Ser Leu Leu Ser Trp Lys Arg Arg Glu Val Cys
35 40 45
Leu Ser Gly Gln Gly Leu Leu Arg Ser Thr Gln Gln Gly Gln Gly Gly
50 55 60
Arg Asp Pro Pro Gly Pro Cys Pro Gly Ser Thr Leu Ser Cys Trp Gln
65 70 75 80
Val Gly His Gln Ala Ser Ala Gln Arg Asn Ser Cys Arg Gln Leu Trp
85 90 95
Thr Pro Cys Leu Thr His Leu Leu Thr Glu Pro Ala Ser Ile Pro
100 105 110

<210> 2555
<211> 368
<212> DNA
<213> Homo sapiens

<400> 2555
ntccggatgg aaaagtaaag accagcaata gccaataacg ccattaacac atacccatat
60
atgttgttaa tgctgcccgg tagttcggtg gcattcttca tgggcaatag tttaatggga
120
gataacgcga ataatggtag tgtcgttcta gtgctcacag acctggtcac ccaaatagaa
180
ggatttatat cctcccatat cctcatttt gtgctcgttg gcctcggcat tgtctttacc
240
gttgccactc gaggtgtaca gttccgcctc ttcgggcaca tgtggcacct catgctcgat
300
tcacggaagc aaaagggcac ctccctctcc agctctcaag cattcacagt gggtctcgat
360
cacgcggn
368

<210> 2556
<211> 102
<212> PRT

<213> Homo sapiens

<400> 2556
Met Leu Leu Met Leu Pro Gly Ser Ser Val Ala Phe Phe Met Gly Asn
1 5 10 15
Ser Leu Met Gly Asp Asn Ala Asn Asn Gly Ser Val Val Leu Val Leu
20 25 30
Thr Asp Leu Val Thr Gln Ile Glu Gly Phe Ile Ser Ser His Ile Leu
35 40 45
Ile Phe Val Leu Val Gly Leu Gly Ile Val Phe Thr Val Ala Thr Arg
50 55 60
Gly Val Gln Phe Arg Leu Phe Gly His Met Trp His Leu Met Leu Asp
65 70 75 80
Ser Arg Lys Gln Lys Gly Thr Ser Leu Ser Ser Ser Gln Ala Phe Thr
85 90 95
Val Gly Leu Asp His Ala
100

<210> 2557
<211> 408
<212> DNA
<213> Homo sapiens

<400> 2557
atcactactc cagttggtga ggcagttctg ggtcgcatct taaatgtgat cggtgagccg
60
attgatgaga tgggcccagt taacgcgaaa gaaaaatggg aaattcaccg tccagctcct
120
aaattcgaag accaagctgt taaagctgag atgttgatga ctggtattaa ggtcgttgat
180
cttcttgcac cttacgcaaa gggtggcaag atcggtctct tcggtggtgc gggcgtaggt
240
aaaacagttt tgattcaaga gttgattcgt aacatcgcta ctgagcacgg tggatactct
300
gtattcgcag gtgtcggcga gcgtactcgc gaaggtaacg atctttgggt tgagatgaaa
360
gaatcaggcg ttatcgcaaa gaccgcactt gtattcggtc agatgaat
408

<210> 2558
<211> 136
<212> PRT
<213> Homo sapiens

<400> 2558
Ile Thr Thr Pro Val Gly Glu Ala Val Leu Gly Arg Ile Leu Asn Val
1 5 10 15
Ile Gly Glu Pro Ile Asp Glu Met Gly Pro Val Asn Ala Lys Glu Lys
20 25 30
Trp Glu Ile His Arg Pro Ala Pro Lys Phe Glu Asp Gln Ala Val Lys
35 40 45
Ala Glu Met Leu Met Thr Gly Ile Lys Val Val Asp Leu Leu Ala Pro
50 55 60
Tyr Ala Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly

65 70 75 80
Lys Thr Val Leu Ile Gln Glu Leu Ile Arg Asn Ile Ala Thr Glu His
85 90 95
Gly Gly Tyr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly
100 105 110
Asn Asp Leu Trp Val Glu Met Lys Glu Ser Gly Val Ile Ala Lys Thr
115 120 125
Ala Leu Val Phe Gly Gln Met Asn
130 135

<210> 2559
<211> 389
<212> DNA
<213> Homo sapiens

<400> 2559
tccttgaaga tgaacatctt tcggctgcaa actgaaaagg atttgaatcc tcagaaaaca
60
gcttttctga aagatcgact gaatgcaata caggaagagc attctaagga cctgaagctg
120
ttgcatctcg aagttatgaa tttgcgccag caactgagag ctgtaaaaga ggaagaagac
180
aaggcacaag atgaggtgca aaggttgact gccactctga agattgcctc gcagacaaag
240
aagaatgcag ccattattga agaggaactg aagaccacaa aacgtaaaat gaaccttaaa
300
attcaagagc ttctagagat gacctcattt ccaagttggt tgaagaaaat aagaacctgc
360
aggatatctt tcaacaggaa catgaagaa
389

<210> 2560
<211> 129
<212> PRT
<213> Homo sapiens

<400> 2560
Ser Leu Lys Met Asn Ile Phe Arg Leu Gln Thr Glu Lys Asp Leu Asn
1 5 10 15
Pro Gln Lys Thr Ala Phe Leu Lys Asp Arg Leu Asn Ala Ile Gln Glu
20 25 30
Glu His Ser Lys Asp Leu Lys Leu Leu His Leu Glu Val Met Asn Leu
35 40 45
Arg Gln Gln Leu Arg Ala Val Lys Glu Glu Glu Asp Lys Ala Gln Asp
50 55 60
Glu Val Gln Arg Leu Thr Ala Thr Leu Lys Ile Ala Ser Gln Thr Lys
65 70 75 80
Lys Asn Ala Ala Ile Ile Glu Glu Glu Leu Lys Thr Thr Lys Arg Lys
85 90 95
Met Asn Leu Lys Ile Gln Glu Leu Leu Glu Met Thr Ser Phe Pro Ser
100 105 110
Trp Leu Lys Lys Ile Arg Thr Cys Arg Ile Ser Phe Asn Arg Asn Met
115 120 125
Lys

<210> 2561
<211> 429
<212> DNA
<213> Homo sapiens

<400> 2561
nnactcacca ctgtggttct actatgcctt ctgaccccgt cttggacttc aactgggaga
60
atgtggagcc atttgaacag gctcctcttc tggagcatat tttcttctgt cacttgtaga
120
aaagctgtat tggattgtga ggcaatgaaa acaaatgaat tcccttctcc atgtttggac
180
tcaaagacta aggtggttat gaagggtcaa aatgtatcta tgttttgttc ccataagaac
240
aaatcactgc agatcaccta ttcattgttt cgacgtaaga cacacctggg aacccaggat
300
ggaaaaggtg aacctgcgat ttttaaccta agcatcacag aagcccatga atcaggcccc
360
tacaaatgca aagcccaagt taccagctgt tcaaaataca gtcgtgactt cagcttcacg
420
attgtcgac
429

<210> 2562
<211> 143
<212> PRT
<213> Homo sapiens

<400> 2562
Xaa Leu Thr Thr Val Val Leu Leu Cys Leu Leu Thr Pro Ser Trp Thr
 1   5   10   15
Ser Thr Gly Arg Met Trp Ser His Leu Asn Arg Leu Leu Phe Trp Ser
            20   25   30
Ile Phe Ser Ser Val Thr Cys Arg Lys Ala Val Leu Asp Cys Glu Ala
        35   40   45
Met Lys Thr Asn Glu Phe Pro Ser Pro Cys Leu Asp Ser Lys Thr Lys
    50   55   60
Val Val Met Lys Gly Gln Asn Val Ser Met Phe Cys Ser His Lys Asn
65   70   75   80
Lys Ser Leu Gln Ile Thr Tyr Ser Leu Phe Arg Arg Lys Thr His Leu
                85   90   95
Gly Thr Gln Asp Gly Lys Gly Glu Pro Ala Ile Phe Asn Leu Ser Ile
            100   105   110
Thr Glu Ala His Glu Ser Gly Pro Tyr Lys Cys Lys Ala Gln Val Thr
        115   120   125
Ser Cys Ser Lys Tyr Ser Arg Asp Phe Ser Phe Thr Ile Val Asp
    130   135   140

<210> 2563
<211> 267
<212> DNA
<213> Homo sapiens

<400> 2563
ggatcccaga cgagtgctgg cagcagtatg ggggccgtgg gggcgacggc caccgtcagc
60
accccggtca ccatccagaa catgacctcc tcttatgtca ccatcacatc ccatgtcctt
120
aaggccttta ccctttggga acaggcagag gccctcacaa ggaagaacaa agaattcttt
180
gctcagctca gcacaaaagt gcgcgtgttg gccctcaaca gcagcctggt ggacctggtg
240
cactacacaa ggcagggcct ccagcgg
267

<210> 2564
<211> 89
<212> PRT
<213> Homo sapiens

<400> 2564
Gly Ser Gln Thr Ser Ala Gly Ser Ser Met Gly Ala Val Gly Ala Thr
1 5 10 15
Ala Thr Val Ser Thr Pro Val Thr Ile Gln Asn Met Thr Ser Ser Tyr
20 25 30
Val Thr Ile Thr Ser His Val Leu Lys Ala Phe Thr Leu Trp Glu Gln
35 40 45
Ala Glu Ala Leu Thr Arg Lys Asn Lys Glu Phe Phe Ala Gln Leu Ser
50 55 60
Thr Lys Val Arg Val Leu Ala Leu Asn Ser Ser Leu Val Asp Leu Val
65 70 75 80
His Tyr Thr Arg Gln Gly Leu Gln Arg
85

<210> 2565
<211> 333
<212> DNA
<213> Homo sapiens

<400> 2565
cttcgcactg ctccgcgagt tcttggggga gtgagcacag cgcgtaagct cagccacgtg
60
tggttcgaat tcgattcctt ggtcaatgcc cgtgacgtgg gcggaatccc caccccgat
120
gggccggtga aatcccagcg actgatccgc agcgacaacc tgcaggccct caccgaggcc
180
gacatcgccc agttgcagca actcggtgtc tccgatgtgg tcgatctgcg ttccacctat
240
gaggtggcca gcgagggccc ggggccgctg accgggcgtg gggtgaccat ccacccccat
300
tccttcctgc ccgaccagca cgccaatgtg cac
333

<210> 2566
<211> 111
<212> PRT

<213> Homo sapiens

<400> 2566
Leu Arg Thr Ala Pro Arg Val Leu Gly Gly Val Ser Thr Ala Arg Lys
1 5 10 15
Leu Ser His Val Trp Phe Glu Phe Asp Ser Leu Val Asn Ala Arg Asp
20 25 30
Val Gly Gly Ile Pro Thr Pro Asp Gly Pro Val Lys Ser Gln Arg Leu
35 40 45
Ile Arg Ser Asp Asn Leu Gln Ala Leu Thr Glu Ala Asp Ile Ala Gln
50 55 60
Leu Gln Gln Leu Gly Val Ser Asp Val Val Asp Leu Arg Ser Thr Tyr
65 70 75 80
Glu Val Ala Ser Glu Gly Pro Gly Pro Leu Thr Gly Arg Gly Val Thr
85 90 95
Ile His Pro His Ser Phe Leu Pro Asp Gln His Ala Asn Val His
100 105 110

<210> 2567
<211> 396
<212> DNA
<213> Homo sapiens

<400> 2567
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agccagttca cagatcaacg tctattcgga accgatcaat ttagtattgg tgggcgctat
120
tctgtacgag gttttagtgg agaagaaacc ttaagaggtg actcgggcta ttatgtacaa
180
aatgaatggg cattaccatt tagaaaacaa caaattactc catatgtagg gatagatatt
240
ggacatgtat gggggccatc tacagaaact caattaggta ataccttaat tggtggtgta
300
gttggtgtac gtggtatggt tggtgacgat gtaaactatg atgtatcact aggaacacca
360
attaagaaac cagaaggttt tgatacagat acgcgt
396

<210> 2568
<211> 132
<212> PRT
<213> Homo sapiens

<400> 2568
Xaa Ile Gln Thr Gly Val Arg Met Gly His Lys Gln Gly Thr Tyr Thr
1 5 10 15
Met Arg Phe Arg Ser Gln Phe Thr Asp Gln Arg Leu Phe Gly Thr Asp
20 25 30
Gln Phe Ser Ile Gly Gly Arg Tyr Ser Val Arg Gly Phe Ser Gly Glu
35 40 45
Glu Thr Leu Arg Gly Asp Ser Gly Tyr Tyr Val Gln Asn Glu Trp Ala
50 55 60
Leu Pro Phe Arg Lys Gln Gln Ile Thr Pro Tyr Val Gly Ile Asp Ile

65 70 75 80
Gly His Val Trp Gly Pro Ser Thr Glu Thr Gln Leu Gly Asn Thr Leu
85 90 95
Ile Gly Gly Val Val Gly Val Arg Gly Met Val Gly Asp Asp Val Asn
100 105 110
Tyr Asp Val Ser Leu Gly Thr Pro Ile Lys Lys Pro Glu Gly Phe Asp
115 120 125
Thr Asp Thr Arg
130

<210> 2569
<211> 330
<212> DNA
<213> Homo sapiens

<400> 2569
cttgctgctg gtgctgatgt gtccatgatt ggccagttcg gcgtcggttt ctactctgcc
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tacctcgtcg ccgatagagt tgtcgtgacc accaagcaca acgatgacga gcagtacgtg
120
tgggagtccc aagcgggcgg gtcgttcact gttactcgtg acacgtcagg ggagcagctt
180
ggcaggggca ctaagatcac actgttcctc aaggacgatc agctggagta ccttgaggag
240
cgtcgcctca aggatctggt caagaagcac tctgagttca tcagctaccc catctccctg
300
tggactgaaa agacaacaga gaaggaaatt
330

<210> 2570
<211> 110
<212> PRT
<213> Homo sapiens

<400> 2570
Leu Ala Ala Gly Ala Asp Val Ser Met Ile Gly Gln Phe Gly Val Gly
1 5 10 15
Phe Tyr Ser Ala Tyr Leu Val Ala Asp Arg Val Val Val Thr Thr Lys
20 25 30
His Asn Asp Asp Glu Gln Tyr Val Trp Glu Ser Gln Ala Gly Gly Ser
35 40 45
Phe Thr Val Thr Arg Asp Thr Ser Gly Glu Gln Leu Gly Arg Gly Thr
50 55 60
Lys Ile Thr Leu Phe Leu Lys Asp Asp Gln Leu Glu Tyr Leu Glu Glu
65 70 75 80
Arg Arg Leu Lys Asp Leu Val Lys Lys His Ser Glu Phe Ile Ser Tyr
85 90 95
Pro Ile Ser Leu Trp Thr Glu Lys Thr Thr Glu Lys Glu Ile
100 105 110

<210> 2571
<211> 335
<212> DNA
<213> Homo sapiens

<400> 2571
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gtgctcctta aacatctcga taatgaacta tctgagctct ttactgagat cgctcgggag
120
aaatgggatg tccgtttagg gcagggaacg acagctatcg accaggtgga gaagcagcgt
180
gaagatgggt cttcctactt cgaaaccacc attacatttg aagacggcag cactgttacc
240
ggtgacgcat tcctagttgc taccggacgt acccctaaca ccgaccgcct tggcctcgac
300
aatggttccg gtgtgaaggt tgaaagggga cgcgt
335

<210> 2572
<211> 111
<212> PRT
<213> Homo sapiens

<400> 2572
Glu Phe Ala Asn Val Phe Ser Gly Met Gly Ser Thr Val Thr Leu Ile
1 5 10 15
Gly Arg Ser Pro Val Leu Leu Lys His Leu Asp Asn Glu Leu Ser Glu
20 25 30
Leu Phe Thr Glu Ile Ala Arg Glu Lys Trp Asp Val Arg Leu Gly Gln
35 40 45
Gly Thr Thr Ala Ile Asp Gln Val Glu Lys Gln Arg Glu Asp Gly Ser
50 55 60
Ser Tyr Phe Glu Thr Thr Ile Thr Phe Glu Asp Gly Ser Thr Val Thr
65 70 75 80
Gly Asp Ala Phe Leu Val Ala Thr Gly Arg Thr Pro Asn Thr Asp Arg
85 90 95
Leu Gly Leu Asp Asn Gly Ser Gly Val Lys Val Glu Arg Gly Arg
100 105 110

<210> 2573
<211> 460
<212> DNA
<213> Homo sapiens

<400> 2573
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gccggatcca taccggaccg tttcgtcagg gtggtcggac atcgacgaca ccgcagatgc
120
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180
cgccactggc acgatgaggg ccatcaccga gaagagaacg gccaccactc gcagaccacc
240
tcgtcccaga agagcgagga cgaaggcgat gacggcgatg accagagccg gtacagccaa
300
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360

cactgaccac gccagtaccg gcagggtcag gatcagcccg acgagaccgg aagtgatgcg
420
tagccaggaa tgacgggagg ttttcgtgtc agccacgcgt
460

<210> 2574
<211> 105
<212> PRT
<213> Homo sapiens

<400> 2574
Met Gly Thr Val Asp Leu Gly Arg Leu Val Arg Ala Gly Ser Ile Pro
1 5 10 15
Asp Arg Phe Val Arg Val Val Gly His Arg Arg His Arg Arg Cys Arg
20 25 30
Asp Asp Val Asp Thr Ser Thr Gly Ala Val Arg Asp Pro Arg Arg Arg
35 40 45
Arg Arg Cys Arg His Trp His Asp Glu Gly His His Arg Glu Glu Asn
50 55 60
Gly His His Ser Gln Thr Thr Ser Ser Gln Lys Ser Glu Asp Glu Gly
65 70 75 80
Asp Asp Gly Asp Asp Gln Ser Arg Tyr Ser Gln Arg Ser His Gln Asn
85 90 95
Gly Gly Asp Glu Gly Glu Gly Ile Val
100 105

<210> 2575
<211> 3954
<212> DNA
<213> Homo sapiens

<400> 2575
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ccactctcgc gcctccgaac agccacaggg gcaaagccct gtcaccccca ggatccggtc
120
atcagggaaa gaggacaggg agaccagaag agggccagct gggacgaggg ggcggacgcc
180
caggaggcaa cttctgagac gcagctcctg agaggggcag ggaccaggcg cgggaggcca
240
gagggggcac agagaacaaa ccccctcaga agtgaagagg agagcggaag gaaccgagag
300
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360
gagaagacgt gtggccgggg gctatcagaa ggaaactggg acggacgggc cgggctcggg
420
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480
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660

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780
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1140
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1320
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1380
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2160
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2220
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2280

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2640
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2760
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3600
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3720
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3780
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3840
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3900

ccgccatact aaacgatcga ggaataaaga cacttggttt ttctaaaaaa aact
3954

<210> 2576
<211> 1016
<212> PRT
<213> Homo sapiens

<400> 2576
Met Ala Pro Arg Thr Leu Trp Ser Cys Tyr Leu Cys Cys Leu Leu Thr
1 5 10 15
Ala Ala Ala Gly Ala Ala Ser Tyr Pro Pro Arg Gly Phe Ser Leu Tyr
20 25 30
Thr Gly Ser Ser Gly Ala Leu Ser Pro Gly Gly Pro Gln Ala Gln Ile
35 40 45
Ala Pro Arg Pro Ala Ser Arg His Arg Asn Trp Cys Ala Tyr Val Val
50 55 60
Thr Arg Thr Val Ser Cys Val Leu Glu Asp Gly Val Glu Thr Tyr Val
65 70 75 80
Lys Tyr Gln Pro Cys Ala Trp Gly Gln Pro Gln Cys Pro Gln Ser Ile
85 90 95
Met Tyr Arg Arg Phe Leu Arg Pro Arg Tyr Arg Val Ala Tyr Lys Thr
100 105 110
Val Thr Asp Met Glu Trp Arg Cys Cys Gln Gly Tyr Gly Gly Asp Asp
115 120 125
Cys Ala Glu Ser Pro Ala Pro Ala Leu Gly Pro Ala Ser Ser Thr Pro
130 135 140
Arg Pro Leu Ala Arg Pro Ala Arg Pro Asn Leu Ser Gly Ser Ser Ala
145 150 155 160
Gly Ser Pro Leu Ser Gly Leu Gly Gly Glu Gly Pro Gly Glu Ser Glu
165 170 175
Lys Val Gln Gln Leu Glu Glu Gln Val Gln Ser Leu Thr Lys Glu Leu
180 185 190
Gln Gly Leu Arg Gly Val Leu Gln Gly Leu Ser Gly Arg Leu Ala Glu
195 200 205
Asp Val Gln Arg Ala Val Glu Thr Ala Phe Asn Gly Arg Gln Gln Pro
210 215 220
Ala Asp Ala Ala Ala Arg Pro Gly Val His Glu Thr Leu Asn Glu Ile
225 230 235 240
Gln His Gln Leu Gln Leu Leu Asp Thr Arg Val Ser Thr His Asp Gln
245 250 255
Glu Leu Gly His Leu Asn Asn His His Gly Gly Ser Ser Ser Ser Gly
260 265 270
Gly Ser Arg Ala Pro Ala Pro Ala Ser Ala Pro Pro Gly Pro Ser Glu
275 280 285
Glu Leu Leu Arg Gln Leu Glu Gln Arg Leu Gln Glu Ser Cys Ser Val
290 295 300
Cys Leu Ala Gly Leu Asp Gly Phe Arg Arg Gln Gln Gln Glu Asp Arg
305 310 315 320
Glu Arg Leu Arg Ala Met Glu Lys Leu Leu Ala Ser Val Glu Glu Arg
325 330 335
Gln Arg His Leu Ala Gly Leu Ala Val Gly Arg Arg Pro Pro Gln Glu
340 345 350
Cys Cys Ser Pro Glu Leu Gly Arg Arg Leu Ala Glu Leu Glu Arg Arg

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        355                 360                 365
Leu Asp Val Val Ala Gly Ser Val Thr Val Leu Ser Gly Arg Arg Gly
    370                 375                 380
Thr Glu Leu Gly Gly Ala Ala Gly Gln Gly Gly His Pro Pro Gly Tyr
385                 390                 395                 400
Thr Ser Leu Ala Ser Arg Leu Ser Arg Leu Glu Asp Arg Phe Asn Ser
                405                 410                 415
Thr Leu Gly Pro Ser Glu Glu Gln Glu Glu Ser Trp Pro Gly Ala Pro
            420                 425                 430
Gly Gly Leu Ser His Trp Leu Pro Ala Ala Arg Gly Arg Leu Glu Gln
        435                 440                 445
Leu Gly Gly Leu Leu Ala Asn Val Ser Gly Glu Leu Gly Gly Arg Leu
    450                 455                 460
Asp Leu Leu Glu Glu Gln Val Ala Gly Ala Met Gln Ala Cys Gly Gln
465                 470                 475                 480
Leu Cys Ser Gly Ala Pro Gly Glu Gln Asp Ser Gln Val Ser Glu Ile
                485                 490                 495
Leu Ser Ala Leu Glu Arg Arg Val Leu Asp Ser Glu Gly Gln Leu Arg
            500                 505                 510
Leu Val Gly Ser Gly Leu His Thr Val Glu Ala Ala Gly Glu Ala Arg
        515                 520                 525
Gln Ala Thr Leu Glu Gly Leu Gln Glu Val Val Gly Arg Leu Gln Asp
    530                 535                 540
Arg Val Asp Ala Gln Asp Glu Thr Ala Ala Glu Phe Thr Leu Arg Leu
545                 550                 555                 560
Asn Leu Thr Ala Ala Arg Leu Gly Gln Leu Glu Gly Leu Leu Gln Ala
                565                 570                 575
His Gly Asp Glu Gly Cys Gly Ala Cys Gly Gly Val Gln Glu Glu Leu
            580                 585                 590
Gly Arg Leu Arg Asp Gly Val Glu Arg Cys Ser Cys Pro Leu Leu Pro
        595                 600                 605
Pro Arg Gly Pro Gly Ala Gly Pro Gly Val Gly Gly Pro Ser Arg Gly
    610                 615                 620
Pro Leu Asp Gly Phe Ser Val Phe Gly Gly Ser Ser Gly Ser Ala Leu
625                 630                 635                 640
Gln Ala Leu Gln Gly Glu Leu Ser Glu Val Ile Leu Ser Phe Ser Ser
                645                 650                 655
Leu Asn Asp Ser Leu Asn Glu Leu Gln Thr Thr Val Glu Gly Gln Gly
            660                 665                 670
Ala Asp Leu Ala Asp Leu Gly Ala Thr Lys Asp Arg Ile Ile Ser Glu
        675                 680                 685
Ile Asn Arg Leu Gln Gln Glu Ala Thr Glu His Ala Thr Glu Ser Glu
    690                 695                 700
Glu Arg Phe Arg Gly Leu Glu Glu Gly Gln Ala Gln Ala Gly Gln Cys
705                 710                 715                 720
Pro Ser Leu Glu Gly Arg Leu Gly Arg Leu Glu Gly Val Cys Glu Arg
                725                 730                 735
Leu Asp Thr Val Ala Gly Gly Leu Gln Gly Leu Arg Glu Gly Leu Ser
            740                 745                 750
Arg His Val Ala Gly Leu Trp Ala Gly Leu Arg Glu Thr Asn Thr Thr
        755                 760                 765
Ser Gln Met Gln Ala Ala Leu Leu Glu Lys Leu Val Gly Gly Gln Ala
    770                 775                 780
Gly Leu Gly Arg Arg Leu Gly Ala Leu Asn Ser Ser Leu Gln Leu Leu
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785                 790                 795                 800
Glu Asp Arg Leu His Gln Leu Ser Leu Lys Asp Leu Thr Gly Pro Ala
                805                 810                 815
Gly Glu Ala Gly Pro Pro Gly Pro Pro Gly Leu Gln Gly Pro Pro Gly
            820                 825                 830
Pro Ala Gly Pro Pro Gly Ser Pro Gly Lys Asp Gly Gln Glu Gly Pro
        835                 840                 845
Ile Gly Pro Pro Gly Pro Gln Gly Glu Gln Gly Val Glu Gly Ala Pro
    850                 855                 860
Ala Ala Pro Val Pro Gln Val Ala Phe Ser Ala Ala Leu Ser Leu Pro
865                 870                 875                 880
Arg Ser Glu Pro Gly Thr Val Pro Phe Asp Arg Val Leu Leu Asn Asp
                885                 890                 895
Gly Gly Tyr Tyr Asp Pro Glu Thr Gly Val Phe Thr Ala Pro Leu Ala
            900                 905                 910
Gly Arg Tyr Leu Leu Ser Ala Val Leu Thr Gly His Arg His Glu Lys
        915                 920                 925
Val Glu Ala Val Leu Ser Arg Ser Asn Gln Gly Val Ala Arg Val Asp
    930                 935                 940
Ser Gly Gly Tyr Glu Pro Glu Gly Leu Glu Asn Lys Pro Val Ala Glu
945                 950                 955                 960
Ser Gln Pro Ser Pro Gly Thr Leu Gly Val Phe Ser Leu Ile Leu Pro
                965                 970                 975
Leu Gln Ala Gly Asp Thr Val Cys Val Asp Leu Val Met Gly Gln Leu
            980                 985                 990
Ala His Ser Glu Glu Pro Leu Thr Ile Phe Ser Gly Ala Leu Leu Tyr
        995                 1000                1005
Gly Asp Pro Glu Leu Glu His Ala
    1010                1015
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<210> 2577
<211> 343
<212> DNA
<213> Homo sapiens

<400> 2577
acgcgtgaag ggggagggtc atggcctcct gggcttcaag gaggagctgg ggctggggtg
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ggggcgtggt gcattcatcc ccggccgcag ctgatctgga gccatctgta gcgaaatgct
120
tgctgagcaa attacgaggg tcaacaggag cagggcagac gcttctccca cctgctggcc
180
agtgttccct cggctaccgt gcactcagcc ccacagtgac ccctgagtgg ataccggccc
240
tgcctgccct gggctctcaa tgggggctcg gggcctcaca gggccagcac gagccacttg
300
ccagggtctc caacagaccc tgagcctggc agtccctggg ccc
343

<210> 2578
<211> 100
<212> PRT
<213> Homo sapiens

<400> 2578
Met Ala Ser Trp Ala Ser Arg Arg Ser Trp Gly Trp Gly Gly Gly Val
1 5 10 15
Val His Ser Ser Pro Ala Ala Ala Asp Leu Glu Pro Ser Val Ala Lys
20 25 30
Cys Leu Leu Ser Lys Leu Arg Gly Ser Thr Gly Ala Gly Gln Thr Leu
35 40 45
Leu Pro Pro Ala Gly Gln Cys Ser Leu Gly Tyr Arg Ala Leu Ser Pro
50 55 60
Thr Val Thr Pro Glu Trp Ile Pro Ala Leu Pro Ala Leu Gly Ser Gln
65 70 75 80
Trp Gly Leu Gly Ala Ser Gln Gly Gln His Glu Pro Leu Ala Arg Val
85 90 95
Ser Asn Arg Pro
100

<210> 2579
<211> 420
<212> DNA
<213> Homo sapiens

<400> 2579
ntcatgatct tcagaagctg tattaatttg gccgcattta tcatcatagt tttttcctat
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ggaagcatgt tttatagtgt tcatcaaagt gccataacag caactgaaat acggaatcaa
120
gttaaaaaag agatgatcct tgccaaacgt tttttcttta tagtatttac tgatgcatta
180
tgctggatac ccatttttgt agtgaaattt ctttcactgc ttcaggtaga aataccaggt
240
accataacct cttgggtagt gatttttatt ctgcccatta acagtgcttt gaacccaatt
300
ctctatactc tgaccacaag accatttaaa gaaatgattc atcggttttg gtataactac
360
agacaaagaa aatctatgga cagcaaaggt cagaaaacag aggctggagt gtgctcgcga
420

<210> 2580
<211> 140
<212> PRT
<213> Homo sapiens

<400> 2580
Xaa Met Ile Phe Arg Ser Cys Ile Asn Leu Ala Ala Phe Ile Ile Ile
1 5 10 15
Val Phe Ser Tyr Gly Ser Met Phe Tyr Ser Val His Gln Ser Ala Ile
20 25 30
Thr Ala Thr Glu Ile Arg Asn Gln Val Lys Lys Glu Met Ile Leu Ala
35 40 45
Lys Arg Phe Phe Phe Ile Val Phe Thr Asp Ala Leu Cys Trp Ile Pro
50 55 60
Ile Phe Val Val Lys Phe Leu Ser Leu Leu Gln Val Glu Ile Pro Gly
65 70 75 80
Thr Ile Thr Ser Trp Val Val Ile Phe Ile Leu Pro Ile Asn Ser Ala

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                85                  90                  95
Leu Asn Pro Ile Leu Tyr Thr Leu Thr Thr Arg Pro Phe Lys Glu Met
            100                 105                 110
Ile His Arg Phe Trp Tyr Asn Tyr Arg Gln Arg Lys Ser Met Asp Ser
        115                 120                 125
Lys Gly Gln Lys Thr Glu Ala Gly Val Cys Ser Arg
    130                 135                 140
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<210> 2581
<211> 459
<212> DNA
<213> Homo sapiens

<400> 2581
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cgtccggtgc acgtccgcgc cgaaggagcc gacacccaga ccacggtgcc cgacacccag
120
cagtttgtat accaggccca ttccctcgac aagattgaga tcattggacg cattctgcag
180
gccaacgacg tcgaaaaggt cattatcttc tgccgcacca agcgtgcatg ccagcggctt
240
tctgacgacc tcgacgaccg cggtttcaaa acccgcgcca tccacggtga tctcacgcag
300
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<213> Homo sapiens

<400> 2582
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Gln Thr Thr Val Pro Asp Thr Gln Gln Phe Val Tyr Gln Ala His Ser
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Glu Lys Val Ile Ile Phe Cys Arg Thr Lys Arg Ala Cys Gln Arg Leu
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Ser Asp Asp Leu Asp Asp Arg Gly Phe Lys Thr Arg Ala Ile His Gly
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Asp Leu Thr Gln Val Ala Arg Glu Lys Ala Leu Lys Lys Phe Arg His
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Gly Glu Ala Thr Ile Leu Val Ala Thr Asp Val Ala Ala Arg Gly Ile
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<211> 1186
<212> PRT
<213> Homo sapiens

<400> 2584
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        35   40   45
His Arg Ser Val Tyr Gly Cys Pro Leu Ala Lys Lys Arg Lys Thr Gln
    50   55   60
Asp Lys Gln Pro Gln Glu Pro Ala Pro Lys Arg Lys Pro Phe Ala Val
65   70   75   80
Lys Ala Asp Ser Ser Ser Val Asp Glu Cys Asp Asp Ser Asp Gly Thr
                85   90   95
Glu Asp Met Asp Glu Lys Glu Glu Asp Glu Gly Glu Glu Tyr Ser Glu
            100   105   110
Asp Asn Asp Glu Pro Gly Asp Glu Asp Glu Glu Asp Glu Glu Gly Asp

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Asp Gly Glu Asp Val Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu
145                 150                 155                 160
Glu Glu Glu Glu Glu Glu Glu Asn Glu Asp His Gln Met Asn Cys His
                165                 170                 175
Asn Thr Arg Ile Met Gln Asp Thr Glu Lys Asp Asp Asn Asn Ser Asp
            180                 185                 190
Glu Tyr Asp Asn Tyr Asp Glu Leu Val Ala Lys Ser Leu Leu Asn Leu
        195                 200                 205
Gly Lys Ile Ala Glu Asp Ala Ala Tyr Arg Ala Arg Thr Glu Ser Glu
    210                 215                 220
Met Asn Ser Asn Thr Ser Asn Ser Leu Glu Asp Asp Ser Asp Lys Asn
225                 230                 235                 240
Glu Asn Leu Gly Arg Lys Ser Glu Leu Ser Leu Asp Leu Asp Ser Asp
                245                 250                 255
Val Val Arg Glu Thr Val Asp Ser Leu Lys Leu Leu Ala Gln Gly His
            260                 265                 270
Gly Val Val Leu Ser Glu Asn Met Asn Asp Arg Asn Tyr Ala Asp Ser
        275                 280                 285
Met Ser Gln Gln Asp Ser Arg Asn Met Asn Tyr Val Met Leu Gly Lys
    290                 295                 300
Pro Met Asn Asn Gly Leu Met Glu Lys Met Val Glu Glu Ser Asp Glu
305                 310                 315                 320
Glu Val Cys Leu Ser Ser Leu Glu Cys Leu Arg Asn Gln Cys Phe Asp
                325                 330                 335
Leu Ala Arg Lys Leu Ser Glu Thr Asn Pro Gln Glu Arg Asn Pro Gln
            340                 345                 350
Gln Asn Met Asn Ile Arg Gln His Val Arg Pro Glu Glu Asp Phe Pro
        355                 360                 365
Gly Arg Thr Pro Asp Arg Asn Tyr Ser Asp Met Leu Asn Leu Met Arg
    370                 375                 380
Leu Glu Glu Gln Leu Ser Pro Arg Ser Arg Val Phe Ala Ser Cys Ala
385                 390                 395                 400
Lys Glu Asp Gly Cys His Glu Arg Asp Asp Asp Thr Thr Ser Val Asn
                405                 410                 415
Ser Asp Arg Ser Glu Glu Val Phe Asp Met Thr Lys Gly Asn Leu Thr
            420                 425                 430
Leu Leu Glu Lys Ala Ile Ala Leu Glu Thr Glu Arg Ala Lys Ala Met
        435                 440                 445
Arg Glu Lys Met Ala Met Glu Ala Gly Arg Arg Asp Asn Met Arg Ser
    450                 455                 460
Tyr Glu Asp Gln Ser Pro Arg Gln Leu Pro Gly Glu Asp Arg Lys Pro
465                 470                 475                 480
Lys Ser Ser Asp Ser His Val Lys Lys Pro Tyr Tyr Gly Lys Asp Pro
                485                 490                 495
Ser Arg Thr Glu Lys Lys Glu Ser Lys Cys Pro Thr Pro Gly Cys Asp
            500                 505                 510
Gly Thr Gly His Val Thr Gly Leu Tyr Pro His His Arg Ser Leu Ser
        515                 520                 525
Gly Cys Pro His Lys Asp Arg Val Pro Pro Glu Ile Leu Ala Met His
    530                 535                 540
Glu Ser Val Leu Lys Cys Pro Thr Pro Gly Cys Thr Gly Arg Gly His
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Asp Val Ser Lys Ser Ser Gln Ala Ser Asp Arg Val Leu Arg Pro Met
        595                 600                 605
Cys Phe Val Lys Gln Leu Glu Ile Pro Gln Tyr Gly Tyr Arg Asn Asn
    610                 615                 620
Val Pro Thr Thr Thr Pro Arg Ser Asn Leu Ala Lys Glu Leu Glu Lys
625                 630                 635                 640
Tyr Ser Lys Thr Ser Phe Glu Tyr Asn Ser Tyr Asp Asn His Thr Tyr
                645                 650                 655
Gly Lys Arg Ala Ile Ala Pro Lys Val Gln Thr Arg Asp Ile Ser Pro
            660                 665                 670
Lys Gly Tyr Asp Asp Ala Lys Arg Tyr Cys Lys Asp Pro Ser Pro Ser
        675                 680                 685
Ser Ser Ser Thr Ser Ser Tyr Ala Pro Ser Ser Ser Ser Asn Leu Ser
    690                 695                 700
Cys Gly Gly Gly Ser Ser Ala Ser Ser Thr Cys Ser Lys Ser Ser Phe
705                 710                 715                 720
Asp Tyr Thr His Asp Met Glu Ala Ala His Met Ala Ala Thr Ala Ile
                725                 730                 735
Leu Asn Leu Ser Thr Arg Cys Arg Glu Met Pro Gln Asn Leu Ser Thr
            740                 745                 750
Lys Pro Gln Asp Leu Cys Ala Thr Arg Asn Pro Asp Met Glu Val Asp
        755                 760                 765
Glu Asn Gly Thr Leu Asp Leu Ser Met Asn Lys Gln Arg Pro Arg Asp
    770                 775                 780
Ser Cys Cys Pro Ile Leu Thr Pro Leu Glu Pro Met Ser Pro Gln Gln
785                 790                 795                 800
Gln Ala Val Met Asn Asn Arg Cys Phe Gln Leu Gly Glu Gly Asp Cys
                805                 810                 815
Trp Asp Leu Pro Val Asp Tyr Thr Lys Met Lys Pro Arg Arg Ile Asp
            820                 825                 830
Glu Asp Glu Ser Lys Asp Ile Thr Pro Glu Asp Leu Asp Pro Phe Gln
        835                 840                 845
Glu Ala Leu Glu Glu Arg Arg Tyr Pro Gly Glu Val Thr Ile Pro Ser
    850                 855                 860
Pro Lys Pro Lys Tyr Pro Gln Cys Lys Glu Ser Lys Lys Asp Leu Ile
865                 870                 875                 880
Thr Leu Ser Gly Cys Pro Leu Ala Asp Lys Ser Ile Arg Ser Met Leu
                885                 890                 895
Ala Thr Ser Ser Gln Glu Leu Lys Cys Pro Thr Pro Gly Cys Asp Gly
            900                 905                 910
Ser Gly His Ile Thr Gly Asn Tyr Ala Ser His Arg Ser Leu Ser Gly
        915                 920                 925
Cys Pro Arg Ala Lys Lys Ser Gly Ile Arg Ile Ala Gln Ser Lys Glu
    930                 935                 940
Asp Lys Glu Asp Gln Glu Pro Ile Arg Cys Pro Val Pro Gly Cys Asp
945                 950                 955                 960
Gly Gln Gly His Ile Thr Gly Lys Tyr Ala Ser His Arg Ser Ala Ser
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Gly Cys Pro Leu Ala Ala Lys Arg Gln Lys Asp Gly Tyr Leu Asn Gly
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Thr Pro Gly Cys Asp Gly Ser Gly His Val Ser Gly Ser Phe Leu Thr
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His Arg Ser Leu Ser Gly Cys Pro Arg Ala Thr Ser Ala Met Lys Lys
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Ala Lys Leu Ser Gly Glu Gln Met Leu Thr Ile Lys Gln Arg Ala Ser
                1045                1050                1055
Asn Gly Ile Glu Asn Asp Glu Glu Ile Lys Gln Leu Asp Glu Glu Ile
            1060                1065                1070
Lys Glu Leu Asn Glu Ser Asn Ser Gln Met Glu Ala Asp Met Ile Lys
        1075                1080                1085
Leu Arg Thr Gln Ile Thr Thr Met Glu Ser Asn Leu Lys Thr Ile Glu
    1090                1095                1100
Glu Glu Asn Lys Val Ile Glu Gln Gln Asn Glu Ser Leu Leu His Glu
1105                1110                1115                1120
Leu Ala Asn Leu Ser Gln Ser Leu Ile His Ser Leu Ala Asn Ile Gln
                1125                1130                1135
Leu Pro His Met Asp Pro Ile Asn Glu Gln Asn Phe Asp Ala Tyr Val
            1140                1145                1150
Thr Thr Leu Thr Glu Met Tyr Thr Asn Gln Asp Arg Tyr Gln Ser Pro
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Glu Asn Lys Ala Leu Leu Glu Asn Ile Lys Gln Ala Val Arg Gly Ile
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Gln Val
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<211> 542
<212> DNA
<213> Homo sapiens

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<211> 122
<212> PRT
<213> Homo sapiens

<400> 2586
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35 40 45
Pro Gln Arg Ala Lys Val Cys Glu His Phe Leu Ser Pro Leu Asn Gly
50 55 60
Leu Ser His Val Ile Leu Thr Arg Leu Leu Cys Phe Ile Thr Ser Val
65 70 75 80
Ser Gly Ala Ser His Pro Arg Glu Glu Trp Trp Gly Cys Arg Leu Thr
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Leu Gly His Leu Ala Ala Ala Ser Val Leu Met Thr Thr Leu Leu Pro
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Gln Ala Leu Leu Leu Asn Val Leu Ala Leu
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<210> 2587
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<212> DNA
<213> Homo sapiens

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<210> 2588
<211> 145
<212> PRT
<213> Homo sapiens

<400> 2588
Xaa Asn Ile His Ala Ala Ile Pro Gly Gly Met Leu Ser Asn Met Glu

```
 1               5                  10                  15
Ser Gln Leu Glu Ala Gln Gly Ala Gly Asp Arg Met Asp Glu Val Met
            20                  25                  30
Lys Glu Val Pro Arg Val Arg Lys Asp Ala Gly Tyr Pro Pro Leu Val
        35                  40                  45
Thr Pro Ser Ser Gln Ile Val Gly Thr Gln Ala Val Phe Asn Val Leu
    50                  55                  60
Met Gly Asn Gly Ser Tyr Lys Asn Leu Thr Ala Glu Phe Ala Asp Leu
65                  70                  75                  80
Met Leu Gly Tyr Tyr Gly Lys Pro Ile Gly Glu Leu Asn Pro Glu Ile
                85                  90                  95
Val Glu Met Ala Lys Lys Gln Thr Gly Lys Glu Pro Ile Asp Cys Arg
            100                 105                 110
Pro Ala Asp Leu Leu Glu Pro Glu Trp Asp Gln Leu Val Glu Gln Ala
        115                 120                 125
Lys Ser Leu Glu Gly Phe Asp Gly Ser Asp Glu Asp Val Leu Thr Asn
    130                 135                 140
Ala
145
```

<210> 2589
<211> 366
<212> DNA
<213> Homo sapiens

<400> 2589
ccggcgaaga aggacatggc catggtcttc ggcgcgactc attacgtcga cccgacggcc
60
ggcgatccgg ttgagcagat cagagcgctg accaggggcc gcggcgtcga tttcgcgatc
120
gaggtcgtcg gcatcgtcga ggtcatggag caggcctact gggcggcgcg acgcggcggc
180
acgatcgtct acgtcggggc gctgggcatc gacgccaagc tggtcctgcc ggcgaacgac
240
ctgcacggcg gcgccaagac gatcatcggc tgcgccaacg gattgggcgc agtgcgcacc
300
gactatgcca agatgatctc gctggtcgag accggacggc tggacctggg cgggatgatc
360
acgcgt
366

<210> 2590
<211> 122
<212> PRT
<213> Homo sapiens

<400> 2590
```
Pro Ala Lys Lys Asp Met Ala Met Val Phe Gly Ala Thr His Tyr Val
 1               5                  10                  15
Asp Pro Thr Ala Gly Asp Pro Val Glu Gln Ile Arg Ala Leu Thr Arg
            20                  25                  30
Gly Arg Gly Val Asp Phe Ala Ile Glu Val Val Gly Ile Val Glu Val
        35                  40                  45
Met Glu Gln Ala Tyr Trp Ala Ala Arg Arg Gly Gly Thr Ile Val Tyr
```

```
    50                  55                  60
Val Gly Ala Leu Gly Ile Asp Ala Lys Leu Val Leu Pro Ala Asn Asp
65                  70                  75                  80
Leu His Gly Gly Ala Lys Thr Ile Ile Gly Cys Ala Asn Gly Leu Gly
                85                  90                  95
Ala Val Arg Thr Asp Tyr Ala Lys Met Ile Ser Leu Val Glu Thr Gly
            100                 105                 110
Arg Leu Asp Leu Gly Gly Met Ile Thr Arg
        115                 120
```

<210> 2591
<211> 341
<212> DNA
<213> Homo sapiens

<400> 2591
acgcgtaaag gcatgacctc accttatcat cagggtcaca cgtgtgttat tctggggctg
60
agcagcccac gagttgtcca gcaccaggcc aggggtcagt cagcaatgag gacagctcct
120
tcctgctcca gggcaggccc tgggcagggc aatgctgggg acacggtggg gagtaggcca
180
cagcttctgt gggggagttc ctatggcagg aggatcatgc ccagcagcgt ggaagagcaa
240
ggggtgaccc tgcactcgag gctcctggga agacggggag ggttgaggtt acatgaggga
300
gaggggtcag ttggtgcatt cacagaacag cagggtggcc a
341

<210> 2592
<211> 109
<212> PRT
<213> Homo sapiens

<400> 2592
```
Met Thr Ser Pro Tyr His Gln Gly His Thr Cys Val Ile Leu Gly Leu
 1               5                  10                  15
Ser Ser Pro Arg Val Val Gln His Gln Ala Arg Gly Gln Ser Ala Met
            20                  25                  30
Arg Thr Ala Pro Ser Cys Ser Arg Ala Gly Pro Gly Gln Gly Asn Ala
        35                  40                  45
Gly Asp Thr Val Gly Ser Arg Pro Gln Leu Leu Trp Gly Ser Ser Tyr
    50                  55                  60
Gly Arg Arg Ile Met Pro Ser Ser Val Glu Glu Gln Gly Val Thr Leu
65                  70                  75                  80
His Ser Arg Leu Leu Gly Arg Arg Gly Gly Leu Arg Leu His Glu Gly
                85                  90                  95
Glu Gly Ser Val Gly Ala Phe Thr Glu Gln Gln Gly Gly
            100                 105
```

<210> 2593
<211> 501
<212> DNA
<213> Homo sapiens

<400> 2593
cgcgtaaggc caccagaaga tttttatgca cagattccgt tgcttcgaga gctaatttcg
60
gcgctttcat ggggttttat ggaggtggat gaatatgagg cggatgatat tatcggtacc
120
ttggcgcgcc aagcggatga agcgggggat tatatgactt atattgtgtc ttcggacctc
180
gatatgctgc aaatcgtaga tgaaaacacc aagatgtatc gaattctgcg gggattttcg
240
gatctcgagg agatggatac tccagcgatt gaagaaaaat atggaatctt gaagtcgcaa
300
tttttggacc tgaaggcgct gaaggggat aattcggata atattccagg cgtaccaggg
360
attggtgaga aaaccgcagt gaaactcttg aatgagtatg gtagcttgga ggggatttat
420
aatcatatca aggaaatttc gggggcgaca cagaagaaat tgattgctgg acgcgaatca
480
gctgagatgt ctcttaagct t
501

<210> 2594
<211> 167
<212> PRT
<213> Homo sapiens

<400> 2594
Arg Val Arg Pro Pro Glu Asp Phe Tyr Ala Gln Ile Pro Leu Leu Arg
1 5 10 15
Glu Leu Ile Ser Ala Leu Ser Trp Gly Phe Met Glu Val Asp Glu Tyr
20 25 30
Glu Ala Asp Asp Ile Ile Gly Thr Leu Ala Arg Gln Ala Asp Glu Ala
35 40 45
Gly Asp Tyr Met Thr Tyr Ile Val Ser Ser Asp Leu Asp Met Leu Gln
50 55 60
Ile Val Asp Glu Asn Thr Lys Met Tyr Arg Ile Leu Arg Gly Phe Ser
65 70 75 80
Asp Leu Glu Glu Met Asp Thr Pro Ala Ile Glu Glu Lys Tyr Gly Ile
85 90 95
Leu Lys Ser Gln Phe Leu Asp Leu Lys Ala Leu Lys Gly Asp Asn Ser
100 105 110
Asp Asn Ile Pro Gly Val Pro Gly Ile Gly Glu Lys Thr Ala Val Lys
115 120 125
Leu Leu Asn Glu Tyr Gly Ser Leu Glu Gly Ile Tyr Asn His Ile Lys
130 135 140
Glu Ile Ser Gly Ala Thr Gln Lys Lys Leu Ile Ala Gly Arg Glu Ser
145 150 155 160
Ala Glu Met Ser Leu Lys Leu
165

<210> 2595
<211> 928
<212> DNA
<213> Homo sapiens

<400> 2595
agatcttcca gatgcaacaa tgatcaatta agacacgcgg cgacatggtg gcccctgcct
60
caccccccag ggatacctgt aatacctgct tcccacttca tgggctacaa tctcatgctg
120
gtcacaattt ctggggctca ctcatataac accaacaaat gggatatttg tgaagaactt
180
cgcctgcggg agcttgaaga agtcaaggcc agagctgctc agatggaaaa gaccatgcgg
240
tggtggtcgg actgcactgc caactggaga gaaaaatgga gtaaagttcg agctgaaagg
300
aacagtgccg gaaaggaagg aagacaactc agaataaaac tagagatggc gatgaaagaa
360
tcggatccac tgaaacagaa acagagtttg ccacttcaga aggaggcatt agaagctaat
420
gttacccagg atctgaagct tcctggcttc gtagaagaat cctgtgaaca tacagaccaa
480
tttcaattga gttcacaaat gcatgagtct atcagagagt atttggtaaa aagacaattt
540
tctacaaagg aggacacaaa taataaggaa caaggtgtgg ttattgattc tctaaaatta
600
agtgaggaga tgaagcccaa tctagatggt gttgatttat tcaacaatgg tggttctgga
660
aacggtgaaa cgaaaactgg gctgagactg aaagcaataa atctgccttt ggaaaatgaa
720
gtaactgaaa tttcagcttt gcaggtgcat ttggatgaat tccaaaaaat cttatggaag
780
gaaagagaaa tgcgcacagc tttggaaaaa gaaatagaga gactggagtc ggctttgtct
840
ctgtggaagt ggaagtatga agaactgaaa gaatcaaagc caaaaaatgt gaaagagttt
900
gacattcttc ttggtcaaca taatgatg
928

<210> 2596
<211> 309
<212> PRT
<213> Homo sapiens

<400> 2596
Arg Ser Ser Arg Cys Asn Asn Asp Gln Leu Arg His Ala Ala Thr Trp
1 5 10 15
Trp Pro Leu Pro His Pro Pro Gly Ile Pro Val Ile Pro Ala Ser His
20 25 30
Phe Met Gly Tyr Asn Leu Met Leu Val Thr Ile Ser Gly Ala His Ser
35 40 45
Tyr Asn Thr Asn Lys Trp Asp Ile Cys Glu Glu Leu Arg Leu Arg Glu
50 55 60
Leu Glu Glu Val Lys Ala Arg Ala Ala Gln Met Glu Lys Thr Met Arg
65 70 75 80
Trp Trp Ser Asp Cys Thr Ala Asn Trp Arg Glu Lys Trp Ser Lys Val
85 90 95
Arg Ala Glu Arg Asn Ser Ala Gly Lys Glu Gly Arg Gln Leu Arg Ile

```
            100                 105                 110
Lys Leu Glu Met Ala Met Lys Glu Ser Asp Pro Leu Lys Gln Lys Gln
        115                 120                 125
Ser Leu Pro Leu Gln Lys Glu Ala Leu Glu Ala Asn Val Thr Gln Asp
    130                 135                 140
Leu Lys Leu Pro Gly Phe Val Glu Glu Ser Cys Glu His Thr Asp Gln
145                 150                 155                 160
Phe Gln Leu Ser Ser Gln Met His Glu Ser Ile Arg Glu Tyr Leu Val
                165                 170                 175
Lys Arg Gln Phe Ser Thr Lys Glu Asp Thr Asn Asn Lys Glu Gln Gly
            180                 185                 190
Val Val Ile Asp Ser Leu Lys Leu Ser Glu Glu Met Lys Pro Asn Leu
        195                 200                 205
Asp Gly Val Asp Leu Phe Asn Asn Gly Gly Ser Gly Asn Gly Glu Thr
    210                 215                 220
Lys Thr Gly Leu Arg Leu Lys Ala Ile Asn Leu Pro Leu Glu Asn Glu
225                 230                 235                 240
Val Thr Glu Ile Ser Ala Leu Gln Val His Leu Asp Glu Phe Gln Lys
                245                 250                 255
Ile Leu Trp Lys Glu Arg Glu Met Arg Thr Ala Leu Glu Lys Glu Ile
            260                 265                 270
Glu Arg Leu Glu Ser Ala Leu Ser Leu Trp Lys Trp Lys Tyr Glu Glu
        275                 280                 285
Leu Lys Glu Ser Lys Pro Lys Asn Val Lys Glu Phe Asp Ile Leu Leu
    290                 295                 300
Gly Gln His Asn Asp
305
```

<210> 2597
<211> 631
<212> DNA
<213> Homo sapiens

<400> 2597
ccatgggtgg gaatgcaaga gacacactct agacttacta gaggagcaag agcaggactt
60
ggctgcacct gcagctgagg gttagcagga attaggagat aacagtagaa tagggctaga
120
ctgaaaaggc ctttgatgcc aggttaggaa atttacattt tatccacaaa atccaaatcc
180
tcctttaata atgagatgtc tttacaagtt tttgggcaag agtggtatgg ctgacctggt
240
gtcctgggaa ggaactgtgt ggggatggtg tgcaggactt acctagggtg ggaaaggcac
300
aagcagcatg gggctgtggc agctaccaga ggtaaaggga catttcaggg aaagacttgg
360
caggacaaga ccttccttgg atggatggat gaataccaga aacagggacc caagagaaag
420
gccgagtttc atagggagag aagatgggtc atgtatgagg catgttgagc ttgtactgat
480
ggtgagacgt ccagtcgaca gtactaccca ctggccagtg agaaatgtgg gaccagggtt
540
caggaggaaa ctggggccgg aaatgagcat ttggaaggcg ccagggtgga agcgggtggt
600

tcactccacg agtgctattt cacttacgcg t
631

<210> 2598
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2598
Met Gly Leu Trp Gln Leu Pro Glu Val Lys Gly His Phe Arg Glu Arg
1 5 10 15
Leu Gly Arg Thr Arg Pro Ser Leu Asp Gly Trp Met Asn Thr Arg Asn
20 25 30
Arg Asp Pro Arg Glu Arg Pro Ser Phe Ile Gly Arg Glu Asp Gly Ser
35 40 45
Cys Met Arg His Val Glu Leu Val Leu Met Val Arg Arg Pro Val Asp
50 55 60
Ser Thr Thr His Trp Pro Val Arg Asn Val Gly Pro Gly Phe Arg Arg
65 70 75 80
Lys Leu Gly Pro Glu Met Ser Ile Trp Lys Ala Pro Gly Trp Lys Arg
85 90 95
Val Val His Ser Thr Ser Ala Ile Ser Leu Thr Arg
100 105

<210> 2599
<211> 356
<212> DNA
<213> Homo sapiens

<400> 2599
nagatcttat acagggacgt gatgttggag aactactgga accttgtttc tctgggactg
60
tgtcattttg atatgaatat tatctccatg ttggaggaag ggaaagagcc ctggactgtg
120
aagagctgtg tgaaaatagc aagaaaacca agaacgcggg aatgtgtcaa aggcgtggtc
180
acagatatcc ctcctaaatg tacaatcaag gatttgctac caaaagagaa gagcagtaca
240
gaagcagtat tccacacagt ggtgttggaa agacacgaaa gccctgacat tgaagacttt
300
tccttcaagg aaccccagaa aaatgtgcat gattttgagt gtcaatggag agatgn
356

<210> 2600
<211> 118
<212> PRT
<213> Homo sapiens

<400> 2600
Xaa Ile Leu Tyr Arg Asp Val Met Leu Glu Asn Tyr Trp Asn Leu Val
1 5 10 15
Ser Leu Gly Leu Cys His Phe Asp Met Asn Ile Ile Ser Met Leu Glu
20 25 30
Glu Gly Lys Glu Pro Trp Thr Val Lys Ser Cys Val Lys Ile Ala Arg

```
        35                  40                  45
Lys Pro Arg Thr Arg Glu Cys Val Lys Gly Val Val Thr Asp Ile Pro
    50                  55                  60
Pro Lys Cys Thr Ile Lys Asp Leu Leu Pro Lys Glu Lys Ser Ser Thr
65                  70                  75                  80
Glu Ala Val Phe His Thr Val Val Leu Glu Arg His Glu Ser Pro Asp
                85                  90                  95
Ile Glu Asp Phe Ser Phe Lys Glu Pro Gln Lys Asn Val His Asp Phe
            100                 105                 110
Glu Cys Gln Trp Arg Asp
        115
```

<210> 2601
<211> 329
<212> DNA
<213> Homo sapiens

<400> 2601
gcgccgatca tgatctacgg cgacgacgtc acccacctgc tcaccgaaga aggcatcgcc
60
tacttgtaca aggcgcgttc cctggaagag cgccaagcga tgatcgccgg cggtggtggg
120
gtcaccgcct tcggcttgcg ccacaacccc aaggacactg cgcgcatgcg ccgcgaaggc
180
ttgatcgcct tgcccgaaga cctcggtatc cgccgcaccg acgccacccg cgaactgttg
240
gccgccaaga gcgtggccga cctggtggag tggtccggtg gcttgtgcaa cccgcccgcc
300
aagttcagga gctggtaaat gcgcgccct
329

<210> 2602
<211> 105
<212> PRT
<213> Homo sapiens

<400> 2602
```
Ala Pro Ile Met Ile Tyr Gly Asp Asp Val Thr His Leu Leu Thr Glu
 1               5                  10                  15
Glu Gly Ile Ala Tyr Leu Tyr Lys Ala Arg Ser Leu Glu Glu Arg Gln
            20                  25                  30
Ala Met Ile Ala Gly Gly Gly Gly Val Thr Ala Phe Gly Leu Arg His
        35                  40                  45
Asn Pro Lys Asp Thr Ala Arg Met Arg Arg Glu Gly Leu Ile Ala Leu
    50                  55                  60
Pro Glu Asp Leu Gly Ile Arg Arg Thr Asp Ala Thr Arg Glu Leu Leu
65                  70                  75                  80
Ala Ala Lys Ser Val Ala Asp Leu Val Glu Trp Ser Gly Gly Leu Cys
                85                  90                  95
Asn Pro Pro Ala Lys Phe Arg Ser Trp
            100                 105
```

<210> 2603
<211> 423

<212> DNA
<213> Homo sapiens

<400> 2603
tcatgatcca ttgctctacc ctttacggtt gtgcacctac gcccaggtcg gtggtcagga
60
gcatcggttc ggtggtaccg aggtcgagga cttccttcac gccgttgttc gcggagggca
120
ggttgtggta agtggtcagg tgggccacga tctgggcact gatcacctcg gtgaaatcga
180
agctctggtt accctgagcg gtcgccgaca cgacacggtc cacaccggag accagaccga
240
tctcggagat gatcgcgtaa ccttcattgt cgtagaggat cttgcacgca tcgatgatgc
300
gcttgatctc cttggcagtg aagatgattt ccatcggggt gttggccgac agatactgac
360
cggagctggt ggtcacctgg gtggaatcca ggtcatccgg aaccgggttc aggttgtccg
420
cgg
423

<210> 2604
<211> 103
<212> PRT
<213> Homo sapiens

<400> 2604
Met Glu Ile Ile Phe Thr Ala Lys Glu Ile Lys Arg Ile Ile Asp Ala
 1   5   10   15
Cys Lys Ile Leu Tyr Asp Asn Glu Gly Tyr Ala Ile Ile Ser Glu Ile
            20   25   30
Gly Leu Val Ser Gly Val Asp Arg Val Val Ser Ala Thr Ala Gln Gly
        35   40   45
Asn Gln Ser Phe Asp Phe Thr Glu Val Ile Ser Ala Gln Ile Val Ala
    50   55   60
His Leu Thr Thr Tyr His Asn Leu Pro Ser Ala Asn Asn Gly Val Lys
65   70   75   80
Glu Val Leu Asp Leu Gly Thr Thr Glu Pro Met Leu Leu Thr Thr Asp
                85   90   95
Leu Gly Val Gly Ala Gln Pro
            100

<210> 2605
<211> 354
<212> DNA
<213> Homo sapiens

<400> 2605
ngggagggag ggcatgtcaa aagcgactgt atccagaggg tttgatttaa acatttttca
60
aaacatatgt ggcaaacagc ggggggaggg gatctcacca acgtttttct ccacttcttc
120
tttgcatgct gggacctgtt ccactttcaa aatgtgtcat tttggaagga aagggaggaa
180

caactacttg aaaggaatac acgtcagtat gagccctttc tcctcagcag aaggttgccc
240
caaagtacct cctctgaggc gagagaaagg agagaggagg agagacagct ttcatcaaat
300
ggggcaccca ggactctagg gagagaggca cgttctcaca aaggcccttt gagc
354

<210> 2606
<211> 101
<212> PRT
<213> Homo sapiens

<400> 2606
Met Ser Lys Ala Thr Val Ser Arg Gly Phe Asp Leu Asn Ile Phe Gln
1 5 10 15
Asn Ile Cys Gly Lys Gln Arg Gly Glu Gly Ile Ser Pro Thr Phe Phe
20 25 30
Ser Thr Ser Ser Leu His Ala Gly Thr Cys Ser Thr Phe Lys Met Cys
35 40 45
His Phe Gly Arg Lys Gly Arg Asn Asn Tyr Leu Lys Gly Ile His Val
50 55 60
Ser Met Ser Pro Phe Ser Ser Ala Glu Gly Cys Pro Lys Val Pro Pro
65 70 75 80
Leu Arg Arg Glu Lys Gly Glu Arg Arg Arg Asp Ser Phe His Gln Met
85 90 95
Gly His Pro Gly Leu
100

<210> 2607
<211> 297
<212> DNA
<213> Homo sapiens

<400> 2607
tgatcaagaa caatgatacg atatcctaac caacagagga agcaacggaa gttgttgttg
60
tttttatgct gtttttttttt tttgagaacg gatcttgccc ctgcccccag gccggaatgg
120
atgacatgga cagaaccccg tcggaaaaaa gccggaatgt gcaaacccaa attcccacca
180
cacgggggcc ctaacaattg gatccatccc cnaaaaaanc cntnncaaaa aaagntaaaa
240
actttttttt ttttaaannn anacccccaa aaaaaccaaa aaaaaaaatt taaaaaa
297

<210> 2608
<211> 95
<212> PRT
<213> Homo sapiens

<400> 2608
Met Ile Arg Tyr Pro Asn Gln Gln Arg Lys Gln Arg Lys Leu Leu Leu
1 5 10 15
Phe Leu Cys Cys Phe Phe Phe Leu Arg Thr Asp Leu Ala Pro Ala Pro

```
            20                  25                  30
Arg Pro Glu Trp Met Thr Trp Thr Glu Pro Arg Arg Lys Lys Ala Gly
        35                  40                  45
Met Cys Lys Pro Lys Phe Pro Pro His Gly Gly Pro Asn Asn Trp Ile
    50                  55                  60
His Pro Xaa Lys Xaa Pro Xaa Gln Lys Lys Xaa Lys Thr Phe Phe Phe
65                  70                  75                  80
Leu Xaa Xaa Xaa Pro Gln Lys Asn Gln Lys Lys Lys Phe Lys Lys
                85                  90                  95
```

<210> 2609
<211> 305
<212> DNA
<213> Homo sapiens

<400> 2609
ncgccatcgg catgatgtca ggcaaagatg atcctggcat ggcaaaggta tacggttttg
60
ttgacacgtc cctgacgatc cctatccgct catctggaga cccatgcgtt ccttggaccc
120
caattgccta cgaaaaaatt ttttttttcc cccccaaaaa acacccccc ctcgcatctg
180
tgaaagttct acctcggggt cgtcatctcg gctgtcatcg tcggcaaatc actcagctgg
240
ccgtaccctt cgtcatcgcc cgggccaccg acctcgacgg cncagcgtgc acggcaacga
300
ccacc
305

<210> 2610
<211> 98
<212> PRT
<213> Homo sapiens

<400> 2610
```
Met Met Ser Gly Lys Asp Asp Pro Gly Met Ala Lys Val Tyr Gly Phe
 1               5                  10                  15
Val Asp Thr Ser Leu Thr Ile Pro Ile Arg Ser Ser Gly Asp Pro Cys
            20                  25                  30
Val Pro Trp Thr Pro Ile Ala Tyr Glu Lys Ile Phe Phe Phe Pro Pro
        35                  40                  45
Lys Lys His Pro Pro Leu Ala Ser Val Lys Val Leu Pro Arg Gly Arg
    50                  55                  60
His Leu Gly Cys His Arg Arg Gln Ile Thr Gln Leu Ala Val Pro Phe
65                  70                  75                  80
Val Ile Ala Arg Ala Thr Asp Leu Asp Gly Xaa Ala Cys Thr Ala Thr
                85                  90                  95
Thr Thr
```

<210> 2611
<211> 342
<212> DNA
<213> Homo sapiens

<400> 2611
gccgccgcga tcgacggcga ctcctcgacc agctgggtgt ccagctcgct gcaaaccgct
60
gtggggcaat ggcttcaggt ggacttcgac catccggtga ccaacgcgac catcaccctg
120
acgcccagcg ccaccgctgt cggagctcag gtgcgccgcg tcgaggtggc aacagccaac
180
ggcaccagca caattcgctt cgaccagccc ggcaagccgc tgacggcggc gctgccctac
240
ggcgagacct catgggtccg gttcaccgcg accggcaccg acgacggctc ccccggcgtg
300
cagttcggca tcaccgactt ctccgtgacg cagtacgacg cg
342

<210> 2612
<211> 114
<212> PRT
<213> Homo sapiens

<400> 2612
Ala Ala Ala Ile Asp Gly Asp Ser Ser Thr Ser Trp Val Ser Ser Ser
1 5 10 15
Leu Gln Thr Ala Val Gly Gln Trp Leu Gln Val Asp Phe Asp His Pro
20 25 30
Val Thr Asn Ala Thr Ile Thr Leu Thr Pro Ser Ala Thr Ala Val Gly
35 40 45
Ala Gln Val Arg Arg Val Glu Val Ala Thr Ala Asn Gly Thr Ser Thr
50 55 60
Ile Arg Phe Asp Gln Pro Gly Lys Pro Leu Thr Ala Ala Leu Pro Tyr
65 70 75 80
Gly Glu Thr Ser Trp Val Arg Phe Thr Ala Thr Gly Thr Asp Asp Gly
85 90 95
Ser Pro Gly Val Gln Phe Gly Ile Thr Asp Phe Ser Val Thr Gln Tyr
100 105 110
Asp Ala

<210> 2613
<211> 414
<212> DNA
<213> Homo sapiens

<400> 2613
acgcgtgtgg gttgtgcaca gggcatggct gctctggaca ggcctgggcc ctgggcatca
60
ttctcctcct ccaaaaggtg agggtctgac ctaatggtac tttgtctgat gttttccaga
120
tatgccccta ctgggaaggg ccaagtgggc aggcagagtc tggggtggag cgaggtgggg
180
ctgggaagca ctcctgcttt tctgctgccc cagaacgaat gcaagttctg gcagcttctc
240
ctcctcctgg gaggaggaaa ggagggctcg cctccaggtc tcaggctgag ggagtgggct
300

ggagaccctc tagatggcca gcagaggctg gcctctgtga gaaggcttcc ttgcgtgact
360
ctggggcccc tcccaggctc tcctcgtggc aggcagggac ttgggccagc atgg
414

<210> 2614
<211> 107
<212> PRT
<213> Homo sapiens

<400> 2614
Met Val Leu Cys Leu Met Phe Ser Arg Tyr Ala Pro Thr Gly Lys Gly
1 5 10 15
Gln Val Gly Arg Gln Ser Leu Gly Trp Ser Glu Val Gly Leu Gly Ser
20 25 30
Thr Pro Ala Phe Leu Leu Pro Gln Asn Glu Cys Lys Phe Trp Gln Leu
35 40 45
Leu Leu Leu Leu Gly Gly Gly Lys Glu Gly Ser Pro Pro Gly Leu Arg
50 55 60
Leu Arg Glu Trp Ala Gly Asp Pro Leu Asp Gly Gln Gln Arg Leu Ala
65 70 75 80
Ser Val Arg Arg Leu Pro Cys Val Thr Leu Gly Pro Leu Pro Gly Ser
85 90 95
Pro Arg Gly Arg Gln Gly Leu Gly Pro Ala Trp
100 105

<210> 2615
<211> 394
<212> DNA
<213> Homo sapiens

<400> 2615
nnngccgccg ccctcggccg cagcgcgctt cttttgcgcn ncgacgtcag ccagaaggcg
60
gacgtcgacg ccatgctgaa ggaaacgctg gcccagttcg gccacatcga tatcctcgtc
120
aacaatgcgg gcgtcacgca tgcggccgat ttcctcgacg tgtgcgaaga cgatttcgac
180
cgggtcatgc gcattaacct gaaatcgatg ttcctgtgcg gccaggccgc ggcgcgcgag
240
atggtcaagc gcaacagcgg ctgcatcatc aacatgtcca gcgtgaatgc ggaactggcc
300
attccgaacc aggtgccgta cgtggtgtcg aaaggcgcca tcaaccagct gaccaaggtc
360
atggccttga acctggcgcc gcacggtgcg cgct
394

<210> 2616
<211> 131
<212> PRT
<213> Homo sapiens

<400> 2616
Xaa Ala Ala Ala Leu Gly Arg Ser Ala Leu Leu Leu Arg Xaa Asp Val

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 1               5                  10                  15
Ser Gln Lys Ala Asp Val Asp Ala Met Leu Lys Glu Thr Leu Ala Gln
            20                  25                  30
Phe Gly His Ile Asp Ile Leu Val Asn Asn Ala Gly Val Thr His Ala
        35                  40                  45
Ala Asp Phe Leu Asp Val Cys Glu Asp Asp Phe Asp Arg Val Met Arg
    50                  55                  60
Ile Asn Leu Lys Ser Met Phe Leu Cys Gly Gln Ala Ala Ala Arg Glu
65                  70                  75                  80
Met Val Lys Arg Asn Ser Gly Cys Ile Ile Asn Met Ser Ser Val Asn
                85                  90                  95
Ala Glu Leu Ala Ile Pro Asn Gln Val Pro Tyr Val Val Ser Lys Gly
            100                 105                 110
Ala Ile Asn Gln Leu Thr Lys Val Met Ala Leu Asn Leu Ala Pro His
        115                 120                 125
Gly Ala Arg
    130
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<210> 2617
<211> 513
<212> DNA
<213> Homo sapiens

<400> 2617
naccggttgg catcatgctc acagcactgg gggttccctt ctttcttttc ctcctcagaa
60
agacattgtg agatgggaaa tatcatggaa acacctatac tttccggctc ccacttgaac
120
gtcaccttgg gaaatcacaa gattctcaat gacgtctccg tatcattcca agcgggagtt
180
atgcacgcca tacttggccc caacggttct gggaagacca ccctggtacg cacgttatgc
240
ggagccctct cccccgagtc ggggagcgtc aaattcgatg gaacggatct atccacgatg
300
tccgcatcct gtatcgcgcg tcgtattgcg atcgtctggc agagcgcgac cgctccctct
360
gacctcaccg tacgtcacct cgttggctac gggagatatg cccacacacc gtggtggcag
420
ataagggaca ccagcgccga cagccatgtg gaacaagcaa tggagctggc cgatgtcacg
480
tgcttcgccg atcgacgcgt caccactctc tca
513

<210> 2618
<211> 171
<212> PRT
<213> Homo sapiens

<400> 2618
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Xaa Arg Leu Ala Ser Cys Ser Gln His Trp Gly Phe Pro Ser Phe Phe
 1               5                  10                  15
Ser Ser Ser Glu Arg His Cys Glu Met Gly Asn Ile Met Glu Thr Pro
            20                  25                  30
Ile Leu Ser Gly Ser His Leu Asn Val Thr Leu Gly Asn His Lys Ile
```

```
        35                  40                  45
Leu Asn Asp Val Ser Val Ser Phe Gln Ala Gly Val Met His Ala Ile
    50                  55                  60
Leu Gly Pro Asn Gly Ser Gly Lys Thr Thr Leu Val Arg Thr Leu Cys
65                  70                  75                  80
Gly Ala Leu Ser Pro Glu Ser Gly Ser Val Lys Phe Asp Gly Thr Asp
                85                  90                  95
Leu Ser Thr Met Ser Ala Ser Cys Ile Ala Arg Arg Ile Ala Ile Val
            100                 105                 110
Trp Gln Ser Ala Thr Ala Pro Ser Asp Leu Thr Val Arg His Leu Val
        115                 120                 125
Gly Tyr Gly Arg Tyr Ala His Thr Pro Trp Trp Gln Ile Arg Asp Thr
    130                 135                 140
Ser Ala Asp Ser His Val Glu Gln Ala Met Glu Leu Ala Asp Val Thr
145                 150                 155                 160
Cys Phe Ala Asp Arg Arg Val Thr Thr Leu Ser
                165                 170
```

<210> 2619
<211> 348
<212> DNA
<213> Homo sapiens

<400> 2619
nnaaatttcg acgaccttga ggttttcctc aagctgttgc cgcgttcggc anccggggaa
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cggatgaacc cgtacaactc ggtgtggagc ggtgtgaccg acggtgacgg gccgcaggaa
120
cagcacgtca ttttccttga taacggtcgt accgacgtgc ttgccgacac ccttggtcgc
180
gaagtgttgc ggtgcatccg gtgtgcttcg tgtatcaata tctgcccggt ttacgagcgg
240
gcgggcggtc acccttacgg ctcggtgtac cccgggccga ttggtgcggt gctcaatccg
300
cagctgcggg gcgtggagca tcccgtcgat cgtggtctgc catacgcg
348

<210> 2620
<211> 116
<212> PRT
<213> Homo sapiens

<400> 2620
```
Xaa Asn Phe Asp Asp Leu Glu Val Phe Leu Lys Leu Leu Pro Arg Ser
 1               5                  10                  15
Ala Xaa Gly Glu Arg Met Asn Pro Tyr Asn Ser Val Trp Ser Gly Val
            20                  25                  30
Thr Asp Gly Asp Gly Pro Gln Glu Gln His Val Ile Phe Leu Asp Asn
        35                  40                  45
Gly Arg Thr Asp Val Leu Ala Asp Thr Leu Gly Arg Glu Val Leu Arg
    50                  55                  60
Cys Ile Arg Cys Ala Ser Cys Ile Asn Ile Cys Pro Val Tyr Glu Arg
65                  70                  75                  80
Ala Gly Gly His Pro Tyr Gly Ser Val Tyr Pro Gly Pro Ile Gly Ala
```

85 90 95
Val Leu Asn Pro Gln Leu Arg Gly Val Glu His Pro Val Asp Arg Gly
100 105 110
Leu Pro Tyr Ala
115

<210> 2621
<211> 1485
<212> DNA
<213> Homo sapiens

<400> 2621
acgcgtgcag gtaaaccaga ggccgtgtga ccagctcagt gctggtttac ggaacaactc
60
ttacttttaa aaattacttg ttcccccaaa ttgttgagtg ccgccgtttg gtttcctatg
120
ttttctttcc ctgttttgat tttgctgaag ggagaggtgg tggtggttag gatcagagct
180
ctcctggcat ccgtggggag gatttgctgg tggtggcttc gggctcatgc ccagacacac
240
tcactgcccc gtctgtccaa ggcctcccct tcccctttgc tggtgggagg agctcgtgtg
300
ctccttggcc gcttactgga agggcgtttt tcagagctgc agggacaggg tgagcagctg
360
aagggctagg agggaagccg gcccccgctc tgcagaagct gcatttcagc tgaatctgtg
420
tttcagcctc agttggttgc accgttagcc cctctcctcc cggatggtca tgtttttgtc
480
acattagaga ataaacagcc acacacacat tttttttcc tttaaaacag taacttggaa
540
atatgaaaag gccagaagga ggagcaaggg ctgttttctg gagtggttga ggtgttgtcc
600
tgcagttgtc attgtcttct ccaccgggct gttcccattt atttcctgtg gaactgaatc
660
cctcctccct ccactccttg ggagcccagg tggtccttgg ccaccattca ggctttccaa
720
gaagccaacc accttggaga ttttttttct tgaatttcgc tgttttcttc tgcttccttt
780
agataaaaag cagctcaaga gaccttatct tagggatgag aaaaacatgc atattaattc
840
catctgagtg attgtcagtg taaggccttt taaaacaaaa gcaagttctt tgttaggaat
900
tggtcaaaat tcatctcttt ctttaagccc atcaactccc aggacggttt gagttactca
960
gttacctaag cttgctattc atccaaatca ttttctagag tcactgtata agggtctatg
1020
agtagctgtg tatgaataaa tattacctgt ctacctcaaa atacacatac tgctgaagca
1080
ttctgtacaa ccgtgtgtta tcacagtgca gttttaagtg taacngttga acttaggcat
1140
tttcctgtgt ggcggaataa gaaaggatnt aacagttaca agcctccaaa ttcagataaa
1200
attaaatcac agttcagatg aaactgaata tcattgtaat aatctcataa tatatatttg
1260

taacttgnta gctatctttg aaatcactgn actttgcaat ggtgctaagc tgatagattt
1320
aaatacacag acgggcgagt ggcgcccgtg tcgatgtctt cagccagtgg tgaccctgct
1380
tttgtaaccg cgttaacctg acaaaacctc agcagcagaa gtccctattt ttctaggagt
1440
ttatcgtgca gacagtcttc actacaggac tcggccctgg ggccc
1485

<210> 2622
<211> 83
<212> PRT
<213> Homo sapiens

<400> 2622
Met Phe Ser Phe Pro Val Leu Ile Leu Leu Lys Gly Glu Val Val Val
1 5 10 15
Val Arg Ile Arg Ala Leu Leu Ala Ser Val Gly Arg Ile Cys Trp Trp
20 25 30
Trp Leu Arg Ala His Ala Gln Thr His Ser Leu Pro Arg Leu Ser Lys
35 40 45
Ala Ser Pro Ser Pro Leu Leu Val Gly Gly Ala Arg Val Leu Leu Gly
50 55 60
Arg Leu Leu Glu Gly Arg Phe Ser Glu Leu Gln Gly Gln Gly Glu Gln
65 70 75 80
Leu Lys Gly

<210> 2623
<211> 3524
<212> DNA
<213> Homo sapiens

<400> 2623
nggatccgaa ttcgcggccg cgtcgactgg agaggacggc gttatttta ttaactggag
60
gcgacggcgg ctgcggcggc ggcgggaccc ccaggcctcc tccggggtat gaaaatcggc
120
agtgggttcc tgagtggcgg cggaggtacc ggcagtagcg gtggtagcgg ctccggcggc
180
ggtggtagtg gcggcggcgg cggcggcggc agcagcggca ggagggcaga gatggaaccc
240
acctttcccc agggtatggt tatgttcaac caccgtcttc ccccggtcac cagcttcacc
300
cggccggcgg ggtcggccgc ccctcccccg caatgcgtgt tatcctcctc tacctccgca
360
gccccggccg ctgagccccc ccctccgcca gccccggaca tgactttcaa gaaggagccg
420
gcggcgtcag ccgcggcctt cccctcgcag aggacctcct gggggttctt gcagtctttg
480
gttagcatca aacaggagaa acccgcggat cctgaggagc agcagtccca ccaccaccat
540
caccaccacc actatggggg gctgttcgct ggagctgaag agaggtctcc aggcctagga
600

ggcggtgaag gggggagtca cggcgtcatc caggacctca gtattctcca ccagcatgtc
660
cagcagcaac cagcccagca ccaccgtgac gtattactca gcagcagtag caggactgat
720
gaccaccatg gcactgagga gccaaagcag gacactaatg tcaaaaaggc aaaaaggcca
780
aagccagaat ctcagggaat caaagccaag aggaagccaa gtgcatcttc caaaccttct
840
ttggttggag atggagaagg tgccatcctc tccccaagtc agaaacctca tatctgtgat
900
cactgtagtg ctgctttccg aagctcctat cacctgcgga gacatgtcct cattcataca
960
ggagaaagac ctttccagtg cagccagtgt agtatgggtt tcattcagaa atacctacta
1020
cagagacatg agaaaattca tagtagagag aagccatttg gatgtgatca gtgcagcatg
1080
aagtttattc agaagtacca tatggagaga cacaagagga cacatagtgg agaaaagcca
1140
tataagtgtg acacttgcca acagtatttt tcaaggactg atagattgtt gaagcacagg
1200
cgcacatgtg gtgaagtcat agttaaagga gccactagtg cagaacctgg gtcatcaaac
1260
cataccaata tgggtaatct ggctgtgttg tctcagggaa atacaagttc ttcaaggaga
1320
aaaacaaagt caaaaagcat agctattgaa aataaggaac agaagaccgg taaaacaaat
1380
gaatcgcaaa tttcaaataa tataaacatg cagagttact cagtagaaat gcctaccgtg
1440
tcttccagtg gaggcataat tggcactgga atagatgaac tgcagaagag ggtgccaaaa
1500
ttgatcttta agaaaggaag cagaaagaat acagataaaa actaccttaa ctttgtgtca
1560
ccattaccag acatagtagg acagaaatcc ttgtctggaa aaccaagtgg ctcacttggc
1620
atagtatcaa ataatagtgt ggagaccatt ggtcttctcc aaagtacaag tggcaaacaa
1680
ggtcagataa gtagtaatta tgatgatgcc atgcagtttt caaagaaaag aagatattta
1740
ccaactgcca gcagcaacag tgccttttct ataaacgtag gacacatggt ctcccaacag
1800
tctgtcattc agtctgcagg tgtcagtgtt ttggacaatg aggcaccatt gtcacttatt
1860
gactcctcag ctctaaatgc tgaaattaaa tcttgtcatg acaagtctgg aattcctgat
1920
gaggttttac aaagtatttt ggatcaatac tccaacaaat cagaaagcca gaaagaggat
1980
cctttcaata ttgcagaacc acgagtggat ttacacacct caggagaaca ctcagaattg
2040
gttcaagaag aaaatttgag cccaggcacc caaacacctt caaatgataa agcaagtatg
2100
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2160
actcttggac acggtttcca atttgtcagt ttgtcttcac ctctccacaa ccacactttg
2220

tttccagaaa aacaaatata cactacgtct cctttggagt gtggtttcgg ccaatctgtt
2280
acctcagtgt tgccatcttc attgccaaag cctccttttg ggatgttgtt tggatctcag
2340
ccaggtcttt atttgtctgc tttggatgct acacatcagc agttgacacc ttcccaggag
2400
ctggatgatc tgatagattc tcagaagaac ttagagactt catcagcctt ccagtcctca
2460
tctcagaaat tgactagcca gaaggaacag aaaaacttag agtcttcaac aggctttcag
2520
attccatctc aggagttagc tagccagata gatcctcaga aagacataga gcctagaaca
2580
acgtatcaga ttgagaactt tgcacaagcg tttggttctc agtttaagtc gggcagcagg
2640
gtgccaatga cctttatcac taactctaat ggagaagtgg accatagagt aaggacttca
2700
gtgtcagatt tctcagggta tacaaatatg atgtctgatg taagtgagcc atgtagtaca
2760
agagtaaaga cacccaccag ccagagttac aggtaaggtc ccaaaagtgg ccaggctgga
2820
ggtcttctaa tgtaattttg ttttattttg agaacactgc cattggaatg tttctacacg
2880
atcctattaa gaataatgtg atgccctttc aatgcaactt ttcatattta gtttattttg
2940
ttagcgtgat tttagctctg tttgtattat gatttttaat caaaatcaat agattaaaaa
3000
tagtttgaca ttcaaagtga caatgtttag caatcaaatt tacatgtata gatcgtcagg
3060
gaatagccca aatgttttaa acgcaaaaaa aaagacaaaa aaaaaccaaa aaaaaaaaac
3120
ctacaaaaaa aactttgttg ctaggattaa ggttattcta attgctttac tctcaggaaa
3180
gtgtaataac gcatgggaat tctgtacgtt atcactgtaa tggaatatcc aatttacaga
3240
tagtatgata tacatttcat catttaagta agggatcgaa aacatttcaa attgctctat
3300
ctgggctgat agacatttcg tcatttaagt aagggatcga agacatttca aattgctatc
3360
tccatctggg ctgatccaaa attctgagat tgttggctac ctatattttg ttgcagcttt
3420
taaatgtact ctgaacttcc aaaccacatt cattccagcc tggtagaaca aatattcttg
3480
gatctttgat caaagcctgg aatgatagct ttaatacaaa aaaa
3524

<210> 2624
<211> 895
<212> PRT
<213> Homo sapiens

<400> 2624
Met Lys Ile Gly Ser Gly Phe Leu Ser Gly Gly Gly Gly Thr Gly Ser
1 5 10 15
Ser Gly Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly

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            20                  25                  30
Gly Gly Ser Ser Gly Arg Arg Ala Glu Met Glu Pro Thr Phe Pro Gln
        35                  40                  45
Gly Met Val Met Phe Asn His Arg Leu Pro Pro Val Thr Ser Phe Thr
    50                  55                  60
Arg Pro Ala Gly Ser Ala Ala Pro Pro Pro Gln Cys Val Leu Ser Ser
65                  70                  75                  80
Ser Thr Ser Ala Ala Pro Ala Ala Glu Pro Pro Pro Pro Pro Ala Pro
                85                  90                  95
Asp Met Thr Phe Lys Lys Glu Pro Ala Ala Ser Ala Ala Ala Phe Pro
            100                 105                 110
Ser Gln Arg Thr Ser Trp Gly Phe Leu Gln Ser Leu Val Ser Ile Lys
        115                 120                 125
Gln Glu Lys Pro Ala Asp Pro Glu Glu Gln Gln Ser His His His His
    130                 135                 140
His His His His Tyr Gly Gly Leu Phe Ala Gly Ala Glu Glu Arg Ser
145                 150                 155                 160
Pro Gly Leu Gly Gly Gly Glu Gly Gly Ser His Gly Val Ile Gln Asp
                165                 170                 175
Leu Ser Ile Leu His Gln His Val Gln Gln Gln Pro Ala Gln His His
            180                 185                 190
Arg Asp Val Leu Leu Ser Ser Ser Ser Arg Thr Asp Asp His His Gly
        195                 200                 205
Thr Glu Glu Pro Lys Gln Asp Thr Asn Val Lys Lys Ala Lys Arg Pro
    210                 215                 220
Lys Pro Glu Ser Gln Gly Ile Lys Ala Lys Arg Lys Pro Ser Ala Ser
225                 230                 235                 240
Ser Lys Pro Ser Leu Val Gly Asp Gly Glu Gly Ala Ile Leu Ser Pro
                245                 250                 255
Ser Gln Lys Pro His Ile Cys Asp His Cys Ser Ala Ala Phe Arg Ser
            260                 265                 270
Ser Tyr His Leu Arg Arg His Val Leu Ile His Thr Gly Glu Arg Pro
        275                 280                 285
Phe Gln Cys Ser Gln Cys Ser Met Gly Phe Ile Gln Lys Tyr Leu Leu
    290                 295                 300
Gln Arg His Glu Lys Ile His Ser Arg Glu Lys Pro Phe Gly Cys Asp
305                 310                 315                 320
Gln Cys Ser Met Lys Phe Ile Gln Lys Tyr His Met Glu Arg His Lys
                325                 330                 335
Arg Thr His Ser Gly Glu Lys Pro Tyr Lys Cys Asp Thr Cys Gln Gln
            340                 345                 350
Tyr Phe Ser Arg Thr Asp Arg Leu Leu Lys His Arg Arg Thr Cys Gly
        355                 360                 365
Glu Val Ile Val Lys Gly Ala Thr Ser Ala Glu Pro Gly Ser Ser Asn
    370                 375                 380
His Thr Asn Met Gly Asn Leu Ala Val Leu Ser Gln Gly Asn Thr Ser
385                 390                 395                 400
Ser Ser Arg Arg Lys Thr Lys Ser Lys Ser Ile Ala Ile Glu Asn Lys
                405                 410                 415
Glu Gln Lys Thr Gly Lys Thr Asn Glu Ser Gln Ile Ser Asn Asn Ile
            420                 425                 430
Asn Met Gln Ser Tyr Ser Val Glu Met Pro Thr Val Ser Ser Ser Gly
        435                 440                 445
Gly Ile Ile Gly Thr Gly Ile Asp Glu Leu Gln Lys Arg Val Pro Lys
```

```
    450                 455                 460
Leu Ile Phe Lys Lys Gly Ser Arg Lys Asn Thr Asp Lys Asn Tyr Leu
470                 475                 480
Asn Phe Val Ser Pro Leu Pro Asp Ile Val Gly Gln Lys Ser Leu Ser
                485                 490                 495
Gly Lys Pro Ser Gly Ser Leu Gly Ile Val Ser Asn Asn Ser Val Glu
            500                 505                 510
Thr Ile Gly Leu Leu Gln Ser Thr Ser Gly Lys Gln Gly Gln Ile Ser
        515                 520                 525
Ser Asn Tyr Asp Asp Ala Met Gln Phe Ser Lys Lys Arg Arg Tyr Leu
    530                 535                 540
Pro Thr Ala Ser Ser Asn Ser Ala Phe Ser Ile Asn Val Gly His Met
545                 550                 555                 560
Val Ser Gln Gln Ser Val Ile Gln Ser Ala Gly Val Ser Val Leu Asp
                565                 570                 575
Asn Glu Ala Pro Leu Ser Leu Ile Asp Ser Ser Ala Leu Asn Ala Glu
            580                 585                 590
Ile Lys Ser Cys His Asp Lys Ser Gly Ile Pro Asp Glu Val Leu Gln
        595                 600                 605
Ser Ile Leu Asp Gln Tyr Ser Asn Lys Ser Glu Ser Gln Lys Glu Asp
    610                 615                 620
Pro Phe Asn Ile Ala Glu Pro Arg Val Asp Leu His Thr Ser Gly Glu
625                 630                 635                 640
His Ser Glu Leu Val Gln Glu Glu Asn Leu Ser Pro Gly Thr Gln Thr
                645                 650                 655
Pro Ser Asn Asp Lys Ala Ser Met Leu Gln Glu Tyr Ser Lys Tyr Leu
            660                 665                 670
Gln Gln Ala Phe Glu Lys Ser Thr Asn Ala Ser Phe Thr Leu Gly His
        675                 680                 685
Gly Phe Gln Phe Val Ser Leu Ser Ser Pro Leu His Asn His Thr Leu
    690                 695                 700
Phe Pro Glu Lys Gln Ile Tyr Thr Thr Ser Pro Leu Glu Cys Gly Phe
705                 710                 715                 720
Gly Gln Ser Val Thr Ser Val Leu Pro Ser Ser Leu Pro Lys Pro Pro
                725                 730                 735
Phe Gly Met Leu Phe Gly Ser Gln Pro Gly Leu Tyr Leu Ser Ala Leu
            740                 745                 750
Asp Ala Thr His Gln Gln Leu Thr Pro Ser Gln Glu Leu Asp Asp Leu
        755                 760                 765
Ile Asp Ser Gln Lys Asn Leu Glu Thr Ser Ser Ala Phe Gln Ser Ser
    770                 775                 780
Ser Gln Lys Leu Thr Ser Gln Lys Glu Gln Lys Asn Leu Glu Ser Ser
785                 790                 795                 800
Thr Gly Phe Gln Ile Pro Ser Gln Glu Leu Ala Ser Gln Ile Asp Pro
                805                 810                 815
Gln Lys Asp Ile Glu Pro Arg Thr Thr Tyr Gln Ile Glu Asn Phe Ala
            820                 825                 830
Gln Ala Phe Gly Ser Gln Phe Lys Ser Gly Ser Arg Val Pro Met Thr
        835                 840                 845
Phe Ile Thr Asn Ser Asn Gly Glu Val Asp His Arg Val Arg Thr Ser
    850                 855                 860
Val Ser Asp Phe Ser Gly Tyr Thr Asn Met Met Ser Asp Val Ser Glu
865                 870                 875                 880
Pro Cys Ser Thr Arg Val Lys Thr Pro Thr Ser Gln Ser Tyr Arg
```

885 890 895

<210> 2625
<211> 1398
<212> DNA
<213> Homo sapiens

<400> 2625
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caccacgaga aacgcctctt ttgcagcagt ttaaggtacg ttaggggtca ccgtgttgca
120
ttgtgggaag tatagggcgg caagcggagg aggcgtggcg agcggatcat ccgcttccgg
180
agtcgaggtt ttcgggcttg taccgcttgg cggtgcggcc tggtgtcggc ttgcaggttc
240
tttctgtgtt tgttctctgc cctgccaagg ccgtagagct ggtgcgtgcg ggtagcgggg
300
ctctccgagg agccgcacgc cggcggcacc atggtccacc tcactactct cctctgcaag
360
gcctaccgtg ggggccactt aaccatccgc cttgccctgg gtggctgcac caatcggccg
420
ttctaccgca ttgtggctgc tcacaacaag tgtcccaggg atggccgttt cgtagagcag
480
ctgggctcct atgatccatt gcccaacagt catggagaaa aactcgttgc cctcaaccta
540
gacaggatcc gtcattggat tggctgcggg gcccacctct ctaagcctat ggaaaagctt
600
ctgggtcttg ctggcttttt ccctctgcat cctatgatga tcacaaatgc tgagagactg
660
cgaaggaaac gggcacgtga agtcctgtta gcttctcaga aaacagatgc agaagctaca
720
gatacagagg ctacagaaac ataaatgagc tgactttagt gagcatagca gtgggaacaa
780
ggtcaaggtc cttttgaaac actgcagcga tcttaatttt gttagatttg gagttcaata
840
aatggagtat cctgagttgc ccttgctctt ctggcctggc ctgcacaggg cccagggaga
900
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960
tcttgggata gacagtggct atgggaggat tggacttttg agttgggctc tgggtctctt
1020
ggacaacttt acaatttact ggcttccaag acttcctgct tcaaaacccc cagccagact
1080
attcatggcc cattcagatc ttcatgttca tcccacaagt gcaagaacag ttaacctttc
1140
ttaattgatt tttgtaattg gaggtttata ttgtcttgcc taatgcatat tctctttttt
1200
tttttttttg agacggagtc ttgttctgtt gccaggaggc cgatgctgca gtgaactgtg
1260
attgttccac tacagtccag cctgggtgac agagaaaaga aaaagaaaac attacataat
1320
ttggctagag cataataatt tgattttctg gtttttgaaa atttgagttg caataaaagg
1380

atatttcagt gtgcgaaa
1398

<210> 2626
<211> 137
<212> PRT
<213> Homo sapiens

<400> 2626
Met Val His Leu Thr Thr Leu Leu Cys Lys Ala Tyr Arg Gly Gly His
1 5 10 15
Leu Thr Ile Arg Leu Ala Leu Gly Gly Cys Thr Asn Arg Pro Phe Tyr
20 25 30
Arg Ile Val Ala Ala His Asn Lys Cys Pro Arg Asp Gly Arg Phe Val
35 40 45
Glu Gln Leu Gly Ser Tyr Asp Pro Leu Pro Asn Ser His Gly Glu Lys
50 55 60
Leu Val Ala Leu Asn Leu Asp Arg Ile Arg His Trp Ile Gly Cys Gly
65 70 75 80
Ala His Leu Ser Lys Pro Met Glu Lys Leu Leu Gly Leu Ala Gly Phe
85 90 95
Phe Pro Leu His Pro Met Met Ile Thr Asn Ala Glu Arg Leu Arg Arg
100 105 110
Lys Arg Ala Arg Glu Val Leu Leu Ala Ser Gln Lys Thr Asp Ala Glu
115 120 125
Ala Thr Asp Thr Glu Ala Thr Glu Thr
130 135

<210> 2627
<211> 320
<212> DNA
<213> Homo sapiens

<400> 2627
acgcgtgaag gggtggtgga atgcacaaaa aaaacacctt gaaggagtgc ctttctcttg
60
acccagagga acgaaagaaa gctgagtcac aaataaacaa ttctgccgtg gaaatgcagg
120
tgcagtcagc cctagccttt ttgggaacag agaatgatgt tgaactgaag ggggcgctag
180
atttagaaac ctgtgagaag caagatataa tgccagaagt ggacaagcag tctggttcgc
240
cagaaagccg agtagaaaac acactgaaca tacatgaaga tttagattag gttaaactca
300
ttgaatatta cctgacttag
320

<210> 2628
<211> 90
<212> PRT
<213> Homo sapiens

<400> 2628
Met Phe Ser Val Phe Ser Thr Arg Leu Ser Gly Glu Pro Asp Cys Leu

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 1               5                  10                  15
Ser Thr Ser Gly Ile Ile Ser Cys Phe Ser Gln Val Ser Lys Ser Ser
            20                  25                  30
Ala Pro Phe Ser Ser Thr Ser Phe Ser Val Pro Lys Lys Ala Arg Ala
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Asp Cys Thr Cys Ile Ser Thr Ala Glu Leu Phe Ile Cys Asp Ser Ala
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<210> 2629
<211> 650
<212> DNA
<213> Homo sapiens

<400> 2629
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<210> 2630
<211> 58
<212> PRT
<213> Homo sapiens

<400> 2630
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<210> 2632
<211> 550
<212> PRT
<213> Homo sapiens

<400> 2632
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35 40 45
Ile Gln Ile Arg Lys Asn Glu Tyr Asp Leu Ile Leu Asn Ser Asp Ile
50 55 60
Asn Ser Asn His Tyr His Gln Trp Phe Tyr Phe Glu Val Ser Gly Met
65 70 75 80
Arg Pro Gly Val Ala Tyr Arg Phe Asn Ile Ile Asn Cys Glu Lys Ser
85 90 95
Asn Ser Gln Phe Asn Tyr Gly Met Gln Pro Leu Met Tyr Ser Val Gln
100 105 110
Glu Ala Leu Asn Ala Arg Pro Trp Trp Ile Arg Met Gly Thr Asp Ile
115 120 125
Cys Tyr Tyr Lys Asn His Phe Ser Arg Ser Ser Val Ala Ala Gly Gly
130 135 140
Gln Lys Gly Lys Ser Tyr Tyr Thr Ile Thr Phe Thr Val Asn Phe Pro
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His Lys Asp Asp Val Cys Tyr Phe Ala Tyr His Tyr Pro Tyr Thr Tyr
165 170 175
Ser Thr Leu Gln Met His Leu Gln Lys Leu Glu Ser Ala His Asn Pro
180 185 190
Gln Gln Ile Tyr Phe Arg Lys Asp Val Leu Cys Glu Thr Leu Ser Gly
195 200 205
Asn Ser Cys Pro Leu Val Thr Ile Thr Ala Met Pro Glu Ser Asn Tyr
210 215 220
Tyr Glu His Ile Cys His Phe Arg Asn Arg Pro Tyr Val Phe Leu Ser

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Thr Leu Glu Tyr Leu Met Ser Asn Asn Pro Thr Ala Gln Ser Leu Leu
            260                 265                 270
Glu Ser Tyr Ile Phe Lys Ile Val Pro Met Leu Asn Pro Asp Gly Val
        275                 280                 285
Ile Asn Gly Asn His Arg Cys Ser Leu Ser Gly Glu Asp Leu Asn Arg
    290                 295                 300
Gln Trp Gln Ser Pro Ser Pro Asp Leu His Pro Thr Ile Tyr His Ala
305                 310                 315                 320
Lys Gly Leu Leu Gln Tyr Leu Ala Ala Val Lys Arg Leu Pro Leu Val
                325                 330                 335
Tyr Cys Asp Tyr His Gly His Ser Arg Lys Lys Asn Val Phe Met Tyr
            340                 345                 350
Gly Cys Ser Ile Lys Glu Thr Val Trp His Thr Asn Asp Asn Ala Thr
        355                 360                 365
Ser Cys Asp Val Val Glu Asp Thr Gly Tyr Arg Thr Leu Pro Lys Ile
    370                 375                 380
Leu Ser His Ile Ala Pro Ala Phe Cys Met Ser Ser Cys Ser Phe Val
385                 390                 395                 400
Val Glu Lys Ser Lys Glu Ser Thr Ala Arg Val Val Val Trp Arg Glu
                405                 410                 415
Ile Gly Val Gln Arg Ser Tyr Thr Met Glu Ser Thr Leu Cys Gly Cys
            420                 425                 430
Asp Gln Gly Lys Tyr Lys Gly Leu Gln Ile Gly Thr Arg Glu Leu Glu
        435                 440                 445
Glu Met Gly Ala Lys Phe Cys Val Gly Leu Leu Arg Leu Lys Arg Leu
    450                 455                 460
Thr Ser Pro Leu Glu Tyr Asn Leu Pro Ser Ser Leu Leu Asp Phe Glu
465                 470                 475                 480
Asn Asp Leu Ile Glu Ser Ser Cys Lys Val Thr Ser Pro Thr Thr Tyr
                485                 490                 495
Val Leu Asp Glu Asp Glu Pro Arg Phe Leu Glu Glu Val Asp Tyr Ser
            500                 505                 510
Ala Glu Ser Asn Asp Glu Leu Asp Ile Glu Leu Ala Glu Asn Val Gly
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<211> 1569
<212> DNA
<213> Homo sapiens

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<210> 2634
<211> 59
<212> PRT
<213> Homo sapiens

<400> 2634
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Ser Phe Ala Glu Glu Leu Ser Arg Ile Leu Glu Lys Arg Lys His Thr
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Gln Leu Val Glu Gln Leu Asp Glu Ser Ser Val
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<210> 2635
<211> 1062
<212> DNA
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<210> 2636

<211> 63
<212> PRT
<213> Homo sapiens

<400> 2636
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Gly Asp Gly Ser Ile Arg Arg Tyr Phe Cys Gly Glu Ala Ala Ala
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<210> 2637
<211> 1045
<212> DNA
<213> Homo sapiens

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<210> 2638
<211> 263
<212> PRT
<213> Homo sapiens

<400> 2638
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35 40 45
Leu Gln Glu Ala Gly Thr Phe Arg His Thr Leu Trp Lys Arg Val Gln
50 55 60
Gly Ala Val Thr Pro Leu Leu Ala Ser Met Ile Ser Phe Ile Asp Arg
65 70 75 80
Asp Gly Asn Leu Glu Leu Leu Thr Arg Pro Asp Thr Pro Pro Trp Ala
85 90 95
Arg Asp Leu Trp Met Phe Ile Phe Ser Asp Thr Met Leu Leu Asn Ile
100 105 110
Pro Leu Val Met Asn Asn Glu Arg His Lys Gly Glu Met Ala Tyr Ile
115 120 125
Val Val Gln Asn His Met Asn Leu Ser Glu Asn Ala Ser Asn Asn Val
130 135 140
Pro Phe Ser Trp Lys Ile Lys Asp Tyr Leu Glu Glu Leu Trp Val Gln
145 150 155 160
Ala Gln Tyr Ile Thr Asp Ala Glu Gly Leu Pro Lys Lys Phe Val Asp
165 170 175
Ile Phe Gln Gln Thr Pro Leu Gly Arg Phe Leu Ala Gln Leu His Gly
180 185 190
Glu Pro Gln Gln Glu Leu Leu Gln Cys Tyr Leu Lys Asp Phe Ile Leu
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Leu Thr Met Arg Val Ser Thr Glu Glu Glu Leu Lys Phe Leu Gln Met
210 215 220
Ala Leu Trp Ser Cys Thr Arg Lys Leu Lys Ala Ala Ser Glu Ala Pro
225 230 235 240
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Arg Ser Gly Leu Gln Asn Phe
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<210> 2639
<211> 3777
<212> DNA
<213> Homo sapiens

<400> 2639
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<212> PRT
<213> Homo sapiens

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Ile Ala Ala Thr Pro Thr Ser Leu Met Glu Ala Gln Ala Glu Gly Pro
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Leu Thr Ala Ile Thr Ile Pro Arg Pro Ser Val Ala Ser Thr Gln Ser
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Thr Ser Gly Ser Phe His Cys Gly Gln Gln Pro Glu Lys Glu Asp Leu
85 90 95
Gln Pro Met Glu Pro Thr Val Glu Leu Tyr Ser Pro Arg Glu Asn Phe
100 105 110
Ser Gly Leu Val Val Thr Glu Gly Glu Pro Pro Ser Gly Gly Ser Arg
115 120 125
Thr Asp Leu Gly Leu Gln Ile Asp His Ile Gly His Asp Met Leu Pro
130 135 140
Asn Ile Arg Glu Ser Asn Lys Ser Gln Asp Leu Gly Pro Lys Glu Leu
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Pro Asp His Asn Arg Leu Val Val Arg Glu Phe Glu Asn Leu Pro Gly
165 170 175
Glu Thr Glu Glu Lys Ser Ile Leu Leu Glu Ser Asp Asn Glu Asp Glu
180 185 190
Lys Leu Ser Arg Gly Gln His Cys Ile Glu Ile Ser Ser Leu Pro Gly
195 200 205
Asp Leu Val Ile Val Glu Lys Asp His Ser Ala Thr Thr Glu Pro Leu
210 215 220
Asp Val Thr Lys Thr Gln Thr Phe Ser Val Val Pro Asn Gln Asp Lys
225 230 235 240
Asn Asn Glu Ile Met Lys Leu Leu Thr Val Gly Thr Ser Glu Ile Ser
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Ser Arg Asp Ile Asp Pro His Val Glu Gly Gln Ile Gly Gln Val Ala

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Gly Lys Arg Glu Lys Ile Thr Pro Arg Asn Gly Glu Leu Phe His Cys
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Val Ser Glu Asn Glu His Gly Ala Pro Thr Arg Lys Asp Met Val Arg
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Ser Ser Phe Val Thr Arg His Ser Arg Ile Pro Val Leu Ala Gln Glu
            340                 345                 350
Ile Asp Ser Thr Leu Glu Ser Ser Ser Pro Val Ser Ala Lys Glu Lys
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Leu Leu Gln Lys Lys Ala Tyr Gln Pro Asp Leu Val Lys Leu Leu Val
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Glu Lys Arg Gln Phe Lys Ser Phe Leu Gly Asp Leu Ser Ser Ala Ser
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Asp Lys Leu Leu Glu Glu Lys Leu Ala Thr Val Pro Ala Pro Phe Cys
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Glu Glu Glu Val Leu Thr Pro Phe Ser Arg Leu Thr Val Asp Ser His
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Leu Ser Arg Ser Ala Glu Asp Ser Phe Leu Ser Pro Ile Ile Ser Gln
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Ser Arg Lys Ser Lys Ile Pro Arg Pro Val Ser Trp Val Asn Thr Asp
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Gln Val Asn Ser Ser Thr Ser Ser Gln Phe Phe Pro Arg Pro Pro Pro
465                 470                 475                 480
Gly Lys Pro Pro Thr Arg Pro Gly Val Glu Ala Arg Leu Arg Arg Tyr
                485                 490                 495
Lys Val Leu Gly Ser Ser Asn Ser Asp Ser Asp Leu Phe Ser Arg Leu
            500                 505                 510
Ala Gln Ile Leu Gln Asn Gly Ser Gln Lys Pro Arg Ser Thr Thr Gln
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Cys Lys Ser Pro Gly Ser Pro His Asn Pro Lys Thr Pro Pro Lys Ser
    530                 535                 540
Pro Val Val Pro Arg Arg Ser Pro Ser Ala Ser Pro Arg Ser Ser Ser
545                 550                 555                 560
Leu Pro Arg Thr Ser Ser Ser Ser Pro Ser Arg Ala Gly Arg Pro His
                565                 570                 575
His Asp Gln Arg Ser Ser Ser Pro His Leu Gly Arg Ser Lys Ser Pro
            580                 585                 590
Pro Ser His Ser Gly Ser Ser Ser Ser Arg Arg Ser Cys Gln Gln Glu
        595                 600                 605
His Cys Lys Pro Ser Lys Asn Gly Leu Lys Gly Ser Gly Ser Leu His
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His His Ser Ala Ser Thr Lys Thr Pro Gln Gly Lys Ser Lys Pro Ala
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Val Thr Val Arg Ile His Gly Ser Met Leu Arg Ala His Arg Cys Val
35 40 45
Leu Ala Ala Gly Ser Pro Phe Phe Gln Asp Lys Leu Leu Leu Gly Tyr
50 55 60
Ser Asp Ile Glu Ile Pro Ser Val Val Ser Val Gln Ser Val Gln Lys
65 70 75 80
Leu Ile Asp Phe Met Tyr Ser Gly Val Leu Arg Val Ser Gln Ser Glu
85 90 95
Ala Leu Gln Ile Leu Thr Ala Ala Ser Ile Leu Gln Ile Lys Thr Val
100 105 110
Ile Asp Glu Cys Thr Arg Ile Val Ser Gln Asn Val Gly Asp Val Phe
115 120 125
Pro Gly Ile Gln Asp Ser Gly Gln Asp Thr Pro Arg Gly Thr Pro Glu
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<210> 2643
<211> 4590
<212> DNA
<213> Homo sapiens

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35 40 45
Arg Pro Asn Leu Thr Ser His Pro Asp Gly Ser Glu Asp Leu Glu Pro
50 55 60
Leu Ala Gly Gly Ser Pro Glu Ala Thr Ser Pro Asp Val Thr Glu Thr
65 70 75 80
Lys Asn Ser Pro Leu Met Glu Asp Phe Phe Glu Glu Gly Phe Ser Gln
85 90 95
Glu Ile Ile Glu Met Leu Ser Lys Asp Gly Phe Trp Asn Ser Asn Phe
100 105 110
Gly Glu Ala Cys Ile Glu Asp Thr Trp Leu Asp Ser Leu Leu Gly Asp
115 120 125
Pro Glu Ser Leu Leu Arg Ser Asp Ile Ala Thr Asn Gly Glu Ser Pro
130 135 140
Thr Glu Cys Lys Ser His Glu Leu Lys Arg Gly Leu Ser Pro Val Ser
145 150 155 160
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165 170 175
Thr Leu Thr Pro Ala Lys Ser Lys Glu Tyr Arg Gly Glu Phe Phe Ser
180 185 190
Tyr Ser Asp His Ser Gln Gln Asp Ser Val Gln Glu Gly Glu Lys Pro
195 200 205
Tyr Gln Cys Ser Glu Cys Gly Lys Ser Phe Ser Gly Ser Tyr Arg Leu
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Thr Gln His Trp Ile Thr His Thr Arg Glu Lys Pro Thr Val His Gln
225 230 235 240
Glu Cys Glu Gln Gly Phe Asp Arg Asn Ala Ser Leu Ser Val Tyr Pro
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Lys Thr His Thr Gly Tyr Lys Phe Tyr Val Cys Asn Glu Tyr Gly Thr
260 265 270
Thr Phe Ser Gln Ser Thr Tyr Leu Trp His Gln Lys Thr His Thr Gly
275 280 285
Glu Lys Pro Cys Lys Ser Gln Asp Ser Asp His Pro Pro Ser His Asp
290 295 300
Thr Gln Pro Gly Glu His Gln Lys Thr His Thr Asp Ser Lys Ser Tyr
305 310 315 320
Asn Cys Asn Glu Cys Gly Lys Ala Phe Thr Arg Ile Phe His Leu Thr
325 330 335
Arg His Gln Lys Ile His Thr Arg Lys Arg Tyr Glu Cys Ser Lys Cys
340 345 350
Gln Ala Thr Phe Asn Leu Arg Lys His Leu Ile Gln His Gln Lys Thr

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His Arg Arg Ile His Thr Gly Tyr Arg Pro His Lys Cys Gln Glu Cys
    450                 455                 460
Val Arg Ser Phe Ser Arg Pro Ser His Leu Met Arg His Gln Ala Ile
465                 470                 475                 480
His Thr Ala Glu Lys Pro Tyr Ser Cys Ala Glu Cys Lys Glu Thr Phe
                485                 490                 495
Ser Asp Asn Asn Arg Leu Val Gln His Gln Lys Met His Thr Val Lys
            500                 505                 510
Thr Pro Tyr Glu Cys Gln Glu Cys Gly Glu Arg Phe Ile Cys Gly Ser
        515                 520                 525
Thr Leu Lys Cys His Glu Ser Val His Ala Arg Glu Lys Gln Gly Phe
    530                 535                 540
Phe Val Ser Gly Lys Ile Leu Asp Gln Asn Pro Glu Gln Lys Glu Lys
545                 550                 555                 560
Cys Phe Lys Cys Asn Lys Cys Glu Lys Thr Phe Ser Cys Ser Lys Tyr
                565                 570                 575
Leu Thr Gln Tyr Glu Arg Ile His Thr Arg Gly Val Lys Pro Phe Glu
            580                 585                 590
Cys Asp Gln Cys Gly Lys Ala Phe Gly Gln Ser Thr Arg Leu Ile His
        595                 600                 605
His Gln Arg Ile His Ser Arg Val Arg Leu Tyr Lys Trp Gly Glu Gln
    610                 615                 620
Gly Lys Ala Ile Ser Ser Ala Ser Leu Ile Lys Leu Gln Ser Phe His
625                 630                 635                 640
Thr Lys Glu His Pro Phe Lys Cys Asn Glu Cys Gly Lys Thr Phe Ser
                645                 650                 655
His Ser Ala His Leu Ser Lys His Gln Leu Ile His Ala Gly Glu Asn
            660                 665                 670
Pro Phe Lys Cys Ser Lys Cys Asp Arg Val Phe Thr Gln Arg Asn Tyr
        675                 680                 685
Leu Val Gln His Glu Arg Thr His Ala Arg Lys Lys Pro Leu Val Cys
    690                 695                 700
Asn Glu Cys Gly Lys Thr Phe Arg Gln Ser Ser Cys Leu Ser Lys His
705                 710                 715                 720
Gln Arg Ile His Ser Gly Glu Lys Pro Tyr Val Cys Asp Tyr Cys Gly
                725                 730                 735
Lys Ala Phe Gly Leu Ser Ala Glu Leu Val Arg His Gln Arg Ile His
            740                 745                 750
Thr Gly Glu Lys Pro Tyr Val Cys Gln Glu Cys Gly Lys Ala Phe Thr
        755                 760                 765
Gln Ser Ser Cys Leu Ser Ile His Arg Arg Val His Thr Gly Glu Lys
    770                 775                 780
Pro Tyr Arg Cys Gly Glu Cys Gly Lys Ala Phe Ala Gln Lys Ala Asn
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785 790 795 800
Leu Thr Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Ser Cys
805 810 815
Asn Val Cys Gly Lys Ala Phe Val Leu Ser Ala His Leu Asn Gln His
820 825 830
Leu Arg Val His Thr Gln Glu Thr Leu Tyr Gln Cys Gln Arg Cys Gln
835 840 845
Lys Ala Phe Arg Cys His Ser Ser Leu Ser Arg His Gln Arg Val His
850 855 860
Asn Lys Gln Gln Tyr Cys Leu
865 870

<210> 2645
<211> 1018
<212> DNA
<213> Homo sapiens

<400> 2645
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120
tgggactcga gctattcctg cagctcagca gacctcctgg ccgtggcaga cttctgcgtt
180
atgacccggc tgctgggcta cgtggacccc ctggatccca gctttgtggc tgccgtcatc
240
accatcacct tcaatccgct ctactggaat gtggttgcac gatgggaaca caagacccgc
300
aagctgagca gggccttcgg atccccctac ctggcctgct actctctaag catcaccatc
360
ctgctcctga acttcctgcg ctcgcactgc ttcacgcagg ccatgctgag ccagcccagg
420
atggagagcc tggacacccc cgcggcctac agcctgggcc tcgcgctcct gggactgggc
480
gtcgtgctcg tgctctccag cttctttgca ctggggttcg ctggaacttt cctaggtgat
540
tacttcggga tcctcaagga ggcgagagtg accgtgttcc ccttcaacat cctggacaac
600
cccatgtact ggggaagcac agccaactac ctgggctggg ccatcatgca cgccagcccc
660
acgggcctgc tcctgacggt gctggtggcc ctcacctaca taatggctct cctatacgaa
720
gagcccttca ccgctgagat ctaccggcag aaagcctccg ggtcccacaa gaggagctga
780
ttgagctgca acagctttgc tgaaggcctg gccagcctcc tggcctgccc caagtggcag
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gccctgcgca gggcgagaat ggtgcctgct gctcagggct cgcccccggc gtgggctgcc
900
ccagtgcctt ggaacctgct gccttgggga ccctggacgt gccgacatat ggccattgag
960
ctccaaccca cacattccca ttcaccaata aaggcaccct gaccccaaaa aaaaaaaa
1018

<210> 2646

<211> 199
<212> PRT
<213> Homo sapiens

<400> 2646
Met Thr Arg Leu Leu Gly Tyr Val Asp Pro Leu Asp Pro Ser Phe Val
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Ala Ala Val Ile Thr Ile Thr Phe Asn Pro Leu Tyr Trp Asn Val Val
20 25 30
Ala Arg Trp Glu His Lys Thr Arg Lys Leu Ser Arg Ala Phe Gly Ser
35 40 45
Pro Tyr Leu Ala Cys Tyr Ser Leu Ser Ile Thr Ile Leu Leu Leu Asn
50 55 60
Phe Leu Arg Ser His Cys Phe Thr Gln Ala Met Leu Ser Gln Pro Arg
65 70 75 80
Met Glu Ser Leu Asp Thr Pro Ala Ala Tyr Ser Leu Gly Leu Ala Leu
85 90 95
Leu Gly Leu Gly Val Val Leu Val Leu Ser Ser Phe Phe Ala Leu Gly
100 105 110
Phe Ala Gly Thr Phe Leu Gly Asp Tyr Phe Gly Ile Leu Lys Glu Ala
115 120 125
Arg Val Thr Val Phe Pro Phe Asn Ile Leu Asp Asn Pro Met Tyr Trp
130 135 140
Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met His Ala Ser Pro
145 150 155 160
Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu Thr Tyr Ile Met Ala
165 170 175
Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile Tyr Arg Gln Lys Ala
180 185 190
Ser Gly Ser His Lys Arg Ser
195

<210> 2647
<211> 1368
<212> DNA
<213> Homo sapiens

<400> 2647
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catgtgacac caaaaggaat taatggtata gactttaaag gggaagcgat aacttttaaa
120
gcaactactg ctggaatcct tgcaacactt tctcattgta ttgaactaat ggttaaacgt
180
gaggacagct ggcagaagag actggataag gaaactgaga agaaaagaag aacagaggaa
240
gcatataaaa atgcaatgac agaacttaag aaaaaatccc actttggagg accagattat
300
gaagaaggcc ctaacagtct gattaatgaa gaagagttct ttgatgctgt tgaagctgct
360
cttgacagac aagataaaat agaagaacag tcacagagtg aaaaggtgag attacattgg
420
cctacatcct tgccctctgg agatgccttt tcttctgtgg ggacacatag atttgtccaa
480

aaggttgaag agatggtgca gaaccacatg acttactcat tacaggatgt aggcggagat
540
gccaattggc agttggttgt agaagaagga gaaatgaagg tatacagaag agaagtagaa
600
gaaaatggga ttgttctgga tcctttaaaa gctacccatg cagttaaagg cgtcacagga
660
catgaagtct gcaattattt ctggaatgtt gacgttcgca atgactggga aacaactata
720
gaaaactttc atgtggtgga aacattagct gataatgcaa tcatcattta tcaaacacac
780
aagagggtgt ggcctgcttc tcagcgagac gtattatatc tttctgtcat tcgaaagata
840
ccagccttga ctgaaaatga ccctgaaact tggatagttt gtaatttttc tgtggatcat
900
gacagtgctc ctctaaacaa ccgatgtgtc cgtgccaaaa taaatgttgc tatgatttgt
960
caaaccttgg taagcccacc agagggaaac caggaaatta gcagggacaa cattctatgc
1020
aagattacat atgtagctaa tgtgaaccct ggaggatggg caccagcctc agtgttaagg
1080
gcagtggcaa agcgagagta tcctaaattt ctaaaacgtt ttacttctta cgtccaagaa
1140
aaaactgcag gaaagcctat tttgttctag tattaacagt gactgaagca aggctgtgtg
1200
acattccatg ttggagaaaa aaagaaaaaa aaagctgaat gctctaagct ggaacgtagg
1260
atctatagcc ttgtctgtgg cccaagacct tggccttgtg tacaaaaatg acaaaatatt
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1368

<210> 2648
<211> 389
<212> PRT
<213> Homo sapiens

<400> 2648
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Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp Phe
20 25 30
Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu Ala
35 40 45
Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser Trp
50 55 60
Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu Glu
65 70 75 80
Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe Gly
85 90 95
Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu Glu
100 105 110
Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu
115 120 125
Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser Leu

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    130                 135                 140
Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val Gln
145                 150                 155                 160
Lys Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp
                165                 170                 175
Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met
            180                 185                 190
Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro
        195                 200                 205
Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val Cys
    210                 215                 220
Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile
225                 230                 235                 240
Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile
                245                 250                 255
Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu
            260                 265                 270
Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro
        275                 280                 285
Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro
    290                 295                 300
Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys
305                 310                 315                 320
Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp
                325                 330                 335
Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly
            340                 345                 350
Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro
        355                 360                 365
Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly
    370                 375                 380
Lys Pro Ile Leu Phe
385
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<210> 2649
<211> 1299
<212> DNA
<213> Homo sapiens

<400> 2649
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gctttcctgc tcctgagttc caggaccgca cgctccgagg aggaccggga cggcctatgg
120
gatgcctggg gcccatggag tgaatgctca cgcacctgcg ggggtggggc ctcctactct
180
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata cagaacatgc
240
agtaatgtgg actgcccacc agaagcaggt gatttccgag ctcagcaatg ctcagctcat
300
aatgatgtca agcaccatgg ccagttttat gaatggcttc ctgtgtctaa tgaccctgac
360
aacccatgtt cactcaagtg ccaagccaaa ggaacaaccc tggttgttga actagcacct
420

aaggtcttag atggtacgcg ttgctataca gaatctttgg atatgtgcat cagtggttta
480
tgccaaattg ttggctgcga tcaccagctg ggaagcaccg tcaaggaaga taactgtggg
540
gtctgcaacg gagatgggtc cacctgccgg ctggtccgag ggcagtataa atcccagctc
600
tccgcaacca aatcggatga tactgtggtt gcaattccct atggaagtag acatattcgc
660
cttgtcttaa aaggtcctga tcacttatat ctggaaacca aaaccctcca ggggactaaa
720
ggtgaaaaca gtctcagctc cacaggaact ttccttgtgg acaattctag tgtggacttc
780
cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc agatttcatt
840
gtcaagattc gtaactcggg ctccgctgac agtacagtcc agttcatctt ctatcaaccc
900
atcatccacc gatggaggga gacggatttc tttccttgct cagcaacctg tggaggaggt
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tatcagctga catcggctga gtgctacgat ctgaggagca accgtgtggt tgctgaccaa
1020
tactgtcact attacccaga gaacatcaaa cccaaaccca agcttcagga gtgcaacttg
1080
gatccttgtc cagccagtga cggatacaag cagatcatgc cttatgacct ctaccatccc
1140
cttcctcggt gggaggccac cccatggacc gcgtgctcct cctcgtgtgg gggggcatc
1200
cagagcccgg gcagtttcct gtgtggagga ggacatccag gggcatgtca cttcagtgga
1260
agagtggaaa tgcatgtaca cccctaagat gcccatcgc
1299

<210> 2650
<211> 428
<212> PRT
<213> Homo sapiens

<400> 2650
Xaa Asp Pro Ser Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu
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Leu Leu Phe Leu Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser
20 25 30
Glu Glu Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu
35 40 45
Cys Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys
50 55 60
Leu Ser Ser Lys Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr Cys
65 70 75 80
Ser Asn Val Asp Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala Gln Gln
85 90 95
Cys Ser Ala His Asn Asp Val Lys His His Gly Gln Phe Tyr Glu Trp
100 105 110
Leu Pro Val Ser Asn Asp Pro Asp Asn Pro Cys Ser Leu Lys Cys Gln
115 120 125
Ala Lys Gly Thr Thr Leu Val Val Glu Leu Ala Pro Lys Val Leu Asp

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    130                 135                 140
Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp Met Cys Ile Ser Gly Leu
145                 150                 155                 160
Cys Gln Ile Val Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu
                165                 170                 175
Asp Asn Cys Gly Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val
            180                 185                 190
Arg Gly Gln Tyr Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr
        195                 200                 205
Val Val Ala Ile Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys
    210                 215                 220
Gly Pro Asp His Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys
225                 230                 235                 240
Gly Glu Asn Ser Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser
                245                 250                 255
Ser Val Asp Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala
            260                 265                 270
Gly Pro Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser
        275                 280                 285
Ala Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg
    290                 295                 300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Gly
305                 310                 315                 320
Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn Arg Val
                325                 330                 335
Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile Lys Pro Lys
            340                 345                 350
Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro Ala Ser Asp Gly
        355                 360                 365
Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His Pro Leu Pro Arg Trp
    370                 375                 380
Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser Ser Cys Gly Gly Gly Ile
385                 390                 395                 400
Gln Ser Pro Gly Ser Phe Leu Cys Gly Gly Gly His Pro Gly Ala Cys
                405                 410                 415
His Phe Ser Gly Arg Val Glu Met His Val His Pro
            420                 425
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<210> 2651
<211> 628
<212> DNA
<213> Homo sapiens

<400> 2651
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120
gagacaggcc gagtgaccaa gacaaaggac gggcatgagg ttcggacctg caaagtggcg
180
gacaaaacag gcagcatcaa tatctctgtc tgggacgatg ttggcaatct gatccagcct
240
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300

tatactggcc gtgggggtga tctgcagaag attggagaat tctgcatgga ttattctgag
360
gttcctaact tcagtgagcc aaacccagag tacagcaccc agcaggcacc caacaaggcg
420
gtgcagaacg acagcaaccc ttcagcttcc cagcctacca ctggaccctc tgctgcctct
480
ccagcctctg agaaccagaa tgggaatgga atgagtgccc caccaggttt ccgggtggtg
540
gcccacatcc ccctcatact ccctcccacc cacccagcac ccgaatcact cgaagccagc
600
ccaaccacac acctgcaggc ccgcctgg
628

<210> 2652
<211> 209
<212> PRT
<213> Homo sapiens

<400> 2652
Tyr Thr Val Leu Pro Ala Gly Leu Val Gly Cys Arg Gly Ser Gly Ser
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Met Thr Thr Glu Thr Phe Val Lys Gly Ile Lys Pro Gly Leu Lys Asn
20 25 30
Leu Asn Leu Ile Phe Ile Val Leu Glu Thr Gly Arg Val Thr Lys Thr
35 40 45
Lys Asp Gly His Glu Val Arg Thr Cys Lys Val Ala Asp Lys Thr Gly
50 55 60
Ser Ile Asn Ile Ser Val Trp Asp Asp Val Gly Asn Leu Ile Gln Pro
65 70 75 80
Gly Asp Ile Ile Arg Leu Thr Lys Gly Tyr Ala Ser Val Phe Lys Gly
85 90 95
Cys Leu Thr Leu Tyr Thr Gly Arg Gly Gly Asp Leu Gln Lys Ile Gly
100 105 110
Glu Phe Cys Met Asp Tyr Ser Glu Val Pro Asn Phe Ser Glu Pro Asn
115 120 125
Pro Glu Tyr Ser Thr Gln Gln Ala Pro Asn Lys Ala Val Gln Asn Asp
130 135 140
Ser Asn Pro Ser Ala Ser Gln Pro Thr Thr Gly Pro Ser Ala Ala Ser
145 150 155 160
Pro Ala Ser Glu Asn Gln Asn Gly Asn Gly Met Ser Ala Pro Pro Gly
165 170 175
Phe Arg Val Val Ala His Ile Pro Leu Ile Leu Pro Pro Thr His Pro
180 185 190
Ala Pro Glu Ser Leu Glu Ala Ser Pro Thr Thr His Leu Gln Ala Arg
195 200 205
Leu

<210> 2653
<211> 2103
<212> DNA
<213> Homo sapiens

<400> 2653

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120
caagctactg accgtactcg ggcgtattag gagccgcgtt ccagcctcac accccacggt
180
gctgttttcg acttcagaaa ggatctagcc tcagcacaga agcgcctcag gcgcggcgca
240
aagctcgagc ggacggcggg ggcggccgga gcctctctcg ggggagccgc gcctgaggag
300
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780
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840
taaacgaatg cagaagagaa gacatttaga aacgagtttc caacagacag atccgtgttg
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1140
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1260
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1380
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1440
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1560
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1620

caaatagcct gcagtgcttc ctgtgaaata gtgaaggagg agggcatttc tgtattccag
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1740
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1860
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1920
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1980
acactgagtt ctgattctaa atgccttctt ctgctgggcg cggtggctca tgcctgtaat
2040
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2100
ggc
2103

<210> 2654
<211> 70
<212> PRT
<213> Homo sapiens

<400> 2654
Tyr Leu Asn Lys Val Gly Val Leu Lys Arg Lys His Phe Pro Gly Ile
 1   5   10   15
Ser Glu Val Asn Phe Leu Arg Phe Glu Cys Cys Phe Lys Thr Leu Ser
            20   25   30
Ser Asp Ser Lys Cys Leu Leu Leu Leu Gly Ala Val Ala His Ala Cys
        35   40   45
Asn Pro Ser Thr Leu Gly Gly Arg Gly Gly Arg Ile Thr Arg Ser Gly
    50   55   60
Asp Arg Asp Tyr Pro Gly
65   70

<210> 2655
<211> 1752
<212> DNA
<213> Homo sapiens

<400> 2655
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caagattagt gcaaataagc tgaaactctg gtacagtagg tgactttatg acagtttccc
120
tcttctttgt gattgctttt ttagagacgg atttttttcc agatttgtgc ttcttgtgtt
180
ttgctttttt tttgatgatc aataacttat tctggatctc aggtttgtaa gacttgaatg
240
caagagaatg aagaccttca cgctttctct gtaagttttc attcaaaaca tctttcaatt
300
tctttttttt ctttttcttc ttttttgccc tcattttagt tagtttgagt ttcttgtggc
360

tctgtagtga ctgctctaat agaatatccc ttacaacttt gtggcagtta atttctggat
420
gatcactgtg acttccattt acatgtattt ggcaagattt tagagtattt tcttttaatg
480
gactgggttc aatctttatt ctggaagctt caccgtattt ttcctgattt tctataaacc
540
ttatttcacc tggactgaga ggctctccaa agccagtaac ttcccctgga ctccttggtt
600
tctctaaatt ttctttacaa caatcagttt ttttaatttc acaaggcctg cgaattctaa
660
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720
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780
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tctccaattt aatccgaggt actctttgta ttttaatggg tggaattgga aattctgggg
900
cctgaaaggg tctctgttta taaatccgta catctgcacc acagaactgt ggaaaatgta
960
cataagcagt ctccaaataa tcataacgaa gaataactgc cctgcattca tggataggct
1020
gtccaagtac agcatcttga acttccttat gtgtatcata cacaaagtca caaagaccct
1080
taagtagcca cacttttgg taaaaaggta gttcgtgaaa aggtttttct tccaatggat
1140
taacttctcc aagaacttta aaaaactgag gacacaaccc cagtttttca gcacagttat
1200
caggattttc agtttgccct acagcagtgt accactgttg tactttctgc ctcagcgctg
1260
cttcccaggt cctataaggc aaagtaggtc ttcgatgtaa ggtaggtctg cgatggggag
1320
gacttaatag agaagtcatt attttcgata gaaaagcatt acactgaggc atcagaagac
1380
aacgttccaa ttcgtaaaag actatttctg gcaaatttag aatttgctga gctaaacaaa
1440
ggaaatgccc aatagctgga atttcccaca tggtctccat acaagttgga gctgcttgag
1500
ctagaagttt tctttcccat tcttctattt ccttttgact agcttcttct gcttcttttc
1560
tttcctgctc ccgaagccta aagaaattta acaaattata ctattattat tcagagggta
1620
ccataaaatg ataaatttta agtatattta tctttagtca aaaaggcaat caactgtcct
1680
agttttattt atttatttat ttgagacaga gtctcgctct gtcccccagg ctgtagtgca
1740
gtgatgcaat ct
1752

<210> 2656
<211> 493
<212> PRT
<213> Homo sapiens

<400> 2656
Met Glu Thr Met Trp Glu Ile Pro Ala Ile Gly His Phe Leu Cys Leu
1 5 10 15
Ala Gln Gln Ile Leu Asn Leu Pro Glu Ile Val Phe Tyr Glu Leu Glu
20 25 30
Arg Cys Leu Leu Met Pro Gln Cys Asn Ala Phe Leu Ser Lys Ile Met
35 40 45
Thr Ser Leu Leu Ser Pro Pro His Arg Arg Pro Thr Leu His Arg Arg
50 55 60
Pro Thr Leu Pro Tyr Arg Thr Trp Glu Ala Ala Leu Arg Gln Lys Val
65 70 75 80
Gln Gln Trp Tyr Thr Ala Val Gly Gln Thr Glu Asn Pro Asp Asn Cys
85 90 95
Ala Glu Lys Leu Gly Leu Cys Pro Gln Phe Phe Lys Val Leu Gly Glu
100 105 110
Val Asn Pro Leu Glu Glu Lys Pro Phe His Glu Leu Pro Phe Tyr Gln
115 120 125
Lys Val Trp Leu Leu Lys Gly Leu Cys Asp Phe Val Tyr Asp Thr His
130 135 140
Lys Glu Val Gln Asp Ala Val Leu Gly Gln Pro Ile His Glu Cys Arg
145 150 155 160
Ala Val Ile Leu Arg Tyr Asp Tyr Leu Glu Thr Ala Tyr Val His Phe
165 170 175
Pro Gln Phe Cys Gly Ala Asp Val Arg Ile Tyr Lys Gln Arg Pro Phe
180 185 190
Gln Ala Pro Glu Phe Pro Ile Pro Pro Ile Lys Ile Gln Arg Val Pro
195 200 205
Arg Ile Lys Leu Glu Lys Leu Lys Cys Asp Tyr Val Ser Thr Ser Asn
210 215 220
Gly Glu His Arg Cys Ser Arg Asp Ser Leu Pro Ser Ser Phe Lys Lys
225 230 235 240
Glu Gln Glu Asn Asn Phe Asp Pro Ala Cys Cys Pro Ala Lys Met Ile
245 250 255
Leu Asp Asn His Asp Ile Ser Val Glu Met Gly Val Lys Ser Asn Tyr
260 265 270
Glu Ile Arg Ile Arg Arg Pro Cys Glu Ile Lys Lys Thr Asp Cys Cys
275 280 285
Lys Glu Asn Leu Glu Lys Pro Arg Ser Pro Gly Glu Val Thr Gly Phe
290 295 300
Gly Glu Pro Leu Ser Pro Gly Glu Ile Arg Phe Ile Glu Asn Gln Glu
305 310 315 320
Lys Tyr Gly Glu Ala Ser Arg Ile Lys Ile Glu Pro Ser Pro Leu Lys
325 330 335
Glu Asn Thr Leu Lys Ser Cys Gln Ile His Val Asn Gly Ser His Ser
340 345 350
Asp His Pro Glu Ile Asn Cys His Lys Val Val Arg Asp Ile Leu Leu
355 360 365
Glu Gln Ser Leu Gln Ser His Lys Lys Leu Lys Leu Thr Lys Met Arg
370 375 380
Ala Lys Lys Lys Lys Lys Lys Lys Lys Lys Leu Lys Asp Val Leu Asn
385 390 395 400
Glu Asn Leu Gln Arg Lys Arg Glu Gly Leu His Ser Leu Ala Phe Lys
405 410 415
Ser Tyr Lys Pro Glu Ile Gln Asn Lys Leu Leu Ile Ile Lys Lys Lys

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            420                 425                 430
Ala Lys His Lys Lys His Lys Ser Gly Lys Lys Ser Val Ser Lys Lys
        435                 440                 445
Ala Ile Thr Lys Lys Arg Lys Thr Val Ile Lys Ser Pro Thr Val Pro
    450                 455                 460
Glu Phe Gln Leu Ile Cys Thr Asn Leu Asp Glu Leu Arg Glu Leu Ile
465                 470                 475                 480
Thr Lys Ile Glu Asn Glu Leu Lys Asp Leu Glu Lys Lys
                485                 490
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<210> 2657
<211> 972
<212> DNA
<213> Homo sapiens

<400> 2657
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aggggtcag agaccacagc ccagtagcct gggacaagcc gcccagtccc tctggtctct
120
gtcctgttgt ctaagggcca aggggcagta gcccctcctc caggggccct gagcacagag
180
gcgtcagatc agagttgcca tcttcaactt gatatgcccc ccacatccca gcagctctgt
240
gggcccaggc tactggcatc cacatgactc ccagggcctg agtccacact gcctgaggac
300
aggagcctca aaactgaaat gcacgtgctt cggaccagcc atccgtgcct gacaatgtcc
360
tatggaaaca cccacacgtg tgcagatcgc tgcaatgaaa gggtccgtca tggggttggg
420
taattccagc tgggaccgcc taggagcgcc atgcagctgt gggaacaagg ttgctgtcca
480
cacagacatg aagggattcc ccgtggaatg aggttagaaa aggaagggca agagtggacg
540
tataagatgc cccatgctgt gtgaaaactg ccatgagaga gagacggagg aaggggggaga
600
aagtgggaga cagagaccaa catctgcact gcctgtgcct gccacactct cccctcgggg
660
ccagagggtg gcctctgggg aggggctggc gagaggggat gccaggcctg ggctgcagca
720
gacttgggtg gtcatggagg atccatgcca tcaacggcag gctggggtgc cctccccggg
780
ccagcaccaa gcatgcatgg ttggtgatgt ggaacttacg cagagcgtgg cggctgggca
840
ggcggctgtg caggggctgg gcatggatat acagggctcg gtagaactcc tggcagtccc
900
gctccccgct ccgctgcagg tggctcagga ggtcacagag ccgcacacgc aaggatgcct
960
tggggttccg ga
972

<210> 2658
<211> 76
<212> PRT

<213> Homo sapiens

<400> 2658
Glu Arg Asp Gly Gly Arg Gly Arg Lys Trp Glu Thr Glu Thr Asn Ile
1 5 10 15
Cys Thr Ala Cys Ala Cys His Thr Leu Pro Ser Gly Pro Glu Gly Gly
20 25 30
Leu Trp Gly Gly Ala Gly Glu Arg Gly Cys Gln Ala Trp Ala Ala Ala
35 40 45
Asp Leu Gly Gly His Gly Gly Ser Met Pro Ser Thr Ala Gly Trp Gly
50 55 60
Ala Leu Pro Gly Pro Ala Pro Ser Met His Gly Trp
65 70 75

<210> 2659
<211> 691
<212> DNA
<213> Homo sapiens

<400> 2659
actagtgaaa gaaacggaag caagatttcc agatgtagca aatgggttta ttacggaaat
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aattcatttt aagaattatt atgatctgaa tgtgaggctg aagaggaaca gaaaagaaag
120
aatggagaga acaccttcaa acgcattgga cccccgctgg agaagcctgt ggagaaggtg
180
cagagggtgg aggccctccc gaggcccgtt ccgcagaacc tgccacagcc acagatgcca
240
ccctatgcct tcgcgcaccc acccttcccc ctgcctcccg tgcggcctgt gttcaacaac
300
ttcccactca acatggggcc tatcccagcc ccgtacgtgc cccctctgcc caacgtgcgg
360
gtcaactatg acttcggtcc catccacatg cccctggagc acaacctgcc catgcacttt
420
ggcccccagc cgcggcatcg cttctgatgg ccccgaatcc ccattgagca gcacaaagcc
480
cgtttggggt aggagtgtgg atggagaacc ctcccccaag gctggtgtct gtaccattgc
540
atcctaagtc agcttgaagg gtaggctggt tttcttccca ccccttttcct agaagggcta
600
ctgctcctgg aagagtggac ggatccataa taaagacgtc ccaaatggtg aaaaaaaaaa
660
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a
691

<210> 2660
<211> 120
<212> PRT
<213> Homo sapiens

<400> 2660
Ser Glu Cys Glu Ala Glu Glu Glu Gln Lys Arg Lys Asn Gly Glu Asn
1 5 10 15
Thr Phe Lys Arg Ile Gly Pro Pro Leu Glu Lys Pro Val Glu Lys Val

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            20                  25                  30
Gln Arg Val Glu Ala Leu Pro Arg Pro Val Pro Gln Asn Leu Pro Gln
        35                  40                  45
Pro Gln Met Pro Pro Tyr Ala Phe Ala His Pro Pro Phe Pro Leu Pro
    50                  55                  60
Pro Val Arg Pro Val Phe Asn Asn Phe Pro Leu Asn Met Gly Pro Ile
65                  70                  75                  80
Pro Ala Pro Tyr Val Pro Pro Leu Pro Asn Val Arg Val Asn Tyr Asp
                85                  90                  95
Phe Gly Pro Ile His Met Pro Leu Glu His Asn Leu Pro Met His Phe
            100                 105                 110
Gly Pro Gln Pro Arg His Arg Phe
        115                 120
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<210> 2661
<211> 1395
<212> DNA
<213> Homo sapiens

<400> 2661
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tgtattggaa aagatgcacc gattgctctt aagaggaaac tggagatgaa agccttgagg
120
gaattagaca gattttctgt tttgaatagc caacacatgt ttgaagtact agctgccatg
180
aatcaccgat ctcttatact cctggatgaa tgcagtaagg tggtcctaga taatatccat
240
gggtgtcctt taagaataat gatcaacata ttgcagtcct gcaaagacct ccagtaccat
300
aatttggatc tcttcaaggg acttgcagat tatgtggctg caactttcga catctggaag
360
ttcagaaaag ttctttttat cctcatttta tttgaaaacc ttggctttcg acctgttggt
420
ttaatggacc tgtttatgaa gagaatagta gaggatcctg aatccctaaa catgaaaaac
480
attctatcta ttcttcatac ttactcttct ctcaatcatg tctacaaatg ccagaacaaa
540
gaacagttcg tggaagttat ggctagtgct ctgactggtt atcttcacac tatttcttct
600
gaaaacttat tggatgcagt atattcattt tgcttgatga attactttcc cctggctcct
660
tttaatcagc ttctgcaaaa agacatcatc agtgagctgc tgacatcaga tgacatgaag
720
aatgcttaca agctgcatac tttggatact tgtctaaaac ttgatgatac tgtctatctg
780
agggacatag ccttgtcact cccacagctg ccgcgggagc tgccatcgtc acatacaaat
840
gcaaaggtgg cagaggtgct gagcagcctt ctgggaggtg aaggacactt ctcaaaggat
900
gtgcacttgc cacacaatta tcatattgat tttgaaatca gaatggacac taacaggaat
960
caagtgctac cactttctga tgtggataca acttctgcta cagatattca aagagtagct
1020

gtgctatgtg tttccagatc tgcttattgt ttgggttcaa gccaccccag aggattcctt
1080
gctatgaaaa tgcggcattt gaatgcaatg ggttttcatg tgatcttggt caataactgg
1140
gagatggaca aactagagat ggaagatgca gtcacatttt tgaagactaa aatctattca
1200
gtagaagctc ttcctgttgc tgctgtaaat gtgcaaagca cacaataaag tgaaaatcaa
1260
ccttttcata ttaggagaca tgcatttgta aaaattaata aagatgacaa gtcagttgtc
1320
aatggaattg agctatctgc taagacaaaa aatgttacct cagttcacta ttaaaattaa
1380
ttttaggagt ggaaa
1395

<210> 2662
<211> 415
<212> PRT
<213> Homo sapiens

<400> 2662

Leu	Val	Asp	Gln	Gln	Val	Trp	Lys	Ile	Glu	Asp	Val	Phe	Thr	Leu	Gln
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Val	Val	Met	Lys	Cys	Ile	Gly	Lys	Asp	Ala	Pro	Ile	Ala	Leu	Lys	Arg
			20					25					30		
Lys	Leu	Glu	Met	Lys	Ala	Leu	Arg	Glu	Leu	Asp	Arg	Phe	Ser	Val	Leu
		35					40					45			
Asn	Ser	Gln	His	Met	Phe	Glu	Val	Leu	Ala	Ala	Met	Asn	His	Arg	Ser
	50					55					60				
Leu	Ile	Leu	Leu	Asp	Glu	Cys	Ser	Lys	Val	Val	Leu	Asp	Asn	Ile	His
65					70					75					80
Gly	Cys	Pro	Leu	Arg	Ile	Met	Ile	Asn	Ile	Leu	Gln	Ser	Cys	Lys	Asp
				85					90					95	
Leu	Gln	Tyr	His	Asn	Leu	Asp	Leu	Phe	Lys	Gly	Leu	Ala	Asp	Tyr	Val
			100					105					110		
Ala	Ala	Thr	Phe	Asp	Ile	Trp	Lys	Phe	Arg	Lys	Val	Leu	Phe	Ile	Leu
		115					120					125			
Ile	Leu	Phe	Glu	Asn	Leu	Gly	Phe	Arg	Pro	Val	Gly	Leu	Met	Asp	Leu
	130					135					140				
Phe	Met	Lys	Arg	Ile	Val	Glu	Asp	Pro	Glu	Ser	Leu	Asn	Met	Lys	Asn
145					150					155					160
Ile	Leu	Ser	Ile	Leu	His	Thr	Tyr	Ser	Ser	Leu	Asn	His	Val	Tyr	Lys
				165					170					175	
Cys	Gln	Asn	Lys	Glu	Gln	Phe	Val	Glu	Val	Met	Ala	Ser	Ala	Leu	Thr
			180					185					190		
Gly	Tyr	Leu	His	Thr	Ile	Ser	Ser	Glu	Asn	Leu	Leu	Asp	Ala	Val	Tyr
		195					200					205			
Ser	Phe	Cys	Leu	Met	Asn	Tyr	Phe	Pro	Leu	Ala	Pro	Phe	Asn	Gln	Leu
	210					215					220				
Leu	Gln	Lys	Asp	Ile	Ile	Ser	Glu	Leu	Leu	Thr	Ser	Asp	Asp	Met	Lys
225					230					235					240
Asn	Ala	Tyr	Lys	Leu	His	Thr	Leu	Asp	Thr	Cys	Leu	Lys	Leu	Asp	Asp
				245					250					255	
Thr	Val	Tyr	Leu	Arg	Asp	Ile	Ala	Leu	Ser	Leu	Pro	Gln	Leu	Pro	Arg

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            260                 265                 270
Glu Leu Pro Ser Ser His Thr Asn Ala Lys Val Ala Glu Val Leu Ser
        275                 280                 285
Ser Leu Leu Gly Gly Glu Gly His Phe Ser Lys Asp Val His Leu Pro
    290                 295                 300
His Asn Tyr His Ile Asp Phe Glu Ile Arg Met Asp Thr Asn Arg Asn
305                 310                 315                 320
Gln Val Leu Pro Leu Ser Asp Val Asp Thr Thr Ser Ala Thr Asp Ile
                325                 330                 335
Gln Arg Val Ala Val Leu Cys Val Ser Arg Ser Ala Tyr Cys Leu Gly
            340                 345                 350
Ser Ser His Pro Arg Gly Phe Leu Ala Met Lys Met Arg His Leu Asn
        355                 360                 365
Ala Met Gly Phe His Val Ile Leu Val Asn Asn Trp Glu Met Asp Lys
    370                 375                 380
Leu Glu Met Glu Asp Ala Val Thr Phe Leu Lys Thr Lys Ile Tyr Ser
385                 390                 395                 400
Val Glu Ala Leu Pro Val Ala Ala Val Asn Val Gln Ser Thr Gln
                405                 410                 415
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<210> 2663
<211> 1024
<212> DNA
<213> Homo sapiens

<400> 2663

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gggaacccgg gagccgaggt aacgaacagc tcggtggcag ggcctgactg ctgcggaggc
120
ctcggcaata ttgattttag acaggcagac ttctgcgtta tgacccggct gctgggctac
180
gtggaccccc tggatcccag ctttgtggct gccgtcatca ccatcacctt caatccgctc
240
tactggaatg tggttgcacg atgggaacac aagacccgca agctgagcag ggccttcgga
300
tccccctacc tggcctgcta ctctctaagc gtcaccatcc tgctcctgaa cttcctgcgc
360
tcgcactgct tcacgcaggc catgctgagc cagcccagga tggagagcct ggacaccccc
420
gcggcctaca gcctgggcct cgcgctcctg ggactgggcg tcgtgctcgt gctctccagc
480
ttctttgcac tggggttcgc tggaactttc ctaggtgatt acttcgggat cctcaaggag
540
gcgagagtga ccgtgttccc cttcaacatc ctggacaacc ccatgtactg gggaagcaca
600
gccaactacc tgggctgggc catcatgcac gccagcccca cgggcctgct cctgacggtg
660
ctggtggccc tcacctacat aatggctctc ctatacgaag agcccttcac cgctgagatc
720
taccggcaga aagcctccgg gtcccacaag aggagctgat tgagctgcaa cagctttgct
780
gaaggcctgg ccagcctccc tcgtgcccca agtggcaggc cctgcgcagg gcgagaatgg
840
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tgcctgctgc tcagggcctc ccccggcgtg ggctgcccca gtgccttgga acctgctgcc
900
ttggggaccc tggacgtgcc gacatatggc cattgagctc caacccacac attcccattc
960
accaataaag gcaccctgac cccaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
1020
aaaa
1024

<210> 2664
<211> 199
<212> PRT
<213> Homo sapiens

<400> 2664
Met Thr Arg Leu Leu Gly Tyr Val Asp Pro Leu Asp Pro Ser Phe Val
 1   5   10   15
Ala Ala Val Ile Thr Ile Thr Phe Asn Pro Leu Tyr Trp Asn Val Val
            20   25   30
Ala Arg Trp Glu His Lys Thr Arg Lys Leu Ser Arg Ala Phe Gly Ser
        35   40   45
Pro Tyr Leu Ala Cys Tyr Ser Leu Ser Val Thr Ile Leu Leu Leu Asn
    50   55   60
Phe Leu Arg Ser His Cys Phe Thr Gln Ala Met Leu Ser Gln Pro Arg
65   70   75   80
Met Glu Ser Leu Asp Thr Pro Ala Ala Tyr Ser Leu Gly Leu Ala Leu
                85   90   95
Leu Gly Leu Gly Val Val Leu Val Leu Ser Ser Phe Phe Ala Leu Gly
            100   105   110
Phe Ala Gly Thr Phe Leu Gly Asp Tyr Phe Gly Ile Leu Lys Glu Ala
        115   120   125
Arg Val Thr Val Phe Pro Phe Asn Ile Leu Asp Asn Pro Met Tyr Trp
    130   135   140
Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met His Ala Ser Pro
145   150   155   160
Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu Thr Tyr Ile Met Ala
                165   170   175
Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile Tyr Arg Gln Lys Ala
            180   185   190
Ser Gly Ser His Lys Arg Ser
        195

<210> 2665
<211> 720
<212> DNA
<213> Homo sapiens

<400> 2665
nnccgcgggc atgtctgtgt gtatgtgtgt gtgtgcacgc gcgtgcatgc atgcatgctg
60
cgaggggagg aagggaagcg tggaaggggg gagagagttg ttgtctagcc tctgagagca
120
gcgccaatgc gaagcgttgc agtcgcttga ctcacctgag gctctccaag gataccttca
180

atgcctgcac tgtaagggag ctgcttttcc cgggtgctgg cgagaacgga agccttcctt
240
tgacgttttt ctaaacatgg gatgcagtct gtgcagcctg cagaagcaag aggagcagta
300
caaattactt atgaagtttg tcaggtcaac ggcagagact tatccagagc aactcatgac
360
caggctgtgg aagctttcaa gacagccaag gagcccatag tggtgcaggt gttgagaaga
420
acaccaagga ccaaaatgtt cacgcctcca tcagagtctc agctggtgga cacgggaacc
480
caaaccgaca tcacctttga acatatcatg gccctcacta agatgtcctc tcccagccca
540
cccgtgctgg atccctatct cttgccagag gagcatccct cagcccatga atactacgat
600
ccaaatgact acattggaga catccatcag gagatggaca gggaggagct ggagctggag
660
gaagtggacc tctacagaat gaacagccag gacaagctgg gcctcactgt gtgctaccgg
720

<210> 2666
<211> 153
<212> PRT
<213> Homo sapiens

<400> 2666
Met Gln Ser Val Gln Pro Ala Glu Ala Arg Gly Ala Val Gln Ile Thr
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Tyr Glu Val Cys Gln Val Asn Gly Arg Asp Leu Ser Arg Ala Thr His
            20   25   30
Asp Gln Ala Val Glu Ala Phe Lys Thr Ala Lys Glu Pro Ile Val Val
        35   40   45
Gln Val Leu Arg Arg Thr Pro Arg Thr Lys Met Phe Thr Pro Pro Ser
    50   55   60
Glu Ser Gln Leu Val Asp Thr Gly Thr Gln Thr Asp Ile Thr Phe Glu
65   70   75   80
His Ile Met Ala Leu Thr Lys Met Ser Ser Pro Ser Pro Pro Val Leu
                85   90   95
Asp Pro Tyr Leu Leu Pro Glu Glu His Pro Ser Ala His Glu Tyr Tyr
            100   105   110
Asp Pro Asn Asp Tyr Ile Gly Asp Ile His Gln Glu Met Asp Arg Glu
        115   120   125
Glu Leu Glu Leu Glu Glu Val Asp Leu Tyr Arg Met Asn Ser Gln Asp
    130   135   140
Lys Leu Gly Leu Thr Val Cys Tyr Arg
145   150

<210> 2667
<211> 289
<212> DNA
<213> Homo sapiens

<400> 2667
nccatgggga atgggatgaa caagatcctg cccggcctgt acatcggcaa cttcaaagat
60

gccagagacg cggaacaatt gagcaagaac aaggggaacc ctttttctgt ttgtccccga
120
tgggtgccag gcctatgttg gaggacaaga catttcaaag aaagtattaa attcattcac
180
gagtgccggc tccgcgggga gagctgcctt gtacactgcc tggccggggt ctccaggagc
240
gtgacactgg tgatcgcata catcatgacc gtcactgact ttggctggg
289

<210> 2668
<211> 96
<212> PRT
<213> Homo sapiens

<400> 2668
Xaa Met Gly Asn Gly Met Asn Lys Ile Leu Pro Gly Leu Tyr Ile Gly
1 5 10 15
Asn Phe Lys Asp Ala Arg Asp Ala Glu Gln Leu Ser Lys Asn Lys Gly
20 25 30
Asn Pro Phe Ser Val Cys Pro Arg Trp Val Pro Gly Leu Cys Trp Arg
35 40 45
Thr Arg His Phe Lys Glu Ser Ile Lys Phe Ile His Glu Cys Arg Leu
50 55 60
Arg Gly Glu Ser Cys Leu Val His Cys Leu Ala Gly Val Ser Arg Ser
65 70 75 80
Val Thr Leu Val Ile Ala Tyr Ile Met Thr Val Thr Asp Phe Gly Trp
85 90 95

<210> 2669
<211> 4285
<212> DNA
<213> Homo sapiens

<400> 2669
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cgcaggtggg gcggttgtca gagcccccctg acgtgggcgc cgggctttta tcggcgattt
120
gatctggcga cctcgggccg gcgcctaaga ggtcagactg cggagcctgc gggtcgccag
180
cggccccgcc gagagccgga ggcaatggat gaacagagcg tggagagcat tgctgaggtt
240
ttccgatgtt tcatttgtat ggagaaattg cgggatgcac gcctgtgtcc tcattgctcc
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aaactgtgtt gtttcagctg tattaggcgc tggctgacag agcagagagc tcaatgtcct
360
cattgccgtg ctccactcca gctacgagaa ctagtaaatt gtcgttgggc agaagaagta
420
acacaacagc ttgatactct tcaactctgc agtctcacca aacatgaaga aaatgaaaag
480
gacaaatgtg aaaatcacca tgaaaaactt agtgtatttt gctggacttg taagaagtgt
540
atctgccatc agtgtgcact ttggggagga atgcatggcg gacatacctt taaacctttg
600

gcagaaattt atgagcaaca cgtcactaaa gtgaatgaag aggtagccaa acttcgtcgg
660
cgtctcatgg aactgatcag cttagttcaa gaagtggaaa ggaatgtaga agctgtaaga
720
aatgcaaaag atgagcgtgt tcgggaaatt aggaatgcag tggagatgat gattgcacgg
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840
caagaaacag agcttttgga atccttactt caggaggtgg agcaccagtt gcggtcttgt
900
agtaagagtg agttgatatc taagagctca gagatcctta tgatgtttca gcaagttcat
960
cggaagccca tggcatcttt tgttaccact cctgttccac cagactttac cagtgaatta
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Glu Gly Met Ser Ser Asp Ser Asp Ile Glu Cys Asp Thr Glu Asn Glu
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Glu Gln Glu Glu His Thr Ser Val Gly Gly Phe His Asp Ser Phe Met
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Val Met Thr Gln Pro Pro Asp Glu Asp Thr His Ser Ser Phe Pro Asp
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Phe Ala Ile Leu Ser Pro Ser Pro Tyr Leu Arg Pro Arg Gly Arg Ala
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His His Pro Pro Ser Arg Leu Gly Gly Gly Arg Ala Pro Ser Trp Pro
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Val Ser Ile Leu Ser Ser Phe Glu Ser Arg Leu Met Lys Leu Glu Asn
50 55 60
Ser Ile Ile Pro Val His Lys Gln Thr Glu Asn Leu Gln Arg Leu Gln
65 70 75 80
Glu Asn Val Glu Lys Thr Leu Ser Cys Leu Asp His Val Ile Ser Tyr
85 90 95
Tyr His Val Ala Ser Asp Thr Glu Lys Ile Ile Arg Glu Gly Pro Thr
100 105 110
Gly Arg Leu Glu Glu Tyr Leu Gly Ser Met Ala Lys Ile Gln Lys Ala
115 120 125
Val Glu Tyr Phe Gln Asp Asn Ser Pro Asp Ser Pro Glu Leu Asn Lys
130 135 140
Val Lys Leu Leu Phe Glu Arg Gly Lys Glu Ala Leu Glu Ser Glu Phe
145 150 155 160
Arg Ser Leu Met Thr Arg His Ser Lys Val Val Ser Pro Val Leu Ile
165 170 175
Leu Asp Leu Ile Ser Gly Asp Asp Asp Leu Glu Ala Gln Glu Asp Val
180 185 190
Thr Leu Glu His Leu Pro Glu Ser Val Leu Gln Asp Val Ile Arg Ile
195 200 205
Ser Arg Trp Leu Val Glu Tyr Gly Arg Asn Gln Asp Phe Met Asn Val
210 215 220
Tyr Tyr Gln Ile Arg Ser Ser Gln Leu Asp Arg Ser Ile Lys Gly Leu
225 230 235 240
Lys Glu His Phe His Lys Ser Ser Ser Ser Ser Gly Val Pro Tyr Ser
245 250 255
Pro Ala Ile Pro Asn Lys Arg Lys Asp Thr Pro Thr Lys Lys Pro Val

```
            260                 265                 270
Lys Arg Pro Gly Thr Ile Arg Lys Ala Gln Asn Leu Leu Lys Gln Tyr
        275                 280                 285
Ser Gln His Gly Leu Asp Gly Lys Lys Gly Gly Ser Asn Leu Ile Pro
    290                 295                 300
Leu Glu Gly Arg Asp Asp Met Leu Asp Val Glu Thr Asp Ala Tyr Ile
305                 310                 315                 320
His Cys Val Ser Ala Phe Val Lys Leu Ala Gln Ser Glu Tyr Gln Leu
                325                 330                 335
Leu Ala Asp Ile Ile Pro Glu His His Gln Lys Lys Thr Phe Asp Ser
            340                 345                 350
Leu Ile Gln Asp Ala Leu Asp Gly Leu Met Leu Glu Gly Glu Asn Ile
        355                 360                 365
Val Ser Ala Ala Arg Lys Ala Ile Val Arg His Asp Phe Ser Thr Val
    370                 375                 380
Leu Thr Val Phe Pro Ile Leu Arg His Leu Lys Gln Thr Lys Pro Glu
385                 390                 395                 400
Phe Asp Gln Val Leu Gln Gly Thr Ala Ala Ser Thr Lys Asn Lys Leu
                405                 410                 415
Pro Gly Leu Ile Thr Ser Met Glu Thr Ile Gly Ala Lys Ala Leu Glu
            420                 425                 430
Asp Phe Ala Asp Asn Ile Lys Asn Asp Pro Asp Lys Glu Tyr Asn Met
        435                 440                 445
Pro Lys Asp Gly Thr Val His Glu Leu Thr Ser Asn Ala Ile Leu Phe
    450                 455                 460
Leu Gln Gln Leu Leu Asp Phe Gln Glu Thr Ala Gly Ala Met Leu Ala
465                 470                 475                 480
Ser Gln Glu Thr Ser Ser Ser Ala Thr Ser Tyr Ser Ser Glu Phe Ser
                485                 490                 495
Lys Arg Leu Leu Ser Thr Tyr Ile Cys Lys Val Leu Gly Asn Leu Gln
            500                 505                 510
Leu Asn Leu Leu Ser Lys Ser Lys Val Tyr Glu Asp Pro Ala Leu Ser
        515                 520                 525
Ala Ile Phe Leu His Asn Asn Tyr Asn Tyr Ile Leu Lys Ser Leu Glu
    530                 535                 540
Lys Ser Glu Leu Ile Gln Leu Val Ala Val Thr Gln Lys Thr Ala Glu
545                 550                 555                 560
Arg Ser Tyr Arg Glu His Ile Glu Gln Gln Ile Gln Thr Tyr Gln Arg
                565                 570                 575
Ser Trp Leu Lys Val Thr Asp Tyr Ile Ala Glu Lys Asn Leu Pro Val
            580                 585                 590
Phe Gln Pro Gly Val Lys Leu Arg Asp Lys Glu Arg Gln Ile Ile Lys
        595                 600                 605
Glu Arg Phe Lys Gly Phe Asn Asp Gly Leu Glu Glu Leu Cys Lys Ile
    610                 615                 620
Gln Lys Ala Trp Ala Ile Pro Asp Thr Glu Gln Arg Asp Arg Ile Arg
625                 630                 635                 640
Gln Ala Gln Lys Thr Ile Val Lys Glu Thr Tyr Gly Ala Phe Leu Gln
                645                 650                 655
Lys Phe Gly Ser Val Pro Phe Thr Lys Asn Pro Glu Lys Tyr Ile Lys
            660                 665                 670
Tyr Gly Val Glu Gln Val Gly Asp Met Ile Asp Arg Leu Phe Asp Thr
        675                 680                 685
Ser Ala
```

690

<210> 2675
<211> 711
<212> DNA
<213> Homo sapiens

<400> 2675
agatctcagt gaagaggacc cttgttcact gtacctcatc aacttcctcc tggacgccac
60
tgtgggcatg ctgctcatct acgtgggggt gcgcgccgtc agcgtcctgg tagagtggca
120
gcagtgggag tccctgcgct tcggcgaata tggagaccct ctgcagtgtg gagcctgggt
180
cgggcagtgc gctctttaca tcgtgatcat gatttttgaa aagtctgtcg tcttcatcgt
240
cctcctccta ctccagtgga aaaaggtggc cctattgaat ccaattgaaa accccgacct
300
gaagctggcc atcgtcatgc tgatcgtccc cttctttgtc aacgctttga tgttttgggt
360
agtggacaat ttcctcatga gaaaggggaa gacgaaagct aagctagaag aaaggggagc
420
caaccaggac tcgaggaatg ggagcaaggt ccgctaccgg agggccgcat cccacgagga
480
gtctgagtct gagatcctga tctcagcgga tgatgagatg gaggagtccg acgtggagga
540
ggacctccgc agactgaccc ccctcaagcc tgtgaagaaa aagaagcacc gctttgggct
600
acccgtatga cacattccca tgctgggggt gacgggaggg ccccgccagc cgctggtgtg
660
cagaggtcat cccacagcat cgttccttac cctctctctg cccttcaccc g
711

<210> 2676
<211> 180
<212> PRT
<213> Homo sapiens

<400> 2676
Met Leu Leu Ile Tyr Val Gly Val Arg Ala Val Ser Val Leu Val Glu
1 5 10 15
Trp Gln Gln Trp Glu Ser Leu Arg Phe Gly Glu Tyr Gly Asp Pro Leu
20 25 30
Gln Cys Gly Ala Trp Val Gly Gln Cys Ala Leu Tyr Ile Val Ile Met
35 40 45
Ile Phe Glu Lys Ser Val Val Phe Ile Val Leu Leu Leu Leu Gln Trp
50 55 60
Lys Lys Val Ala Leu Leu Asn Pro Ile Glu Asn Pro Asp Leu Lys Leu
65 70 75 80
Ala Ile Val Met Leu Ile Val Pro Phe Phe Val Asn Ala Leu Met Phe
85 90 95
Trp Val Val Asp Asn Phe Leu Met Arg Lys Gly Lys Thr Lys Ala Lys
100 105 110
Leu Glu Glu Arg Gly Ala Asn Gln Asp Ser Arg Asn Gly Ser Lys Val

```
        115                 120                 125
Arg Tyr Arg Arg Ala Ala Ser His Glu Glu Ser Glu Ser Glu Ile Leu
    130                 135                 140
Ile Ser Ala Asp Asp Glu Met Glu Glu Ser Asp Val Glu Glu Asp Leu
145                 150                 155                 160
Arg Arg Leu Thr Pro Leu Lys Pro Val Lys Lys Lys Lys His Arg Phe
                165                 170                 175
Gly Leu Pro Val
            180
```

<210> 2677
<211> 735
<212> DNA
<213> Homo sapiens

<400> 2677
ngcgcgccag gaccgctcct gcaccgaggg tgcccgccgc gctatggagg ccttccagag
60
ggccgctggt gagggcggcc cgggccgcgg tggggcacgg cgcggtgcca gggtgttgca
120
gagccccttt tgcagggcag gagctgggga gtggttagga catcagtccc tcaggtaggg
180
ggagtgagca catcaggtcc atatgtgtcc caggagcatc cctagctggc cgccctgagt
240
gctgcatggg gcagagatgg gcaggtacac ggccctgcct gtgtgagcac ccctccctcc
300
gctggggcct tcagcctcct gagggagaac ttctcccatg cgccgagccc agacatgagc
360
gctgcgtccc tctgcgcact ggagcagctc atgatggccc aggcccagga atgtgtgttt
420
gagggcctct caccacctgc ctccatggcc ccccaagact gcctggccca gctgcgcctg
480
gcgcaggagg ccgcccaggt gagctcgggc acccgtgtca ggatgcaggg ggtggggccg
540
agctggggtc agagcccagg tccaggcatg cgtgagctct cccacctcct tccttgtgtg
600
tcagccccga gccagctgtt gtcctgctcc ctgggggggc tggtcaggaa cctggggacc
660
cgagcctctg cctccaggga atggcacaaa gcagcaggaa ctgaggtgcc agggaggctg
720
ctgggatggt ggtcg
735

<210> 2678
<211> 170
<212> PRT
<213> Homo sapiens

<400> 2678
```
Leu Ala Ala Leu Ser Ala Ala Trp Gly Arg Asp Gly Gln Val His Gly
 1               5                  10                  15
Pro Ala Cys Val Ser Thr Pro Pro Ser Ala Gly Ala Phe Ser Leu Leu
            20                  25                  30
Arg Glu Asn Phe Ser His Ala Pro Ser Pro Asp Met Ser Ala Ala Ser
```

```
        35                  40                  45
Leu Cys Ala Leu Glu Gln Leu Met Met Ala Gln Ala Gln Glu Cys Val
    50                  55                  60
Phe Glu Gly Leu Ser Pro Pro Ala Ser Met Ala Pro Gln Asp Cys Leu
65                  70                  75                  80
Ala Gln Leu Arg Leu Ala Gln Glu Ala Ala Gln Val Ser Ser Gly Thr
                85                  90                  95
Arg Val Arg Met Gln Gly Val Gly Pro Ser Trp Gly Gln Ser Pro Gly
            100                 105                 110
Pro Gly Met Arg Glu Leu Ser His Leu Leu Pro Cys Val Ser Ala Pro
        115                 120                 125
Ser Gln Leu Leu Ser Cys Ser Leu Gly Gly Leu Val Arg Asn Leu Gly
    130                 135                 140
Thr Arg Ala Ser Ala Ser Arg Glu Trp His Lys Ala Ala Gly Thr Glu
145                 150                 155                 160
Val Pro Gly Arg Leu Leu Gly Trp Trp Ser
                165                 170
```

<210> 2679
<211> 560
<212> DNA
<213> Homo sapiens

<400> 2679
agccgcccca cctcctgttc cattataatc ttattttggt tatgttgata caacacaatc
60
tgtccttcca agtgatcacc ggagtccaga tatttctgtc aagtcagcca accaggaagg
120
ggctgcagac aaagtgcggc aacagggact ccaccaggcc atggagctca tcccacaaga
180
cgcctcaccg cacaggaggg ctgaccccag ggaaacgtgt caccaggaca cagcacgaag
240
ctcaaaaggg gctagcatgc tctgtgcagc tgccagactc tgccctgaag aatcacaggg
300
cactctagtg agcgctgcag cagccagcag gccctggatg gccaggtgtg cagtggggag
360
gcacaggggg tgcaccagga cgcagccaga cctgggccag ttcgcgccga ctcttctcca
420
ttccagaggt ccaggaagca cctgtcaatg tggaagtcag aatgctcagg ccaaataccg
480
agatcaacta actattcagg ttgaaccaga ggcctgggcg ggggcatcca actgcccacc
540
cgtcagactg agggacgcgt
560

<210> 2680
<211> 133
<212> PRT
<213> Homo sapiens

<400> 2680
```
Met Glu Leu Ile Pro Gln Asp Ala Ser Pro His Arg Arg Ala Asp Pro
 1               5                  10                  15
Arg Glu Thr Cys His Gln Asp Thr Ala Arg Ser Ser Lys Gly Ala Ser
```

```
            20                  25                  30
Met Leu Cys Ala Ala Ala Arg Leu Cys Pro Glu Glu Ser Gln Gly Thr
        35                  40                  45
Leu Val Ser Ala Ala Ala Ala Ser Arg Pro Trp Met Ala Arg Cys Ala
    50                  55                  60
Val Gly Arg His Arg Gly Cys Thr Arg Thr Gln Pro Asp Leu Gly Gln
65                  70                  75                  80
Phe Ala Pro Thr Leu Leu His Ser Arg Gly Pro Gly Ser Thr Cys Gln
                85                  90                  95
Cys Gly Ser Gln Asn Ala Gln Ala Lys Tyr Arg Asp Gln Leu Thr Ile
            100                 105                 110
Gln Val Glu Pro Glu Ala Trp Ala Gly Ala Ser Asn Cys Pro Pro Val
        115                 120                 125
Arg Leu Arg Asp Ala
    130
```

<210> 2681
<211> 585
<212> DNA
<213> Homo sapiens

<400> 2681
gattctctag tagccctaat tctacccatc tggctactaa ttcaaacttt cttccttcac
60
atctgtttgt ggacttctcc aatataacta gtatgcctgg gctcattctg cttcttctct
120
tctggaatag tttatttcat gaccatgtgc agaggggtg atggggcaag cctcacaagc
180
cccggaggtc tgtggctgag gtgtaccttg gctttgttgc ctggaactgc tctgactctg
240
ctcttcgctc tttcctgggc tgtgtcacta cagctctgac tcctttccac cttggagttt
300
agcttccctg ccaggaaagc taaggagtag gagttgttct tggaaacaaa tgccgagcga
360
tgtgtctgtg tcatctggcc tcgagaaggt tcttcattct ctgaatctga gagacgtgca
420
ggacaacgtt ccagatttgt tttcagtact aatggttcat ctctttttt ctgttcatcc
480
attttccttt tccctgtttc tgtatcctct ggtaacagct tgtggatttg atcttcagag
540
ggtttttcct cttgtaactt ttcttctctc agctttctca agctt
585

<210> 2682
<211> 116
<212> PRT
<213> Homo sapiens

<400> 2682
```
Met Asp Glu Gln Lys Lys Arg Asp Glu Pro Leu Val Leu Lys Thr Asn
 1               5                  10                  15
Leu Glu Arg Cys Pro Ala Arg Leu Ser Asp Ser Glu Asn Glu Glu Pro
            20                  25                  30
Ser Arg Gly Gln Met Thr Gln Thr His Arg Ser Ala Phe Val Ser Lys
```

```
        35                  40                  45
Asn Asn Ser Tyr Ser Leu Ala Phe Leu Ala Gly Lys Leu Asn Ser Lys
    50                  55                  60
Val Glu Arg Ser Gln Ser Cys Ser Asp Thr Ala Gln Glu Arg Ala Lys
65                  70                  75                  80
Ser Arg Val Arg Ala Val Pro Gly Asn Lys Ala Lys Val His Leu Ser
                85                  90                  95
His Arg Pro Pro Gly Leu Val Arg Leu Ala Pro Ser Pro Pro Leu His
            100                 105                 110
Met Val Met Lys
        115
```

<210> 2683
<211> 498
<212> DNA
<213> Homo sapiens

<400> 2683
nacgcgttac actgactcca aaactctcct tggtggccta ggtgaaacct catggccaac
60
atcacctgga tggccaacca cactggaagg ttggatttca tcctcatggg actcttcaga
120
cgatccaaac atccagctct acttagtgtg gtcatctttg tggttttcct gatggcgttg
180
tctgaaaatg ctgtcctgat ccttctgata cactgtgaca cctacctcca cacccccatg
240
tacttttttca tcagtcaatt gtctctcatg gacatggcgt acatttctgt cactgtgccc
300
aagatgctcc tggaccaggt catgggtgtg aataagatct cagcccctga gtgtgggatg
360
cagatgttcc tctatctgac actagcaggt tcggaatttt tccttctagc caccatggcc
420
tatgaccgct acgtggccat ctgccatcct ctccgttacc ctgtcctcat gaaccatagg
480
gtctgtcttt tcctggca
498

<210> 2684
<211> 149
<212> PRT
<213> Homo sapiens

<400> 2684
```
Met Ala Asn Ile Thr Trp Met Ala Asn His Thr Gly Arg Leu Asp Phe
 1               5                  10                  15
Ile Leu Met Gly Leu Phe Arg Arg Ser Lys His Pro Ala Leu Leu Ser
            20                  25                  30
Val Val Ile Phe Val Val Phe Leu Met Ala Leu Ser Glu Asn Ala Val
        35                  40                  45
Leu Ile Leu Leu Ile His Cys Asp Thr Tyr Leu His Thr Pro Met Tyr
    50                  55                  60
Phe Phe Ile Ser Gln Leu Ser Leu Met Asp Met Ala Tyr Ile Ser Val
65                  70                  75                  80
Thr Val Pro Lys Met Leu Leu Asp Gln Val Met Gly Val Asn Lys Ile
```

```
                85                  90                  95
Ser Ala Pro Glu Cys Gly Met Gln Met Phe Leu Tyr Leu Thr Leu Ala
            100                 105                 110
Gly Ser Glu Phe Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val
        115                 120                 125
Ala Ile Cys His Pro Leu Arg Tyr Pro Val Leu Met Asn His Arg Val
    130                 135                 140
Cys Leu Phe Leu Ala
145
```

<210> 2685
<211> 391
<212> DNA
<213> Homo sapiens

<400> 2685
ngccggctgc acacgctgcc acctgggctg cctcgaaatg tccatgtgct gaaggtcaag
60
cgcaatgagc tggctgccct ggcacgaggg gcgctggcgg gcatggctca gcttcgggaa
120
ctctacctca caggcaaccg actgcgaagc cgggccctgg gcccccgtgc ctgggtggac
180
ctcgcccatc tgcagttgct ggacatcgcc gggaatcagc tcacagagat cccggagggg
240
ctcccccccat cgctggagta tctgtacctg cagaataaca agattagcgc tgttcctgcc
300
agcgcctttg actctactcc caacctcaag gggatctttc tcaggttcaa caagctggct
360
gtgggctccg tagtagaaag cgccttccgg a
391

<210> 2686
<211> 130
<212> PRT
<213> Homo sapiens

<400> 2686
```
Xaa Arg Leu His Thr Leu Pro Pro Gly Leu Pro Arg Asn Val His Val
 1               5                  10                  15
Leu Lys Val Lys Arg Asn Glu Leu Ala Ala Leu Ala Arg Gly Ala Leu
            20                  25                  30
Ala Gly Met Ala Gln Leu Arg Glu Leu Tyr Leu Thr Gly Asn Arg Leu
        35                  40                  45
Arg Ser Arg Ala Leu Gly Pro Arg Ala Trp Val Asp Leu Ala His Leu
    50                  55                  60
Gln Leu Leu Asp Ile Ala Gly Asn Gln Leu Thr Glu Ile Pro Glu Gly
65                  70                  75                  80
Leu Pro Pro Ser Leu Glu Tyr Leu Tyr Leu Gln Asn Asn Lys Ile Ser
                85                  90                  95
Ala Val Pro Ala Ser Ala Phe Asp Ser Thr Pro Asn Leu Lys Gly Ile
            100                 105                 110
Phe Leu Arg Phe Asn Lys Leu Ala Val Gly Ser Val Val Glu Ser Ala
        115                 120                 125
Phe Arg
```

130

<210> 2687
<211> 399
<212> DNA
<213> Homo sapiens

<400> 2687
nagtgcaaga aatgtttaat acaagagatt gaaccctacc aaaatgggag gtttagcctc
60
caggaatggg agtgcaataa atctctaata caagagattg agcctcacca acctccagga
120
tgggaaatga caggtaagac agggactaca aaagaccaag cagacaataa aattcccccc
180
gacagtccgc taggccttat gttaagatac cggaaagata atgaaaggac caaacacaag
240
aaaagacagc aaatgataaa atattgctgg tttatttgga ctaaggaacc catcctgaaa
300
cctttggtct tttggccaca gttagggttg agcggggact ggatatgcca actcctaatc
360
cagtatgtaa aggataaaag tccagtttct caagaggag
399

<210> 2688
<211> 91
<212> PRT
<213> Homo sapiens

<400> 2688
Met Thr Gly Lys Thr Gly Thr Thr Lys Asp Gln Ala Asp Asn Lys Ile
 1   5   10   15
Pro Pro Asp Ser Pro Leu Gly Leu Met Leu Arg Tyr Arg Lys Asp Asn
            20   25   30
Glu Arg Thr Lys His Lys Lys Arg Gln Gln Met Ile Lys Tyr Cys Trp
        35   40   45
Phe Ile Trp Thr Lys Glu Pro Ile Leu Lys Pro Leu Val Phe Trp Pro
    50   55   60
Gln Leu Gly Leu Ser Gly Asp Trp Ile Cys Gln Leu Leu Ile Gln Tyr
65   70   75   80
Val Lys Asp Lys Ser Pro Val Ser Gln Glu Glu
                85   90

<210> 2689
<211> 560
<212> DNA
<213> Homo sapiens

<400> 2689
gcacccattc aagttgggtt agttggcttc tgtttggtgt ttgctacacc cctgtgttgt
60
gccctgtttc ctcagaaaag atacaaaaat gtgggtctca ccaagttgcc caggctggtc
120
tcaaactcct ggcctcaaga aatcctcctg gttcagcctc acaaagctcc gagattacag
180

ttgcatgtct gtgacaagct tggaggccga gttgcaagct aagatccaag agagccatcc
240
tgaattgcga cgcgtgtact tcaataaggg attgtaaagc agggaggaaa cctctgcagc
300
tcattctgcc actgcaaagc tggtgtagcc atgctggtga gaaaaatcct gttcaacctg
360
ggttggtata tcgtctttga aaaacaatga ctataaaagc tacaggaaag gtatttcagg
420
acgtttattg aaggcattgg tggagctctc tgtatgtgtt ttgctctgca gggaactcaa
480
agttggcatt cccgtcacgg atgagaatgg gaaccgcttg ggggagtcgg cgaacgctgc
540
gaaacaagcc atcacgccag
560

<210> 2690
<211> 73
<212> PRT
<213> Homo sapiens

<400> 2690
Ala Pro Ile Gln Val Gly Leu Val Gly Phe Cys Leu Val Phe Ala Thr
1 5 10 15
Pro Leu Cys Cys Ala Leu Phe Pro Gln Lys Arg Tyr Lys Asn Val Gly
20 25 30
Leu Thr Lys Leu Pro Arg Leu Val Ser Asn Ser Trp Pro Gln Glu Ile
35 40 45
Leu Leu Val Gln Pro His Lys Ala Pro Arg Leu Gln Leu His Val Cys
50 55 60
Asp Lys Leu Gly Gly Arg Val Ala Ser
65 70

<210> 2691
<211> 532
<212> DNA
<213> Homo sapiens

<400> 2691
gatctcatct gtacacactt catggatggc atgaatgagc tggcgattgc ttacatcctg
60
caggggtgc tgaaggccct cgactacatc caccacatgg gatatgtaca caggagtgtc
120
aaagccagcc acatcctgat ctctgtggat gggaaggtct acctgtctgg tttgcgcagc
180
aacctcagca tgataagcca tgggcagcgg cagcgagtgg tccacgattt tcccaagtac
240
agtgtcaagg ttctgccgtg gctcagcccc gaggtcctcc agcagaatct ccagggttat
300
gatgccaagt ctgacatcta cagtgtggga atcacagcct gtgaactggc caacggccat
360
gtcccctta aggatatgcc tgccacccag atgctgctag agaaactgaa cggcacagtg
420
ccctgcctgt tggataccag caccatcccc gctgaggagc tgaccatgag ccctcgcgc
480

tcagtggcca actctggcct gagtgacagc ctgaccacca gcacaccccg gg
532

<210> 2692
<211> 177
<212> PRT
<213> Homo sapiens

<400> 2692
Asp Leu Ile Cys Thr His Phe Met Asp Gly Met Asn Glu Leu Ala Ile
1 5 10 15
Ala Tyr Ile Leu Gln Gly Val Leu Lys Ala Leu Asp Tyr Ile His His
20 25 30
Met Gly Tyr Val His Arg Ser Val Lys Ala Ser His Ile Leu Ile Ser
35 40 45
Val Asp Gly Lys Val Tyr Leu Ser Gly Leu Arg Ser Asn Leu Ser Met
50 55 60
Ile Ser His Gly Gln Arg Gln Arg Val Val His Asp Phe Pro Lys Tyr
65 70 75 80
Ser Val Lys Val Leu Pro Trp Leu Ser Pro Glu Val Leu Gln Gln Asn
85 90 95
Leu Gln Gly Tyr Asp Ala Lys Ser Asp Ile Tyr Ser Val Gly Ile Thr
100 105 110
Ala Cys Glu Leu Ala Asn Gly His Val Pro Phe Lys Asp Met Pro Ala
115 120 125
Thr Gln Met Leu Leu Glu Lys Leu Asn Gly Thr Val Pro Cys Leu Leu
130 135 140
Asp Thr Ser Thr Ile Pro Ala Glu Glu Leu Thr Met Ser Pro Ser Arg
145 150 155 160
Ser Val Ala Asn Ser Gly Leu Ser Asp Ser Leu Thr Thr Ser Thr Pro
165 170 175
Arg

<210> 2693
<211> 798
<212> DNA
<213> Homo sapiens

<400> 2693
gcgttccaga atctcaccag ccttgtggtg ctgcatttgc ataacaaccg catccagcat
60
ctggggaccc acagcttcga ggggctgcac aatctggaga cactagacct gaattataac
120
aagctgcagg agttccctgt ggccatccgg accctgggca gactgcagga actggggttc
180
cataacaaca acatcaaggc catcccagaa aaggccttca tggggaaccc tctgctacag
240
acgatacact tttatgataa cccaatccag tttgtgggaa gatcggcatt ccagtacctg
300
cctaaactcc acacactatc tctgaatggt gccatggaca tccaggagtt tccagatctc
360
aaaggcacca ccagcctgga gatcctgacc ctgacccgcg caggcatccg gctgctccca
420

tcggggatgt gccaacagct gcccaggctc cgagtcctgg aactgtctca caatcaaatt
480
gaggagctgc ccagcctgca caggtgtcag aaattggagg aaatcggcct ccaacacaac
540
cgcatctggg aaattggagc tgacaccttc agccagctga gctccctgca agccctggat
600
ttaaggtgga acgccatccg gtccatccac cccgaggcct tctccaccct gcactccctg
660
gtcaagctgg acctgacaga caaccagctg accacactgc ccctggctgg acttgggggc
720
ttgatgcatc tgaagctcaa agggaacctt gctctctccc aggccttctc caaggacagt
780
ttcccaaaac tgaggatc
798

<210> 2694
<211> 266
<212> PRT
<213> Homo sapiens

<400> 2694
Ala Phe Gln Asn Leu Thr Ser Leu Val Val Leu His Leu His Asn Asn
1 5 10 15
Arg Ile Gln His Leu Gly Thr His Ser Phe Glu Gly Leu His Asn Leu
20 25 30
Glu Thr Leu Asp Leu Asn Tyr Asn Lys Leu Gln Glu Phe Pro Val Ala
35 40 45
Ile Arg Thr Leu Gly Arg Leu Gln Glu Leu Gly Phe His Asn Asn Asn
50 55 60
Ile Lys Ala Ile Pro Glu Lys Ala Phe Met Gly Asn Pro Leu Leu Gln
65 70 75 80
Thr Ile His Phe Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala
85 90 95
Phe Gln Tyr Leu Pro Lys Leu His Thr Leu Ser Leu Asn Gly Ala Met
100 105 110
Asp Ile Gln Glu Phe Pro Asp Leu Lys Gly Thr Thr Ser Leu Glu Ile
115 120 125
Leu Thr Leu Thr Arg Ala Gly Ile Arg Leu Leu Pro Ser Gly Met Cys
130 135 140
Gln Gln Leu Pro Arg Leu Arg Val Leu Glu Leu Ser His Asn Gln Ile
145 150 155 160
Glu Glu Leu Pro Ser Leu His Arg Cys Gln Lys Leu Glu Glu Ile Gly
165 170 175
Leu Gln His Asn Arg Ile Trp Glu Ile Gly Ala Asp Thr Phe Ser Gln
180 185 190
Leu Ser Ser Leu Gln Ala Leu Asp Leu Arg Trp Asn Ala Ile Arg Ser
195 200 205
Ile His Pro Glu Ala Phe Ser Thr Leu His Ser Leu Val Lys Leu Asp
210 215 220
Leu Thr Asp Asn Gln Leu Thr Thr Leu Pro Leu Ala Gly Leu Gly Gly
225 230 235 240
Leu Met His Leu Lys Leu Lys Gly Asn Leu Ala Leu Ser Gln Ala Phe
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Ser Lys Asp Ser Phe Pro Lys Leu Arg Ile

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<210> 2695
<211> 2265
<212> DNA
<213> Homo sapiens

<400> 2695
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2265

<210> 2696
<211> 663
<212> PRT
<213> Homo sapiens

<400> 2696
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Ala Val Cys Val Leu Gly Thr Leu Thr Gln Leu Asp Ile Cys Ser Ser
20 25 30
Ala Pro Glu Asp Cys Thr Ser Phe Ser Ile Asn Ala Ser Pro Gly Val
35 40 45
Val Val Asp Ile Ala His Ser Pro Pro Ala Lys Lys Lys Ser Thr Gly
50 55 60
Ser Ser Thr Trp Pro Leu Asp Pro Gly Val Glu Val Thr Leu Thr Met
65 70 75 80
Lys Ala Ala Ser Gly Ser Thr Gly Asp Gln Lys Val Gln Ile Ser Tyr
85 90 95
Tyr Gly Pro Lys Thr Pro Pro Val Lys Ala Leu Leu Tyr Leu Thr Ala
100 105 110
Val Glu Ile Ser Leu Cys Ala Asp Ile Thr Arg Thr Gly Lys Val Lys
115 120 125
Pro Thr Arg Ala Val Lys Asp Gln Arg Thr Trp Thr Trp Gly Pro Cys

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    130                 135                 140
Gly Gln Gly Ala Ile Leu Leu Val Asn Cys Asp Arg Asp Asn Leu Glu
145                 150                 155                 160
Ser Ser Ala Met Asp Cys Glu Asp Asp Glu Val Leu Asp Ser Glu Asp
                165                 170                 175
Leu Gln Asp Met Ser Leu Met Thr Leu Ser Thr Lys Thr Pro Lys Asp
            180                 185                 190
Phe Phe Thr Asn His Thr Leu Val Leu His Val Ala Arg Ser Glu Met
        195                 200                 205
Asp Lys Val Arg Val Phe Gln Ala Thr Arg Gly Lys Leu Ser Ser Lys
    210                 215                 220
Cys Ser Val Val Leu Gly Pro Lys Trp Pro Ser His Tyr Leu Met Val
225                 230                 235                 240
Pro Gly Gly Lys His Asn Met Asp Phe Tyr Val Glu Ala Leu Ala Phe
                245                 250                 255
Pro Asp Thr Asp Phe Pro Gly Leu Ile Thr Leu Thr Ile Ser Leu Leu
            260                 265                 270
Asp Thr Ser Asn Leu Glu Leu Pro Glu Ala Val Val Phe Gln Asp Ser
        275                 280                 285
Val Val Phe Arg Val Ala Pro Trp Ile Met Thr Pro Asn Thr Gln Pro
    290                 295                 300
Pro Gln Glu Val Tyr Ala Cys Ser Ile Phe Glu Asn Glu Asp Phe Leu
305                 310                 315                 320
Lys Ser Val Thr Thr Leu Ala Met Lys Ala Lys Cys Lys Leu Thr Ile
                325                 330                 335
Cys Pro Glu Glu Glu Asn Met Asp Asp Gln Trp Met Gln Asp Glu Met
            340                 345                 350
Glu Ile Gly Tyr Ile Gln Ala Pro His Lys Thr Leu Pro Val Val Phe
        355                 360                 365
Asp Ser Pro Arg Asn Arg Gly Leu Lys Glu Phe Pro Ile Lys Arg Val
    370                 375                 380
Met Gly Pro Asp Phe Gly Tyr Val Thr Arg Gly Pro Gln Thr Gly Gly
385                 390                 395                 400
Ile Ser Gly Leu Asp Ser Phe Gly Asn Leu Glu Val Ser Pro Pro Val
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Thr Val Arg Gly Lys Glu Tyr Pro Leu Gly Arg Ile Leu Phe Gly Asp
            420                 425                 430
Ser Cys Tyr Pro Ser Asn Asp Ser Arg Gln Met His Gln Ala Leu Gln
        435                 440                 445
Asp Phe Leu Ser Ala Gln Gln Val Gln Ala Pro Val Lys Leu Tyr Ser
    450                 455                 460
Asp Trp Leu Ser Val Gly His Val Asp Glu Phe Leu Ser Phe Val Pro
465                 470                 475                 480
Ala Pro Asp Arg Lys Gly Phe Arg Leu Leu Leu Ala Ser Pro Arg Ser
                485                 490                 495
Cys Tyr Lys Leu Phe Gln Glu Gln Gln Asn Glu Gly His Gly Glu Ala
            500                 505                 510
Leu Leu Phe Glu Gly Ile Lys Lys Lys Lys Gln Gln Lys Ile Lys Asn
        515                 520                 525
Ile Leu Ser Asn Lys Thr Leu Arg Glu His Asn Ser Phe Val Glu Arg
    530                 535                 540
Cys Ile Asp Trp Asn Arg Glu Leu Leu Lys Arg Glu Leu Gly Leu Ala
545                 550                 555                 560
Glu Ser Asp Ile Ile Asp Ile Pro Gln Leu Phe Lys Leu Lys Glu Phe
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                565                 570                 575
Ser Lys Ala Glu Ala Phe Phe Pro Asn Met Val Asn Met Leu Val Leu
            580                 585                 590
Gly Lys His Leu Gly Ile Pro Lys Pro Phe Gly Pro Val Ile Asn Gly
        595                 600                 605
Arg Cys Cys Leu Glu Glu Lys Val Cys Ser Leu Leu Glu Pro Leu Gly
    610                 615                 620
Leu Gln Cys Thr Phe Ile Asn Asp Phe Phe Thr Tyr His Ile Arg His
625                 630                 635                 640
Gly Glu Val His Cys Gly Thr Asn Val Arg Arg Lys Pro Phe Ser Phe
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Lys Trp Trp Asn Met Val Pro
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<210> 2697
<211> 2468
<212> DNA
<213> Homo sapiens

<400> 2697

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gtaactgacc ccaggaacat tctgttaacc aacgaacaac tcgagagtgc gagaaaaata
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480
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960
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1020
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<210> 2698
<211> 332
<212> PRT

<213> Homo sapiens

<400> 2698

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            20                  25                  30
Gly Arg Ala Asn His Phe Phe Thr Val Thr Asp Pro Arg Asn Ile Leu
        35                  40                  45
Leu Thr Asn Glu Gln Leu Glu Ser Ala Arg Lys Ile Val His Asp Tyr
    50                  55                  60
Arg Gln Gly Ile Val Pro Pro Gly Leu Thr Glu Asn Glu Leu Trp Arg
65                  70                  75                  80
Ala Lys Tyr Ile Tyr Asp Ser Ala Phe His Pro Asp Thr Gly Glu Lys
                85                  90                  95
Met Ile Leu Ile Gly Arg Met Ser Ala Gln Val Pro Met Asn Met Thr
            100                 105                 110
Ile Thr Gly Cys Met Met Thr Phe Tyr Arg Thr Thr Pro Ala Val Leu
        115                 120                 125
Phe Trp Gln Trp Ile Asn Gln Ser Phe Asn Ala Val Val Asn Tyr Thr
    130                 135                 140
Asn Arg Ser Gly Asp Ala Pro Leu Thr Val Asn Glu Leu Gly Thr Ala
145                 150                 155                 160
Tyr Val Ser Ala Thr Thr Gly Ala Val Ala Thr Ala Leu Gly Leu Asn
                165                 170                 175
Ala Leu Thr Lys His Val Ser Pro Leu Ile Gly Arg Phe Val Pro Phe
            180                 185                 190
Ala Ala Val Ala Ala Ala Asn Cys Ile Asn Ile Pro Leu Met Arg Gln
        195                 200                 205
Arg Glu Leu Lys Val Gly Ile Pro Val Thr Asp Glu Asn Gly Asn Arg
    210                 215                 220
Leu Gly Glu Ser Ala Asn Ala Ala Lys Gln Ala Ile Thr Gln Val Val
225                 230                 235                 240
Val Ser Arg Ile Leu Met Ala Ala Pro Gly Met Ala Ile Pro Pro Phe
                245                 250                 255
Ile Met Asn Thr Leu Glu Lys Lys Ala Phe Leu Lys Arg Phe Pro Trp
            260                 265                 270
Met Ser Ala Pro Ile Gln Val Gly Leu Val Gly Phe Cys Leu Val Phe
        275                 280                 285
Ala Thr Pro Leu Cys Cys Ala Leu Phe Pro Gln Lys Ser Ser Met Ser
    290                 295                 300
Val Thr Ser Leu Glu Ala Glu Leu Gln Ala Lys Ile Gln Glu Ser His
305                 310                 315                 320
Pro Glu Leu Arg Arg Val Tyr Phe Asn Lys Gly Leu
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<210> 2699
<211> 974
<212> DNA
<213> Homo sapiens

<400> 2699

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aaaaaaaaaa aaaa
974

<210> 2700
<211> 177
<212> PRT
<213> Homo sapiens

<400> 2700
Met Pro Leu Pro Asp Thr Met Phe Cys Ala Gln Gln Ile His Ile Pro
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Pro Glu Leu Pro Asp Ile Leu Lys Gln Phe Thr Lys Ala Ala Ile Arg
20 25 30
Thr Gln Pro Ala Asp Val Leu Arg Trp Ser Ala Gly Tyr Phe Ser Ala
35 40 45
Leu Ser Arg Gly Asp Pro Leu Pro Val Lys Asp Arg Met Glu Met Pro
50 55 60
Val Ala Thr Gln Lys Thr Asp Thr Gly Leu Thr Gln Gly Leu Leu Lys
65 70 75 80
Val Leu His Lys Gln Cys His His Lys Arg Tyr Val Glu Leu Thr Asp
85 90 95
Leu Glu Gln Lys Trp Lys Asn Leu Cys Leu Pro Lys Glu Lys Phe Lys
100 105 110
Ala Leu Leu Gln Leu Asp Pro Cys Glu Asn Lys Ile Lys Trp Ile Asn

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        115                 120                 125
Phe Leu Ala Leu Gly Cys Ser Met Leu Gly Gly Ser Leu Asn Thr Ala
    130                 135                 140
Leu Lys His Leu Cys Glu Ile Leu Thr Asp Asp Pro Glu Ala Gly Pro
145                 150                 155                 160
Leu Ala Ser Pro Ser Arg Arg Phe Pro Thr Phe Thr Ala Thr Trp Pro
                165                 170                 175
Asp
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<210> 2701
<211> 646
<212> DNA
<213> Homo sapiens

<400> 2701
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120
agcacactga gaggatgatt taagaaaaac tggctgggca cggtgtccca tgcctgtaat
180
cccagcactt tgggaggcca aaatgccagc agctcttcct tgccagagat gatctgaccc
240
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300
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360
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420
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480
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540
ctggagagag atcgattgaa atacgaatcc cagaaatcta aatccagcag cgtggctgtc
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646

<210> 2702
<211> 92
<212> PRT
<213> Homo sapiens

<400> 2702
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Leu Gly Pro Gly Asp Gln Glu Ser Arg Trp Lys Gln Tyr Leu Glu Asp
            20                  25                  30
Glu Arg Ile Ala Leu Phe Leu Gln Asn Glu Glu Phe Met Lys Glu Leu
        35                  40                  45
Gln Arg Asn Arg Asp Phe Leu Leu Ala Leu Glu Arg Asp Arg Leu Lys
    50                  55                  60
Tyr Glu Ser Gln Lys Ser Lys Ser Ser Ser Val Ala Val Gly Asn Asp
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65 70 75 80
Phe Gly Phe Ser Ser Pro Val Pro Gly Thr Gly Asp
85 90

<210> 2703
<211> 610
<212> DNA
<213> Homo sapiens

<400> 2703
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120
ataaaatgca aaccacccct ctgtagcaac tcacccatct gcatcgcccg tgaatgttcg
180
ggcccttggg gaaaagggct cttgccccca gaaggaacct tgctcccaag gcctttgctg
240
ggggaggggc ccaaagggga ggcctccaag ttcccctctt tctttgatct ttctcttgtc
300
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360
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420
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480
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<210> 2704
<211> 108
<212> PRT
<213> Homo sapiens

<400> 2704
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Lys Ala Ile Lys Ala Gly Ile Lys Cys Lys Pro Pro Leu Cys Ser Asn
35 40 45
Ser Pro Ile Cys Ile Ala Arg Glu Cys Ser Gly Pro Trp Gly Lys Gly
50 55 60
Leu Leu Pro Pro Glu Gly Thr Leu Leu Pro Arg Pro Leu Leu Gly Glu
65 70 75 80
Gly Pro Lys Gly Glu Ala Ser Lys Phe Pro Leu Phe Phe Asp Leu Ser
85 90 95
Leu Val His Leu Pro Gln Ala His Pro Ala Ala Ser
100 105

<210> 2705
<211> 843
<212> DNA
<213> Homo sapiens

<400> 2705
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120
gacatcaaca tccaggaacc tcgctgggac caaagtactt tcctgggcag agcccggcac
180
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420
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720
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<213> Homo sapiens

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Thr Val Thr Asp Pro Arg Asn Leu Leu Leu Ser Gly Ala Gln Leu Glu
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Ala Ser Arg Asn Ile Val Gln Asn Tyr Arg Ala Gly Val Val Thr Pro
    50   55   60
Gly Ile Thr Glu Asp Gln Leu Trp Arg Ala Lys Tyr Val Tyr Asp Ser
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Ala Phe His Pro Asp Thr Gly Glu Lys Val Val Leu Ile Gly Arg Met

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Phe Tyr Arg Lys Thr Pro Thr Val Val Phe Trp Gln Trp Val Asn Gln
        115                 120                 125
Ser Phe Asn Ala Ile Val Asn Tyr Ser Asn Arg Ser Gly Asp Thr Pro
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Ile Thr Val Arg Gln Leu Gly Thr Ala Tyr Val Ser Ala Thr Thr Gly
145                 150                 155                 160
Ala Val Ala Thr Ala Leu Gly Leu Lys Ser Leu Thr Lys His Leu Pro
                165                 170                 175
Pro Leu Val Gly Arg Phe Val Pro Phe Ala Ala Val Ala Ala Ala Asn
            180                 185                 190
Cys Ile Asn Ile Pro Leu Met Arg Gln Arg Glu Leu Gln Val Gly Ile
        195                 200                 205
Pro Val Thr Asp Glu Ala Gly Gln Arg Leu Gly His Ser Val Thr Ala
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        35   40   45
Pro Phe Asp Phe Arg Arg Phe Asp Ile Tyr Arg Lys Val Pro Lys Asp
    50   55   60
Leu Thr Gln Pro Thr Tyr Thr Gly Ala Ile Ile Ser Ile Cys Cys Cys
65   70   75   80
Leu Phe Ile Leu Phe Leu Phe Leu Ser Glu Leu Thr Gly Phe Ile Thr
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Thr Glu Val Val Asn Glu Leu Tyr Val Asp Asp Pro Asp Lys Asp Ser
            100   105   110
Gly Gly Lys Ile Asp Val Ser Leu Asn Ile Ser Leu Pro Asn Leu His
        115   120   125
Cys Glu Leu Val Gly Leu Asp Ile Gln Asp Glu Met Gly Arg His Glu
    130   135   140
Val Gly His Ile Asp Asn Ser Met Lys Ile Pro Leu Asn Asn Gly Ala
145   150   155   160
Gly Cys Arg Phe Glu Gly Gln Phe Ser Ile Asn Lys Val Pro Gly Asn
                165   170   175
Phe His Val Ser Thr His Ser Ala Thr Ala Gln Pro Gln Asn Pro Asp
            180   185   190
Met Thr His Val Ile His Lys Leu Ser Phe Gly Asp Thr Leu Gln Val
        195   200   205
Gln Asn Ile His Gly Ala Phe Asn Ala Leu Gly Gly Ala Asp Arg Leu
    210   215   220
Thr Ser Asn Pro Leu Ala Ser His Asp Tyr Ile Leu Lys Ile Val Pro

225 230 235 240
Thr Val Tyr Glu Asp Lys Ser Gly Lys Gln Arg Tyr Ser Tyr Gln Tyr
245 250 255
Thr Val Ala Asn Lys Glu Tyr Val Ala Tyr Ser His Thr Gly Arg Ile
260 265 270
Ile Pro Ala Ile Trp Phe Arg Tyr Asp Leu Ser Pro Ile Thr Val Lys
275 280 285
Tyr Thr Glu Arg Arg Gln Pro Leu Tyr Arg Phe Ile Thr Thr Ile Cys
290 295 300
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Ala Ser Gly Gln Ala Lys Ser Ser Ser Lys Glu Ser Lys Asp Ser Lys
50 55 60
Thr Ser Ser Lys Asp Asp Lys Gly Ser Thr Ser Ser Thr Ser Gly Ser
65 70 75 80
Ser Gly Ser Ser Thr Lys Asn Ile Trp Val Ser Gly Leu Ser Ser Asn
85 90 95
Thr Lys Ala Ala Asp Leu Lys Asn Leu Phe Gly Lys Tyr Gly Lys Val
100 105 110
Leu Ser Ala Lys Val Val Thr Asn Ala Arg Ser Pro Gly Ala Lys Cys
115 120 125
Tyr Gly Ile Val Thr Met Ser Ser Ser Thr Glu Val Ser Arg Cys Ile
130 135 140
Ala His Leu His Arg Thr Glu Leu His Gly Gln Leu Ile Ser Val Glu
145 150 155 160
Lys Val Lys Gly Asp Pro Ser Lys Lys Glu Met Lys Lys Glu Asn Asp
165 170 175
Glu Lys Ser Ser Ser Arg Ser Ser Gly Asp Lys Lys Asn Thr Ser Asp
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Arg Ser Ser Lys Thr Gln Ala Ser Val Lys Lys Glu Glu Lys Arg Ser
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6420
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<211> 2096
<212> PRT

<213> Homo sapiens

<400> 2712

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Arg Lys Ile Gln His Val Lys Asn Glu Leu Cys His Met Leu Ser Leu
        35                  40                  45
Glu Glu Val Ala Pro Val Leu Gln Gln Thr Leu Leu Gln Asp Asn Leu
    50                  55                  60
Leu Gly Arg Val His Phe Asp Gln Phe Lys Glu Ala Leu Ile Leu Ile
65                  70                  75                  80
Leu Ser Arg Thr Leu Ser Asp Glu Glu His Phe Gln Glu Pro Asp Cys
                85                  90                  95
Ser Leu Glu Ala Gln Pro Arg Tyr Val Arg Gly Glu Lys Pro Tyr Gly
            100                 105                 110
Arg Arg Ser Leu Pro Glu Phe Gln Glu Ser Val Glu Glu Phe Pro Glu
        115                 120                 125
Val Thr Val Ile Glu Pro Leu Asp Glu Glu Ala Arg Pro Ser His Ile
    130                 135                 140
Pro Ala Gly Asp Cys Ser Glu His Trp Lys Thr Gln Arg Ser Glu Glu
145                 150                 155                 160
Tyr Glu Ala Glu Gly Gln Leu Arg Phe Trp Asn Pro Asp Asp Leu Asn
                165                 170                 175
Ala Ser Gln Ser Gly Ser Ser Pro Pro Gln Asp Trp Ile Glu Glu Lys
            180                 185                 190
Leu Gln Gln Val Cys Glu Asp Leu Gly Ile Thr Pro Asp Gly His Leu
        195                 200                 205
Asn Arg Lys Lys Leu Val Ser Ile Cys Glu Gln Tyr Gly Leu Gln Asn
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Val Asp Gly Glu Met Leu Glu Glu Val Phe His Asn Leu Asp Pro Asp
225                 230                 235                 240
Gly Thr Met Ser Val Glu Asp Phe Phe Tyr Gly Leu Phe Lys Asn Gly
                245                 250                 255
Lys Ser Leu Thr Pro Ser Ala Ser Thr Pro Tyr Arg Gln Leu Lys Arg
            260                 265                 270
His Leu Ser Met Gln Ser Phe Asp Glu Ser Gly Arg Arg Thr Thr Thr
        275                 280                 285
Ser Ser Ala Thr Thr Ser Thr Ile Gly Phe Arg Val Phe Ser Cys Leu
    290                 295                 300
Asp Asp Gly Met Gly His Ala Ser Val Glu Arg Ile Leu Asp Thr Trp
305                 310                 315                 320
Gln Glu Glu Gly Ile Glu Asn Ser Gln Glu Ile Leu Lys Ala Leu Asp
                325                 330                 335
Phe Ser Leu Asp Gly Asn Ile Asn Leu Thr Glu Leu Thr Leu Ala Leu
            340                 345                 350
Glu Asn Glu Leu Leu Val Thr Lys Asn Ser Ile His Gln Ala Ala Leu
        355                 360                 365
Ala Ser Phe Lys Ala Glu Ile Arg His Leu Leu Glu Arg Val Asp Gln
    370                 375                 380
Val Val Arg Glu Lys Arg Ser Tyr Gly Arg Ile Trp Thr Ala Glu Lys
385                 390                 395                 400
Leu Lys Ser Leu Met Ala Ser Glu Val Asp Asp His Asp Ala Ala Ile
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                405                 410                 415
Glu Arg Arg Asn Glu Tyr Asn Leu Arg Lys Leu Asp Glu Glu Tyr Lys
            420                 425                 430
Glu Arg Ile Ala Ala Leu Lys Asn Glu Leu Arg Lys Glu Arg Glu Gln
        435                 440                 445
Ile Leu Gln Gln Ala Gly Lys Gln Arg Leu Glu Leu Glu Gln Glu Ile
    450                 455                 460
Glu Lys Ala Lys Thr Glu Glu Asn Tyr Ile Arg Asp Arg Leu Ala Leu
465                 470                 475                 480
Ser Leu Lys Glu Asn Ser Arg Leu Glu Asn Glu Leu Leu Glu Asn Ala
                485                 490                 495
Glu Lys Leu Ala Glu Tyr Glu Asn Leu Thr Asn Lys Leu Gln Arg Asn
            500                 505                 510
Leu Glu Asn Val Leu Ala Glu Lys Phe Gly Asp Leu Asp Pro Ser Ser
        515                 520                 525
Ala Glu Phe Phe Leu Gln Glu Glu Arg Leu Thr Gln Met Arg Asn Glu
    530                 535                 540
Tyr Glu Arg Gln Cys Arg Val Leu Gln Asp Gln Val Asp Glu Leu Gln
545                 550                 555                 560
Ser Glu Leu Glu Glu Tyr Arg Ala Gln Gly Arg Val Leu Arg Leu Pro
                565                 570                 575
Leu Lys Asn Ser Pro Ser Glu Glu Val Glu Ala Asn Ser Gly Gly Ile
            580                 585                 590
Glu Pro Glu His Gly Leu Gly Ser Glu Glu Cys Asn Pro Leu Asn Met
        595                 600                 605
Ser Ile Glu Ala Glu Leu Val Ile Glu Gln Met Lys Glu Gln His His
    610                 615                 620
Arg Asp Ile Cys Cys Leu Arg Leu Glu Leu Glu Asp Lys Val Arg His
625                 630                 635                 640
Tyr Glu Lys Gln Leu Asp Glu Thr Val Val Ser Cys Lys Lys Ala Gln
                645                 650                 655
Glu Asn Met Lys Gln Arg His Glu Asn Glu Thr His Thr Leu Glu Glu
            660                 665                 670
Gln Ile Ser Asp Leu Lys Met Lys Ile Ala Glu Leu Gln Gly Gln Ala
        675                 680                 685
Ala Val Leu Lys Glu Ala His His Glu Ala Thr Cys Arg His Glu Glu
    690                 695                 700
Glu Lys Lys Gln Leu Gln Val Lys Leu Glu Glu Glu Lys Thr His Leu
705                 710                 715                 720
Gln Glu Lys Leu Arg Leu Gln His Glu Met Glu Leu Lys Ala Arg Leu
                725                 730                 735
Thr Gln Ala Gln Ala Ser Phe Gly Arg Glu Arg Glu Gly Leu Gln Ser
            740                 745                 750
Ser Ala Trp Thr Glu Glu Lys Val Arg Gly Leu Thr Gln Glu Leu Glu
        755                 760                 765
Gln Phe His Gln Glu Gln Leu Thr Ser Leu Val Glu Lys His Thr Leu
    770                 775                 780
Glu Lys Glu Glu Leu Arg Lys Glu Leu Leu Glu Lys His Gln Arg Glu
785                 790                 795                 800
Leu Gln Glu Gly Arg Glu Lys Met Glu Thr Glu Cys Asn Arg Arg Thr
                805                 810                 815
Ser Gln Ile Glu Ala Gln Phe Gln Ser Asp Cys Gln Lys Val Thr Glu
            820                 825                 830
Arg Cys Glu Ser Ala Leu Gln Ser Leu Glu Gly Arg Tyr Arg Gln Glu
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        835                 840                 845
Leu Lys Asp Leu Gln Glu Gln Gln Arg Glu Glu Lys Ser Gln Trp Glu
    850                 855                 860
Phe Glu Lys Asp Glu Leu Thr Gln Glu Cys Ala Glu Ala Gln Glu Leu
870                 875                 880
Leu Lys Glu Thr Leu Lys Arg Glu Lys Thr Thr Ser Leu Val Leu Thr
                885                 890                 895
Gln Glu Arg Glu Met Leu Glu Lys Thr Tyr Lys Asp His Leu Asn Ser
            900                 905                 910
Met Val Val Glu Arg Gln Gln Leu Leu Gln Asp Leu Glu Asp Leu Arg
        915                 920                 925
Asn Val Ser Glu Thr Gln Gln Ser Leu Leu Ser Asp Gln Ile Leu Glu
    930                 935                 940
Leu Lys Ser Ser His Lys Arg Glu Leu Arg Glu Arg Glu Glu Val Leu
945                 950                 955                 960
Cys Gln Gln Gly Val Ser Glu Gln Leu Ala Ser Gln Arg Leu Glu Arg
                965                 970                 975
Leu Glu Met Glu His Asp Gln Glu Arg Gln Glu Met Met Ser Lys Leu
            980                 985                 990
Leu Ala Met Glu Asn Ile His Lys Ala Thr Cys Glu Thr Ala Asp Arg
        995                 1000                1005
Glu Arg Ala Glu Met Ser Thr Glu Ile Ser Arg Leu Gln Ser Lys Ile
    1010                1015                1020
Lys Glu Met Gln Gln Ala Thr Ser Pro Leu Ser Met Leu Gln Ser Gly
1025                1030                1035                1040
Cys Gln Val Ile Gly Glu Glu Glu Val Glu Gly Asp Gly Ala Leu Ser
                1045                1050                1055
Leu Leu Gln Lys Gly Glu Gln Leu Leu Glu Glu Asn Gly Asp Val Leu
            1060                1065                1070
Leu Ser Leu Gln Arg Ala His Glu Gln Ala Val Lys Glu Asn Val Lys
        1075                1080                1085
Met Ala Thr Glu Ile Ser Arg Leu Gln Gln Arg Leu Gln Lys Leu Glu
    1090                1095                1100
Pro Gly Leu Val Met Ser Ser Cys Leu Asp Glu Pro Ala Thr Glu Phe
1105                1110                1115                1120
Phe Gly Asn Thr Ala Glu Gln Thr Glu Pro Phe Leu Gln Gln Asn Arg
                1125                1130                1135
Thr Lys Gln Val Glu Gly Val Thr Arg Arg His Val Leu Ser Asp Leu
            1140                1145                1150
Glu Asp Asp Glu Val Arg Asp Leu Gly Ser Thr Gly Thr Ser Ser Val
        1155                1160                1165
Gln Arg Gln Glu Val Lys Ile Glu Glu Ser Glu Ala Ser Val Glu Gly
    1170                1175                1180
Phe Ser Glu Leu Glu Asn Ser Glu Glu Thr Arg Thr Glu Ser Trp Glu
1185                1190                1195                1200
Leu Lys Asn His Ile Ser Leu Leu Gln Glu Gln Leu Met Met Phe Cys
                1205                1210                1215
Ala Asp Cys Asp Leu Ala Ser Glu Lys Lys Gln Glu Leu Leu Phe Asp
            1220                1225                1230
Val Ser Val Leu Lys Lys Lys Leu Lys Ile Leu Glu Arg Ile Pro Glu
        1235                1240                1245
Ala Ser Pro Arg Tyr Lys Leu Leu Tyr Glu Asp Val Ser Arg Glu Asn
    1250                1255                1260
Asp Cys Leu Gln Glu Glu Leu Glu Met Met Glu Thr Arg Tyr Asp Glu
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1265 1270 1275 1280
Ala Leu Glu Asn Asn Lys Glu Leu Thr Ala Glu Val Phe Arg Leu Gln
1285 1290 1295
Asp Glu Leu Lys Lys Met Glu Glu Val Thr Glu Thr Phe Leu Ser Leu
1300 1305 1310
Glu Lys Ser Tyr Asp Glu Val Lys Ile Glu Asn Glu Glu Leu Asn Val
1315 1320 1325
Leu Val Leu Arg Leu Gln Gly Lys Ile Glu Lys Leu Xaa Thr Arg Ala
1330 1335 1340
Trp Ser Ser Gly Val Thr Ala Ala Tyr Gly Lys Xaa Ser Leu Glu Asn
1345 1350 1355 1360
Leu Glu Ile Glu Pro Asp Gly Asn Ile Leu Gln Leu Asn Gln Thr Leu
1365 1370 1375
Glu Glu Cys Val Pro Arg Val Arg Ser Val His His Val Ile Glu Glu
1380 1385 1390
Cys Lys Gln Glu Asn Gln Tyr Leu Glu Gly Asn Thr Gln Leu Leu Glu
1395 1400 1405
Lys Val Lys Ala His Glu Ile Ala Trp Leu His Gly Thr Ile Gln Thr
1410 1415 1420
His Gln Glu Arg Pro Arg Val Gln Asn Gln Val Ile Leu Glu Glu Asn
1425 1430 1435 1440
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1445 1450 1455
Ile Ala Glu Leu Glu Leu Glu Lys Thr Lys Leu Gln Glu Leu Thr Arg
1460 1465 1470
Lys Leu Lys Glu Arg Val Pro Ile Leu Val Lys Gln Lys Asp Val Leu
1475 1480 1485
Ser Pro Gly Lys Lys Glu Glu Glu Leu Lys Ala Met Met His Asp Leu
1490 1495 1500
Gln Ile Pro Cys Ser Glu Met Gln Gln Lys Val Glu Leu Leu Lys Tyr
1505 1510 1515 1520
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1525 1530 1535
Thr Thr Leu Asn Glu Glu Asp Ser Ile Ser Asn Leu Lys Leu Gly Thr
1540 1545 1550
Leu Asn Gly Ser Gln Glu Glu Met Trp Gln Lys Thr Glu Ser Val Lys
1555 1560 1565
Gln Glu Asn Ala Ala Val Leu Lys Met Val Glu Asn Leu Lys Lys Gln
1570 1575 1580
Ile Ser Glu Leu Lys Ile Lys Asn Gln Gln Leu Asp Leu Glu Asn Thr
1585 1590 1595 1600
Glu Leu Ser Gln Lys Asn Ser Pro Asn Gln Glu Lys Leu Gln Glu Leu
1605 1610 1615
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1620 1625 1630
Asn Ser Ala Leu Glu Glu Arg Glu Gln Glu Lys Phe Asn Leu Lys Glu
1635 1640 1645
Glu Pro Glu Arg Cys Lys Val Gln Ser Ser Thr Leu Val Ser Ser Leu
1650 1655 1660
Glu Ala Glu Leu Ser Glu Val Lys Ile Gln Thr His Ile Val Gln Gln
1665 1670 1675 1680
Glu Asn Pro Leu Leu Gln Asp Glu Leu Glu Lys Met Lys Gln Leu His
1685 1690 1695
Arg Cys Pro Asp Leu Ser Asn Phe Gln Gln Lys Ile Ser Ser Val Leu

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            1700                1705                1710
Ser Tyr Asn Glu Lys Leu Leu Lys Glu Lys Glu Ala Leu Ser Glu Glu
        1715                1720                1725
Leu Asn Ser Cys Val Asp Lys Leu Ala Lys Ser Ser Leu Leu Glu His
    1730                1735                1740
Arg Ile Ala Thr Met Lys Gln Glu Gln Lys Ser Trp Glu His Gln Ser
1745                1750                1755                1760
Ala Ser Leu Lys Thr Gln Leu Val Ala Ser Gln Glu Lys Val Gln Asn
                1765                1770                1775
Leu Glu Asp Thr Val Gln Asn Val Asn Leu Gln Met Ser Arg Met Lys
            1780                1785                1790
Ser Asp Pro Arg Val Thr Gln Gln Glu Lys Glu Ala Leu Lys Gln Glu
        1795                1800                1805
Val Met Pro Leu His Lys Gln Leu Gln Asn Ser Val Xaa Lys Ser Trp
    1810                1815                1820
Ala Pro Glu Ile Ala Thr His Pro Ser Gly Leu His Asn Gln Gln Lys
1825                1830                1835                1840
Arg Leu Ser Trp Asp Lys Leu Asp His Leu Met Asn Glu Glu Gln Gln
                1845                1850                1855
Leu Leu Trp Gln Glu Asn Glu Arg Leu Gln Thr Met Val Gln Asn Thr
            1860                1865                1870
Lys Ala Glu Leu Thr His Ser Arg Glu Lys Val Arg Gln Leu Glu Ser
        1875                1880                1885
Asn Leu Leu Pro Lys His Gln Lys His Leu Asn Pro Ser Gly Thr Met
    1890                1895                1900
Asn Pro Thr Glu Gln Glu Lys Leu Ser Leu Lys Arg Glu Cys Asp Gln
1905                1910                1915                1920
Phe Gln Lys Glu Gln Ser Pro Ala Asn Arg Lys Val Ser Gln Met Asn
                1925                1930                1935
Ser Leu Glu Gln Glu Leu Glu Thr Ile His Leu Glu Asn Glu Gly Leu
            1940                1945                1950
Lys Lys Lys Gln Val Lys Leu Asp Glu Gln Leu Met Glu Met Gln His
        1955                1960                1965
Leu Arg Ser Thr Ala Thr Pro Ser Pro Ser Pro His Ala Trp Asp Leu
    1970                1975                1980
Gln Leu Leu Gln Gln Gln Ala Cys Pro Met Val Pro Arg Glu Gln Phe
1985                1990                1995                2000
Leu Gln Leu Gln Arg Gln Leu Leu Gln Ala Glu Arg Ile Asn Gln His
                2005                2010                2015
Leu Gln Glu Glu Leu Glu Asn Arg Thr Ser Glu Thr Asn Thr Pro Gln
            2020                2025                2030
Gly Asn Gln Glu Gln Leu Val Thr Val Met Glu Glu Arg Met Ile Glu
        2035                2040                2045
Val Glu Gln Lys Leu Lys Leu Val Lys Arg Leu Leu Gln Glu Lys Val
    2050                2055                2060
Asn Gln Leu Lys Glu Gln Val Ser Leu Pro Gly His Leu Cys Ser Pro
2065                2070                2075                2080
Thr Ser His Ser Ser Phe Asn Ser Ser Phe Thr Ser Leu Tyr Cys His
                2085                2090                2095
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<212> DNA
<213> Homo sapiens

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120
gccgccggaa gcttctcgga ggagcagttc tgggaggcct gcgccgagct ccagcagccc
180
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240
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300
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360
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420
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480
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720
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780
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840
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900
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960
gctcactcgt ctgcttcctt tctcgctccc cccatcctgg gctgggctgc cttcttctac
1020
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1080
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1140
acaacaaaat ttaagaatga ctatttgggc gggctggctc ttttgcagct tgtgatttct
1200
tccagcttgg gaggggctgc tggaagtggc atttcgttca gagctgactt tcagtgcacc
1260
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1320
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1380
gttatgatgc cagaccattt ggagaagtat cagaggcctg accggacaca taatacgaca
1440
accacatttt tcctcatcat ccatgaggaa atggatgatt tctcttttcc atatgtcact
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1560

atggctgtgg cagctagcaa aagcaaagat gctttgtgca tagccttgtg aaaaagtatc
1620
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gttcacagcc aggtaaaatt taactggtgg cttaatgact ctgcaccttt ttctcaggaa
1740
ttctgcctaa gttgtctgcc ttttctacca ccaaaaagac ttttagtttt ctatgctttc
1800
tcctgaattt tggtagggta aggtatttct atgtcaaagg cacagccttg atgatctcag
1860
ggaaaaattt taatcactgt gtataatgat actgaacctt gattaataac agaaattcag
1920
gatgtaaagc cacagaatgg gatttattaa tgtgggatac ctcagactgt ttgttttctt
1980
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2040
aaaaaaaaaa aaaaaaaaaa aaaaaa
2066

<210> 2714
<211> 214
<212> PRT
<213> Homo sapiens

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Cys Ala Glu Leu Gln Gln Pro Ala Leu Ala Gly Ala Asp Trp Gln Leu
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Leu Val Glu Thr Ser Gly Ile Ser Ile Tyr Arg Leu Leu Asp Lys Lys
35 40 45
Thr Gly Leu Tyr Glu Tyr Lys Val Phe Gly Val Leu Glu Asp Cys Ser
50 55 60
Pro Thr Leu Leu Ala Asp Ile Tyr Met Asp Ser Asp Tyr Arg Lys Gln
65 70 75 80
Trp Asp Gln Tyr Val Lys Glu Leu Tyr Glu Gln Glu Cys Asn Gly Glu
85 90 95
Thr Val Val Tyr Trp Glu Val Lys Tyr Pro Phe Pro Met Ser Asn Arg
100 105 110
Asp Tyr Val Tyr Leu Arg Gln Arg Arg Asp Leu Asp Met Glu Gly Arg
115 120 125
Lys Ile His Val Ile Leu Ala Arg Ser Thr Ser Met Pro Gln Leu Gly
130 135 140
Glu Arg Ser Gly Val Ile Arg Val Lys Gln Tyr Lys Gln Ser Leu Ala
145 150 155 160
Ile Glu Ser Asp Gly Lys Lys Gly Ser Lys Val Phe Met Tyr Tyr Phe
165 170 175
Asp Asn Pro Gly Gly Gln Ile Pro Ser Trp Leu Ile Asn Trp Ala Ala
180 185 190
Lys Asn Gly Val Pro Asn Phe Leu Lys Asp Met Ala Arg Ala Cys Gln
195 200 205
Asn Tyr Leu Lys Lys Thr
210

<210> 2715
<211> 378
<212> DNA
<213> Homo sapiens

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120
gaggaagagg aagaagaaga gatggatgta gatgaagcca caggggcagt taagaagcac
180
aatggtgttg gaggcagtcc ccctaagtcc aagttactgt ttagtaacac agcagctcaa
240
aaattaagag gaatggatga agtatacaac ctcttctatg tcaacaacaa ctggtatatt
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378

<210> 2716
<211> 126
<212> PRT
<213> Homo sapiens

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Lys Ile Lys Gln Ile Met His His Phe Ile Pro Asp Leu Leu Phe Ala
            20   25   30
Gln Arg Gly Asp Leu Ser Asp Val Glu Glu Glu Glu Glu Glu Glu Met
        35   40   45
Asp Val Asp Glu Ala Thr Gly Ala Val Lys Lys His Asn Gly Val Gly
    50   55   60
Gly Ser Pro Pro Lys Ser Lys Leu Leu Phe Ser Asn Thr Ala Ala Gln
65   70   75   80
Lys Leu Arg Gly Met Asp Glu Val Tyr Asn Leu Phe Tyr Val Asn Asn
                85   90   95
Asn Trp Tyr Ile Phe Met Arg Leu His Gln Ile Leu Cys Leu Arg Leu
            100   105   110
Leu Arg Ile Cys Ser Gln Ala Glu Arg Gln Ile Glu Glu Glu
        115   120   125

<210> 2717
<211> 2076
<212> DNA
<213> Homo sapiens

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tttaatacaa tagttattaa cgattagtgt tgagaaaatt atttccctct acatacaaaa
120

atacagattt gaacactatg aaaaagatca agacaagtac catgaaaaac tggtccttca
180
aatgaaaggg ggaaaattga gggcaatgtg aggctttgcc tgctgtcggg gacaaatcaa
240
tagcagcaaa gctttggggc cccaacccac tccatacata cagacttgaa cccaaaagcc
300
aggccagcca ggggacgccc acccagggct tccacgtcag ctgaaaaacc aaacacataa
360
acctaagttt gcccaacggg catcgcctca gaaagcccac agttgtgtct ttaaactgcc
420
gaaatgaaag agacttgatg agtaaaatgt gatagttgtt aacattgccc cccaaaagtg
480
ccaccaggtg aagtaccacg gagaaatcat attggaaagt tactacttag ccatctgact
540
tgacttcctt ggttatcaaa taattacata ttctgaccct tcagaaggac accaaaagct
600
acaatttttat gtttcaatcc atctgtacct tcatttgcaa tggctcagct agtttactca
660
agggttttgg gaccagacat aactcacgtc ctgcaggaag gagaagcaaa aggagccggt
720
gaagagtacg tgtctgtgtc ttggtgtcat ctagctcctc acagcaaaca gcctgttttg
780
ttcagcctga agcctggaaa aggccgccga gcctagccag agcatccaca acgaaccaat
840
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900
cactctgcag tggcaggaag gccatgcctc tgcaggacgc tcgcactgat tctggaaggg
960
cccaggccag agaatacact tgggctcagt tcaccagccc aaaccacagg ggaaggagcc
1020
ggacaccggc ctctcaccat tttacaccca aagacaggag gtcagggctc tgatgctact
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cttctgtttg taaaatatgg aaccactttc tttgtactgt ttgaggtgag cagtggctcc
1140
aaactgagca agtggttaaa aaatgccaaa tgcaattata ctgacttata attatttcac
1200
agaaatatac tcttactctc agactattta ataagcagg aacaagatgc aggagaagca
1260
gcagcagaga ggaaagagga atagccaggg aatttttttt gttttttttc ttctttaaaa
1320
tacatacgaa gtgtaaagag aaaatggcca aaacctcaaa actaccattg ttgaaaacaa
1380
tattaaaagg acacaatcta aaatcatgct acaaaaatag tgttatcttg tttaactaaa
1440
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1500
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1560
aaaatagtca tacttgtaaa taaatagttt agtgtttctg ccatgggttc ctgaacccct
1620
acaaatttca acatatacaa atagtttcaa ttcctaccat tctcttagag ggaaccacgt
1680
caaacaaaat caagttagga aaagcactga ttttatccaa gtaggtcaat ttgaggcaag
1740

attcaaaaac tcattttaaa atgggttaca gagtgaaaga gttgggaaca ggcagccccc
1800
tttgggcctg ggtcagccta cgagtccatc ccaggtgtcc tgccctcaca tctgccagcc
1860
ctcaggccgg ccaggtctcc cttcaaaccc tgagtatttg ccttcctcac ttctgcgaag
1920
aggggaacag aatcttgaag cttgcaaaat cgattctgga aaaagcaggc aagcaaagca
1980
gggcctgtgg ggggaagcag cgtgagtcag gcctcaccct ggtgcaaggg caccagcagg
2040
tctccctcct ctcccctcct caccatccct acgcgt
2076

<210> 2718
<211> 110
<212> PRT
<213> Homo sapiens

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Ala Val Ala Gly Arg Pro Cys Leu Cys Arg Thr Leu Ala Leu Ile Leu
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Glu Gly Pro Arg Pro Glu Asn Thr Leu Gly Leu Ser Ser Pro Ala Gln
35 40 45
Thr Thr Gly Glu Gly Ala Gly His Arg Pro Leu Thr Ile Leu His Pro
50 55 60
Lys Thr Gly Gly Gln Gly Ser Asp Ala Thr Leu Leu Phe Val Lys Tyr
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<210> 2719
<211> 546
<212> DNA
<213> Homo sapiens

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420

gccaccagcg tccttttga gagcacccca gtttatccca atgctggtcg gtactgggag
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<212> PRT
<213> Homo sapiens

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His Val Leu Val Ala His Arg Thr Asp Asn Lys Val His Met Gly Asp
35 40 45
Leu Asp Val Pro Leu Glu Gln Glu Met Ala Lys Glu Asp Pro Val Cys
50 55 60
Ala Pro Glu Ser Met Gly Ser Glu Asp Met Leu Phe Met Leu Tyr Thr
65 70 75 80
Ser Gly Ser Thr Gly Met Pro Lys Gly Ile Val His Thr Gln Ala Gly
85 90 95
Tyr Leu Leu Tyr Ala Ala Leu Thr His Lys Leu Val Phe Asp His Gln
100 105 110
Pro Gly Asp Ile Phe Gly Cys Val Ala Asp Ile Gly Trp Ile Thr Gly
115 120 125
His Ser Tyr Val Val Tyr Gly Pro Leu Cys Asn Gly Ala Thr Ser Val
130 135 140
Leu Phe Glu Ser Thr Pro Val Tyr Pro Asn Ala Gly Arg Tyr Trp Glu
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Val Arg Leu Leu Leu Lys
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<210> 2721
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<212> DNA
<213> Homo sapiens

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<211> 508
<212> PRT
<213> Homo sapiens

<400> 2722
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35 40 45
Tyr Gly Gln Thr His Tyr Tyr His Gln Arg Gln Asn Ser Asp Asp Lys
50 55 60
Leu Asn Gly Trp Gln Asn Ser Arg Asp Ser Gly Ile Cys Ile Asn Ala
65 70 75 80
Ser Asn Trp Gln Asp Lys Ser Met Gly Cys Glu Asn Gly His Val Pro
85 90 95
Leu Tyr Ser Ser Ser Ser Ser Val Pro Thr Thr Ile Asn Thr Ile Gly Thr
100 105 110
Ser Thr Ser Thr Asn Val Pro Ala Trp Leu Lys Ser Leu Arg Leu His
115 120 125
Lys Tyr Ala Ala Leu Phe Ser Gln Met Thr Tyr Glu Glu Met Met Ala
130 135 140
Leu Thr Glu Cys Gln Leu Glu Ala Gln Asn Val Thr Lys Gly Ala Arg
145 150 155 160
His Lys Ile Val Ile Ser Ile Gln Lys Leu Lys Glu Arg Gln Asn Leu

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                165                 170                 175
Leu Lys Ser Leu Glu Arg Asp Ile Ile Glu Gly Gly Ser Leu Arg Ile
            180                 185                 190
Pro Leu Gln Glu Leu His Gln Met Ile Leu Thr Pro Ile Lys Ala Tyr
        195                 200                 205
Ser Ser Pro Ser Thr Thr Pro Glu Ala Arg Arg Arg Glu Pro Gln Ala
    210                 215                 220
Pro Arg Gln Pro Ser Leu Met Gly Pro Glu Ser Gln Ser Pro Asp Cys
225                 230                 235                 240
Lys Asp Gly Ala Ala Ala Thr Gly Ala Thr Ala Thr Pro Ser Ala Gly
                245                 250                 255
Ala Ser Gly Gly Leu Gln Pro His Gln Leu Ser Ser Cys Asp Gly Glu
            260                 265                 270
Leu Ala Val Ala Pro Leu Pro Glu Gly Asp Leu Pro Gly Gln Phe Thr
        275                 280                 285
Arg Val Met Gly Lys Val Cys Thr Gln Leu Leu Val Ser Arg Pro Asp
    290                 295                 300
Glu Glu Asn Ile Ser Ser Tyr Leu Gln Leu Ile Asp Lys Cys Leu Ile
305                 310                 315                 320
His Glu Ala Phe Thr Glu Thr Gln Lys Lys Arg Leu Leu Ser Trp Lys
                325                 330                 335
Gln Gln Val Gln Lys Leu Phe Arg Ser Phe Pro Arg Lys Thr Leu Leu
            340                 345                 350
Asp Ile Ser Gly Tyr Arg Gln Gln Arg Asn Arg Gly Phe Gly Gln Ser
        355                 360                 365
Asn Ser Leu Pro Thr Ala Gly Ser Val Gly Gly Gly Met Gly Arg Arg
    370                 375                 380
Asn Pro Arg Gln Tyr Gln Ile Pro Ser Arg Asn Val Pro Ser Ala Arg
385                 390                 395                 400
Leu Gly Leu Leu Gly Thr Ser Gly Phe Val Ser Ser Asn Gln Arg Asn
                405                 410                 415
Thr Thr Ala Thr Pro Thr Ile Met Lys Gln Gly Arg Gln Asn Leu Trp
            420                 425                 430
Phe Ala Asn Pro Gly Gly Ser Asn Ser Met Pro Ser Arg Thr His Ser
        435                 440                 445
Ser Val Gln Arg Thr Arg Ser Leu Pro Val His Thr Ser Pro Gln Asn
    450                 455                 460
Met Leu Met Phe Gln Gln Pro Glu Phe Gln Leu Pro Val Thr Glu Pro
465                 470                 475                 480
Asp Ile Asn Asn Arg Leu Glu Ser Leu Cys Leu Ser Met Thr Glu His
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Ala Leu Gly Asp Gly Val Asp Arg Thr Ser Thr Ile
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<210> 2723
<211> 1221
<212> DNA
<213> Homo sapiens

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120

cccaacacat tctggagtgc tgctgaggat gggcttatcc gccagtatga ccttcgagag
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420
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480
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1221

<210> 2724
<211> 404
<212> PRT
<213> Homo sapiens

<400> 2724
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Thr Ile His Met Phe Gly Asp His Thr Asn Arg Val Lys Arg Ile Ala
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Thr Ala Pro Met Trp Pro Asn Thr Phe Trp Ser Ala Ala Glu Asp Gly
35 40 45
Leu Ile Arg Gln Tyr Asp Leu Arg Glu Asn Ser Lys His Ser Glu Val
50 55 60
Leu Ile Asp Leu Thr Glu Tyr Cys Gly Gln Leu Val Glu Ala Lys Cys

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65                  70                  75                  80
Leu Thr Val Asn Pro Gln Asp Asn Asn Cys Leu Ala Val Gly Ala Ser
                85                  90                  95
Gly Pro Phe Val Arg Leu Tyr Asp Ile Arg Met Ile His Asn His Arg
            100                 105                 110
Lys Ser Met Lys Gln Ser Pro Ser Ala Gly Val His Thr Phe Cys Asp
        115                 120                 125
Arg Gln Lys Pro Leu Pro Asp Gly Ala Ala Gln Tyr Tyr Val Ala Gly
    130                 135                 140
His Leu Pro Val Lys Leu Pro Asp Tyr Asn Asn Arg Leu Arg Val Leu
145                 150                 155                 160
Val Ala Thr Tyr Val Thr Phe Ser Pro Asn Gly Thr Glu Leu Leu Val
                165                 170                 175
Asn Met Gly Gly Glu Gln Val Tyr Leu Phe Asp Leu Thr Tyr Lys Gln
            180                 185                 190
Arg Pro Tyr Thr Phe Leu Leu Pro Arg Lys Cys His Ser Ser Gly Glu
        195                 200                 205
Val Gln Asn Gly Lys Met Ser Thr Asn Gly Val Ser Asn Gly Val Ser
    210                 215                 220
Asn Gly Leu His Leu His Ser Asn Gly Phe Arg Leu Pro Glu Ser Arg
225                 230                 235                 240
Gly His Val Ser Pro Gln Val Glu Leu Pro Pro Tyr Leu Glu Arg Val
                245                 250                 255
Lys Gln Gln Ala Asn Glu Ala Phe Ala Cys Gln Gln Trp Thr Gln Ala
            260                 265                 270
Ile Gln Leu Tyr Ser Lys Ala Val Gln Arg Ala Pro His Asn Ala Met
        275                 280                 285
Leu Tyr Gly Asn Arg Ala Ala Ala Tyr Met Lys Arg Lys Trp Asp Gly
    290                 295                 300
Asp His Tyr Asp Ala Leu Arg Asp Cys Leu Lys Ala Ile Ser Leu Asn
305                 310                 315                 320
Pro Cys His Leu Lys Ala His Phe Arg Leu Ala Arg Cys Leu Phe Glu
                325                 330                 335
Leu Lys Tyr Val Ala Glu Ala Leu Glu Cys Leu Asp Asp Phe Lys Gly
            340                 345                 350
Lys Phe Pro Glu Gln Ala His Ser Ser Ala Cys Asp Ala Leu Gly Arg
        355                 360                 365
Asp Ile Thr Ala Ala Leu Phe Ser Lys Asn Asp Gly Glu Glu Lys Lys
    370                 375                 380
Gly Pro Gly Gly Gly Ala Pro Val Arg Leu Arg Ser Thr Ser Arg Lys
385                 390                 395                 400
Gly Cys Thr Arg
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<210> 2725
<211> 856
<212> DNA
<213> Homo sapiens

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120

aaggttctta aagaagtcag ggtgcaggat gagaacaacg tttgttttga gtgtggcgcg
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<210> 2726
<211> 148
<212> PRT
<213> Homo sapiens

<400> 2726
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Val Ser Val Thr Tyr Gly Ile Trp Ile Cys Leu Glu Cys Ser Gly Arg
35 40 45
His Arg Gly Leu Gly Val His Leu Ser Phe Val Arg Ser Val Thr Met
50 55 60
Asp Lys Trp Lys Asp Ile Glu Leu Glu Lys Met Lys Ala Gly Gly Asn
65 70 75 80
Ala Lys Phe Arg Glu Phe Leu Glu Ser Gln Glu Asp Tyr Asp Pro Cys
85 90 95
Trp Ser Leu Gln Glu Lys Tyr Asn Ser Arg Ala Ala Ala Leu Phe Arg
100 105 110
Asp Lys Val Val Ala Leu Ala Glu Gly Arg Glu Trp Ser Leu Glu Ser
115 120 125
Ser Pro Ala Gln Asn Trp Thr Pro Pro Gln Pro Arg Thr Leu Pro Ser
130 135 140
Met Val His Arg
145

<210> 2727
<211> 1119
<212> DNA
<213> Homo sapiens

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480
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720
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780
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900
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960
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1020
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1119

<210> 2728
<211> 221
<212> PRT
<213> Homo sapiens

<400> 2728
Met Val Lys Ser Val Leu Asp Lys Thr Lys His Ser Val Glu Ser Met
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Ile Thr Thr Leu Asp Pro Gly Met Ala Pro Tyr Ile Lys Ser Gly Gly

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            20                  25                  30
Glu Leu Asp Ile Val Val Thr Ser Asn Lys Glu Val Lys Val Ala Ala
        35                  40                  45
Val Arg Asp Ala Phe Gln Glu Val Phe Gly Leu Ala Val Val Val Gly
    50                  55                  60
Glu Ala Gly Gln Ser Asn Ile Ala Pro Gln Pro Val Gly Tyr Ala Ala
65                  70                  75                  80
Gly Leu Lys Gly Ala Gln Glu Arg Ile Asp Ser Leu Arg Arg Thr Gly
                85                  90                  95
Val Ile His Glu Lys Gln Thr Ala Val Ser Val Glu Asn Phe Ile Ala
            100                 105                 110
Glu Leu Leu Pro Asp Lys Trp Phe Asp Ile Gly Cys Leu Val Val Glu
        115                 120                 125
Asp Pro Val His Gly Ile His Leu Glu Thr Phe Thr Gln Ala Thr Pro
    130                 135                 140
Val Pro Leu Glu Phe Val Gln Gln Ala Gln Ser Leu Thr Pro Gln Asp
145                 150                 155                 160
Tyr Asn Leu Arg Trp Ser Gly Leu Leu Val Thr Val Gly Glu Val Leu
                165                 170                 175
Glu Lys Ser Leu Leu Asn Val Ser Arg Thr Asp Trp His Met Ala Phe
            180                 185                 190
Thr Gly Met Ser Arg Arg Gln Met Ile Tyr Ser Ala Ala Arg Ala Ile
        195                 200                 205
Ala Gly Met Tyr Lys Gln Arg Leu Pro Pro Arg Thr Val
    210                 215                 220
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<210> 2729
<211> 393
<212> DNA
<213> Homo sapiens

<400> 2729
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gagccccctc acttcccctg cttacagaaa ctgctggatt atctcacacg gatgatgccg
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393

<210> 2730
<211> 92
<212> PRT
<213> Homo sapiens

<400> 2730
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            20                  25                  30
Leu Asp Gln Cys Ala Glu Asp Phe Arg Glu Pro Pro His Phe Pro Cys
        35                  40                  45
Leu Gln Lys Leu Leu Asp Tyr Leu Thr Arg Met Met Pro Gly Ser Asp
    50                  55                  60
Pro Glu Arg Arg Ala Gln Asn Leu Leu Glu Gln Phe Gln Lys Gln Glu
65                  70                  75                  80
Val Glu Thr Asp Asn Gly Leu Pro Asn Thr Ile Ser
                85                  90
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<210> 2731
<211> 447
<212> DNA
<213> Homo sapiens

<400> 2731
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120
atcggtgtca cctgcgtgtt tcccatcgac ctggccaaga ccaggctgca gaaccagcag
180
aacggccagc gcgtgtacac gagcatgtcc gactgcctca tcaagaccgt ccgctccgag
240
ggctacttcg gcatgtaccg gggagctgct gtgaacttga ccctcgtcac ccccgagaag
300
gccatcaagc tggcagccaa cgacttcttc cgacatcagc tctctaagga cgggcagaag
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420
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447

<210> 2732
<211> 125
<212> PRT
<213> Homo sapiens

<400> 2732
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Ala Asp Gln Pro Ala Ser Gln Ala His Gln Trp Arg His Arg Gly Leu
 1               5                  10                  15
Ile Gly Val Thr Cys Val Phe Pro Ile Asp Leu Ala Lys Thr Arg Leu
            20                  25                  30
Gln Asn Gln Gln Asn Gly Gln Arg Val Tyr Thr Ser Met Ser Asp Cys
        35                  40                  45
Leu Ile Lys Thr Val Arg Ser Glu Gly Tyr Phe Gly Met Tyr Arg Gly
    50                  55                  60
Ala Ala Val Asn Leu Thr Leu Val Thr Pro Glu Lys Ala Ile Lys Leu
65                  70                  75                  80
Ala Ala Asn Asp Phe Phe Arg His Gln Leu Ser Lys Asp Gly Gln Lys
                85                  90                  95
Leu Thr Leu Leu Lys Glu Met Leu Ala Gly Cys Gly Ala Gly Thr Cys
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100 105 110
Gln Val Ile Val Thr Thr Pro Met Glu Met Leu Lys Ile
115 120 125

<210> 2733
<211> 3619
<212> DNA
<213> Homo sapiens

<400> 2733
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120
ccccagcacc catgtcaccc ccaacagctg gactgcccgc tggccatgga gcggatcaag
180
gaggaccggc ccatcaccat caaggacgac aagggcaacc tcaaccgctg catcgcagac
240
gtggtctcgc tcttcatcac ggtcatggac aagctgcgcc tggcggagct gacggtggac
300
gagttcctag cttcgggctt tgactccgag tccgaatccg agtccgaaaa ttctccacaa
360
gcggagacac gggaagcacg cgaggctgcc cggagtccgg ataagccggg cgggagcccc
420
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540
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1260
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1320

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1380
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2940

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3480
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3619

<210> 2734
<211> 790
<212> PRT
<213> Homo sapiens

<400> 2734
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Gly Asn Leu Asn Arg Cys Ile Ala Asp Val Val Ser Leu Phe Ile Thr
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Val Met Asp Lys Leu Arg Leu Ala Glu Leu Thr Val Asp Glu Phe Leu
35 40 45
Ala Ser Gly Phe Asp Ser Glu Ser Glu Ser Glu Ser Glu Asn Ser Pro
50 55 60
Gln Ala Glu Thr Arg Glu Ala Arg Glu Ala Ala Arg Ser Pro Asp Lys
65 70 75 80
Pro Gly Gly Ser Pro Ser Ala Ser Arg Arg Lys Gly Arg Ala Ser Glu
85 90 95
His Lys Asp Gln Leu Ser Arg Leu Lys Asp Arg Asp Pro Glu Phe Tyr
100 105 110
Lys Phe Leu Gln Glu Asn Asp Gln Ser Leu Leu Asn Phe Ser Asp Ser
115 120 125
Asp Ser Ser Glu Glu Glu Glu Gly Pro Phe His Ser Leu Pro Asp Val
130 135 140
Leu Glu Glu Ala Ser Glu Glu Glu Asp Gly Ala Glu Glu Gly Glu Asp
145 150 155 160
Gly Asp Arg Val Pro Arg Gly Leu Lys Gly Lys Lys Asn Ser Val Pro
165 170 175
Val Thr Val Ala Met Val Glu Arg Trp Lys Gln Ala Ala Lys Gln Arg

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            180                 185                 190
Leu Thr Pro Lys Leu Phe His Glu Val Val Gln Ala Phe Arg Ala Ala
        195                 200                 205
Val Ala Thr Thr Arg Gly Asp Gln Glu Ser Ala Glu Ala Asn Lys Phe
    210                 215                 220
Gln Val Thr Asp Ser Ala Ala Phe Asn Ala Leu Val Thr Phe Cys Ile
225                 230                 235                 240
Arg Asp Leu Ile Gly Cys Leu Gln Lys Leu Leu Phe Gly Lys Val Ala
                245                 250                 255
Lys Asp Ser Ser Arg Met Leu Gln Pro Ser Ser Ser Pro Leu Trp Gly
            260                 265                 270
Lys Leu Arg Val Asp Ile Lys Ala Tyr Leu Gly Ser Ala Ile Gln Leu
        275                 280                 285
Val Ser Cys Leu Ser Glu Thr Thr Val Leu Ala Ala Val Leu Arg His
    290                 295                 300
Ile Ser Val Leu Val Pro Cys Phe Leu Thr Phe Pro Lys Gln Cys Arg
305                 310                 315                 320
Met Leu Leu Lys Arg Met Val Val Val Trp Ser Thr Gly Glu Glu Ser
                325                 330                 335
Leu Arg Val Leu Ala Phe Leu Val Leu Ser Arg Val Cys Arg His Lys
            340                 345                 350
Lys Asp Thr Phe Leu Gly Pro Val Leu Lys Gln Met Tyr Ile Thr Tyr
        355                 360                 365
Val Arg Asn Cys Lys Phe Thr Ser Pro Gly Ala Leu Pro Phe Ile Ser
    370                 375                 380
Phe Met Gln Trp Thr Leu Thr Glu Leu Leu Ala Leu Glu Pro Gly Val
385                 390                 395                 400
Ala Tyr Gln His Ala Phe Leu Tyr Ile Arg Gln Leu Ala Ile His Leu
                405                 410                 415
Arg Asn Ala Met Thr Thr Arg Lys Lys Glu Thr Tyr Gln Ser Val Tyr
            420                 425                 430
Asn Trp Gln Tyr Val His Cys Leu Phe Leu Trp Cys Arg Val Leu Ser
        435                 440                 445
Thr Ala Gly Pro Ser Glu Ala Leu Gln Pro Leu Val Tyr Pro Leu Ala
    450                 455                 460
Gln Val Ile Ile Gly Cys Ile Lys Leu Ile Pro Thr Ala Arg Phe Tyr
465                 470                 475                 480
Pro Leu Arg Met His Cys Ile Arg Ala Leu Thr Leu Leu Ser Gly Ser
                485                 490                 495
Ser Gly Ala Phe Ile Pro Val Leu Pro Phe Ile Leu Glu Met Phe Gln
            500                 505                 510
Gln Val Asp Phe Asn Arg Lys Pro Gly Arg Met Ser Ser Lys Pro Ile
        515                 520                 525
Asn Phe Ser Val Ile Leu Lys Leu Ser Asn Val Asn Leu Gln Glu Lys
    530                 535                 540
Ala Tyr Arg Asp Gly Leu Val Glu Gln Leu Tyr Asp Leu Thr Leu Glu
545                 550                 555                 560
Tyr Leu His Ser Gln Ala His Cys Ile Gly Phe Pro Glu Leu Val Leu
                565                 570                 575
Pro Val Val Leu Gln Leu Lys Ser Phe Leu Arg Glu Cys Lys Val Ala
            580                 585                 590
Asn Tyr Cys Arg Gln Val Gln Gln Leu Leu Gly Lys Val Gln Glu Asn
        595                 600                 605
Ser Ala Tyr Ile Cys Ser Arg Arg Gln Arg Val Ser Phe Gly Val Ser
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610 615 620
Glu Gln Gln Ala Val Glu Ala Trp Glu Lys Leu Thr Arg Glu Glu Gly
625 630 635 640
Thr Pro Leu Thr Leu Tyr Tyr Ser His Trp Arg Lys Leu Arg Asp Arg
645 650 655
Glu Ile Gln Leu Glu Ile Ser Gly Lys Glu Arg Val Arg Leu Gly Glu
660 665 670
Gly Thr Trp Leu Glu Asp Leu Asn Phe Pro Glu Ile Lys Arg Arg Lys
675 680 685
Met Ala Asp Arg Lys Asp Glu Asp Arg Lys Gln Phe Lys Asp Leu Phe
690 695 700
Asp Leu Asn Ser Ser Glu Glu Asp Asp Thr Glu Gly Phe Leu Glu Arg
705 710 715 720
Gly Ile Leu Gly Pro Leu Ser Thr Arg His Gly Val Glu Asp Asp Glu
725 730 735
Glu Asp Glu Glu Glu Gly Glu Glu Asp Ser Ser Asn Ser Glu Gly Glu
740 745 750
Trp Ser Trp Asp Gly Asp Pro Asp Ala Glu Ala Gly Leu Ala Pro Gly
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770 775 780
Gln Leu Ser Glu Asp Asp
785 790

<210> 2735
<211> 1666
<212> DNA
<213> Homo sapiens

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240
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480
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540
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600
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660
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720

aactcttcga aaacctgctg gtgctgagtc ctgtgtgggg caccccacac gacacccctc
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1020
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1666

<210> 2736
<211> 218
<212> PRT
<213> Homo sapiens

<400> 2736
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Phe His Ser Ser His Ile Ser Thr Ile Gly Val Asp Phe Lys Met Lys
35 40 45
Thr Ile Glu Val Asp Gly Ile Lys Val Arg Ile Gln Ile Trp Asp Thr
50 55 60
Ala Gly Gln Glu Arg Tyr Gln Thr Ile Thr Lys Gln Tyr Tyr Arg Arg
65 70 75 80
Ala Gln Gly Ile Phe Leu Val Tyr Asp Ile Ser Ser Glu Arg Ser Tyr
85 90 95
Gln His Ile Met Lys Trp Val Ser Asp Val Asp Glu Tyr Ala Pro Glu
100 105 110
Gly Val Gln Lys Ile Leu Ile Gly Asn Lys Ala Asp Glu Glu Gln Lys

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        115                 120                 125
Arg Gln Val Gly Arg Glu Gln Gly Gln Gln Lys Cys Pro Ser Leu Gln
    130                 135                 140
Leu Ala Lys Glu Tyr Gly Met Asp Phe Tyr Glu Thr Ser Ala Cys Thr
145                 150                 155                 160
Asn Leu Asn Ile Lys Glu Ser Phe Thr Arg Leu Thr Glu Leu Val Leu
                165                 170                 175
Gln Ala His Arg Lys Glu Leu Glu Gly Leu Arg Met Arg Ala Ser Asn
            180                 185                 190
Glu Leu Ala Leu Ala Glu Leu Glu Glu Glu Glu Gly Lys Pro Glu Gly
        195                 200                 205
Pro Ala Asn Ser Ser Lys Thr Cys Trp Cys
    210                 215
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<210> 2737
<211> 898
<212> DNA
<213> Homo sapiens

<400> 2737
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360
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840
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898

<210> 2738
<211> 299
<212> PRT

<213> Homo sapiens

<400> 2738
Xaa Pro Val Cys Ala Thr Cys Ala Gly Phe Gly Gly Arg Cys His Arg
1 5 10 15
His Arg Ile Arg Arg Ala Glu Glu His Ala Glu Glu Leu Arg Asn Lys
20 25 30
Ile Val Asp Gln Cys Glu Arg Leu Gln Leu Gln Ser Ala Ala Ile Thr
35 40 45
Lys Tyr Val Ala Asp Val Leu Pro Gly Lys Asn Gln Arg Ala Val Ser
50 55 60
Met Ala Ser Ala Ala Arg Glu Leu Val Ile Gln Arg Leu Ser Leu Val
65 70 75 80
Arg Ser Leu Cys Glu Ser Glu Glu Gln Arg Leu Leu Glu Gln Val His
85 90 95
Gly Glu Glu Glu Arg Ala His Gln Ser Ile Leu Thr Gln Arg Val His
100 105 110
Trp Ala Glu Ala Leu Gln Lys Leu Asp Thr Ile Arg Thr Gly Leu Val
115 120 125
Gly Met Leu Thr His Leu Asp Asp Leu Gln Leu Ile Gln Lys Glu Gln
130 135 140
Glu Ile Phe Glu Arg Thr Glu Glu Ala Glu Gly Ile Leu Asp Pro Gln
145 150 155 160
Glu Ser Glu Met Leu Asn Phe Asn Glu Lys Cys Thr Arg Ser Pro Leu
165 170 175
Leu Thr Gln Leu Trp Ala Thr Ala Val Leu Gly Ser Leu Ser Gly Thr
180 185 190
Glu Asp Ile Arg Ile Asp Glu Arg Thr Val Ser Pro Phe Leu Gln Leu
195 200 205
Ser Asp Asp Arg Lys Thr Leu Thr Ser Ala Pro Arg Ser Gln Arg Cys
210 215 220
Ala Asp Gly Pro Glu Arg Phe Asp His Trp Pro Asn Ala Leu Ala Ala
225 230 235 240
Thr Ser Phe Gln Asn Gly Leu His Ala Trp Met Val Asn Val Gln Asn
245 250 255
Ser Cys Ala Tyr Lys Val Gly Val Ala Ser Gly His Leu Pro Arg Lys
260 265 270
Gly Ser Gly Ser Asp Cys Arg Leu Gly His Asn Ala Phe Ser Trp Val
275 280 285
Phe Ser Arg Tyr Asp Gln Glu Phe Arg Phe Ser
290 295

<210> 2739
<211> 1501
<212> DNA
<213> Homo sapiens

<400> 2739
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gccgaggaca agagcatccg gctcggcttg tttctcatca tctccggcgt cgtgtcgctc
120
ttcatcttcg gcttctgctg gctgagtccc gcgctgcagg atctgcaagc cacggaggcc
180

aattgcacgg tgctgtcggt gcagcagatc ggcgaggtgt tcgagtgcac cttcacctgt
240
ggcgccgact gcaggggcac ctcgcagtac ccctgcgtcc aggtctacgt gaacaactct
300
gagtccaact ctagggcgct gctgcacagc gacgagcacc agctcctgac caaccccaag
360
tgctcctata tccctccctg taagagagaa aatcagaaga atttggaaag tgtcatgaat
420
tggcaacagt actggaaaga tgagattggt tcccagccat ttacttgcta ttttaatcaa
480
catcaaagac cagatgatgt gcttctgcat cgcactcatg atgagattgt cctcctgcat
540
tgcttcctct ggcccctggt gacatttgtg gtgggcgttc tcattgtggt cctgaccatc
600
tgtgccaaga gcttggcggt caaggcggaa gccatgaaga agcgcaagtt ctcttaaagg
660
ggaaggaggc ttgtagaaag caaagtacag aagctgtact catcggcacg cgtccacctg
720
cggaacctgt gtttcctggc gcaggagatg gacagggcca cgacagggct ctgagaggct
780
catccctcag tggcaacaga aacaggcaca actggaagac ttggaacctc aaagcttgta
840
ttccatctgc tgtagcaatg gctaaagggt caagatctta gctgtatgga gtaactattt
900
cagaaaaccc tataagaagt tcattttctt tcaaaagtaa cagtatatta tttgtacagt
960
gtagtataca aaccattatg atttatgcta cttaaaaata ttaaaataga gtggtctgtg
1020
ttattttcta tttccttttt tatgcttaga acaccagggt tttaaaaaaa aaaaaaggtg
1080
aggacatctg ggtctcattt gcttctgcta ggttaaactt ttacttgaca acaaggattc
1140
ctgctgaagt ctgaacctta ctgtgtaacc ctcagtttcc actattaaag agtatctttt
1200
gacgtcctgc ttggaaaatg aatagtatac tggtaactca gtctccagtc acctctgtgt
1260
ctcttaagca agagattcta aaagattggg aaaacatatc ctccaaaacc tgcctttgcc
1320
taaccattat ttttcaccag attacttctt aagagaggga ggtgattctg aagaaggctt
1380
ctatctcaaa aagcactggg cttccttatt catctgttct tgttgttttt gacggagtta
1440
aaaaagtttg tgtgcaatac aatataaatg atgtgaagga cactcttaaa aaaaaaaaaa
1500
a
1501

<210> 2740
<211> 218
<212> PRT
<213> Homo sapiens

<400> 2740
Glu Ser Arg Arg Glu Trp Gly Ala Met Ala Lys Leu Arg Val Ala Tyr

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 1               5                  10                  15
Glu Tyr Thr Glu Ala Glu Asp Lys Ser Ile Arg Leu Gly Leu Phe Leu
            20                  25                  30
Ile Ile Ser Gly Val Val Ser Leu Phe Ile Phe Gly Phe Cys Trp Leu
        35                  40                  45
Ser Pro Ala Leu Gln Asp Leu Gln Ala Thr Glu Ala Asn Cys Thr Val
    50                  55                  60
Leu Ser Val Gln Gln Ile Gly Glu Val Phe Glu Cys Thr Phe Thr Cys
65                  70                  75                  80
Gly Ala Asp Cys Arg Gly Thr Ser Gln Tyr Pro Cys Val Gln Val Tyr
                85                  90                  95
Val Asn Asn Ser Glu Ser Asn Ser Arg Ala Leu Leu His Ser Asp Glu
            100                 105                 110
His Gln Leu Leu Thr Asn Pro Lys Cys Ser Tyr Ile Pro Pro Cys Lys
        115                 120                 125
Arg Glu Asn Gln Lys Asn Leu Glu Ser Val Met Asn Trp Gln Gln Tyr
    130                 135                 140
Trp Lys Asp Glu Ile Gly Ser Gln Pro Phe Thr Cys Tyr Phe Asn Gln
145                 150                 155                 160
His Gln Arg Pro Asp Asp Val Leu Leu His Arg Thr His Asp Glu Ile
                165                 170                 175
Val Leu Leu His Cys Phe Leu Trp Pro Leu Val Thr Phe Val Val Gly
            180                 185                 190
Val Leu Ile Val Val Leu Thr Ile Cys Ala Lys Ser Leu Ala Val Lys
        195                 200                 205
Ala Glu Ala Met Lys Lys Arg Lys Phe Ser
    210                 215
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<210> 2741
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 2741

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aaggctcgag ggaaagtgag tgagatcatc aacaatgcca ttgtgcacta ccgagatgac
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ttggatctgc agaacctcat tgattttggc cagaaaaagt ttagctgctg tggagggatt
120
tcctacaagg actggtctca gaacatgtat ttcaactgct cagaagacaa ccccagtcga
180
gagcgctgct ctgtgcctta ctcctgttgc ttgcctactc ctgaccaggc agtgatcaac
240
actatgtgtg gccaaggtat gcaggccttt gactacttgg aagctagcaa agtcatctac
300
accaatggct gtattgacaa gttggtcaac tggatacaca gcaacctatt cttacttggt
360
ggtgtggctc taggcctggc catcccccag ctggtgggaa ttctgctgtc ccagatccta
420
gtgaatcaga tcaaagatca gatcaagcta cagctctaca accagcagca ccgggctgac
480
ccatggtact gagaatccat cctgcacctc ctcaccatgg aaactggcaa gcctcataaa
540
cgaacagcag tgggtgctga aagcagcacc aaatggagat ttggattcca gccccccagt
600
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gacagcccag tgggaagaag caaactccag atgggcagaa ggcagggtgc acaggtggct
660
ccagtctcag gaggatgcgc ctcctctccc ccatcccagc cctcagcatt gtgccagagt
720
gataccctta agtgtttggg tttatgtttt cagttttgtt tgggaaacag cagttgcaca
780
gagagttggg ggtactgctg ctgccttttc accgaggcac tgccaccacc agctctagca
840
gggatgctcc tgagcttggc ggacatactt agatcctaac gtgccagtga gacctggctg
900
tggagagtag cactggcagc cctgcctgga ctccacttgg catgatacca gctccagaag
960
ggaagggagt ggagcaggca gtgaggagag agcctggggg tcggctgggg acagccgtat
1020
gtgctaggta ggagtggagg gagatatgtt taccaaatgc ctgtcctgcc atcctcccag
1080
gtagtcagag tgagctacat cctgccccgc cttcatttcc atggaaacat ggcagctagg
1140
acacggggta tacaacagca gccaaattct tccccacctc ccttacttcg aaaaaaagtt
1200
tggaaccctg gtccctatac tctgcagtca gaagtgggac tgagccatac atgcccttga
1260
attcctcccc gtctggccct ccctctccag caagcagggt tttctttaac ttggcagtgt
1320
gcagaggaga agtggtaaca cccccacccc attcccctgc atcggagctc agtattccta
1380
cagggtaaga ggtaggaatc ttgctgggac gaggggagcc agaagtggca ataaaagcgt
1440
gttgacctgg gcaaaaaaaa aaaaaaaaaa aaagaaaaaa aaaaaaa
1487

<210> 2742
<211> 163
<212> PRT
<213> Homo sapiens

<400> 2742
Lys Ala Arg Gly Lys Val Ser Glu Ile Ile Asn Asn Ala Ile Val His
1 5 10 15
Tyr Arg Asp Asp Leu Asp Leu Gln Asn Leu Ile Asp Phe Gly Gln Lys
20 25 30
Lys Phe Ser Cys Cys Gly Gly Ile Ser Tyr Lys Asp Trp Ser Gln Asn
35 40 45
Met Tyr Phe Asn Cys Ser Glu Asp Asn Pro Ser Arg Glu Arg Cys Ser
50 55 60
Val Pro Tyr Ser Cys Cys Leu Pro Thr Pro Asp Gln Ala Val Ile Asn
65 70 75 80
Thr Met Cys Gly Gln Gly Met Gln Ala Phe Asp Tyr Leu Glu Ala Ser
85 90 95
Lys Val Ile Tyr Thr Asn Gly Cys Ile Asp Lys Leu Val Asn Trp Ile
100 105 110
His Ser Asn Leu Phe Leu Leu Gly Gly Val Ala Leu Gly Leu Ala Ile
115 120 125
Pro Gln Leu Val Gly Ile Leu Leu Ser Gln Ile Leu Val Asn Gln Ile

```
    130                 135                 140
Lys Asp Gln Ile Lys Leu Gln Leu Tyr Asn Gln Gln His Arg Ala Asp
145                 150                 155                 160
Pro Trp Tyr


<210> 2743
<211> 384
<212> DNA
<213> Homo sapiens

<400> 2743
ngaattctcc cctcggcctc ccgagactcg ggtgtcctgt ctccccccgg agcctcccaa
60
gactccggtg tccagtctcc gcccggagcc tccagagact ggagtgtccc atctccgccc
120
acagcctccc aagactcagg tgtccagtct ccacctggag cctccagaga ctggagtgtc
180
ccatctccgc ccagagccta ccaagactga ggtgtccagt ctccacctgg agcctcccga
240
gactggagtg gcccatctct acctggagcc tcctgggact ggagtgtctc atctctgccc
300
agagcctccc aagactcgcg tatctcatct ccatcgggag cctcctgaga ctggagtgcc
360
tgatctctgc ctggagcctc ccaa
384

<210> 2744
<211> 69
<212> PRT
<213> Homo sapiens

<400> 2744
Xaa Ile Leu Pro Ser Ala Ser Arg Asp Ser Gly Val Leu Ser Pro Pro
 1               5                  10                  15
Gly Ala Ser Gln Asp Ser Gly Val Gln Ser Pro Pro Gly Ala Ser Arg
            20                  25                  30
Asp Trp Ser Val Pro Ser Pro Pro Thr Ala Ser Gln Asp Ser Gly Val
        35                  40                  45
Gln Ser Pro Pro Gly Ala Ser Arg Asp Trp Ser Val Pro Ser Pro Pro
    50                  55                  60
Arg Ala Tyr Gln Asp
65

<210> 2745
<211> 769
<212> DNA
<213> Homo sapiens

<400> 2745
gaattccacc ttccctcctg cagtgctgag aggcagcgag gacggagagg acagcggcat
60
ctctaggctc ttctgagagg gacagagaaa gaatagaaat gtgccctaaa agcataaatg
120
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agtatcacct gagaaaatta ggcattcccg tcttggaaac acgtctctgt gagtttgcat
180
ttcatttggc ttggagccct ggctcgatgc ctcatggatc tttctcccca aggagggacg
240
tcttgagggg tccgagcctc aggccaagga cccctgatgc agactctgga atccctggcc
300
caaaggcctg tctgggccca tctggggctg aggacacaca gatacataat gacacctgca
360
gaaatgtatt ctctgaggac acttagaata tgaggaagag ggtgtggccc aaccctcact
420
tcacctgggg aggggcttct tccggacagt agacaccctg cccgtgcaga gagatgtcat
480
gggggcacct gctctccctg atagatgctg agagcatcca gaaacttcca gaccagccct
540
ctcaccacac ccagaagagg cctttcccat ctggagagaa gcttccagac cagcccttca
600
cacaccacag ccaggagggg cctttcccac ctgggagaga aacttccaga ccagcccctc
660
ataccacagc caagaggggc ctttctcacc tggagagaaa cttccagacc agcccctcac
720
accacagcca agaggggcct ttccccccgg gagagaaact tccagacca
769

<210> 2746
<211> 98
<212> PRT
<213> Homo sapiens

<400> 2746
Met Ser Trp Gly His Leu Leu Ser Leu Ile Asp Ala Glu Ser Ile Gln
1 5 10 15
Lys Leu Pro Asp Gln Pro Ser His His Thr Gln Lys Arg Pro Phe Pro
20 25 30
Ser Gly Glu Lys Leu Pro Asp Gln Pro Phe Thr His His Ser Gln Glu
35 40 45
Gly Pro Phe Pro Pro Gly Arg Glu Thr Ser Arg Pro Ala Pro His Thr
50 55 60
Thr Ala Lys Arg Gly Leu Ser His Leu Glu Arg Asn Phe Gln Thr Ser
65 70 75 80
Pro Ser His His Ser Gln Glu Gly Pro Phe Pro Pro Gly Glu Lys Leu
85 90 95
Pro Asp

<210> 2747
<211> 1100
<212> DNA
<213> Homo sapiens

<400> 2747
tttttcttct ccaggcccag ggccccggcc agtgcccagc cccgctggga gccccggcca
60
gcaccacgga cggcgcccag gaagcccgag tccccctgga cgggggcctt ctggattccg
120

aggcccccgg caggttcgcc caagggctgc ttcgcttgcg tgtccaagcc ccctgccctg
180
caggctccgg cggcccctgc ccctgagccc tcggcctctc ccccgatggc gcccacactg
240
ttccccatgg agtccaagag cagcaagacc gacagcgtgc gggctgccgg cgcgcccccc
300
gcctgcaagc acctagccga gaagaagacg atgaccaacc ccacgaccgt catcgaggtc
360
tacccggaca ccaccgaggt gaacgactat tacctgtggt ccatcttcaa cttcgtctac
420
ctcaacttct gctgcctggg cttcatcgcc ttggcctact ccctcaaagt gcgagacaag
480
aagcttctca atgacctgaa tggagccgtg gaggatgcaa agacggcccg gctgttcaac
540
atcaccagtt ctgccctggc agcctcctgc atcatcctcg tcttcatctt cctgcggtac
600
cccctcaccg actactaagg cccgccaggc acggctgctg gcggagacaa gcactgagac
660
atgtttattc tcatggtccc tgaaacgcag gatcccatga ggttggggca gggcagggct
720
tcttgtcctg gggccccctt gagctgtgaa ctgggcagca aggccatcag aagctgagta
780
cagcaagggg gcagtgagct tggccctcag tccacccccc ccgcctcctg gcctccaccc
840
tgcctgtgtc tggggcctgg gggcttctcc cctcgctgct gcaccctggc ttccagcgtc
900
tgtgtccctg ccctcacgtg ccccttccca ggctcctggg gcccccttgga cctgacacct
960
agcaggaagg gcttatgcaa aattgtccca ggttgggagg actcactctg tgctccccga
1020
ccctgcctcc tccacgatgt gaccccgctc agagcccttg tgtctgtgaa ctttcaatga
1080
aatacccatg cagctccaaa
1100

<210> 2748
<211> 205
<212> PRT
<213> Homo sapiens

<400> 2748
Phe Phe Phe Ser Arg Pro Arg Ala Pro Ala Ser Ala Gln Pro Arg Trp
1 5 10 15
Glu Pro Arg Pro Ala Pro Arg Thr Ala Pro Arg Lys Pro Glu Ser Pro
20 25 30
Trp Thr Gly Ala Phe Trp Ile Pro Arg Pro Pro Ala Gly Ser Pro Lys
35 40 45
Gly Cys Phe Ala Cys Val Ser Lys Pro Pro Ala Leu Gln Ala Pro Ala
50 55 60
Ala Pro Ala Pro Glu Pro Ser Ala Ser Pro Pro Met Ala Pro Thr Leu
65 70 75 80
Phe Pro Met Glu Ser Lys Ser Ser Lys Thr Asp Ser Val Arg Ala Ala
85 90 95
Gly Ala Pro Pro Ala Cys Lys His Leu Ala Glu Lys Lys Thr Met Thr

```
            100                 105                 110
Asn Pro Thr Thr Val Ile Glu Val Tyr Pro Asp Thr Thr Glu Val Asn
        115                 120                 125
Asp Tyr Tyr Leu Trp Ser Ile Phe Asn Phe Val Tyr Leu Asn Phe Cys
    130                 135                 140
Cys Leu Gly Phe Ile Ala Leu Ala Tyr Ser Leu Lys Val Arg Asp Lys
145                 150                 155                 160
Lys Leu Leu Asn Asp Leu Asn Gly Ala Val Glu Asp Ala Lys Thr Ala
                165                 170                 175
Arg Leu Phe Asn Ile Thr Ser Ser Ala Leu Ala Ala Ser Cys Ile Ile
            180                 185                 190
Leu Val Phe Ile Phe Leu Arg Tyr Pro Leu Thr Asp Tyr
        195                 200                 205
```

<210> 2749
<211> 2050
<212> DNA
<213> Homo sapiens

<400> 2749
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gcgccattcg gcagcgcctt gtgggtctat aatctactta gcacagagag tgtcttctaa
120
gtacttcaca tccttctctg cagatgctct gacctttgac ccctgccgtt cagctctagg
180
gcccgtgcag gccacaccat gaacacctcc ccaggcacgg tgggcagtga cccggtcatc
240
ctggccactg caggctacga ccacaccgtg cgcttctggc aggcccacag cggcatctgc
300
acccggacgg tgcagcacca ggactcccag gtgaatgcct tggaggtcac accggaccgc
360
agcatgattg ctgctgcagt tcagcctgtg tccctaggtt accagcacat ccgcatgtat
420
gatctcaact ccaataaccc taaccccatc atcagctacg acggcgtcaa caagaacatc
480
gcgtctgtgg gcttccacga agacggccgc tggatgtaca cgggcggcga ggactgcaca
540
gccaggatct gggacctcag gtcccggaac ctgcagtgcc agcggatctt ccaggtgaac
600
gcacccatta actgcgtgtg cctgcacccc aaccaggcag agctcatcgt gggtgaccag
660
agcggggcta tccacatctg ggacttgaaa acagaccaca acgagcagct gatccctgag
720
cccgaggtct ccatcacgtc cgcccacatc gatcccgacg ccagctacat ggcagctgtc
780
aatagcaccg gaaactgcta tgtctggaat ccgacggggg gcattggtga cgaggtgacc
840
cagctcatcc ccaagactaa gatccctgcc cacacgcgct acgccctgca gtgtcgcttc
900
agccccgact ccacgctcct cgccacctgc tcggctgatc agacgtgcaa gatctggagg
960
acgtccaact tctccctgat gacggagctg agcatcaaga gcggcaaccc cggggagtcc
1020

tcccgcggct ggatgtgggg ctgcgccttc tcgggggact cccagtacat cgtcactgct
1080
tcctcggaca acctggcccg gctctggtgt gtggagactg gagagatcaa gagagagtat
1140
ggcggccacc agaaggctgt tgtctgcctg gccttcaatg acagtgtgct gggctagcct
1200
gtgacccctc gggactgcct ggtgcaggtg gtggcagctg gagggaccca tgcagcaccc
1260
aggtcagagc agaccctccc ctgccggcct gcgccagctg gacctgatgg ccccctgtgg
1320
cgccttgacc tgctgggcca ggctgccctg ggactctcag cccccagttg cttatccaga
1380
tgtgacagag ctcgacccaa gccaggctgc acactcctgg actgggctag cctgcactgc
1440
ctgggaaagt cggccgaggg cccaaagctg ctgaggggtc tgaggctggt gcccaccccc
1500
aagctagtgt gttctctgcc cctccctgcc cgcgtttcag ggcctcggtc catagagaac
1560
accaccacca tggccaggtg gaagggttta ttagtccctg ccagcagctg tcctccctgg
1620
tgcaggtggc ctggccagcc cactggattg gggacgggcc aggctgggcc aggtcggggg
1680
ctcagtctgg gaggtaataa aagcagaccg acacgcagat gttgctcggg aagcagatgt
1740
cgatgcagag ataaatcagc cgctgtctcc ggggcccctc tgctcgccgg gcccagtaga
1800
tgggggtcct catgcacagg cgctgcacca aagcccccgc ctgggcggta gccacttacg
1860
aggctcccct gcactgccag cagctcctgg gtgtggtggg tgtcctggct ggggacccaa
1920
gcctcttgga ccttggaggt atccaccagc agccgcaggt ctcccgatca ctgtcctcca
1980
tcaggcggag gaagcagacc tggtgctcct cagggcggta acagatgcag ccgctctgcc
2040
cgtcgaacag
2050

<210> 2750
<211> 332
<212> PRT
<213> Homo sapiens

<400> 2750
Met Asn Thr Ser Pro Gly Thr Val Gly Ser Asp Pro Val Ile Leu Ala
1 5 10 15
Thr Ala Gly Tyr Asp His Thr Val Arg Phe Trp Gln Ala His Ser Gly
20 25 30
Ile Cys Thr Arg Thr Val Gln His Gln Asp Ser Gln Val Asn Ala Leu
35 40 45
Glu Val Thr Pro Asp Arg Ser Met Ile Ala Ala Ala Val Gln Pro Val
50 55 60
Ser Leu Gly Tyr Gln His Ile Arg Met Tyr Asp Leu Asn Ser Asn Asn
65 70 75 80
Pro Asn Pro Ile Ile Ser Tyr Asp Gly Val Asn Lys Asn Ile Ala Ser

```
                85                  90                  95
Val Gly Phe His Glu Asp Gly Arg Trp Met Tyr Thr Gly Gly Glu Asp
            100                 105                 110
Cys Thr Ala Arg Ile Trp Asp Leu Arg Ser Arg Asn Leu Gln Cys Gln
        115                 120                 125
Arg Ile Phe Gln Val Asn Ala Pro Ile Asn Cys Val Cys Leu His Pro
    130                 135                 140
Asn Gln Ala Glu Leu Ile Val Gly Asp Gln Ser Gly Ala Ile His Ile
145                 150                 155                 160
Trp Asp Leu Lys Thr Asp His Asn Glu Gln Leu Ile Pro Glu Pro Glu
                165                 170                 175
Val Ser Ile Thr Ser Ala His Ile Asp Pro Asp Ala Ser Tyr Met Ala
            180                 185                 190
Ala Val Asn Ser Thr Gly Asn Cys Tyr Val Trp Asn Leu Thr Gly Gly
        195                 200                 205
Ile Gly Asp Glu Val Thr Gln Leu Ile Pro Lys Thr Lys Ile Pro Ala
    210                 215                 220
His Thr Arg Tyr Ala Leu Gln Cys Arg Phe Ser Pro Asp Ser Thr Leu
225                 230                 235                 240
Leu Ala Thr Cys Ser Ala Asp Gln Thr Cys Lys Ile Trp Arg Thr Ser
                245                 250                 255
Asn Phe Ser Leu Met Thr Glu Leu Ser Ile Lys Ser Gly Asn Pro Gly
            260                 265                 270
Glu Ser Ser Arg Gly Trp Met Trp Gly Cys Ala Phe Ser Gly Asp Ser
        275                 280                 285
Gln Tyr Ile Val Thr Ala Ser Ser Asp Asn Leu Ala Arg Leu Trp Cys
    290                 295                 300
Val Glu Thr Gly Glu Ile Lys Arg Glu Tyr Gly Gly His Gln Lys Ala
305                 310                 315                 320
Val Val Cys Leu Ala Phe Asn Asp Ser Val Leu Gly
                325                 330
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<210> 2751
<211> 1877
<212> DNA
<213> Homo sapiens

<400> 2751
nntcatgagc cagcacaact gctccaagga tggccccacc tcgcagccac gcctgcgcac
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gctcccaccn ggccggagac agccaggagc gctcggacag ccccgagatc tgccattacg
120
agaagagctt tcacaagcac tcggccaccc ccaactacac gcactgtggc ctcttcgggg
180
acccacacct caggactttc accgaccgct tccagacctg caaggtgcag ggcgcctggc
240
cgctcatcga caataattac ctgaacgtgc aggtcaccaa cacgcctgtg ctgcccagct
300
cagcggccac tgccaccagc aagctcacca tcatcttcaa gaacttccag gagtgtgtgg
360
accagaaggt gtaccaggct gagatggacg agctcccggc cgccttcgtg gatggctcta
420
agaacggtgg ggacaagcac ggggccaaca gcctgaagat cactgagaag gtgtcaggcc
480

agcacgtgga gatccaggcc aagtacatcg gcaccaccat cgtggtgcgc caggtgggcc
540
gctacctgac ctttgccgtc cgcatgccag aggaagtggt caatgctgtg gaggactggg
600
acagccaggg tctctacctc tgcctgcggg gctgcccccc caaccagcag atcgacttcc
660
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<213> Homo sapiens

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<213> Homo sapiens

<400> 2754

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Cys His Thr Val Val Pro Glu Lys Asp Gly Asp Asn Ile Ile Tyr Gln
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Ala Ser Ser Pro Asp Glu Ala Ala Leu Val Lys Gly Ala Lys Lys Leu
65                  70                  75                  80
Gly Phe Val Phe Thr Ala Arg Thr Pro Phe Ser Val Ile Ile Glu Ala
                85                  90                  95
Met Gly Gln Glu Gln Thr Phe Gly Ile Leu Asn Val Leu Glu Phe Ser
            100                 105                 110
Ser Asp Arg Lys Arg Met Ser Val Ile Val Arg Thr Pro Ser Gly Arg
        115                 120                 125
Leu Arg Leu Tyr Cys Lys Gly Ala Asp Asn Val Ile Phe Glu Arg Leu
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Ser Lys Asp Ser Lys Tyr Met Glu Glu Thr Leu Cys His Leu Glu Tyr
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Phe Ala Thr Glu Gly Leu Arg Thr Leu Cys Val Ala Tyr Ala Asp Leu
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Ser Glu Gly Asn Glu Tyr Glu Glu Trp Leu Lys Val Tyr Gln Glu Ala
            180                 185                 190
Ser Thr Ile Leu Lys Asp Arg Ala Gln Arg Leu Glu Glu Cys Tyr Glu
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Ile Ile Glu Lys Asn Leu Leu Leu Leu Gly Ala Thr Ala Ile Glu Asp
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Arg Leu Gln Ala Gly Val Pro Glu Thr Ile Ala Thr Leu Leu Lys Ala
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Glu Ile Lys Ile Trp Val Leu Thr Gly Asp Lys Gln Glu Thr Ala Ile
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Asn Ile Gly Tyr Ser Cys Arg Leu Val Ser Gln Asn Met Ala Leu Ile
            260                 265                 270
Leu Leu Lys Gly Asp Ser Leu Asp Ala Thr Arg Ala Ala Ile Thr Gln
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His Cys Thr Asp Leu Gly Asn Leu Leu Gly Lys Glu Asn Asp Val Ala
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Arg Arg Ser Phe Leu Asp Leu Ala Leu Ser Cys Lys Ala Val Ile Cys
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Ala Leu Pro Pro Phe Thr Leu Gly Ile Phe Glu Arg Ser Cys Thr Gln
465                 470                 475                 480
Glu Ser Met Leu Arg Phe Pro Gln Leu Tyr Lys Ile Thr Gln Asn Gly
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Glu Gly Phe Asn Thr Lys Val Phe Trp Gly His Cys Ile Asn Ala Leu
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Val His Ser Leu Ile Leu Phe Trp Phe Pro Met Lys Ala Leu Glu His
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Pro Thr Ile Pro Ile Ala Pro Asp Met Arg Gly Gln Ala Thr Met Val
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Cys Leu Ile Glu Asp Val Ala Trp Arg Ala Ala Lys His Thr Cys Lys
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Lys Thr Leu Leu Glu Glu Val Gln Glu Leu Glu Thr Lys Ser Arg Val
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Leu Gly Lys Ala Val Leu Arg Asp Ser Asn Gly Lys Arg Leu Asn Glu
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Arg Asp Arg Leu Ile Lys Arg Leu Gly Arg Lys Thr Pro Pro Thr Leu
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Phe Arg Gly Ser Ser Leu Gln Gln Gly Val Pro His Gly Tyr Ala Phe
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Ala Lys Glu Asn Leu Lys Lys Ile Gln Glu Met Glu Lys Ser Asp Glu
50 55 60
Ser Ser Thr Asp Leu Glu Glu Leu Lys Asn Ala Asp Trp Ala Arg Phe
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85 90 95
Val Gln Glu Arg Gln Tyr Asn Pro Leu Pro Ile Glu Tyr Gln Leu Thr
100 105 110
Pro Tyr Glu Met Leu Met Asp Asp Ile Arg Cys Lys Arg Tyr Thr Leu
115 120 125
Arg Lys Val Met Val Asn Gly Asp Ile Pro Pro Arg Leu Lys Lys Ser
130 135 140
Ala His Glu Ile Ile Leu Asp Phe Ile Arg Ser Arg Pro Pro Leu Asn
145 150 155 160
Pro Val Ser Ala Arg Lys Leu Lys Pro Thr Pro Pro Arg Pro Arg Ser
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225 230 235 240
Pro Ala Gln Arg Lys Lys Leu Leu Arg Ala Pro Thr Leu Ala Glu Leu
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Gln Pro Glu Arg Arg Gln Pro Pro Gln Arg Arg His Ser Ile Glu Lys
305 310 315 320
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325 330 335
Ser Arg Ser Leu Glu Glu Phe Cys Tyr Pro Val Glu Cys Leu Ala Leu
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Gly Lys Leu Cys Phe Cys Cys Arg Thr Arg Arg Phe Ser Phe Phe Thr
385 390 395 400
Trp Ser Tyr Thr Cys Gln Phe Cys Lys Arg Pro Val Cys Ser Gln Cys
405 410 415
Cys Lys Lys Met Arg Leu Pro Ser Lys Pro Tyr Ser Thr Leu Pro Ile

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Arg Phe Ser Ser Lys Ser Lys Ser Met Asp Lys Ser Asp Glu Glu Leu
465                 470                 475                 480
Gln Phe Pro Lys Glu Leu Met Glu Asp Trp Ser Thr Met Glu Val Cys
                485                 490                 495
Val Asp Cys Lys Lys Phe Ile Ser Glu Ile Ile Ser Ser Ser Arg Arg
            500                 505                 510
Ser Leu Val Leu Ala Asn Lys Arg Ala Arg Leu Lys Arg Lys Thr Gln
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tcctgcaggg actgacctct gagttatcca aaggccgacc tggggaaaga ctgattttga
120
ggttttaata gttttcagat gcttcaagtg ttgtgaacag agacttgttt ggattatgca
180
tttctcagct agactaaata aatgctagca atggatacgt gcaaacatgt tgggcagctg
240
cagcttgctc aagaccattc cagcctcaac cctcagaaat ggcactgtgt ggactgcaac
300
acgaccgagt ccatttgggc ttgccttagc tgctcccatg ttgcctgtgg aagatatatt
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gagatgtacg ttttttgtta cctttgtga
449

<210> 2758
<211> 82
<212> PRT
<213> Homo sapiens

<400> 2758
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Met Leu Ala Met Asp Thr Cys Lys His Val Gly Gln Leu Gln Leu Ala
 1               5                  10                  15
Gln Asp His Ser Ser Leu Asn Pro Gln Lys Trp His Cys Val Asp Cys
            20                  25                  30
Asn Thr Thr Glu Ser Ile Trp Ala Cys Leu Ser Cys Ser His Val Ala
        35                  40                  45
Cys Gly Arg Tyr Ile Glu Glu His Ala Leu Lys His Phe Gln Glu Ser
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```
    50                  55                  60
Ser His Pro Val Ala Leu Glu Val Asn Glu Met Tyr Val Phe Cys Tyr
65                  70                  75                  80
Leu Cys
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<210> 2759
<211> 688
<212> DNA
<213> Homo sapiens

<400> 2759
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gagaccaagc ccagccaagg tcccgctgat ggttcccggc ctgagcccca gcgcccacga
120
aaccgccccc acttccagcg gagacggcag caggcccctg gcccccagca ggcccctggc
180
ccccggcagc ccgcagcccc tgagacctca gcccctgtca acagtgggga ccccaccacc
240
accatcctgg agtgattcca actcaactca aaggacaccc agagctgcca tctggtatct
300
gccagttttt ccaaatgacc tgtaccctac ccagtaccct gctccccctt tcccataatt
360
catgacatca aaacatcagc ttttcacctt ttccttgaga ctcaggaggg ccaaagcaac
420
agcctttggc ttttttctct ttttcttccc tctcccctag catgggttga aggaagggag
480
ccatccttac tgttcagaga cagcaactcc ctcccgtaac tcaggctgag aaggaaccag
540
ccagctctta cctcctcctg gttgcttttc ttgcccccac cccaagttta tttttgtttt
600
cccccggccc cctacctctg aagccatttt atgatctgtc atgtgccacc tgagcctcca
660
gtaaaaacaa aaacaggaaa aaaaaaaa
688

<210> 2760
<211> 84
<212> PRT
<213> Homo sapiens

<400> 2760
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Tyr Arg Ser Pro Phe Arg Pro Arg Pro Arg Gln Gln Pro Thr Thr Glu
 1               5                  10                  15
Gly Gly Asp Gly Glu Thr Lys Pro Ser Gln Gly Pro Ala Asp Gly Ser
            20                  25                  30
Arg Pro Glu Pro Gln Arg Pro Arg Asn Arg Pro Tyr Phe Gln Arg Arg
        35                  40                  45
Arg Gln Gln Ala Pro Gly Pro Gln Gln Ala Pro Gly Pro Arg Gln Pro
    50                  55                  60
Ala Ala Pro Glu Thr Ser Ala Pro Val Asn Ser Gly Asp Pro Thr Thr
65                  70                  75                  80
Thr Ile Leu Glu
```

<210> 2761
<211> 922
<212> DNA
<213> Homo sapiens

<400> 2761
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120
cccataactg agggcaataa agagccagat aagacctggg tgaaaaaggg agagcccctc
180
ccggtaaaac tgaactcttc tacagaagca aatgtgatta aagaggctct agactcctct
240
ttggaatcta ctctggacaa cagctgtcaa ggtgcacaaa tggataataa atctgaagtt
300
cagttgtggc tgttaaagag aattcaggta cccattgaag atatacttcc ttcaaaagaa
360
gaaaaaagca agaccccacc catgttcctg tgcatcaaag tgggaaaacc aatgagaaaa
420
tcctttgcca ctcacactgc agccatggtc cagcagtacg gcaaacggag aaagcagcca
480
gagtactggt ttgctgttcc tcgggagagg gtggatcatt tgtacacatt ctttgttcag
540
tggtctcccg atgtctatgg aaaagatgcc aaagagcaag gctttgtggt ggtggagaag
600
gaagaactga acatgattga caacttcttc agtgagccaa caaccaagag ctgggagatc
660
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720
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780
cgctgggccc gccccttttcc tgcaagggtg caagggtatc catggagact ggcctatagc
840
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900
cctgtcctat tggtcatcaa ag
922

<210> 2762
<211> 307
<212> PRT
<213> Homo sapiens

<400> 2762
Thr Arg Glu Gly Pro Gln Val Ser Glu Asn Leu Gln Lys Thr Glu Leu
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Ser Asp Gly Lys Ser Ile Glu Pro Gly Gly Ile Asp Ile Thr Leu Ser
20 25 30
Ser Ser Leu Ser Gln Ala Gly Asp Pro Ile Thr Glu Gly Asn Lys Glu
35 40 45
Pro Asp Lys Thr Trp Val Lys Lys Gly Glu Pro Leu Pro Val Lys Leu

```
    50                  55                  60
Asn Ser Ser Thr Glu Ala Asn Val Ile Lys Glu Ala Leu Asp Ser Ser
65                  70                  75                  80
Leu Glu Ser Thr Leu Asp Asn Ser Cys Gln Gly Ala Gln Met Asp Asn
                85                  90                  95
Lys Ser Glu Val Gln Leu Trp Leu Leu Lys Arg Ile Gln Val Pro Ile
            100                 105                 110
Glu Asp Ile Leu Pro Ser Lys Glu Glu Lys Ser Lys Thr Pro Pro Met
        115                 120                 125
Phe Leu Cys Ile Lys Val Gly Lys Pro Met Arg Lys Ser Phe Ala Thr
    130                 135                 140
His Thr Ala Ala Met Val Gln Gln Tyr Gly Lys Arg Arg Lys Gln Pro
145                 150                 155                 160
Glu Tyr Trp Phe Ala Val Pro Arg Glu Arg Val Asp His Leu Tyr Thr
                165                 170                 175
Phe Phe Val Gln Trp Ser Pro Asp Val Tyr Gly Lys Asp Ala Lys Glu
            180                 185                 190
Gln Gly Phe Val Val Val Glu Lys Glu Glu Leu Asn Met Ile Asp Asn
        195                 200                 205
Phe Phe Ser Glu Pro Thr Thr Lys Ser Trp Glu Ile Ile Thr Val Glu
    210                 215                 220
Glu Ala Lys Arg Arg Lys Ser Thr Cys Ser Tyr Tyr Glu Asp Glu Asp
225                 230                 235                 240
Glu Glu Val Leu Pro Val Leu Arg Pro Pro Arg Ala Phe Trp Glu Asn
                245                 250                 255
Lys Pro Leu Asn Arg Trp Ala Arg Pro Phe Pro Ala Arg Val Gln Gly
            260                 265                 270
Tyr Pro Trp Arg Leu Ala Tyr Ser Thr Leu Glu His Gly Thr Ser Leu
        275                 280                 285
Lys Thr Leu Tyr Arg Lys Ser Ala Ser Leu Asp Ser Pro Val Leu Leu
    290                 295                 300
Val Ile Lys
305
```

<210> 2763
<211> 2210
<212> DNA
<213> Homo sapiens

<400> 2763
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gttcttgttg gatcacaaac aacctaattg acagtctatc gccaacatcc acaaacacag
120
caaacagtcc agtcctgcag accacacagg gtacatctag agggttctac ttgcatcacc
180
cacacttcca ctcctgtgaa acaactgtct tgggcatgag aagggccagg ataggccagg
240
tgaatggcag gctgcccaac aaccccaatc ccaaaccaac ctcccaggcc atgggcccaa
300
gtccctgcag gaagatgcta ataggtacaa caggtagaac atgtagacac aaacatctag
360
tttatttttt ctgactgtaa ccaaagtcag caaaagaaac aacaaaactt cagtgcccta
420

gaaatcctcc tggattcaat gacaacacat caatggccgg gcacagggtt ggattccttt
480
tatgaaatca ccttataatc tctcatcatc ccaggacagt gccttttggg actgcatgaa
540
tctttaatag ctacaccaca ttttctcatc ctttaagtta tgacagacag gttatctctc
600
tccaagagca tcaggttaga tgctctttca ctcttacaaa ctgtcaggtg gagggagaat
660
cacgacatca ttcataaata actgtggagt ctgggatgct ggctgaaggc atctccagga
720
aggactggag ggcgattttg ctaaagggct gctcactgct catttcactg catgccgctt
780
ttctcacttt ggttgggagt ttgaaggacc atgtaatcac agagattaga gctccctgtg
840
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900
tctgtgagct gtattcgcat cagcgccgga gcctcagaaa gaatgcgtgt ttacactctg
960
tactctccaa tgggtaatat ttatcataga aatctaatac atattcttca gtcttgaatc
1020
caaacttctg gtacagtagc atagcggggt tgcttgctga gacgtgaagg gttacgtcct
1080
tgcccatgca ggtctgaatc agatgataga tcatgaaagt tgcaatccct gctcttctcc
1140
attcagggtg gacgaacaga aatgaaatgt aagcttcatt gtatttcaca tcaggaacca
1200
tgaagccaaa ggcaatgatg actttttttat aaagaacaac aacactgaag tctgggtact
1260
gcagacactc agacaggtca atgccaggcc aaaaaaactc ctgacacatg gagttgatcg
1320
ttgggatgtg atttggccgc acataacagt aatcgagagg tgcgtcgggc tccggcgtcc
1380
agtgagggtc gctcctgtgc aggtgggaac gaatctgtga caggagctgc agtttgggtg
1440
gctttgtttc ataatcacgc ctgatataag gtttcaagat ccgagaggta taagggctga
1500
caatactctg gtccacagcc atatcttctg atcctaccaa gcgatacaaa aacttggtgg
1560
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1620
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1680
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1740
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tccgagcttc cggagtcatg gcaacagcac cgggacaagc ttccagcctc ttgagcagca
1860
gcttttcctc gtagatgctc acgggagtat acctgggctc tttcggcttt gtgtccttct
1920
ccagctgagg cttcctcttt tctctagccc ttgtttgcaa agatgtgttt gaatctgtgt
1980
cttcactgtc aatatccatc ctgtcgggtt tttcctcctc actctctacc tcctgcttta
2040

tctgttcagg gcctctgacc ttctttctgc ccccaaccac tggcccagaa gctactgacc
2100
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2160
cgtcatcatg aaacaaggct tgtgggggca tcacatctgg aatcagatct
2210

<210> 2764
<211> 423
<212> PRT
<213> Homo sapiens

<400> 2764

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Gly	Val	Ile	Asp	Pro	Gly	Met	Glu	Tyr	Val	Pro	Pro	Pro	Ala	Gly	Ser
			20					25					30		
Val	Ala	Ser	Gly	Pro	Val	Val	Gly	Gly	Arg	Lys	Lys	Val	Arg	Gly	Pro
		35					40					45			
Glu	Gln	Ile	Lys	Gln	Glu	Val	Glu	Ser	Glu	Glu	Glu	Lys	Pro	Asp	Arg
	50					55					60				
Met	Asp	Ile	Asp	Ser	Glu	Asp	Thr	Asp	Ser	Asn	Thr	Ser	Leu	Gln	Thr
65					70					75					80
Arg	Ala	Arg	Glu	Lys	Arg	Lys	Pro	Gln	Leu	Glu	Lys	Asp	Thr	Lys	Pro
				85					90					95	
Lys	Glu	Pro	Arg	Tyr	Thr	Pro	Val	Ser	Ile	Tyr	Glu	Glu	Lys	Leu	Leu
			100					105					110		
Leu	Lys	Arg	Leu	Glu	Ala	Cys	Pro	Gly	Ala	Val	Ala	Met	Thr	Pro	Glu
		115					120					125			
Ala	Arg	Arg	Leu	Lys	Arg	Lys	Leu	Ile	Val	Arg	Gln	Ala	Lys	Arg	Asp
	130					135					140				
Arg	Gly	Leu	Pro	Leu	Phe	Asp	Leu	Asp	Gln	Val	Val	Asn	Ala	Ala	Leu
145					150					155					160
Leu	Leu	Val	Asp	Gly	Ile	Tyr	Gly	Ala	Lys	Glu	Gly	Gly	Ile	Ser	Arg
				165					170					175	
Leu	Pro	Ala	Gly	Gln	Ala	Thr	Tyr	Arg	Thr	Thr	Cys	Gln	Asp	Phe	Arg
			180					185					190		
Ile	Leu	Asp	Arg	Tyr	Gln	Thr	Ser	Leu	Pro	Ser	Arg	Lys	Gly	Phe	Arg
		195					200					205			
His	Gln	Thr	Thr	Lys	Phe	Leu	Tyr	Arg	Leu	Val	Gly	Ser	Glu	Asp	Met
	210					215					220				
Ala	Val	Asp	Gln	Ser	Ile	Val	Ser	Pro	Tyr	Thr	Ser	Arg	Ile	Leu	Lys
225					230					235					240
Pro	Tyr	Ile	Arg	Arg	Asp	Tyr	Glu	Thr	Lys	Pro	Pro	Lys	Leu	Gln	Leu
				245					250					255	
Leu	Ser	Gln	Ile	Arg	Ser	His	Leu	His	Arg	Ser	Asp	Pro	His	Trp	Thr
			260					265					270		
Pro	Glu	Pro	Asp	Ala	Pro	Leu	Asp	Tyr	Cys	Tyr	Val	Arg	Pro	Asn	His
		275					280					285			
Ile	Pro	Thr	Ile	Asn	Ser	Met	Cys	Gln	Glu	Phe	Phe	Trp	Pro	Gly	Ile
	290					295					300				
Asp	Leu	Ser	Glu	Cys	Leu	Gln	Tyr	Pro	Asp	Phe	Ser	Val	Val	Val	Leu
305					310					315					320
Tyr	Lys	Lys	Val	Ile	Ile	Ala	Phe	Gly	Phe	Met	Val	Pro	Asp	Val	Lys

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                325                 330                 335
Tyr Asn Glu Ala Tyr Ile Ser Phe Leu Phe Val His Pro Glu Trp Arg
            340                 345                 350
Arg Ala Gly Ile Ala Thr Phe Met Ile Tyr His Leu Ile Gln Thr Cys
        355                 360                 365
Met Gly Lys Asp Val Thr Leu His Val Ser Ala Ser Asn Pro Ala Met
    370                 375                 380
Leu Leu Tyr Gln Lys Phe Gly Phe Lys Thr Glu Glu Tyr Val Leu Asp
385                 390                 395                 400
Phe Tyr Asp Lys Tyr Tyr Pro Leu Glu Ser Thr Glu Cys Lys His Ala
                405                 410                 415
Phe Phe Leu Arg Leu Arg Arg
            420
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<210> 2765
<211> 582
<212> DNA
<213> Homo sapiens

<400> 2765
tctgggtgtg gagccttatt attcaccact ttggcaggtg tctcagtggc ttacttaccc
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agtggagggg caggatggca cggccacttg gggcttgggg gcgctccggc tgccgtaccg
180
tggctgcaag cctaaaccgg gcttgggccc atcctgagca gcccagggtt tgttcagctc
240
ccggcttctg gccactcggc atcgccagag tctccaggcc agcacagggc cacagatggc
300
aagtccaaga agcaggcacc cgctgaccac cactgccccg atagttgcag aggccaggcc
360
aggggcgcag ctgacctcca ggaaggcaga gaggttgtgc tgggagctgg ttgtgtccca
420
gcagagcaga ggcttctggc cagagcagtt gtctcggcgg atgtcgtgcc aggactccag
480
ggcacagttg cagtcggcct gcaggtcaag gtcacagcgg gcggccagcg ccccatccac
540
acgagacaag gggttgcgta gcacgttcag gacctcaagc tt
582

<210> 2766
<211> 100
<212> PRT
<213> Homo sapiens

<400> 2766
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Met Gly Arg Trp Pro Pro Ala Val Thr Leu Thr Cys Arg Pro Thr Ala
 1               5                  10                  15
Thr Val Pro Trp Ser Pro Gly Thr Thr Ser Ala Glu Thr Thr Ala Leu
            20                  25                  30
Ala Arg Ser Leu Cys Ser Ala Gly Thr Gln Pro Ala Pro Ser Thr Thr
        35                  40                  45
Ser Leu Pro Ser Trp Arg Ser Ala Ala Pro Leu Ala Trp Pro Leu Gln
```

```
    50                  55                  60
Leu Ser Gly Gln Trp Trp Ser Ala Gly Ala Cys Phe Leu Asp Leu Pro
65                  70                  75                  80
Ser Leu Ala Leu Cys Trp Pro Gly Asp Ser Gly Asp Ala Glu Trp Pro
                85                  90                  95
Glu Ala Gly Ser
            100

<210> 2767
<211> 1202
<212> DNA
<213> Homo sapiens

<400> 2767
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atcacttctg atgactccct ggagcacact gacagttcag atgtgtcgac cctgcagaat
120
gactcagcct acgacagcaa cgaccctgat gtggaatcca acagcagcag tggcatcagc
180
tctcccagca ggcagcccca ggtgcccatg gccacagctg ctggcttgga tagcgcgggc
240
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360
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420
ccccgggtag gctctcgttt ggaaagtgag gaggctgaag acccatttcc agaggaggtc
480
ttccctgcag tgcaaggcaa aaccaagagg ccggtggacc tgaagatcaa gaacttggcc
540
ccgggttcgg tgctcccgcg ggcactggtt ctcaaagcct tctccagcag ctcgctggac
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720
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780
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960
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1020
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1080
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1200
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ag
1202

<210> 2768
<211> 282
<212> PRT
<213> Homo sapiens

<400> 2768
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20 25 30
Ser Leu Ala Gln Pro Asp Arg Arg Tyr Ser Glu Pro Ser Met Pro Ser
35 40 45
Ser Gln Glu Cys Leu Glu Ser Arg Val Thr Asn Gln Thr Leu Thr Lys
50 55 60
Ser Glu Gly Asp Phe Pro Val Pro Arg Val Gly Ser Arg Leu Glu Ser
65 70 75 80
Glu Glu Ala Glu Asp Pro Phe Pro Glu Glu Val Phe Pro Ala Val Gln
85 90 95
Gly Lys Thr Lys Arg Pro Val Asp Leu Lys Ile Lys Asn Leu Ala Pro
100 105 110
Gly Ser Val Leu Pro Arg Ala Leu Val Leu Lys Ala Phe Ser Ser Ser
115 120 125
Ser Leu Asp Ala Ser Ser Asp Ser Ser Pro Val Ala Ser Pro Ser Ser
130 135 140
Pro Lys Arg Asn Phe Phe Ser Arg His Gln Ser Phe Thr Thr Lys Thr
145 150 155 160
Glu Lys Gly Lys Pro Ser Arg Glu Ile Lys Lys His Ser Met Ser Phe
165 170 175
Thr Phe Ala Pro His Lys Lys Val Leu Thr Lys Asn Leu Ser Ala Gly
180 185 190
Ser Gly Lys Ser Gln Asp Phe Thr Arg Asp His Val Pro Arg Gly Val
195 200 205
Arg Lys Glu Ser Gln Leu Ala Gly Arg Ile Val Gln Glu Asn Gly Cys
210 215 220
Glu Thr His Asn Gln Thr Ala Arg Gly Phe Cys Leu Arg Pro His Ala
225 230 235 240
Leu Ser Val Asp Asp Val Phe Gln Gly Ala Asp Trp Glu Arg Pro Gly
245 250 255
Ser Pro Pro Ser Tyr Glu Glu Ala Met Gln Gly Pro Ala Ala Arg Leu
260 265 270
Val Ala Ser Gln Gln Phe Gln Phe Leu Ala
275 280

<210> 2769
<211> 1286
<212> DNA
<213> Homo sapiens

<400> 2769
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120
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180
tacgacgagg gcgacccctc tgagaagctg gagctggtga caggcaccaa cgtgtacatc
240
acaagggcgc agctgatgaa ctgccacgtc agcgcaggca cgcggcacaa ggtcctactg
300
cggcggctcc tggcctcctt ctttgaccgg aacacgctgg ccaacagctg cggcaccggc
360
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420
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480
gcggccgaca tgtgcaccaa cgcccgccgc gtcgtgcgca agagctggat gcccaaggtc
540
aaggtgctca aggctgagga tgacgcctac accaccttca tcagtgaaac gggcaagatc
600
gagccggaca tgatgggtgt ggagcatggc ttcgagaccg ccagccacga gggcgaggcg
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720
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1020
cccctcccca ggcctnaggc cacctcgcgg aagccttcag cctccgcccc tcactgcagc
1080
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1140
cttccacgtc tccaaaagcg ccttcctgtc accctcgtct atccctgcgc ctgggggctg
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1260
tgcacaaccg acctcaggtg gccggc
1286

<210> 2770
<211> 228
<212> PRT
<213> Homo sapiens

<400> 2770
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Ala Glu Lys Val Glu Ala Leu Pro Glu Gln Val Ala Pro Glu Ser Arg
20 25 30
Asn Arg Ile Arg Val Arg Gln Asp Leu Ala Ser Leu Pro Ala Glu Leu

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        35                  40                  45
Ile Asn Gln Ile Gly Asn Arg Cys His Pro Lys Leu Tyr Asp Glu Gly
    50                  55                  60
Asp Pro Ser Glu Lys Leu Glu Leu Val Thr Gly Thr Asn Val Tyr Ile
65                  70                  75                  80
Thr Arg Ala Gln Leu Met Asn Cys His Val Ser Ala Gly Thr Arg His
                85                  90                  95
Lys Val Leu Leu Arg Arg Leu Leu Ala Ser Phe Phe Asp Arg Asn Thr
            100                 105                 110
Leu Ala Asn Ser Cys Gly Thr Gly Ile Arg Ser Ser Thr Asn Asp Pro
        115                 120                 125
Arg Arg Lys Pro Leu Asp Ser Arg Val Leu His Ala Val Lys Tyr Tyr
    130                 135                 140
Cys Gln Asn Phe Ala Pro Asn Phe Lys Glu Ser Glu Met Asn Ala Ile
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Ala Ala Asp Met Cys Thr Asn Ala Arg Arg Val Val Arg Lys Ser Trp
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Met Pro Lys Val Lys Val Leu Lys Ala Glu Asp Asp Ala Tyr Thr Thr
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Phe Ile Ser Glu Thr Gly Lys Ile Glu Pro Asp Met Met Gly Val Glu
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<210> 2771
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<212> DNA
<213> Homo sapiens

<400> 2771

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<213> Homo sapiens

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        35   40   45
Thr Thr Leu Gly Thr Leu Arg Lys Phe Pro Gly Ser Lys Leu Ala Glu
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Met Phe Ser Ser Leu Ala Lys Ala Ser Thr Asp Ala Glu Gly Arg Phe
65   70   75   80
Phe Ile Asp Arg Pro Ser Thr Tyr Phe Arg Pro Ile Leu Asp Tyr Leu
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Arg Thr Gly Gln Val Pro Thr Gln His Ile Pro Glu Val Tyr Arg Glu

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            100                 105                 110
Ala Gln Phe Tyr Glu Ile Lys Pro Leu Val Lys Leu Leu Glu Asp Met
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Val Pro Gly Tyr Ser Glu Asn Leu Glu Leu Met Val Arg Leu Ala Arg
145                 150                 155                 160
Ala Glu Ala Ile Thr Ala Arg Lys Ser Ser Val Leu Val Cys Leu Val
                165                 170                 175
Glu Thr Glu Glu Gln Asp Ala Tyr Tyr Ser Glu Val Leu Cys Phe Leu
            180                 185                 190
Gln Asp Lys Lys Met Phe Lys Ser Val Val Lys Phe Gly Pro Trp Lys
        195                 200                 205
Ala Val Leu Asp Asn Ser Asp Leu Met His Cys Leu Glu Met Asp Ile
    210                 215                 220
Lys Ala Gln Gly Tyr Lys Val Phe Ser Lys Phe Tyr Leu Thr Tyr Pro
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<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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35 40 45
Gly Ile Met Arg Ser Lys Lys Pro Lys Lys His Pro Lys Val Ala Val
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Lys Ala Lys Pro Ser Pro Arg Leu Thr Ile Phe Asp Glu Glu Val Asp
65 70 75 80
Pro Asp Glu Gly Leu Phe Gly Pro Gly Arg Lys Leu Ser Pro Gln Asp
85 90 95
Pro Ser Glu Asp Val Ser Ser Met Asp Pro Leu Lys Leu Phe Asp Asp
100 105 110
Pro Asp Leu Gly Gly Ala Ile Pro Leu Gly Asp Ser Leu Leu Leu Pro
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Ala Ala Cys Glu Ser Gly Gly Pro Thr Pro Ser Leu Ser His Arg Asp
130 135 140
Ala Ser Lys Glu Leu Phe Arg Gln Ile Gln Lys Glu Pro
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<210> 2775
<211> 3139
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

<400> 2776
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Trp Thr His Pro Ile Thr Asp Gln Leu Arg Ala Met Asn Lys Ala Ala
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His Gln Glu Ser Thr Glu His Val Leu Ser Gly Gly Val Val Val Ser
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Ala Ile Phe Phe Ile Leu Ser Ala Asn Ile Leu Ser Ser Pro Ser Lys
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Arg Gly Gln Lys Gly Thr Leu Ile Gly Tyr Ser Pro Glu Gly Thr Pro
100 105 110
Leu Tyr Asn Phe Met Gly Asp Ala Phe Gln His Ser Ser Gln Ser Ile
115 120 125
Pro Arg Phe Ile Lys Glu Ser Leu Lys Gln Ile Leu Glu Glu Ser Asp
130 135 140
Ser Arg Gln Ile Phe Tyr Phe Leu Cys Leu Asn Leu Leu Phe Thr Phe
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Gly Tyr Gly Arg Ile Glu Ile Leu Ser Gly Phe Ile Asn Gly Leu Phe
    210                 215                 220
Leu Ile Val Ile Ala Phe Phe Val Phe Met Glu Ser Val Ala Arg Leu
225                 230                 235                 240
Ile Asp Pro Pro Glu Leu Asp Thr His Met Leu Thr Pro Val Ser Val
                245                 250                 255
Gly Gly Leu Ile Val Asn Leu Ile Gly Ile Cys Ala Phe Ser His Ala
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His Ser His Ala His Gly Ala Ser Gln Gly Ser Cys His Ser Ser Asp
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Arg Ile His Ser Leu Ile Glu Gln Phe Gly Trp Phe Ile Ala Asp Ser
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<212> DNA
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675 680 685
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780
gaaacgctgc ctgggtggaa agcagacacc acaggcgcca ggaggtggga ggacctgccc
840
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900
gttggtgttg gcaagtcaag agagtcgatg atccagctgt tttagtcgca gactgagctg
960
atcccaacag gccctggcag cgtctggact tgtgtaaaca gcagcagtca cgttcctcgg
1020

ccgccacaac caacaccaaa gcaggaaaac cattttctgt acttttatat ttctgttcaa
1080
cctgttggtt tctacaatga ttttaaacat tggaaagcca gccttgtgta tatttttaaa
1140
aattatattc aaaatgagcc aaagtgctca gagaccttct atgacacatt agtgtcacat
1200
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1260
aaaaaaaa
1268

<210> 2782
<211> 314
<212> PRT
<213> Homo sapiens

<400> 2782
Val Asp Gly Leu Gln Glu Val Gln Arg Gln Ala Gln Glu Gly Lys Asn
 1   5   10   15
Ile Gly Thr Thr Lys Lys Gly Ile Gly Pro Thr Tyr Ser Ser Lys Ala
            20   25   30
Ala Arg Thr Gly Leu Arg Ile Cys Asp Leu Leu Ser Asp Phe Asp Glu
        35   40   45
Phe Ser Ser Arg Phe Lys Asn Leu Ala His Gln His Gln Ser Met Phe
    50   55   60
Pro Thr Leu Glu Ile Asp Ile Glu Gly Gln Leu Lys Arg Leu Lys Gly
65   70   75   80
Phe Ala Glu Arg Ile Arg Pro Met Val Arg Asp Gly Val Tyr Phe Met
                85   90   95
Tyr Glu Ala Leu His Gly Pro Pro Lys Lys Ile Leu Val Glu Gly Ala
            100   105   110
Asn Ala Ala Leu Leu Asp Ile Asp Phe Gly Thr Tyr Pro Phe Val Thr
        115   120   125
Ser Ser Asn Cys Thr Val Gly Gly Val Cys Thr Gly Leu Gly Ile Pro
    130   135   140
Pro Gln Asn Ile Gly Asp Val Tyr Gly Val Val Lys Ala Tyr Thr Thr
145   150   155   160
Arg Val Gly Ile Gly Ala Phe Pro Thr Glu Gln Ile Asn Glu Ile Gly
                165   170   175
Gly Leu Leu Gln Thr Arg Gly His Glu Trp Gly Val Thr Thr Gly Arg
            180   185   190
Lys Arg Arg Cys Gly Trp Leu Asp Leu Met Ile Leu Arg Tyr Ala His
        195   200   205
Met Val Asn Gly Phe Thr Ala Leu Ala Leu Thr Lys Leu Asp Ile Leu
    210   215   220
Asp Val Leu Gly Glu Val Lys Val Gly Val Ser Tyr Lys Leu Asn Gly
225   230   235   240
Lys Arg Ile Pro Tyr Phe Pro Ala Asn Gln Glu Met Leu Gln Lys Val
                245   250   255
Glu Val Glu Tyr Glu Thr Leu Pro Gly Trp Lys Ala Asp Thr Thr Gly
            260   265   270
Ala Arg Arg Trp Glu Asp Leu Pro Pro Gln Ala Gln Asn Tyr Ile Arg
        275   280   285
Phe Val Glu Asn His Val Gly Val Ala Val Lys Trp Val Gly Val Gly

290 295 300
Lys Ser Arg Glu Ser Met Ile Gln Leu Phe
305 310

<210> 2783
<211> 2376
<212> DNA
<213> Homo sapiens

<400> 2783
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120
gttgatgtag aagattatta cccagctttc ctggacatgg tgcggagcct gctggatggc
180
aacatagact catcacagta tgaagattca ctgagagaga tgttcaccat tcatgcctac
240
attgccttta ccatggacaa actgatccag agcattgtca gacagctgca gcatatcgtg
300
agtgatgaga tctgtgtgca ggtgactgac ctttacctgg cagaaaataa taatggggcc
360
accggaggcc agctgaacac acagaactca aggagcctcc tggagtcaac gtatcagcgg
420
aaagctgagc agctaatgtc agatgagaat tgctttaagc ttatgtttat tcagagccaa
480
ggccaggtcc agctgactat tgagcttctg gacacagaag aggagaattc ggatgaccct
540
gtggaagcag agcgctggtc agactacgtg gagcgataca tgaattcaga tactacctcg
600
cctgagcttc gtgaacatct agcacagaaa ccagtatttc tccccaggaa tctacggcgg
660
atccggaagt gtcaacgtgg tcgagagcag caggaaaagg aagggaagga aggaaacagc
720
aagaagacca tggagaatgt ggatagtctg gataagctgg agtgtagatt caagctgaat
780
tcctacaaga tggtgtatgt gatcaaatca gaggactata tgtatcggag gaccgccctg
840
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900
tgggtagata aatggaccaa ggagcatgtg ccccgtgaaa tggcagcaga gaccagcaag
960
tggctcatgg gtgaggggct ggagggcctg gtgccctgta ccaccacctg tgatacagag
1020
accctgcatt ttgtgagcat taacaagtat cgtgtcaaat acggcacagt attcaaagcc
1080
ccttaactgc aaagccagag cagataactt ggggtgtgtg tggggatgtg tgtgtgggcc
1140
tatgcactca cacactgaag aaacaaggaa gatgcctttc aagcctcact gggcctctct
1200
gggacatggc cacctgacct gtgtgtggct ggtgcagcct ggcaccaagt gggctacctg
1260
ttaggaacat gaatacctta caaagctgaa gctggaactt ttcccaaagg gttttgggta
1320

tagcctgccc tggaggggaa ggaagtccat gcaagcaaag acatgcagtt tgcttgcaca
1380
caccagcaga gctaagactg gagtctcctg tggcctaact ttcaatgagg gaaccggatg
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ctgttcacac tttgactgga tggagatgca tttacaaaac agactggaga aggacttaat
1500
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1560
aaaagctgga tttgattttt ttttctggt cactcgagca catctaagat cacccattag
1620
gttttatctg ggacctgcag tttggctttg ggattgatca tcttgtggat tttattcctg
1680
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1740
tcagttgtcc tttttagctc ccgtggaact gttttgtatc tgcctcttta ctagtctacc
1800
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1860
taacttgttt ttttgtacat aatgtacata ctgtcaattt tttattaaaa gaaatatgct
1920
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1980
tagtacctat gaacagatgt acaagacatt tattacactt tttaccaaag ggagttacca
2040
ttgtagtact tttgtgtaaa acttgtcttc ccctttgccc ccaacttttt ttttttttt
2100
ttgtaaataa ataaagcttg gttcttactt aaggaaaaaa ctctcaaccc acgtcccttg
2160
tcctcaccag aaaatactgt gaagcaggga ttttgacttc agttccttat ccagggtaga
2220
aacaggattt tgcttaaaat acttgttact tgtcccaaat caaaatattc caaaatctta
2280
gaatacttaa gtcttttagt acgtgttttt ttcccttgtt caaataatct gaaaatattt
2340
tatatttggg taagttgtca agctatgtag tttgta
2376

<210> 2784
<211> 361
<212> PRT
<213> Homo sapiens

<400> 2784
Ala Glu Arg Gln Ile Glu Glu Glu Asn Arg Glu Arg Glu Trp Glu Arg
1 5 10 15
Glu Val Leu Gly Ile Lys Arg Asp Lys Ser Asp Ser Pro Ala Ile Gln
20 25 30
Leu Arg Leu Lys Glu Pro Met Asp Val Asp Val Glu Asp Tyr Tyr Pro
35 40 45
Ala Phe Leu Asp Met Val Arg Ser Leu Leu Asp Gly Asn Ile Asp Ser
50 55 60
Ser Gln Tyr Glu Asp Ser Leu Arg Glu Met Phe Thr Ile His Ala Tyr
65 70 75 80
Ile Ala Phe Thr Met Asp Lys Leu Ile Gln Ser Ile Val Arg Gln Leu

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                85                  90                  95
Gln His Ile Val Ser Asp Glu Ile Cys Val Gln Val Thr Asp Leu Tyr
            100                 105                 110
Leu Ala Glu Asn Asn Asn Gly Ala Thr Gly Gly Gln Leu Asn Thr Gln
        115                 120                 125
Asn Ser Arg Ser Leu Leu Glu Ser Thr Tyr Gln Arg Lys Ala Glu Gln
    130                 135                 140
Leu Met Ser Asp Glu Asn Cys Phe Lys Leu Met Phe Ile Gln Ser Gln
145                 150                 155                 160
Gly Gln Val Gln Leu Thr Ile Glu Leu Leu Asp Thr Glu Glu Glu Asn
                165                 170                 175
Ser Asp Asp Pro Val Glu Ala Glu Arg Trp Ser Asp Tyr Val Glu Arg
            180                 185                 190
Tyr Met Asn Ser Asp Thr Thr Ser Pro Glu Leu Arg Glu His Leu Ala
        195                 200                 205
Gln Lys Pro Val Phe Leu Pro Arg Asn Leu Arg Arg Ile Arg Lys Cys
    210                 215                 220
Gln Arg Gly Arg Glu Gln Gln Glu Lys Glu Gly Lys Glu Gly Asn Ser
225                 230                 235                 240
Lys Lys Thr Met Glu Asn Val Asp Ser Leu Asp Lys Leu Glu Cys Arg
                245                 250                 255
Phe Lys Leu Asn Ser Tyr Lys Met Val Tyr Val Ile Lys Ser Glu Asp
            260                 265                 270
Tyr Met Tyr Arg Arg Thr Ala Leu Leu Arg Ala His Gln Ser His Glu
        275                 280                 285
Arg Val Ser Lys Arg Leu His Gln Arg Phe Gln Ala Trp Val Asp Lys
    290                 295                 300
Trp Thr Lys Glu His Val Pro Arg Glu Met Ala Ala Glu Thr Ser Lys
305                 310                 315                 320
Trp Leu Met Gly Glu Gly Leu Glu Gly Leu Val Pro Cys Thr Thr Thr
                325                 330                 335
Cys Asp Thr Glu Thr Leu His Phe Val Ser Ile Asn Lys Tyr Arg Val
            340                 345                 350
Lys Tyr Gly Thr Val Phe Lys Ala Pro
        355                 360
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<210> 2785
<211> 492
<212> DNA
<213> Homo sapiens

<400> 2785
gccgcggttc ggacccgccg gcgacatggc cagctccgga gaggacatat ccaatgatga
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tgatgacatg cacctgcag cagccgggat ggcagacggg gtccacctcc tagggttctc
120
tgatgagatc ctccttcaca tcctgagtca cgtccccagc acagatctga ttctgaacgt
180
ccggcgtacc tgtcggaagc ttgcagccct gtgccttgac aagagcctca tccacaccgt
240
gttgctgcaa aaggactatc aggcgagcga ggacaaagtg aggcagctgg tgaaggagat
300
cggccgggag atccagcagc tgagcatggc tggctgctac tggctgcctg gctccaccgt
360

ggaacacgtg gcccgctgcc cgcagcctgg tgaaggtgaa cctctcgggc tgccacctca
420
cttccctgcg cctctacaag atgctctcgg ccctgcagca cctgcgctcg ctggccatcg
480
acgtgagccc cg
492

<210> 2786
<211> 155
<212> PRT
<213> Homo sapiens

<400> 2786
Met Ala Ser Ser Gly Glu Asp Ile Ser Asn Asp Asp Asp Asp Met His
1 5 10 15
Pro Ala Ala Ala Gly Met Ala Asp Gly Val His Leu Leu Gly Phe Ser
20 25 30
Asp Glu Ile Leu Leu His Ile Leu Ser His Val Pro Ser Thr Asp Leu
35 40 45
Ile Leu Asn Val Arg Arg Thr Cys Arg Lys Leu Ala Ala Leu Cys Leu
50 55 60
Asp Lys Ser Leu Ile His Thr Val Leu Leu Gln Lys Asp Tyr Gln Ala
65 70 75 80
Ser Glu Asp Lys Val Arg Gln Leu Val Lys Glu Ile Gly Arg Glu Ile
85 90 95
Gln Gln Leu Ser Met Ala Gly Cys Tyr Trp Leu Pro Gly Ser Thr Val
100 105 110
Glu His Val Ala Arg Cys Pro Gln Pro Gly Glu Gly Glu Pro Leu Gly
115 120 125
Leu Pro Pro His Phe Pro Ala Pro Leu Gln Asp Ala Leu Gly Pro Ala
130 135 140
Ala Pro Ala Leu Ala Gly His Arg Arg Glu Pro
145 150 155

<210> 2787
<211> 299
<212> DNA
<213> Homo sapiens

<400> 2787
ngtctttaga caatgactcg ggacagtgga atgaaacaga agcatgctgc atcaacctca
60
atgtggggag aagagccgta ctctgacata tcagttgcta aaacacgtgc agggcatgcc
120
acaatgcaca gacatggcag tatccttctg gtgggaggga gtcaccattt gctctgccct
180
gccctctgct gggtgctctt acaggtgcta ctgcatccag cgcttgaaac aattctgtgg
240
ggtattgatt ctgaagagat cactgatggc cgtgatttct tgcctcagct tacccagat
299

<210> 2788
<211> 95
<212> PRT

<213> Homo sapiens

<400> 2788
Met Thr Arg Asp Ser Gly Met Lys Gln Lys His Ala Ala Ser Thr Ser
1 5 10 15
Met Trp Gly Glu Glu Pro Tyr Ser Asp Ile Ser Val Ala Lys Thr Arg
20 25 30
Ala Gly His Ala Thr Met His Arg His Gly Ser Ile Leu Leu Val Gly
35 40 45
Gly Ser His His Leu Leu Cys Pro Ala Leu Cys Trp Val Leu Leu Gln
50 55 60
Val Leu Leu His Pro Ala Leu Glu Thr Ile Leu Trp Gly Ile Asp Ser
65 70 75 80
Glu Glu Ile Thr Asp Gly Arg Asp Phe Leu Pro Gln Leu Thr Gln
85 90 95

<210> 2789
<211> 492
<212> DNA
<213> Homo sapiens

<400> 2789
nggaccccag ctgctccttt ttgaaggaaa tctgctcgct cagggagtcg atgcggccga
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gctgctggaa ggagtgcacc aggaggctgc cggggtccgg gagcccatgc tccagtgcct
120
gcgaggccag gctgtgcagt ggggccagca ccagctgcag cttctcctcc agcaggtcca
180
ccctggactg cagcctctgc acttcttcct tcattgcact gtccactcct gcgggcagag
240
ccaggcgctg ggtcacggcc ggccggctcc ccacccacac ccccagggct ccctcctgtc
300
cccagggaga ggcagagcca gaagactcag gcccaggcct ctgccacccc cgctgcctgc
360
ctggcgctgg ccagaggtct caggctatgc cgcctaagta cgtcggggcg ggtggctctg
420
cgcagaggct cagggtcccg gccacgctga gggaggtcaa ggctgaggtc tcagcggccc
480
tcgttccgaa tt
492

<210> 2790
<211> 141
<212> PRT
<213> Homo sapiens

<400> 2790
Arg Lys Ser Ala Arg Ser Gly Ser Arg Cys Gly Arg Ala Ala Gly Arg
1 5 10 15
Ser Ala Pro Gly Gly Cys Arg Gly Pro Gly Ala His Ala Pro Val Pro
20 25 30
Ala Arg Pro Gly Cys Ala Val Gly Pro Ala Pro Ala Ala Ser Pro
35 40 45
Pro Ala Gly Pro Pro Trp Thr Ala Ala Ser Ala Leu Leu Pro Ser Leu

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    50                  55                  60
His Cys Pro Leu Leu Arg Ala Glu Pro Gly Ala Gly Ser Arg Pro Ala
65                  70                  75                  80
Gly Ser Pro Pro Thr Pro Pro Gly Leu Pro Pro Val Pro Arg Glu Arg
                85                  90                  95
Gln Ser Gln Lys Thr Gln Ala Gln Ala Ser Ala Thr Pro Ala Ala Cys
            100                 105                 110
Leu Ala Leu Ala Arg Gly Leu Arg Leu Cys Arg Leu Ser Thr Ser Gly
        115                 120                 125
Arg Val Ala Leu Arg Arg Gly Ser Gly Ser Arg Pro Arg
    130                 135                 140
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<210> 2791
<211> 1271
<212> DNA
<213> Homo sapiens

<400> 2791
nntgtacagg ggatgcagaa tcaatgaaag agataaacaa acatcagagt actgtcagac
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atagaggact ggataataca tttgtgtctt tctacatagt ggtatagaaa tatcaggtcc
120
ccaaattccc atttttcttc caatcacatt taaaatttca atatgttgca ggcagtatgt
180
gtaagattat atccaaatat ttactcctgg ttgctcctct tgggcaagct gtgaatatga
240
tcaaaatatt taaagaagga agaaggtaaa gatctaaaat atgacatgaa aatacccaga
300
gaagtgtgcc taaattagca ttagggtttg agggatccta aggatgacaa aaagggactc
360
ttctattgaa ttcgtggttg atgctcagcg atagtaacaa tcctgcctcc cctaacatct
420
tcctcccctt ccagcagctt cacagaacat ggttgatgag gtaacttagg ggatgcacag
480
ggtgtggcca gaagacccct ttccctatag accactatga gccctgaaag atttatgagg
540
taatgttcac ttcatcctgt gcttcttttc ctagatgtga actatgaaga ctttactttc
600
accataccag atgtagagga ctcaagtcag agaccagatc agggacccca gagacctcct
660
cctgaaggac tcctacctag acccccctggt gatagtggta accaagatga tggtcctcag
720
cagagaccac caaaaccagg aggccatcac cgccatcctc ccccacctcc ttttcaaaat
780
cagcaacgac caccccaacg aggacaccgt caactctctc taccccgatt tccttctgtc
840
agcctgcagg aagcatcatc attcttccgg agggacagac cagcaagaca tccccaggag
900
caaccactct ggtaatctag aattcagtgg cagaaaataa ataagaagat aacttccttc
960
agaaagccat gacattgaaa taatgtggtc ataactcttt cttcagtata ccaataaaat
1020
attaatagca tgcggaagaa agaatggttt gcatccacat ggagagtgta ccatttagag
1080

gtaacaggga gaggagaggg tgtgccatca agaggcaaca tggaggtgtt tcaaacctat
1140
gcatcttgtt ataaatatat ctttgctcac atgaatttta cttgttaatt agcctggctg
1200
gggtgaatgg taacaggaga gaaatggaag agaataggga gcactgcgcc agcattaaca
1260
gctcactgtc t
1271

<210> 2792
<211> 123
<212> PRT
<213> Homo sapiens

<400> 2792
Cys Ser Leu His Pro Val Leu Leu Phe Leu Asp Val Asn Tyr Glu Asp
1 5 10 15
Phe Thr Phe Thr Ile Pro Asp Val Glu Asp Ser Ser Gln Arg Pro Asp
20 25 30
Gln Gly Pro Gln Arg Pro Pro Pro Glu Gly Leu Leu Pro Arg Pro Pro
35 40 45
Gly Asp Ser Gly Asn Gln Asp Asp Gly Pro Gln Gln Arg Pro Pro Lys
50 55 60
Pro Gly Gly His His Arg His Pro Pro Pro Pro Pro Phe Gln Asn Gln
65 70 75 80
Gln Arg Pro Pro Gln Arg Gly His Arg Gln Leu Ser Leu Pro Arg Phe
85 90 95
Pro Ser Val Ser Leu Gln Glu Ala Ser Ser Phe Phe Arg Arg Asp Arg
100 105 110
Pro Ala Arg His Pro Gln Glu Gln Pro Leu Trp
115 120

<210> 2793
<211> 847
<212> DNA
<213> Homo sapiens

<400> 2793
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gtggtccctc gggtgaaaca gaaagcggga gctacgcgga gagggagcga agagcggggc
120
tgaggcggcg gcgtcactgc caggaaacaa ccccaacagt cagcgcgccg gcggccgcgg
180
cggccctgag agctgactct gcagctgagg tagagagaca acgatcagga accctaagaa
240
gaggcgccag aggagccgcc ttctgcctca gaacggcgtg actcggagaa ttggagcgtt
300
attcagtata ttaatgtctt attgataatg gcagaacatc caccactact ggatacaact
360
cagatcttaa gtagtgatat ttctcttttg tctgccccta ttgtaagtgc agatggaaca
420
caacaggtta ttctggtaca agttaaccca ggagaagcat ttacaataag aagagaagat
480

ggacagtttc agtgcattac aggtcctgct caggttccaa tgatgtcccc aaatggttct
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gtgcctccta tctatgtgcc tcctggatat gccccacagg ttattgaaga caatggtgtt
600
cgaagagttg tcgtggtccc tcaggcacca gagtttcacc ctggtagtca cacagttctc
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caccgttctc cacatcctcc tctacctggt ttcattcctg tcccaactat gatgccgcct
720
caccacgtca tatgtactca cccgtgactg gagctggaga catgacaaca cagtatatgc
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840
cacgcgt
847

<210> 2794
<211> 139
<212> PRT
<213> Homo sapiens

<400> 2794
Met Ala Glu His Pro Pro Leu Leu Asp Thr Thr Gln Ile Leu Ser Ser
 1   5   10   15
Asp Ile Ser Leu Leu Ser Ala Pro Ile Val Ser Ala Asp Gly Thr Gln
            20   25   30
Gln Val Ile Leu Val Gln Val Asn Pro Gly Glu Ala Phe Thr Ile Arg
        35   40   45
Arg Glu Asp Gly Gln Phe Gln Cys Ile Thr Gly Pro Ala Gln Val Pro
    50   55   60
Met Met Ser Pro Asn Gly Ser Val Pro Pro Ile Tyr Val Pro Pro Gly
65   70   75   80
Tyr Ala Pro Gln Val Ile Glu Asp Asn Gly Val Arg Arg Val Val Val
                85   90   95
Val Pro Gln Ala Pro Glu Phe His Pro Gly Ser His Thr Val Leu His
            100   105   110
Arg Ser Pro His Pro Pro Leu Pro Gly Phe Ile Pro Val Pro Thr Met
        115   120   125
Met Pro Pro His His Val Ile Cys Thr His Pro
    130   135

<210> 2795
<211> 1022
<212> DNA
<213> Homo sapiens

<400> 2795
ngccggcgct gccagcagtt gtagagcagg ccaagcgcaa tgatgatgat gcagatggcc
60
ccaatgacca ccagcaccac gaagagcgtg ccgtagtcgc tgcgcacctg gctggcccgc
120
gcctggcagc tgctggttgt ggaatagttc tggatgccaa tctcctccag gctcctgcgg
180
atgtcaccca gcatggaaag gacatcttga gtgggcacca ccccctgctc gcccaccagt
240

gtcatgagaa ggtgctgctc cttctcgctg ggcttgctca gagagatgtg ccaggcccca
300
tggtggccac tgccatggcg gggcagcacc tcttccacca gggccaggag ctgtggcccc
360
cggtgctgcc ggaacacctc acagtctatg ttctctgtca tgttcagaat gatgtagttt
420
ttcccagcca gattgctcca gtccttgcag atcacctgcg tagaatccca gggtatcctg
480
gattgagctt cagctgcctg cccttctagg agctgctggt tgagatcttc ttgtcccaag
540
gtagcagagg aaggtgtcag ttccatgtct ccaggggcca gtggggaaga ggctgaggtt
600
ctagagccaa ggggatcttc atctgggtgc tcggccccac tgggagctgt ggtttgaggg
660
aatgaaggca aggccggcac ctcctcgtgc tggccagaca aaccagctgc tcctgcagtg
720
gcttcctcgc ttgcttcctg aggagcctcg aactctaccc caagccctgc agctggcagc
780
actgtggcct ctgcctcttg gctggtggag tcctggtccc ccggagtcac tgtagttggg
840
gtgactgaag gcagcagcaa gctgggcccc atgctgctct ccacctcatc aggtgagnna
900
gaaaagtcac ggacctgagg cttggcttct tcttgggatc cattcacagg gagcagctcc
960
tcctcttcct cctcctcttg tttctctacc tcttccttct ccctctcctc cccttcacgc
1020
gt
1022

<210> 2796
<211> 56
<212> PRT
<213> Homo sapiens

<400> 2796
Ala Ser Ala Ala Cys Pro Ser Arg Ser Cys Trp Leu Arg Ser Ser Cys
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Pro Lys Val Ala Glu Glu Gly Val Ser Ser Met Ser Pro Gly Ala Ser
            20   25   30
Gly Glu Glu Ala Glu Val Leu Glu Pro Arg Gly Ser Ser Ser Gly Cys
        35   40   45
Ser Ala Pro Leu Gly Ala Val Val
    50   55

<210> 2797
<211> 475
<212> DNA
<213> Homo sapiens

<400> 2797
cggccgctgc tgattgcctt cagcgcctgc accacggtgc tggtggccgt gcacctgttc
60
gccctcctca tcagcacctg catcctgccc aatgtggagg ccgtgagcaa catccacaac
120

ctgaactcca tcagcgagtc cccgcatgag cgcatgcacc cctacatcga gctggcctgg
180
ggcttctcca ccgtgcttgg catcctactc ttcctggccg aggtggtgct gctctgctgg
240
atcaagttcc tccccgtgga tgcccggcgc cagcctggcc ccccacctgg ccctgggagt
300
cacacgggct ggcaggccgc cctggtgtcc accatcatca tggtgcccgt gggcctcatc
360
ttcgtggtct tcaccatcca cttctaccgc tccctggtgc gccacaaaac ggagcgccac
420
aaccgcgaga tcgaggagct ccacaagctc aaggtccagc tggacgggca tgagc
475

<210> 2798
<211> 158
<212> PRT
<213> Homo sapiens

<400> 2798
Arg Pro Leu Leu Ile Ala Phe Ser Ala Cys Thr Thr Val Leu Val Ala
1 5 10 15
Val His Leu Phe Ala Leu Leu Ile Ser Thr Cys Ile Leu Pro Asn Val
20 25 30
Glu Ala Val Ser Asn Ile His Asn Leu Asn Ser Ile Ser Glu Ser Pro
35 40 45
His Glu Arg Met His Pro Tyr Ile Glu Leu Ala Trp Gly Phe Ser Thr
50 55 60
Val Leu Gly Ile Leu Leu Phe Leu Ala Glu Val Val Leu Leu Cys Trp
65 70 75 80
Ile Lys Phe Leu Pro Val Asp Ala Arg Arg Gln Pro Gly Pro Pro Pro
85 90 95
Gly Pro Gly Ser His Thr Gly Trp Gln Ala Ala Leu Val Ser Thr Ile
100 105 110
Ile Met Val Pro Val Gly Leu Ile Phe Val Val Phe Thr Ile His Phe
115 120 125
Tyr Arg Ser Leu Val Arg His Lys Thr Glu Arg His Asn Arg Glu Ile
130 135 140
Glu Glu Leu His Lys Leu Lys Val Gln Leu Asp Gly His Glu
145 150 155

<210> 2799
<211> 2872
<212> DNA
<213> Homo sapiens

<400> 2799
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180
tcatgggtca tgtctccttt tttattctgc tgcatgatgg ttggaggtgg cgaagacacc
240

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360
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420
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480
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540
atcatcccat tggccctgcc ttgcaagctg gtcattccaa accgagaccc cacagatgaa
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720
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780
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840
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900
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gccatcgtca acttcgtctc caaggtcatg ctgaatgccg gccaaaagag atgaaccctg
1080
ccccttgccc agggccagtg ccatggggaa ggggcttgtg gggaggggac ccatgaatcc
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1200
caacgtgggg agagggaagt gaattgcaga ggggaggggg aaaagagaga gagagagaga
1260
gagagagaga gagagagaga gagaaagatg gaggagaaga acttggattc ccctgggtag
1320
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1380
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1440
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1620
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1740
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1860

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1920
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1980
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gctggggatt gagtcttgct gctctgccca gccctgttct attctgcagg gtccctgtgt
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2340
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2460
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2580
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2640
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2700
acatgagaca tactgacaga atctgtaagc taataaaatg taagaaaagg ttaaaaaaag
2760
aataggtaaa ttgacaagaa gtatttattg tttttccata ttgctttatt gccttccttg
2820
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2872

<210> 2800
<211> 294
<212> PRT
<213> Homo sapiens

<400> 2800
Met Ser Pro Phe Leu Phe Cys Cys Met Met Val Gly Gly Gly Glu Asp
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Thr Phe Met Ala Ser Pro Tyr Lys Pro Glu Ile Ser Arg Glu Gln Ala
20 25 30
Ile Ala Leu Leu Lys Asp Gln Glu Pro Gly Ala Phe Ile Ile Arg Asp
35 40 45
Ser His Ser Phe Arg Gly Ala Tyr Gly Leu Ala Met Lys Val Ser Ser
50 55 60
Pro Pro Pro Thr Ile Met Gln Gln Asn Lys Lys Gly Asp Met Thr His
65 70 75 80
Glu Leu Val Arg His Phe Leu Ile Glu Thr Gly Pro Arg Gly Val Lys
85 90 95
Leu Lys Gly Cys Pro Asn Glu Pro Asn Phe Gly Ser Leu Ser Ala Leu

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            100                 105                 110
Val Tyr Gln His Ser Ile Ile Pro Leu Ala Leu Pro Cys Lys Leu Val
        115                 120                 125
Ile Pro Asn Arg Asp Pro Thr Asp Glu Ser Lys Asp Ser Ser Gly Pro
    130                 135                 140
Ala Asn Ser Thr Ala Asp Leu Leu Lys Gln Gly Ala Ala Cys Asn Val
145                 150                 155                 160
Leu Phe Ile Asn Ser Val Asp Met Glu Ser Leu Thr Gly Pro Gln Ala
                165                 170                 175
Ile Ser Lys Ala Thr Ser Glu Thr Leu Ala Ala Asp Pro Thr Pro Ala
            180                 185                 190
Ala Thr Ile Val His Phe Lys Val Ser Ala Gln Gly Ile Thr Leu Thr
        195                 200                 205
Asp Asn Gln Arg Lys Leu Phe Phe Arg Arg His Tyr Pro Leu Asn Thr
    210                 215                 220
Val Thr Phe Cys Asp Leu Asp Pro Gln Glu Arg Lys Trp Met Lys Thr
225                 230                 235                 240
Glu Gly Gly Ala Pro Ala Lys Leu Phe Gly Phe Val Ala Arg Lys Gln
                245                 250                 255
Gly Ser Thr Thr Asp Asn Ala Cys His Leu Phe Ala Glu Leu Asp Pro
            260                 265                 270
Asn Gln Pro Ala Ser Ala Ile Val Asn Phe Val Ser Lys Val Met Leu
        275                 280                 285
Asn Ala Gly Gln Lys Arg
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<210> 2801
<211> 549
<212> DNA
<213> Homo sapiens

<400> 2801
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ttcagcacac cagtggggca gtgcctcgaa aaggcaacag atggctccct gcaaagtgag
180
gattggacgt tgaatatgga gatctgtgac atcatcaatg agacggagga agggccaaag
240
gatgccattc gagccctgaa gaagcggctc aacgggaacc ggaactacag agaggtgatg
300
ctggcattaa cagtgctgga gacatgtgtg aagaactgtg gccaccgctt ccacatcctt
360
gtggccaacc gagatttcat cgacagtgtt ctggtcaaaa ttatatctcc caagaacaac
420
cctcccacca ttgtacagga caaagtgctt gctctgatcc aggcatgggc tgatgccttt
480
cgaagcagtc ctgatctcac cggcgttgtg cacatatatg aggagctgaa gaggaaaggg
540
gttgaattc
549

<210> 2802

<211> 151
<212> PRT
<213> Homo sapiens

<400> 2802
Met Glu Phe Leu Leu Gly Asn Pro Phe Ser Thr Pro Val Gly Gln Cys
1 5 10 15
Leu Glu Lys Ala Thr Asp Gly Ser Leu Gln Ser Glu Asp Trp Thr Leu
20 25 30
Asn Met Glu Ile Cys Asp Ile Ile Asn Glu Thr Glu Glu Gly Pro Lys
35 40 45
Asp Ala Ile Arg Ala Leu Lys Lys Arg Leu Asn Gly Asn Arg Asn Tyr
50 55 60
Arg Glu Val Met Leu Ala Leu Thr Val Leu Glu Thr Cys Val Lys Asn
65 70 75 80
Cys Gly His Arg Phe His Ile Leu Val Ala Asn Arg Asp Phe Ile Asp
85 90 95
Ser Val Leu Val Lys Ile Ile Ser Pro Lys Asn Asn Pro Pro Thr Ile
100 105 110
Val Gln Asp Lys Val Leu Ala Leu Ile Gln Ala Trp Ala Asp Ala Phe
115 120 125
Arg Ser Ser Pro Asp Leu Thr Gly Val Val His Ile Tyr Glu Glu Leu
130 135 140
Lys Arg Lys Gly Val Glu Phe
145 150

<210> 2803
<211> 459
<212> DNA
<213> Homo sapiens

<400> 2803
nccatggcca cgcctgggct ccagcagcat cagcagcccc caggaccggg gaggcacagg
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tggcccccac cacccggagg agcagctcct gcccctgtcc gggggatgac tgattctcct
120
ccgccagccg tagggtgtgt gctgtccggg ctcacgggga ccctgtctcc gagtcgttcg
180
tgcagcgtgt gtaccagccc ttcctcacca cctgcgacgg gcaccgggcc tgcagcacct
240
accgcaatat gccagccgcc atgccggaac ggagggagct gtgtccagcc tggccgctgc
300
cgctgccctg caggatggcg gggtgacact tgccagtcag atgtggacna gtgcaatgaa
360
ggaagaagtg cagaggctgc agtccagggt ggacctgctg gaggagaagc tgcagctggt
420
actggcccca ctgcacagcc tggcctcgca ggcactgga
459

<210> 2804
<211> 153
<212> PRT
<213> Homo sapiens

<400> 2804
Xaa Met Ala Thr Pro Gly Leu Gln Gln His Gln Gln Pro Pro Gly Pro
1 5 10 15
Gly Arg His Arg Trp Pro Pro Pro Pro Gly Gly Ala Ala Pro Ala Pro
20 25 30
Val Arg Gly Met Thr Asp Ser Pro Pro Pro Ala Val Gly Cys Val Leu
35 40 45
Ser Gly Leu Thr Gly Thr Leu Ser Pro Ser Arg Ser Cys Ser Val Cys
50 55 60
Thr Ser Pro Ser Ser Pro Pro Ala Thr Gly Thr Gly Pro Ala Ala Pro
65 70 75 80
Thr Ala Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln
85 90 95
Pro Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
100 105 110
Ser Asp Val Asp Xaa Cys Asn Glu Gly Arg Ser Ala Glu Ala Ala Val
115 120 125
Gln Gly Gly Pro Ala Gly Gly Glu Ala Ala Ala Gly Thr Gly Pro Thr
130 135 140
Ala Gln Pro Gly Leu Ala Gly Thr Gly
145 150

<210> 2805
<211> 771
<212> DNA
<213> Homo sapiens

<400> 2805
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aagtttaatc agacctgctc acacttcaga atagagaaga ttgagaggat ccagaatcca
120
gatctctgga atagctacca ggcaaagaaa aaaactatgg atgccaagaa tggccagaca
180
atgaatgaga agcaactctt ccatgggaca gatgccggct ccgtgccaca cgtcaatcga
240
aatggcttta accgcagcta tgccggaaag aatgctgtgg catatggaaa gggaacctat
300
tttgctgtca atgccaatta ttctgccaat gatacgtact ccagaccaga tgcaaatggg
360
agaaagcatg tgtattatgt gcgagtactt actggaatct atacacatgg aaatcattca
420
ttaattgtgc ctccttcaaa gaaccctcaa aatcctactg acctgtatga cactgtcaca
480
gataatgtgc accatccaag tttatttgtg gcattttatg actaccaagc atacccagag
540
taccttatta cgtttagaaa ataacacttt ggtatccttc ccacaaaatt attctccatt
600
tgtacatatc tagttgtaaa acaagtttta gctttttttt ttaattcctc ttaacagatt
660
tttctaatat ccaaggatca ttctttgtcg ctgcagtcag atctttcttc agcttctctt
720
tcataatgga aatgaactta ttatcttgag agccaaataa cttggaaatt t
771

<210> 2806
<211> 187
<212> PRT
<213> Homo sapiens

<400> 2806
Xaa Asn Phe Cys Val Val Glu Leu Leu Pro Ser Asp Pro Glu Tyr Asn
1 5 10 15
Thr Val Ala Ser Lys Phe Asn Gln Thr Cys Ser His Phe Arg Ile Glu
20 25 30
Lys Ile Glu Arg Ile Gln Asn Pro Asp Leu Trp Asn Ser Tyr Gln Ala
35 40 45
Lys Lys Lys Thr Met Asp Ala Lys Asn Gly Gln Thr Met Asn Glu Lys
50 55 60
Gln Leu Phe His Gly Thr Asp Ala Gly Ser Val Pro His Val Asn Arg
65 70 75 80
Asn Gly Phe Asn Arg Ser Tyr Ala Gly Lys Asn Ala Val Ala Tyr Gly
85 90 95
Lys Gly Thr Tyr Phe Ala Val Asn Ala Asn Tyr Ser Ala Asn Asp Thr
100 105 110
Tyr Ser Arg Pro Asp Ala Asn Gly Arg Lys His Val Tyr Tyr Val Arg
115 120 125
Val Leu Thr Gly Ile Tyr Thr His Gly Asn His Ser Leu Ile Val Pro
130 135 140
Pro Ser Lys Asn Pro Gln Asn Pro Thr Asp Leu Tyr Asp Thr Val Thr
145 150 155 160
Asp Asn Val His His Pro Ser Leu Phe Val Ala Phe Tyr Asp Tyr Gln
165 170 175
Ala Tyr Pro Glu Tyr Leu Ile Thr Phe Arg Lys
180 185

<210> 2807
<211> 1660
<212> DNA
<213> Homo sapiens

<400> 2807
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120
cccaggtgct cagggccgcc tgtgaatgca ggtgccttgt cccaaacaga ggacatatta
180
atagggccat gatttcctgt tgccacaatt ttgccaaggc aggctggcac cagaacacca
240
aagaagggaa attatagtgg agtagcagtt tgtgaatctg gagtccttgg ttcaatcaca
300
gaacaagtag ggagaggagc caggacctag gccttcaggt tttcagcaag gaaggactct
360
caggccatcc ttgcagttca gttaacagga ggaagcaagg atccccagag agctggagta
420
ctctgactct cggatagaaa ggcaggacaa tcggagcctg gggttcacgt gagtcaggaa
480

agggagctct ccacactgga atcgctgtag ccgaggaggt tctaatggga cgatcttcga
540
cggtttcctt tccagctcaa aagaaagcac aataggacgg aggacagagg ggctagtaca
600
aagtgtccag aggaacatgg tcatgggctc gtcaaccctg gctgaagact caagttgggc
660
tccaggccct gcaaactgca agaccactct gcctggcact tggacgaaat ctaggaggga
720
ggcccactct ctaggacaca gccctagtgc tgctgccaca tggtgattcc tacaggtcac
780
cacggcttcg gcagtcccat cctccaccag gagcctgatg atggcctggc ttatagctgt
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ctgcgtaggg caagtggagc ccaggcgagt gcactttccc tgccggcaga tgctggtaca
900
ataagcacac acccagaaga gctgaaggct gaagacagag acgatatggc aagaggcagt
960
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1020
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1080
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1140
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1260
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1380
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1500
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1560
agcggggcca ggagctacga gtcggtacac ctgtcccggg tgcaagaact caaaccagcg
1620
gactgaagag ccaaagaaaa tgaggtgaac cctctgatca
1660

<210> 2808
<211> 390
<212> PRT
<213> Homo sapiens

<400> 2808
Met Leu Phe Glu Lys Asp Gly Ser Ser Cys Ile Ser Arg Arg Pro Leu
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Glu Leu Ala Gly Cys Ala Ser Cys Leu Thr Val Gln Asp Asn Trp Thr
            20   25   30
Leu Glu Leu Glu Ser Ser Gln Asp Ile Gln Asp Val Leu Asp Ala Asn
        35   40   45
Lys Ser Leu Pro Glu Ser Ser Leu Thr Asp Leu Leu Ser Asp Asn Phe

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    50                  55                  60
Thr Asp Ser Leu Val Ser Phe Ser Ala Glu Ile Leu Ser Arg Thr Leu
65                  70                  75                  80
Cys Glu Pro Leu Val Ala Ser Leu Trp Met Lys Leu Gly Asn Thr Gly
                85                  90                  95
Ala Met Arg Arg Cys Val Lys Leu Thr Val Ala Leu Glu Thr Ala Glu
            100                 105                 110
Cys Glu Phe Pro Pro His Leu Asp Val Tyr Ile Glu Asp Pro His Leu
        115                 120                 125
Pro Pro Ser Leu Gly Leu Leu Pro Gly Ala Arg Val His Phe Ser Gln
    130                 135                 140
Leu Glu Lys Arg Val Ser Arg Ser His Asn Val Tyr Cys Cys Phe Arg
145                 150                 155                 160
Ser Ser Thr Tyr Val Gln Val Leu Ser Phe Pro Pro Glu Thr Thr Ile
                165                 170                 175
Ser Val Pro Leu Pro His Ile Tyr Leu Ala Glu Leu Leu Gln Gly Gly
            180                 185                 190
Gln Ser Pro Phe Gln Ala Thr Ala Ser Cys His Ile Val Ser Val Phe
        195                 200                 205
Ser Leu Gln Leu Phe Trp Val Cys Ala Tyr Cys Thr Ser Ile Cys Arg
    210                 215                 220
Gln Gly Lys Cys Thr Arg Leu Gly Ser Thr Cys Pro Thr Gln Thr Ala
225                 230                 235                 240
Ile Ser Gln Ala Ile Ile Arg Leu Leu Val Glu Asp Gly Thr Ala Glu
                245                 250                 255
Ala Val Val Thr Cys Arg Asn His His Val Ala Ala Ala Leu Gly Leu
            260                 265                 270
Cys Pro Arg Glu Trp Ala Ser Leu Leu Asp Phe Val Gln Val Pro Gly
        275                 280                 285
Arg Val Val Leu Gln Phe Ala Gly Pro Gly Ala Gln Leu Glu Ser Ser
    290                 295                 300
Ala Arg Val Asp Glu Pro Met Thr Met Phe Leu Trp Thr Leu Cys Thr
305                 310                 315                 320
Ser Pro Ser Val Leu Arg Pro Ile Val Leu Ser Phe Glu Leu Glu Arg
                325                 330                 335
Lys Pro Ser Lys Ile Val Pro Leu Glu Pro Pro Arg Leu Gln Arg Phe
            340                 345                 350
Gln Cys Gly Glu Leu Pro Phe Leu Thr His Val Asn Pro Arg Leu Arg
        355                 360                 365
Leu Ser Cys Leu Ser Ile Arg Glu Ser Glu Tyr Ser Ser Ser Leu Gly
    370                 375                 380
Ile Leu Ala Ser Ser Cys
385                 390
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<210> 2809
<211> 1502
<212> DNA
<213> Homo sapiens

<400> 2809
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120

actgttaagc gctggcccag tccccccacc ccacccagcc gtgtactgcc tgggctcccc
180
tcaaagggaa atttttacgg aaacatcttg gcagcaagtg gaaaaagatc tatggcccat
240
gaaccaactg aaaactccaa gaaccctctg tctgcctctg ccagcagcga gtcctaagcg
300
cagaatccag agctcgtagc tgtcctcagc tgtaactact gtttcagaat gttgctgctg
360
catacatttg tcatgtcagc cagccagctc cgtgggtgag agtgtgcgtg tgcgcgtgtc
420
tgtgtgtgtg tgcgtctgtg tgtgcgtgtc tgtgtgtgtg cacgtctgtg cgtctgtgtg
480
tgcgcgtctg tgtgcgcgtg tgtctgtgcg tgtgtgcgtc tgtgtgtgcg tctgtgcgcg
540
tgtgtgtgcg cgtctgtgtg tatgtgtgca cgcgccngcg tctgtgtgtg cacgtgcgtg
600
nntctctgca cgcgtgtctg tgtatgtgtg cacgcgtgtg tctgtgtgtg tgcacgcgcg
660
tgcacgtcac caccggagca tttagggttt ggtacaagat ggttctaaaa tggcaaaggt
720
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780
atcgcaagca ttcagactgg acgaccggct cgtattccga tcagtcgctt ccattgttag
840
catcgtacac gattgtgatt tttatgtcaa aagaagccaa aacttgcaat actattttta
900
gcagacaaaa aaaagaacta agtataaaat gtataaatat ttttgacttg aacatttgga
960
tggcactggg tgcaagtaga gcatccatcc ttcggatgga atgtttggaa aaaagagact
1020
tttaaaaagg agacggttgt tttaaagagt ctgtttaggg gttaaagtac tgtaactcac
1080
gactgttaaa aaataaattt tcctgtgctg taaaggaagg tttcacagta ccactgagtt
1140
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1200
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1260
gttacttttt agccatggct gacattgtat caataactaa aactgaaaca ttcaaaagcg
1320
aacagggaaa ccgagggctt caagcgtgct cagagccgtt tcagacagtg gaaatccatg
1380
acaaacaaaa ggatgtgatc attaattgta aagcgctttg taaaattcac atttacaaaa
1440
taataaagtc agttcaaacc taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
1500
aa
1502

<210> 2810
<211> 102
<212> PRT
<213> Homo sapiens

<400> 2810
Glu Cys Ala Cys Ala Arg Val Cys Val Cys Val Arg Leu Cys Val Arg
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Val Cys Val Cys Ala Arg Leu Cys Val Cys Val Cys Ala Ser Val Cys
20 25 30
Ala Cys Val Cys Ala Cys Val Arg Leu Cys Val Arg Leu Cys Ala Cys
35 40 45
Val Cys Ala Ser Val Cys Met Cys Ala Arg Ala Xaa Val Cys Val Cys
50 55 60
Thr Cys Val Xaa Leu Cys Thr Arg Val Cys Val Cys Val His Ala Cys
65 70 75 80
Val Cys Val Cys Ala Arg Ala Cys Thr Ser Pro Pro Glu His Leu Gly
85 90 95
Phe Gly Thr Arg Trp Phe
100

<210> 2811
<211> 591
<212> DNA
<213> Homo sapiens

<400> 2811
nnacgcgtgt aggttgggtg cacttacaag taagtataaa ctgctcttca attcaagttt
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attaatgctg ccccacccca gggttttaat ccggtctggg cagaagcggg cgataaaagc
120
caaaggagac cataaagtgt aggatatttc ctggttagtg gctgccgggt aatcacgatg
180
catccatctt cctcggcgtc gcagccctca gtagccagaa ggcagtctcc ttccctgggg
240
ggcaaaagcc ccgagcccag cctgcccngt tgccccgctc ccgcggtgga tgaacctcaa
300
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360
gcgccactga ggcccagacc gggggaagga gaccctgtca ctcgggagcg gagccctgtc
420
ccgggagcga cggaaatgcc tcctccacgc cccaaggttc ctgctccgcc aggcccaacc
480
ggaaggagtc ctcgggccgc agtggggcac caccgggccg ccggccctcc aggctgcgtg
540
gggccttctc tcagtgggca actggggagc tagcccgggg cggccgcaag c
591

<210> 2812
<211> 131
<212> PRT
<213> Homo sapiens

<400> 2812
Met His Pro Ser Ser Ser Ala Ser Gln Pro Ser Val Ala Arg Arg Gln
1 5 10 15
Ser Pro Ser Leu Gly Gly Lys Ser Pro Glu Pro Ser Leu Pro Xaa Cys
20 25 30
Pro Ala Pro Ala Val Asp Glu Pro Gln Pro Xaa Ser Gln Ala Pro Pro

```
        35                  40                  45
Gly Pro Arg Val Pro Gly Pro Pro Arg Pro Trp Gly Ala Ala Pro Leu
    50                  55                  60
Arg Pro Arg Pro Gly Glu Gly Asp Pro Val Thr Arg Glu Arg Ser Pro
65                  70                  75                  80
Val Pro Gly Ala Thr Glu Met Pro Pro Pro Arg Pro Lys Val Pro Ala
                85                  90                  95
Pro Pro Gly Pro Thr Gly Arg Ser Pro Arg Ala Ala Val Gly His His
            100                 105                 110
Arg Ala Ala Gly Pro Pro Gly Cys Val Gly Pro Ser Leu Ser Gly Gln
        115                 120                 125
Leu Gly Ser
    130
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<210> 2813
<211> 2417
<212> DNA
<213> Homo sapiens

<400> 2813
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tgcctgagtt tgaagagagt taaccactgg aatctctcat gttgtttatt ccctccaaaa
120
tgctgcagtt cagtgttgtc ccagatttta tgcttgtgct tagatttctc tgttctctaa
180
tttgttaagt ttgtctttaa tatttcacag gctttcttga tcatggatgg tgaagatata
240
ccagattttt caagtttaaa ggaggaaact gcttattgga aggaactttc cttgaagtat
300
aagcaaagct tccaggaagc tcgggatgag ctagttgaat tccaggaagg aagcagagaa
360
ttagaagcag agttggaggc acaattagta caggctgaac aaagaaatag agacttgcag
420
gctgataacc aaagactgaa atatgaagtg gaggcattaa aggagaagct agagcatcaa
480
tatgcacaga gctataagca ggtctcagtg ttagaagatg atttaagtca gactcgggcc
540
attaaggagc agttgcataa gtatgtgaga gagctggagc aggccaacga cgacctggag
600
cgagccaaaa gggcaacaat agtttcactg gaaactttga acaaactaaa ccaggccatt
660
gaacgaaatg catttttaga aagtgaactt gatgaaaagg aatctttgtt ggtctctgta
720
cagaggttaa aggatgaagc aagagattta aggcaagaac tagcagttcg ggaaagacaa
780
caggaagtaa ctagaaagtc ggctcctagc tctccaactc tagactgtga aaagatggac
840
tccgccgtcc aagcatcact ttctttgcca gctacccctg ttggcaaagg aacggagaac
900
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960
gctaggatat cagcactaaa catcgtgggg gatctcttac ggaaagtagg ggctttagaa
1020

tccaaattag cagcttgcag gaattttgca aaggaccaag catcacgaaa atcctatatt
1080
tcagggaatg ttaactgtgg ggtgctgaat ggcaatggca caaagttctc tcgatcaggg
1140
catacatctt tcttcgacaa aggggcagta aacggctttg accccgctcc tcctcctcct
1200
ggtctgggct cctcgcgtcc atcgtcagcg ccgggtatgt gcctctcagt gtgtgagtgc
1260
ctagcctcca ggggggctcc tgccctcctc caacaaccca ggacacccac gcctcacccc
1320
tcggtgcctg ggcccagccc cgtgcccctc cgtctgcctc cgcacggctg gcagagggca
1380
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1440
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1500
ggtcgcaagg tgatacatac gtgtattact tggtcactgg atgcagaagt acccattcat
1560
cacacctgcc ccatagcccc cactctgctg tactgatagg atttagttgt gttttaggac
1620
attgcaaatc ttctagaagt tctcccccaa atcaggtcaa tgtgtgccct cctgagctcc
1680
cacccaggca tctccagtgc tcatgatcat gtgtccccca actccacccc tcacagtttg
1740
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1800
ctgattttac ttaagcagct accattccat ggacttgcct cccagagcag cacaatgccc
1860
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1920
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1980
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2040
cgtcccgttg tgttaggaag ggtgagtggc tggttccagg gtgggccggt gccagctccg
2100
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2160
tactgtttac atttgtttta ttgtacatag gtttgtaaac attattgcct gagatatttg
2220
tatataactt gggctttgta gcttttattt attcagaacg catacggcat gttaatgact
2280
ctgatggtgt cctcctctgg gcagctgtat aggatcatca tgtggttaca aaaaatactt
2340
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2400
aaaaaaaaaa aaaaaaa
2417

<210> 2814
<211> 471
<212> PRT
<213> Homo sapiens

<400> 2814
Phe Val Lys Phe Val Phe Asn Ile Ser Gln Ala Phe Leu Ile Met Asp
1 5 10 15
Gly Glu Asp Ile Pro Asp Phe Ser Ser Leu Lys Glu Glu Thr Ala Tyr
20 25 30
Trp Lys Glu Leu Ser Leu Lys Tyr Lys Gln Ser Phe Gln Glu Ala Arg
35 40 45
Asp Glu Leu Val Glu Phe Gln Glu Gly Ser Arg Glu Leu Glu Ala Glu
50 55 60
Leu Glu Ala Gln Leu Val Gln Ala Glu Gln Arg Asn Arg Asp Leu Gln
65 70 75 80
Ala Asp Asn Gln Arg Leu Lys Tyr Glu Val Glu Ala Leu Lys Glu Lys
85 90 95
Leu Glu His Gln Tyr Ala Gln Ser Tyr Lys Gln Val Ser Val Leu Glu
100 105 110
Asp Asp Leu Ser Gln Thr Arg Ala Ile Lys Glu Gln Leu His Lys Tyr
115 120 125
Val Arg Glu Leu Glu Gln Ala Asn Asp Asp Leu Glu Arg Ala Lys Arg
130 135 140
Ala Thr Ile Val Ser Leu Glu Thr Leu Asn Lys Leu Asn Gln Ala Ile
145 150 155 160
Glu Arg Asn Ala Phe Leu Glu Ser Glu Leu Asp Glu Lys Glu Ser Leu
165 170 175
Leu Val Ser Val Gln Arg Leu Lys Asp Glu Ala Arg Asp Leu Arg Gln
180 185 190
Glu Leu Ala Val Arg Glu Arg Gln Gln Glu Val Thr Arg Lys Ser Ala
195 200 205
Pro Ser Ser Pro Thr Leu Asp Cys Glu Lys Met Asp Ser Ala Val Gln
210 215 220
Ala Ser Leu Ser Leu Pro Ala Thr Pro Val Gly Lys Gly Thr Glu Asn
225 230 235 240
Thr Phe Pro Ser Pro Lys Ala Ile Pro Asn Gly Phe Gly Thr Ser Pro
245 250 255
Leu Thr Pro Ser Ala Arg Ile Ser Ala Leu Asn Ile Val Gly Asp Leu
260 265 270
Leu Arg Lys Val Gly Ala Leu Glu Ser Lys Leu Ala Ala Cys Arg Asn
275 280 285
Phe Ala Lys Asp Gln Ala Ser Arg Lys Ser Tyr Ile Ser Gly Asn Val
290 295 300
Asn Cys Gly Val Leu Asn Gly Asn Gly Thr Lys Phe Ser Arg Ser Gly
305 310 315 320
His Thr Ser Phe Phe Asp Lys Gly Ala Val Asn Gly Phe Asp Pro Ala
325 330 335
Pro Pro Pro Pro Gly Leu Gly Ser Ser Arg Pro Ser Ser Ala Pro Gly
340 345 350
Met Cys Leu Ser Val Cys Glu Cys Leu Ala Ser Arg Gly Ala Pro Ala
355 360 365
Leu Leu Gln Gln Pro Arg Thr Pro Thr Pro His Pro Ser Val Pro Gly
370 375 380
Pro Ser Pro Val Pro Leu Arg Leu Pro Pro His Gly Trp Gln Arg Ala
385 390 395 400
Gly Cys Met Gln Trp Arg Leu Leu Gly Pro Ala Gln Pro Arg Asn Ser
405 410 415
Ala Arg Tyr Gln Tyr Trp Leu Phe Ser Leu Leu Ala Val Val Pro Leu

420 425 430
Val Ser His Asp Cys Thr Phe Val Gly Arg Lys Val Ile His Thr Cys
435 440 445
Ile Thr Trp Ser Leu Asp Ala Glu Val Pro Ile His His Thr Cys Pro
450 455 460
Ile Ala Pro Thr Leu Leu Tyr
465 470

<210> 2815
<211> 1421
<212> DNA
<213> Homo sapiens

<400> 2815
ncagcggagg agagagtggg cgccaccgtg gggctgtccc accggtggag gctccagcgg
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agatgagctg ggcaggcctc gcggagcaag tgcaaactgc acccgcgtcc tgggggcatc
120
tgcggggaga cttaggggtc atgctttgtg ccccaggcca cccagaggag aaggccaccc
180
cgcctggagg cacaggccat gaggggctct caggaggtgc tgctgatgtg gcttctggtg
240
ttggcagtgg gcggcacaga gcacgcctac cggcccggcc gtagggtgtg tgctgtccgg
300
gctcacgggg accctgtctc cgagtcgttc gtgcagcgtg tgtaccagcc cttcctcacc
360
acctgcgacg ggcaccgggc ctgcagcacc taccgaacca tctataggac cgcctaccgc
420
cgcagccctg ggctggcccc tgccaggcct cgctacgcgt gctgccccgg ctggaagagg
480
accagcgggc ttcctggggc ctgtggagca gcaatatgcc agccgccatg ccggaacgga
540
gggagctgtg tccagcctgg ccgctgccgc tgccctgcag gatggcgggg tgacacttgc
600
cagtcagatg tggatgaatg cagtgctagg aggggcggct gtccccagcg ctgcgtcaac
660
accgccggca gttactggtg ccagtgttgg gaggggcaca gcctgtctgc agacggtaca
720
ctctgtgtgc ccaagggagg gccccccagg gtggccccca acccgacagg agtggacagt
780
gcaatgaagg aagaagtgca gaggctgcag tccagggtgg acctgctgga ggagaagctg
840
cagctggtgc tggccccact gcacagcctg gcctcgcagg caggagcatg ggctcccgga
900
ccccggcagc ctcctggtgc actccttcca gcagctcggc cgcatcgact ccctgagcga
960
gcagatttcc ttcctggagg agcagctggg gtcctgctcc tgcaagaaag actcngtgac
1020
tgcccagcgc cccaggctgg actgagcccc tcacgccgcc ctgcagcccc catgcccctg
1080
cccaacatgc tgggggtcca gaagccacct cggggtgact gagcggaagg ccaggcaggg
1140
ccttcctcct cttcctcctc cccttcctca ggaggctccc cagaccctgg catgggatgg
1200

gctgggatct tctctgtgaa tccacccctg gctaccccca ccctggctac cccaacggca
1260
tcccaaggcc aggtgggccc tcagctgagg gaaggtacga gctccctgct ggagcctggg
1320
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1380
tgaccccccag cacaataaaa atgaaacgtg aaaaaaaaaa a
1421

<210> 2816
<211> 307
<212> PRT
<213> Homo sapiens

<400> 2816
Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu Ala
1 5 10 15
Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala
20 25 30
Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val
35 40 45
Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr
50 55 60
Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala
65 70 75 80
Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser
85 90 95
Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg
100 105 110
Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly
115 120 125
Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg
130 135 140
Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp
145 150 155 160
Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys
165 170 175
Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val
180 185 190
Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp
195 200 205
Leu Leu Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu
210 215 220
Ala Ser Gln Ala Gly Ala Trp Ala Pro Gly Pro Arg Gln Pro Pro Gly
225 230 235 240
Ala Leu Leu Pro Ala Ala Arg Pro His Arg Leu Pro Glu Arg Ala Asp
245 250 255
Phe Leu Pro Gly Gly Ala Ala Gly Val Leu Leu Leu Gln Glu Arg Leu
260 265 270
Xaa Asp Cys Pro Ala Pro Gln Ala Gly Leu Ser Pro Ser Arg Arg Pro
275 280 285
Ala Ala Pro Met Pro Leu Pro Asn Met Leu Gly Val Gln Lys Pro Pro
290 295 300
Arg Gly Asp

305

<210> 2817
<211> 219
<212> DNA
<213> Homo sapiens

<400> 2817
nntggctttt ctgtctctct ctcttttttt cttgtagatc acgagctgct caggcaagag
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ctgaacacgc ggtttctggt gcagagcgcc gagcggcctg gcgcctccct gggcccgggg
120
gttctgctgc gggcggagtt ccatcagcac cagcacacac accagcacac gcaccaacac
180
acacaccagc accaacacac attcgccccc ttcacgcgt
219

<210> 2818
<211> 73
<212> PRT
<213> Homo sapiens

<400> 2818
Xaa Gly Phe Ser Val Ser Leu Ser Phe Phe Leu Val Asp His Glu Leu
1 5 10 15
Leu Arg Gln Glu Leu Asn Thr Arg Phe Leu Val Gln Ser Ala Glu Arg
20 25 30
Pro Gly Ala Ser Leu Gly Pro Gly Val Leu Leu Arg Ala Glu Phe His
35 40 45
Gln His Gln His Thr His Gln His Thr His Gln His Thr His Gln His
50 55 60
Gln His Thr Phe Ala Pro Phe Thr Arg
65 70

<210> 2819
<211> 730
<212> DNA
<213> Homo sapiens

<400> 2819
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60
gatcgaggcc tccaagggaa atatggcaaa acaggctcag caggggccag gggccacact
120
ggacccaaag ggcagaaggg ctccatgggg gcccctgggg agcggtgcaa gagccactac
180
gccgcctttt cggtgggccg ggaagcccat gcacagcaac cactactacc agacgtgatc
240
ttcgacacgg agttcgtgaa cctctacgac cacttcaaca tgttcaccgg caagttctac
300
tgctacgtgc ccggcctcta cttcttcagc ctcaacgtgc acacctggaa ccagaaggag
360
acctacctgc acatcatgaa gaacgaggag gaggtggtga tcttgttcgc gcaggtgggc
420

gaccgcagca tcatgcaaag ccagagcctg atgctggagc tgcgagagca ggaccaggtg
480
tgggtacgcc tctacaaggg cgaacgtgag aacgccatct tcagcgagga gctggacacc
540
tacatcacct tcagtggcta cctggtcaag cacgccaccg agccctagct ggccggccac
600
ctcctttcct ctcgccacct tccacccctg cgctgtgctg accccaccgc ctcttccccg
660
atccctggac tccgactccc tggctttggc attcagtgag acgccctgca cacacagaaa
720
gccaaagcga
730

<210> 2820
<211> 195
<212> PRT
<213> Homo sapiens

<400> 2820
Xaa Thr Ala Val Pro Gln Ile Asn Ile Thr Ile Leu Lys Gly Glu Lys
 1   5   10   15
Gly Asp Arg Gly Asp Arg Gly Leu Gln Gly Lys Tyr Gly Lys Thr Gly
            20   25   30
Ser Ala Gly Ala Arg Gly His Thr Gly Pro Lys Gly Gln Lys Gly Ser
        35   40   45
Met Gly Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser
    50   55   60
Val Gly Arg Glu Ala His Ala Gln Gln Pro Leu Leu Pro Asp Val Ile
65   70   75   80
Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met Phe Thr
                85   90   95
Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe Ser Leu Asn
            100   105   110
Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His Ile Met Lys Asn
        115   120   125
Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val Gly Asp Arg Ser Ile
    130   135   140
Met Gln Ser Gln Ser Leu Met Leu Glu Leu Arg Glu Gln Asp Gln Val
145   150   155   160
Trp Val Arg Leu Tyr Lys Gly Glu Arg Glu Asn Ala Ile Phe Ser Glu
                165   170   175
Glu Leu Asp Thr Tyr Ile Thr Phe Ser Gly Tyr Leu Val Lys His Ala
            180   185   190
Thr Glu Pro
        195

<210> 2821
<211> 1746
<212> DNA
<213> Homo sapiens

<400> 2821
nnagactgca gttcctcgct tacctgtgca gtctaatttt gagctgcctc tttgtagtct
60

taaaaggcag gagcttcgtg ttgtgggtct gctaacccgt acgtttccgt gggcaagtcg
120
tgtgtactcc tcgccatggc acaactccaa acacgtttct acactgataa caagaaatat
180
gcagtagatg atgttccttt ctcaatccct gccacctcag aagttgctga ccttagtaat
240
attatcaata aattgctgga gaccaaaaat gagctccaca aacatgtgga gtttgatttc
300
ctcatcaagg gccagtttct tcgaatgccc ttggacaaac acatggaaat ggaagacatc
360
tcatcagaag aagttgtgga aatagaatac gtggagaagt atactgcacc ccagccagag
420
caatgcatgt tccatgatga ctggatcagt tcaattaaag gggcagagga atggatcttg
480
actggttctt atggtaagac ttctcggatc tggtccttgg aaggaaagtc aataatgaca
540
attgtgggac atacggatgt tgtaaaagat gtggcctggg tgaaaaaaga tagtttgtcc
600
tgcttattan ttgagtgctt ctatggatca gactattctc ttatgggagt ggaatgtaga
660
gagaaacaaa gtgaaagccc tacactgctg nntagaggtc atgctggaag tgtagattct
720
atagctgttg atggctcagg aactaaattt tgcagtggct cctgggataa gatgctaaag
780
atctggtcta cagtccctac agatgaagaa gatgaaatgg aggagtccac aaatcgacca
840
agaaagaaac agaagacaga acagttggga ctaacaagga ctcccatagt gaccctctct
900
ggccacatgg aggcagtttc ctcagttctg tggtcagatg ctgaagaaat ctgcagtgca
960
tcttgggacc atacaattag agtgtgggat gttgagtctg gcagtcttaa gtcaactttg
1020
acaggaaata aagtgtttaa ttgtatttcc tattctccac tttgtaaacg tttagcatct
1080
ggaagcacag ataggcatat cagactgtgg gatccccgaa ctaaagatgg ttctttggtg
1140
tcgctgtccc taacgtcaca tactggttgg gtgacatcag taaaatggtc tcctacccat
1200
gaacagcagc tgatttcagg atctttagat aacattgtta agctgtggga tacaagaagt
1260
tgtaaggctc ctctctatga tctggctgct catgaagaca aagttctgag tgtagactgg
1320
acagacacag ggctacttct gagtggagga gcagacaata aattgtattc ctacagatat
1380
tcacctacca cttcccatgt tggggcatga aagtgaacaa taatttgact atagagatta
1440
tttctgtaaa tgaaattggt agagaaccat gaaattacat agatgcagat gcagaaagca
1500
gccttttgaa gtttatataa tgttttcacc cttcataaca gctaacgtat cacttttttct
1560
tattttgtat ttataataag ataggttgtg tttataaaat acaaactgtg gcatacattc
1620
tctatacaaa cttgaaatta aactgagttt tacatttctc tttaaaggta ttggtttgaa
1680

ttcagatttg ctttttttatt tttatttgtt ttttttttga gatggagtat tgctctgttg
1740
cctagg
1746

<210> 2822
<211> 424
<212> PRT
<213> Homo sapiens

<400> 2822
Met Ala Gln Leu Gln Thr Arg Phe Tyr Thr Asp Asn Lys Lys Tyr Ala
 1   5   10   15
Val Asp Asp Val Pro Phe Ser Ile Pro Ala Thr Ser Glu Val Ala Asp
            20   25   30
Leu Ser Asn Ile Ile Asn Lys Leu Leu Glu Thr Lys Asn Glu Leu His
        35   40   45
Lys His Val Glu Phe Asp Phe Leu Ile Lys Gly Gln Phe Leu Arg Met
    50   55   60
Pro Leu Asp Lys His Met Glu Met Glu Asp Ile Ser Ser Glu Glu Val
65   70   75   80
Val Glu Ile Glu Tyr Val Glu Lys Tyr Thr Ala Pro Gln Pro Glu Gln
                85   90   95
Cys Met Phe His Asp Asp Trp Ile Ser Ser Ile Lys Gly Ala Glu Glu
            100   105   110
Trp Ile Leu Thr Gly Ser Tyr Gly Lys Thr Ser Arg Ile Trp Ser Leu
        115   120   125
Glu Gly Lys Ser Ile Met Thr Ile Val Gly His Thr Asp Val Val Lys
    130   135   140
Asp Val Ala Trp Val Lys Lys Asp Ser Leu Ser Cys Leu Leu Xaa Glu
145   150   155   160
Cys Phe Tyr Gly Ser Asp Tyr Ser Leu Met Gly Val Glu Cys Arg Glu
                165   170   175
Lys Gln Ser Glu Ser Pro Thr Leu Leu Xaa Arg Gly His Ala Gly Ser
            180   185   190
Val Asp Ser Ile Ala Val Asp Gly Ser Gly Thr Lys Phe Cys Ser Gly
        195   200   205
Ser Trp Asp Lys Met Leu Lys Ile Trp Ser Thr Val Pro Thr Asp Glu
    210   215   220
Glu Asp Glu Met Glu Glu Ser Thr Asn Arg Pro Arg Lys Lys Gln Lys
225   230   235   240
Thr Glu Gln Leu Gly Leu Thr Arg Thr Pro Ile Val Thr Leu Ser Gly
                245   250   255
His Met Glu Ala Val Ser Ser Val Leu Trp Ser Asp Ala Glu Glu Ile
            260   265   270
Cys Ser Ala Ser Trp Asp His Thr Ile Arg Val Trp Asp Val Glu Ser
        275   280   285
Gly Ser Leu Lys Ser Thr Leu Thr Gly Asn Lys Val Phe Asn Cys Ile
    290   295   300
Ser Tyr Ser Pro Leu Cys Lys Arg Leu Ala Ser Gly Ser Thr Asp Arg
305   310   315   320
His Ile Arg Leu Trp Asp Pro Arg Thr Lys Asp Gly Ser Leu Val Ser
                325   330   335
Leu Ser Leu Thr Ser His Thr Gly Trp Val Thr Ser Val Lys Trp Ser

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            340                 345                 350
Pro Thr His Glu Gln Gln Leu Ile Ser Gly Ser Leu Asp Asn Ile Val
        355                 360                 365
Lys Leu Trp Asp Thr Arg Ser Cys Lys Ala Pro Leu Tyr Asp Leu Ala
    370                 375                 380
Ala His Glu Asp Lys Val Leu Ser Val Asp Trp Thr Asp Thr Gly Leu
385                 390                 395                 400
Leu Leu Ser Gly Gly Ala Asp Asn Lys Leu Tyr Ser Tyr Arg Tyr Ser
                405                 410                 415
Pro Thr Thr Ser His Val Gly Ala
            420
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<210> 2823
<211> 461
<212> DNA
<213> Homo sapiens

<400> 2823
cggccgcagc cttccccttt actcctggct gacaccatga actgctccca cgttcacccc
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gttgtgtctg tcagtggggg aaggggcgg aaccctcatg ctggggttcg ggtggacgtg
120
ggtgggtggt gacccctgtt gggaggcaga cacagtcaca ggcgtcgccc ttgggaaggg
180
cagccggaga agctggccct gtgtgggcct gggcctgtag ggtttcccag tggctttgcg
240
gagccagaga gctggatggc acctggtcca gccaagcaaa gccccgaggg caggggctgg
300
atggggacac gcacatgtcc cttggccacg acaaaatggc agtgatgctg cttgccttcc
360
tgcagcatct gtgaggatca aatgcgtgca cctacgcaaa gcatccgcac atagcaagtg
420
ctcacctagc acaggagccc cgtgctcctc ccaagtctca g
461

<210> 2824
<211> 81
<212> PRT
<213> Homo sapiens

<400> 2824
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Met Cys Val Ser Pro Ser Ser Pro Cys Pro Arg Gly Phe Ala Trp Leu
 1               5                  10                  15
Asp Gln Val Pro Ser Ser Ser Leu Ala Pro Gln Ser His Trp Glu Thr
            20                  25                  30
Leu Gln Ala Gln Ala His Thr Gly Pro Ala Ser Pro Ala Ala Leu Pro
        35                  40                  45
Lys Gly Asp Ala Cys Asp Cys Val Cys Leu Pro Thr Gly Val Thr Thr
    50                  55                  60
His Pro Arg Pro Pro Glu Pro Gln His Glu Gly Ser Ala Pro Phe Pro
65                  70                  75                  80
His
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<210> 2825
<211> 1520
<212> DNA
<213> Homo sapiens

<400> 2825
tgtctaacac ttgcttgcta caaaggccat ttggatatgg ttcgctttct acttgaagct
60
ggtgcagatc aagagcacaa aacagatgag atgcacactg ccttaatgga ggcctgcatg
120
gatggacatg tagaggtggc acgtttgctt ttggatagtg gtgctcaagt gaacatgcct
180
gcagattcat ttgaatctcc attgacgcta gctgcctgtg gaggacatgt tgaattggca
240
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<210> 2826
<211> 506
<212> PRT
<213> Homo sapiens

<400> 2826
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Leu Leu Leu Asp Ser Gly Ala Gln Val Asn Met Pro Ala Asp Ser Phe
50 55 60
Glu Ser Pro Leu Thr Leu Ala Ala Cys Gly Gly His Val Glu Leu Ala
65 70 75 80
Ala Leu Leu Ile Glu Arg Gly Ala Asn Leu Glu Glu Val Asn Asp Glu
85 90 95
Gly Tyr Thr Pro Leu Met Glu Ala Ala Arg Glu Gly His Glu Glu Met
100 105 110
Val Ala Leu Leu Leu Ser Thr Arg Ser Xaa Ile Ser Met His Arg Gln
115 120 125
Lys Lys Leu Lys Lys Leu Leu Leu Thr Leu Ala Cys Cys Gly Gly Phe
130 135 140
Leu Glu Val Ala Asp Phe Leu Ile Lys Ala Gly Ala Asp Ile Glu Leu
145 150 155 160
Gly Cys Ser Thr Pro Leu Met Glu Ala Ala Gln Glu Gly His Leu Glu
165 170 175
Leu Val Lys Tyr Leu Leu Ala Ala Gly Ala Asn Val His Ala Thr Thr
180 185 190
Ala Thr Gly Asp Thr Ala Leu Thr Tyr Ala Cys Glu Asn Gly His Thr
195 200 205
Asp Val Ala Asp Val Leu Leu Gln Ala Gly Ala Asp Leu Asp Lys Gln
210 215 220
Glu Asp Met Lys Thr Ile Leu Glu Gly Ile Asp Pro Ala Lys His Leu
225 230 235 240
Glu His Glu Ser Glu Gly Gly Arg Thr Pro Leu Met Lys Ala Ala Arg
245 250 255
Ala Gly His Val Cys Thr Val Gln Phe Leu Ile Ser Lys Gly Ala Asn
260 265 270
Val Asn Arg Thr Thr Ala Asn Asn Asp His Thr Val Leu Ser Leu Ala
275 280 285
Cys Ala Gly Gly His Leu Ala Val Val Glu Leu Leu Leu Ala His Gly
290 295 300
Ala Asp Pro Thr His Arg Leu Lys Asp Gly Ser Thr Met Leu Ile Glu
305 310 315 320
Ala Ala Lys Gly Gly His Thr Ser Val Val Cys Tyr Leu Leu Asp Tyr
325 330 335
Pro Asn Asn Leu Leu Ser Ala Pro Pro Pro Asp Val Thr Gln Leu Thr

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Pro Pro Ser His Asp Leu Asn Arg Ala Pro Arg Val Pro Val Gln Ala
        355                 360                 365
Leu Pro Met Val Val Pro Pro Gln Glu Pro Asp Lys Pro Pro Ala Asn
    370                 375                 380
Val Ala Thr Thr Leu Pro Ile Arg Asn Lys Ala Ala Ser Lys Gln Lys
385                 390                 395                 400
Ser Ser Ser His Leu Pro Ala Asn Ser Gln Asp Val Gln Gly Tyr Ile
                405                 410                 415
Thr Asn Gln Ser Pro Glu Ser Ile Val Glu Glu Ala Gln Gly Lys Leu
            420                 425                 430
Thr Glu Leu Glu Gln Arg Ile Lys Glu Ala Ile Glu Lys Asn Ala Gln
        435                 440                 445
Leu Gln Ser Leu Glu Leu Ala His Ala Asp Gln Leu Thr Lys Glu Lys
    450                 455                 460
Ile Glu Glu Leu Asn Lys Thr Arg Glu Glu Gln Ile Gln Lys Lys Gln
465                 470                 475                 480
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<210> 2827
<211> 481
<212> DNA
<213> Homo sapiens

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481

<210> 2828
<211> 160
<212> PRT
<213> Homo sapiens

<400> 2828
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            20                  25                  30
Leu Tyr Pro Gly Gly Cys Gln Gln Leu Leu His Leu Cys Val Gln Gln
        35                  40                  45
Pro Leu Gln Leu Leu Gln Val Glu Phe Leu Arg Leu Asn Thr His Glu
    50                  55                  60
Asp Pro Gln Leu Leu Glu Ala Thr Leu Ala Gln Leu Pro Gln Asn Leu
65                  70                  75                  80
Ser Cys Leu Arg Ser Leu Val Leu Lys Arg Gly Gln Arg Arg Asp Thr
                85                  90                  95
Leu Gly Ala Cys Leu Arg Gly Ala Leu Thr Asn Leu Pro Ala Gly Leu
            100                 105                 110
Ser Gly Leu Ala His Leu Ala His Leu Asp Leu Ser Phe Asn Ser Leu
        115                 120                 125
Glu Thr Leu Pro Ala Cys Val Leu Gln Met Arg Gly Leu Gly Ala Leu
    130                 135                 140
Leu Leu Ser His Asn Cys Leu Ser Glu Leu Pro Glu Ala Leu Gly Ala
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<210> 2829
<211> 3648
<212> DNA
<213> Homo sapiens

<400> 2829

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<210> 2830
<211> 668
<212> PRT
<213> Homo sapiens

<400> 2830
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            20   25   30
Lys Gln Gln Asp Leu Ser Ile Ala Met Val Val Thr Ser Arg Glu Val
        35   40   45
Leu Ser Ala Leu Ser Gln Leu Val Pro Cys Val Gly Cys Arg Arg Ser
    50   55   60
Val Glu Arg Leu Phe Ser Gln Leu Val Glu Ser Gly Asn Pro Ala Leu

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65                  70                  75                  80
Glu Pro Leu Thr Val Gly Pro Lys Gly Val Leu Ser Val Thr Arg Ser
                85                  90                  95
Cys Met Thr Asp Ala Lys Lys Leu Tyr Thr Leu Phe Tyr Val His Gly
            100                 105                 110
Ser Lys Leu Asn Asp Met Ile Asp Ala Ile Pro Lys Ser Lys Lys Asn
        115                 120                 125
Lys Arg Cys Gln Leu His Ser Leu Asp Thr His Lys Pro Lys Pro Leu
    130                 135                 140
Gly Gly Cys Trp Met Asp Val Trp Glu Leu Met Ser Gln Glu Cys Arg
145                 150                 155                 160
Asp Glu Val Val Leu Ile Asp Ser Ser Cys Leu Leu Glu Thr Leu Glu
                165                 170                 175
Thr Tyr Leu Arg Lys His Arg Phe Cys Thr Asp Cys Lys Asn Lys Val
            180                 185                 190
Leu Arg Ala Tyr Asn Ile Leu Ile Gly Glu Leu Asp Cys Ser Lys Glu
        195                 200                 205
Lys Gly Tyr Cys Ala Ala Leu Tyr Glu Gly Leu Arg Cys Cys Pro His
    210                 215                 220
Glu Arg His Ile His Val Cys Cys Glu Thr Asp Phe Ile Ala His Leu
225                 230                 235                 240
Leu Gly Arg Ala Glu Pro Glu Phe Ala Gly Gly Tyr Glu Arg Arg Glu
                245                 250                 255
Arg His Ala Lys Thr Ile Asp Ile Ala Gln Glu Glu Val Leu Thr Cys
            260                 265                 270
Leu Gly Ile His Leu Tyr Glu Arg Leu His Arg Ile Trp Gln Lys Leu
        275                 280                 285
Arg Ala Glu Glu Gln Thr Trp Gln Met Leu Phe Tyr Leu Gly Val Asp
    290                 295                 300
Ala Leu Arg Lys Ser Phe Glu Met Thr Val Glu Lys Val Gln Gly Ile
305                 310                 315                 320
Ser Arg Leu Glu Gln Leu Cys Glu Glu Phe Ser Glu Glu Glu Arg Val
                325                 330                 335
Arg Glu Leu Lys Gln Glu Lys Lys Arg Gln Lys Arg Lys Asn Arg Arg
            340                 345                 350
Lys Asn Lys Cys Val Cys Asp Ile Pro Thr Pro Leu Gln Thr Ala Asp
        355                 360                 365
Glu Lys Glu Val Ser Gln Glu Lys Glu Thr Asp Phe Ile Glu Asn Ser
    370                 375                 380
Ser Cys Lys Ala Cys Gly Ser Thr Glu Asp Gly Asn Thr Cys Val Glu
385                 390                 395                 400
Val Ile Val Thr Asn Glu Asn Thr Ser Cys Thr Cys Pro Ser Ser Gly
                405                 410                 415
Asn Leu Leu Gly Ser Pro Lys Ile Lys Lys Gly Leu Ser Pro His Cys
            420                 425                 430
Asn Gly Ser Asp Cys Gly Tyr Ser Ser Ser Met Glu Gly Ser Glu Thr
        435                 440                 445
Gly Ser Arg Glu Gly Ser Asp Val Ala Cys Thr Glu Gly Ile Cys Asn
    450                 455                 460
His Asp Glu His Gly Asp Asp Ser Cys Val His His Cys Glu Asp Lys
465                 470                 475                 480
Glu Asp Asp Gly Asp Ser Cys Val Glu Cys Trp Ala Asn Ser Glu Glu
                485                 490                 495
Asn Asp Thr Lys Gly Lys Asn Lys Lys Lys Lys Lys Lys Ser Lys Ile
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Leu Lys Cys Asp Glu His Ile Gln Lys Leu Gly Ser Cys Ile Thr Asp
        515                 520                 525
Pro Gly Asn Arg Glu Thr Ser Gly Asn Thr Met His Thr Val Phe His
    530                 535                 540
Arg Asp Lys Thr Lys Asp Thr His Pro Glu Ser Cys Cys Ser Ser Glu
545                 550                 555                 560
Lys Gly Gly Gln Pro Leu Pro Trp Phe Glu His Arg Lys Asn Val Pro
                565                 570                 575
Gln Phe Ala Glu Pro Thr Glu Thr Leu Phe Gly Pro Asp Ser Gly Lys
            580                 585                 590
Gly Ala Lys Ser Leu Val Glu Leu Leu Asp Glu Ser Glu Cys Thr Ser
        595                 600                 605
Asp Glu Glu Ile Phe Ile Ser Gln Asp Glu Ile Gln Ser Phe Met Ala
    610                 615                 620
Asn Asn Gln Ser Phe Tyr Ser Asn Arg Glu Gln Tyr Arg Gln His Leu
625                 630                 635                 640
Lys Glu Lys Phe Asn Lys Tyr Cys Arg Leu Asn Asp His Lys Arg Pro
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<210> 2831
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<212> DNA
<213> Homo sapiens

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3360
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3420
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3480
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3540
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3600
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3660
ccaagatttt gaaggaaatg agtggccagc gccagggccc aggccatgtg gcctgcccag
3720
cctcaatgtc acttggtggc ggggtggggt gggggtgggc agcagcatcc cagccttgag
3780
atgcttcact ttccttctct gtaaccagac tttgaaaaat tgttcgtttc atcaggctct
3840
gttcctcaat ggccttttgc tacgtgcctc ccgagaaatt tgtctttttg tataaatgac
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3960
aaaaaaaaaa aaaaaaaaaa aaaaaa
3986

<210> 2832
<211> 611
<212> PRT
<213> Homo sapiens

<400> 2832
Leu Leu Pro His Pro Gly Leu Gly Phe Gln Arg Arg Gly Pro Gly Arg
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Ser Val Ile Phe Ser Gln Trp Gly Cys Gly Phe Ser Leu Cys Pro Gly
20 25 30
Gly Thr Arg Thr Ser Ser Gly Arg Leu Arg Arg Leu Gly Asp Ser Ser
35 40 45
Gly Pro Ala Leu Lys Arg Ser Phe Glu Val Glu Glu Val Glu Thr Pro
50 55 60
Asn Ser Thr Pro Pro Arg Arg Val Gln Thr Pro Leu Leu Arg Ala Thr
65 70 75 80
Val Ala Ser Ser Thr Gln Lys Phe Gln Asp Leu Gly Val Lys Asn Ser
85 90 95
Glu Pro Ser Ala Arg His Val Asp Ser Leu Ser Gln Arg Ser Pro Lys
100 105 110
Ala Ser Leu Arg Arg Val Glu Leu Ser Gly Pro Lys Ala Ala Glu Pro
115 120 125
Val Ser Arg Arg Thr Glu Leu Ser Ile Asp Ile Ser Ser Lys Gln Val
130 135 140
Glu Asn Ala Gly Ala Ile Gly Pro Ser Arg Phe Gly Leu Lys Arg Ala
145 150 155 160
Glu Val Leu Gly His Lys Thr Pro Glu Pro Ala Pro Arg Arg Thr Glu
165 170 175
Ile Thr Ile Val Lys Pro Gln Glu Ser Ala His Arg Arg Met Glu Pro
180 185 190
Pro Ala Ser Lys Val Pro Glu Val Pro Thr Ala Pro Ala Thr Asp Ala
195 200 205
Ala Pro Lys Arg Val Glu Ile Gln Met Pro Lys Pro Ala Glu Ala Pro
210 215 220
Thr Ala Pro Ser Pro Ala Gln Thr Leu Glu Asn Ser Glu Pro Ala Pro
225 230 235 240
Val Ser Gln Leu Gln Ser Arg Leu Glu Pro Lys Pro Gln Pro Pro Val
245 250 255
Ala Glu Ala Thr Pro Arg Ser Gln Glu Ala Thr Glu Ala Ala Pro Ser
260 265 270
Cys Val Gly Asp Met Ala Asp Thr Pro Arg Asp Ala Gly Leu Lys Gln
275 280 285
Ala Pro Ala Ser Arg Asn Glu Lys Ala Pro Val Asp Phe Gly Tyr Val
290 295 300
Gly Ile Asp Ser Ile Leu Glu Gln Met Arg Arg Lys Ala Met Lys Gln
305 310 315 320
Gly Phe Glu Phe Asn Ile Met Val Val Gly Gln Ser Gly Leu Gly Lys
325 330 335
Ser Thr Leu Ile Asn Thr Leu Phe Lys Ser Lys Ile Ser Arg Lys Ser
340 345 350
Val Gln Pro Thr Ser Glu Glu Arg Ile Pro Lys Thr Ile Glu Ile Lys
355 360 365
Ser Ile Thr His Asp Ile Glu Glu Lys Gly Val Arg Met Lys Leu Thr

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    370                 375                 380
Val Ile Asp Thr Pro Gly Phe Gly Asp His Ile Asn Asn Glu Asn Cys
385                 390                 395                 400
Trp Gln Pro Ile Met Lys Phe Ile Asn Asp Gln Tyr Glu Lys Tyr Leu
                405                 410                 415
Gln Glu Glu Val Asn Ile Asn Arg Lys Lys Arg Ile Pro Asp Thr Arg
            420                 425                 430
Val His Cys Cys Leu Tyr Phe Ile Pro Ala Thr Gly His Ser Leu Arg
        435                 440                 445
Pro Leu Asp Ile Glu Phe Met Lys Arg Leu Ser Lys Val Val Asn Ile
    450                 455                 460
Val Pro Val Ile Ala Lys Ala Asp Thr Leu Thr Leu Glu Glu Arg Val
465                 470                 475                 480
His Phe Lys Gln Arg Ile Thr Ala Asp Leu Leu Ser Asn Gly Ile Asp
                485                 490                 495
Val Tyr Pro Gln Lys Glu Phe Asp Glu Asp Ser Glu Asp Arg Leu Val
            500                 505                 510
Asn Glu Lys Phe Arg Glu Met Ile Pro Phe Ala Val Val Gly Ser Asp
        515                 520                 525
His Glu Tyr Gln Val Asn Gly Lys Arg Ile Leu Gly Arg Lys Thr Lys
    530                 535                 540
Trp Gly Thr Ile Glu Val Glu Asn Thr Thr His Cys Glu Phe Ala Tyr
545                 550                 555                 560
Leu Arg Asp Leu Leu Ile Arg Thr His Met Gln Asn Ile Lys Asp Ile
                565                 570                 575
Thr Ser Ser Ile His Phe Glu Ala Tyr Arg Val Lys Arg Leu Asn Glu
            580                 585                 590
Gly Ser Ser Ala Met Ala Asn Gly Val Glu Glu Lys Glu Pro Glu Ala
        595                 600                 605
Pro Glu Met
    610
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<210> 2833
<211> 420
<212> DNA
<213> Homo sapiens

<400> 2833
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120
ctccggctgc tcaggtcccc aacgctccgg ggccatggag gtgcttccgg ccggaatgtg
180
actactggga gtctcgggga gccgcagtgg ctgagggtag ccaccggggg gcgccctgga
240
acatcgccgg ccttgttctc cggacgtggg gcagccaccg gggggcgcca gggaggacgc
300
ttcgatacca aatgcctcgc ggctgccact tggggacgcc ttcctggtcc cgaagaaaca
360
ctcccaggac aggacagctg gaacggggtc cccagcaggg ccggactggg catgtgcgcc
420

<210> 2834

<211> 117
<212> PRT
<213> Homo sapiens

<400> 2834
Met Leu Gly Ser Leu Val Leu Arg Arg Lys Ala Leu Ala Pro Arg Leu
1 5 10 15
Leu Leu Arg Leu Leu Arg Ser Pro Thr Leu Arg Gly His Gly Gly Ala
20 25 30
Ser Gly Arg Asn Val Thr Thr Gly Ser Leu Gly Glu Pro Gln Trp Leu
35 40 45
Arg Val Ala Thr Gly Gly Arg Pro Gly Thr Ser Pro Ala Leu Phe Ser
50 55 60
Gly Arg Gly Ala Ala Thr Gly Gly Arg Gln Gly Gly Arg Phe Asp Thr
65 70 75 80
Lys Cys Leu Ala Ala Ala Thr Trp Gly Arg Leu Pro Gly Pro Glu Glu
85 90 95
Thr Leu Pro Gly Gln Asp Ser Trp Asn Gly Val Pro Ser Arg Ala Gly
100 105 110
Leu Gly Met Cys Ala
115

<210> 2835
<211> 938
<212> DNA
<213> Homo sapiens

<400> 2835
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gcccaaggcg ggggagtggg gaagagaggg aagggagagc ccccgcagga agtacatgaa
120
tgagtgggtt actgctgcgg gcaactggga ctccatcctg ctgggcatcc tctgagagtt
180
tatgtagaat acacttcaga attgtcctgc tcaaggacaa tgaagctgag gtcctgctcc
240
ttattgactc agggttgctg ctcctgggga cattaacccc ccaacacttc tagcttgccc
300
agtgcactga ctgagcacac agctgtggcc accagagaac ctctttgggc tgtgatacag
360
gaaaccatcg gtgtgcatgg taactctcta gcagtgtcct tcatgccggg acatggggac
420
acgggcaggc actgctggca tctgctaacc ccggaggccc atacttcaga accggtcagc
480
tgggccaagg cctctctaag gcccagcggc tctcatgggc aaatgtcagg tgacacagag
540
tcagagaccc tgagtgtgcg aggggaagat attggtgaag acctgttctc tgaggccctg
600
ggccgggcag tggggcagtg ggcgggggcc aagctgctgg accatggctg tgtggagagc
660
agcattctgg attcctctgc gggctctgct ccccactacg aggtgtttgt ggcgctgagg
720
gggctgagga atctgtcaga ggaaaatcga gacaagctgg accactgcct tcaggaagcc
780

tctccccgct acaagtccct gcggttctgg ggcagcgtgg gccctgcaga gtccacctgg
840
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900
tcccctctggg acctctccgg atggggagtc cttggcca
938

<210> 2836
<211> 178
<212> PRT
<213> Homo sapiens

<400> 2836
Met Pro Gly His Gly Asp Thr Gly Arg His Cys Trp His Leu Leu Thr
1 5 10 15
Pro Glu Ala His Thr Ser Glu Pro Val Ser Trp Ala Lys Ala Ser Leu
20 25 30
Arg Pro Ser Gly Ser His Gly Gln Met Ser Gly Asp Thr Glu Ser Glu
35 40 45
Thr Leu Ser Val Arg Gly Glu Asp Ile Gly Glu Asp Leu Phe Ser Glu
50 55 60
Ala Leu Gly Arg Ala Val Gly Gln Trp Ala Gly Ala Lys Leu Leu Asp
65 70 75 80
His Gly Cys Val Glu Ser Ser Ile Leu Asp Ser Ser Ala Gly Ser Ala
85 90 95
Pro His Tyr Glu Val Phe Val Ala Leu Arg Gly Leu Arg Asn Leu Ser
100 105 110
Glu Glu Asn Arg Asp Lys Leu Asp His Cys Leu Gln Glu Ala Ser Pro
115 120 125
Arg Tyr Lys Ser Leu Arg Phe Trp Gly Ser Val Gly Pro Ala Glu Ser
130 135 140
Thr Trp Trp Cys Pro Glu Ser Ser Pro Ala Pro Pro Pro Ser Ser Pro
145 150 155 160
Gln Arg Pro Pro Arg Pro Ser Leu Trp Asp Leu Ser Gly Trp Gly Val
165 170 175
Leu Gly

<210> 2837
<211> 1250
<212> DNA
<213> Homo sapiens

<400> 2837
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gttttcacaa tggaggactc cggaaagact ttcagctccg aggaggaaga agctaactat
120
tggaaagatc tggcgatgac ctacaaacag agggcagaaa atacgcaaga ggaactccga
180
gaattccagg agggaagccg agaatatgaa gctgaattgg agacgcagct gcaacaaatt
240
gaaaccagga acagagacct cctgtccgaa aataaccgcc ttcgcatgga gctggaaacc
300

atcaaggaga agtttgaagt gcagcactct gaaggctacc ggcagatctc agccttggag
360
gatgacctcg cgcagaccaa agccattaaa gaccaattgc agaaatacat cagagagctg
420
gagcaagcaa atgacgccct ggaaagagcc aagcgcgcca cgatcatgtc tctcgaagac
480
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540
gaaaaagaga atctcctgga atctgttcag agactgaagg atgaagccag agatttgcgg
600
caggaactgg ccgtgcagca gaagcaggag aaacccagga cccccatgcc cagctcagtg
660
gaagctgaga ggacagacac agctgtgcag gccacgggct ccgtgccgtc cacgcccatt
720
gctcaccgag gacccagctc aagtttaaac acacctggga gcttcagacg tggcctggac
780
gacntccacc gggggacccc cctcacacct gcggcccgga tatcagccct caacattgtg
840
ggagacctac tgcggaaagt cggggcactg gagtccaaac tcgcttcctg ccggaacctc
900
gtgtacgatc agtccccaaa ccgaacaggt ggcccagcct ctgggcggag cagcaagaac
960
agagatggcg gggagagacg gccaagcagc accagcgtgc ctttgggtga taaggggtca
1020
gtaccttcta ataaacctct cgctggcggg gagaacccgc ctgccccagg caagagacac
1080
tcacccccag cccacagcca tgtgtctttt taaattatag gattatttca gcaaaccttа
1140
tcctctcctc tgctccctgc aggcagcatt aggtggtgtc ttgtggcttg aacaaagggc
1200
tagagagagg gtcttgtttt gtgagacagg gtctcgctct gtcacctagg
1250

<210> 2838
<211> 370
<212> PRT
<213> Homo sapiens

<400> 2838
Xaa Leu Pro Ser Ser Pro Leu Leu Glu His His Ala Thr Arg Arg Val
1 5 10 15
Ile Ser Ser Pro Val Phe Thr Met Glu Asp Ser Gly Lys Thr Phe Ser
20 25 30
Ser Glu Glu Glu Glu Ala Asn Tyr Trp Lys Asp Leu Ala Met Thr Tyr
35 40 45
Lys Gln Arg Ala Glu Asn Thr Gln Glu Glu Leu Arg Glu Phe Gln Glu
50 55 60
Gly Ser Arg Glu Tyr Glu Ala Glu Leu Glu Thr Gln Leu Gln Gln Ile
65 70 75 80
Glu Thr Arg Asn Arg Asp Leu Leu Ser Glu Asn Asn Arg Leu Arg Met
85 90 95
Glu Leu Glu Thr Ile Lys Glu Lys Phe Glu Val Gln His Ser Glu Gly
100 105 110
Tyr Arg Gln Ile Ser Ala Leu Glu Asp Asp Leu Ala Gln Thr Lys Ala

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        115                 120                 125
Ile Lys Asp Gln Leu Gln Lys Tyr Ile Arg Glu Leu Glu Gln Ala Asn
    130                 135                 140
Asp Ala Leu Glu Arg Ala Lys Arg Ala Thr Ile Met Ser Leu Glu Asp
145                 150                 155                 160
Phe Glu Gln Arg Leu Asn Gln Ala Ile Glu Arg Asn Ala Phe Leu Glu
                165                 170                 175
Ser Glu Leu Asp Glu Lys Glu Asn Leu Leu Glu Ser Val Gln Arg Leu
            180                 185                 190
Lys Asp Glu Ala Arg Asp Leu Arg Gln Glu Leu Ala Val Gln Gln Lys
        195                 200                 205
Gln Glu Lys Pro Arg Thr Pro Met Pro Ser Ser Val Glu Ala Glu Arg
    210                 215                 220
Thr Asp Thr Ala Val Gln Ala Thr Gly Ser Val Pro Ser Thr Pro Ile
225                 230                 235                 240
Ala His Arg Gly Pro Ser Ser Ser Leu Asn Thr Pro Gly Ser Phe Arg
                245                 250                 255
Arg Gly Leu Asp Asp Xaa His Arg Gly Thr Pro Leu Thr Pro Ala Ala
            260                 265                 270
Arg Ile Ser Ala Leu Asn Ile Val Gly Asp Leu Leu Arg Lys Val Gly
        275                 280                 285
Ala Leu Glu Ser Lys Leu Ala Ser Cys Arg Asn Leu Val Tyr Asp Gln
    290                 295                 300
Ser Pro Asn Arg Thr Gly Gly Pro Ala Ser Gly Arg Ser Ser Lys Asn
305                 310                 315                 320
Arg Asp Gly Gly Glu Arg Arg Pro Ser Ser Thr Ser Val Pro Leu Gly
                325                 330                 335
Asp Lys Gly Ser Val Pro Ser Asn Lys Pro Leu Ala Gly Gly Glu Asn
            340                 345                 350
Pro Pro Ala Pro Gly Lys Arg His Ser Pro Pro Ala His Ser His Val
        355                 360                 365
Ser Phe
    370
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<210> 2839
<211> 606
<212> DNA
<213> Homo sapiens

<400> 2839

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tgccaaatcc agtttacagt agctatagat ttcgccgcca caaacgggga ccccaggaac
120
agctgttcct tgcactacat ccacccttac caacccaatg agtatctgaa agctttggta
180
gctgtggggg agatttgcca agactatgac agtgacaaaa tgttccctgc ctttgggttt
240
ggcgccagga tacctccaga gtacacggtc tctcatgact ttgcaatcaa ctttaatgaa
300
gacaacccag aatgtgcagg aattcaagga gttgtggaag cctatcagag ctgtcttcct
360
aagctccaac tctacggtcc caccaacatt gcccccatca tccagaaggt tgccaagtca
420
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gcgtcagagg aaactaacac caaagaggca tcgcaatact tcatcctgct gatcctgaca
480
gatggtgtta tcacagacat gggcgacacc cgggaggcca ttgtccatgc ctcccacctc
540
cccatgtcag tcatcatcgt gggagtaggg aacgctgact tcagtgacat gcagatgctg
600
gacggt
606

<210> 2840
<211> 202
<212> PRT
<213> Homo sapiens

<400> 2840
Ile Leu Asn Leu Cys Lys Ile His Lys Met His Ser Phe Leu Asp Tyr
1 5 10 15
Ile Met Gly Gly Cys Gln Ile Gln Phe Thr Val Ala Ile Asp Phe Ala
20 25 30
Ala Thr Asn Gly Asp Pro Arg Asn Ser Cys Ser Leu His Tyr Ile His
35 40 45
Pro Tyr Gln Pro Asn Glu Tyr Leu Lys Ala Leu Val Ala Val Gly Glu
50 55 60
Ile Cys Gln Asp Tyr Asp Ser Asp Lys Met Phe Pro Ala Phe Gly Phe
65 70 75 80
Gly Ala Arg Ile Pro Pro Glu Tyr Thr Val Ser His Asp Phe Ala Ile
85 90 95
Asn Phe Asn Glu Asp Asn Pro Glu Cys Ala Gly Ile Gln Gly Val Val
100 105 110
Glu Ala Tyr Gln Ser Cys Leu Pro Lys Leu Gln Leu Tyr Gly Pro Thr
115 120 125
Asn Ile Ala Pro Ile Ile Gln Lys Val Ala Lys Ser Ala Ser Glu Glu
130 135 140
Thr Asn Thr Lys Glu Ala Ser Gln Tyr Phe Ile Leu Leu Ile Leu Thr
145 150 155 160
Asp Gly Val Ile Thr Asp Met Gly Asp Thr Arg Glu Ala Ile Val His
165 170 175
Ala Ser His Leu Pro Met Ser Val Ile Ile Val Gly Val Gly Asn Ala
180 185 190
Asp Phe Ser Asp Met Gln Met Leu Asp Gly
195 200

<210> 2841
<211> 2065
<212> DNA
<213> Homo sapiens

<400> 2841
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tcaccccagc cccccggctc tgcacccact gtgctgccca caggagtggt cctgcccatg
120
gaagggccag ttcaggtggc cggagctcct gagctgccct aggggactgc tgtgggtctg
180

aggtggtgat gtcccccacg gctgcctgcg cctgagcccc cacgcatcca cccctggggc
240
cactctgctg ttcaggagca cccacccgtg tcctcgacca tgagcagccc cccagcttac
300
cctggcatca ggatctcagg gtgccgggcc cttggagcag aaggcagcaa tgcagagtcc
360
ctggacaggc tcctgccacc tgtgggcact gggcgctctc cccggaagcg gaccaccagc
420
cagtgcaagt cagagcctcc cctgctgcgt acaagcaagc gtaccatcta caccgccggg
480
cggccgccct ggtacaatga acacggcacg caatccaaag aggccttcgc catcggcttg
540
ggaggcggca gtgcctctgg gaagaccact gtggccagaa tgatcatcga ggccctggat
600
gtgccctggg tggtcttgct gtccatggac tccttctaca aggtgctcca cagcctcccc
660
caccaggtgc tgactgagca gcagcaggaa caggccgcac acaacaactt caacttcgac
720
cacccagatg cctttgactt cgacctcatc atttccaccc tcaagaagct gaagcagggg
780
aagagtgtca aggtgcccat ttatgacttc accacgcaca gccggaagaa ggactggaaa
840
acactgtatg gtgcaaacgt catcatcttt gagggcatca tggcctttgc tgacaagaca
900
ctgttggagc tcctggacat gaagatcttt gtggacacag actccgacat ccgcctggta
960
cggcggctgc gccgggacat cagtgagcgc ggccgggaca tcgagggtgt catcaagcag
1020
tacaacaagt ttgtcaagcc ctccttcgac cagtacatcc agcccaccat gcgcctggca
1080
gacatcgtgg tccccagagg gagcggcaac acggtggcca tcgacctgat tgtgcagcac
1140
gtgcacagcc agctggagga gcgtgaactc agcgtcaggg ctgcgctggc ctcggcacac
1200
cagtgccacc cgctgccccg gacgctgagc gtcctgaaga gcacgccgca ggtacggggc
1260
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1320
agactgatgc ggctgctcat cgagcacgcg ctctccttcc tgccctttca ggactgcgtc
1380
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1440
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1500
gacgtgcgca tcggcaccat cctcatccag accaaccagc ttaccgggga gcccgagctc
1560
cactacctga ggctgcccaa ggacatcagc gatgaccacg tgatcctcat ggactgcacc
1620
gtgtccacgg gcgcggcggc catgatggca gtgcgcgtgc tcctggacca cgacgtgcct
1680
gaggacaaga tctttttgct gtcgctgctc atggcagaga tgggcgtgca ctcagtggcc
1740
tatgcatttc cgcgagtgag aatcatcacc acggcggtgg acaagcgggt caatgacctt
1800

ttccgcatca tcccaggcat tgggaacttt ggcgaccgct actttgggac agacgcggtc
1860
cccgatggca gtgacgagga ggaagtggcc tacacgggtt agctgcccag tgagccatcc
1920
cgtccccacc accctcctcc tgcctcctga cccaggactg ctgaatacaa agatgttaat
1980
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2040
aaaaatgaaa aaaaaaaaaa aaaaa
2065

<210> 2842
<211> 540
<212> PRT
<213> Homo sapiens

<400> 2842
Met Ser Ser Pro Pro Ala Tyr Pro Gly Ile Arg Ile Ser Gly Cys Arg
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Ala Leu Gly Ala Glu Gly Ser Asn Ala Glu Ser Leu Asp Arg Leu Leu
20 25 30
Pro Pro Val Gly Thr Gly Arg Ser Pro Arg Lys Arg Thr Thr Ser Gln
35 40 45
Cys Lys Ser Glu Pro Pro Leu Leu Arg Thr Ser Lys Arg Thr Ile Tyr
50 55 60
Thr Ala Gly Arg Pro Pro Trp Tyr Asn Glu His Gly Thr Gln Ser Lys
65 70 75 80
Glu Ala Phe Ala Ile Gly Leu Gly Gly Gly Ser Ala Ser Gly Lys Thr
85 90 95
Thr Val Ala Arg Met Ile Ile Glu Ala Leu Asp Val Pro Trp Val Val
100 105 110
Leu Leu Ser Met Asp Ser Phe Tyr Lys Val Leu His Ser Leu Pro His
115 120 125
Gln Val Leu Thr Glu Gln Gln Gln Glu Gln Ala Ala His Asn Asn Phe
130 135 140
Asn Phe Asp His Pro Asp Ala Phe Asp Phe Asp Leu Ile Ile Ser Thr
145 150 155 160
Leu Lys Lys Leu Lys Gln Gly Lys Ser Val Lys Val Pro Ile Tyr Asp
165 170 175
Phe Thr Thr His Ser Arg Lys Lys Asp Trp Lys Thr Leu Tyr Gly Ala
180 185 190
Asn Val Ile Ile Phe Glu Gly Ile Met Ala Phe Ala Asp Lys Thr Leu
195 200 205
Leu Glu Leu Leu Asp Met Lys Ile Phe Val Asp Thr Asp Ser Asp Ile
210 215 220
Arg Leu Val Arg Arg Leu Arg Arg Asp Ile Ser Glu Arg Gly Arg Asp
225 230 235 240
Ile Glu Gly Val Ile Lys Gln Tyr Asn Lys Phe Val Lys Pro Ser Phe
245 250 255
Asp Gln Tyr Ile Gln Pro Thr Met Arg Leu Ala Asp Ile Val Val Pro
260 265 270
Arg Gly Ser Gly Asn Thr Val Ala Ile Asp Leu Ile Val Gln His Val
275 280 285
His Ser Gln Leu Glu Glu Arg Glu Leu Ser Val Arg Ala Ala Leu Ala

```
    290                 295                 300
Ser Ala His Gln Cys His Pro Leu Pro Arg Thr Leu Ser Val Leu Lys
305                 310                 315                 320
Ser Thr Pro Gln Val Arg Gly Met His Thr Ile Ile Arg Asp Lys Glu
                325                 330                 335
Thr Ser Arg Asp Glu Phe Ile Phe Tyr Ser Lys Arg Leu Met Arg Leu
            340                 345                 350
Leu Ile Glu His Ala Leu Ser Phe Leu Pro Phe Gln Asp Cys Val Val
        355                 360                 365
Gln Thr Pro Gln Gly Gln Asp Tyr Ala Gly Lys Cys Tyr Ala Gly Lys
    370                 375                 380
Gln Ile Thr Gly Val Ser Ile Leu Arg Ala Gly Glu Thr Met Glu Pro
385                 390                 395                 400
Ala Leu Arg Ala Val Cys Lys Asp Val Arg Ile Gly Thr Ile Leu Ile
                405                 410                 415
Gln Thr Asn Gln Leu Thr Gly Glu Pro Glu Leu His Tyr Leu Arg Leu
            420                 425                 430
Pro Lys Asp Ile Ser Asp Asp His Val Ile Leu Met Asp Cys Thr Val
        435                 440                 445
Ser Thr Gly Ala Ala Ala Met Met Ala Val Arg Val Leu Leu Asp His
    450                 455                 460
Asp Val Pro Glu Asp Lys Ile Phe Leu Leu Ser Leu Leu Met Ala Glu
465                 470                 475                 480
Met Gly Val His Ser Val Ala Tyr Ala Phe Pro Arg Val Arg Ile Ile
                485                 490                 495
Thr Thr Ala Val Asp Lys Arg Val Asn Asp Leu Phe Arg Ile Ile Pro
            500                 505                 510
Gly Ile Gly Asn Phe Gly Asp Arg Tyr Phe Gly Thr Asp Ala Val Pro
        515                 520                 525
Asp Gly Ser Asp Glu Glu Glu Val Ala Tyr Thr Gly
    530                 535                 540
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<210> 2843
<211> 497
<212> DNA
<213> Homo sapiens

<400> 2843
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120
caaagcccag aatttgaagc tcaaagttcc aaattccagg aaggtgcgga gatgcttctg
180
aaccccgagg aaaagagtcc tttgaatatc tccgtaggag ttcacccccc ggactccttc
240
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300
cccacagggg ccctgctgtc tacaccgcag tttgagatgc ttcagaatcc cctgggtctc
360
acaggagccc ttcgaggtcc aggtcggcgg ggtggccggg cccggggtgg gcagggccct
420
cggcctaaca tctgtggcat ctgggggaag agcttcgggc gggactaccc tgatccagca
480

caggcatcca caccggt
497

<210> 2844
<211> 165
<212> PRT
<213> Homo sapiens

<400> 2844
Pro Arg Tyr Glu Pro Gln Ser Pro Gly Tyr Glu Pro Arg Ser Pro Gly
1 5 10 15
Tyr Glu Pro Arg Ser Pro Gly Tyr Glu Ser Glu Ser Ser Arg Tyr Glu
20 25 30
Ser Gln Asn Thr Glu Leu Lys Thr Gln Ser Pro Glu Phe Glu Ala Gln
35 40 45
Ser Ser Lys Phe Gln Glu Gly Ala Glu Met Leu Leu Asn Pro Glu Glu
50 55 60
Lys Ser Pro Leu Asn Ile Ser Val Gly Val His Pro Leu Asp Ser Phe
65 70 75 80
Thr Gln Gly Phe Gly Glu Gln Pro Thr Gly Asp Leu Pro Ile Gly Pro
85 90 95
Pro Phe Glu Met Pro Thr Gly Ala Leu Leu Ser Thr Pro Gln Phe Glu
100 105 110
Met Leu Gln Asn Pro Leu Gly Leu Thr Gly Ala Leu Arg Gly Pro Gly
115 120 125
Arg Arg Gly Gly Arg Ala Arg Gly Gly Gln Gly Pro Arg Pro Asn Ile
130 135 140
Cys Gly Ile Trp Gly Lys Ser Phe Gly Arg Asp Tyr Pro Asp Pro Ala
145 150 155 160
Gln Ala Ser Thr Pro
165

<210> 2845
<211> 934
<212> DNA
<213> Homo sapiens

<400> 2845
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accgtgtgcg cacgggctgt gcttctcggc tggacacaga gtttggggag gccacttccc
120
ttcaccaagg ctcggggttc tatagcccct ttctgggaca gctgcatggg atccggcctc
180
tcaggcccca cggtgggtgc gggggctgtg gaaaggtctc agctgcaggg ggatgaatgt
240
gacctccagt tgcaacgtct ccccccgcgt gagtggggtt atcaggccta gctcaccttg
300
tgtgcagtca gtgtcgagtg ccacctgcgt actggatgct gctctcagtg ctgcggtgcc
360
acagcacaca aaaatagttc tcacgttgcc gtggagagac aagcagtcaa cgcagatata
420
tcctgtggca agtgatggta aatgctgtgg caagaaagca ggttctggag gtgaagggcg
480

gtgggggaga cagggcaggg aaggtgagca gcggtctgag agtcccttgt ggcacctcgt
540
gggcattagc caaagccgtc ctgatcccaa gggacagggc agggaaggtg agtagtggtc
600
cgagagtccc ttgtggcacc tcatgggcat cggtcaaagc cgtcatgacc ccgaggatgt
660
gccaggagtc agggcctctc ctcctacgtg ggcctgaagg ggctgctgta attcaggagg
720
gtaggcttgg gatgaagggt ctggaatttc tgtctgccag cattagccta atgcaaatct
780
tttcctattc ttttctattg agttaaaggt cctggtggca ttgtcgggtg gggcacattg
840
ctgttgtcat agggctgttt gccttgtgtt tcgtggagcc ccattgctga gcttacaacg
900
tcactctgct ctcagctccc acggcctaac catg
934

<210> 2846
<211> 149
<212> PRT
<213> Homo sapiens

<400> 2846
Met Pro Met Arg Cys His Lys Gly Leu Ser Asp His Tyr Ser Pro Ser
1 5 10 15
Leu Pro Cys Pro Leu Gly Ser Gly Arg Leu Trp Leu Met Pro Thr Arg
20 25 30
Cys His Lys Gly Leu Ser Asp Arg Cys Ser Pro Ser Leu Pro Cys Leu
35 40 45
Pro His Arg Pro Ser Pro Pro Glu Pro Ala Phe Leu Pro Gln His Leu
50 55 60
Pro Ser Leu Ala Thr Gly Tyr Ile Cys Val Asp Cys Leu Ser Leu His
65 70 75 80
Gly Asn Val Arg Thr Ile Phe Val Cys Cys Gly Thr Ala Ala Leu Arg
85 90 95
Ala Ala Ser Ser Thr Gln Val Ala Leu Asp Thr Asp Cys Thr Gln Gly
100 105 110
Glu Leu Gly Leu Ile Thr Pro Leu Thr Arg Gly Glu Thr Leu Gln Leu
115 120 125
Glu Val Thr Phe Ile Pro Leu Gln Leu Arg Pro Phe His Ser Pro Arg
130 135 140
Thr His Arg Gly Ala
145

<210> 2847
<211> 2830
<212> DNA
<213> Homo sapiens

<400> 2847
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gtcccctcca tagcaacagt tcctccttgc ctcacaactt cagctccatt aattcgccgt
120

cagctctcac atgaccacga atctgttggc cctcctagcc tggatgctca gcccaactca
180
aagacagaaa gatcaaaatc atatgatgag ggtctggatg attacagaga agatgcaaaa
240
ttgtccttta agcacgtatc tagtctgaag ggaatcaaga tcgcagacag ccaaaagtca
300
tcagaagact ctgggtccag aaaagattct tcctcagagg tcttcagtga tgctgccaag
360
gaagggtggc ttcatttccg acccccttgtc accgataagg gcaagcgagt tggtggaagt
420
attcggccat ggaaacagat gtatgttgtc cttcggggtc attcacttta cctgtacaaa
480
gataaaagag agcagacgac tccgtctgag gaagagcagc ccatcagtgt taatgcttgc
540
ttgatagaca tctcttacag tgagaccaag aggaaaaatg tgtttcgact caccacgtcc
600
gactgtgaat gcctgtttca ggctgaagac agagatgata tgctagcttg gatcaagacg
660
atccaggaga gcagcaacct aaacgaagag gacactggag tcactaacag ggatctaatt
720
agtcgaagaa taaaagaata caacaatctg atgagcaaag cagaacagtt gccaaaaaca
780
cctcgccaga gtctcagcat caggcaaact ttgcttggtg ctaaatcaga gccaaagact
840
caaagcccac actctccgaa ggaagagtcg gaaaggaaac ttctcagtaa agatgatacc
900
agtcccccaa aagacaaagg cacatggaga aaaggcattc caagtatcat gagaaagaca
960
tttgagaaaa agccaactgc tacaggaact ttcggcgtcc gactagatga ctgcccacca
1020
gctcatacta atcggtatat tccattaata gttgacatat gttgcaaatt agttgaagaa
1080
agaggtcttg aatatacagg tatttataga gttcctggaa ataatgcagc catctcaagt
1140
atgcaagaag aactcaacaa gggaatggct gatattgata tacaagatga taaatggcga
1200
gatttgaatg tgataagcag tttactaaaa tccttcttca gaaaactccc tgagcctctc
1260
ttcacaaatg ataaatatgc tgattttatt gaagccaatc gtaaagaaga tcctctagat
1320
cgtctgaaaa cattaaaaag actaattcac gatttgcctg aacatcatta tgaaacactt
1380
aagttccttt cagctcatct gaagacagtg gcagaaaatt cagaaaaaaa taagatggaa
1440
ccaagaaacc tagcaatagt gtttggtccc acccttgttc gaacatcaga agacaacatg
1500
acccacatgg tcacccacat gcctgaccag tacaagattg tagaaacgct catccagcac
1560
catgactggt ttttcacaga agaaggtgct gaagagcctc ttacaacagt gcaggaggaa
1620
agcacagtag actcccagcc agtgccaaac atagatcatt tactcaccaa cattggaagg
1680
acaggagtct ccccaggaga tgtatcagat tcagctacta gtgactcaac aaaatctaag
1740

ggttcttggg gatctggaaa ggatcagtat agcagggaac tgcttgtgtc ctccatcttt
1800
gcagctgcta gtcgcaagag gaagaagccg aaagaaaaag cacagcctag cagctcagaa
1860
gatgaactgg acaatgtatt ttttaagaaa gaaaatgtgg aacagtgtca caatgatact
1920
aaagaggagt ccaaaaaaga aagtgagaca ctgggcagaa aacagaagat catcattgcc
1980
aaagaaaaca gcactaggaa agaccccagc acgacaaaag atgaaaagat atcactagga
2040
aaagagagca cgccttctga agaaccctca ccaccacaca actcaaaaca caacaagtca
2100
ccaactctca gctgtcgctt tgccatcctg aaagagagcc ccaggtcact tctggcacag
2160
aagtcctccc accttgaaga gacaggctct gactctggca ctttgctcag cacgtcttcc
2220
caggcctccc tggcaaggtt ttccatgaag aaatcaacca gtccagaaac gaaacatagc
2280
gagtttttgg ccaacgtcag caccatcacc tcagattatt ccaccacatc gtctgctaca
2340
tacttgacta gcctggactc cagtcgactg agccctgagg tgcaatccgt ggcagagagc
2400
aaggggacg aggcagatga cgagagaagc gaactcatca gtgaagggcg gcctgtggaa
2460
accgacagcg ggaacgagtt tcccattttc cccacagcct tgacttcaga gaggcttttc
2520
cgaggagaac tgcaaaaagt gactaagagc agccggagaa attctgaatg aagtgaagta
2580
agttgcaccg agggaagttt aacatcaagt ttagatagcc ggagacagct cttcagttcc
2640
cataaactca tcacatgtga tactctctcc aggaaaaaat cagcgagatt caagtcagac
2700
agtggaagtc taggagatgc caagaacgag aaagaaacac cttcattaac taaagtgttt
2760
gatgttatga aaaaaggaaa gtcaactggg agtttactga cacccaccag aggcgaatcc
2820
gaaaaacagg
2830

<210> 2848
<211> 856
<212> PRT
<213> Homo sapiens

<400> 2848
Xaa Asp His Asp Ile Ala His Ile Pro Ala Ser Ala Val Ile Ser Ala
1 5 10 15
Ser Thr Ser Gln Val Pro Ser Ile Ala Thr Val Pro Pro Cys Leu Thr
20 25 30
Thr Ser Ala Pro Leu Ile Arg Arg Gln Leu Ser His Asp His Glu Ser
35 40 45
Val Gly Pro Pro Ser Leu Asp Ala Gln Pro Asn Ser Lys Thr Glu Arg
50 55 60
Ser Lys Ser Tyr Asp Glu Gly Leu Asp Asp Tyr Arg Glu Asp Ala Lys

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65                  70                  75                  80
Leu Ser Phe Lys His Val Ser Ser Leu Lys Gly Ile Lys Ile Ala Asp
                85                  90                  95
Ser Gln Lys Ser Ser Glu Asp Ser Gly Ser Arg Lys Asp Ser Ser Ser
            100                 105                 110
Glu Val Phe Ser Asp Ala Ala Lys Glu Gly Trp Leu His Phe Arg Pro
        115                 120                 125
Leu Val Thr Asp Lys Gly Lys Arg Val Gly Gly Ser Ile Arg Pro Trp
    130                 135                 140
Lys Gln Met Tyr Val Val Leu Arg Gly His Ser Leu Tyr Leu Tyr Lys
145                 150                 155                 160
Asp Lys Arg Glu Gln Thr Thr Pro Ser Glu Glu Glu Gln Pro Ile Ser
                165                 170                 175
Val Asn Ala Cys Leu Ile Asp Ile Ser Tyr Ser Glu Thr Lys Arg Lys
            180                 185                 190
Asn Val Phe Arg Leu Thr Thr Ser Asp Cys Glu Cys Leu Phe Gln Ala
        195                 200                 205
Glu Asp Arg Asp Asp Met Leu Ala Trp Ile Lys Thr Ile Gln Glu Ser
    210                 215                 220
Ser Asn Leu Asn Glu Glu Asp Thr Gly Val Thr Asn Arg Asp Leu Ile
225                 230                 235                 240
Ser Arg Arg Ile Lys Glu Tyr Asn Asn Leu Met Ser Lys Ala Glu Gln
                245                 250                 255
Leu Pro Lys Thr Pro Arg Gln Ser Leu Ser Ile Arg Gln Thr Leu Leu
            260                 265                 270
Gly Ala Lys Ser Glu Pro Lys Thr Gln Ser Pro His Ser Pro Lys Glu
        275                 280                 285
Glu Ser Glu Arg Lys Leu Leu Ser Lys Asp Asp Thr Ser Pro Pro Lys
    290                 295                 300
Asp Lys Gly Thr Trp Arg Lys Gly Ile Pro Ser Ile Met Arg Lys Thr
305                 310                 315                 320
Phe Glu Lys Lys Pro Thr Ala Thr Gly Thr Phe Gly Val Arg Leu Asp
                325                 330                 335
Asp Cys Pro Pro Ala His Thr Asn Arg Tyr Ile Pro Leu Ile Val Asp
            340                 345                 350
Ile Cys Cys Lys Leu Val Glu Glu Arg Gly Leu Glu Tyr Thr Gly Ile
        355                 360                 365
Tyr Arg Val Pro Gly Asn Asn Ala Ala Ile Ser Ser Met Gln Glu Glu
    370                 375                 380
Leu Asn Lys Gly Met Ala Asp Ile Asp Ile Gln Asp Asp Lys Trp Arg
385                 390                 395                 400
Asp Leu Asn Val Ile Ser Ser Leu Leu Lys Ser Phe Phe Arg Lys Leu
                405                 410                 415
Pro Glu Pro Leu Phe Thr Asn Asp Lys Tyr Ala Asp Phe Ile Glu Ala
            420                 425                 430
Asn Arg Lys Glu Asp Pro Leu Asp Arg Leu Lys Thr Leu Lys Arg Leu
        435                 440                 445
Ile His Asp Leu Pro Glu His His Tyr Glu Thr Leu Lys Phe Leu Ser
    450                 455                 460
Ala His Leu Lys Thr Val Ala Glu Asn Ser Glu Lys Asn Lys Met Glu
465                 470                 475                 480
Pro Arg Asn Leu Ala Ile Val Phe Gly Pro Thr Leu Val Arg Thr Ser
                485                 490                 495
Glu Asp Asn Met Thr His Met Val Thr His Met Pro Asp Gln Tyr Lys
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            500                 505                 510
Ile Val Glu Thr Leu Ile Gln His His Asp Trp Phe Phe Thr Glu Glu
        515                 520                 525
Gly Ala Glu Glu Pro Leu Thr Thr Val Gln Glu Glu Ser Thr Val Asp
    530                 535                 540
Ser Gln Pro Val Pro Asn Ile Asp His Leu Leu Thr Asn Ile Gly Arg
545                 550                 555                 560
Thr Gly Val Ser Pro Gly Asp Val Ser Asp Ser Ala Thr Ser Asp Ser
                565                 570                 575
Thr Lys Ser Lys Gly Ser Trp Gly Ser Gly Lys Asp Gln Tyr Ser Arg
            580                 585                 590
Glu Leu Leu Val Ser Ser Ile Phe Ala Ala Ala Ser Arg Lys Arg Lys
        595                 600                 605
Lys Pro Lys Glu Lys Ala Gln Pro Ser Ser Ser Glu Asp Glu Leu Asp
    610                 615                 620
Asn Val Phe Phe Lys Lys Glu Asn Val Glu Gln Cys His Asn Asp Thr
625                 630                 635                 640
Lys Glu Glu Ser Lys Lys Glu Ser Glu Thr Leu Gly Arg Lys Gln Lys
                645                 650                 655
Ile Ile Ile Ala Lys Glu Asn Ser Thr Arg Lys Asp Pro Ser Thr Thr
            660                 665                 670
Lys Asp Glu Lys Ile Ser Leu Gly Lys Glu Ser Thr Pro Ser Glu Glu
        675                 680                 685
Pro Ser Pro Pro His Asn Ser Lys His Asn Lys Ser Pro Thr Leu Ser
    690                 695                 700
Cys Arg Phe Ala Ile Leu Lys Glu Ser Pro Arg Ser Leu Leu Ala Gln
705                 710                 715                 720
Lys Ser Ser His Leu Glu Glu Thr Gly Ser Asp Ser Gly Thr Leu Leu
                725                 730                 735
Ser Thr Ser Ser Gln Ala Ser Leu Ala Arg Phe Ser Met Lys Lys Ser
            740                 745                 750
Thr Ser Pro Glu Thr Lys His Ser Glu Phe Leu Ala Asn Val Ser Thr
        755                 760                 765
Ile Thr Ser Asp Tyr Ser Thr Thr Ser Ser Ala Thr Tyr Leu Thr Ser
    770                 775                 780
Leu Asp Ser Ser Arg Leu Ser Pro Glu Val Gln Ser Val Ala Glu Ser
785                 790                 795                 800
Lys Gly Asp Glu Ala Asp Asp Glu Arg Ser Glu Leu Ile Ser Glu Gly
                805                 810                 815
Arg Pro Val Glu Thr Asp Ser Gly Asn Glu Phe Pro Ile Phe Pro Thr
            820                 825                 830
Ala Leu Thr Ser Glu Arg Leu Phe Arg Gly Glu Leu Gln Lys Val Thr
        835                 840                 845
Lys Ser Ser Arg Arg Asn Ser Glu
    850                 855
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<210> 2849
<211> 380
<212> DNA
<213> Homo sapiens

<400> 2849
gcgcgcgtgg agagggcgcg ggagttggca ttcggtggtc ctggcagtta gctgagcacg
60

ccctctgagc cgctcggtgg acaccaggca ctctagtagg cctggcctac ccagaaacag
120
caggagagag aagaaacagg ccagctgtga gaagccaagg acaccgagtc ggtcatggca
180
cctaaggcgg caaaggggge caagccagag ccagcaccag ctccacctcc acccggggcc
240
aaacccgagg aagacaagaa ggacggtaag gagccatcgg acaaacctca aaaggcggtg
300
caggaccata aggagccatc ggacaaacct caaaaggcgg tgcagcccaa gcacgaagtg
360
ggcacgaagg aggggtgtcg
380

<210> 2850
<211> 76
<212> PRT
<213> Homo sapiens

<400> 2850
Glu Ala Lys Asp Thr Glu Ser Val Met Ala Pro Lys Ala Ala Lys Gly
1 5 10 15
Ala Lys Pro Glu Pro Ala Pro Ala Pro Pro Pro Pro Gly Ala Lys Pro
20 25 30
Glu Glu Asp Lys Lys Asp Gly Lys Glu Pro Ser Asp Lys Pro Gln Lys
35 40 45
Ala Val Gln Asp His Lys Glu Pro Ser Asp Lys Pro Gln Lys Ala Val
50 55 60
Gln Pro Lys His Glu Val Gly Thr Lys Glu Gly Cys
65 70 75

<210> 2851
<211> 2459
<212> DNA
<213> Homo sapiens

<400> 2851
nntgatcaga gttcgactct tgcccaacac tctgttgaac tgactttacc caatcatcat
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ccatttcata gagatttgct ccgatatgcc aagctgatgg agtggctaaa gagtacagat
120
tatggaaaat atgaaggact aacaaagaat tacatggatt atttatcccg actatatgaa
180
agagaaatca aagatttctt tgaagttgca aagatcaaga tgactggcac aactaaagaa
240
agcaagaagt ttggtcttca tggaagttcg gggaaattaa ctggatctac ttctagtcta
300
aataagctca gtgttcagag ttcagggaat cgcagatctc agtcatcttc cctgttggat
360
atgggaaaca tgtctgcctc tgatctcgat gttgctgaca ggaccaaatt tgataagatc
420
tttgaacagg tactaagtga actggagccc ctatgtctgg cagaacagga cttcataagt
480
aaatttttca aactacagca acatcaaagt gtgcctggaa ctatgaaatt ttaagactga
540

gcaggctttt gctatatcaa tactagtcaa attgttggtc ttttattatg taaagtgcct
600
gaataatttt tgcaggctga agcagaggac ctggatggag gaacattatc acggcaacat
660
aattgtggca caccactgcc tgtttcatct gagaaagata tgatccgcca gatgatgatt
720
aaaatatttc gctgcattga gccagagctg aacaacctaa ttgcattagg agacaaaatt
780
gatagcttta actctcttta tatgttagtc aaaatgagtc atcatgtgtg gactgcacaa
840
aatgtggacc ctgcttcttt cctaagtact acattgggaa atgttttggt gactgtcaaa
900
aggaactttg acaaatgcat tagtaaccaa ataaggcaaa tggaagaagt aaagatctca
960
aaaaagagta aagttggaat tcttccattt gttgctgaat ttgaagaatt tgctggactt
1020
gcagaatcaa tcttcaaaaa tgctgagcgt cgtggagacc tggataaagc atacaccaaa
1080
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1140
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1200
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1260
tcttatgtca tttactcttt aggacaacct cttgaaaaac taaatcattt ctttgaaggt
1320
gttgaagctc gcgtggcaca gggcataagg gaggaggaag taagttacca acttgcattt
1380
aacaaacaag aacttcgtaa agtcattaag gagtaccctg gaaaggaagt aaaaaaaggt
1440
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1500
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1560
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1620
gattattgtt ccagcattgc acagtcccac taaaccttgt gaaagaagaa aagataactg
1680
aatgaagcat ttgagtataa cagacactat accaaaatac caagcaactg ttttgagaac
1740
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1800
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1860
ctaacttaag cattcatgtc accataaaat gcctttagca tttctcaatg actggatggg
1920
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1980
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2040
ctgtacaaaa ttgtttttt cacactaaca aatgtgtata tggagaagag ggctcatgtg
2100
atgatcattt gtgaacttag atttttgagg attatgtgac tagtaataaa tgtgaaataa
2160

attttcaaaa aagttgacat ttgaaaaaaa aattagtaac caaataaggc aaatggaaga
2220
agtaaagatc tcaaaaaaga gtaaagttgg aattcttcca tttgttgctg aatttgaaga
2280
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2340
agcatacacc aaacttatca gaggagtatt tgtcaatgtg gagaaagtag caaatgaaag
2400
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2459

<210> 2852
<211> 317
<212> PRT
<213> Homo sapiens

<400> 2852
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Leu Asn Asn Leu Ile Ala Leu Gly Asp Lys Ile Asp Ser Phe Asn Ser
20 25 30
Leu Tyr Met Leu Val Lys Met Ser His His Val Trp Thr Ala Gln Asn
35 40 45
Val Asp Pro Ala Ser Phe Leu Ser Thr Thr Leu Gly Asn Val Leu Val
50 55 60
Thr Val Lys Arg Asn Phe Asp Lys Cys Ile Ser Asn Gln Ile Arg Gln
65 70 75 80
Met Glu Glu Val Lys Ile Ser Lys Lys Ser Lys Val Gly Ile Leu Pro
85 90 95
Phe Val Ala Glu Phe Glu Glu Phe Ala Gly Leu Ala Glu Ser Ile Phe
100 105 110
Lys Asn Ala Glu Arg Arg Gly Asp Leu Asp Lys Ala Tyr Thr Lys Leu
115 120 125
Ile Arg Gly Val Phe Val Asn Val Glu Lys Val Ala Asn Glu Ser Gln
130 135 140
Lys Thr Pro Arg Asp Val Val Met Met Glu Asn Phe His His Ile Phe
145 150 155 160
Ala Thr Leu Ser Arg Leu Lys Ile Ser Cys Leu Glu Ala Glu Lys Lys
165 170 175
Glu Ala Lys Gln Lys Tyr Thr Asp His Leu Gln Ser Tyr Val Ile Tyr
180 185 190
Ser Leu Gly Gln Pro Leu Glu Lys Leu Asn His Phe Phe Glu Gly Val
195 200 205
Glu Ala Arg Val Ala Gln Gly Ile Arg Glu Glu Glu Val Ser Tyr Gln
210 215 220
Leu Ala Phe Asn Lys Gln Glu Leu Arg Lys Val Ile Lys Glu Tyr Pro
225 230 235 240
Gly Lys Glu Val Lys Lys Gly Leu Asp Asn Leu Tyr Lys Lys Val Asp
245 250 255
Lys His Leu Cys Glu Glu Glu Asn Leu Leu Gln Val Val Trp His Ser
260 265 270
Met Gln Asp Glu Phe Ile Arg Gln Tyr Lys His Phe Glu Gly Leu Ile
275 280 285
Ala Arg Cys Tyr Pro Gly Ser Gly Val Thr Met Glu Phe Thr Ile Gln

290 295 300
Asp Ile Leu Asp Tyr Cys Ser Ser Ile Ala Gln Ser His
305 310 315

<210> 2853
<211> 4993
<212> DNA
<213> Homo sapiens

<400> 2853
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agagggcgcg gggaccgtca gcagcacctt agctacaatc gttcagctat tctcggaaga
120
gagaagggag agggaggagg ccggggcggg agtgggggct gtcaccctcg gaccccggcg
180
tgagaggggc cgtgcggccg gacgtcctcg gggtgggccc ccagtcggtg gccgaagacc
240
tacagctcag gcccctgggt cccaaatttc caggctttgc ccctcctcct ttctcagata
300
cccgggtaac agtcctcata gtccagatat ccgggactcg ggtcccaacc tctctaaacc
360
tgggtctctg tttcatagat tttcaaatat caggttcagg cccctgcgtg caccagtatc
420
cggggttcat tccccgggcg tttcaaatat cggattcagt ctccatcccg ttcagatatt
480
cggggttcag accccacaat cagaaatccg gaattcggca gctgtcgccc tcgacgaggg
540
ggaggactgg accgcgaggt cagattaggt tgtcaccccc tcccctccag gggaggcttc
600
ccgggcccgc ccctcaggaa gggcgaaagc cgaggaagag gtggcaaggg gaaaggtctc
660
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720
ggggcaccat agtgacccct accaggccag gccccactct cagggccccc aggggccacc
780
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840
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900
gccgtatact ttgcccggga tgtccggaat agtgaggtgg tggccatcaa gaagatgtcc
960
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1020
cagaagctcc ggcatcccaa caccattcag taccggggct gttacctgag ggagcacacg
1080
gcttggctgg taatggagta ttgcctgggc tcagcttctg accttctaga agtgcacaag
1140
aaaccccttc aggaggtaga gatcgcagct gtgacccatg gggcgcttca gggcctggca
1200
tatctgcact cccacaacat gatccatagg gatgtgaagg ctggaaacat cctgctgtca
1260
gagccagggt tagtgaagct aggggacttt ggttctgcgt ccatcatggc acctgccaac
1320

tccttcgtgg gcaccccata ctggatggca cccgaggtga tcctggccat ggatgagggg
1380
cagtacgatg gcaaagtgga cgtctggtcc ttggggataa cctgcatcga gctggctgaa
1440
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50 55 60
Gln Ser Asn Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Arg Phe Leu
65 70 75 80
Gln Lys Leu Arg His Pro Asn Thr Ile Gln Tyr Arg Gly Cys Tyr Leu
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Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala
100 105 110
Ser Asp Leu Leu Glu Val His Lys Lys Pro Leu Gln Glu Val Glu Ile
115 120 125
Ala Ala Val Thr His Gly Ala Leu Gln Gly Leu Ala Tyr Leu His Ser
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His Asn Met Ile His Arg Asp Val Lys Ala Gly Asn Ile Leu Leu Ser
145 150 155 160
Glu Pro Gly Leu Val Lys Leu Gly Asp Phe Gly Ser Ala Ser Ile Met
165 170 175
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180 185 190
Val Ile Leu Ala Met Asp Glu Gly Gln Tyr Asp Gly Lys Val Asp Val
195 200 205
Trp Ser Leu Gly Ile Thr Cys Ile Glu Leu Ala Glu Arg Lys Pro Pro
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Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile Ala Gln Asn
225 230 235 240
Glu Ser Pro Val Leu Gln Ser Gly His Trp Ser Glu Tyr Phe Arg Asn

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Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Ile Leu Phe Gln Glu Ala
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Pro Asn Gly Pro Gly Ala Glu Ala Pro Glu Glu Glu Glu Glu Ala Glu
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Pro Tyr Met His Arg Ala Gly Thr Leu Thr Ser Leu Glu Ser Ser His
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Ser Val Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser Ser Ser Val
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His Arg Leu Pro Gly Ser Asp Asn Leu Tyr Asp Asp Pro Tyr Gln Pro
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Glu Ala Gln Arg Ala Gly Phe Gly Ala Glu Ala Glu Lys Leu Ala Arg
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Ala Ala Leu Leu Glu Ala Gln Lys Arg Thr Tyr Lys Leu Arg Lys Glu
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Gln Leu Lys Glu Glu Leu Gln Glu Asn Pro Ser Thr Pro Lys Arg Glu
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Lys Ala Glu Trp Leu Leu Arg Gln Lys Glu Gln Leu Gln Gln Cys Gln
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740 745 750
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Leu Cys Lys Gly Trp Asn Trp Arg Leu Ala Arg Ala Ser Gln Gly Leu
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Leu Val Thr Val Ser Arg Asn Pro Leu Glu Glu Thr Ser Ala Leu Ser
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Val Glu Thr Pro Ser Tyr Val Lys Val Ser Gly Ala Ala Pro Val Ser
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Ile Glu Ala Gly Ser Ala Val Gly Lys Thr Thr Ser Phe Ala Gly Ser
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Ser Ala Ser Ser Tyr Ser Pro Ser Glu Ala Ala Leu Lys Asn Phe Thr
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Pro Ser Glu Thr Pro Thr Met Asp Ile Ala Thr Lys Gly Pro Phe Pro
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Thr Ser Arg Asp Pro Leu Pro Ser Val Pro Pro Thr Thr Thr Asn Ser
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Ser Arg Gly Thr Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys
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Ala Gln Ser Cys Tyr Pro Val Thr Thr Lys His Glu Cys Ser Asp Lys

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Leu Trp Lys Asn Asn Leu Pro Ile Met Val Glu Met Met Leu Leu Pro
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Asp Cys Cys Tyr Ser Asp Asp Gly Pro Thr Thr Glu Gly Ile Asp Leu
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Asn Asp Pro Ala Ile Lys Gln Asp Ala Leu Leu Leu Glu Arg Trp Ile
        115                 120                 125
Leu Glu Pro Val Pro Arg Gln Asn Gly Asp Arg Phe Ile Glu Glu Lys
    130                 135                 140
Thr Leu Leu Leu Ala Val Arg Ser Phe Val Phe Phe Ser Gln Leu Ser
145                 150                 155                 160
Ala Trp Leu Ser Val Ser His Gly Ala Ile Pro Arg Asn Ile Leu Tyr
                165                 170                 175
Arg Ile Ser Ala Ala Asp Val Asp Leu Gln Trp Asn Phe Ser Gln Thr
            180                 185                 190
Pro Ile Glu His Val Phe Pro Val Pro Asn Val Ser His Asn Val Ala
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Leu Lys Val Ser Gly Gln Ser Leu Ala Gln Thr Ile
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<212> DNA
<213> Homo sapiens

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<210> 2860
<211> 343
<212> PRT
<213> Homo sapiens

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Thr Met His Gln Pro Pro Glu Ser Thr Ala Ala Ala Ala Ala Ala Ala
            20   25   30
Asp Ile Ser Ala Arg Lys Met Ala His Pro Ala Met Phe Pro Arg Arg
        35   40   45
Gly Ser Gly Ser Gly Ser Ala Ser Ala Leu Asn Ala Ala Gly Thr Gly
    50   55   60
Val Gly Ser Asn Ala Thr Ser Ser Glu Asp Phe Pro Pro Pro Ser Leu
65   70   75   80
Leu Gln Pro Pro Pro Pro Ala Ala Ser Ser Thr Ser Gly Pro Gln Pro
                85   90   95
Pro Pro Pro Gln Ser Leu Asn Leu Leu Ser Gln Ala Gln Leu Gln Ala
            100   105   110
Gln Pro Leu Ala Pro Gly Gly Thr Gln Met Lys Lys Lys Ser Gly Phe
        115   120   125
Gln Ile Thr Ser Val Thr Pro Ala Gln Ile Ser Ala Ser Ile Ser Ser
    130   135   140
Asn Asn Ser Ile Ala Glu Asp Thr Glu Ser Tyr Asp Asp Leu Asp Glu
145   150   155   160
Ser His Thr Glu Asp Leu Ser Ser Ser Glu Ile Leu Asp Val Ser Leu
                165   170   175
Ser Arg Ala Thr Asp Leu Gly Glu Pro Glu Arg Ser Ser Ser Glu Glu
            180   185   190
Thr Leu Asn Asn Phe Gln Glu Ala Glu Thr Pro Gly Ala Val Ser Pro
        195   200   205
Asn Gln Pro His Leu Pro Gln Pro His Leu Pro His Leu Pro Gln Gln
    210   215   220
Asn Val Val Ile Asn Gly Asn Ala His Pro His His Leu His His His
225   230   235   240
His Gln Ile His His Gly His His Leu Gln His Gly His His His Pro
                245   250   255
Ser His Val Ala Val Ala Ser Ala Ser Ile Thr Gly Gly Pro Pro Ser
            260   265   270
Ser Pro Val Ser Arg Lys Leu Ser Thr Thr Gly Ser Ser Asp Ser Ile
        275   280   285
Thr Pro Val Ala Pro Thr Ser Ala Val Ser Ser Ser Gly Ser Pro Ala

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    290                 295                 300
Ser Val Met Thr Asn Met Arg Ala Pro Ser Thr Thr Gly Gly Ile Gly
305                 310                 315                 320
Ile Asn Ser Val Thr Gly Thr Ser Thr Val Asn Asn Val Asn Ile Thr
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Ala Val Gly Ser Phe Asn Ser
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<210> 2861
<211> 756
<212> DNA
<213> Homo sapiens

<400> 2861
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<210> 2862
<211> 252
<212> PRT
<213> Homo sapiens

<400> 2862
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Ser Leu Asp Glu Asp Leu Ser Phe His Ser Pro Ser Leu Asp Leu Val
            20                  25                  30
Ser Glu Ala Leu Ala Val Ile Asn Asn Gly Asn Lys Gly Pro Pro Val
        35                  40                  45
Gly Ser Arg Ile Ser Met Pro Thr Thr Lys Pro Arg Pro Gly Leu Arg
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    50                  55                  60
Glu Glu Lys Leu Ala Ser Ile Met Ser Lys Leu Pro Leu Ala Thr Pro
65                  70                  75                  80
Lys Lys Leu Asp Ser Thr Gln Thr Thr His Ser Ser Ser Leu Ile Ala
                85                  90                  95
Gly His Thr Gly Pro Val Pro Lys Lys Pro Gln Asp Leu Ala His Thr
            100                 105                 110
Gly Ile Ser Ser Gly Leu Ile Ala Gly Ser Ser Ile Gln Asn Pro Lys
        115                 120                 125
Val Ser Leu Glu Pro Leu Pro Ala Arg Leu Leu Gln Gln Gly Leu Gln
    130                 135                 140
Arg Ser Ser Gln Ile His Thr Ser Ser Ser Ser Gln Thr His Val Ser
145                 150                 155                 160
Ser Ser Ser Gln Ala Gln Ile Ala Ala Ser Ser His Ala Leu Gly Thr
                165                 170                 175
Ser Glu Ala Gln Asp Ala Ser Ser Leu Thr Gln Val Thr Lys Val His
            180                 185                 190
Gln His Ser Ala Val Gln Gln Asn Tyr Val Ser Pro Leu Gln Ala Thr
        195                 200                 205
Ile Ser Lys Ser Gln Thr Asn Pro Val Val Lys Leu Ser Asn Asn Pro
    210                 215                 220
Gln Leu Ser Cys Ser Ser Ser Leu Ile Lys Thr Ser Asp Lys Pro Leu
225                 230                 235                 240
Met Tyr Arg Leu Pro Leu Ser Thr Pro Phe Thr Arg
                245                 250
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<210> 2863
<211> 711
<212> DNA
<213> Homo sapiens

<400> 2863

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660
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711

<210> 2864
<211> 237
<212> PRT
<213> Homo sapiens

<400> 2864
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Ser Gly Arg Ile Val Trp Ser Pro Ala Val Pro Gly Ile Pro Val Arg
35 40 45
Ser Ser Ser Leu Pro Leu Phe Ser Asp Ala Met Pro Ala Pro Thr Gln
50 55 60
Leu Phe Phe Pro Leu Ile Arg Asn Cys Glu Leu Ser Arg Ile Tyr Gly
65 70 75 80
Thr Ala Cys Tyr Cys His His Lys His Leu Cys Cys Ser Ser Ser Tyr
85 90 95
Ile Pro Gln Ser Arg Leu Arg Tyr Thr Pro His Pro Ala Tyr Ala Thr
100 105 110
Phe Cys Arg Pro Lys Glu Asn Trp Trp Gln Tyr Thr Gln Gly Arg Arg
115 120 125
Tyr Ala Ser Thr Pro Gln Lys Phe Tyr Leu Thr Pro Pro Gln Val Asn
130 135 140
Ser Ile Leu Lys Ala Asn Glu Tyr Ser Phe Lys Val Pro Glu Phe Asp
145 150 155 160
Gly Lys Asn Val Ser Ser Ile Leu Gly Phe Asp Ser Asn Gln Leu Pro
165 170 175
Ala Asn Ala Pro Ile Glu Asp Arg Arg Ser Ala Ala Thr Cys Leu Gln
180 185 190
Thr Arg Gly Met Leu Leu Gly Val Phe Asp Gly His Ala Gly Cys Ala
195 200 205
Cys Ser Gln Ala Val Ser Glu Arg Leu Phe Tyr Tyr Ile Ala Val Ser
210 215 220
Leu Leu Pro His Glu Thr Leu Leu Glu Ile Glu Asn Ala
225 230 235

<210> 2865
<211> 585
<212> DNA
<213> Homo sapiens

<400> 2865
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240

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420
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585

<210> 2866
<211> 134
<212> PRT
<213> Homo sapiens

<400> 2866
Glu Arg Arg Ser Ser Arg Arg Gln Arg Gln Phe Phe Lys Phe Leu Arg
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Ser Met Ser Ser Val Tyr Leu Gln Cys Lys Val Leu Ile Cys Asp Ser
20 25 30
Ser Asp His Gln Ser Arg Cys Asn Gln Gly Cys Val Ser Arg Ser Lys
35 40 45
Arg Asp Ile Ser Ser Tyr Lys Trp Lys Thr Asp Ser Ile Ile Gly Pro
50 55 60
Ile Arg Leu Lys Arg Asp Arg Ser Ala Ser Gly Asn Ser Gly Phe Gln
65 70 75 80
His Glu Thr His Ala Glu Glu Thr Pro Asn Gln Pro Phe Asn Ser Val
85 90 95
His Leu Phe Ser Phe Met Val Leu Ala Leu Asn Val Val Thr Val Ala
100 105 110
Thr Ile Thr Val Arg His Phe Val Asn Gln Arg Ala Asp Tyr Lys Tyr
115 120 125
Gln Lys Leu Gln Asn Tyr
130

<210> 2867
<211> 444
<212> DNA
<213> Homo sapiens

<400> 2867
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<210> 2868
<211> 84
<212> PRT
<213> Homo sapiens

<400> 2868
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Lys Gly Glu Glu Leu Ser Ala Ala Ala Ile Lys Arg Ile Val Ala Thr
            20   25   30
Ala Lys Ala Ser Gly Lys Lys Leu Gln Lys Val Thr Leu Lys Val Ser
        35   40   45
Pro Arg Gly Ile Ile Leu His Pro Gly His His Pro Ala Pro Arg Gln
    50   55   60
His Cys Cys His Ser Arg Leu Val Ala Ala Ala Pro Arg Pro Cys Trp
65   70   75   80
Trp Cys Trp Arg

<210> 2869
<211> 5811
<212> DNA
<213> Homo sapiens

<400> 2869
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<210> 2870
<211> 258
<212> PRT
<213> Homo sapiens

<400> 2870
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Ser Lys Arg Phe Lys Thr Met Ser Pro Ser Gln Met Ile Met Pro Asn
35 40 45
Val Met Glu Met Ile Ala Ala Leu Gly Pro Gly Pro Ser Pro Tyr Pro
50 55 60
Leu Pro Pro Pro Pro Gly Gly Thr Asn Ser Asn Asp Tyr Ser Ser Gln
65 70 75 80
Gly Asn Asn Tyr Gln Gly His Gly Asn Phe Asp Phe Pro His Gly Asn
85 90 95
Pro Gly Gly Thr Ser Met Asn Asp Phe Met His Gly Pro Pro Gln Leu
100 105 110
Ser His Pro Pro Asp Met Pro Asn Asn Met Ala Ala Leu Glu Lys Pro
115 120 125
Leu Ser His Pro Met Gln Glu Thr Met Pro His Ala Gly Ser Ser Asp
130 135 140
Gln Pro His Pro Ser Ile Gln Gln Gly Leu His Val Pro His Pro Ser
145 150 155 160
Ser Gln Ser Gly Pro Pro Leu His His Ser Gly Ala Pro Pro Pro Pro
165 170 175
Pro Ser Gln Pro Pro Arg Gln Pro Pro Gln Ala Ala Pro Ser Ser His
180 185 190
Pro His Ser Asp Leu Thr Phe Asn Pro Ser Ser Ala Leu Glu Gly Gln
195 200 205
Ala Gly Ala Gln Gly Ala Ser Asp Met Pro Glu Pro Ser Leu Asp Leu
210 215 220
Leu Pro Glu Leu Thr Asn Pro Asp Glu Leu Leu Ser Tyr Leu Asp Pro
225 230 235 240
Pro Asp Leu Pro Ser Asn Ser Asn Asp Asp Leu Leu Ser Leu Phe Glu
245 250 255
Asn Asn

<210> 2871
<211> 786

<212> DNA
<213> Homo sapiens

<400> 2871
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attaacactg ctggtgcaga gatgctgtat tggactgtag gggagctgac tggagtgaac
180
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600
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660
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786

<210> 2872
<211> 153
<212> PRT
<213> Homo sapiens

<400> 2872
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Ile Ser Pro Asp Ala Phe Phe Gln Ile Asn Thr Ala Gly Ala Glu Met
35 40 45
Leu Tyr Trp Thr Val Gly Glu Leu Thr Gly Val Asn Ser Asp Thr Ile
50 55 60
Leu Leu Asp Ile Cys Cys Gly Thr Gly Val Ile Gly Leu Pro Leu Ala
65 70 75 80
Gln His Thr Ser Arg Val Leu Gly Ile Glu Leu Leu Glu Gln Ala Val
85 90 95
Glu Asp Ala Arg Trp Thr Ala Ala Phe Asn Gly Ile Thr Asn Ser Glu
100 105 110
Phe His Thr Gly Gln Ala Glu Lys Ile Leu Pro Gly Leu Leu Lys Ser
115 120 125
Lys Glu Asp Gly Gln Ser Ile Val Ala Val Val Asn Pro Ala Arg Ala

130 135 140
Gly Leu Arg Lys Asp Glu Gln Leu Phe
145 150

<210> 2873
<211> 1187
<212> DNA
<213> Homo sapiens

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240
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300
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360
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480
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720
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1187

<210> 2874
<211> 248
<212> PRT

<213> Homo sapiens

<400> 2874

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Lys Leu Lys Ala Ser Ser Arg Thr Ser Ala Leu Leu Ser Gly Phe Ala
        35                  40                  45
Met Val Ala Met Val Glu Val Gln Leu Asp Ala Asp His Asp Tyr Pro
    50                  55                  60
Pro Gly Leu Leu Ile Ala Phe Ser Ala Cys Thr Thr Val Leu Val Ala
65                  70                  75                  80
Gly His Leu Phe Ala Leu Met Ile Ser Thr Cys Ile Leu Pro Asn Ile
                85                  90                  95
Glu Ala Val Ser Asn Cys Thr Ile Ser Thr Arg Lys Glu Ser Pro His
            100                 105                 110
Glu Arg Met His Arg His Ile Glu Leu Ala Trp Ala Phe Ser Thr Val
        115                 120                 125
Ile Gly Thr Leu Leu Phe Leu Ala Glu Val Val Leu Leu Cys Trp Val
    130                 135                 140
Lys Phe Leu Pro Leu Lys Lys Gln Pro Gly Gln Pro Arg Pro Thr Ser
145                 150                 155                 160
Lys Pro Pro Ala Ser Gly Ala Ala Ala Asn Val Ser Thr Ser Gly Ile
                165                 170                 175
Thr Pro Gly Gln Ala Ala Ala Ile Ala Ser Thr Thr Ile Met Val Pro
            180                 185                 190
Phe Gly Leu Ile Phe Ile Val Phe Ala Val His Phe Tyr Arg Ser Leu
        195                 200                 205
Val Ser His Lys Thr Asp Arg Gln Phe Gln Glu Leu Asn Glu Leu Ala
    210                 215                 220
Glu Phe Ala Arg Leu Gln Asp Gln Leu Asp His Arg Gly Asp His Pro
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Leu Thr Pro Gly Ser His Tyr Ala
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<210> 2875
<211> 593
<212> DNA
<213> Homo sapiens

<400> 2875

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caaggctttg gttttacatt aagacatttt attgtttatc ccccagagtc tgcaattcaa
240
ttttcatata aggatgaaga aaatggaaac agaggaggaa aacaaagaaa ccgcttggaa
300
ccaatggata ccatatttgt taagcaagtt aaagaaggag gacctgcttt tgaagctgga
360
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420
tcccaagtaa ttgctttaat tcaaaacagt gatacaacat tggaacttag tgttatgcca
480
aaagatgaag acattctcca agtggtaagt tttatttatt catatatgag ttgttttaca
540
gtcatgaatg ttcggaaaat atttttgaga tggaagtatt aaagatggaa ttc
593

<210> 2876
<211> 193
<212> PRT
<213> Homo sapiens

<400> 2876
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Glu Gln Ser Glu Thr Val Ser Leu Ser Glu Asp Glu Thr Phe Ser Trp
35 40 45
Pro Gly Pro Lys Thr Val Thr Leu Lys Arg Thr Ser Gln Gly Phe Gly
50 55 60
Phe Thr Leu Arg His Phe Ile Val Tyr Pro Pro Glu Ser Ala Ile Gln
65 70 75 80
Phe Ser Tyr Lys Asp Glu Glu Asn Gly Asn Arg Gly Gly Lys Gln Arg
85 90 95
Asn Arg Leu Glu Pro Met Asp Thr Ile Phe Val Lys Gln Val Lys Glu
100 105 110
Gly Gly Pro Ala Phe Glu Ala Gly Leu Cys Thr Gly Asp Arg Ile Ile
115 120 125
Lys Val Asn Gly Glu Ser Val Ile Gly Lys Thr Tyr Ser Gln Val Ile
130 135 140
Ala Leu Ile Gln Asn Ser Asp Thr Thr Leu Glu Leu Ser Val Met Pro
145 150 155 160
Lys Asp Glu Asp Ile Leu Gln Val Val Ser Phe Ile Tyr Ser Tyr Met
165 170 175
Ser Cys Phe Thr Val Met Asn Val Arg Lys Ile Phe Leu Arg Trp Lys
180 185 190
Tyr

<210> 2877
<211> 1921
<212> DNA
<213> Homo sapiens

<400> 2877
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180

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720
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780
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840
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1740
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1800

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1920
a
1921

<210> 2878
<211> 451
<212> PRT
<213> Homo sapiens

<400> 2878
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Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg Lys Asp
35 40 45
Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Thr Pro Ala Arg Thr
50 55 60
Ser Glu Leu Pro Leu Val Met Trp Leu Gln Gly Gly Pro Gly Gly Ser
65 70 75 80
Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser Asp
85 90 95
Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu Phe
100 105 110
Val Asp Asn Pro Val Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser Gly
115 120 125
Ala Tyr Ala Lys Asp Leu Ala Met Val Ala Ser Asp Met Met Val Leu
130 135 140
Leu Lys Thr Phe Phe Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe
145 150 155 160
Tyr Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly
165 170 175
Leu Glu Leu Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe
180 185 190
Ala Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val
195 200 205
Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys
210 215 220
Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala Val
225 230 235 240
Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala Glu
245 250 255
Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr Asn Ile Leu
260 265 270
Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser Leu Glu Phe Thr
275 280 285
Gln Ser His Leu Val Cys Leu Cys Gln Arg His Val Arg His Leu Gln
290 295 300
Arg Asp Ala Leu Ser Gln Leu Met Asn Gly Pro Ile Arg Lys Lys Leu
305 310 315 320
Lys Ile Ile Pro Glu Asp Gln Ser Trp Gly Gly Gln Ala Thr Asn Val

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                325                 330                 335
Phe Val Asn Met Glu Glu Asp Phe Met Lys Pro Val Ile Asp Ile Val
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Asp Thr Leu Leu Glu Ala Gly Val Asn Val Thr Val Tyr Asn Gly Gln
        355                 360                 365
Leu Asp Leu Ile Val Asp Thr Ile Gly Gln Glu Ala Trp Val Arg Lys
    370                 375                 380
Leu Lys Trp Pro Glu Leu Ser Arg Phe Asn Gln Leu Lys Trp Lys Ala
385                 390                 395                 400
Leu Tyr Ser Asp Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser
                405                 410                 415
Tyr Lys Asn Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val
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Pro Ser Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr
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Gln Gln Glu
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<210> 2879
<211> 1352
<212> DNA
<213> Homo sapiens

<400> 2879
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gagccggtca atggcaagga ggagcaggaa cgggacctcc tggagaagac gcgcctgctg
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1352

<210> 2880
<211> 376
<212> PRT
<213> Homo sapiens

<400> 2880
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35 40 45
Asp Trp Tyr Leu Val Thr Gly Ser Ser Leu Thr Cys Thr Pro Gly Pro
50 55 60
Ala Arg Gly Glu Arg Pro Pro Arg Leu Gly Leu Pro Thr Pro Gly Val
65 70 75 80
Pro Val Xaa Asp Lys Tyr Ala Pro Lys Leu Asp Ser Pro Tyr Phe Arg
85 90 95
His Ser Ser Val Ser Phe Phe Pro Ser Phe Pro Pro Ala Ile Pro Gly
100 105 110
Leu Pro Thr Leu Leu Pro His Pro Gly Pro Phe Gly Ser Leu Gln Gly
115 120 125
Ala Phe Gln Pro Lys Thr Ser Ser Pro Ile Glu Val Ala Arg Arg Ala
130 135 140
Gly Ala Val His Thr Leu Leu Gln Lys Ala Pro Gly Val Ser Asp Pro
145 150 155 160
Tyr Arg Ala Val Val Lys Lys Pro Gly Arg Trp Cys Ala Val His Val
165 170 175
Gln Ile Ala Trp Gln Ile Tyr Arg His Gln Gln Lys Ile Lys Glu Met
180 185 190
Gln Leu Asp Pro His Lys Leu Glu Val Gly Ala Lys Leu Asp Leu Phe
195 200 205
Gly Arg Pro Pro Ala Pro Gly Val Phe Ala Gly Phe His Tyr Pro Gln
210 215 220
Asp Leu Ala Arg Pro Leu Phe Pro Ser Thr Gly Ala Ala His Pro Ala
225 230 235 240
Ser Asn Pro Phe Gly Pro Ser Ala His Pro Gly Ser Phe Leu Pro Thr

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                245                 250                 255
Gly Pro Leu Thr Asp Pro Phe Ser Arg Pro Ser Thr Phe Gly Gly Leu
            260                 265                 270
Gly Ser Leu Ser Ser His Ala Phe Gly Gly Leu Gly Ser His Ala Leu
        275                 280                 285
Ala Pro Gly Gly Ser Ile Phe Ala Pro Lys Glu Gly Ser Ser Val Leu
    290                 295                 300
Gly Leu Pro Ser Pro His Glu Ala Trp Ser Arg Leu His Arg Ala Pro
305                 310                 315                 320
Pro Ser Phe Pro Ala Pro Pro Pro Trp Pro Lys Ser Val Asp Ala Glu
                325                 330                 335
Arg Val Ser Ala Leu Thr Asn His Asp Arg Glu Pro Val Asn Gly Lys
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Glu Glu Gln Glu Arg Asp Leu Leu Glu Lys Thr Arg Leu Leu Ser Arg
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<210> 2881
<211> 3021
<212> DNA
<213> Homo sapiens

<400> 2881

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900
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1920
aaacaaaacc tcgtcattaa agacaaattt atcagaagat gggtgcacaa agaaggcttt
1980
agtggcttca agaggtatgt gaccgctgcc gaggacaagg agcttgaagc caagatcgca
2040
gttgttgaaa agtataacat caggattcca gagctggtgc aaaggataga aaaatgccat
2100
atagaagatt tggactttgc agagtacatt ctgggcactg tgcacaaagc caaaggcctg
2160
gagtttgaca ctgtgcatgt tttggatgat tttgtgaaag tgccttgtgc ccggcataac
2220
ctgccccagc ttccgcactt cagagttgag tcattttctg aggatgaatg gaatttactg
2280
tatgttgcag taactcgagc caagaagcgt ctcatcatga ccaaatcatt ggaaaacatt
2340
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2400
ggcgtggtgc gctgctgcgt gggacagtgc aacaatgcca tccctgttga caccgtcctt
2460
accatgaaga agctgcccat cacctatagc aacaggaagg aaaacaaggg gggctacctc
2520

tgccactcct gtgcggagca gcgcatcggg cccctggcgt tcctgacagc ctccccggag
2580
caggtgcgcg ccatggagcg cactgtggag aacatcgtac tgccccggca tgaggccctg
2640
ctcttcctcg tcttctgagg acaaggcgca cgttctccgc agtgcagagc agcttgccga
2700
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2760
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2820
cctacagaca gccagtctcc acttgcctcc cctctggatg tatctggtca gggaagtggg
2880
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2940
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3000
aaaaaaaaaa aaaaaaaaaa a
3021

<210> 2882
<211> 96
<212> PRT
<213> Homo sapiens

<400> 2882
Gly Gln Gly Ala Arg Ser Pro Gln Cys Arg Ala Ala Cys Arg Gly Pro
1 5 10 15
Arg Val Lys Lys Ala Ser Glu Gly Gly Phe Cys Ser Leu Arg Leu Trp
20 25 30
Val His Pro Gln His Phe Leu Arg Lys Arg Thr Pro Ala Gln Ala Gly
35 40 45
Pro Ala Ile Ser Pro Leu Pro Thr Asp Ser Gln Ser Pro Leu Ala Ser
50 55 60
Pro Leu Asp Val Ser Gly Gln Gly Ser Gly Gly Cys Ser Phe Asp Lys
65 70 75 80
Lys Lys Lys Lys Phe Tyr Val Phe Lys Leu Leu Leu Gln Asp Phe Asn
85 90 95

<210> 2883
<211> 516
<212> DNA
<213> Homo sapiens

<400> 2883
gagaaggagg acaggggtga gtactccccc gcacttgccc tgcccagcct ccggggctgc
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taccacgagg ggccggctgg tggtgcggcg gcggcaccga gcagtgtgga cacgtacccg
120
tacgggctgc ccacacctcc tgaaatgtct cccctggacg tgctggagcc ggagcagacc
180
ttcttctcct ccccctgcca ggaggagcat ggccatcccc gccgcatccc ccacctgcca
240
gggcacccgt actcaccgga gtacgcccca agccctctcc actgtagcca ccccctgggc
300

tccctggccc ttggccagtc ccccggcgtc tccatgatgt cccctgtacc cggctgtccc
360
ccatctcctg cctattactc cccggccacc taccacccac tccactccaa cctccaagcc
420
cacctgggcc agctttcccc gcctcctgag caccctggct tcgacgccct ggatcaactg
480
aaccagggtg aactcctggg ggacatggat cgcaat
516

<210> 2884
<211> 172
<212> PRT
<213> Homo sapiens

<400> 2884
Glu Lys Glu Asp Arg Gly Glu Tyr Ser Pro Ala Leu Ala Leu Pro Ser
1 5 10 15
Leu Arg Gly Cys Tyr His Glu Gly Pro Ala Gly Gly Ala Ala Ala Ala
20 25 30
Pro Ser Ser Val Asp Thr Tyr Pro Tyr Gly Leu Pro Thr Pro Pro Glu
35 40 45
Met Ser Pro Leu Asp Val Leu Glu Pro Glu Gln Thr Phe Phe Ser Ser
50 55 60
Pro Cys Gln Glu Glu His Gly His Pro Arg Arg Ile Pro His Leu Pro
65 70 75 80
Gly His Pro Tyr Ser Pro Glu Tyr Ala Pro Ser Pro Leu His Cys Ser
85 90 95
His Pro Leu Gly Ser Leu Ala Leu Gly Gln Ser Pro Gly Val Ser Met
100 105 110
Met Ser Pro Val Pro Gly Cys Pro Pro Ser Pro Ala Tyr Tyr Ser Pro
115 120 125
Ala Thr Tyr His Pro Leu His Ser Asn Leu Gln Ala His Leu Gly Gln
130 135 140
Leu Ser Pro Pro Pro Glu His Pro Gly Phe Asp Ala Leu Asp Gln Leu
145 150 155 160
Asn Gln Gly Glu Leu Leu Gly Asp Met Asp Arg Asn
165 170

<210> 2885
<211> 807
<212> DNA
<213> Homo sapiens

<400> 2885
aagcttcagg gcattgggca tttcangaat accattcgag aaatgttttc tcagttcgca
60
gagtttgatg atgaactgga tagcatggct ccagtgggga gagatgcaga aacattgcaa
120
aagcaaaagg aaactataaa agcctttcta aagaaactag aagccctcat agcaagcaat
180
gacaatgcca ataaaacctg caagatgatg ttagccacag aagaaacctc tcctgacctt
240
gttggaatca aaagggactt ggaggcctta agcaaacaat gcaacaagtt actggaccga
300

gcccaagcca gagaagagca ggttgaaggg acaattaagc gccttgaaga attttacagc
360
aaattgaaag aatttttctat tctgctccag aaagccgaag aacatgaaga gtcacaaggt
420
cctgttggta tggaaacgga gacaattaat cagcagctta acatgttcaa ggtattccag
480
aaagaagaga ttgaaccctt gcaaggtaaa cagcaagatg taaactggtt aggtcaaggc
540
cttattcaga gtgctgccaa aagcactagc actcagggct tggagcatga cctggatgat
600
gtcaatgcac ggtggaagac tctcaataag aaggtggctc agcgagcagc ccagctgcag
660
gaggccttgc tgcactgtgg gaggttccag gatgccctgg agtccctgct cagctggatg
720
gtggacactg aggagcttgt ggccaatcag aagcccccgt cggctgagtt caaagtggta
780
aaggacaaga tacaagaaca aaagctt
807

<210> 2886
<211> 269
<212> PRT
<213> Homo sapiens

<400> 2886
Lys Leu Gln Gly Ile Gly His Phe Xaa Asn Thr Ile Arg Glu Met Phe
1 5 10 15
Ser Gln Phe Ala Glu Phe Asp Asp Glu Leu Asp Ser Met Ala Pro Val
20 25 30
Gly Arg Asp Ala Glu Thr Leu Gln Lys Gln Lys Glu Thr Ile Lys Ala
35 40 45
Phe Leu Lys Lys Leu Glu Ala Leu Ile Ala Ser Asn Asp Asn Ala Asn
50 55 60
Lys Thr Cys Lys Met Met Leu Ala Thr Glu Glu Thr Ser Pro Asp Leu
65 70 75 80
Val Gly Ile Lys Arg Asp Leu Glu Ala Leu Ser Lys Gln Cys Asn Lys
85 90 95
Leu Leu Asp Arg Ala Gln Ala Arg Glu Glu Gln Val Glu Gly Thr Ile
100 105 110
Lys Arg Leu Glu Glu Phe Tyr Ser Lys Leu Lys Glu Phe Ser Ile Leu
115 120 125
Leu Gln Lys Ala Glu Glu His Glu Glu Ser Gln Gly Pro Val Gly Met
130 135 140
Glu Thr Glu Thr Ile Asn Gln Gln Leu Asn Met Phe Lys Val Phe Gln
145 150 155 160
Lys Glu Glu Ile Glu Pro Leu Gln Gly Lys Gln Gln Asp Val Asn Trp
165 170 175
Leu Gly Gln Gly Leu Ile Gln Ser Ala Ala Lys Ser Thr Ser Thr Gln
180 185 190
Gly Leu Glu His Asp Leu Asp Asp Val Asn Ala Arg Trp Lys Thr Leu
195 200 205
Asn Lys Lys Val Ala Gln Arg Ala Ala Gln Leu Gln Glu Ala Leu Leu
210 215 220
His Cys Gly Arg Phe Gln Asp Ala Leu Glu Ser Leu Leu Ser Trp Met

225 230 235 240
Val Asp Thr Glu Glu Leu Val Ala Asn Gln Lys Pro Pro Ser Ala Glu
245 250 255
Phe Lys Val Val Lys Asp Lys Ile Gln Glu Gln Lys Leu
260 265

<210> 2887
<211> 1945
<212> DNA
<213> Homo sapiens

<400> 2887
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gcagcgactc cgaaggtgtt aactgtctgg cctatgatga agccatcatg gctcagcagg
120
accgaattca gcaagagatt gctgtgcaga accctctggt gtcagagcgg ctggagctct
180
cggtcctata caaggagtat gctgaagatg acaacatcta tcaacagaag atcaaggacc
240
tccacaaaaa gtactcgtac atccgcaaga ccaggcctga cggcaactgt ttctatcggg
300
ctttcggatt ctcccacttg gaggcactgc tggatgacag caaggagttg cagcggtgag
360
aagggtgggc actgggcacc gaggcaggtg ggtgtctacc tcctccccgg gcgagtagga
420
tgtgtctcga gtagggtgtc tccctccttc ccgggcgatg ggctggactc tggccttgcc
480
aggcggggca gtgctgtctc ggccctggcg tctgggctgg tcgaggagcc catgctgggc
540
ccgcctttcc atcccacccc caggttcaag gctgtgtctg ccaagagcaa ggaagacctg
600
gtgtcccagg gcttcactga attcacaatt gaggatttcc acaacacgtt catggacctg
660
attgagcagg tggagaagca gacctctgtc gccgacctgc tggcctcctt caatgaccag
720
agcacctccg actaccttgt ggtctacctg cggctgctca cctcgggcta cctgcagcgc
780
gagagcaagt tcttcgagca cttcatcgag ggtggacgga ctgtcaagga gttctgccag
840
caggaggtgg agcccatgtg caaggagagc gaccacatcc acatcattgc gctggcccag
900
gccctcagcg tgtccatcca ggtggagtac atggaccgcg gcgagggcgg caccaccaat
960
ccgcacatct tccctgaggg ctccgagccc aaggtctacc ttctctaccg gcctggacac
1020
tacgatatcc tctacaaata gggctggctc cagcccgctg ctgccctgct gccccctct
1080
gccaggcgct agacatgtac agaggttttt ctgtggttgt aaatggtcct atttcacccc
1140
cttcttcctg tcacatgacc ccccccatg ttttattaaa gggggtgctg gtggtgagcc
1200
gtgtgtgcgt gtccctgctc tgctgcccgc ctggctgctc tgtctgctgc cccctccccc
1260

caggtgggtc cccctgcttt tcacctatct actcctgagc ttccccaaca ggagcaggtt
1320
tgaggggcca ggcctcttgg aggcccctcc tgcttcgttg ggttctgctt ccttcccttc
1380
ttagctggct caggggcttc tatgggatcc tggaagttcc ttagggactt gcccagggtc
1440
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1500
ccccagaccc cagcttcctg ccctccaccg ggagtctgca tggttgggag tcctgggtgg
1560
aggggccttt gtgaggctgg acccggctca gggcaggtgg aggagctggg cctcccacag
1620
ggtgcccggg cagtgccatc ctggtggggg agggcagcct tcaaacgtgt ggggtctaca
1680
gtcctcaggt ctaggcaggg ctgccggttc tccacctccc catccgcccc aggccccctg
1740
cctgtgcctg ccttgcaccc cctctgcttg ggccacggtg tctctgcatt gcctgccttt
1800
ttgccttcac ctcttttctt ccccgccccc tgcacattcg gggtctcagc ccccaggctg
1860
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1920
aaaaaaaaaa aaaaaaaaaa aaaaa
1945

<210> 2888
<211> 315
<212> PRT
<213> Homo sapiens

<400> 2888
Met Met Lys Pro Ser Trp Leu Ser Arg Thr Glu Phe Ser Lys Arg Leu
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Leu Cys Arg Thr Leu Trp Cys Gln Ser Gly Trp Ser Ser Arg Ser Tyr
            20   25   30
Thr Arg Ser Met Leu Lys Met Thr Thr Ser Ile Asn Arg Arg Ser Arg
        35   40   45
Thr Ser Thr Lys Ser Thr Arg Thr Ser Ala Arg Pro Gly Leu Thr Ala
    50   55   60
Thr Val Ser Ile Gly Leu Ser Asp Ser Pro Thr Trp Arg His Cys Trp
65   70   75   80
Met Thr Ala Arg Ser Cys Ser Gly Glu Lys Gly Gly His Trp Ala Pro
                85   90   95
Arg Gln Val Gly Val Tyr Leu Leu Pro Gly Arg Val Gly Cys Val Ser
            100   105   110
Ser Arg Val Ser Pro Ser Phe Pro Gly Asp Gly Leu Asp Ser Gly Leu
        115   120   125
Ala Arg Arg Gly Ser Ala Val Ser Ala Leu Ala Ser Gly Leu Val Glu
    130   135   140
Glu Pro Met Leu Gly Pro Pro Phe His Pro Thr Pro Arg Phe Lys Ala
145   150   155   160
Val Ser Ala Lys Ser Lys Glu Asp Leu Val Ser Gln Gly Phe Thr Glu
                165   170   175
Phe Thr Ile Glu Asp Phe His Asn Thr Phe Met Asp Leu Ile Glu Gln

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            180                 185                 190
Val Glu Lys Gln Thr Ser Val Ala Asp Leu Leu Ala Ser Phe Asn Asp
        195                 200                 205
Gln Ser Thr Ser Asp Tyr Leu Val Val Tyr Leu Arg Leu Leu Thr Ser
    210                 215                 220
Gly Tyr Leu Gln Arg Glu Ser Lys Phe Phe Glu His Phe Ile Glu Gly
225                 230                 235                 240
Gly Arg Thr Val Lys Glu Phe Cys Gln Gln Glu Val Glu Pro Met Cys
                245                 250                 255
Lys Glu Ser Asp His Ile His Ile Ile Ala Leu Ala Gln Ala Leu Ser
            260                 265                 270
Val Ser Ile Gln Val Glu Tyr Met Asp Arg Gly Glu Gly Gly Thr Thr
        275                 280                 285
Asn Pro His Ile Phe Pro Glu Gly Ser Glu Pro Lys Val Tyr Leu Leu
    290                 295                 300
Tyr Arg Pro Gly His Tyr Asp Ile Leu Tyr Lys
305                 310                 315
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<210> 2889
<211> 614
<212> DNA
<213> Homo sapiens

<400> 2889
gtgcacctcc ccgaggtgca gctgccgaaa gtgtcagaga ttcggctgcc ggaaatgcaa
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gtgnccgaag ttcccgacgt gcatcttccg aagncaccag aggtgaagct gcccagggct
120
ccggaggtgc agctaaaggc caccaaggca gaacaggcag aagggatgga atttggcttc
180
aagatgccca agatgaccat gcccaagcta gggagggcag agtccccatc acgtggcaag
240
ccaggcgagg cgggtgctga ggtctcaggg aagctggtaa cacttccctg tctgcagcca
300
gaggtggatg gtgaggctca tgtgggtgtc ccctctctca ctctgccttc agtggagcta
360
gacctgccag gagcacttgg cctgcagggg caggtcccag ccgctaaaat gggcaaggga
420
gagcgggcgg agggccccga ggtggcagca ggggtcaggg aagtgggctt ccgagtgccc
480
tctgttgaaa ttgtcacccc acagctgccc gccgtggaaa ttgaggaagg gcggctggag
540
atgatagaga caaaagtcaa gccctcttcc aagttctcct tacctaagtt tggactctcg
600
ggaccaaagg tggc
614

<210> 2890
<211> 204
<212> PRT
<213> Homo sapiens

<400> 2890
Val His Leu Pro Glu Val Gln Leu Pro Lys Val Ser Glu Ile Arg Leu

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 1               5                  10                  15
Pro Glu Met Gln Val Xaa Glu Val Pro Asp Val His Leu Pro Lys Xaa
            20                  25                  30
Pro Glu Val Lys Leu Pro Arg Ala Pro Glu Val Gln Leu Lys Ala Thr
        35                  40                  45
Lys Ala Glu Gln Ala Glu Gly Met Glu Phe Gly Phe Lys Met Pro Lys
    50                  55                  60
Met Thr Met Pro Lys Leu Gly Arg Ala Glu Ser Pro Ser Arg Gly Lys
65                  70                  75                  80
Pro Gly Glu Ala Gly Ala Glu Val Ser Gly Lys Leu Val Thr Leu Pro
                85                  90                  95
Cys Leu Gln Pro Glu Val Asp Gly Glu Ala His Val Gly Val Pro Ser
            100                 105                 110
Leu Thr Leu Pro Ser Val Glu Leu Asp Leu Pro Gly Ala Leu Gly Leu
        115                 120                 125
Gln Gly Gln Val Pro Ala Ala Lys Met Gly Lys Gly Glu Arg Ala Glu
    130                 135                 140
Gly Pro Glu Val Ala Ala Gly Val Arg Glu Val Gly Phe Arg Val Pro
145                 150                 155                 160
Ser Val Glu Ile Val Thr Pro Gln Leu Pro Ala Val Glu Ile Glu Glu
                165                 170                 175
Gly Arg Leu Glu Met Ile Glu Thr Lys Val Lys Pro Ser Ser Lys Phe
            180                 185                 190
Ser Leu Pro Lys Phe Gly Leu Ser Gly Pro Lys Val
        195                 200
```

<210> 2891
<211> 565
<212> DNA
<213> Homo sapiens

<400> 2891
tttttttttt tttttttttt tttttttttt tttttttttc ccatgctccc actggtttat
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ttcaacccca aatattttcc aacagaagta gaaaacaggg catattaaac aaacaacaaa
120
ccaaccaacc aacaaaacta aaagtgatac tgacacagtt caggtgataa gcaggaaaat
180
gggattatca gacaccggct ctttggcaca cactgcgaag tcagcccctc tgcccagtct
240
ggaaaagcaa cggcgtaagt caatgtgatg aagaggtcca gcctctcgtc gggaacttgg
300
ccgcaaaatg ggtaatgctt ttctgtagga tgtggagtgt agctggtgtt gcaatggtgt
360
tttgctcagg gctcggcaca gacgtcctcc ggccttccac tgcgatgttg ctctttggtc
420
tcttaacaac atggggacga ggtgggcgca cctttccaaa gtggactgtg atttggccgc
480
cgttcttctc ggagcttggg gttccttgcc ctccaccagt ggggacggtg cagtctttgg
540
cagctgctct tctggggtgg gggcc
565

<210> 2892

<211> 90
<212> PRT
<213> Homo sapiens

<400> 2892
Met Leu Leu Arg Asp Gln Arg Ala Thr Ser Gln Trp Lys Ala Gly Gly
1 5 10 15
Arg Leu Cys Arg Ala Leu Ser Lys Thr Pro Leu Gln His Gln Leu His
20 25 30
Ser Thr Ser Tyr Arg Lys Ala Leu Pro Ile Leu Arg Pro Ser Ser Arg
35 40 45
Arg Glu Ala Gly Pro Leu His His Ile Asp Leu Arg Arg Cys Phe Ser
50 55 60
Arg Leu Gly Arg Gly Ala Asp Phe Ala Val Cys Ala Lys Glu Pro Val
65 70 75 80
Ser Asp Asn Pro Ile Phe Leu Leu Ile Thr
85 90

<210> 2893
<211> 2270
<212> DNA
<213> Homo sapiens

<400> 2893
cacaactctt cacccattcc ctgccccctt ctggatacgc tgcctgttct ttctgtgcct
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agccctgtcc aagctctatg agacctctct ctgcctgcag tctgtttctg ctgtacctcc
120
tcaattctgg cctgtgctct tctagggaga ctagatgtat gcaccaccca gaaactgcca
180
gtagggagca ccctacaggc atgacttggc agctaggcca tgtttatttc ccttggtggg
240
gcacccgaca ggcagagttt attccctcag cttgggggtg gcagtggtgg tggtagtgct
300
aggggttact gcaggcaggt ttctgtttct ttgcatcccg ggactggctt gttctcacct
360
ttttgttctg tccctctctg gtgtatttac tttctctctt tttgcattgt tctcagcctt
420
ccatctgcat ctcttcatct ctgcctctct tgcctgcatt tcctcaatct tgattgtccc
480
tgcctcttcc tctgccattc cctctcttcc ccctcagtct gtggctctgc ctccctgtct
540
cactctccct ataactggcc tctccctgcc cagaccttcc tggacgagct gcatgagaca
600
gggcagctgc actctatgtc cacctggatg gagctatatc cagcagtcag cactgatgtc
660
cgctttgcca acatgctggg ccagccgggc tccacccctc tggacttatt caagttctat
720
gtggaggagt tgaaggcacg attccatgat gaaaagaaga tcattaagga catccttaag
780
gaccggggct tctgcgtgga ggtgaacacg gcctttgagg acttcgccca cgtcataagc
840
tttgacaaga gggctgccgc actggacgca ggcaacatca agctgacctt caatagtctg
900

ctggagaaag cagaggcacg ggagagggag cgggagaagg aggaggcacg caggatgcgg
960
cgcagggaag ctgcctttcg aagcatgctg aggcaggctg tgcctgctct ggagctaggc
1020
actgcctggg aagaggtccg tgagcgtttt gtgtgtgact cagcctttga gcagatcacc
1080
ctggagtcgg agcggatccg gctcttccgg gagttcctac aggtgctgga gactgaatgc
1140
cagcacctcc acaccaaagg ccgaaagcat ggcaggaaag gcaagaagca ccatcacaag
1200
cgttcccact caccctcagg ctctgagtca gaagaagagg agctgccccc accatctctc
1260
cggcccccca agcggaggag gcggaacccc tcagagtcag gctctgagcc ctcttcctca
1320
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1380
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1440
agaagacaca agtcgaatag tcctgagagt gagacagacc ctgaggagaa agctggcaag
1500
gagagcgatg agaaagaaca agaacaggac aaggacaggg agctccaaca ggcagagctc
1560
cctaaccgtt ccccaggctt tggaatcaag aaggagaaga caggctggga cacgtcagaa
1620
agtgagctga gtgagggtga gctggagagg cggcggcgga cactcctaca gcagctggat
1680
gatcaccagt gacccaatga gctgttctct gcctcgggtc tgtgtgaggc catggctcct
1740
gggccaccct caccgtctgc ctcagacttc ttccttagtc tggtctgtgt ccacttttc
1800
taaagtaacc ccacccccag cacaccattg ttggcacctc tcaaggttgc tcttggtgtt
1860
caagggtccc ctactccctg gactagtgca gtccttgccc tcagccccag accagagatg
1920
ggtggtatat gccatgtggg gtgggtgatg ccagtagata aaagtgtgag agaaggggtc
1980
tccagggaag agtcacaggc tgttggacgc agcctgggtg gcagagggca gggtcatcac
2040
cctctagcat cagtgcctgc tcctgcctgc cctggccctg aggctccacc acttcttcct
2100
ccacccagga cctaatgtac gtgtgttttg ttttttgttt tttaaataac aatatttata
2160
acatgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
2220
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaag
2270

<210> 2894
<211> 490
<212> PRT
<213> Homo sapiens

<400> 2894
Met Phe Ile Ser Leu Gly Gly Ala Pro Asp Arg Gln Ser Leu Phe Pro

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 1               5                  10                  15
Gln Leu Gly Gly Gly Ser Gly Gly Gly Ser Ala Arg Gly Tyr Cys Arg
            20                  25                  30
Gln Val Ser Val Ser Leu His Pro Gly Thr Gly Leu Phe Ser Pro Phe
        35                  40                  45
Cys Ser Val Pro Leu Trp Cys Ile Tyr Phe Leu Ser Phe Cys Ile Val
    50                  55                  60
Leu Ser Leu Pro Ser Ala Ser Leu His Leu Cys Leu Ser Cys Leu His
65                  70                  75                  80
Phe Leu Asn Leu Asp Cys Pro Cys Leu Phe Leu Cys His Ser Leu Ser
                85                  90                  95
Ser Pro Ser Val Cys Gly Ser Ala Ser Leu Ser His Ser Pro Tyr Asn
            100                 105                 110
Trp Pro Leu Pro Ala Gln Thr Phe Leu Asp Glu Leu His Glu Thr Gly
        115                 120                 125
Gln Leu His Ser Met Ser Thr Trp Met Glu Leu Tyr Pro Ala Val Ser
    130                 135                 140
Thr Asp Val Arg Phe Ala Asn Met Leu Gly Gln Pro Gly Ser Thr Pro
145                 150                 155                 160
Leu Asp Leu Phe Lys Phe Tyr Val Glu Glu Leu Lys Ala Arg Phe His
                165                 170                 175
Asp Glu Lys Lys Ile Ile Lys Asp Ile Leu Lys Asp Arg Gly Phe Cys
            180                 185                 190
Val Glu Val Asn Thr Ala Phe Glu Asp Phe Ala His Val Ile Ser Phe
        195                 200                 205
Asp Lys Arg Ala Ala Ala Leu Asp Ala Gly Asn Ile Lys Leu Thr Phe
    210                 215                 220
Asn Ser Leu Leu Glu Lys Ala Glu Ala Arg Glu Arg Glu Arg Glu Lys
225                 230                 235                 240
Glu Glu Ala Arg Arg Met Arg Arg Arg Glu Ala Ala Phe Arg Ser Met
                245                 250                 255
Leu Arg Gln Ala Val Pro Ala Leu Glu Leu Gly Thr Ala Trp Glu Glu
            260                 265                 270
Val Arg Glu Arg Phe Val Cys Asp Ser Ala Phe Glu Gln Ile Thr Leu
        275                 280                 285
Glu Ser Glu Arg Ile Arg Leu Phe Arg Glu Phe Leu Gln Val Leu Glu
    290                 295                 300
Thr Glu Cys Gln His Leu His Thr Lys Gly Arg Lys His Gly Arg Lys
305                 310                 315                 320
Gly Lys Lys His His His Lys Arg Ser His Ser Pro Ser Gly Ser Glu
                325                 330                 335
Ser Glu Glu Glu Glu Leu Pro Pro Pro Ser Leu Arg Pro Pro Lys Arg
            340                 345                 350
Arg Arg Arg Asn Pro Ser Glu Ser Gly Ser Glu Pro Ser Ser Ser Leu
        355                 360                 365
Asp Ser Val Glu Ser Gly Gly Ala Ala Leu Gly Gly Arg Gly Ser Pro
    370                 375                 380
Ser Ser His Leu Leu Gly Ala Asp His Gly Leu Arg Lys Ala Lys Lys
385                 390                 395                 400
Pro Lys Lys Lys Thr Lys Lys Arg Arg His Lys Ser Asn Ser Pro Glu
                405                 410                 415
Ser Glu Thr Asp Pro Glu Glu Lys Ala Gly Lys Glu Ser Asp Glu Lys
            420                 425                 430
Glu Gln Glu Gln Asp Lys Asp Arg Glu Leu Gln Gln Ala Glu Leu Pro
```

```
        435                 440                 445
Asn Arg Ser Pro Gly Phe Gly Ile Lys Lys Glu Lys Thr Gly Trp Asp
    450                 455                 460
Thr Ser Glu Ser Glu Leu Ser Glu Gly Glu Leu Glu Arg Arg Arg Arg
465                 470                 475                 480
Thr Leu Leu Gln Gln Leu Asp Asp His Gln
                485                 490
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<210> 2895
<211> 697
<212> DNA
<213> Homo sapiens

<400> 2895
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120
tgcaggcggt agcacgtctc cagcatcaac ctgaagtccg ccacgaactc ggtgatgccc
180
ccgtactggc cgctggcgaa cttctcttcc atctgcagca gacacatgcc ctgtccgggc
240
tgctgcggga aggcgcgacc gccccggccc ccgctgcgcg gcccttctgc cacctcctcc
300
tgccgcggtg gcaacgcccc ccaagggctg cagaaagggg gcggtgaggc cccggtgctt
360
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420
gctccttgca gcaaccgcct ccgatcccca tcgcctccat ctcttcctcc tgatcgtccg
480
cgtcctccag cgaggaggca ctccttccgt gggccggccc tgaggtctgg gccgccgctg
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ccacctcctc ctcgtcgtcc tctccttcgg ccgccggtgg cggccgctct tcctccccag
600
ccggctccat cgctcccggc gtcccgggca cactcatgcc ccggcaggcc taggctgggc
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697

<210> 2896
<211> 174
<212> PRT
<213> Homo sapiens

<400> 2896
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Met Pro Pro Tyr Trp Pro Leu Ala Asn Phe Ser Ser Ile Cys Ser Arg
 1               5                  10                  15
His Met Pro Cys Pro Gly Cys Cys Gly Lys Ala Arg Pro Pro Arg Pro
            20                  25                  30
Pro Leu Arg Gly Pro Ser Ala Thr Ser Ser Cys Arg Gly Gly Asn Ala
        35                  40                  45
Pro Gln Gly Leu Gln Lys Gly Gly Gly Glu Ala Pro Val Leu Leu Leu
    50                  55                  60
Gln Glu Leu Ala Gln Asp Ala Val Ala Pro Ala Val Ala Arg Arg Ser
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65 70 75 80
Ala Pro Ala Pro Cys Ser Asn Arg Leu Arg Ser Pro Ser Pro Pro Ser
85 90 95
Leu Pro Pro Asp Arg Pro Arg Pro Pro Ala Arg Arg His Ser Phe Arg
100 105 110
Gly Pro Ala Leu Arg Ser Gly Pro Pro Leu Pro Pro Pro Pro Arg Arg
115 120 125
Pro Leu Leu Arg Pro Pro Val Ala Ala Ala Leu Pro Pro Gln Pro Ala
130 135 140
Pro Ser Leu Pro Ala Ser Arg Ala His Ser Cys Pro Gly Arg Pro Arg
145 150 155 160
Leu Gly Gly Val Glu Gln Pro Leu Glu Val Leu Gly Asp Ala
165 170

<210> 2897
<211> 3184
<212> DNA
<213> Homo sapiens

<400> 2897
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aatatggaat agatatttca tatctatatt tggaaaacac ataataggga aataactgcc
120
ctataattgt atgagaagaa taaaaacagt tcctttagaa ttcttattgt tttctctatt
180
ctttttcagg ctaagacaat gcatagcttt tggttgatac aggtaaccct ggttaccact
240
aaagggtgat ccccttcaga taataaaccc atttaactcc agtctcactc ccttcaccag
300
gagggcagct cacagtcagc ttggtggtga tgggggtttt gctgccagat gggtttcctt
360
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420
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480
aggggatgat tatgctgtac ccggctcgga tcgagaaggg accttggggc ttgggaggca
540
gagccattcc aaagaggggg atgatatact ctccacctgc gagcgatgat aggatcagga
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720
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780
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840
tcagatagag ctcatattgg tagtaaccca agtcagtgtt gtgcaaagtt agtcttccga
900
aggtttctcc agctttcagg ggctgaaatt caaatgagaa cgtgccctcg gagttggcag
960
gcaccacaaa ctgggagggc agggcgatgt cgggcatccg gcattccgtg gagaaggtca
1020

ccgagtaggg cagagggttc tccaacttga tggaggctga cgcaacttgc cggactgggg
1080
tcaccatctc gatggttttg atgatgcctg aagggatgac cctgaaactc acattgtagt
1140
acaagaactc atttgtcacc tcgtttcgga agatcacctt tgcagcgtac gttccctcct
1200
tgtgggaaaa gaagttcagc ttgtagtctt tcttagagcc agacagtaca tcaatgtaat
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caaggccctt catagtgatg cttaggtccg gcttctctgg tttcagtatt tccacgatga
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1800
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1920
taaaccttgc acccacatcg cctgtgttca acatgaggat gcgacgcgtg gcttgcgtct
1980
gatacaccac gggtccaaag ggaatatgtt cctggtccag tgagatctcc agggcctggc
2040
agcagccgct aaggaggaag agggggcgca ggagccccat gcattccatg aacacttcct
2100
cagagaaggg agggacacgc ttcttcgggg caaagatgac ttccagttta cagacttctt
2160
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2220
ctggaattgt gaacagaatg gactgattaa atgtgagctg ggccaggctg ttgttcatga
2280
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2460
gataaaaagt tattggaatc tccaatgtgt ttcctggctt taccacatca acacgggagt
2520
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2640

tcccaaagtt gtagctggtg aaggagaaat ggatagccgg gctcacagca cagcctgaga
2700
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2760
cacacttctt taatggttga aaagacaggg tggcatgtac actctgtcct acatccacag
2820
tgctgtcgat gggtgaaaat tccaagtact gcagcaaggt tttggagcca cacagctgtg
2880
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2940
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3060
catttaatgt cacagggtgg actttctttt ccacattgca gatcaaatta aagttcacat
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agcc
3184

<210> 2898
<211> 933
<212> PRT
<213> Homo sapiens

<400> 2898
Met Asn Val Glu Ile Lys Cys Lys Asp Arg Thr Gly Ser Ile Thr Leu
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Leu Thr Pro Asn Gln Thr Asn Ile Ile Asn Phe Tyr Glu Val Glu Leu
20 25 30
Asn Glu Cys Val Gln Cys Glu Phe Asn Phe Ile Asn Thr Gly Lys Phe
35 40 45
Thr Phe Ser Phe Gln Ala Gln Leu Cys Gly Ser Lys Thr Leu Leu Gln
50 55 60
Tyr Leu Glu Phe Ser Pro Ile Asp Ser Thr Val Asp Val Gly Gln Ser
65 70 75 80
Val His Ala Thr Leu Ser Phe Gln Pro Leu Lys Lys Cys Val Leu Thr
85 90 95
Asp Leu Glu Leu Ile Ile Lys Ile Ser His Gly Pro Thr Phe Met Cys
100 105 110
Asn Ile Ser Gly Cys Ala Val Ser Pro Ala Ile His Phe Ser Phe Thr
115 120 125
Ser Tyr Asn Phe Gly Thr Cys Phe Ile Tyr Gln Ala Gly Met Pro Pro
130 135 140
Tyr Lys Gln Thr Leu Val Ile Thr Asn Lys Glu Glu Thr Pro Met Ser
145 150 155 160
Ile Asp Cys Leu Tyr Thr Asn Thr Thr His Leu Glu Val Asn Ser Arg
165 170 175
Val Asp Val Val Lys Pro Gly Asn Thr Leu Glu Ile Pro Ile Thr Phe
180 185 190
Tyr Pro Arg Glu Ser Ile Asn Tyr Gln Glu Leu Ile Pro Phe Glu Ile
195 200 205
Asn Gly Leu Ser Gln Gln Thr Val Glu Ile Lys Gly Lys Gly Thr Glu

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    210                 215                 220
Met Lys Ile Leu Val Leu Asp Pro Ala Asn Arg Ile Val Lys Leu Gly
225                 230                 235                 240
Ala Val Leu Pro Gly Gln Val Val Lys Arg Thr Val Ser Ile Met Asn
                245                 250                 255
Asn Ser Leu Ala Gln Leu Thr Phe Asn Gln Ser Ile Leu Phe Thr Ile
            260                 265                 270
Pro Glu Leu Gln Glu Pro Lys Val Leu Thr Leu Ala Pro Phe His Asn
        275                 280                 285
Ile Thr Leu Lys Pro Lys Glu Val Cys Lys Leu Glu Val Ile Phe Ala
    290                 295                 300
Pro Lys Lys Arg Val Pro Pro Phe Ser Glu Glu Val Phe Met Glu Cys
305                 310                 315                 320
Met Gly Leu Leu Arg Pro Leu Phe Leu Leu Ser Gly Cys Cys Gln Ala
                325                 330                 335
Leu Glu Ile Ser Leu Asp Gln Glu His Ile Pro Phe Gly Pro Val Val
            340                 345                 350
Tyr Gln Thr Gln Ala Thr Arg Arg Ile Leu Met Leu Asn Thr Gly Asp
        355                 360                 365
Val Gly Ala Arg Phe Lys Trp Asp Ile Lys Lys Phe Glu Pro His Phe
    370                 375                 380
Ser Ile Ser Pro Glu Glu Gly Tyr Ile Thr Ser Gly Met Glu Val Ser
385                 390                 395                 400
Phe Glu Val Thr Tyr His Pro Thr Glu Val Gly Lys Glu Ser Leu Cys
                405                 410                 415
Lys Asn Ile Leu Cys Tyr Ile Gln Gly Gly Ser Pro Leu Ser Leu Thr
            420                 425                 430
Leu Ser Gly Val Cys Val Gly Pro Pro Ala Val Lys Glu Val Val Asn
        435                 440                 445
Phe Thr Cys Gln Val Arg Ser Lys His Thr Gln Thr Ile Leu Leu Ser
    450                 455                 460
Asn Arg Thr Asn Gln Thr Trp Asn Leu His Pro Ile Phe Glu Gly Glu
465                 470                 475                 480
His Trp Glu Gly Pro Glu Phe Ile Thr Leu Glu Ala His Gln Gln Asn
                485                 490                 495
Lys Pro Tyr Glu Ile Thr Tyr Arg Pro Arg Thr Met Asn Leu Glu Asn
            500                 505                 510
Arg Lys His Gln Gly Thr Leu Phe Phe Pro Leu Pro Asp Gly Thr Gly
        515                 520                 525
Trp Leu Tyr Ala Leu His Gly Thr Ser Glu Leu Pro Lys Ala Val Ala
    530                 535                 540
Asn Ile Tyr Arg Glu Val Pro Cys Lys Thr Pro Tyr Thr Glu Leu Leu
545                 550                 555                 560
Pro Ile Thr Asn Trp Leu Asn Lys Pro Gln Arg Phe Arg Val Ile Val
                565                 570                 575
Glu Ile Leu Lys Pro Glu Lys Pro Asp Leu Ser Ile Thr Met Lys Gly
            580                 585                 590
Leu Asp Tyr Ile Asp Val Leu Ser Gly Ser Lys Lys Asp Tyr Lys Leu
        595                 600                 605
Asn Phe Phe Ser His Lys Glu Gly Thr Tyr Ala Ala Lys Val Ile Phe
    610                 615                 620
Arg Asn Glu Val Thr Asn Glu Phe Leu Tyr Tyr Asn Val Ser Phe Arg
625                 630                 635                 640
Val Ile Pro Ser Gly Ile Ile Lys Thr Ile Glu Met Val Thr Pro Val
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                645                 650                 655
Arg Gln Val Ala Ser Ala Ser Ile Lys Leu Glu Asn Pro Leu Pro Tyr
            660                 665                 670
Ser Val Thr Phe Ser Thr Glu Cys Arg Met Pro Asp Ile Ala Leu Pro
        675                 680                 685
Ser Gln Phe Val Val Pro Ala Asn Ser Glu Gly Thr Phe Ser Phe Glu
    690                 695                 700
Phe Gln Pro Leu Lys Ala Gly Glu Thr Phe Gly Arg Leu Thr Leu His
705                 710                 715                 720
Asn Thr Asp Leu Gly Tyr Tyr Gln Tyr Glu Leu Tyr Leu Lys Ala Thr
                725                 730                 735
Pro Ala Leu Pro Glu Lys Pro Val His Phe Gln Thr Val Leu Gly Ser
            740                 745                 750
Ser Gln Ile Ile Leu Val Lys Phe Ile Asn Tyr Thr Arg Gln Arg Thr
        755                 760                 765
Glu Tyr Tyr Cys Arg Thr Asp Cys Thr Asp Phe His Ala Glu Lys Leu
    770                 775                 780
Ile Asn Ala Ala Pro Gly Gly Gln Gly Gly Thr Glu Ala Ser Val Glu
785                 790                 795                 800
Val Leu Phe Glu Pro Ser His Leu Gly Glu Thr Lys Gly Ile Leu Ile
                805                 810                 815
Leu Ser Ser Leu Ala Gly Gly Glu Tyr Ile Ile Pro Leu Phe Gly Met
            820                 825                 830
Ala Leu Pro Pro Lys Pro Gln Gly Pro Phe Ser Ile Arg Ala Gly Tyr
        835                 840                 845
Ser Ile Ile Ile Pro Phe Lys Asn Val Phe Tyr His Met Val Thr Phe
    850                 855                 860
Ser Ile Ile Val Asp Asn Pro Ala Phe Thr Ile Arg Ala Gly Glu Ser
865                 870                 875                 880
Val Arg Pro Lys Lys Ile Asn Asn Ile Thr Val Ser Phe Glu Gly Asn
                885                 890                 895
Pro Ser Gly Ser Lys Thr Pro Ile Thr Thr Lys Leu Thr Val Ser Cys
            900                 905                 910
Pro Pro Gly Glu Gly Ser Glu Thr Gly Val Lys Trp Val Tyr Tyr Leu
        915                 920                 925
Lys Gly Ile Thr Leu
    930
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<210> 2899
<211> 876
<212> DNA
<213> Homo sapiens

<400> 2899
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gggtaccatg gacgtgggcg aacttctgag ctaccaggag ggtcattgcg aggagcagta
120
gagctgcact gccgaatgtc gtagccacta gccacatagg ctgttgattg cttgaaatgt
180
gactagtctg aattgagaaa tactcccaac aggggcacaa aacgtccccg ggatgatgag
240
gaagaagaac tgaagacacg ccgcaagcaa actggtactc gagaacgcgg ccgctatcgg
300

gaagaagaaa tgactgtggt ggaggaagcg gatgatgaca aaaaaaggct gctgcagatt
360
attgacagag atggggaaga ggaagaggaa gaggaggagc cattggatga aagctcagtg
420
aagaaaatga tcctcacatt tgaaaagaga tcatataaaa accaagaatt gcggattaag
480
tttccagaca atccagagaa gttcatggaa tccgagctgg acctaaatga catcattcag
540
gagatgcacg tggtggccac catgccagac ctgtaccacc ttctggtgga gctgaatgct
600
gtacagtcgc ttctcggctt gctcggacac gataatacag atgtgtccat agctgtggtc
660
gatttgcttc aggaattaac agatatagac accctccatg agagtgaaga gggagcagaa
720
gtgctcatcg atgctctggt ggatgggcag gtggtagcac tgctggtaca gaatctggag
780
cgcctggatg agtctgtgaa agaggaggca gatggcgtcc acaacactct ggctattgtg
840
gaaaacatgg ctgagttccg gcctgagatg tgtaca
876

<210> 2900
<211> 189
<212> PRT
<213> Homo sapiens

<400> 2900
Met Thr Val Val Glu Glu Ala Asp Asp Asp Lys Lys Arg Leu Leu Gln
 1   5   10   15
Ile Ile Asp Arg Asp Gly Glu Glu Glu Glu Glu Glu Glu Glu Pro Leu
            20   25   30
Asp Glu Ser Ser Val Lys Lys Met Ile Leu Thr Phe Glu Lys Arg Ser
        35   40   45
Tyr Lys Asn Gln Glu Leu Arg Ile Lys Phe Pro Asp Asn Pro Glu Lys
    50   55   60
Phe Met Glu Ser Glu Leu Asp Leu Asn Asp Ile Ile Gln Glu Met His
65   70   75   80
Val Val Ala Thr Met Pro Asp Leu Tyr His Leu Leu Val Glu Leu Asn
                85   90   95
Ala Val Gln Ser Leu Leu Gly Leu Leu Gly His Asp Asn Thr Asp Val
            100   105   110
Ser Ile Ala Val Val Asp Leu Leu Gln Glu Leu Thr Asp Ile Asp Thr
        115   120   125
Leu His Glu Ser Glu Glu Gly Ala Glu Val Leu Ile Asp Ala Leu Val
    130   135   140
Asp Gly Gln Val Val Ala Leu Leu Val Gln Asn Leu Glu Arg Leu Asp
145   150   155   160
Glu Ser Val Lys Glu Glu Ala Asp Gly Val His Asn Thr Leu Ala Ile
                165   170   175
Val Glu Asn Met Ala Glu Phe Arg Pro Glu Met Cys Thr
            180   185

<210> 2901
<211> 756

<212> DNA
<213> Homo sapiens

<400> 2901
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ccgcccgtcc agagcctgaa gggcgaggat gctgaggaat ccttggagga ggaggaggcg
120
ctggaccctc tgggcattat gcgctccaag aagcccaaga aacatcccaa agtggccgtg
180
aaagccaagc cctcgccccg gctcaccatc tttgacgagg aggtggaccc tgatgagggg
240
ctctttggcc cgggcaggaa gctgtctcca caggacccct cggaggacgt gtcatccatg
300
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360
ctcctgctgc cggccgcctg tgagagtgga gggcccacac ccagcctcag ccacagggac
420
gcctccaagg aactgttcag gtaccacctg tccccagcgg cgcttggcca gctctgagag
480
tgtcctggac agagccaagg gcccggctca ttgcccagtc tcagccccag cctcctctga
540
ggggaggacc ccaggcctgt gaaaagtaga agcctgtggg tgcacattgg gtgagaggcg
600
gtgaaggggg ctgaggggga ggnaantcgc ccagggctgc tcagctagtt ccagaaagag
660
agaactttgt gtgcacaacc agtctttctt ttcacaatca tattttaaca gtttatgtaa
720
agaataatta aattatataa ttgccagggc aaaaaa
756

<210> 2902
<211> 158
<212> PRT
<213> Homo sapiens

<400> 2902
Thr Arg Arg Arg Gly Ala Phe Asp Phe Phe Glu Lys Gln Asp Gln Val
 1   5   10   15
Ala Glu Glu Gly Pro Pro Val Gln Ser Leu Lys Gly Glu Asp Ala Glu
            20   25   30
Glu Ser Leu Glu Glu Glu Glu Ala Leu Asp Pro Leu Gly Ile Met Arg
        35   40   45
Ser Lys Lys Pro Lys Lys His Pro Lys Val Ala Val Lys Ala Lys Pro
    50   55   60
Ser Pro Arg Leu Thr Ile Phe Asp Glu Glu Val Asp Pro Asp Glu Gly
65   70   75   80
Leu Phe Gly Pro Gly Arg Lys Leu Ser Pro Gln Asp Pro Ser Glu Asp
                85   90   95
Val Ser Ser Met Asp Pro Leu Lys Leu Phe Asp Asp Pro Asp Leu Gly
            100   105   110
Gly Ala Ile Pro Leu Gly Asp Ser Leu Leu Leu Pro Ala Ala Cys Glu
        115   120   125
Ser Gly Gly Pro Thr Pro Ser Leu Ser His Arg Asp Ala Ser Lys Glu

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    130                 135                 140
Leu Phe Arg Tyr His Leu Ser Pro Ala Ala Leu Gly Gln Leu
145                 150                 155

<210> 2903
<211> 542
<212> DNA
<213> Homo sapiens

<400> 2903
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accacctatt tctctgggaa ttgtaccatg gaagatgcca aattggccca ggactttctg
120
gactcacaga acctcagtgc ctacaacacc cggctcttca aagaggtcga tggagaaggg
180
aagccctact acgaggtgcg gctggcttct gtgcttggct cagagccttc cctggactct
240
gaggtgactt ccaagctgaa gagctatgaa ttccggggaa gccctttcca ggtgacccgg
300
ggggactacg cgcccatcct ccagaaggtg gtggagcagc tggagaaagc caaggcctat
360
gcagccaaca gccaccaggg gcagatgctg gcccagtata tagagagctt cacccagggc
420
tccatcgagg cccacaagag gggctcccgc ttctggatcc aggacaaagg cccccatcgt
480
ggagaggtga ggcgccagct ccaccccacc tgccccctcc tgcctgcccc tccttcacgc
540
gt
542

<210> 2904
<211> 180
<212> PRT
<213> Homo sapiens

<400> 2904
Lys Leu Met Phe Ser Leu Tyr Pro Arg Leu Arg His Leu Gly Leu Gly
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Lys Glu Gly Ile Thr Thr Tyr Phe Ser Gly Asn Cys Thr Met Glu Asp
            20                  25                  30
Ala Lys Leu Ala Gln Asp Phe Leu Asp Ser Gln Asn Leu Ser Ala Tyr
        35                  40                  45
Asn Thr Arg Leu Phe Lys Glu Val Asp Gly Glu Gly Lys Pro Tyr Tyr
    50                  55                  60
Glu Val Arg Leu Ala Ser Val Leu Gly Ser Glu Pro Ser Leu Asp Ser
65                  70                  75                  80
Glu Val Thr Ser Lys Leu Lys Ser Tyr Glu Phe Arg Gly Ser Pro Phe
                85                  90                  95
Gln Val Thr Arg Gly Asp Tyr Ala Pro Ile Leu Gln Lys Val Val Glu
            100                 105                 110
Gln Leu Glu Lys Ala Lys Ala Tyr Ala Ala Asn Ser His Gln Gly Gln
        115                 120                 125
Met Leu Ala Gln Tyr Ile Glu Ser Phe Thr Gln Gly Ser Ile Glu Ala
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130 135 140
His Lys Arg Gly Ser Arg Phe Trp Ile Gln Asp Lys Gly Pro His Arg
145 150 155 160
Gly Glu Val Arg Arg Gln Leu His Pro Thr Cys Pro Leu Leu Pro Ala
165 170 175
Pro Pro Ser Arg
180

<210> 2905
<211> 814
<212> DNA
<213> Homo sapiens

<400> 2905
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gtcacaagat ccttcttctg tattacaaat tctgccactt tgtttcagaa ctgggtatca
120
ggattcctcc tctgcccagg tttctgctgt ccccccaaaa gaaagacatg tagctgggca
180
tggtggtaca catctgtggt cccagttact caggaggctg aggcaggagg attgcttgag
240
cccaggtgtt caaggttgca gtgggctgtg aatgctctac ttcactccag cctgagcaac
300
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360
ctggaaatgg gcttcggggt ggttaaccaa gcccagggaa acttgcgtgg cccagcatct
420
tccgtccgct gcaggaggag cacacgcccc cggcccgggt cagcaagacg cgagaaagcg
480
gccacgccgg gcgtccggga gctgaggctg gagggcgcct ggcaggcagg gcggggccca
540
ggcggcggga gtgcttatga ccggcgctgg ggggaacttc tggacgtcaa ggggccacta
600
taaagcggca cagtcttgag ccttcgctct tcacctaagt cagtgagcgc ccttcgcaaa
660
gcctctgtgg aggtaaccat tgggggttcg cctccaaatc caggaatgca cctcaaaaat
720
gctcctacac cgtaagaccg tgtccttcaa tgcaaagggg actgtgcggc gaggcaccga
780
caagccgtag ccctgagacc actcaaagcc tgca
814

<210> 2906
<211> 200
<212> PRT
<213> Homo sapiens

<400> 2906
Phe Ser Tyr Pro Ser Phe Val Tyr Leu Gly Thr Phe Thr Leu Val Asp
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Asn Arg Ile Pro Val Thr Arg Ser Phe Phe Cys Ile Thr Asn Ser Ala
20 25 30
Thr Leu Phe Gln Asn Trp Val Ser Gly Phe Leu Leu Cys Pro Gly Phe

```
        35                  40                  45
Cys Cys Pro Pro Lys Arg Lys Thr Cys Ser Trp Ala Trp Trp Tyr Thr
    50                  55                  60
Ser Val Val Pro Val Thr Gln Glu Ala Glu Ala Gly Gly Leu Leu Glu
65                  70                  75                  80
Pro Arg Cys Ser Arg Leu Gln Trp Ala Val Asn Ala Leu Leu His Ser
                85                  90                  95
Ser Leu Ser Asn Arg Ala Arg Pro Arg Pro Ser Ser Arg Leu Ser Ile
            100                 105                 110
Pro Pro Pro Gln His Pro Phe Leu Leu Glu Met Gly Phe Gly Val Val
        115                 120                 125
Asn Gln Ala Gln Gly Asn Leu Arg Gly Pro Ala Ser Ser Val Arg Cys
    130                 135                 140
Arg Arg Ser Thr Arg Pro Arg Pro Gly Ser Ala Arg Arg Glu Lys Ala
145                 150                 155                 160
Ala Thr Pro Gly Val Arg Glu Leu Arg Leu Glu Gly Ala Trp Gln Ala
                165                 170                 175
Gly Arg Gly Pro Gly Gly Gly Ser Ala Tyr Asp Arg Arg Trp Gly Glu
            180                 185                 190
Leu Leu Asp Val Lys Gly Pro Leu
        195                 200
```

<210> 2907
<211> 379
<212> DNA
<213> Homo sapiens

<400> 2907
ntgagaccct gtctcaaagt aaaaaattct gaaaaatgct atgaccgtga gtgaccggcc
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atcagcaggc tgtgatctgc cgaaactcat gacagcgagc ctcaatggct gggtcttaag
120
aaacagcatc ttcacttttc ccaggctgct ttccaatttc caacactgtc cccaagatta
180
caaaggcaaa ggaattcttc ccttaatgtt ggacggtcct gagactgctc caccctgggc
240
tcattacact gggaccagct ttaagcttcc ctgttcaacg cggagagctc cacagcccag
300
gacgacagag cagatgatgg cacgacgccc tcaaaaccca gacaggcctt cttggcttgc
360
cctggccgat gccaccggt
379

<210> 2908
<211> 113
<212> PRT
<213> Homo sapiens

<400> 2908
```
Met Thr Val Ser Asp Arg Pro Ser Ala Gly Cys Asp Leu Pro Lys Leu
 1               5                  10                  15
Met Thr Ala Ser Leu Asn Gly Trp Val Leu Arg Asn Ser Ile Phe Thr
            20                  25                  30
Phe Pro Arg Leu Leu Ser Asn Phe Gln His Cys Pro Gln Asp Tyr Lys
```

```
        35                  40                  45
Gly Lys Gly Ile Leu Pro Leu Met Leu Asp Gly Pro Glu Thr Ala Pro
    50                  55                  60
Pro Trp Ala His Tyr Thr Gly Thr Ser Phe Lys Leu Pro Cys Ser Thr
65                  70                  75                  80
Arg Arg Ala Pro Gln Pro Arg Thr Thr Glu Gln Met Met Ala Arg Arg
                85                  90                  95
Pro Gln Asn Pro Asp Arg Pro Ser Trp Leu Ala Leu Ala Asp Ala Thr
            100                 105                 110
Gly
```

<210> 2909
<211> 2420
<212> DNA
<213> Homo sapiens

<400> 2909
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60
gctttaaaaa aaaaaaaaaa gacacatttt ttgaaagata ttcttagtgt tgtgacctgg
120
cattgggccc ctgtgagcgg gacggtggct gagaccgcct gctgtggctt tgcgagttct
180
ctgcactcac tggcaggggt ttggtgggaa acggggaagc tttggcatgg ttctgtccag
240
ttgcttataa tcaagaataa tgagttttga ggtttacaaa gagcagaagt aacatttata
300
cggctggcat ttgacaaaag attgctgata atatactcat tccaggaagt gtaaaaatgc
360
tttaaaggaa tgataatttg tacttactgt ttatggggac tagatatatt agaattatag
420
catcattatg gggacatagt gtttccctat aaattcagaa attctctggt tgatgtaaaa
480
tcatacttcc tggttttact taattagtaa agaaataaat aaattagagt aacatttagt
540
caggtagagt tactcctttt tccccttctt tattaataaa ttttatttt agcacaatca
600
tttacccaaa aagagagttt gagaatgttc gagaatctct accactcggt aaccatgctg
660
gctgttatat cagaaaaatc cataaacata cacagcagcg agctgttttc acaagacttc
720
ctgctaataa acacaacact ttctcctcca ctcagatggg agcctcagat gccaaaacgc
780
agatgtgcca actaactata ggctcgttgc taagcagaga aacctatcaa gtttgtccag
840
caaattcgat tgtacagtgg gatggcgtct gctctgcggc cttggacagg gagccactgg
900
tctgtgctgc tgtcccctga ggcaggtcga agctggtggc ccttagaggg caggtaaaat
960
ggttctcatg ggttagaaca taagggcttt gagaaaaaat gcaaaaggtc tcattgaaat
1020
tggaggccta tgtgaatctg tttacatgga ggcatactga gatctcgttc tgtgcttagg
1080

tgaactgcag gtctcacgct ggctgcatga cttggtgccc cctggctggc tgagccactg
1140
cctgccacct tctcatacca ttacgtgggg gtctaaagag gacatcatcc ccaaccaaag
1200
aatagtgaga gagaaaatcc caaacatttg agacagggtt caaaagcacc cagacgcctt
1260
ctgtctcttt cccagttccc atctggctag ggactgtgaa tcagaattca gaatctgtgc
1320
tgccctgagg ggacaggcac ccaaatgcaa taaataacac caagctcagg acccagccac
1380
tgaccttcct ccaccactgc tgcgggttat tcctcgatgg gaactgaagg atccaaggga
1440
ggaatccgtt ccgcccccaa acctccctgc acaacatcga atgcgggagt ctggctgctg
1500
cttctgcaca ggacagagcc tccagtcttt tgcttgagag catcatttat ggcatggact
1560
gggaacgcaa tgtgttcaca caaatgcacg acaattgtac atcagcatct ttacaatatt
1620
aaaggagtca tatacaagtc tacagccatt gtacacagga tggtgatggc tggggagccc
1680
cgcccaccag tcctctgcag tttctccacc ggagaacact tggggagctg tcacaaggcc
1740
agggggggtc catctttggg cctgtcgtgg ggcaggcagc aggtctgcaa ggactcctca
1800
gggccagtcc tcactggaat caggggtcaa gagcgccagg tctgcctgtg tctgggtctc
1860
atcggcaggc tagtgtaaca acgtgaatta aaactgtgca tattcgcatg agaaaactgg
1920
agctggggat ggctccctga gctggggacc tagaagacgc tgctgacaga tgggcccctt
1980
catggtgggg cccattcctg aggtaacgtg cagccctgag gctggtccga acgggaggag
2040
acttctccag cagcccaggt gccagtccac acagacagga ctggaagccc ctgggcagca
2100
ggtcaggtga cccggggagt gcagcctgag cccccaacgg cagcaaacgt gaaggtctca
2160
ggtggttaca gaatcactca gccctcaggc ccccaccact ctcctcccag cagccctgca
2220
gcacacatcc ctgcatctgt cccgagagcc ccagccctgc aggcatctgg gcctgaatgc
2280
caggcagctg gtccaccctg cagccatgct gcacgtctga ctgagaactg agcaccagat
2340
aaagaagcat tggtccttgt cagcctctct gacttttgca gttagggctg catccattta
2400
aatatgtaga aaaatagcca
2420

<210> 2910
<211> 153
<212> PRT
<213> Homo sapiens

<400> 2910
Met Gly Thr Glu Gly Ser Lys Gly Gly Ile Arg Ser Ala Pro Lys Pro

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 1               5                  10                  15
Pro Cys Thr Thr Ser Asn Ala Gly Val Trp Leu Leu Leu Leu His Arg
            20                  25                  30
Thr Glu Pro Pro Val Phe Cys Leu Arg Ala Ser Phe Met Ala Trp Thr
        35                  40                  45
Gly Asn Ala Met Cys Ser His Lys Cys Thr Thr Ile Val His Gln His
    50                  55                  60
Leu Tyr Asn Ile Lys Gly Val Ile Tyr Lys Ser Thr Ala Ile Val His
65                  70                  75                  80
Arg Met Val Met Ala Gly Glu Pro Arg Pro Pro Val Leu Cys Ser Phe
                85                  90                  95
Ser Thr Gly Glu His Leu Gly Ser Cys His Lys Ala Arg Gly Gly Pro
            100                 105                 110
Ser Leu Gly Leu Ser Trp Gly Arg Gln Gln Val Cys Lys Asp Ser Ser
        115                 120                 125
Gly Pro Val Leu Thr Gly Ile Arg Gly Gln Glu Arg Gln Val Cys Leu
    130                 135                 140
Cys Leu Gly Leu Ile Gly Arg Leu Val
145                 150
```

<210> 2911
<211> 1327
<212> DNA
<213> Homo sapiens

<400> 2911

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120
gctgcggagc ccgggaagcg gagcgagggc gggaagaccc ccgtggcccg gagcagcgga
180
ggcgggggct gggcagaccc ccgaacgtgc ctgagcctgc tgtcgctggg gacgtgcctg
240
ggcctggcct ggtttgtatt tcagcagtca gaaaaatttg caaaggtgga aaaccaatac
300
cagttactga aactagaaac caatgaattc caacaacttc aaagtaaaat cagtttaatt
360
tcagaaaagt ggcagaaatc tgaagctatc atggaacaat tgaagtcttt tcaaataatt
420
gctcatctaa agcgtctaca ggaagaaatt aatgaggtaa aaacttggtc caataggata
480
actgaaaaac aggatatact gaacaacagt ctgacgacgc tttctcaaga cattacaaaa
540
gtagaccaaa gtacaacttc catggcaaaa gatgttggtc tcaagattac aagtgtaaaa
600
acagatatac gacggatttc aggtttagta actgatgtaa tatcattgac agattctgtg
660
caagaactag aaaataaaat agagaaagta gaaaaaaata cagtaaaaaa tataggtgat
720
cttctttcaa gcagtattga tcgaacagca acgctccgaa agacagcatc tgaaaattca
780
caaagaatta actctgttaa gaagacgcta accgaactaa agagtgactt cgacaaacat
840
```

acagatagat ttctaagctt agaaggtgac agagccaaag ttctgaagac agtgactttt
900
gcaaatgatc taaaaccaaa ggtgtataat ctaaagaagg acttttcccg tttagaacca
960
ttagtaaatg atttaacact acgcattggg agattggtta ccgacttact acaaagagag
1020
aaagaaattg ctttcttaag tgaaaaaata tctaatttaa caatagtcca agctgagatt
1080
aaggatatta aagatgaaat agcacacatt tcagatatga attagtttga cattattgag
1140
attagactaa ggtaattttt ttaatgggac ctctcatgag aagactggta aatcaaaaat
1200
aatgatattt tggagcaaaa gtcattttat atttaatcct attttgtaca gtaaaaataa
1260
aactttaaaa caggttgatt ttccaaaata aatatgctaa aacctatttt tgcaacttta
1320
aaaaaaa
1327

<210> 2912
<211> 350
<212> PRT
<213> Homo sapiens

<400> 2912
Met Ser Glu Val Lys Ser Arg Lys Lys Ser Gly Pro Lys Gly Ala Pro
1 5 10 15
Ala Ala Glu Pro Gly Lys Arg Ser Glu Gly Gly Lys Thr Pro Val Ala
20 25 30
Arg Ser Ser Gly Gly Gly Gly Trp Ala Asp Pro Arg Thr Cys Leu Ser
35 40 45
Leu Leu Ser Leu Gly Thr Cys Leu Gly Leu Ala Trp Phe Val Phe Gln
50 55 60
Gln Ser Glu Lys Phe Ala Lys Val Glu Asn Gln Tyr Gln Leu Leu Lys
65 70 75 80
Leu Glu Thr Asn Glu Phe Gln Gln Leu Gln Ser Lys Ile Ser Leu Ile
85 90 95
Ser Glu Lys Trp Gln Lys Ser Glu Ala Ile Met Glu Gln Leu Lys Ser
100 105 110
Phe Gln Ile Ile Ala His Leu Lys Arg Leu Gln Glu Glu Ile Asn Glu
115 120 125
Val Lys Thr Trp Ser Asn Arg Ile Thr Glu Lys Gln Asp Ile Leu Asn
130 135 140
Asn Ser Leu Thr Thr Leu Ser Gln Asp Ile Thr Lys Val Asp Gln Ser
145 150 155 160
Thr Thr Ser Met Ala Lys Asp Val Gly Leu Lys Ile Thr Ser Val Lys
165 170 175
Thr Asp Ile Arg Arg Ile Ser Gly Leu Val Thr Asp Val Ile Ser Leu
180 185 190
Thr Asp Ser Val Gln Glu Leu Glu Asn Lys Ile Glu Lys Val Glu Lys
195 200 205
Asn Thr Val Lys Asn Ile Gly Asp Leu Leu Ser Ser Ser Ile Asp Arg
210 215 220
Thr Ala Thr Leu Arg Lys Thr Ala Ser Glu Asn Ser Gln Arg Ile Asn

```
225                 230                 235                 240
Ser Val Lys Lys Thr Leu Thr Glu Leu Lys Ser Asp Phe Asp Lys His
                245                 250                 255
Thr Asp Arg Phe Leu Ser Leu Glu Gly Asp Arg Ala Lys Val Leu Lys
            260                 265                 270
Thr Val Thr Phe Ala Asn Asp Leu Lys Pro Lys Val Tyr Asn Leu Lys
        275                 280                 285
Lys Asp Phe Ser Arg Leu Glu Pro Leu Val Asn Asp Leu Thr Leu Arg
    290                 295                 300
Ile Gly Arg Leu Val Thr Asp Leu Leu Gln Arg Glu Lys Glu Ile Ala
305                 310                 315                 320
Phe Leu Ser Glu Lys Ile Ser Asn Leu Thr Ile Val Gln Ala Glu Ile
                325                 330                 335
Lys Asp Ile Lys Asp Glu Ile Ala His Ile Ser Asp Met Asn
            340                 345                 350
```

<210> 2913
<211> 361
<212> DNA
<213> Homo sapiens

<400> 2913
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atccagcaac tgaggaccaa catccagctt cctgcctgcc tccgtgtcat tggctacctg
120
cggcgcatgg acgtcttcac tgaggctgag ttgagggtga agtttcttca ggcccgagat
180
gcttggctcc ggtccatcct gactgccatt cctaatgatg atccctattt ccatattaca
240
aaaaccatcg agggcctccc gtgtccatct ctttgatatc atcacccagt accgggccat
300
cttctcagac gaggacccac tgctgccccc tgccatgggt gagcacactg ggatgagagt
360
g
361

<210> 2914
<211> 112
<212> PRT
<213> Homo sapiens

<400> 2914
```
Met Ala Gly Gly Ser Ser Gly Ser Ser Ser Glu Lys Met Ala Arg Tyr
 1               5                  10                  15
Trp Val Met Ile Ser Lys Arg Trp Thr Arg Glu Ala Leu Asp Gly Phe
            20                  25                  30
Cys Asn Met Glu Ile Gly Ile Ile Ile Arg Asn Gly Ser Gln Asp Gly
        35                  40                  45
Pro Glu Pro Ser Ile Ser Gly Leu Lys Lys Leu His Pro Gln Leu Ser
    50                  55                  60
Leu Ser Glu Asp Val His Ala Pro Gln Val Ala Asn Asp Thr Glu Ala
65                  70                  75                  80
Gly Arg Lys Leu Asp Val Gly Pro Gln Leu Leu Asp Gln Leu Ala Gln
```

```
                85                  90                  95
His Gln Leu His Gly Leu Ala His Phe Val His Asp Ala Leu Asp Asp
            100                 105                 110
```

<210> 2915
<211> 1782
<212> DNA
<213> Homo sapiens

<400> 2915
caagaggatc accttaaaca cttaagaacc ctcgaaaaaa cattagaaaa aatggagaga
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caaaaaaggc agcagcaggc agcacagata agactgatcc aagaggtgga actcaaagct
120
tcagctgccg atagagaaat atacttactt agaacttccc ttcatcgaga aagagaacaa
180
gcgcaacaac ttcatcaact tcttgcattg aaagaacagg aacacaggaa ggaacttgaa
240
acaagggagt tttttactga tgctgacttc caggatgcct tagctaaaga aatagccaaa
300
gaagagaaaa agcatgagca aatgataaaa gaataccaag agaaaattga cgtgttaagc
360
cagcagtata tggatttaga aaatgaattc cgtattgctt taactgttga agccagaaga
420
tttcaagatg ttaaagatgg ttttgaaaat gttgcaactg agttagcaaa gagcaaacat
480
gctcttattt gggctcaacg aaaagaaaat gagtcttcct ctttaattaa agatctgacc
540
tgtatggtaa aggaacaaaa aacaaaactg gcagaagttt ctaaattgaa acaagaaaca
600
gcagcaaatt tacagaatca aatcaacacc cttgaaattt taattgaaga tgacaagcag
660
aagagtattc aaatagaact tctcaagcac gaaaaagtcc agcttatttc tgagctagca
720
gccaaggaat cactaatatt tggtttaagg acagaaagaa aagtatgggg acatgagctg
780
gcacaacaag gatcttctct agcccaaaat cgtggaaaat tggaggctca aattgagagt
840
ttatctagag agaatgaatg tctgcgaaag acaaatgaaa gtgatagtga tgcattaaga
900
ataaagtgca aaatcataga cgaccaaact gaaactatta gaaaattaaa agattgttta
960
caagaaaaag atgaacacat caaaagatta caagaaaaga tcacagaaat agaaaaatgc
1020
actcaagaac aacttgatga aaaatcttca caactggatg aggtacttga gaagttggaa
1080
aggcacaatg aaagaaaaga aaaactaaaa caacagttga aaggaaagga agtagaactt
1140
gaagaaatca gaaaagctta cagtacactg aatcggaagt ggcatgataa aggagaactt
1200
ctatgtcatc ttgaaacaca agtaaaagaa gtgaaagaaa aatttgaaaa caaggaaaag
1260
aaacttaaag cggaaagaga caaaagtatt gaactacaaa agaatgcaat ggaaaaactt
1320

catagtatgg atgatgcctt taaaagacaa gttgatgcaa ttgttgaagc tcatcaagct
1380
gaaatagcac agctggccaa tgaaaagcag aagtgtattg attctgcaaa tttaaaggtc
1440
catcaaattg aaaaagaaat gcgtgaactt ttggaagaaa catgcaagaa caaaaaaaca
1500aaattaagca acttgctttt gctttaaatg aaattcagca agatatgtga 1560
tggttctgag aatgaattta attgaaatag accagcagac ctattgtaaa aatgattaaa
1620
tattgtaata gtagtaactg ctatgacttt gaaatgtctc tttctatàca tttcattatg
1680
aatatatttt taaagacttt tgatcaagta tttattaatt gtataggttt tttataataa
1740
attgttgaca attttgtcta ttagaaaaaa ctaaaaaaaa aa
1782

<210> 2916
<211> 519
<212> PRT
<213> Homo sapiens

<400> 2916

Gln	Glu	Asp	His	Leu	Lys	His	Leu	Arg	Thr	Leu	Glu	Lys	Thr	Leu	Glu
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Lys	Met	Glu	Arg	Gln	Lys	Arg	Gln	Gln	Gln	Ala	Ala	Gln	Ile	Arg	Leu
			20					25					30		
Ile	Gln	Glu	Val	Glu	Leu	Lys	Ala	Ser	Ala	Ala	Asp	Arg	Glu	Ile	Tyr
		35					40					45			
Leu	Leu	Arg	Thr	Ser	Leu	His	Arg	Glu	Arg	Glu	Gln	Ala	Gln	Gln	Leu
	50					55					60				
His	Gln	Leu	Leu	Ala	Leu	Lys	Glu	Gln	Glu	His	Arg	Lys	Glu	Leu	Glu
65					70					75					80
Thr	Arg	Glu	Phe	Phe	Thr	Asp	Ala	Asp	Phe	Gln	Asp	Ala	Leu	Ala	Lys
				85					90					95	
Glu	Ile	Ala	Lys	Glu	Glu	Lys	Lys	His	Glu	Gln	Met	Ile	Lys	Glu	Tyr
			100					105					110		
Gln	Glu	Lys	Ile	Asp	Val	Leu	Ser	Gln	Gln	Tyr	Met	Asp	Leu	Glu	Asn
		115					120					125			
Glu	Phe	Arg	Ile	Ala	Leu	Thr	Val	Glu	Ala	Arg	Arg	Phe	Gln	Asp	Val
	130					135					140				
Lys	Asp	Gly	Phe	Glu	Asn	Val	Ala	Thr	Glu	Leu	Ala	Lys	Ser	Lys	His
145					150					155					160
Ala	Leu	Ile	Trp	Ala	Gln	Arg	Lys	Glu	Asn	Glu	Ser	Ser	Ser	Leu	Ile
				165					170					175	
Lys	Asp	Leu	Thr	Cys	Met	Val	Lys	Glu	Gln	Lys	Thr	Lys	Leu	Ala	Glu
			180					185					190		
Val	Ser	Lys	Leu	Lys	Gln	Glu	Thr	Ala	Ala	Asn	Leu	Gln	Asn	Gln	Ile
		195					200					205			
Asn	Thr	Leu	Glu	Ile	Leu	Ile	Glu	Asp	Asp	Lys	Gln	Lys	Ser	Ile	Gln
	210					215					220				
Ile	Glu	Leu	Leu	Lys	His	Glu	Lys	Val	Gln	Leu	Ile	Ser	Glu	Leu	Ala
225					230					235					240
Ala	Lys	Glu	Ser	Leu	Ile	Phe	Gly	Leu	Arg	Thr	Glu	Arg	Lys	Val	Trp
				245					250					255	
Gly	His	Glu	Leu	Ala	Gln	Gln	Gly	Ser	Ser	Leu	Ala	Gln	Asn	Arg	Gly

```
            260                 265                 270
Lys Leu Glu Ala Gln Ile Glu Ser Leu Ser Arg Glu Asn Glu Cys Leu
        275                 280                 285
Arg Lys Thr Asn Glu Ser Asp Ser Asp Ala Leu Arg Ile Lys Cys Lys
    290                 295                 300
Ile Ile Asp Asp Gln Thr Glu Thr Ile Arg Lys Leu Lys Asp Cys Leu
305                 310                 315                 320
Gln Glu Lys Asp Glu His Ile Lys Arg Leu Gln Glu Lys Ile Thr Glu
                325                 330                 335
Ile Glu Lys Cys Thr Gln Glu Gln Leu Asp Glu Lys Ser Ser Gln Leu
            340                 345                 350
Asp Glu Val Leu Glu Lys Leu Glu Arg His Asn Glu Arg Lys Glu Lys
        355                 360                 365
Leu Lys Gln Gln Leu Lys Gly Lys Glu Val Glu Leu Glu Glu Ile Arg
    370                 375                 380
Lys Ala Tyr Ser Thr Leu Asn Arg Lys Trp His Asp Lys Gly Glu Leu
385                 390                 395                 400
Leu Cys His Leu Glu Thr Gln Val Lys Glu Val Lys Glu Lys Phe Glu
                405                 410                 415
Asn Lys Glu Lys Lys Leu Lys Ala Glu Arg Asp Lys Ser Ile Glu Leu
            420                 425                 430
Gln Lys Asn Ala Met Glu Lys Leu His Ser Met Asp Asp Ala Phe Lys
        435                 440                 445
Arg Gln Val Asp Ala Ile Val Glu Ala His Gln Ala Glu Ile Ala Gln
    450                 455                 460
Leu Ala Asn Glu Lys Gln Lys Cys Ile Asp Ser Ala Asn Leu Lys Val
465                 470                 475                 480
His Gln Ile Glu Lys Glu Met Arg Glu Leu Leu Glu Glu Thr Cys Lys
                485                 490                 495
Asn Lys Lys Thr Met Glu Ala Lys Ile Lys Gln Leu Ala Phe Ala Leu
            500                 505                 510
Asn Glu Ile Gln Gln Asp Met
        515
```

<210> 2917
<211> 2636
<212> DNA
<213> Homo sapiens

<400> 2917
ncctgcgtgt gccaccgctg gttccagccg gccatcccct cctggctgca gaagacgtac
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aacgaggccc tggcgcgggt gcagcggnct gtgcagatgg atgagctggt gcccctgggt
120
gaactgacca agcacagcac atcagcggtg gatctatcca ctngctttgc ccagatcagc
180
cacactgccc ggcagctgga ctggccagac ccagaggagg ccttcatgat taccgtcaag
240
tttgtggagg acacctgtcg cctggccctg gtgtactgca gccttataaa ggcccgggcc
300
cgcgagctct cttcaggcca gaaggaccaa ggccaggcag ccaacatgct gtgtgtggtg
360
gtgaatgaca tggagcagct gcggctggtg atcggcaagt tgcccgccca gctggcatgg
420

gaggccctgg agcagcgggt aggggccgtg ctggagcagg ggcagctgca gaacacgctg
480
catgcccagc tgcagagcgc gctggccggg ctgggccatg agatccgcac tggcgtccgc
540
accctggccg agcagttgga ggtgggcatc gccaagcaca tccagaaact ggtgggcgtc
600
agggagtctg tcctgcctga ggatgccatt ctgcccctga tgaagttcct ggaggtggag
660
ctttgctaca tgaacaccaa cttggtgcag gagaacttca gcagcctcct gaccctgctc
720
tggacccaca cactcacagt gctggtggag gcggccgcct cccagcgcag ctcatccctg
780
gcttccaaca ggctgaagat tgccctgcag aacctggaga tctgcttcca cgctgagggc
840
tgtggcctgc cacccaaggc cctgcacact gccaccttcc aggctctgca gagggacctg
900
gagctgcagg cggcctccag ccgggaactc atccggaagt acttctgcag ccgaatccag
960
cagcaggcag aaaccacctc tgaggagctg ggggctgtga cagtcaaggc ctcctaccgc
1020
gcctctgagc agaagctgcg tgtggagctg ctcagcgcct ccagcctgct gcccctggac
1080
tccaatggct ccagcgaccc ctttgtccag ctgaccttgg agcccaggca tgagttccct
1140
gagctggccg cccgggagac ccagaagcac aagaaggacc ttcacccatt gtttgatgag
1200
acctttgaat tcctggtgcc tgctgagccg tgccgcaagg ctggggcatg cctcctgctc
1260
accgtgctgg actacgacac gctgggggcc gacgacctgg aaggcgaggc cttcctgccg
1320
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1380
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1440
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1500
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1680
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1740
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1980
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2040

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2100
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2160
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2220
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2280
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2340
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2400
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2460
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2520
gagcaggggc ctccccaggg tgcaggttga ggcctgaggg ctgctcttga gacagtaggg
2580
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2636

<210> 2918
<211> 509
<212> PRT
<213> Homo sapiens

<400> 2918
Xaa Cys Val Cys His Arg Trp Phe Gln Pro Ala Ile Pro Ser Trp Leu
 1   5   10   15
Gln Lys Thr Tyr Asn Glu Ala Leu Ala Arg Val Gln Arg Xaa Val Gln
            20   25   30
Met Asp Glu Leu Val Pro Leu Gly Glu Leu Thr Lys His Ser Thr Ser
        35   40   45
Ala Val Asp Leu Ser Thr Xaa Phe Ala Gln Ile Ser His Thr Ala Arg
    50   55   60
Gln Leu Asp Trp Pro Asp Pro Glu Glu Ala Phe Met Ile Thr Val Lys
65   70   75   80
Phe Val Glu Asp Thr Cys Arg Leu Ala Leu Val Tyr Cys Ser Leu Ile
                85   90   95
Lys Ala Arg Ala Arg Glu Leu Ser Ser Gly Gln Lys Asp Gln Gly Gln
            100   105   110
Ala Ala Asn Met Leu Cys Val Val Val Asn Asp Met Glu Gln Leu Arg
        115   120   125
Leu Val Ile Gly Lys Leu Pro Ala Gln Leu Ala Trp Glu Ala Leu Glu
    130   135   140
Gln Arg Val Gly Ala Val Leu Glu Gln Gly Gln Leu Gln Asn Thr Leu
145   150   155   160
His Ala Gln Leu Gln Ser Ala Leu Ala Gly Leu Gly His Glu Ile Arg
                165   170   175
Thr Gly Val Arg Thr Leu Ala Glu Gln Leu Glu Val Gly Ile Ala Lys
            180   185   190
His Ile Gln Lys Leu Val Gly Val Arg Glu Ser Val Leu Pro Glu Asp
        195   200   205
Ala Ile Leu Pro Leu Met Lys Phe Leu Glu Val Glu Leu Cys Tyr Met

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    210                 215                 220
Asn Thr Asn Leu Val Gln Glu Asn Phe Ser Ser Leu Leu Thr Leu Leu
225                 230                 235                 240
Trp Thr His Thr Leu Thr Val Leu Val Glu Ala Ala Ala Ser Gln Arg
                245                 250                 255
Ser Ser Ser Leu Ala Ser Asn Arg Leu Lys Ile Ala Leu Gln Asn Leu
            260                 265                 270
Glu Ile Cys Phe His Ala Glu Gly Cys Gly Leu Pro Pro Lys Ala Leu
        275                 280                 285
His Thr Ala Thr Phe Gln Ala Leu Gln Arg Asp Leu Glu Leu Gln Ala
    290                 295                 300
Ala Ser Ser Arg Glu Leu Ile Arg Lys Tyr Phe Cys Ser Arg Ile Gln
305                 310                 315                 320
Gln Gln Ala Glu Thr Thr Ser Glu Glu Leu Gly Ala Val Thr Val Lys
                325                 330                 335
Ala Ser Tyr Arg Ala Ser Glu Gln Lys Leu Arg Val Glu Leu Leu Ser
            340                 345                 350
Ala Ser Ser Leu Leu Pro Leu Asp Ser Asn Gly Ser Ser Asp Pro Phe
        355                 360                 365
Val Gln Leu Thr Leu Glu Pro Arg His Glu Phe Pro Glu Leu Ala Ala
    370                 375                 380
Arg Glu Thr Gln Lys His Lys Lys Asp Leu His Pro Leu Phe Asp Glu
385                 390                 395                 400
Thr Phe Glu Phe Leu Val Pro Ala Glu Pro Cys Arg Lys Ala Gly Ala
                405                 410                 415
Cys Leu Leu Leu Thr Val Leu Asp Tyr Asp Thr Leu Gly Ala Asp Asp
            420                 425                 430
Leu Glu Gly Glu Ala Phe Leu Pro Leu Arg Glu Val Pro Gly Leu Ser
        435                 440                 445
Gly Ser Glu Glu Pro Gly Glu Val Pro Gln Thr Arg Leu Pro Leu Thr
    450                 455                 460
Tyr Pro Ala Pro Asn Gly Asp Pro Ile Leu Gln Leu Leu Glu Gly Arg
465                 470                 475                 480
Lys Gly Asp Arg Glu Ala Gln Val Phe Val Arg Leu Arg Arg His Arg
                485                 490                 495
Ala Lys Gln Ala Ser Gln His Ala Leu Arg Pro Ala Pro
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<210> 2919
<211> 455
<212> DNA
<213> Homo sapiens

<400> 2919
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120
aggactagct ttggagacgg gcgttggtca agcagcaggg agaggagttt ggacacacaa
180
gctggctggc tcaggatggc tttacctatg tggctccttg agagatcatt gagaagacta
240
aggacatcct ggagcgcgtc attcccagca gcctggttgc cacagcactc tgtggctcgg
300

gcaagatggt tagtgagaag gctggacacc tgccgggcca gacctgagtg cacagcctct
360
gtggagccac cttcctcttt ttcccactca aaacaacgga tggcaagcac ctggaaggca
420
gcccaagcca tggtggccac cttctgcttc ttggt
455

<210> 2920
<211> 143
<212> PRT
<213> Homo sapiens

<400> 2920
Met Ala Trp Ala Ala Phe Gln Val Leu Ala Ile Arg Cys Phe Glu Trp
 1   5   10   15
Glu Lys Glu Glu Gly Gly Ser Thr Glu Ala Val His Ser Gly Leu Ala
            20   25   30
Arg Gln Val Ser Ser Leu Leu Thr Asn His Leu Ala Arg Ala Thr Glu
        35   40   45
Cys Cys Gly Asn Gln Ala Ala Gly Asn Asp Ala Leu Gln Asp Val Leu
    50   55   60
Ser Leu Leu Asn Asp Leu Ser Arg Ser His Ile Gly Lys Ala Ile Leu
65   70   75   80
Ser Gln Pro Ala Cys Val Ser Lys Leu Leu Ser Leu Leu Leu Asp Gln
                85   90   95
Arg Pro Ser Pro Lys Leu Val Leu Ile Ile Leu Gln Leu Cys Arg Ala
            100   105   110
Ala Leu Pro Leu Met Ser Val Glu Asp Cys Gly Asn Val Glu Leu Pro
        115   120   125
Pro Trp Ser Tyr Ser Val Pro Ser Leu Asn Ser Glu Gln Glu Asp
    130   135   140

<210> 2921
<211> 1855
<212> DNA
<213> Homo sapiens

<400> 2921
gggcccggag cggggccttg gaggcccagc ccgcgcggcg acgtctccgc gtggcgtcac
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ggcaccgact gacggccacc caccatggcc gcagaccagc gcccgaaggc cgacacgctg
120
gccctgaggc aacggctcat cagctcttcc tgcagactct ttttcccga ggatcctgtt
180
aagattgtcc gggcccaagg gcagtacatg tacgatgaac agggggcaga atacatcgat
240
tgcatcagca atgtggcgca cgttgggcac tgccaccctc tcgtggtcca agcagcacat
300
gagcagaacc aggtgctcaa caccaacagc cggtacctgc atgacaacat cgtggactat
360
gcgcagaggc tgtcagagac cctgccggag cagctctgtg tgttctattt cctgaattct
420
gggtcagaag ccaatgacct ggccctgagg ctggctcgcc actacacggg acaccaggac
480

gtggtggtat tagatcatgc gtatcacggc cacctgagct ccctgattga catcagtccc
540
tacaagttcc gcaacctgga tggccagaag gagtgggtcc acgtggcacc tctcccagac
600
acctaccggg gcccctaccg gnngaggacc accccaaccc agctatggnc ctatgccaac
660
gaggtgaaac gtgtggtcag cagtgcacag gagaagggca ggaagattgc agccttcttc
720
gctgagtctc tgcccagtgt gggagggcag atcattcccc ctgctggcta cttctcccaa
780
gtggcagagc acatccgcaa ggccggaggg gtctttgttg cagatgagat ccaggttggc
840
tttggccggg taggcaagca cttctgggcc ttccagctcc agggaaaaga cttcgtccct
900
gacatcgtca ccatgggcaa gtccattggc aacggccacc ctgttgcctg cgtggccgca
960
acccagcctg tggcgagggc atttgaagcc accggcgttg agtacttcaa cacgtttggg
1020
ggcagcccag tgtcctgcgc tgtggggctg gccgtcctga atgtcttgga gaaggagcag
1080
ctccaggatc atgccaccag tgtaggcagc ttcctgatgc agctcctctg gcagcaaaaa
1140
atcagacatc ccatcgtcgg ggatgtcagg ggtgttgggc tcttcattgg tgtggatctg
1200
atcaaagatg aggccacaag gacaccagca actgaagagg canntgtcta cttggtatca
1260
aggctgaagg agaactacgt tttgctgagc actgatggcc ctgggaggaa catcctgaag
1320
tttaagcccc caatgtgctt cagcctggac aatgcacggc aggtggtggc aaagctggat
1380
gccattctga ctgacatgga agagaaggtg agaagttgtg aaacgctgag gctccagccc
1440
taagccagcc ctgctctgcc taagtgtact ccagaagaaa ctcatctcat ccaaatacac
1500
gctattgaga aggcgagcct gacctccctc ttacagataa agtcagcttt cagaggctca
1560
gggtgggggg gcctgcccga ggccataatg ctacccaccc cctcctccta accactggtc
1620
tgttggaata acccagatgt ctgcatcccc tcaagtcagt caatttcctt tctgtccact
1680
gggggtggaa tggggtaggg tgggatactt taaagtgctc ctgcttaaat aaattagacc
1740
agaccagtgt atttctaaag aaaatcctga catgcacacc cattaaaaat agtacatttt
1800
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1855

<210> 2922
<211> 452
<212> PRT
<213> Homo sapiens

<400> 2922
Met Ala Ala Asp Gln Arg Pro Lys Ala Asp Thr Leu Ala Leu Arg Gln

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 1               5                  10                  15
Arg Leu Ile Ser Ser Ser Cys Arg Leu Phe Phe Pro Glu Asp Pro Val
            20                  25                  30
Lys Ile Val Arg Ala Gln Gly Gln Tyr Met Tyr Asp Glu Gln Gly Ala
        35                  40                  45
Glu Tyr Ile Asp Cys Ile Ser Asn Val Ala His Val Gly His Cys His
    50                  55                  60
Pro Leu Val Val Gln Ala Ala His Glu Gln Asn Gln Val Leu Asn Thr
65                  70                  75                  80
Asn Ser Arg Tyr Leu His Asp Asn Ile Val Asp Tyr Ala Gln Arg Leu
                85                  90                  95
Ser Glu Thr Leu Pro Glu Gln Leu Cys Val Phe Tyr Phe Leu Asn Ser
            100                 105                 110
Gly Ser Glu Ala Asn Asp Leu Ala Leu Arg Leu Ala Arg His Tyr Thr
        115                 120                 125
Gly His Gln Asp Val Val Val Leu Asp His Ala Tyr His Gly His Leu
    130                 135                 140
Ser Ser Leu Ile Asp Ile Ser Pro Tyr Lys Phe Arg Asn Leu Asp Gly
145                 150                 155                 160
Gln Lys Glu Trp Val His Val Ala Pro Leu Pro Asp Thr Tyr Arg Gly
                165                 170                 175
Pro Tyr Arg Xaa Arg Thr Thr Pro Thr Gln Leu Trp Xaa Tyr Ala Asn
            180                 185                 190
Glu Val Lys Arg Val Val Ser Ser Ala Gln Glu Lys Gly Arg Lys Ile
        195                 200                 205
Ala Ala Phe Phe Ala Glu Ser Leu Pro Ser Val Gly Gly Gln Ile Ile
    210                 215                 220
Pro Pro Ala Gly Tyr Phe Ser Gln Val Ala Glu His Ile Arg Lys Ala
225                 230                 235                 240
Gly Gly Val Phe Val Ala Asp Glu Ile Gln Val Gly Phe Gly Arg Val
                245                 250                 255
Gly Lys His Phe Trp Ala Phe Gln Leu Gln Gly Lys Asp Phe Val Pro
            260                 265                 270
Asp Ile Val Thr Met Gly Lys Ser Ile Gly Asn Gly His Pro Val Ala
        275                 280                 285
Cys Val Ala Ala Thr Gln Pro Val Ala Arg Ala Phe Glu Ala Thr Gly
    290                 295                 300
Val Glu Tyr Phe Asn Thr Phe Gly Gly Ser Pro Val Ser Cys Ala Val
305                 310                 315                 320
Gly Leu Ala Val Leu Asn Val Leu Glu Lys Glu Gln Leu Gln Asp His
                325                 330                 335
Ala Thr Ser Val Gly Ser Phe Leu Met Gln Leu Leu Trp Gln Gln Lys
            340                 345                 350
Ile Arg His Pro Ile Val Gly Asp Val Arg Gly Val Gly Leu Phe Ile
        355                 360                 365
Gly Val Asp Leu Ile Lys Asp Glu Ala Thr Arg Thr Pro Ala Thr Glu
    370                 375                 380
Glu Ala Xaa Val Tyr Leu Val Ser Arg Leu Lys Glu Asn Tyr Val Leu
385                 390                 395                 400
Leu Ser Thr Asp Gly Pro Gly Arg Asn Ile Leu Lys Phe Lys Pro Pro
                405                 410                 415
Met Cys Phe Ser Leu Asp Asn Ala Arg Gln Val Val Ala Lys Leu Asp
            420                 425                 430
Ala Ile Leu Thr Asp Met Glu Glu Lys Val Arg Ser Cys Glu Thr Leu
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435 440 445
Arg Leu Gln Pro
450

<210> 2923
<211> 572
<212> DNA
<213> Homo sapiens

<400> 2923
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gtacaggagg gaccctgaaa atgtccttaa agcctcctcc atgtaagaaa ctggcaggcc
120
tggagccccc cccccgtggg accacccctcc ttccagcaaa atgccggcca agctcaagga
180
gaaacagcgt ttattgtgga ggggagctgg gcggggctca gcctcggaga actggcagta
240
cagccgcccc agcctcggct ccacccatag ccggaacggg atctccagga tggcagagaa
300
gccttcagcc agcgttgggg cctcgaactg cttcctggca gtggtgggaa cagtgaggga
360
cagcctggat catgtggccc agccagtgcc cctgcccccc gctatcccca acagtacctg
420
tagccataca tgaccatgtc tgacacgggg atatgagagg agtccgtcat ctctcgaaac
480
cggttgttgt ggcgcgcctg ctccagagtg gcggtgaaga ggaagcagcg gcaggggacg
540
cccgcggctc gggcacactg gacgtacctg gc
572

<210> 2924
<211> 91
<212> PRT
<213> Homo sapiens

<400> 2924
Met Ser Leu Lys Pro Pro Pro Cys Lys Lys Leu Ala Gly Leu Glu Pro
1 5 10 15
Leu Pro Arg Gly Thr Thr Leu Leu Pro Ala Lys Cys Arg Pro Ser Ser
20 25 30
Arg Arg Asn Ser Val Tyr Cys Gly Gly Glu Leu Gly Gly Ala Gln Pro
35 40 45
Arg Arg Thr Gly Ser Thr Ala Ala Pro Ala Ser Ala Pro Pro Ile Ala
50 55 60
Gly Thr Gly Ser Pro Gly Trp Gln Arg Ser Leu Gln Pro Ala Leu Gly
65 70 75 80
Pro Arg Thr Ala Ser Trp Gln Trp Trp Glu Gln
85 90

<210> 2925
<211> 1999
<212> DNA
<213> Homo sapiens

<400> 2925
ngcgcgccag gggggggctg ctggggtgtt tgtcgcagcg ggttttcctc ggcggtttgc
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ggagctgcta ggatggagca ggttgcggag ggagcaaggg tgaccgcagt ccctgtgtca
120
gctgccgaca gcactgagga gttggccgaa gtcgaagaag gagttggagt agtgggcgaa
180
gataatgacg cagccgcgag aggagcggag gcctttggcg acagtgagga ggacggagag
240
gatgtgttcg aggtggagaa gatcctggac atgaagaccg agggggggtaa agttctttac
300
aaagttcgct ggaaaggcta tacatcggat gatgatacct gggagcccga gattcacctg
360
gaggactgta aagaagtgct tcttgaattt aggaagaaaa ttgcagagaa caaagccaaa
420
gcagtcagga aggatattca gagactatcc ttaaataacg acatatttga ggcgaactct
480
gatagcgatc agcaaagtga gacaaaagaa gatacttccc caaagaagaa aaagaaaaaa
540
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600
aagctaaaag acaagtccaa accagacctg gagagctcct tggaaagttt agtttttgat
660
ttaaggacaa agaaaagaat ttctgaagcc aaagaagaac taaaggagtc caaaaagccc
720
aaaaaagatg aagtaaaaga aacaaaagaa ttaaagaaag ttaaaaaggg tgaaataaga
780
gatttaaaga cgaaaacaag agaagatccc aaagaaaata gaaaaacaaa aaaagaaaaa
840
tttgtcgaat cccaggtgga atctgaatca agtgtactta atgattctcc ctttccagag
900
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960
agagagagag cagggcagga catggggctg gagcatggct ttgagaagcc cctagacagt
1020
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1320
gaaaaatatc agaaaaggca tgattctgac aaggaagaaa aaggcagaaa agagccaaaa
1380
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1440
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1500
accatagacg atcacaaaac caaggaaaac aaacagtcac ttaaagaaag gagaaacacc
1560

agagacgaaa cggatacttg ggcatacatt gctgcagaag gtgatcagga ggttttagac
1620
agcgtgtgcc aagcagatga gaattcaggt gagtttggaa tcattttgta gaatttttca
1680
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1740
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1800
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1860
ctcagcacgt atagaaatta aaagatttct gattttctac cttacctact cttacctggc
1920
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1980
ttatttgtat tttacccctt
1999

<210> 2926
<211> 305
<212> PRT
<213> Homo sapiens

<400> 2926
Lys Lys Val Lys Lys Gly Glu Ile Arg Asp Leu Lys Thr Lys Thr Arg
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Glu Asp Pro Lys Glu Asn Arg Lys Thr Lys Lys Glu Lys Phe Val Glu
20 25 30
Ser Gln Val Glu Ser Glu Ser Ser Val Leu Asn Asp Ser Pro Phe Pro
35 40 45
Glu Asp Asp Asn Glu Gly Leu His Ser Asp Ser Arg Glu Glu Lys Gln
50 55 60
Asn Thr Lys Ser Ala Arg Glu Arg Ala Gly Gln Asp Met Gly Leu Glu
65 70 75 80
His Gly Phe Glu Lys Pro Leu Asp Ser Ala Met Ser Ala Glu Glu Asp
85 90 95
Thr Asp Val Arg Gly Arg Arg Lys Lys Lys Thr Pro Arg Lys Ala Glu
100 105 110
Asp Thr Arg Glu Asn Arg Lys Leu Glu Asn Lys Asn Ala Phe Leu Glu
115 120 125
Lys Lys Thr Val Pro Lys Lys Gln Arg Asn Gln Asp Arg Ser Lys Ser
130 135 140
Ala Ala Glu Leu Glu Lys Leu Met Pro Val Ser Ala Gln Thr Pro Lys
145 150 155 160
Gly Arg Arg Leu Ser Gly Glu Glu Arg Gly Leu Trp Ser Thr Asp Ser
165 170 175
Ala Glu Glu Asp Lys Glu Thr Lys Arg Asn Glu Ser Lys Glu Lys Tyr
180 185 190
Gln Lys Arg His Asp Ser Asp Lys Glu Glu Lys Gly Arg Lys Glu Pro
195 200 205
Lys Gly Leu Lys Thr Leu Lys Glu Ile Arg Asn Ala Phe Asp Leu Phe
210 215 220
Lys Leu Thr Pro Glu Glu Lys Asn Asp Val Ser Glu Asn Asn Arg Lys
225 230 235 240
Arg Glu Glu Ile Pro Leu Asp Phe Lys Thr Ile Asp Asp His Lys Thr

245 250 255
Lys Glu Asn Lys Gln Ser Leu Lys Glu Arg Arg Asn Thr Arg Asp Glu
260 265 270
Thr Asp Thr Trp Ala Tyr Ile Ala Ala Glu Gly Asp Gln Glu Val Leu
275 280 285
Asp Ser Val Cys Gln Ala Asp Glu Asn Ser Gly Glu Phe Gly Ile Ile
290 295 300
Leu
305

<210> 2927
<211> 1084
<212> DNA
<213> Homo sapiens

<400> 2927
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120
ggtgttaact gtctggccta tgatgaagcc atcatggctc agcaggaccg aattcagcaa
180
gagattgctg tgcagaaccc tctggtgtca gagcggctgg agctctcggt cctatacaag
240
gagtatgctg aagatgacaa catctatcaa cagaagatca aggacctcca caaaaagtac
300
tcgtacatcc gcaagaccag gcctgacggc aactgtttct atcgggcttt cggattctcc
360
cacttggagg cactgctgga tgacagcaag gagttgcagc ggttcaaggc tgtgtctgcc
420
aagagcaagg aagacctggt gtcccagggc ttcactgaat tcacaattga ggatttccac
480
aacacgttca tggacctgat tgagcaggtg gagaagcaga cctctgtcgc cgacctgctg
540
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600
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660
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720
atcattgcgc tggcccaggc cctcagcgtg tccatccagg tggagtacat ggaccgcggc
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gagggcggca ccaccaatcc gcacatcttc cctgagggct ccgagcccaa ggtctacctt
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960
atggtcctat ttcacccccc tcttcctgtc acatgacccc cccccatgtt ttattaaagg
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1080
aaaa
1084

<210> 2928
<211> 292
<212> PRT
<213> Homo sapiens

<400> 2928
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Ser Leu Arg Pro Ala Thr Phe Ser Gly Val Asn Cys Leu Ala Tyr Asp
35 40 45
Glu Ala Ile Met Ala Gln Gln Asp Arg Ile Gln Gln Glu Ile Ala Val
50 55 60
Gln Asn Pro Leu Val Ser Glu Arg Leu Glu Leu Ser Val Leu Tyr Lys
65 70 75 80
Glu Tyr Ala Glu Asp Asp Asn Ile Tyr Gln Gln Lys Ile Lys Asp Leu
85 90 95
His Lys Lys Tyr Ser Tyr Ile Arg Lys Thr Arg Pro Asp Gly Asn Cys
100 105 110
Phe Tyr Arg Ala Phe Gly Phe Ser His Leu Glu Ala Leu Leu Asp Asp
115 120 125
Ser Lys Glu Leu Gln Arg Phe Lys Ala Val Ser Ala Lys Ser Lys Glu
130 135 140
Asp Leu Val Ser Gln Gly Phe Thr Glu Phe Thr Ile Glu Asp Phe His
145 150 155 160
Asn Thr Phe Met Asp Leu Ile Glu Gln Val Glu Lys Gln Thr Ser Val
165 170 175
Ala Asp Leu Leu Ala Ser Phe Asn Asp Gln Ser Thr Ser Asp Tyr Leu
180 185 190
Val Val Tyr Leu Arg Leu Leu Thr Ser Gly Tyr Leu Gln Arg Glu Ser
195 200 205
Lys Phe Phe Glu His Phe Ile Glu Gly Gly Arg Thr Val Lys Glu Phe
210 215 220
Cys Gln Gln Glu Val Glu Pro Met Cys Lys Glu Ser Asp His Ile His
225 230 235 240
Ile Ile Ala Leu Ala Gln Ala Leu Ser Val Ser Ile Gln Val Glu Tyr
245 250 255
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Ile Leu Tyr Lys
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<210> 2929
<211> 4920
<212> DNA
<213> Homo sapiens

<400> 2929
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420
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<210> 2930
<211> 1166
<212> PRT
<213> Homo sapiens

<400> 2930
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Val Ser Ser Ala Ala Asp Ser Val Glu Ser Thr Ala Phe Ile Met Glu
35 40 45
Gln Lys Glu Asn Met Ile Asp Lys Asp Val Glu Leu Ser Val Val Leu
50 55 60
Pro Gly Asp Ile Ile Lys Ser Thr Thr Val His Gly Ser Lys Pro Met
65 70 75 80
Met Asp Leu Leu Ile Phe Leu Cys Ala Gln Tyr His Leu Asn Pro Ser
85 90 95
Ser Tyr Thr Ile Asp Leu Leu Ser Ala Glu Gln Asn His Ile Lys Phe
100 105 110
Lys Pro Asn Thr Pro Ile Gly Met Leu Glu Val Glu Lys Val Ile Leu
115 120 125
Lys Pro Lys Met Leu Asp Lys Lys Lys Pro Thr Pro Ile Ile Pro Glu
130 135 140
Lys Thr Val Arg Val Val Ile Asn Phe Lys Lys Thr Gln Lys Thr Ile
145 150 155 160
Val Arg Val Ser Pro His Ala Ser Leu Gln Glu Leu Ala Pro Ile Ile
165 170 175
Cys Ser Lys Cys Glu Phe Asp Pro Leu His Thr Leu Leu Leu Lys Asp
180 185 190
Tyr Gln Ser Gln Glu Pro Leu Asp Leu Thr Lys Ser Leu Asn Asp Leu
195 200 205
Gly Leu Arg Glu Leu Tyr Ala Met Asp Val Asn Arg Glu Ser Cys Gln
210 215 220
Ile Ser Gln Asn Leu Asp Ile Met Lys Glu Lys Glu Asn Lys Gly Phe
225 230 235 240
Phe Ser Phe Phe Gln Arg Ser Lys Lys Lys Arg Asp Gln Thr Ala Ser
245 250 255
Ala Pro Ala Thr Pro Leu Val Asn Lys His Arg Pro Thr Phe Thr Arg
260 265 270
Ser Asn Thr Ile Ser Lys Pro Tyr Ile Ser Asn Thr Leu Pro Ser Asp
275 280 285
Ala Pro Lys Lys Arg Arg Ala Pro Leu Pro Pro Met Pro Ala Ser Gln
290 295 300
Ser Val Pro Gln Asp Leu Ala His Ile Gln Glu Arg Pro Ala Ser Cys
305 310 315 320
Ile Val Lys Ser Met Ser Val Asp Glu Thr Asp Lys Ser Pro Cys Glu
325 330 335
Ala Gly Arg Val Arg Ala Gly Ser Leu Gln Leu Ser Ser Met Ser Ala
340 345 350
Gly Asn Ser Ser Leu Arg Arg Thr Lys Arg Lys Ala Pro Ser Pro Pro
355 360 365
Ser Lys Ile Pro Pro His Gln Ser Asp Glu Asn Ser Arg Val Thr Ala

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    370                 375                 380
Leu Gln Pro Val Asp Gly Val Pro Pro Asp Ser Ala Ser Glu Ala Asn
385                 390                 395                 400
Ser Pro Glu Glu Leu Ser Ser Pro Glu Thr Phe His Pro Gly Leu Ser
                405                 410                 415
Ser Gln Glu Gln Cys Thr Ala Pro Lys Leu Met Glu Glu Thr Ser Val
            420                 425                 430
Phe Glu Cys Pro Gly Thr Pro Glu Ala Ala Ile Thr Ser Leu Thr Ser
        435                 440                 445
Gly Ile Ser Ser Asp Tyr Ser Leu Glu Glu Ile Asp Glu Lys Glu Glu
    450                 455                 460
Leu Ser Glu Val Pro Lys Val Glu Ala Glu Asn Ile Ser Pro Lys Ser
465                 470                 475                 480
Gln Asp Ile Pro Phe Val Ser Thr Asp Ile Ile Asn Thr Leu Lys Asn
                485                 490                 495
Asp Pro Asp Ser Ala Leu Gly Asn Gly Ser Gly Glu Phe Ser Gln Asn
            500                 505                 510
Ser Met Glu Glu Lys Gln Glu Thr Lys Ser Thr Asp Gly Gln Glu Pro
        515                 520                 525
His Ser Val Val Tyr Asp Thr Ser Asn Gly Lys Lys Val Val Asp Ser
    530                 535                 540
Ile Arg Asn Leu Lys Ser Leu Gly Pro Asn Gln Glu Asn Val Gln Asn
545                 550                 555                 560
Glu Ile Ile Val Tyr Pro Glu Asn Thr Glu Asp Asn Met Lys Asn Gly
                565                 570                 575
Val Lys Lys Thr Glu Ile Asn Val Glu Gly Val Ala Lys Asn Asn Asn
            580                 585                 590
Ile Asp Met Glu Val Glu Arg Pro Ser Asn Ser Glu Ala His Glu Thr
        595                 600                 605
Asp Thr Ala Ile Ser Tyr Lys Glu Asn His Leu Ala Ala Ser Ser Val
    610                 615                 620
Pro Asp Gln Lys Leu Asn Gln Pro Ser Ala Glu Lys Thr Lys Asp Ala
625                 630                 635                 640
Ala Ile Gln Thr Thr Pro Ser Cys Asn Ser Phe Asp Gly Lys His Gln
                645                 650                 655
Asp His Asn Leu Ser Asp Ser Lys Val Glu Glu Cys Val Gln Thr Ser
            660                 665                 670
Asn Asn Asn Ile Ser Thr Gln His Ser Cys Leu Ser Ser Gln Asp Ser
        675                 680                 685
Val Asn Thr Ser Arg Glu Phe Arg Ser Gln Gly Thr Leu Ile Ile His
    690                 695                 700
Ser Glu Asp Pro Leu Thr Val Lys Asp Pro Ile Cys Ala His Gly Asn
705                 710                 715                 720
Asp Asp Leu Leu Pro Pro Val Asp Arg Ile Asp Lys Asn Ser Thr Ala
                725                 730                 735
Ser Tyr Leu Lys Asn Tyr Pro Leu Tyr Arg Gln Asp Tyr Asn Pro Lys
            740                 745                 750
Pro Lys Pro Ser Asn Glu Ile Thr Arg Glu Tyr Ile Pro Lys Ile Gly
        755                 760                 765
Met Thr Thr Tyr Lys Ile Val Pro Pro Lys Ser Leu Glu Ile Ser Lys
    770                 775                 780
Asp Trp Gln Ser Glu Thr Ile Glu Tyr Lys Asp Asp Gln Asp Met His
785                 790                 795                 800
Ala Leu Gly Lys Lys His Thr His Glu Asn Val Lys Glu Thr Ala Ile
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                805                 810                 815
Gln Thr Glu Asp Ser Ala Ile Ser Glu Ser Pro Glu Glu Pro Leu Pro
            820                 825                 830
Asn Leu Lys Pro Lys Pro Asn Leu Arg Thr Glu His Gln Val Pro Ser
        835                 840                 845
Ser Val Ser Ser Pro Asp Asp Ala Met Val Ser Pro Leu Lys Pro Ala
    850                 855                 860
Pro Lys Met Thr Arg Asp Thr Gly Thr Ala Pro Phe Ala Pro Asn Leu
865                 870                 875                 880
Glu Glu Ile Asn Asn Ile Leu Glu Ser Lys Phe Lys Ser Arg Ala Ser
                885                 890                 895
Asn Ala Gln Ala Lys Pro Ser Ser Phe Phe Leu Gln Met Gln Lys Arg
            900                 905                 910
Val Ser Gly His Tyr Val Thr Ser Ala Ala Ala Lys Ser Val His Ala
        915                 920                 925
Ala Pro Asn Pro Ala Pro Lys Glu Leu Thr Asn Lys Glu Ala Glu Arg
    930                 935                 940
Asp Met Leu Pro Ser Pro Glu Gln Thr Leu Ser Pro Leu Ser Lys Met
945                 950                 955                 960
Pro His Ser Val Pro Gln Pro Leu Val Glu Lys Thr Asp Asp Asp Val
                965                 970                 975
Ile Gly Gln Ala Pro Ala Glu Ala Ser Pro Pro Pro Ile Ala Pro Lys
            980                 985                 990
Pro Val Thr Ile Pro Ala Ser Gln Val Ser Thr Gln Asn Leu Lys Thr
        995                 1000                1005
Leu Lys Thr Phe Gly Ala Pro Arg Pro Tyr Ser Ser Ser Gly Pro Ser
    1010                1015                1020
Pro Phe Ala Leu Ala Val Val Lys Arg Ser Gln Ser Phe Ser Lys Glu
1025                1030                1035                1040
Arg Thr Glu Ser Pro Ser Ala Ser Ala Leu Val Gln Pro Pro Ala Asn
                1045                1050                1055
Thr Glu Glu Gly Lys Thr His Ser Val Asn Lys Phe Val Asp Ile Pro
            1060                1065                1070
Gln Leu Gly Val Ser Asp Lys Glu Asn Asn Ser Ala His Asn Glu Gln
        1075                1080                1085
Asn Ser Gln Ile Pro Thr Pro Thr Asp Gly Pro Ser Phe Thr Val Met
    1090                1095                1100
Arg Gln Ser Ser Leu Thr Phe Gln Ser Ser Asp Pro Glu Gln Met Arg
1105                1110                1115                1120
Gln Ser Leu Leu Thr Ala Ile Arg Ser Gly Glu Ala Ala Ala Lys Leu
                1125                1130                1135
Lys Arg Val Thr Ile Pro Ser Asn Thr Ile Ser Val Asn Gly Arg Ser
            1140                1145                1150
Arg Leu Ser His Ser Met Ser Pro Asp Ala Gln Asp Gly His
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<210> 2931
<211> 625
<212> DNA
<213> Homo sapiens

<400> 2931
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120
ttagagatct tcgaagccat attttctcca gatgttttgg gatgaggaga cacaacaaca
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gtgtttttag gttcactctg atgagttgcc atgaaatcaa accaatctaa actgtcatct
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360
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420
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480
aagcagcagt ctctgctgat aaaccagact cagtactgac tcatcatgtc cccaggaacc
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600
cacagtgcac agtcccttca cgcgt
625

<210> 2932
<211> 90
<212> PRT
<213> Homo sapiens

<400> 2932
Met Cys Glu Pro Gly Gln Arg Ser Lys Val Asp Ile Gly Leu Leu Pro
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Ser Pro Gly Glu Thr Gly Val Pro Trp Arg Ala Asp Asn Val Glu Ser
            20   25   30
Asn Lys Lys Lys Arg Leu Ala Leu Asp Ser Glu Ala Ala Val Ser Ala
        35   40   45
Asp Lys Pro Asp Ser Val Leu Thr His His Val Pro Arg Asn Leu Gln
    50   55   60
Lys Leu Cys Lys Glu Arg Ala Gln Lys Leu Cys Arg Asn Ser Thr Arg
65   70   75   80
Val Pro Ala Gln Cys Thr Val Pro Ser Arg
                85   90

<210> 2933
<211> 688
<212> DNA
<213> Homo sapiens

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gatgaggaaa ggatggtaca gagctctcct ccaatatctg gtgaagacaa caaatgggag
120
cgagaaagtc aagaaacgac tagagaactt ctgaaagtta aagacagatt aattgaagta
180
gaaagaaata atgctacact gcaagcagag aagcaagcgt tgaaaactca actgaagcaa
240

cttgagacac agaacaataa tttgcaggct cagattcttg cacttcagag gcagacagtg
300
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360
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420
cagtcttcct tagaaaatga aaatgaatct gtaatcaaag agcgagaaga cctaaaatct
480
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540
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688

<210> 2934
<211> 229
<212> PRT
<213> Homo sapiens

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Lys Gln Arg Gln Asp Glu Glu Arg Met Val Gln Ser Ser Pro Pro Ile
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Ser Gly Glu Asp Asn Lys Trp Glu Arg Glu Ser Gln Glu Thr Thr Arg
35 40 45
Glu Leu Leu Lys Val Lys Asp Arg Leu Ile Glu Val Glu Arg Asn Asn
50 55 60
Ala Thr Leu Gln Ala Glu Lys Gln Ala Leu Lys Thr Gln Leu Lys Gln
65 70 75 80
Leu Glu Thr Gln Asn Asn Asn Leu Gln Ala Gln Ile Leu Ala Leu Gln
85 90 95
Arg Gln Thr Val Ser Leu Gln Glu Gln Asn Thr Thr Leu Gln Thr Gln
100 105 110
Asn Ala Lys Leu Gln Val Glu Asn Ser Thr Leu Asn Ser Gln Ser Thr
115 120 125
Ser Leu Met Asn Gln Asn Ala Gln Leu Leu Ile Gln Gln Ser Ser Leu
130 135 140
Glu Asn Glu Asn Glu Ser Val Ile Lys Glu Arg Glu Asp Leu Lys Ser
145 150 155 160
Leu Tyr Asp Ser Leu Ile Lys Asp His Glu Lys Leu Glu Leu Leu His
165 170 175
Glu Arg Gln Ala Ser Glu Tyr Glu Ser Leu Ile Ser Lys His Gly Thr
180 185 190
Leu Lys Ser Ala His Lys Asn Leu Glu Val Glu His Arg Asp Leu Glu
195 200 205
Asp Arg Tyr Asn Gln Leu Leu Lys Gln Lys Gly Gln Leu Glu Asp Leu
210 215 220
Glu Lys Met Leu Lys
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<210> 2935
<211> 1200
<212> DNA
<213> Homo sapiens

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aactctaaaa gataaagcaa gaaatgtcaa gtaggttttg cacattgggc tgctttaggc
180
tgtgccctct gattcttctg gtgtactcat gatactctcc cttggtgccc tccaggctga
240
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300
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360
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480
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540
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600
tcagaggact cagcgtcagg atccgatgag tagaaacgga ggaaggttct ctttgcgctt
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720
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780
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840
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gcaccatctg caacgatcca ccagggcgaa gaagaaggac cacttgatat ctgggctgtt
960
gtgaaacctg gaaataccaa ggaaaaaatt gcattctttg catcccacca gtgtagtaac
1020
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1080
aggaaaaaat caggggatct taaaaaagcc aaggtacagg tggaaaggat gagggaggtt
1140
aacagcaggt gctaccaacc tgagcctttt gcatgtggca ttgagcactg ttctgtgcac
1200

<210> 2936
<211> 109
<212> PRT
<213> Homo sapiens

<400> 2936
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Val Lys Val Lys Met Glu Lys Lys Ser Thr Pro Ser Arg Gly Ser Ser
        35                  40                  45
Ser Lys Ser Ser Ser Arg Gln Leu Ser Glu Ser Phe Lys Ser Lys Glu
    50                  55                  60
Phe Val Ser Ser Asp Glu Ser Ser Ser Gly Glu Asn Lys Ser Lys Lys
65                  70                  75                  80
Lys Arg Arg Arg Ser Glu Asp Ser Glu Glu Glu Glu Leu Ala Ser Thr
                85                  90                  95
Pro Pro Ser Ser Glu Asp Ser Ala Ser Gly Ser Asp Glu
            100                 105
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<210> 2937
<211> 749
<212> DNA
<213> Homo sapiens

<400> 2937
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cgagtcaaaa agctgacatg tcgggtaaaa attaaagaag caacggggct gcccttaaac
120
ctctcaaatt ttgtcttctg tcaatacaca ttctgggacc agtgtgagtc tacggtggct
180
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240
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300
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360
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420
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<210> 2938
<211> 249
<212> PRT
<213> Homo sapiens

<400> 2938
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Glu Ala Thr Gly Leu Pro Leu Asn Leu Ser Asn Phe Val Phe Cys Gln
        35                  40                  45
Tyr Thr Phe Trp Asp Gln Cys Glu Ser Thr Val Ala Ala Pro Val Val
    50                  55                  60
Asp Pro Glu Val Pro Ser Pro Gln Ser Lys Asp Ala Gln Tyr Thr Val
65                  70                  75                  80
Thr Phe Ser His Cys Lys Asp Tyr Val Val Asn Val Thr Glu Glu Phe
                85                  90                  95
Leu Glu Phe Ile Ser Asp Gly Ala Leu Ala Ile Glu Val Trp Gly His
            100                 105                 110
Arg Cys Ala Gly Asn Gly Ser Ser Ile Trp Glu Val Asp Ser Leu His
        115                 120                 125
Ala Lys Thr Arg Thr Leu His Asp Arg Trp Asn Glu Val Thr Arg Arg
    130                 135                 140
Ile Glu Met Trp Ile Ser Ile Leu Glu Leu Asn Glu Leu Gly Glu Tyr
145                 150                 155                 160
Ala Ala Val Glu Leu His Gln Ala Lys Asp Val Asn Thr Gly Gly Ile
                165                 170                 175
Phe Gln Leu Arg Gln Gly His Ser Arg Arg Val Gln Val Thr Val Lys
            180                 185                 190
Pro Val Gln His Ser Gly Thr Leu Pro Leu Met Val Glu Ala Ile Leu
        195                 200                 205
Ser Val Ser Ile Gly Cys Val Thr Ala Arg Ser Thr Lys Leu Gln Arg
    210                 215                 220
Gly Leu Asp Ser Tyr Gln Arg Asp Asp Glu Asp Gly Asp Asp Met Asp
225                 230                 235                 240
Ser Tyr Gln Glu Glu Asp Leu Asn Cys
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<210> 2939
<211> 2405
<212> DNA
<213> Homo sapiens

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120
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acagaggaga agccactgtt gccaggacag acgcctgagg cggccaagac tcactctgtg
240
gagacaccat acggctctgt cactttcact gtctatggca cccccaaacc caaacgccca
300
gcgatcctta cctaccacga tgtgggactc aactataaat cttgcttcca gccactgttt
360
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420
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480

cttgcagaca tgatcccttg cgtcctgcag tacctaaatt tctctacaat aattggagtt
540
ggtgttggag ctggagccta catcctggcg agatatgctc ttaaccaccc ggacactgtt
600
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660
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720
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1320
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1380
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1440
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1800
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1920
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1980
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2040
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2100

tgaaccaatg tcccttcagc acctcccagg ttagatatgg gggaggtgag ggctgggtcc
2160
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2220
gaagaaagat ttccagactc gactgctctg ggaccagggt gtcatgagcg taaaatgggc
2280
aagggagagc gggcggaggg ccccgaggtg gcagcagggg tcagggaagt gggcttccga
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2405

<210> 2940
<211> 357
<212> PRT
<213> Homo sapiens

<400> 2940
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Tyr Gly Ser Val Thr Phe Thr Val Tyr Gly Thr Pro Lys Pro Lys Arg
35 40 45
Pro Ala Ile Leu Thr Tyr His Asp Val Gly Leu Asn Tyr Lys Ser Cys
50 55 60
Phe Gln Pro Leu Phe Gln Phe Glu Asp Met Gln Glu Ile Ile Gln Asn
65 70 75 80
Phe Val Arg Val His Val Asp Ala Pro Gly Met Glu Glu Gly Ala Pro
85 90 95
Val Phe Pro Leu Gly Tyr Gln Tyr Pro Ser Leu Asp Gln Leu Ala Asp
100 105 110
Met Ile Pro Cys Val Leu Gln Tyr Leu Asn Phe Ser Thr Ile Ile Gly
115 120 125
Val Gly Val Gly Ala Gly Ala Tyr Ile Leu Ala Arg Tyr Ala Leu Asn
130 135 140
His Pro Asp Thr Val Glu Gly Leu Val Leu Ile Asn Ile Asp Pro Asn
145 150 155 160
Ala Lys Gly Trp Met Asp Trp Ala Ala His Lys Leu Thr Gly Leu Thr
165 170 175
Ser Ser Ile Pro Glu Met Ile Leu Gly His Leu Phe Ser Gln Glu Glu
180 185 190
Leu Ser Gly Asn Ser Glu Leu Ile Gln Lys Tyr Arg Asn Ile Ile Thr
195 200 205
His Ala Pro Asn Leu Asp Asn Ile Glu Leu Tyr Trp Asn Ser Tyr Asn
210 215 220
Asn Arg Arg Asp Leu Asn Phe Glu Arg Gly Gly Asp Ile Thr Leu Arg
225 230 235 240
Cys Pro Val Met Leu Val Val Gly Asp Gln Ala Pro His Glu Asp Ala
245 250 255
Val Val Glu Cys Asn Ser Lys Leu Asp Pro Thr Gln Thr Ser Phe Leu
260 265 270
Lys Met Ala Asp Ser Gly Gly Gln Pro Gln Leu Thr Gln Pro Gly Lys

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        275                 280                 285
Leu Thr Glu Ala Phe Lys Tyr Phe Leu Gln Gly Met Gly Tyr Met Ala
    290                 295                 300
Ser Ser Cys Met Thr Arg Leu Ser Arg Ser Arg Thr Ala Ser Leu Thr
305                 310                 315                 320
Ser Ala Ala Ser Val Asp Gly Asn Arg Ser Arg Ser Arg Thr Leu Ser
                325                 330                 335
Gln Ser Ser Glu Ser Gly Thr Leu Ser Ser Gly Pro Pro Gly His Thr
            340                 345                 350
Met Glu Val Ser Cys
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<210> 2941
<211> 847
<212> DNA
<213> Homo sapiens

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240
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300
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360
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480
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600
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660
ctggggctgc tgcaggaccc ccaggcctga gcccagcacc cgctccaccc cagccagctg
720
ggcagggccg gtgtgggggct ggagccaggc agctagccca ggacggagca agggaagacc
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840
ggtgcac
847

<210> 2942
<211> 229
<212> PRT
<213> Homo sapiens

<400> 2942
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Gly Gly Asn Ala Pro Cys Ile Leu Gln Leu Asp Leu Gln His Leu His
20 25 30
Gly Arg Gly His Asp His Leu Ala Gly Ala Ser Pro Thr Ala Arg Gln
35 40 45
His Leu Phe Lys Gln Gly Gln Leu Ser Ala Gln Gly Gly Ala Gln Pro
50 55 60
Ser Val Glu Ala Pro Ala Ala Pro Arg Pro Thr Ala Thr Gln Leu Thr
65 70 75 80
Arg Asp Leu Leu Arg Ser Arg Gly Ile Ala Gly Leu Tyr Lys Gly Leu
85 90 95
Gly Ala Thr Leu Leu Arg Asp Val Pro Phe Ser Val Val Tyr Phe Pro
100 105 110
Leu Phe Ala Asn Leu Asn Gln Leu Gly Arg Pro Ala Ser Glu Glu Lys
115 120 125
Ser Pro Phe Tyr Val Ser Phe Leu Ala Gly Cys Val Ala Gly Ser Ala
130 135 140
Ala Ala Val Ala Val Asn Pro Cys Asp Val Val Lys Thr Arg Leu Gln
145 150 155 160
Ser Leu Gln Arg Gly Val Asn Glu Asp Thr Tyr Ser Gly Ile Leu Asp
165 170 175
Cys Ala Arg Lys Ile Leu Arg His Glu Gly Pro Ser Ala Phe Leu Lys
180 185 190
Gly Ala Tyr Cys Arg Ala Leu Val Ile Ala Pro Leu Phe Gly Ile Ala
195 200 205
Gln Val Val Tyr Phe Leu Gly Ile Ala Glu Ser Leu Leu Gly Leu Leu
210 215 220
Gln Asp Pro Gln Ala
225

<210> 2943
<211> 1501
<212> DNA
<213> Homo sapiens

<400> 2943
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120
tctagtgttt gggtttcttc gcggctgctc aagatgaacc gactcttcgg gaaagcgaaa
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240
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aagaagatga gagagggtcc tgcaaagaat atggtcaagc agaaagcctt gcgagtttta
360
aagcaaaaga ggatgtatga gcagcagcgg gacaatcttg ccaacagtca ttcaacatgg
420
aacgccaatt ataccatcca gtctttgaag gacaccaaga ccacggttga tgctatgaaa
480

ctgggagtaa aggaaatgaa gaaggcatac aagcaagtga agatcgacca gattgaggat
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ttacaagacc agctagagga tatgatggaa gatgcaaatg aaatccaaga agcactgagt
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cgcagttatg gcaccccaga actggatgaa gatgatttag aagcagagtt ggatgcacta
660
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720
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900
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1320
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1380
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1500
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1501

<210> 2944
<211> 218
<212> PRT
<213> Homo sapiens

<400> 2944
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            20   25   30
Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln
        35   40   45
Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys
    50   55   60
Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp
65   70   75   80
Asn Leu Ala Asn Ser His Ser Thr Trp Asn Ala Asn Tyr Thr Ile Gln

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                85                  90                  95
Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val
            100                 105                 110
Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu
        115                 120                 125
Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile
    130                 135                 140
Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp
145                 150                 155                 160
Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp
                165                 170                 175
Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro
            180                 185                 190
Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp
        195                 200                 205
Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser
    210                 215
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<210> 2945
<211> 3331
<212> DNA
<213> Homo sapiens

<400> 2945

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180
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240
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420
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780
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900
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1020
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2520

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3331

<210> 2946
<211> 463
<212> PRT
<213> Homo sapiens

<400> 2946
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Lys Arg Thr Thr Pro Leu Gln Thr His Ser Ile Ile Ile Ser Asp Gln
35 40 45
Val Pro Ser Asp Gln Asp Ala His Gln Tyr Leu Arg Leu Arg Asp Gln
50 55 60
Ser Glu Ala Thr Gln Val Met Ala Glu Pro Gly Glu Gly Gly Ser Glu
65 70 75 80
Thr Val Ala Leu Pro Pro Pro Pro Pro Ser Glu Glu Gly Gly Val Pro
85 90 95
Gln Asp Ala Ala Gly Arg Gly Gly Thr Pro Gln Ile Arg Val Val Gly
100 105 110
Gly Arg Gly His Val Ala Ile Lys Ala Gly Gln Glu Glu Gly Gln Pro
115 120 125
Pro Ala Glu Gly Leu Ala Ala Ala Ser Val Val Met Ala Ala Asp Arg
130 135 140
Ser Leu Lys Lys Gly Val Gln Gly Gly Glu Lys Ala Leu Glu Ile Cys

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145                 150                 155                 160
Gly Ala Gln Arg Ser Ala Ser Glu Leu Thr Ala Gly Ala Glu Ala Glu
                165                 170                 175
Ala Glu Glu Val Lys Thr Gly Lys Cys Ala Thr Val Ser Ala Ala Val
            180                 185                 190
Ala Glu Arg Glu Ser Ala Glu Val Val Val Lys Glu Gly Leu Ala Glu
        195                 200                 205
Lys Glu Val Met Glu Glu Gln Met Glu Val Glu Glu Gln Pro Pro Glu
    210                 215                 220
Gly Glu Glu Ile Glu Val Ala Glu Glu Asp Arg Leu Glu Glu Glu Ala
225                 230                 235                 240
Arg Glu Glu Glu Gly Pro Trp Pro Leu His Glu Ala Leu Arg Met Asp
                245                 250                 255
Pro Leu Glu Ala Ile Gln Leu Glu Leu Asp Thr Val Asn Ala Gln Ala
            260                 265                 270
Asp Arg Ala Phe Gln Gln Leu Glu His Lys Phe Gly Arg Met Arg Arg
        275                 280                 285
His Tyr Leu Glu Arg Arg Asn Tyr Ile Ile Gln Asn Ile Pro Gly Phe
    290                 295                 300
Trp Met Thr Ala Phe Arg Asn His Pro Gln Leu Ser Ala Met Ile Arg
305                 310                 315                 320
Gly Gln Asp Ala Glu Met Leu Arg Tyr Ile Thr Asn Leu Glu Val Lys
                325                 330                 335
Glu Leu Arg His Pro Arg Thr Gly Cys Lys Phe Lys Phe Phe Phe Arg
            340                 345                 350
Arg Asn Pro Tyr Phe Arg Asn Lys Leu Ile Val Lys Glu Tyr Glu Val
        355                 360                 365
Arg Ser Ser Gly Arg Val Val Ser Leu Ser Thr Pro Ile Ile Trp Arg
    370                 375                 380
Arg Gly His Glu Pro Gln Ser Phe Ile Arg Arg Asn Gln Asp Leu Ile
385                 390                 395                 400
Cys Ser Phe Phe Thr Trp Phe Ser Asp His Ser Leu Pro Glu Ser Asp
                405                 410                 415
Lys Ile Ala Glu Ile Ile Lys Glu Asp Leu Trp Pro Asn Pro Leu Gln
            420                 425                 430
Tyr Tyr Leu Leu Arg Glu Gly Val Arg Arg Ala Arg Arg Arg Pro Leu
        435                 440                 445
Arg Glu Pro Val Glu Ile Pro Arg Pro Phe Gly Phe Gln Ser Gly
    450                 455                 460
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<210> 2947
<211> 997
<212> DNA
<213> Homo sapiens

<400> 2947
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120
ccttcatgca ggaaccacat caaatcaagc tgcagcttga tcgccttcaa ctccgaccgt
180
cctggtgtac tgggcattgt gcctctgcaa ggccaaggag aggacaagcg acgcgtggcc
240

cacctgggct gccattcaga cctagtcacc gacttggact tctcgccctt tgatgacttc
300
ctcctggcca caggctcggc tgacaggacg gtaaaactct ggcgactgcc agggcctggc
360
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420
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480
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540
cagagcgccg tctggagccg agatggagcc ctggtgggca cggcgtgcaa ggacaagcag
600
ctgcagatct ttgaccccag aacaaagccg cgggcctctc agagcacgca ggcccatgag
660
aacagcaggg atagccggct ggcatggatg ggcacctggg agcaccttgt gtctactgga
720
ttcaaccaga tgcgtgagcg cgaagtgaag ctgtgggaca cgcggttctt ctccagcgcc
780
ctggcctccc tcaccttgga cacctcgctt gggtgtctcg tgcctctgct ggaccctgac
840
tctgggctcc tggtcctggc aggaaagggc gagaggcagc tgtactgtta cgaggtggtc
900
ccgcagcagc cggcgctgag cccagtgacc cagtgtgtcc tggagagcgt gctgcgtggg
960
gctgcccttg tgccccggca ggcgctggcc gtcatga
997

<210> 2948
<211> 332
<212> PRT
<213> Homo sapiens

<400> 2948
Xaa Ala Ser Ala Ala Val Pro Val Ala Met Asn Arg Phe Arg Val Ser
 1   5   10   15
Lys Phe Arg His Thr Glu Ala Arg Pro Pro Arg Arg Glu Ser Trp Ile
            20   25   30
Ser Asp Ile Arg Ala Gly Thr Ala Pro Ser Cys Arg Asn His Ile Lys
        35   40   45
Ser Ser Cys Ser Leu Ile Ala Phe Asn Ser Asp Arg Pro Gly Val Leu
    50   55   60
Gly Ile Val Pro Leu Gln Gly Gln Gly Glu Asp Lys Arg Arg Val Ala
65   70   75   80
His Leu Gly Cys His Ser Asp Leu Val Thr Asp Leu Asp Phe Ser Pro
                85   90   95
Phe Asp Asp Phe Leu Leu Ala Thr Gly Ser Ala Asp Arg Thr Val Lys
            100   105   110
Leu Trp Arg Leu Pro Gly Pro Gly Gln Ala Leu Pro Ser Ala Pro Gly
        115   120   125
Val Val Leu Gly Pro Glu Asp Leu Pro Val Glu Val Leu Gln Phe His
    130   135   140
Pro Thr Ser Asp Gly Ile Leu Val Ser Ala Ala Gly Thr Thr Val Lys
145   150   155   160
Val Trp Asp Ala Ala Lys Gln Gln Pro Leu Thr Glu Leu Ala Ala His

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                165                 170                 175
Gly Asp Leu Val Gln Ser Ala Val Trp Ser Arg Asp Gly Ala Leu Val
            180                 185                 190
Gly Thr Ala Cys Lys Asp Lys Gln Leu Gln Ile Phe Asp Pro Arg Thr
        195                 200                 205
Lys Pro Arg Ala Ser Gln Ser Thr Gln Ala His Glu Asn Ser Arg Asp
    210                 215                 220
Ser Arg Leu Ala Trp Met Gly Thr Trp Glu His Leu Val Ser Thr Gly
225                 230                 235                 240
Phe Asn Gln Met Arg Glu Arg Glu Val Lys Leu Trp Asp Thr Arg Phe
                245                 250                 255
Phe Ser Ser Ala Leu Ala Ser Leu Thr Leu Asp Thr Ser Leu Gly Cys
            260                 265                 270
Leu Val Pro Leu Leu Asp Pro Asp Ser Gly Leu Leu Val Leu Ala Gly
        275                 280                 285
Lys Gly Glu Arg Gln Leu Tyr Cys Tyr Glu Val Val Pro Gln Gln Pro
    290                 295                 300
Ala Leu Ser Pro Val Thr Gln Cys Val Leu Glu Ser Val Leu Arg Gly
305                 310                 315                 320
Ala Ala Leu Val Pro Arg Gln Ala Leu Ala Val Met
                325                 330
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<210> 2949
<211> 880
<212> DNA
<213> Homo sapiens

<400> 2949
actagtatca ctcctcccag tggagccttt tctggggatt tagctgaatc cttgtgagta
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120
ggcactgtgt ggtcttggtc ataggtactt tggattttcc catttacttt tttacttcca
180
acaacagtct tgtgattgaa aatcttactc caaattccac cttccacatt gtctttcact
240
ccaaattcat aaactgtgtt gggctttagg ttttccacaa ttgtttcagg ggctggacag
300
atttgaaaaa tccacttctt ttctttatcc ttttctcgat agcgaattgt ataaaatctg
360
tcattgggac agtgacttgg caatgtccag tcatggtgtg ggttgatgag gaaaccccag
420
gacaggaaga ctgagctcgg tgtcagagtg ccaaccacca gctgcagagg tttgcgagaa
480
cgagttttac ctgaacatga cttcttttga cttggaggtg gagcaggtcg cacaactatc
540
agatatttcg gctctgcatc aactatagct tctgtgaatt tcccttcagc gggaagaggg
600
aagtactggt ttggtgatac attgctgcca tatcccagga gaagaccttc aagctttaca
660
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720
ttgaggtttg gccttttacc ttttggcaat ttctgtgcat ttcccagggc tagtgtaata
780

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840
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880

<210> 2950
<211> 279
<212> PRT
<213> Homo sapiens

<400> 2950
Met Arg Gly Gly Lys Cys Asn Met Leu Ser Ser Leu Gly Cys Leu Leu
1 5 10 15
Leu Cys Gly Ser Ile Thr Leu Ala Leu Gly Asn Ala Gln Lys Leu Pro
20 25 30
Lys Gly Lys Arg Pro Asn Leu Lys Val His Ile Asn Thr Thr Ser Asp
35 40 45
Ser Ile Leu Leu Lys Phe Leu Arg Pro Ser Pro Asn Val Lys Leu Glu
50 55 60
Gly Leu Leu Leu Gly Tyr Gly Ser Asn Val Ser Pro Asn Gln Tyr Phe
65 70 75 80
Pro Leu Pro Ala Glu Gly Lys Phe Thr Glu Ala Ile Val Asp Ala Glu
85 90 95
Pro Lys Tyr Leu Ile Val Val Arg Pro Ala Pro Pro Pro Ser Gln Lys
100 105 110
Lys Ser Cys Ser Gly Lys Thr Arg Ser Arg Lys Pro Leu Gln Leu Val
115 120 125
Val Gly Thr Leu Thr Pro Ser Ser Val Phe Leu Ser Trp Gly Phe Leu
130 135 140
Ile Asn Pro His His Asp Trp Thr Leu Pro Ser His Cys Pro Asn Asp
145 150 155 160
Arg Phe Tyr Thr Ile Arg Tyr Arg Glu Lys Asp Lys Glu Lys Lys Trp
165 170 175
Ile Phe Gln Ile Cys Pro Ala Pro Glu Thr Ile Val Glu Asn Leu Lys
180 185 190
Pro Asn Thr Val Tyr Glu Phe Gly Val Lys Asp Asn Val Glu Gly Gly
195 200 205
Ile Trp Ser Lys Ile Phe Asn His Lys Thr Val Val Gly Ser Lys Lys
210 215 220
Val Asn Gly Lys Ile Gln Ser Thr Tyr Asp Gln Asp His Thr Val Pro
225 230 235 240
Ala Tyr Val Pro Arg Lys Leu Ile Pro Ile Thr Ile Ile Lys Gln Val
245 250 255
Ile Gln Asn Val Thr His Lys Asp Ser Ala Lys Ser Pro Glu Lys Ala
260 265 270
Pro Leu Gly Gly Val Ile Leu
275

<210> 2951
<211> 3478
<212> DNA
<213> Homo sapiens

<400> 2951

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ccccctggcc agccctggcc ccagcctctg ccggagccct ctgtggaggc agagcagtgc
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240
aggccatgga caggctgccc cgctgacggc cagggtgaag catgtgagga gccgccccgg
300
agccaagcag gagggaagag gctttcatag attctattca caaagaataa ccaccatttt
360
gcaaggacca tgaggccact gtgcgtgaca tgctggtggc tcggactgct ggctgccatg
420
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480
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540
ttcattgtgc cccagcagcg ggtcacgggt gccatctgcg tcaactccaa ggagcctgag
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gtgcttctgg agaaccgagt gcataagcag gagctagagc tgctcaacaa tgagctgctc
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1080
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1680
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2280
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2400
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2700
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2760
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3180
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3300
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3360
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3420
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3478

<210> 2952
<211> 493
<212> PRT
<213> Homo sapiens

<400> 2952
Met Arg Pro Leu Cys Val Thr Cys Trp Trp Leu Gly Leu Leu Ala Ala
1 5 10 15
Met Gly Ala Val Ala Gly Gln Glu Asp Gly Phe Glu Gly Thr Glu Glu
20 25 30
Gly Ser Pro Arg Glu Phe Ile Tyr Leu Asn Arg Tyr Lys Arg Ala Gly
35 40 45
Glu Ser Gln Asp Lys Cys Thr Tyr Thr Phe Ile Val Pro Gln Gln Arg
50 55 60
Val Thr Gly Ala Ile Cys Val Asn Ser Lys Glu Pro Glu Val Leu Leu
65 70 75 80
Glu Asn Arg Val His Lys Gln Glu Leu Glu Leu Leu Asn Asn Glu Leu
85 90 95
Leu Lys Gln Lys Arg Gln Ile Glu Thr Leu Gln Gln Leu Val Glu Val
100 105 110
Asp Gly Gly Ile Val Ser Glu Val Lys Leu Leu Arg Lys Glu Ser Arg
115 120 125
Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu
130 135 140
Ile Ile Arg Lys Arg Asp Asn Ala Leu Glu Leu Ser Gln Leu Glu Asn
145 150 155 160
Arg Ile Leu Asn Gln Thr Ala Asp Met Leu Gln Leu Ala Ser Lys Tyr
165 170 175
Lys Asp Leu Glu His Lys Phe Gln His Leu Ala Met Leu Ala His Asn
180 185 190
Gln Ser Glu Ile Ile Ala Gln Leu Glu Glu His Cys Gln Arg Val Pro
195 200 205
Ser Ala Arg Pro Val Pro Gln Pro Pro Pro Ala Ala Pro Pro Arg Val
210 215 220
Tyr Gln Pro Pro Thr Tyr Asn Arg Ile Ile Asn Gln Ile Ser Thr Asn
225 230 235 240
Glu Ile Gln Ser Asp Gln Asn Leu Lys Val Leu Pro Pro Pro Leu Pro
245 250 255
Thr Met Pro Thr Leu Thr Ser Leu Pro Ser Ser Thr Asp Lys Pro Ser
260 265 270
Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly His Asp Thr
275 280 285
Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn Arg Leu Met Gln
290 295 300
Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly Trp Thr Val Ile Gln

305 310 315 320
Arg Arg Leu Asp Gly Ser Val Asn Phe Phe Arg Asn Trp Glu Thr Tyr
325 330 335
Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu Gly Leu Glu
340 345 350
Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn Tyr Lys Leu Leu Val Thr
355 360 365
Met Glu Asp Trp Ser Gly Arg Lys Val Phe Ala Glu Tyr Ala Ser Phe
370 375 380
Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys Leu Arg Leu Gly Arg Tyr
385 390 395 400
His Gly Asn Ala Gly Asp Ser Phe Thr Trp His Asn Gly Lys Gln Phe
405 410 415
Thr Thr Leu Asp Arg Asp His Asp Val Tyr Thr Gly Asn Cys Ala His
420 425 430
Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu
435 440 445
Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg Tyr Gln Asp
450 455 460
Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser Leu Lys Lys
465 470 475 480
Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His
485 490

<210> 2953
<211> 1377
<212> DNA
<213> Homo sapiens

<400> 2953
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cgagctcgag cagccaaccc cgggcgcgtc ggggccatgg acggcctgag gcagcgcgtg
120
gagcacttcc tggagcaaag gaacctggtc accgaagtgc tgggggcgct ggaggccaag
180
accggggtgg agaagcggta tctggctgca ggagccgtca ctctgctaag cctgtatctg
240
ctgttcggct acggagcgtc tctgctgtgc aatctcatcg gatttgtgta ccccgcatat
300
gcctcaatca aagctatcga gagcccaagc aaggacgacg acactgtgtg gctcacctac
360
tgggtggtgt acgccctgtt tgggctggcc gagttcttca gcgatctact cctgtcctgg
420
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480
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540
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600
ataaccagga acgtcaagcc aagccagacc ccgcagccga aggacaagtg aagcagcccc
660
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720

ccacagagtc ttcagcgcat cccccaacag cagcccctgc cagtccctcg ggtccaggca
780
aggccctggg ggtctcctta aatgccacct cgggcaagtc ccagtcccag tcctcggcca
840
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960
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1020
tgcagccacc caacgtcacc tccagcccgg tctcacccat ggtccagtct cccagcagca
1080
gcaacatccc cacgcagccc cccagcaagt cctctggcaa gccggaggac gcagccccca
1140
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1200
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1260
agatcacctg cagctggcca caccacaggc ccccgtgcct gcagcactac tggtgcctga
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1377

<210> 2954
<211> 181
<212> PRT
<213> Homo sapiens

<400> 2954
Leu Arg Gln Arg Val Glu His Phe Leu Glu Gln Arg Asn Leu Val Thr
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Glu Val Leu Gly Ala Leu Glu Ala Lys Thr Gly Val Glu Lys Arg Tyr
20 25 30
Leu Ala Ala Gly Ala Val Thr Leu Leu Ser Leu Tyr Leu Leu Phe Gly
35 40 45
Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Val Tyr Pro Ala
50 55 60
Tyr Ala Ser Ile Lys Ala Ile Glu Ser Pro Ser Lys Asp Asp Asp Thr
65 70 75 80
Val Trp Leu Thr Tyr Trp Val Val Tyr Ala Leu Phe Gly Leu Ala Glu
85 90 95
Phe Phe Ser Asp Leu Leu Leu Ser Trp Phe Pro Phe Tyr Tyr Val Gly
100 105 110
Lys Cys Ala Phe Leu Leu Phe Cys Met Ala Pro Arg Pro Trp Asn Gly
115 120 125
Ala Leu Met Leu Tyr Gln Arg Val Val Arg Pro Leu Phe Leu Arg His
130 135 140
His Gly Ala Val Asp Arg Ile Met Asn Asp Leu Ser Gly Arg Ala Leu
145 150 155 160
Asp Ala Ala Ala Gly Ile Thr Arg Asn Val Lys Pro Ser Gln Thr Pro
165 170 175
Gln Pro Lys Asp Lys
180

<210> 2955
<211> 295
<212> DNA
<213> Homo sapiens

<400> 2955
acgcgtgaag gggtgagaat atgttttccc tggctcaact taccacacct caatgcctac
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agatgtgtta tcacctaact gttcacttgt ttctgtcatg tgttttcatg tccatttcac
120
aaggcatgcc ctgcccctgt ctcactttcc ccttattctg gcatatcaac tcgtatttcc
180
caatttccca ctataaaggg catacagtgc taccacttcc tctctcctcc aaaatagctt
240
ctccaccatt ctcactcatt atagggatta gcaagcaagc cgctgctcaa gccag
295

<210> 2956
<211> 91
<212> PRT
<213> Homo sapiens

<400> 2956
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Tyr His Leu Thr Val His Leu Phe Leu Ser Cys Val Phe Met Ser Ile
            20   25   30
Ser Gln Gly Met Pro Cys Pro Cys Leu Thr Phe Pro Leu Phe Trp His
        35   40   45
Ile Asn Ser Tyr Phe Pro Ile Ser His Tyr Lys Gly His Thr Val Leu
    50   55   60
Pro Leu Pro Leu Ser Ser Lys Ile Ala Ser Pro Pro Phe Ser Leu Ile
65   70   75   80
Ile Gly Ile Ser Lys Gln Ala Ala Ala Gln Ala
                85   90

<210> 2957
<211> 4724
<212> DNA
<213> Homo sapiens

<400> 2957
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gtgtggggtg ttggatgaag actgttgttc aattcagggg ccggtggggc tgagggtttc
120
tgtgggggaa gacctgatac cgccaggccc cgaagccctt caggagccag tcggtggggg
180
tcctcactta cagggtaaaa acggggtctc tgaggtgggc cctgaccagg aaacgctgag
240
ccgggacctc gcgtgattct cggaacccga ggagaagcgg cgtccggggc tatggctgtg
300
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360

ggagaagatg agtatgccaa cgttgatgcc attgttgtat cagtgggtgt tgatgaagaa
420
attgtttatg ccaaatcaac tgccttacag acatggctct ttggttatga actaactgat
480
actatcatgg tcttttgtga tgacaaaatc atctttatgg ccagcaagaa aaaagtggag
540
ttcttgaaac agattgccaa cactaagggc aatgagaatg ctaatggagc ccctgccatc
600
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660
gccattaaag aaagcaagaa tggcaagaag attggagtgt tcagcaaaga caaattccct
720
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Ser Thr Ala Leu Gln Thr Trp Leu Phe Gly Tyr Glu Leu Thr Asp Thr
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Ala Asn Gly Ala Pro Ala Ile Thr Leu Leu Ile Arg Glu Lys Asn Glu
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Ser Asn Lys Ser Ser Phe Asp Lys Met Ile Glu Ala Ile Lys Glu Ser
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Lys Asn Gly Lys Lys Ile Gly Val Phe Ser Lys Asp Lys Phe Pro Gly
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Glu Phe Met Lys Ser Trp Asn Asp Cys Leu Asn Lys Glu Gly Phe Asp
145                 150                 155                 160
Lys Ile Asp Ile Ser Ala Val Val Ala Tyr Thr Ile Ala Val Lys Glu
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Asp Gly Glu Leu Asn Leu Met Lys Lys Ala Ala Ser Ile Thr Ser Glu
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Val Phe Asn Lys Phe Phe Lys Glu Arg Val Met Glu Ile Val Asp Ala
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Asp Glu Lys Val Arg His Ser Lys Leu Ala Glu Ser Val Glu Lys Ala
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Ile Glu Glu Lys Lys Tyr Leu Ala Gly Ala Asp Pro Ser Thr Val Glu
225                 230                 235                 240
Met Cys Tyr Pro Pro Ile Ile Gln Ser Gly Gly Asn Tyr Asn Leu Lys
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Phe Ser Val Val Ser Asp Lys Asn His Met His Phe Gly Ala Ile Thr
            260                 265                 270
Cys Ala Met Gly Ile Arg Phe Lys Ser Tyr Cys Ser Asn Leu Val Arg
        275                 280                 285
Thr Leu Met Val Asp Pro Ser Gln Glu Val Gln Glu Asn Tyr Asn Phe
    290                 295                 300
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Lys Ile Cys Asp Val Tyr Asn Ala Val Met Asp Val Val Lys Lys Gln
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Gly Ile Glu Phe Arg Glu Gly Ser Leu Val Ile Asn Ser Lys Asn Gln
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Tyr Lys Leu Lys Lys Gly Met Val Phe Ser Ile Asn Leu Gly Phe Ser
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Asp Val Gln Phe Tyr Thr Glu Val Gly Glu Ile Thr Thr Asp Leu Gly
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Lys His Gln His Met His Asp Arg Asp Asp Leu Tyr Ala Glu Gln Met
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Ser Lys Lys Val Thr Met Ile Asn Ala Ile Pro Val Ala Ser Leu Asp
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Pro Ile Lys Glu Trp Leu Asn Ser Cys Asp Leu Lys Tyr Thr Glu Gly
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Lys Glu Ser Leu Gly Ser Glu Glu Glu Ser Gly Lys Asp Trp Asp Glu
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Leu Glu Glu Glu Ala Arg Lys Ala Asp Arg Glu Ser Arg Tyr Glu Glu
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Glu Glu Glu Gln Ser Arg Ser Met Ser Arg Lys Arg Lys Ala Ser Val
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Leu Glu Thr Leu Leu Arg Tyr Tyr Asp Gln Ile Cys Ser Ile Glu Pro
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Lys Phe Pro Phe Ser Glu Asn Gln Ile Cys Leu Thr Phe Thr Trp Lys
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Asp Ala Phe Asp Lys Gly Ser Leu Phe Gly Gly Ser Val Lys Leu Ala
100 105 110
Leu Ala Ser Leu Gly Tyr Glu Lys Ser Cys Val Leu Phe Asn Cys Ala
115 120 125
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Gly Thr Lys Phe Tyr Asn Glu Leu Thr Glu Ile Leu Val Arg Phe Gln
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Pro Thr Pro Pro Thr Pro Ala Pro Arg Thr Met Pro Pro Thr Lys Pro
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820 825 830
Tyr Pro Pro Val Tyr His Gln Ser Pro Gly Gln Ala Pro Tyr Pro Gly
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<210> 2961
<211> 434
<212> DNA
<213> Homo sapiens

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Gln Gln Leu Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala
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<212> DNA
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<211> 115
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<213> Homo sapiens

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65 70 75 80
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<211> 386
<212> PRT
<213> Homo sapiens

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Thr Arg Arg Tyr Tyr Lys Glu Lys Phe Gly Ile Thr Asp Leu Pro Arg
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Ile Asp Val Ser Lys Arg Glu Pro Pro Pro Val Lys Gln Glu Leu Pro
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Pro Tyr Asn Gly Phe Gly Leu Val Glu Asp Ser Ala Gln Asn Cys Phe
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Ala Leu Ile Pro Lys Ala Pro Lys Lys Asp Val Ile Lys Met Leu Val
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Asp Met Ile Ser Ile Phe Glu Pro Pro Val Arg Asn Ser Gly Ile Ile
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Tyr Val Leu Lys Tyr Met Glu Ser Asn Ala Ala Gln Tyr Ser Pro Glu
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Cys Lys Asp Asn Ile Arg Glu Ala Phe Gln Ile Tyr Asp Lys Glu Ala
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Ser Gly Tyr Val Asp Arg Asp Met Phe Phe Lys Ile Cys Glu Ser Leu
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Asn Val Pro Val Asp Asp Ser Leu Val Lys Glu Leu Leu Arg Met Cys
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<212> DNA
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<400> 2967
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<213> Homo sapiens

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Ile Ile Ala Val Val Leu Gly Val Ile Trp Gly Val Leu Pro Leu Arg
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Gly Phe Leu Gly Ile Ala Gly Phe Cys Leu Ile Asn Ala Gly Val Leu

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Tyr Leu Tyr Phe Ser Asn Tyr Leu Gln Ile Asp Glu Glu Glu Tyr Gly
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<212> PRT
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<210> 2972
<211> 632
<212> PRT

<213> Homo sapiens

<400> 2972

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Lys Lys Met Lys Arg Lys Phe Tyr Ser Trp Glu Glu Cys Met Asn Leu
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Arg Glu Val Lys Ser Leu Lys Lys Leu Asn His Ala Asn Val Val Lys
    50                  55                  60
Leu Lys Glu Val Ile Arg Glu Asn Asp His Leu Tyr Phe Ile Phe Glu
65                  70                  75                  80
Tyr Met Lys Glu Asn Leu Tyr Gln Leu Ile Lys Glu Arg Asn Lys Leu
                85                  90                  95
Phe Pro Glu Ser Ala Ile Arg Asn Ile Met Tyr Gln Ile Leu Gln Gly
            100                 105                 110
Leu Ala Phe Ile His Lys His Gly Phe Phe His Arg Asp Leu Lys Pro
        115                 120                 125
Glu Asn Leu Leu Cys Met Gly Pro Glu Leu Val Lys Ile Ala Asp Phe
    130                 135                 140
Gly Leu Ala Arg Glu Ile Arg Ser Lys Pro Pro Tyr Thr Asp Tyr Val
145                 150                 155                 160
Ser Thr Arg Trp Tyr Arg Ala Pro Glu Val Leu Leu Arg Ser Thr Asn
                165                 170                 175
Tyr Ser Ser Pro Ile Asp Val Trp Ala Val Gly Cys Ile Met Ala Glu
            180                 185                 190
Val Tyr Thr Leu Arg Pro Leu Phe Pro Gly Ala Ser Glu Ile Asp Thr
        195                 200                 205
Ile Phe Lys Ile Cys Gln Val Leu Gly Thr Pro Lys Lys Thr Asp Trp
    210                 215                 220
Pro Glu Gly Tyr Gln Leu Ser Ser Ala Met Asn Phe Arg Trp Pro Gln
225                 230                 235                 240
Cys Val Pro Asn Asn Leu Lys Thr Leu Ile Pro Asn Ala Ser Ser Glu
                245                 250                 255
Ala Val Gln Leu Leu Arg Asp Met Leu Gln Trp Asp Pro Lys Lys Arg
            260                 265                 270
Pro Thr Ala Ser Gln Ala Leu Arg Tyr Pro Tyr Phe Gln Val Gly His
        275                 280                 285
Pro Leu Gly Ser Thr Thr Gln Asn Leu Gln Asp Ser Glu Lys Pro Gln
    290                 295                 300
Lys Gly Ile Leu Glu Lys Ala Gly Pro Pro Pro Tyr Ile Lys Pro Val
305                 310                 315                 320
Pro Pro Ala Gln Pro Pro Ala Lys Pro His Thr Arg Ile Ser Ser Arg
                325                 330                 335
Gln His Gln Ala Ser Gln Pro Pro Leu His Leu Thr Tyr Pro Tyr Lys
            340                 345                 350
Ala Glu Val Ser Arg Thr Asp His Pro Ser His Leu Gln Glu Asp Lys
        355                 360                 365
Pro Ser Pro Leu Leu Phe Pro Ser Leu His Asn Lys His Pro Gln Ser
    370                 375                 380
Lys Ile Thr Ala Gly Leu Glu His Lys Asn Gly Glu Ile Lys Pro Lys
385                 390                 395                 400
Ser Arg Arg Arg Trp Gly Leu Ile Ser Arg Ser Thr Lys Asp Ser Asp
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420 425 430
Ile Asp Leu Lys Asn Lys Lys Arg Gln Ser Asp Asp Thr Leu Cys Arg
435 440 445
Phe Glu Ser Val Leu Asp Leu Lys Pro Ser Glu Pro Val Gly Thr Gly
450 455 460
Asn Ser Ala Pro Thr Gln Thr Ser Tyr Gln Arg Arg Asp Thr Pro Thr
465 470 475 480
Leu Arg Ser Ala Ala Lys Gln His Tyr Leu Lys His Ser Arg Tyr Leu
485 490 495
Pro Gly Ile Ser Ile Arg Asn Gly Ile Leu Ser Asn Pro Gly Lys Glu
500 505 510
Phe Ile Pro Pro Asn Pro Trp Ser Ser Ser Gly Leu Ser Gly Lys Ser
515 520 525
Ser Gly Thr Met Ser Val Ile Ser Lys Val Asn Ser Val Gly Ser Ser
530 535 540
Ser Thr Ser Ser Ser Gly Leu Thr Gly Asn Tyr Val Pro Ser Phe Leu
545 550 555 560
Lys Lys Glu Ile Gly Ser Ala Met Gln Arg Val His Leu Ala Pro Ile
565 570 575
Pro Asp Pro Ser Pro Gly Tyr Ser Ser Leu Lys Ala Met Arg Pro His
580 585 590
Pro Gly Arg Pro Phe Phe His Thr Gln Pro Arg Ser Thr Pro Gly Leu
595 600 605
Ile Pro Arg Pro Pro Ala Ala Gln Pro Val His Gly Arg Thr Asp Trp
610 615 620
Ala Ser Lys Tyr Ala Ser Arg Arg
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<211> 858
<212> DNA
<213> Homo sapiens

<400> 2973
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180
gcctactcct ctcatgaccc agaggcacta acgcgggaac tccaggagca tgtgaaaagg
240
gtgactgctc catacaaaac ccccaggaag gtggcctttg tttcagaact gccaaagacg
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gtttctggaa agatccaaag gagtaaattg cgaagtcagg agtgggggaa atgaggtgca
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420
gtccccatgg ggagcatcat ctcttcgacc ctaaagatgt caaaggtgtg cagcttccaa
480
acggcatccc caggatcact gggcaatgct ggaaagagca aaagaatatc attggccctg
540

atcacataga tgctgcgccg cctagcaaat gcttggtggt tcgacttctc cctctgtctg
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660
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720
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<210> 2974
<211> 117
<212> PRT
<213> Homo sapiens

<400> 2974
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35 40 45
Gly Glu Val Val Lys Ala Phe Ile Val Leu Thr Pro Ala Tyr Ser Ser
50 55 60
His Asp Pro Glu Ala Leu Thr Arg Glu Leu Gln Glu His Val Lys Arg
65 70 75 80
Val Thr Ala Pro Tyr Lys Thr Pro Arg Lys Val Ala Phe Val Ser Glu
85 90 95
Leu Pro Lys Thr Val Ser Gly Lys Ile Gln Arg Ser Lys Leu Arg Ser
100 105 110
Gln Glu Trp Gly Lys
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<210> 2975
<211> 1425
<212> DNA
<213> Homo sapiens

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acaccagaat cccagccaga tactccgcct ggcacccctc tggtgtccca agatgagaag
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agagatgctg agctgccgaa gaagcgtatg gggaagtcaa accccggctg ggagaacttg
240
gagaagttgc tagtgttcac cgcagctggg gtgaaaccgg ggnncaaggt ggctggcttt
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gatctggacg ggacgctcat caccacacgc tctgggaagg tctttcccac tggccccagt
360

gactggagga tcttgtaccc agagattccc cgtaagctcc gagagctgga agccgagggc
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<210> 2976
<211> 328
<212> PRT
<213> Homo sapiens

<400> 2976

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			20					25					30		
Thr	Leu	Arg	Trp	Glu	Glu	Thr	Arg	Thr	Pro	Glu	Ser	Gln	Pro	Asp	Thr
		35					40					45			
Pro	Pro	Gly	Thr	Pro	Leu	Val	Ser	Gln	Asp	Glu	Lys	Arg	Asp	Ala	Glu
	50					55					60				
Leu	Pro	Lys	Lys	Arg	Met	Gly	Lys	Ser	Asn	Pro	Gly	Trp	Glu	Asn	Leu
65					70					75					80
Glu	Lys	Leu	Leu	Val	Phe	Thr	Ala	Ala	Gly	Val	Lys	Pro	Gly	Xaa	Lys

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                85                  90                  95
Val Ala Gly Phe Asp Leu Asp Gly Thr Leu Ile Thr Thr Arg Ser Gly
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Lys Val Phe Pro Thr Gly Pro Ser Asp Trp Arg Ile Leu Tyr Pro Glu
        115                 120                 125
Ile Pro Arg Lys Leu Arg Glu Leu Glu Ala Glu Gly Tyr Lys Leu Val
    130                 135                 140
Ile Phe Thr Asn Gln Met Ser Ile Gly Arg Gly Lys Leu Pro Ala Glu
145                 150                 155                 160
Glu Phe Lys Ala Lys Val Glu Ala Val Val Glu Lys Leu Gly Val Pro
                165                 170                 175
Phe Gln Val Leu Val Ala Thr His Ala Gly Leu Tyr Arg Lys Pro Val
            180                 185                 190
Thr Gly Met Trp Asp His Leu Gln Glu Gln Ala Asn Asp Gly Thr Pro
        195                 200                 205
Ile Ser Ile Gly Asp Ser Ile Phe Val Gly Asp Ala Ala Gly Arg Pro
    210                 215                 220
Ala Asn Trp Ala Pro Gly Arg Lys Lys Lys Asp Phe Ser Cys Ala Asp
225                 230                 235                 240
Arg Leu Phe Ala Leu Asn Leu Gly Leu Pro Phe Ala Thr Pro Glu Glu
                245                 250                 255
Phe Phe Leu Lys Trp Pro Ala Ala Gly Phe Glu Leu Pro Ala Phe Asp
            260                 265                 270
Pro Arg Thr Val Ser Arg Ser Gly Pro Leu Cys Leu Pro Glu Ser Arg
        275                 280                 285
Ala Leu Leu Ser Ala Ser Pro Glu Val Val Val Ala Val Gly Phe Pro
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Tyr Val His Val Thr Gly Thr Arg
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<210> 2977
<211> 1420
<212> DNA
<213> Homo sapiens

<400> 2977

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480
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<210> 2978
<211> 369
<212> PRT
<213> Homo sapiens

<400> 2978
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35 40 45
Ala His Val Asp Val Gln Thr Leu Ser Ser Gln Leu Ala Val Thr Val
50 55 60
Gly Pro Gly Glu Arg Arg Ile Gly Pro Gly Glu Pro Leu Glu Leu Leu
65 70 75 80
Cys Asn Val Ser Gly Ala Leu Pro Pro Ala Gly Arg His Ala Ala Tyr
85 90 95
Ser Val Gly Trp Glu Met Ala Pro Ala Gly Ala Pro Gly Pro Gly Arg
100 105 110
Leu Val Ala Gln Leu Asp Thr Glu Gly Val Gly Ser Leu Xaa Ala Leu

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        115                 120                 125
Ala Met Arg Ala Asp Xaa Ile Ala Met Glu Lys Val Ala Ser Arg Thr
    130                 135                 140
Tyr Arg Leu Arg Leu Glu Ala Ala Arg Pro Gly Asp Ala Gly Thr Tyr
145                 150                 155                 160
Arg Cys Leu Ala Lys Ala Tyr Val Arg Gly Ser Gly Thr Arg Leu Arg
                165                 170                 175
Glu Ala Ala Ser Ala Arg Ser Arg Pro Leu Pro Val His Val Arg Glu
            180                 185                 190
Glu Gly Val Val Leu Glu Ala Val Ala Trp Leu Ala Gly Gly Thr Val
        195                 200                 205
Tyr Arg Gly Glu Thr Ala Ser Leu Leu Cys Asn Ile Ser Val Arg Gly
    210                 215                 220
Gly Pro Pro Gly Leu Arg Leu Ala Ala Ser Trp Trp Val Glu Arg Pro
225                 230                 235                 240
Glu Asp Gly Glu Leu Ser Ser Val Pro Ala Gln Leu Val Gly Gly Val
                245                 250                 255
Gly Gln Asp Gly Val Ala Glu Leu Gly Val Arg Pro Gly Gly Gly Pro
            260                 265                 270
Val Ser Val Glu Leu Val Gly Pro Arg Ser His Arg Leu Arg Leu His
        275                 280                 285
Ser Leu Gly Pro Glu Asp Glu Gly Val Tyr His Cys Ala Pro Ser Ala
    290                 295                 300
Trp Val Gln His Ala Asp Tyr Ser Trp Tyr Gln Ala Gly Ser Ala Arg
305                 310                 315                 320
Ser Gly Pro Val Thr Val Tyr Pro Tyr Met His Ala Leu Asp Thr Leu
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Phe Val Pro Leu Leu Val Gly Thr Gly Val Ala Leu Val Thr Gly Ala
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Thr Val Leu Gly Thr Ile Thr Cys Cys Phe Met Lys Arg Leu Arg Lys
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<210> 2979
<211> 2191
<212> DNA
<213> Homo sapiens

<400> 2979

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420
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1860
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1980
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2040

ccagcagccg cgcaggtttc cccactggct gcaatggccc taccaaaagc catgttgcat
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2191

<210> 2980
<211> 140
<212> PRT
<213> Homo sapiens

<400> 2980
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20 25 30
Gly Thr Glu His Gly Gln Pro Phe Ala Arg Gly Trp Gly Ala Trp Gly
35 40 45
Asn Ala Arg Arg Ala Arg Val Gly Arg Ala Glu Cys Leu Leu Ser Gly
50 55 60
Arg Pro Pro Thr Ala Val Leu Pro Arg Leu Val Glu Asn Leu Lys Ala
65 70 75 80
Arg Val Pro Val Pro Gly His Thr Glu Pro Leu Trp Ser Glu Gly Thr
85 90 95
Ala Pro Gly Gln Gly Leu Trp Ser His Ala Pro Ala Asp Gly Ser Leu
100 105 110
Met Asn Leu Ile Arg Thr Leu Val Gly Ala Val Val Phe Glu Leu Leu
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Ser Met Cys Phe Gly Asp Gly Ala Gly Ala Ala Cys
130 135 140

<210> 2981
<211> 617
<212> DNA
<213> Homo sapiens

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ccggagcagg aggctgccga ggcagattta tccaatatgg aaagggtatc tctctcgacg
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gcagaccccc aaggagtgac ctatgctgag ctaagcacca gcgccctgtc tgaggcagct
420
tcagacacca cccaggagcc cccaggatct catgaatatg cggcactgaa agtgtagcaa
480

gaagacagcc ctggccacta aaagaggggg gatcgtgctg gccaaggtta tcggaaatct
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<210> 2982
<211> 107
<212> PRT
<213> Homo sapiens

<400> 2982
Lys Gln Thr Pro Glu Pro Ser Leu Ser Pro Ser Ser Ala Ala Ser Pro
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Ser Phe Ser Ser Ser Ser Gln Ser Ser Ser Ser Thr Asp Ala Xaa Gln
20 25 30
His Ser Ser Ser Ser Glu Glu Ser Thr Lys Arg Thr Ser His Ser Lys
35 40 45
Leu Pro Glu Gln Glu Ala Ala Glu Ala Asp Leu Ser Asn Met Glu Arg
50 55 60
Val Ser Leu Ser Thr Ala Asp Pro Gln Gly Val Thr Tyr Ala Glu Leu
65 70 75 80
Ser Thr Ser Ala Leu Ser Glu Ala Ala Ser Asp Thr Thr Gln Glu Pro
85 90 95
Pro Gly Ser His Glu Tyr Ala Ala Leu Lys Val
100 105

<210> 2983
<211> 614
<212> DNA
<213> Homo sapiens

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120
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180
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240
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300
cgtgcagtgg ccgagggttt tctgctggtc tattccatca cagactatga cagctacttg
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420
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480
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600

agtggggaaa gaag
614

<210> 2984
<211> 204
<212> PRT
<213> Homo sapiens

<400> 2984
Arg Pro Leu Ser Met Ser Gly His Phe Leu Leu Ala Pro Ile Pro Glu
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Ser Ser Ser Asp Tyr Leu Leu Pro Lys Asp Ile Lys Leu Ala Val Leu
20 25 30
Gly Ala Gly Arg Val Gly Lys Ser Ala Met Ile Val Arg Phe Leu Thr
35 40 45
Lys Arg Phe Ile Gly Asp Tyr Glu Pro Asn Thr Gly Lys Leu Tyr Ser
50 55 60
Arg Leu Val Tyr Val Glu Gly Asp Gln Leu Ser Leu Gln Ile Gln Asp
65 70 75 80
Thr Pro Gly Gly Val Gln Ile Gln Asp Ser Leu Pro Gln Val Val Asp
85 90 95
Ser Leu Gln Met Arg Ala Val Ala Glu Gly Phe Leu Leu Val Tyr Ser
100 105 110
Ile Thr Asp Tyr Asp Ser Tyr Leu Ser Ile Arg Pro Leu Tyr Gln His
115 120 125
Ile Arg Lys Val His Pro Asp Ser Lys Ala Pro Val Ile Ile Val Gly
130 135 140
Asn Lys Gly Asp Leu Leu His Ala Arg Gln Val Gln Thr Gln Asp Gly
145 150 155 160
Ile Gln Leu Ala Asn Glu Leu Gly Ser Leu Phe Leu Glu Ile Ser Thr
165 170 175
Ser Glu Asn Tyr Glu Asp Val Cys Asp Val Phe Gln His Leu Cys Lys
180 185 190
Glu Val Ser Lys Met His Gly Leu Ser Gly Glu Arg
195 200

<210> 2985
<211> 4547
<212> DNA
<213> Homo sapiens

<400> 2985
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300
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360

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1980

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<210> 2986
<211> 988
<212> PRT
<213> Homo sapiens

<400> 2986
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Gln Glu Val Phe Lys Pro Glu Asn Ile Ser Leu Arg Asn Lys Leu Arg
20 25 30
Glu Leu Cys Val Lys Leu Met Phe Leu His Pro Val Asp Tyr Gly Arg
35 40 45
Lys Ala Glu Glu Leu Leu Trp Arg Lys Val Tyr Tyr Glu Val Ile Gln
50 55 60
Leu Ile Lys Thr Asn Lys Lys His Ile His Ser Arg Ser Thr Leu Glu
65 70 75 80
Cys Ala Tyr Arg Thr His Leu Val Ala Gly Ile Gly Phe Tyr Gln His
85 90 95
Leu Leu Leu Tyr Ile Gln Ser His Tyr Gln Leu Glu Leu Gln Cys Cys
100 105 110
Ile Asp Trp Thr His Val Thr Asp Pro Leu Ile Gly Cys Lys Lys Pro

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        115                 120                 125
Val Ser Ala Ser Gly Lys Glu Met Asp Trp Ala Gln Met Ala Cys His
    130                 135                 140
Arg Cys Leu Val Tyr Leu Gly Asp Leu Ser Arg Tyr Gln Asn Glu Leu
145                 150                 155                 160
Ala Gly Val Asp Thr Glu Leu Leu Ala Glu Arg Phe Tyr Tyr Gln Ala
                165                 170                 175
Leu Ser Val Ala Pro Gln Ile Gly Met Pro Phe Asn Gln Leu Gly Thr
            180                 185                 190
Leu Ala Gly Ser Lys Tyr Tyr Asn Val Glu Ala Met Tyr Cys Tyr Leu
        195                 200                 205
Arg Cys Ile Gln Ser Glu Val Ser Phe Glu Gly Ala Tyr Gly Asn Leu
    210                 215                 220
Lys Arg Leu Tyr Asp Lys Ala Ala Lys Met Tyr His Gln Leu Lys Lys
225                 230                 235                 240
Cys Glu Thr Arg Lys Leu Ser Pro Gly Lys Lys Arg Cys Lys Asp Ile
                245                 250                 255
Lys Arg Leu Leu Val Asn Phe Met Tyr Leu Gln Ser Leu Leu Gln Pro
            260                 265                 270
Lys Ser Ser Ser Val Asp Ser Glu Leu Thr Ser Leu Cys Gln Ser Val
        275                 280                 285
Leu Glu Asp Phe Asn Leu Cys Leu Phe Tyr Leu Pro Ser Ser Pro Asn
    290                 295                 300
Leu Ser Leu Ala Ser Glu Asp Glu Glu Glu Tyr Glu Ser Gly Tyr Ala
305                 310                 315                 320
Phe Leu Pro Asp Leu Leu Ile Phe Gln Met Val Ile Ile Cys Leu Met
                325                 330                 335
Cys Val His Ser Leu Glu Arg Ala Gly Ser Lys Gln Tyr Ser Ala Ala
            340                 345                 350
Ile Ala Phe Thr Leu Ala Leu Phe Ser His Leu Val Asn His Val Asn
        355                 360                 365
Ile Arg Leu Gln Ala Glu Leu Glu Glu Gly Glu Asn Pro Val Pro Ala
    370                 375                 380
Phe Gln Ser Asp Gly Thr Asp Glu Pro Glu Ser Lys Glu Pro Val Glu
385                 390                 395                 400
Lys Glu Glu Glu Pro Asp Pro Glu Pro Pro Pro Val Thr Pro Gln Val
                405                 410                 415
Gly Glu Gly Arg Lys Ser Arg Lys Phe Ser Arg Leu Ser Cys Leu Arg
            420                 425                 430
Arg Arg Arg His Pro Pro Lys Val Gly Asp Asp Ser Asp Leu Ser Glu
        435                 440                 445
Gly Phe Glu Ser Asp Ser Ser His Asp Ser Ala Arg Ala Ser Glu Gly
    450                 455                 460
Ser Asp Ser Gly Ser Asp Lys Ser Leu Glu Gly Gly Gly Thr Ala Phe
465                 470                 475                 480
Asp Ala Glu Thr Asp Ser Glu Met Asn Ser Gln Glu Ser Arg Ser Asp
                485                 490                 495
Leu Glu Asp Met Glu Glu Glu Glu Gly Thr Arg Ser Pro Thr Leu Glu
            500                 505                 510
Pro Pro Arg Gly Arg Ser Glu Ala Pro Asp Ser Leu Asn Gly Pro Leu
        515                 520                 525
Gly Pro Ser Glu Ala Ser Ile Ala Ser Asn Leu Gln Ala Met Ser Thr
    530                 535                 540
Gln Met Phe Gln Thr Lys Arg Cys Phe Arg Leu Ala Pro Thr Phe Ser
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Asn Leu Leu Leu Gln Pro Thr Thr Asn Pro His Thr Ser Ala Ser His
                565                 570                 575
Arg Pro Cys Val Asn Gly Asp Val Asp Lys Pro Ser Glu Pro Ala Ser
            580                 585                 590
Glu Glu Gly Ser Glu Ser Glu Gly Ser Glu Ser Ser Gly Arg Ser Cys
        595                 600                 605
Arg Asn Glu Arg Ser Ile Gln Glu Lys Leu Gln Val Leu Met Ala Glu
    610                 615                 620
Gly Leu Leu Pro Ala Val Lys Val Phe Leu Asp Trp Leu Arg Thr Asn
625                 630                 635                 640
Pro Asp Leu Ile Ile Val Cys Ala Gln Ser Ser Gln Ser Leu Trp Asn
                645                 650                 655
Arg Leu Ser Val Leu Leu Asn Leu Leu Pro Ala Ala Gly Glu Leu Gln
            660                 665                 670
Glu Ser Gly Leu Ala Leu Cys Pro Glu Val Gln Asp Leu Leu Glu Gly
        675                 680                 685
Cys Glu Leu Pro Asp Leu Pro Ser Ser Leu Leu Leu Pro Glu Asp Met
    690                 695                 700
Ala Leu Arg Asn Leu Pro Pro Leu Arg Ala Ala His Arg Arg Phe Asn
705                 710                 715                 720
Phe Asp Thr Asp Arg Pro Leu Leu Ser Thr Leu Glu Glu Ser Val Val
                725                 730                 735
Arg Ile Cys Cys Ile Arg Ser Phe Gly His Phe Ile Ala Arg Leu Gln
            740                 745                 750
Gly Ser Ile Leu Gln Phe Asn Pro Glu Val Gly Ile Phe Val Ser Ile
        755                 760                 765
Ala Gln Ser Glu Gln Glu Ser Leu Leu Gln Gln Ala Gln Ala Gln Phe
    770                 775                 780
Arg Met Ala Gln Glu Glu Ala Arg Arg Asn Arg Leu Met Arg Asp Met
785                 790                 795                 800
Ala Gln Leu Arg Leu Gln Leu Glu Val Ser Gln Leu Glu Gly Ser Leu
                805                 810                 815
Gln Gln Pro Lys Ala Gln Ser Ala Met Ser Pro Tyr Leu Val Pro Asp
            820                 825                 830
Thr Gln Ala Leu Cys His His Leu Pro Val Ile Arg Gln Leu Ala Thr
        835                 840                 845
Ser Gly Arg Phe Ile Val Ile Ile Pro Arg Thr Val Ile Asp Gly Leu
    850                 855                 860
Asp Leu Leu Lys Lys Glu His Pro Gly Ala Arg Asp Gly Ile Arg Tyr
865                 870                 875                 880
Leu Glu Ala Glu Phe Lys Lys Gly Asn Arg Tyr Ile Arg Cys Gln Lys
                885                 890                 895
Glu Val Gly Lys Ser Phe Glu Arg His Lys Leu Lys Arg Gln Asp Ala
            900                 905                 910
Asp Ala Trp Thr Leu Tyr Lys Ile Leu Asp Ser Cys Lys Gln Leu Thr
        915                 920                 925
Leu Ala Gln Gly Ala Gly Glu Glu Asp Pro Ser Gly Met Val Thr Ile
    930                 935                 940
Ile Thr Gly Leu Pro Leu Asp Asn Pro Ser Val Leu Ser Gly Pro Met
945                 950                 955                 960
Gln Ala Ala Leu Gln Ala Ala Ala His Ala Ser Val Asp Ile Lys Asn
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Val Leu Asp Phe Tyr Lys Gln Trp Lys Glu Ile Gly
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980 985

<210> 2987
<211> 1016
<212> DNA
<213> Homo sapiens

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120
gaaaggcggt cctgaaattc acaggggaga gcggatattc caggaggcag tctaagttat
180
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240
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300
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900
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1016

<210> 2988
<211> 95
<212> PRT
<213> Homo sapiens

<400> 2988
Trp Ser Leu Thr Leu Ser Pro Arg Leu Glu Cys Ser Gly Thr Ile Ser
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Ala His Cys Lys Leu His Leu Pro Gly Ser His His Pro Pro Ala Ser
20 25 30
Ala Ser Arg Val Ala Gly Thr Thr Gly Thr Arg His Asn Ala Arg Leu

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        35                  40                  45
Phe Phe Val Phe Leu Val Glu Met Gly Phe His Tyr Val Ser Gln Asp
    50                  55                  60
Gly Leu Asp Leu Leu Thr Ser Leu Leu Ala Xaa Leu Arg Leu Pro Lys
65                  70                  75                  80
Cys Trp Asn Tyr Xaa Arg Glu Thr Pro Arg Leu Val Ser Ile Lys
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<210> 2989
<211> 1185
<212> DNA
<213> Homo sapiens

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720
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780
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840
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900
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960
ttatttacac cctgtttgtg aagtggctgt gttcaccctg ggtggacacg gaatgttttt
1020
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1080
agctttttgt atctgtaggt ttaatatctg tgtatgtaag caaacttgga tgcaaaatat
1140
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1185

<210> 2990
<211> 114
<212> PRT
<213> Homo sapiens

<400> 2990
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1 5 10 15
Lys Ser Leu Glu Leu Val Ser Phe Glu Glu Val Ala Val His Phe Thr
20 25 30
Trp Glu Glu Trp Gln Asp Leu Asp Asp Ala Gln Arg Thr Leu Tyr Arg
35 40 45
Asp Val Met Leu Glu Thr Tyr Ser Ser Leu Val Ser Leu Gly His Cys
50 55 60
Ile Thr Lys Pro Glu Met Ile Phe Lys Leu Glu Gln Gly Ala Glu Pro
65 70 75 80
Trp Ile Val Glu Glu Thr Leu Asn Leu Arg Leu Ser Gly Gly Ser Lys
85 90 95
Lys Gln Val Phe Ser Gly Ile Cys His Arg Ser Leu Val Glu Leu Gln
100 105 110
Glu Val

<210> 2991
<211> 980
<212> DNA
<213> Homo sapiens

<400> 2991
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120
ttggtgggct ccagctgacc cctccagagc ccctgagtgg tggcggtctg cagtcctcag
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240
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360
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420
agcgtttcct tcatgccgcc attcatcact gtctcagtta ccttgtctgt actttctgca
480
tcctcctctc cgtcagagct ggcttccatg gccacactgc ctgccgcttc tggctgcact
540
gccagggcag ccgcactggg agtcagaggg tccatgggtt cagtgctggt ttccatttcc
600
actggagaat tactccttaa agaatctttt gtgctttctc agggaagagt gaactctgaa
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aaagaagccc agcccgtctc tttagttggc atcggctcct ctgtgctcca gacatcagat
720

cccacagaat ccaatggagc accgtgggtt gtttccattg ggacatcaaa gttagctgac
780
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catatatctt cctcatcaga
980

<210> 2992
<211> 64
<212> PRT
<213> Homo sapiens

<400> 2992
Val Val Ala Val Cys Ser Pro Gln Ser Ala Ala Ala Asp Val Thr Arg
1 5 10 15
His Thr Gly Pro Phe Thr Glu Val Ser Pro Gly Ala Leu Gly Trp Pro
20 25 30
Val Leu Cys Ser Gly Leu Leu Leu Gly Gly Leu Gly Ala Ala His Phe
35 40 45
Ala Ser Ala Val Ser Gly His Ser Ser Ala Ser Leu Gln Ala Ala Ser
50 55 60

<210> 2993
<211> 687
<212> DNA
<213> Homo sapiens

<400> 2993
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120
cgatacctca agtttgacat cgagattgga cgtggctcct tcaagacggt gtatcgaggg
180
ctagacaccg acaccacagt ggaggtggcc tggtgtgagc tgcagactcg gaaactgtct
240
agagctgagc ggcagcgctt ctcagaggag gtggagatgc tcaaggggct gcagcacccc
300
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360
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420
atgaagccgc gggtccttca gcgctggagc cgccaaatcc tgcggggact tcatttccta
480
cactcccggg ttcctcccat cctgcaccgg gatctcaagt gcgacaatgt ctttatcacg
540
ggacctactg gctctgtcaa aatcggggac ctgggcctgg ccacgctcaa gcgcgcctcc
600
tttgccaaga gtgtcatcgg gaccccggaa ttcatggccc ccgagatgta cgaggaaaag
660

tacgatgagg ccgtggacgt gtacgcg
687

<210> 2994
<211> 229
<212> PRT
<213> Homo sapiens

<400> 2994
Xaa Cys Pro Arg Ser Arg Glu Pro Leu Met Val Thr Glu Ala Val Ala
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Leu Glu Arg Arg Arg Glu Gln Glu Glu Lys Glu Asp Met Glu Thr Gln
20 25 30
Ala Val Ala Thr Ser Pro Asp Gly Arg Tyr Leu Lys Phe Asp Ile Glu
35 40 45
Ile Gly Arg Gly Ser Phe Lys Thr Val Tyr Arg Gly Leu Asp Thr Asp
50 55 60
Thr Thr Val Glu Val Ala Trp Cys Glu Leu Gln Thr Arg Lys Leu Ser
65 70 75 80
Arg Ala Glu Arg Gln Arg Phe Ser Glu Glu Val Glu Met Leu Lys Gly
85 90 95
Leu Gln His Pro Asn Ile Val Arg Phe Tyr Asp Ser Trp Lys Ser Val
100 105 110
Leu Arg Gly Gln Val Cys Ile Val Leu Val Thr Glu Leu Met Thr Ser
115 120 125
Gly Thr Leu Lys Thr Tyr Leu Arg Arg Phe Arg Glu Met Lys Pro Arg
130 135 140
Val Leu Gln Arg Trp Ser Arg Gln Ile Leu Arg Gly Leu His Phe Leu
145 150 155 160
His Ser Arg Val Pro Pro Ile Leu His Arg Asp Leu Lys Cys Asp Asn
165 170 175
Val Phe Ile Thr Gly Pro Thr Gly Ser Val Lys Ile Gly Asp Leu Gly
180 185 190
Leu Ala Thr Leu Lys Arg Ala Ser Phe Ala Lys Ser Val Ile Gly Thr
195 200 205
Pro Glu Phe Met Ala Pro Glu Met Tyr Glu Glu Lys Tyr Asp Glu Ala
210 215 220
Val Asp Val Tyr Ala
225

<210> 2995
<211> 1879
<212> DNA
<213> Homo sapiens

<400> 2995
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taataaaatt aagcagtcaa aagaagtagc aaaaacaaga tagtcattca tatatacaga
120
acatatagat tcatttctag ttgattcaat cctatttatg tatttaaaat acaaaataat
180
ggccatctgg ctagttccaa cggtagagca tgagactctt aaaatacaaa atacatctta
240

atgtgtcaag aagaccacag ttagcaccag gaaaggaact ttactttagc ttctgattac
300
ttttttattt ttatttttac tttattatta ttattattat ttttgagatg gagtctcact
360
ctgntcaccc aggctggaat acagtggtgt gatctcagct cactgcaacc tccacctccc
420
aggttcaagc gattctcctg cctcagcctc ctgagtagct gggactctga tagatgcctg
480
ccaccacacc cgggtgattt ttgtattttt agtagagacg gggtttcgcc atgttgctca
540
ggctggtctc gaactcccga cctcaagtga cttgctcacc ttggcctccc aaagtgctgg
600
gattacaggt gtgagccact gcacccagcc tggcagtcaa ttttaagcct cctatttccc
660
aggttttagc ttaataatcc tcattagttt ttcagatttt tgtcagtctt gttttggggc
720
tattttgcct tagtgggcct aaacagaata ttaaaatata ttaataatcc atactgagag
780
tagagtataa atgggtttct cactccttag ggacacgagt ggaaacaata catcccatga
840
acacaggtga atgtccctgg ttatccctga gctgggcagt ttcacacaat catttttttct
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ctgaggccaa agtctgtggt ttgatcatct tagcagcttc cagaacagaa agtaggttta
960
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1020
ccacgaaaac tcccccaagg atgaagcctt ctccttccag gtttccagag aagcctccgt
1080
tccaggctcg gaagaagttg taccacactc ccagacggat aaatcccata aacatcatct
1140
tccgcctttg tggaccatag aacttttttct tttcatccag gaagatttct cctttgaaat
1200
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1320
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1440
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1500
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1560
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1620
cgcccgggcg ctaaggggcc aaaccgcccg gcccggaggg tcccaggggc gggccccgga
1680
gtacctggag gatatagacc tgaaaacact ggagaaggaa ccaaggactt tcaaagcaaa
1740
ggagctatgg gaaaaaaatg gagctgtgat tatggccgtg cggaggccag gctgtttcct
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1860

ccccctctat gcagtggta
1879

<210> 2996
<211> 101
<212> PRT
<213> Homo sapiens

<400> 2996
His Gln Glu Arg Asn Phe Thr Leu Ala Ser Asp Tyr Phe Phe Ile Phe
1 5 10 15
Ile Phe Thr Leu Leu Leu Leu Leu Leu Phe Leu Arg Trp Ser Leu Thr
20 25 30
Leu Xaa Thr Gln Ala Gly Ile Gln Trp Cys Asp Leu Ser Ser Leu Gln
35 40 45
Pro Pro Pro Pro Arg Phe Lys Arg Phe Ser Cys Leu Ser Leu Leu Ser
50 55 60
Ser Trp Asp Ser Asp Arg Cys Leu Pro Pro His Pro Gly Asp Phe Cys
65 70 75 80
Ile Phe Ser Arg Asp Gly Val Ser Pro Cys Cys Ser Gly Trp Ser Arg
85 90 95
Thr Pro Asp Leu Lys
100

<210> 2997
<211> 800
<212> DNA
<213> Homo sapiens

<400> 2997
actcagatgg gcaccatcag tgctagacaa gaattctatt cctcttatcc aggcctccca
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gagccatcca aagtgacatc tccagtggtc acctcttcca ccataaaaga cattgtttct
120
acaaccatac ctgcttcctc tgagataaca agaattgaga tggagtcaac atccaccctg
180
acccccacac caagggagac cagcacctcc caggagatcc actcagccac aaagccaagc
240
actgttcctt acaaggcact cactagtgcc acgattgagg actccatgac acaagtcatg
300
tcctctagca gaggacctag ccctgatcag tccacaatgt cacaagacat atccactgaa
360
gtgatcacca ggctctctac ctcccccatc aagacagaat ctacagaaat gaccattacc
420
acccaaacag ggtctcctgg ggctacatca aggggtaccc ttaccttgga cacttcaaca
480
acttttatgt cagggaccca ctcaactgca tctcaaagat tttcacactc acagatgacc
540
gctcttatga gtagaactcc tggagatgtg ccatggctaa cccatccctc tggggaagag
600
cccgcctctg cctctttctc actggcttca cctgtcttga cctcattttt ttcgtttttt
660
gcccattccc aaaaacctcc acctttttttg gttcctgggc aaacttttc cctagggctg
720

gggaaaccca aaatgtgggg ccaacccaga actgaaacat tccccccaat ggacaacctt
780
tttgaaaagg gccccttttgc
800

<210> 2998
<211> 266
<212> PRT
<213> Homo sapiens

<400> 2998
Thr Gln Met Gly Thr Ile Ser Ala Arg Gln Glu Phe Tyr Ser Ser Tyr
1 5 10 15
Pro Gly Leu Pro Glu Pro Ser Lys Val Thr Ser Pro Val Val Thr Ser
20 25 30
Ser Thr Ile Lys Asp Ile Val Ser Thr Thr Ile Pro Ala Ser Ser Glu
35 40 45
Ile Thr Arg Ile Glu Met Glu Ser Thr Ser Thr Leu Thr Pro Thr Pro
50 55 60
Arg Glu Thr Ser Thr Ser Gln Glu Ile His Ser Ala Thr Lys Pro Ser
65 70 75 80
Thr Val Pro Tyr Lys Ala Leu Thr Ser Ala Thr Ile Glu Asp Ser Met
85 90 95
Thr Gln Val Met Ser Ser Ser Arg Gly Pro Ser Pro Asp Gln Ser Thr
100 105 110
Met Ser Gln Asp Ile Ser Thr Glu Val Ile Thr Arg Leu Ser Thr Ser
115 120 125
Pro Ile Lys Thr Glu Ser Thr Glu Met Thr Ile Thr Thr Gln Thr Gly
130 135 140
Ser Pro Gly Ala Thr Ser Arg Gly Thr Leu Thr Leu Asp Thr Ser Thr
145 150 155 160
Thr Phe Met Ser Gly Thr His Ser Thr Ala Ser Gln Arg Phe Ser His
165 170 175
Ser Gln Met Thr Ala Leu Met Ser Arg Thr Pro Gly Asp Val Pro Trp
180 185 190
Leu Thr His Pro Ser Gly Glu Glu Pro Ala Ser Ala Ser Phe Ser Leu
195 200 205
Ala Ser Pro Val Leu Thr Ser Phe Phe Ser Phe Phe Ala His Ser Gln
210 215 220
Lys Pro Pro Pro Phe Leu Val Pro Gly Gln Thr Phe Ser Leu Gly Leu
225 230 235 240
Gly Lys Pro Lys Met Trp Gly Gln Pro Arg Thr Glu Thr Phe Pro Pro
245 250 255
Met Asp Asn Leu Phe Glu Lys Gly Pro Phe
260 265

<210> 2999
<211> 550
<212> DNA
<213> Homo sapiens

<400> 2999
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acccccttgc cactttggcc ccctccaggc tttgggcact gacaagcatg ggaaggaggc
120
tgaggggtgc actgaggaca gcccagtgct ggcctgcagg caccccttaa catgaacagc
180
ctggtcacca tgaacagcag caggaggcag acaggctcct gggtggaaag aagctggtcc
240
acagtgaaga cccacctcca agccagggaa agcctgaagc ctgggggatg ggtcgccagt
300
cccagaaacc gcaagggcaa cttgtggtgc ttttccctgg gcccacccat ggccgcccat
360
ggacgaattg gcatgcactt tctcccctct gaggcccata aaagcccctg ggctcagcca
420
gagctgagcg gatatcagga cgacaagctg cacagaggta ctacccatac caaggcctcc
480
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540
cagggtctcc
550

<210> 3000
<211> 167
<212> PRT
<213> Homo sapiens

<400> 3000
Met Cys Ser Ser Gln Gln Arg Gly Gly Leu Gly Met Gly Ser Thr Ser
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Val Gln Leu Val Val Leu Ile Ser Ala Gln Leu Trp Leu Ser Pro Gly
            20   25   30
Ala Phe Met Gly Leu Arg Gly Glu Lys Val His Ala Asn Ser Ser Met
        35   40   45
Gly Gly His Gly Trp Ala Gln Gly Lys Ala Pro Gln Val Ala Leu Ala
    50   55   60
Val Ser Gly Thr Gly Asp Pro Ser Pro Arg Leu Gln Ala Phe Pro Gly
65   70   75   80
Leu Glu Val Gly Leu His Cys Gly Pro Ala Ser Phe His Pro Gly Ala
                85   90   95
Cys Leu Pro Pro Ala Ala Val His Gly Asp Gln Ala Val His Val Lys
            100   105   110
Gly Cys Leu Gln Ala Ser Thr Gly Leu Ser Ser Val His Pro Ser Ala
        115   120   125
Ser Phe Pro Cys Leu Ser Val Pro Lys Ala Trp Arg Gly Pro Lys Trp
    130   135   140
Gln Gly Gly Trp His Val Ser Thr Thr Pro Ser Met Cys Thr Leu Ser
145   150   155   160
Trp Ala Val Thr Ala Pro Gly
                165

<210> 3001
<211> 1092
<212> DNA
<213> Homo sapiens

<400> 3001

agatctttgt gaggcctgaa tgaaatggcc ccattcagaa ttccccagga tgtcatccat
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aatagctctg cctggctgag tttgaaaggt cactgttctg tttcagcgtt gagatgcctt
120
gaagtacaga ggttgagccc ctatgtatgc ctgggggagt cccagaaagt ggaatcccaa
180
ccttgctcag ctcaccagtg tttcttctat aacccagaca ttgcaaagac agcagtaccc
240
actgaggcat ccagcccagc tcaggccctg ccacccnnca gtaccaaagc atcattgtca
300
ggcaagggat acagaacaca gtgctctcac cagactgcag cttgggggac acccagcacg
360
gagagaagct gaggcggaac tgcactatct accggccctg gttctccccc tacagctact
420
tcgtgtgtgc agacaaagag agccagctgg aggcctatga cttcccagag gtgcagcagg
480
atgagggcaa gtgggacaac tgcctttctg aggacatggc tgagaacatc tgttcgtcct
540
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600
actccatcac atcccaggac atcctaatgg cttccaggtg gcacccagca cagcagaatg
660
gctacaagtg cgtggcctgc tgccgcatgt accccaccct ggacttcctc aagagccaca
720
tcaagagggg cttcagggag ggcttcagct gcaaggtgta ctaccgcaag ctcaaagccc
780
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840
ccttcaatag tcctgctgaa caccttaggc aaattggcgg tgaagcctac ttatgtctct
900
agagagatgc caataaagtt agtcacagcc ttctgtccag tctgaggtca ccccgcacag
960
cctgctgtcc ttcccagaac ccggctctca tcacctttgg ctaatggttg cctagcaaca
1020
ccaggcacac accctcccct ttctctcttt taaaaataaa gacaatactt gaagtttggg
1080
aaaatcaaaa aa
1092

<210> 3002
<211> 115
<212> PRT
<213> Homo sapiens

<400> 3002
Met Ala Pro Phe Arg Ile Pro Gln Asp Val Ile His Asn Ser Ser Ala
1 5 10 15
Trp Leu Ser Leu Lys Gly His Cys Ser Val Ser Ala Leu Arg Cys Leu
20 25 30
Glu Val Gln Arg Leu Ser Pro Tyr Val Cys Leu Gly Glu Ser Gln Lys
35 40 45
Val Glu Ser Gln Pro Cys Ser Ala His Gln Cys Phe Phe Tyr Asn Pro
50 55 60
Asp Ile Ala Lys Thr Ala Val Pro Thr Glu Ala Ser Ser Pro Ala Gln

65 70 75 80
Ala Leu Pro Pro Xaa Ser Thr Lys Ala Ser Leu Ser Gly Lys Gly Tyr
85 90 95
Arg Thr Gln Cys Ser His Gln Thr Ala Ala Trp Gly Thr Pro Ser Thr
100 105 110
Glu Arg Ser
115

<210> 3003
<211> 474
<212> DNA
<213> Homo sapiens

<400> 3003
gcgcgccatg gagccccggg cggttgcaga agccgtggag acgggtgagg aggatgtgat
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tatggaagct ctgcggtcat acaaccagga gcactcccag agcttcacgt ttgatgatgc
120
ccaacaggag gaccggaaga gactggcgga gctgctggtc tccgtcctgg aacagggctt
180
gccacctcc caccgtgtca tctggctgca gagtgtccga atcctgtccc gggaccgcaa
240
ctgcctggac ccgttcacca gccgccagag cctgcaggca ctagcctgct atgctgacat
300
ctctgtctct gaggggtccg tcccagagtc cgcagacatg gatgttgtac tggagtccct
360
caagtgcctg tgcaacctcg tgctcagcag ccctgtggca cagatgctgg cagcagaggc
420
ccgcctagtg gtgaagctca cagagcgtgt ggggctgtac cgtgagagga gctc
474

<210> 3004
<211> 155
<212> PRT
<213> Homo sapiens

<400> 3004
Met Glu Pro Arg Ala Val Ala Glu Ala Val Glu Thr Gly Glu Glu Asp
1 5 10 15
Val Ile Met Glu Ala Leu Arg Ser Tyr Asn Gln Glu His Ser Gln Ser
20 25 30
Phe Thr Phe Asp Asp Ala Gln Gln Glu Asp Arg Lys Arg Leu Ala Glu
35 40 45
Leu Leu Val Ser Val Leu Glu Gln Gly Leu Pro Pro Ser His Arg Val
50 55 60
Ile Trp Leu Gln Ser Val Arg Ile Leu Ser Arg Asp Arg Asn Cys Leu
65 70 75 80
Asp Pro Phe Thr Ser Arg Gln Ser Leu Gln Ala Leu Ala Cys Tyr Ala
85 90 95
Asp Ile Ser Val Ser Glu Gly Ser Val Pro Glu Ser Ala Asp Met Asp
100 105 110
Val Val Leu Glu Ser Leu Lys Cys Leu Cys Asn Leu Val Leu Ser Ser
115 120 125
Pro Val Ala Gln Met Leu Ala Ala Glu Ala Arg Leu Val Val Lys Leu

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    130                 135                 140
Thr Glu Arg Val Gly Leu Tyr Arg Glu Arg Ser
145                 150                 155

<210> 3005
<211> 799
<212> DNA
<213> Homo sapiens

<400> 3005
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gacaacagtg acaacgtgga actcaagttc aatctggacc agtacgtcaa caagcggtac
120
ccaggcctcg tgaagattgt ccgcaacagc cggcgggaag gactgatccg cgcgcggctg
180
cagggctgga aggcggccac cgccccagtc gtcggcttct ttgatgccca cgtcgagttc
240
aacacgggct gggccgagcc cgcactgtcg cggatccgag aggaccggcg tcgcatcgtg
300
ctgccagcca tcgacaacat caagtacagc acgtttgagg tgcagcagta tgcgaacgcc
360
gcccatggct acaactgggg cctctggtgc atgtacatca tccccccgca ggactggctg
420
gaccgcggcg acgagtcagc acccatcagg accccagcca tgatcggctg ctccttcgta
480
gtggaccgcg agtacttcgg agacattggg ctgctggacc ccggcatgga ggtgtatggc
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ggcgagaacg tagaactggg catgagggtg tggcagtgtg gcggcagcat ggaggtgctg
600
ccctgctccc gcgtggccca catcgagcgc accaggaagc cctacaacaa cgacattgac
660
tactacgcca agcgcaacgc cctgcgcacc gccgaggtgt ggatggatga cttcaagtcc
720
cacgtgtaca tggcctggaa catccccatg tcgaacccag gggtggactt cggggacgtg
780
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799

<210> 3006
<211> 266
<212> PRT
<213> Homo sapiens

<400> 3006
Val His Ser Val Val Asn His Thr Pro Ser Gln Leu Leu Lys Glu Val
 1               5                  10                  15
Ile Leu Val Asp Asp Asn Ser Asp Asn Val Glu Leu Lys Phe Asn Leu
            20                  25                  30
Asp Gln Tyr Val Asn Lys Arg Tyr Pro Gly Leu Val Lys Ile Val Arg
        35                  40                  45
Asn Ser Arg Arg Glu Gly Leu Ile Arg Ala Arg Leu Gln Gly Trp Lys
    50                  55                  60
Ala Ala Thr Ala Pro Val Val Gly Phe Phe Asp Ala His Val Glu Phe
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65                  70                  75                  80
Asn Thr Gly Trp Ala Glu Pro Ala Leu Ser Arg Ile Arg Glu Asp Arg
                85                  90                  95
Arg Arg Ile Val Leu Pro Ala Ile Asp Asn Ile Lys Tyr Ser Thr Phe
            100                 105                 110
Glu Val Gln Gln Tyr Ala Asn Ala Ala His Gly Tyr Asn Trp Gly Leu
        115                 120                 125
Trp Cys Met Tyr Ile Ile Pro Pro Gln Asp Trp Leu Asp Arg Gly Asp
    130                 135                 140
Glu Ser Ala Pro Ile Arg Thr Pro Ala Met Ile Gly Cys Ser Phe Val
145                 150                 155                 160
Val Asp Arg Glu Tyr Phe Gly Asp Ile Gly Leu Leu Asp Pro Gly Met
                165                 170                 175
Glu Val Tyr Gly Gly Glu Asn Val Glu Leu Gly Met Arg Val Trp Gln
            180                 185                 190
Cys Gly Gly Ser Met Glu Val Leu Pro Cys Ser Arg Val Ala His Ile
        195                 200                 205
Glu Arg Thr Arg Lys Pro Tyr Asn Asn Asp Ile Asp Tyr Tyr Ala Lys
    210                 215                 220
Arg Asn Ala Leu Arg Thr Ala Glu Val Trp Met Asp Asp Phe Lys Ser
225                 230                 235                 240
His Val Tyr Met Ala Trp Asn Ile Pro Met Ser Asn Pro Gly Val Asp
                245                 250                 255
Phe Gly Asp Val Ser Glu Arg Leu Ala Leu
            260                 265
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<210> 3007
<211> 536
<212> DNA
<213> Homo sapiens

<400> 3007
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300
attgcagcat acaacttgtg tgcaggtgct gtgaagtgcc tcttggagca gggagcaaat
360
cctgcattta ggaatgacaa aggacagatc cctgctgatg ttgttccaga cccagtagat
420
atgccgttag agatggctga cgccgcagcc actgctaagg aaatcaagca gatgcttcta
480
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536

<210> 3008
<211> 163
<212> PRT

<213> Homo sapiens

<400> 3008

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Met Thr Leu Leu His Tyr Thr Cys Lys Ser Gly Ala His Gly Ile Gly
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Asp Val Glu Thr Ala Val Lys Phe Ala Thr Gln Leu Ile Asp Leu Gly
            20                  25                  30
Ala Asp Ile Ser Leu Arg Ser Arg Trp Thr Asn Met Asn Ala Leu His
        35                  40                  45
Tyr Ala Ala Tyr Phe Asp Val Pro Glu Leu Ile Arg Val Ile Leu Lys
    50                  55                  60
Thr Ser Lys Pro Lys Asp Val Asp Ala Pro Cys Ser Asp Phe Asn Phe
65                  70                  75                  80
Gly Thr Ala Leu His Ile Ala Ala Tyr Asn Leu Cys Ala Gly Ala Val
                85                  90                  95
Lys Cys Leu Leu Glu Gln Gly Ala Asn Pro Ala Phe Arg Asn Asp Lys
            100                 105                 110
Gly Gln Ile Pro Ala Asp Val Val Pro Asp Pro Val Asp Met Pro Leu
        115                 120                 125
Glu Met Ala Asp Ala Ala Ala Thr Ala Lys Glu Ile Lys Gln Met Leu
    130                 135                 140
Leu Asp Ala Val Pro Leu Ser Cys Asn Ile Ser Lys Ala Met Leu Pro
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Pro Ser Arg
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<210> 3009
<211> 1335
<212> DNA
<213> Homo sapiens

<400> 3009

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240
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300
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420
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660
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cttaagatga acacattgag cagtaaccgg gcaaacatgc tgaaagaagt acagctcatg
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840
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<210> 3010
<211> 310
<212> PRT
<213> Homo sapiens

<400> 3010
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Ser Gln Val Gly Arg Val Trp Pro Ser Ser Tyr Arg Ala Leu Ile Ser
35 40 45
Ala Phe Ser Arg Leu Thr Arg Leu Asp Asp Phe Thr Cys Lys Lys Ile
50 55 60
Gly Ser Gly Phe Phe Ser Glu Val Phe Lys Val Arg His Arg Ala Ser
65 70 75 80
Gly Gln Val Met Ala Leu Lys Met Asn Thr Leu Ser Ser Asn Arg Ala
85 90 95
Asn Met Leu Lys Glu Val Gln Leu Met Asn Arg Leu Ser His Pro Asn
100 105 110
Ile Leu Arg Phe Met Gly Val Cys Val His Gln Gly Gln Leu His Ala
115 120 125
Leu Thr Glu Tyr Ile Asn Ser Gly Asn Leu Glu Gln Leu Leu Asp Ser
130 135 140
Asn Leu His Leu Pro Trp Thr Val Arg Val Lys Leu Ala Tyr Asp Ile
145 150 155 160
Ala Val Gly Leu Ser Tyr Leu His Phe Lys Gly Ile Phe His Arg Asp
165 170 175
Leu Thr Ser Lys Asn Cys Leu Ile Lys Arg Asp Glu Asn Gly Tyr Ser

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            180                 185                 190
Ala Val Val Ala Asp Phe Gly Leu Ala Glu Lys Ile Pro Asp Val Ser
        195                 200                 205
Met Gly Ser Glu Lys Leu Ala Val Val Gly Ser Pro Phe Trp Met Ala
    210                 215                 220
Pro Glu Val Leu Arg Asp Glu Pro Tyr Asn Glu Lys Ala Asp Val Phe
225                 230                 235                 240
Ser Tyr Gly Ile Ile Leu Cys Glu Ile Ile Val Arg Ile Gln Ala Asp
                245                 250                 255
Pro Asp Tyr Leu Pro Arg Thr Glu Asn Phe Gly Leu Asp Tyr Asp Ala
            260                 265                 270
Phe Gln His Met Val Gly Asp Cys Pro Pro Asp Phe Leu Gln Leu Thr
        275                 280                 285
Phe Asn Cys Cys Asn Val Ser Val Phe Leu Pro Leu Pro Phe Ile Arg
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Gly Trp Leu Asn Pro Phe
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<210> 3011
<211> 3253
<212> DNA
<213> Homo sapiens

<400> 3011
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2520

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3253

<210> 3012
<211> 870
<212> PRT
<213> Homo sapiens

<400> 3012
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Glu Ser Pro Asp Glu Leu Ser Phe Arg Lys Gly Asp Ile Met Thr Val
20 25 30
Leu Glu Gln Asp Thr Gln Gly Leu Asp Gly Trp Trp Leu Cys Ser Leu
35 40 45
His Gly Arg Gln Gly Ile Val Pro Gly Asn Arg Leu Lys Ile Leu Val
50 55 60
Gly Met Tyr Asp Lys Lys Pro Ala Gly Pro Gly Ser Gly Pro Pro Ala
65 70 75 80
Thr Pro Ala Gln Pro Gln Pro Gly Leu His Ala Pro Ala Pro Pro Ala
85 90 95
Ser Gln Tyr Thr Pro Met Leu Pro Asn Thr Tyr Gln Pro Gln Pro Asp
100 105 110
Ser Val Tyr Leu Val Pro Thr Pro Ser Lys Ala Gln Gln Gly Leu Tyr
115 120 125
Gln Val Pro Gly Pro Ser Pro Gln Phe Gln Ser Pro Pro Ala Lys Gln
130 135 140
Thr Ser Thr Phe Ser Lys Gln Thr Pro His His Pro Phe Pro Ser Pro
145 150 155 160
Ala Thr Asp Leu Tyr Gln Val Pro Pro Gly Pro Gly Gly Pro Ala Gln

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                165                 170                 175
Asp Ile Tyr Gln Val Pro Pro Ser Ala Gly Met Gly His Asp Ile Tyr
            180                 185                 190
Gln Val Pro Pro Ser Met Asp Thr Arg Ser Trp Glu Gly Thr Lys Pro
        195                 200                 205
Pro Ala Lys Val Val Val Pro Thr Arg Val Gly Gln Gly Tyr Val Tyr
    210                 215                 220
Glu Ala Ala Gln Pro Glu Gln Asp Glu Tyr Asp Ile Pro Arg His Leu
225                 230                 235                 240
Leu Ala Pro Gly Pro Gln Asp Ile Tyr Asp Val Pro Pro Val Arg Gly
                245                 250                 255
Leu Leu Pro Ser Gln Tyr Gly Gln Glu Val Tyr Asp Thr Pro Pro Met
            260                 265                 270
Ala Val Lys Gly Pro Asn Gly Arg Asp Pro Leu Leu Glu Val Tyr Asp
        275                 280                 285
Val Pro Pro Ser Val Glu Lys Gly Leu Pro Pro Ser Asn His His Ala
    290                 295                 300
Val Tyr Asp Val Pro Pro Ser Val Ser Lys Asp Val Pro Asp Gly Pro
305                 310                 315                 320
Leu Leu Arg Glu Glu Thr Tyr Asp Val Pro Pro Ala Phe Ala Lys Ala
                325                 330                 335
Lys Pro Phe Asp Pro Ala Arg Thr Pro Leu Val Leu Gly Ala Pro Pro
            340                 345                 350
Pro Asp Ser Pro Pro Ala Glu Asp Val Tyr Tyr Val Pro Pro Pro Ala
        355                 360                 365
Pro Asp Leu Tyr Asp Val Pro Pro Gly Leu Arg Arg Pro Gly Pro Gly
    370                 375                 380
Thr Leu Tyr Asp Val Pro Arg Glu Arg Val Leu Pro Pro Glu Val Ala
385                 390                 395                 400
Asp Gly Gly Val Val Asp Ser Gly Val Tyr Ala Val Pro Pro Pro Ala
                405                 410                 415
Glu Arg Glu Ala Pro Ala Glu Gly Lys Arg Leu Ser Ala Ser Ser Thr
            420                 425                 430
Gly Ser Thr Arg Ser Ser Gln Ser Ala Ser Ser Leu Glu Val Ala Gly
        435                 440                 445
Pro Gly Arg Glu Pro Leu Glu Leu Glu Val Ala Val Glu Ala Leu Ala
    450                 455                 460
Arg Leu Gln Gln Gly Val Ser Ala Thr Val Ala His Leu Leu Asp Leu
465                 470                 475                 480
Ala Gly Ser Ala Gly Ala Thr Gly Gly Trp Arg Ser Pro Ser Glu Pro
                485                 490                 495
Gln Glu Pro Leu Val Gln Asp Leu Gln Ala Ala Val Ala Ala Val Gln
            500                 505                 510
Ser Ala Val His Glu Leu Leu Glu Phe Ala Arg Ser Ala Val Gly Asn
        515                 520                 525
Ala Ala His Thr Ser Asp Arg Ala Leu His Ala Lys Leu Ser Arg Gln
    530                 535                 540
Leu Gln Lys Met Glu Asp Val His Gln Thr Leu Val Ala His Gly Gln
545                 550                 555                 560
Ala Leu Asp Ala Gly Arg Gly Gly Ser Gly Ala Thr Leu Glu Asp Leu
                565                 570                 575
Asp Arg Leu Val Ala Cys Ser Arg Ala Val Pro Glu Asp Ala Lys Gln
            580                 585                 590
Leu Ala Ser Phe Leu His Gly Asn Ala Ser Leu Leu Phe Arg Arg Thr
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595 600 605
Lys Ala Thr Ala Pro Gly Pro Glu Gly Gly Gly Thr Leu His Pro Asn
610 615 620
Pro Thr Asp Lys Thr Ser Ser Ile Gln Ser Arg Pro Leu Pro Ser Pro
625 630 635 640
Pro Lys Phe Thr Ser Gln Asp Ser Pro Asp Gly Gln Tyr Glu Asn Ser
645 650 655
Glu Gly Gly Trp Met Glu Asp Tyr Asp Tyr Val His Leu Gln Gly Lys
660 665 670
Glu Glu Phe Glu Lys Thr Gln Lys Glu Leu Leu Glu Lys Gly Asn Ile
675 680 685
Thr Arg Gln Gly Lys Ser Gln Leu Glu Leu Gln Gln Leu Lys Gln Phe
690 695 700
Glu Arg Leu Glu Gln Glu Val Ser Arg Pro Ile Asp His Asp Leu Ala
705 710 715 720
Asn Trp Thr Pro Ala Gln Pro Leu Ala Pro Gly Arg Thr Gly Gly Leu
725 730 735
Gly Pro Ser Asp Arg Gln Leu Leu Leu Phe Tyr Leu Glu Gln Cys Glu
740 745 750
Ala Asn Leu Thr Thr Leu Thr Asn Ala Val Asp Ala Phe Phe Thr Ala
755 760 765
Val Ala Thr Asn Gln Pro Pro Lys Ile Phe Val Ala His Ser Lys Phe
770 775 780
Val Ile Leu Ser Ala His Lys Leu Val Phe Ile Gly Asp Thr Leu Ser
785 790 795 800
Arg Gln Ala Lys Ala Ala Asp Val Arg Ser Gln Val Thr His Tyr Ser
805 810 815
Asn Leu Leu Cys Asp Leu Leu Arg Gly Ile Val Ala Thr Thr Lys Ala
820 825 830
Ala Ala Leu Gln Tyr Pro Ser Pro Ser Ala Ala Gln Asp Met Val Glu
835 840 845
Arg Val Lys Glu Leu Gly His Ser Thr Gln Gln Phe Arg Arg Val Leu
850 855 860
Gly Gln Leu Ala Ala Ala
865 870

<210> 3013
<211> 248
<212> DNA
<213> Homo sapiens

<400> 3013
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120
gaccaggtgc tggaggagca gaccaaggca gcgcagcagg ctgggtgggg cctcctcctt
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atcgatgc
248

<210> 3014

<211> 82
<212> PRT
<213> Homo sapiens

<400> 3014
Xaa Arg Val Lys Gly Thr Val Val Ile Phe Asp Glu Ala His Asn Val
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Glu Lys Met Cys Glu Glu Ser Ala Ser Phe Asp Leu Thr Pro His Asp
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Leu Ala Ser Gly Leu Asp Val Ile Asp Gln Val Leu Glu Glu Gln Thr
35 40 45
Lys Ala Ala Gln Gln Ala Gly Trp Gly Leu Leu Leu Ala Arg Arg Trp
50 55 60
Val Ala Pro Pro Arg Pro Thr Val Ile Leu Leu Arg Leu Glu Gly Ala
65 70 75 80
Ile Asp

<210> 3015
<211> 438
<212> DNA
<213> Homo sapiens

<400> 3015
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120
ccggagaagc attttcacaa ctaaacttga cctgacccag ctgcacggtg actggctcca
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240
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300
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438

<210> 3016
<211> 103
<212> PRT
<213> Homo sapiens

<400> 3016
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20 25 30
Lys Pro Pro Trp Gln Leu Cys Pro Arg Ala Phe Ala Phe Cys His Arg
35 40 45
Val Pro Gly Gly Met Val His Pro Ile Phe Leu Glu Pro Val Thr Val

50 55 60
Gln Leu Gly Gln Val Lys Phe Ser Cys Glu Asn Ala Ser Pro Asp Thr
65 70 75 80
Arg Cys Val Gly Gln Leu Ser Ile Pro Ser Pro Arg Met Pro Trp Gly
85 90 95
Arg Leu Gln Ala Arg Tyr Val
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<210> 3017
<211> 4796
<212> DNA
<213> Homo sapiens

<400> 3017
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300
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420
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1200

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4560
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4680
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4796

<210> 3018
<211> 104
<212> PRT
<213> Homo sapiens

<400> 3018
Cys His Leu Glu Gln Val His Leu Lys Pro Ile Pro Lys Asp Thr Pro
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Thr Thr Pro Thr Pro Thr Leu Ala Cys Pro Ser Pro Gln Cys Ala Phe
20 25 30
Gln Arg Trp Ile Thr Ile Gln His Arg Trp Ser Ser Ala Leu His Cys
35 40 45
Gln Gly Leu Thr Pro Thr Pro Gly Ala Leu Pro Asn Tyr Leu Lys Val
50 55 60
Lys Ala Asn Arg Ala Ile Pro Gln Ala Val Thr Ser Thr Arg Leu Gly
65 70 75 80
Thr Thr Lys Pro Pro Cys Thr Ile Thr Pro Pro Cys Arg Ala Val Arg
85 90 95
Ser Thr Ser Pro Arg Leu Pro Thr
100

<210> 3019
<211> 882
<212> DNA
<213> Homo sapiens

<400> 3019
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120
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180
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240
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300
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360
gagctgtgag cgggactgcc aggagttcta ccgagccctg tatatccatg cccagccccc
420

gcacagccgc ctgcccagcc gccacgctct gcagaactca gattgcacag agctagactc
480
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720
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780
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840
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882

<210> 3020
<211> 58
<212> PRT
<213> Homo sapiens

<400> 3020
Gln Gly Thr His Glu Leu Pro Gly Trp Pro Gly Pro Cys Cys Gly Thr
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Gly Pro Ala Pro Val Leu Leu Ser Ala Arg Pro Gln Gly Pro Ala Arg
20 25 30
Asp Pro Ala Arg Pro Arg Phe Leu Ala Cys His His Arg Gln Thr Cys
35 40 45
Gln Pro Leu Pro Ala Gly Leu Pro Gly Arg
50 55

<210> 3021
<211> 1008
<212> DNA
<213> Homo sapiens

<400> 3021
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120
gggcatgtgg gtgccttggg gtagggtaaa ggttccatct tgatcgcggt ggtgtttccc
180
aagtgtatac actcaccaaa actatactta gaactcaaaa ctcgccaaat atatacttaa
240
aatggatgca gttggttatg tataaattat acctcaataa agttgattaa aaacatcaat
300
tcctcagaaa attcttttct gaccactccc ctctcagacg aggtcgggcc tcctggtatg
360
catacccata cccactacaa cctgtattta tttttttga aacatggtct ctttctgtcg
420
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480

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600
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660
tccgcggact acggttctgg ctcgctagct ctggaaggga gcaccgggag ggaatggtgg
720
caactcccaa ggaggggacc cagggatccg agaaaggaag acttggggta ggtggggttg
780
gattttgact ggagagaaga aagggtcagg agtgcagggc gggtacctgg ggagctgcgt
840
ggactcgcgc agacgggaag caggcgcgtg ctggcggtga cctggggccg gagaggaacg
900
ctgggtcccc tccttgggag ttgccaccat tccctcccgg tgctcccttc cagagctagc
960
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1008

<210> 3022
<211> 94
<212> PRT
<213> Homo sapiens

<400> 3022
Met His Thr His Thr His Tyr Asn Leu Tyr Leu Phe Phe Leu Lys His
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Gly Leu Phe Leu Ser Ser Arg Leu Glu Cys Ser Gly Ala Ile Met Asp
            20   25   30
His Cys Ser Leu Asp Leu Pro Gly Ser Ser Asp Pro Pro Gly Ser Pro
        35   40   45
Pro Val Ala Gly Thr Thr Gly Ala Leu Pro His Arg Lys Ala His Phe
    50   55   60
Leu Glu Ala Glu Thr Glu Ala Pro Ser Gly Lys Gly Asp Pro Pro Gly
65   70   75   80
Met Arg Gly Ala Gln Arg Ala Ala Thr Trp Gly Pro Thr Arg
                85   90

<210> 3023
<211> 1834
<212> DNA
<213> Homo sapiens

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aacttctatt ttggtgttca aagatcggga taaatatgta agtggagaat tcaggtaagt
120
tcagattttt ccctccagtt ggtttaattt ctatttccta aaacattaaa ataataatgg
180
aatgattgaa ataataaaca tttttcttat tcaagatttc gtcatggcta ttgtaaagga
240
aaccctagga aaatggtgaa aacttgggca gaaaaagaaa tgaggaactt aatcaggcta
300

aacacagcag agataccatg tccagaacca ataatgctaa gaagtcatgt tcttgtcatg
360
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420
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480
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600
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660
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720
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780
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900
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960
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1140
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1260
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1320
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1380
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1440
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1620
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1740
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1834

<210> 3024

<211> 347
<212> PRT
<213> Homo sapiens

<400> 3024
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Gly Asn Pro Arg Lys Met Val Lys Thr Trp Ala Glu Lys Glu Met Arg
20 25 30
Asn Leu Ile Arg Leu Asn Thr Ala Glu Ile Pro Cys Pro Glu Pro Ile
35 40 45
Met Leu Arg Ser His Val Leu Val Met Ser Phe Ile Gly Lys Asp Asp
50 55 60
Met Pro Ala Pro Leu Leu Lys Asn Val Gln Leu Ser Glu Ser Lys Ala
65 70 75 80
Arg Glu Leu Tyr Leu Gln Val Ile Gln Tyr Met Arg Arg Met Tyr Gln
85 90 95
Asp Ala Arg Leu Val His Ala Asp Leu Ser Glu Phe Asn Met Leu Tyr
100 105 110
His Gly Gly Gly Val Tyr Ile Ile Asp Val Ser Gln Ser Val Glu His
115 120 125
Asp His Pro His Ala Leu Glu Phe Leu Arg Lys Asp Cys Ala Asn Val
130 135 140
Asn Asp Phe Phe Met Arg His Ser Val Ala Val Met Thr Val Arg Glu
145 150 155 160
Leu Phe Glu Phe Val Thr Asp Pro Ser Ile Thr His Glu Asn Met Asp
165 170 175
Ala Tyr Leu Ser Lys Ala Met Glu Ile Ala Ser Gln Arg Thr Lys Glu
180 185 190
Glu Arg Ser Ser Gln Asp His Val Asp Glu Glu Val Phe Lys Arg Ala
195 200 205
Tyr Ile Pro Arg Thr Leu Asn Glu Val Lys Asn Tyr Glu Arg Asp Met
210 215 220
Asp Ile Ile Met Lys Leu Lys Glu Glu Asp Met Ala Met Asn Ala Gln
225 230 235 240
Gln Asp Asn Ile Leu Pro Asp Cys Tyr Arg Ile Glu Glu Arg Phe Val
245 250 255
Arg Ser Ser Glu Gly Pro Cys Thr Leu Glu Asn Gln Val Glu Glu Arg
260 265 270
Thr Cys Ser Asp Ser Glu Asp Ile Gly Ser Ser Glu Cys Ser Asp Thr
275 280 285
Asp Ser Glu Glu Gln Gly Asp His Ala Arg Pro Lys Lys His Thr Thr
290 295 300
Asp Pro Asp Ile Asp Lys Lys Glu Arg Lys Lys Met Val Lys Glu Ala
305 310 315 320
Gln Arg Glu Lys Arg Lys Asn Lys Ile Pro Lys His Val Lys Lys Arg
325 330 335
Lys Glu Lys Thr Ala Lys Thr Lys Lys Gly Lys
340 345

<210> 3025
<211> 1370
<212> DNA
<213> Homo sapiens

<400> 3025
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tcaagagaag ataaaaattg aaactgctaa tcatctagta ctactgctaa gccgctccaa
120
agcttctgaa gcatctaggt gatcttctta aatctttgac aggaaagagt aggaaacttt
180
ttggcagact tttacctggt gaatggactt gttttagaat caaggaaaag aagagaacat
240
ctcagtgaag aggatattct tcgaaataag gccatcatgg agagtttgag taaaggtgga
300
aacataatgg aacagaattt tgagccgatt cgaagacagt ctcttacacc tcctcctcag
360
aacactatta catgggaaga atatatatct gctgaaaatg gaaaagctcc tcatctgggt
420
agagaattgg tgtgcaaaga gagtaagaaa acgtttaaag ctacgatagc catgagccag
480
gaatttccct tagggataga gttattattg aatgttttag aagtagtagc tcccttcaag
540
cactttaaca agcttagaga atttgttcag atgaagcttc ctccaggctt tcctgtaaaa
600
ttagatatac ctgtgtttcc cacaatcaca gccactgtga cttttcagga gtttcgatac
660
gatgaatttg atggctccat ctttactata cctgatgact acaaggaaga cccaagccgt
720
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780
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840
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900
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1020
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1260
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1320
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1370

<210> 3026
<211> 152
<212> PRT
<213> Homo sapiens

<400> 3026
Met Glu Ser Leu Ser Lys Gly Gly Asn Ile Met Glu Gln Asn Phe Glu
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Pro Ile Arg Arg Gln Ser Leu Thr Pro Pro Pro Gln Asn Thr Ile Thr
20 25 30
Trp Glu Glu Tyr Ile Ser Ala Glu Asn Gly Lys Ala Pro His Leu Gly
35 40 45
Arg Glu Leu Val Cys Lys Glu Ser Lys Lys Thr Phe Lys Ala Thr Ile
50 55 60
Ala Met Ser Gln Glu Phe Pro Leu Gly Ile Glu Leu Leu Leu Asn Val
65 70 75 80
Leu Glu Val Val Ala Pro Phe Lys His Phe Asn Lys Leu Arg Glu Phe
85 90 95
Val Gln Met Lys Leu Pro Pro Gly Phe Pro Val Lys Leu Asp Ile Pro
100 105 110
Val Phe Pro Thr Ile Thr Ala Thr Val Thr Phe Gln Glu Phe Arg Tyr
115 120 125
Asp Glu Phe Asp Gly Ser Ile Phe Thr Ile Pro Asp Asp Tyr Lys Glu
130 135 140
Asp Pro Ser Arg Phe Pro Asp Leu
145 150

<210> 3027
<211> 1154
<212> DNA
<213> Homo sapiens

<400> 3027
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cgcagacggc ggcctccgcg gcgctctcca gtcatggact accggcggct tctcatgagc
180
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240
aagacagtca aagagaagga tgacattctg tttgaagacc ttcaagacaa tgtgaatgag
300
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360
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420
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600
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660
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720
aaagaagcta atgtatacca tgctagcaca gcaaatggag agagcagagc aatcaaaatt
780

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840
tttcgtcatg gctattgtaa aggaaaccct aggaaaatgg tgaaaacttg ggcagaaaaa
900
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960
ctaagaagtc atgttcttgt catgagtttc atcggtaaag atgacatttc ttttcattca
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1154

<210> 3028
<211> 331
<212> PRT
<213> Homo sapiens

<400> 3028
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Lys Glu Lys Asp Asp Ile Leu Phe Glu Asp Leu Gln Asp Asn Val Asn
35 40 45
Glu Asn Gly Glu Gly Glu Ile Glu Asp Glu Glu Glu Glu Gly Tyr Asp
50 55 60
Asp Asp Asp Asp Asp Trp Asp Trp Asp Glu Gly Val Gly Lys Leu Ala
65 70 75 80
Lys Gly Tyr Val Trp Asn Gly Gly Ser Asn Pro Gln Ala Asn Arg Gln
85 90 95
Thr Ser Asp Ser Ser Ser Ala Lys Met Ser Thr Pro Ala Asp Lys Val
100 105 110
Leu Arg Lys Phe Glu Asn Lys Ile Asn Leu Asp Lys Leu Asn Val Thr
115 120 125
Asp Ser Val Ile Asn Lys Val Thr Glu Lys Ser Arg Gln Lys Glu Ala
130 135 140
Asp Met Tyr Arg Ile Lys Asp Lys Ala Asp Arg Ala Thr Val Glu Gln
145 150 155 160
Val Leu Asp Pro Arg Thr Arg Met Ile Leu Phe Lys Met Leu Thr Arg
165 170 175
Gly Ile Ile Thr Glu Ile Asn Gly Cys Ile Ser Thr Gly Lys Glu Ala
180 185 190
Asn Val Tyr His Ala Ser Thr Ala Asn Gly Glu Ser Arg Ala Ile Lys
195 200 205
Ile Tyr Lys Thr Ser Ile Leu Val Phe Lys Asp Arg Asp Lys Tyr Val
210 215 220
Ser Gly Clu Phe Arg Phe Arg His Gly Tyr Cys Lys Gly Asn Pro Arg
225 230 235 240
Lys Met Val Lys Thr Trp Ala Glu Lys Glu Met Arg Asn Leu Ile Arg
245 250 255
Leu Asn Thr Ala Glu Ile Pro Cys Pro Glu Pro Ile Met Leu Arg Ser

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            260                 265                 270
His Val Leu Val Met Ser Phe Ile Gly Lys Asp Asp Ile Ser Phe His
        275                 280                 285
Ser Arg Pro Ala Pro Leu Leu Lys Asn Val Gln Leu Ser Glu Ser Lys
    290                 295                 300
Ala Arg Glu Leu Tyr Leu Gln Val Ile Gln Tyr Met Arg Arg Met Tyr
305                 310                 315                 320
Gln Asp Ala Arg Leu Val His Ala Asp Arg Arg
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<210> 3029
<211> 344
<212> DNA
<213> Homo sapiens

<400> 3029
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ctgaaaagat tcgattttga ttatacaacc atgcatagga ttaaactgaa tgatcgaatg
120
acatttcccg aggaactaga tatgagtact tttattgatg ttgaagatga aaaatctcct
180
cagactgaaa gttgcactga caggggagca gaaaatgaag gtagttgtca cagtgatcag
240
atgagcaacg atttctccaa tgatgatggt gttgatgaag gaatctgttt tgaaaccaat
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344

<210> 3030
<211> 114
<212> PRT
<213> Homo sapiens

<400> 3030
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Thr Arg Asp Ala Arg Lys Gly Leu Arg Phe Leu His Phe Pro Tyr Leu
 1               5                  10                  15
Leu Thr Leu Gln Leu Lys Arg Phe Asp Phe Asp Tyr Thr Thr Met His
            20                  25                  30
Arg Ile Lys Leu Asn Asp Arg Met Thr Phe Pro Glu Glu Leu Asp Met
        35                  40                  45
Ser Thr Phe Ile Asp Val Glu Asp Glu Lys Ser Pro Gln Thr Glu Ser
    50                  55                  60
Cys Thr Asp Arg Gly Ala Glu Asn Glu Gly Ser Cys His Ser Asp Gln
65                  70                  75                  80
Met Ser Asn Asp Phe Ser Asn As$_1$ Asp Gly Val Asp Glu Gly Ile Cys
                85                  90                  95
Phe Glu Thr Asn Ser Gly Thr Glu Lys Ile Ser Lys Ser Gly Pro Glu
            100                 105                 110
Lys Asn
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<210> 3031
<211> 567

<212> DNA
<213> Homo sapiens

<400> 3031
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cctccccctt cctattttgc cacgttttac tcgtgcacac cccggatgaa ccgcagattg
120
gttggtcctg atgttattcc cctgccacac atctacggag ctcgaatcaa aggtgtggaa
180
gtgttctgtc ctctggatcc cccgccgcca tatgaagctg tggtgagcca gatggaccag
240
gagcagggat cttcattcca aatgtcagaa ggatcagaag ctgctgtgat cccattggat
300
ctgggctgca cacaagtgac tcaagatggg gacattccta acatacctgc cgaagaaaat
360
gcatccacct caactcccag ttcaaccctg gtgcgtccta tcagaagccg gagagccctc
420
ccacccttga ggaccaggtc gaagagtgac cctgtgctcc atccttctga ggagagagct
480
gccccagtgc tcagctgtga agctgcaaca cagactgaaa ggagactgga tctggctgca
540
gtgactctga ggagaggctt gagatct
567

<210> 3032
<211> 189
<212> PRT
<213> Homo sapiens

<400> 3032
Ala Glu Glu Ala Glu Asp His Gly Arg Ile Pro Asp Pro Asp Asp Phe
 1   5   10   15
Val Pro Pro Val Pro Pro Pro Ser Tyr Phe Ala Thr Phe Tyr Ser Cys
            20   25   30
Thr Pro Arg Met Asn Arg Arg Leu Val Gly Pro Asp Val Ile Pro Leu
        35   40   45
Pro His Ile Tyr Gly Ala Arg Ile Lys Gly Val Glu Val Phe Cys Pro
    50   55   60
Leu Asp Pro Pro Pro Pro Tyr Glu Ala Val Val Ser Gln Met Asp Gln
65   70   75   80
Glu Gln Gly Ser Ser Phe Gln Met Ser Glu Gly Ser Glu Ala Ala Val
                85   90   95
Ile Pro Leu Asp Leu Gly Cys Thr Gln Val Thr Gln Asp Gly Asp Ile
            100   105   110
Pro Asn Ile Pro Ala Glu Glu Asn Ala Ser Thr Ser Thr Pro Ser Ser
        115   120   125
Thr Leu Val Arg Pro Ile Arg Ser Arg Arg Ala Leu Pro Pro Leu Arg
    130   135   140
Thr Arg Ser Lys Ser Asp Pro Val Leu His Pro Ser Glu Glu Arg Ala
145   150   155   160
Ala Pro Val Leu Ser Cys Glu Ala Ala Thr Gln Thr Glu Arg Arg Leu
                165   170   175
Asp Leu Ala Ala Val Thr Leu Arg Arg Gly Leu Arg Ser

180 185

<210> 3033
<211> 821
<212> DNA
<213> Homo sapiens

<400> 3033
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120
tactatgata aattatttaa ggaatactgc atagcagatc tcagtaaata taaagaaaat
180
aagtttggat ttaggtggcg agtagaaaaa gaagtaattt caggaaaagg tcaatttttc
240
tgtggaaata aatattgtga taaaaaagaa ggcttaaaga gttgggaagt taattttggt
300
tatattgagc atggtgagaa gagaaatgca cttgttaaat taaggttatg ccaagaatgt
360
tccattaaat taaatttcca tcacaggaga aaagaaatca agtcaaaaaa aagaaaagat
420
aaaaccaaaa aagactgtga agagtcatca ataaaaaat ccagattatc ttctgcagaa
480
gaggcctcca agaaaaaaga taaaggacat tcatcttcaa agaaatctga agattctcta
540
cttagaaact ctgatgagga agaaagtgct tcagaatctg aactttggaa gggtccacta
600
ccagagacag atgaaaaatc acaggaagaa gaatttgatg agtattttca ggatttgttt
660
ctatgagacg agagagagaa gcctccgctc cttaatgtga aacttcatga agttttaaac
720
ctcatgcaat ttgaaattcc atctacgtct ttatctgcaa gttacagctt ctgtgctttg
780
tcttcgcaac tacaaatcca ggttctctca gcaacaacac a
821

<210> 3034
<211> 221
<212> PRT
<213> Homo sapiens

<400> 3034
Xaa Arg Val Lys Gly Glu Asn Asp Lys Thr Asp Leu Asp Val Ile Arg
1 5 10 15
Glu Asn His Arg Phe Leu Trp Asn Glu Glu Asp Glu Met Asp Met Thr
20 25 30
Trp Glu Lys Arg Leu Ala Lys Lys Tyr Tyr Asp Lys Leu Phe Lys Glu
35 40 45
Tyr Cys Ile Ala Asp Leu Ser Lys Tyr Lys Glu Asn Lys Phe Gly Phe
50 55 60
Arg Trp Arg Val Glu Lys Glu Val Ile Ser Gly Lys Gly Gln Phe Phe
65 70 75 80
Cys Gly Asn Lys Tyr Cys Asp Lys Lys Glu Gly Leu Lys Ser Trp Glu

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                85                  90                  95
Val Asn Phe Gly Tyr Ile Glu His Gly Glu Lys Arg Asn Ala Leu Val
            100                 105                 110
Lys Leu Arg Leu Cys Gln Glu Cys Ser Ile Lys Leu Asn Phe His His
        115                 120                 125
Arg Arg Lys Glu Ile Lys Ser Lys Lys Arg Lys Asp Lys Thr Lys Lys
    130                 135                 140
Asp Cys Glu Glu Ser Ser His Lys Lys Ser Arg Leu Ser Ser Ala Glu
145                 150                 155                 160
Glu Ala Ser Lys Lys Lys Asp Lys Gly His Ser Ser Ser Lys Lys Ser
                165                 170                 175
Glu Asp Ser Leu Leu Arg Asn Ser Asp Glu Glu Glu Ser Ala Ser Glu
            180                 185                 190
Ser Glu Leu Trp Lys Gly Pro Leu Pro Glu Thr Asp Glu Lys Ser Gln
        195                 200                 205
Glu Glu Glu Phe Asp Glu Tyr Phe Gln Asp Leu Phe Leu
    210                 215                 220
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<210> 3035
<211> 878
<212> DNA
<213> Homo sapiens

<400> 3035
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120
cctcagacca cgacaggggc ctcccacaca cggctcgcag aacctgtgca aggagaacca
180
caaaggatga gcactctggc ccacccaaaa ccatggcagc cctgagggca cagactggac
240
accctgcaga gtctcactct gtcattcagg gtggagtgca atggcgcaat ctcagctcac
300
tgcaacctcc cactcccggg ctcaagcaat tctcctgacc cacactcagg cccagctcct
360
tcccagactg tcatcctctt tctagaagga aacagggacc ctgggggtcg gggatggccc
420
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480
atgctctgcc ccatggctac ccgctgctgc ctgcaaggtt ccagagtcac gtccccagtg
540
agtctctgac ccggcggcca gcacaccagt gtgaatcacg tgtgtcccca gtgagtctct
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gacccggcgg ccagcgcacc agtgtgaatc acatgcgtcc ccagtgagtc tctgacccgg
660
cgaccagagc accagtgtga atcacatgcg tccccggtga gtctctgcag ggtgtccagt
720
ctgtgccctc agggctgcca tggttttggg tgggccagag tgctcatcct ttgtggttct
780
ccttgcacaa gttctgcgag ccatgtgtgg gaggcccctg tcgtggtctg aggacgtccc
840
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878

<210> 3036
<211> 65
<212> PRT
<213> Homo sapiens

<400> 3036
Gly His Arg Leu Asp Thr Leu Gln Ser Leu Thr Leu Ser Phe Arg Val
1 5 10 15
Glu Cys Asn Gly Ala Ile Ser Ala His Cys Asn Leu Pro Leu Pro Gly
20 25 30
Ser Ser Asn Ser Pro Asp Pro His Ser Gly Pro Ala Pro Ser Gln Thr
35 40 45
Val Ile Leu Phe Leu Glu Gly Asn Arg Asp Pro Gly Gly Arg Gly Trp
50 55 60
Pro
65

<210> 3037
<211> 3538
<212> DNA
<213> Homo sapiens

<400> 3037
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120
ctcaagctca tagtagatgc tttcctacag cagttaccca actgtgtcaa ccgagatctg
180
atagacaagg cagcaatgga ttttttgcatg aacatgaaca caaaagcaaa caggaagaag
240
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300
agattggttg ctacattgca tccctgcatg tctgatgtag cagaggatct ttgttccatg
360
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420
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480
acactgcatt gtttaaagat gcttctgtca gacttctctc atcaccatat tgaaatggca
540
tgcaccctgc tggagacatg tggacggttt cttttcagat ctccagaatc tcacctgagg
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660
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720
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1260
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2820
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3420
caaaacttgt aaagttgtaa catttcacat ggaaatgctg cccaatcttc accagcttca
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3538

<210> 3038
<211> 697
<212> PRT
<213> Homo sapiens

<400> 3038
Pro Asn Cys Val Asn Arg Asp Leu Ile Asp Lys Ala Ala Met Asp Phe
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Cys Met Asn Met Asn Thr Lys Ala Asn Arg Lys Lys Leu Val Arg Ala
20 25 30
Leu Phe Ile Val Pro Arg Gln Arg Leu Asp Leu Leu Pro Phe Tyr Ala
35 40 45
Arg Leu Val Ala Thr Leu His Pro Cys Met Ser Asp Val Ala Glu Asp
50 55 60
Leu Cys Ser Met Leu Arg Gly Asp Phe Arg Phe His Val Arg Lys Lys
65 70 75 80
Asp Gln Ile Asn Ile Glu Thr Lys Asn Lys Thr Val Arg Phe Ile Gly
85 90 95
Glu Leu Thr Lys Phe Lys Met Phe Thr Lys Asn Asp Thr Leu His Cys

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                100                 105                 110
Leu Lys Met Leu Leu Ser Asp Phe Ser His His His Ile Glu Met Ala
        115                 120                 125
Cys Thr Leu Leu Glu Thr Cys Gly Arg Phe Leu Phe Arg Ser Pro Glu
    130                 135                 140
Ser His Leu Arg Thr Ser Val Leu Leu Glu Gln Met Met Arg Lys Lys
145                 150                 155                 160
Gln Ala Met His Leu Asp Ala Arg Tyr Val Thr Met Val Glu Asn Ala
                165                 170                 175
Tyr Tyr Tyr Cys Asn Pro Pro Pro Ala Glu Lys Thr Val Lys Lys Lys
            180                 185                 190
Arg Pro Pro Leu Gln Glu Tyr Val Arg Lys Leu Leu Tyr Lys Asp Leu
        195                 200                 205
Ser Lys Val Thr Thr Glu Lys Val Leu Arg Gln Met Arg Lys Leu Pro
    210                 215                 220
Trp Gln Asp Gln Glu Val Lys Asp Tyr Val Ile Cys Cys Met Ile Asn
225                 230                 235                 240
Ile Trp Asn Val Lys Tyr Asn Ser Ile His Cys Val Ala Asn Leu Leu
                245                 250                 255
Ala Gly Leu Val Leu Tyr Gln Glu Asp Val Gly Ile His Val Val Asp
            260                 265                 270
Gly Val Leu Glu Asp Ile Arg Leu Gly Met Glu Val Asn Gln Pro Lys
        275                 280                 285
Phe Asn Gln Arg Arg Ile Ser Ser Ala Lys Phe Leu Gly Glu Leu Tyr
    290                 295                 300
Asn Tyr Arg Met Val Glu Ser Ala Val Ile Phe Arg Thr Leu Tyr Ser
305                 310                 315                 320
Phe Thr Ser Phe Gly Val Asn Pro Asp Gly Ser Pro Ser Ser Leu Asp
                325                 330                 335
Pro Pro Glu His Leu Phe Arg Ile Arg Leu Val Cys Thr Ile Leu Asp
            340                 345                 350
Thr Cys Gly Gln Tyr Phe Asp Arg Gly Ser Ser Lys Arg Lys Leu Asp
        355                 360                 365
Cys Phe Leu Val Tyr Phe Gln Arg Tyr Val Trp Trp Lys Lys Ser Leu
    370                 375                 380
Glu Val Trp Thr Lys Asp His Pro Phe Pro Ile Asp Ile Asp Tyr Met
385                 390                 395                 400
Ile Ser Asp Thr Leu Glu Leu Leu Arg Pro Lys Ile Lys Leu Cys Asn
                405                 410                 415
Ser Leu Glu Glu Ser Ile Arg Gln Val Gln Asp Leu Glu Arg Glu Phe
            420                 425                 430
Leu Ile Lys Leu Gly Leu Val Asn Asp Lys Asp Ser Lys Asp Phe Met
        435                 440                 445
Thr Glu Gly Glu Asn Leu Glu Glu Asp Glu Glu Glu Glu Glu Gly Gly
    450                 455                 460
Ala Glu Thr Glu Glu Gln Ser Gly Asn Glu Ser Glu Val Asn Glu Pro
465                 470                 475                 480
Glu Glu Glu Glu Gly Ser Asp Asn Asp Asp Asp Glu Gly Glu Glu Glu
                485                 490                 495
Glu Glu Glu Asn Thr Asp Tyr Leu Thr Asp Ser Asn Lys Glu Asn Glu
            500                 505                 510
Thr Asp Glu Glu Asn Thr Glu Val Met Ile Lys Gly Gly Gly Leu Lys
        515                 520                 525
His Val Pro Cys Val Glu Asp Glu Asp Phe Ile Gln Ala Leu Asp Lys
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    530                 535                 540
Met Met Leu Glu Asn Leu Gln Gln Arg Ser Gly Glu Ser Val Lys Val
545                 550                 555                 560
His Gln Leu Asp Val Ala Ile Pro Leu His Leu Lys Ser Gln Leu Arg
                565                 570                 575
Lys Gly Pro Pro Leu Gly Gly Gly Glu Gly Glu Ala Glu Ser Ala Asp
            580                 585                 590
Thr Met Pro Phe Val Met Leu Thr Arg Lys Gly Asn Lys Gln Gln Phe
        595                 600                 605
Lys Ile Leu Asn Val Pro Met Ser Ser Gln Leu Ala Ala Asn His Trp
    610                 615                 620
Asn Gln Gln Gln Ala Glu Gln Glu Glu Arg Met Arg Met Lys Lys Leu
625                 630                 635                 640
Thr Leu Asp Ile Asn Glu Arg Gln Glu Gln Glu Asp Tyr Gln Glu Met
                645                 650                 655
Leu Gln Ser Leu Ala Gln Arg Pro Ala Pro Ala Asn Thr Asn Arg Glu
            660                 665                 670
Arg Arg Pro Arg Tyr Gln His Pro Lys Gly Ala Pro Asn Ala Asp Leu
        675                 680                 685
Ile Phe Lys Thr Gly Gly Arg Arg Arg
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<210> 3039
<211> 1836
<212> DNA
<213> Homo sapiens

<400> 3039

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120
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720
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780
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1740
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gagtcccaga ccgcgacagc tcagctgcgg aaattg
1836

<210> 3040
<211> 142
<212> PRT
<213> Homo sapiens

<400> 3040
Thr Leu Cys His Cys Leu Asp Leu His Ile Arg Ala Ala Leu Met Pro
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Leu Pro Asp Thr Ala Thr Gly Leu Asp Trp Thr His Leu Val Asp Ala
20 25 30
Ala Arg Ala Phe Glu Asp Gln Arg Val Ala Ser Phe Cys Thr Leu Thr
35 40 45
Asp Met Gln His Gly Gln Asp Leu Glu Gly Ala Gln Glu Leu Pro Leu
50 55 60
Cys Val Asp Pro Gly Ser Gly Lys Glu Phe Met Asp Thr Thr Gly Glu
65 70 75 80
Arg Ser Pro Ser Pro Leu Thr Gly Lys Val Asn Gln Leu Glu Leu Ile

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                85                  90                  95
Leu Arg Gln Leu Gln Thr Asp Leu Arg Lys Glu Lys Gln Asp Lys Ala
            100                 105                 110
Gly Leu Gln Ala Glu Val Gln His Leu Arg Gln Asp Asn Met Arg Leu
        115                 120                 125
Gln Glu Glu Ser Gln Thr Ala Thr Ala Gln Leu Arg Lys Leu
    130                 135                 140
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<210> 3041
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 3041
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540
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600
ggccgcattc accggttcgt ggagaagcca caggtgtttg tgtccaataa gatcaacgca
660
ggcatgtaca tcctgagccc tgcagtgctg cggcgcatcc agctgcagcc tacgtccatt
720
gagaaggagg tcttccccat tatggccaag gaggggcagc tatatgccat ggagttacag
780
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840
cagtcactga ggcagaagca gcctgagcgg ctgtgctcag gccctggcat tgtgggcaac
900
gtgctggtgg acccaagtgc ccgcatcggc cagaactgca gcattggccc caatgtgagc
960
ctgggacctg gcgtggtggt cgaagatggt gtgtgtatcc ggcggtgcac ggtgctgcgg
1020
gatgcccgga tccgttccca ttcctggctt gagtcctgca ttgtgggctg gcgctgccgc
1080
gtgggtcagt gggtacgcat ggagaacgtg acagtgctgg gtgaggacgt catagttaat
1140
gatgagctct acctcaacgg agccagcgtg ctgccccaca agtctattgg cgagtcagtg
1200

ccagagcctc gtatcatcat gtgaggggat gcagtggggc tggccgagcc ccggttttcc
1260
catcagcaag gggagtgctg gcctgacaca tcagaagacc ctggacttgt cattatttgt
1320
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1380
ctggcaggat ccctgctggg cacaccccac aaaccccact ccctcaagaa gggccagggc
1440
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1500
aaaaaaaaaa aa
1512

<210> 3042
<211> 360
<212> PRT
<213> Homo sapiens

<400> 3042
Met Lys Ala Leu Ile Leu Val Gly Gly Tyr Gly Thr Arg Leu Arg Pro
1 5 10 15
Leu Thr Leu Ser Thr Pro Lys Pro Leu Val Asp Phe Cys Asn Lys Pro
20 25 30
Ile Leu Leu His Gln Val Glu Ala Leu Ala Ala Ala Gly Val Asp His
35 40 45
Val Ile Leu Ala Val Ser Tyr Met Ser Gln Val Leu Glu Lys Glu Met
50 55 60
Lys Ala Gln Glu Gln Arg Leu Gly Ile Arg Ile Ser Met Ser His Glu
65 70 75 80
Glu Glu Pro Leu Gly Thr Ala Gly Pro Leu Ala Leu Ala Arg Asp Leu
85 90 95
Leu Ser Glu Thr Ala Asp Pro Phe Phe Val Leu Asn Ser Asp Val Ile
100 105 110
Cys Asp Phe Pro Phe Gln Ala Met Val Gln Phe His Arg His His Gly
115 120 125
Gln Glu Gly Ser Ile Leu Val Thr Lys Val Glu Glu Pro Ser Lys Tyr
130 135 140
Gly Val Val Val Cys Glu Ala Asp Thr Gly Arg Ile His Arg Phe Val
145 150 155 160
Glu Lys Pro Gln Val Phe Val Ser Asn Lys Ile Asn Ala Gly Met Tyr
165 170 175
Ile Leu Ser Pro Ala Val Leu Arg Arg Ile Gln Leu Gln Pro Thr Ser
180 185 190
Ile Glu Lys Glu Val Phe Pro Ile Met Ala Lys Glu Gly Gln Leu Tyr
195 200 205
Ala Met Glu Leu Gln Gly Phe Trp Met Asp Ile Gly Gln Pro Lys Asp
210 215 220
Phe Leu Thr Gly Met Cys Leu Phe Leu Gln Ser Leu Arg Gln Lys Gln
225 230 235 240
Pro Glu Arg Leu Cys Ser Gly Pro Gly Ile Val Gly Asn Val Leu Val
245 250 255
Asp Pro Ser Ala Arg Ile Gly Gln Asn Cys Ser Ile Gly Pro Asn Val
260 265 270
Ser Leu Gly Pro Gly Val Val Val Glu Asp Gly Val Cys Ile Arg Arg

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        275                 280                 285
Cys Thr Val Leu Arg Asp Ala Arg Ile Arg Ser His Ser Trp Leu Glu
    290                 295                 300
Ser Cys Ile Val Gly Trp Arg Cys Arg Val Gly Gln Trp Val Arg Met
305                 310                 315                 320
Glu Asn Val Thr Val Leu Gly Glu Asp Val Ile Val Asn Asp Glu Leu
                325                 330                 335
Tyr Leu Asn Gly Ala Ser Val Leu Pro His Lys Ser Ile Gly Glu Ser
            340                 345                 350
Val Pro Glu Pro Arg Ile Ile Met
        355                 360
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<210> 3043
<211> 394
<212> DNA
<213> Homo sapiens

<400> 3043
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tctcatgatg ccagcgcttc ctcttcactg gcgtctgacc caggagcagt ccagaatcag
120
cttctctgac ctcactccaa ctcacgtgtc tttgacactt taagggactt cctgttttag
180
ggtcttctgg ctgggtgtca ttgaatgggc agtgattctc taactttaga ctgatgttcc
240
ccagcctttg tttggggact cggaggcaga gtagacagtt acccttaccc ctgggttggg
300
gagggtcata ttcctggtat ccccaggagg tcaacagggg cttcattttt ctgagggact
360
agagggtctt gtggagctcc tgggacagag atct
394

<210> 3044
<211> 115
<212> PRT
<213> Homo sapiens

<400> 3044
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Met Lys Pro Leu Leu Thr Ser Trp Gly Tyr Gln Glu Tyr Asp Pro Pro
 1               5                  10                  15
Gln Pro Arg Gly Lys Gly Asn Cys Leu Leu Cys Leu Arg Val Pro Lys
            20                  25                  30
Gln Arg Leu Gly Asn Ile Ser Leu Lys Leu Glu Asn His Cys Pro Phe
        35                  40                  45
Asn Asp Thr Gln Pro Glu Asp Pro Lys Thr Gly Ser Pro Leu Lys Cys
    50                  55                  60
Gln Arg His Val Ser Trp Ser Glu Val Arg Glu Ala Asp Ser Gly Leu
65                  70                  75                  80
Leu Leu Gly Gln Thr Pro Val Lys Arg Lys Arg Trp His His Glu Thr
                85                  90                  95
Ser Ser Phe Ser Pro Cys Leu Trp Leu Lys Ala Arg Ala Ser Arg Ser
            100                 105                 110
Lys Glu Ile
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115

<210> 3045
<211> 605
<212> DNA
<213> Homo sapiens

<400> 3045
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60
gaagaaattc tttgttacaa gctgctatcc atgtccaggg ccaaacatga atcctattgc
120
tcttgggagc cgctggcttg cttatgcaga aaacaagttg attcgatgtc atcagtcccg
180
tggtggagcc tgtggagaca acattcagtc ttatactgcc acagtcatta gtgctgctaa
240
aacattgaaa agtggcctga caatggtagg gaaagtggtg actcagctga caggcacact
300
gccttcaggt gtgacagaag atgatgttgc catccacagt aattcacggc ggagtccttt
360
ggtcccaggc atcatcacag ttattgacac cgaaaccgtg gagagggcca ggtgtttgtg
420
agtgaggatc ttgacagtga tggcattgtg gcccacttcc ctgcccatga gaagccagtg
480
tgctgcatgg cttttaatac aagtggaatg cttctagtca caacagacac ccttggccat
540
gactttcatg tcttccaaat tctgactcat ccttggtcct catctacgga gagacgacaa
600
cgcgt
605

<210> 3046
<211> 72
<212> PRT
<213> Homo sapiens

<400> 3046
His Arg Asn Arg Gly Glu Gly Gln Val Phe Val Ser Glu Asp Leu Asp
1 5 10 15
Ser Asp Gly Ile Val Ala His Phe Pro Ala His Glu Lys Pro Val Cys
20 25 30
Cys Met Ala Phe Asn Thr Ser Gly Met Leu Leu Val Thr Thr Asp Thr
35 40 45
Leu Gly His Asp Phe His Val Phe Gln Ile Leu Thr His Pro Trp Ser
50 55 60
Ser Ser Thr Glu Arg Arg Gln Arg
65 70

<210> 3047
<211> 391
<212> DNA
<213> Homo sapiens

<400> 3047

attttggagg agaggaagaa tgaaatgacc caagtcatta cccgaaccca agaggagaaa
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ctggaacatg tccgtgctct gatcaaaaag tattctgatc atttggagaa cgtctcaaag
120
ttggttgagt caggaattca gtttatggat gagccagaaa tggcagtgtt tctgcagaat
180
gccaaaaccc tgctaaaaaa aatctcggaa gcatcaaagg catttcagat ggagaaaata
240
gaacatggct atgagaacat gaaccacttc acagtcaacc tcaatagaga agaaaagata
300
atacgtgaaa ttgactttta cagagaagat gaagatgaag aagaagaaga aggcggagaa
360
ggagaaaaag aagagaagga gaagtgggag a
391

<210> 3048
<211> 122
<212> PRT
<213> Homo sapiens

<400> 3048
Met Thr Gln Val Ile Thr Arg Thr Gln Glu Glu Lys Leu Glu His Val
1 5 10 15
Arg Ala Leu Ile Lys Lys Tyr Ser Asp His Leu Glu Asn Val Ser Lys
20 25 30
Leu Val Glu Ser Gly Ile Gln Phe Met Asp Glu Pro Glu Met Ala Val
35 40 45
Phe Leu Gln Asn Ala Lys Thr Leu Leu Lys Lys Ile Ser Glu Ala Ser
50 55 60
Lys Ala Phe Gln Met Glu Lys Ile Glu His Gly Tyr Glu Asn Met Asn
65 70 75 80
His Phe Thr Val Asn Leu Asn Arg Glu Glu Lys Ile Ile Arg Glu Ile
85 90 95
Asp Phe Tyr Arg Glu Asp Glu Asp Glu Glu Glu Glu Glu Gly Gly Glu
100 105 110
Gly Glu Lys Glu Glu Lys Glu Lys Trp Glu
115 120

<210> 3049
<211> 599
<212> DNA
<213> Homo sapiens

<400> 3049
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tttcagatgt tcctggttcg ccgggacagc agctcgaagc agctggtgct ctgtgtccac
120
tttccttctc tgaacgaaag ctcggccgag gtgctcgaat acaccattaa ggaagaaaag
180
tcgatattgt acctggaagg ctcggctctt gtgtttgagg acatcttcag attgattgcg
240
ttctactgtg tcagtagaga cttactgccc ttcacactgc ggctacccca ggccatcctt
300

gaggccagca gcttcacgga ccttgagacc atcgccaacc tgggtctggg tttctgggac
360
tcctcgctga atcctccaca agaaagaggg aagccagcag agcccccaag agaccgggcc
420
cccggattcc ccctagtctc cagcctcagg cccacagccc atgacgcaaa ctgtgcctgt
480
gaaatcgagc tgtcggtagg aaatgaccgc ctgtggtttg tgaatcctat tttcatcgag
540
gactgcagca gcgccctgcc caccgaccag ccacctcttg gaaattgccc ttcacgcgt
599

<210> 3050
<211> 177
<212> PRT
<213> Homo sapiens

<400> 3050
Met Phe Leu Val Arg Arg Asp Ser Ser Ser Lys Gln Leu Val Leu Cys
 1   5   10   15
Val His Phe Pro Ser Leu Asn Glu Ser Ser Ala Glu Val Leu Glu Tyr
            20   25   30
Thr Ile Lys Glu Glu Lys Ser Ile Leu Tyr Leu Glu Gly Ser Ala Leu
        35   40   45
Val Phe Glu Asp Ile Phe Arg Leu Ile Ala Phe Tyr Cys Val Ser Arg
    50   55   60
Asp Leu Leu Pro Phe Thr Leu Arg Leu Pro Gln Ala Ile Leu Glu Ala
65   70   75   80
Ser Ser Phe Thr Asp Leu Glu Thr Ile Ala Asn Leu Gly Leu Gly Phe
                85   90   95
Trp Asp Ser Ser Leu Asn Pro Pro Gln Glu Arg Gly Lys Pro Ala Glu
            100   105   110
Pro Pro Arg Asp Arg Ala Pro Gly Phe Pro Leu Val Ser Ser Leu Arg
        115   120   125
Pro Thr Ala His Asp Ala Asn Cys Ala Cys Glu Ile Glu Leu Ser Val
    130   135   140
Gly Asn Asp Arg Leu Trp Phe Val Asn Pro Ile Phe Ile Glu Asp Cys
145   150   155   160
Ser Ser Ala Leu Pro Thr Asp Gln Pro Pro Leu Gly Asn Cys Pro Ser
                165   170   175
Arg

<210> 3051
<211> 820
<212> DNA
<213> Homo sapiens

<400> 3051
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60
agacgatgga aacattgcca gtgaagacag ctccctctca gatgcccttg ttcttgagga
120
tgaagactct caggttacca gcacaatatc ccccctacat tctcctcaca agggactccc
180

tcctcggcca ccgtcgcaca acaggcctcc tcctccccag tccctggagg gactccgaca
240
gatgcactat caccgncaac gactatgaca agtcacccat caagcccaaa atgtggagtg
300
agtcctcttt agatgaaccc tatgagaagg tcaagaagcg ctcctctcac agccattcca
360
gcagccacaa gcgcttcccc agcacaggaa gctgtgcgga agccggcgga ggaagcaact
420
ccttgcagaa cagccccatc cgcggcctcc cgcactggaa ctcccagtcc agcatgccgt
480
ccacgccaga cctgcgggtc cggagtcccc actacgtcca ttccacgagg tcggtggaca
540
tcagccccac ccgactgcac agcctcgcac tgcactttag gcaccggagc tccagcctgg
600
agtcccaggg caagctcctg ggctcggaaa acgacaccgg gagccccgac ttctacaccc
660
cgcggactcg tagcagcaac ggctcagacc ccatggacga ctgctcgtcg tgcaccagcc
720
actcgagctc ggagcactac tacccggcgc agatgaacgc caactactcc acgctggccg
780
aggactcgcc gtccaaggcg cggctgcatg gatattcgac
820

<210> 3052
<211> 62
<212> PRT
<213> Homo sapiens

<400> 3052
Arg Leu Ser Gly Tyr Gln His Asn Ile Pro Pro Thr Phe Ser Ser Gln
 1   5   10   15
Gly Thr Pro Ser Ser Ala Thr Val Ala Gln Gln Ala Ser Ser Ser Pro
            20   25   30
Val Pro Gly Gly Thr Pro Thr Asp Ala Leu Ser Pro Xaa Thr Thr Met
        35   40   45
Thr Ser His Pro Ser Ser Pro Lys Cys Gly Val Ser Pro Leu
    50   55   60

<210> 3053
<211> 2625
<212> DNA
<213> Homo sapiens

<400> 3053
agtggctgnt cagaacatac atctntcatg ctttcattgt ctcaccaaga gaagccagaa
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gagcctccga catctaatga atgcttagaa gatataaccg taaaagatgg actttctctc
120
cagtttaaaa gatttagaga aactgtacca acttgggata caataagaga tgaagaagat
180
gttcttgatg agctcttgca gtatttgggt gttactagtc ctgaatgctt acagagaact
240
ggaatctcac ttaatattcc tgctccacaa cctgtgtgca tttctgaaaa acaagaaaat
300

gatgttatta atgctatcct taagcaacat acagaagaaa aagaatttgt tgagaagcac
360
tttaatgact taaacatgaa agctgtggaa caagatgaac caatacctca aaaacctcag
420
tcagcatttt attattgcag attgcttctt agtatattgg gaatgaattc ctgggacaaa
480
cggaggagct ttcatctcct gaagaaaaat gaaaagctac ttagagaact taggaacttg
540
gattcaaggc agtgccgaga gacacacaag attgcagtat tttatgttgc tgaaggacaa
600
gaagacaaac actccattct caccaataca ggaggaagtc aagcatatga agattttgta
660
gctggtcttg gttgggaggt aaatcttaca aaccattgtg gttttatggg aggactacaa
720
aaaaacaaaa gcactggatt gaccactcca tattttgcta cctctacagt agaggtaata
780
tttcacgtgt caacaagaat gccttctgat tctgatgatt ctttgaccaa aaaattgaga
840
catttgggaa atgatgaagt gcacattgtt tggtcagagc atactagaga ctacaggaga
900
ggaattattc ccacagaatt tggtgatgtc cttattgtaa tatatccaat gaaaaatcac
960
atgttcagta ttcagataat gaaaaaacca gaggttccct tctttggtcc ccttttgat
1020
ggtgctattg tgaatggaaa ggttctaccc attatggtta gagcaacagc tataaatgca
1080
agccgtgctc tgaaatctct gattccattg tatcaaaact tctatgagga gagagcacga
1140
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1200
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1260
gttctgttta tctgaaggct cctacccaga gattctaccc agtgaaactc ccacagcaac
1320
gcaggtagat ggggctgacc tggcctctcc aatgtctcct cgaactagca aaagccgcat
1380
gtccatgaag ctgcgtcgtt cctctggctc agccaataaa tcctaaggag acaagcagcc
1440
cagcagtgat cagcagtagc caccttagca cgaacatagg gttaaccctt tcaggccttc
1500
atgtctgcca taacatgcat gtttcttcct gtacatttat ttgagaaaac actggattta
1560
aataatttta aataatttgt agcttaatat taaagattta agttatttat tgtttcattt
1620
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1680
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1740
gccaaaatac aattggacaa ttagtctcat tatttattgt gccccattgc aactttatgg
1800
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1860
acagcaaaag atgtacctgt taatacacag aatgtgtaca gattatttgt tatgacaata
1920

aaacactcaa aataaatggt ctttagcatc tcaaattcca actgaaatca ttttagtatt
1980
aactcttctt cccaaagcaa tgtctcattt cttggctgtg caggtgatgc catgttatat
2040
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2220
tggggaagaa aagaaggaaa attttctgat ataaatatgt tgttcaaatt atgagtatta
2280
tttaaaaaag aaaaaggaac ataacccagg agtctaagtt aaatctaata ttgttaatac
2340
tgaacttgca ggtccaggtt ggtatacatt ccaccctcta gaagtatttt cttacagtag
2400
ataagctgct cacattttgt tttgaatggg catctcctga ggaaatgtag catgacattg
2460
gtactaactg catgtgtaaa tacatcatac tggcaaaccg taaaatataa attatgtatc
2520
atcattcatg tagtatctat aatttgtaac agtgggggggg aaagatgaca tggtatttaa
2580
taatacaata aaaatattct tatcacttcc taaaaaaaaa aaaaa
2625

<210> 3054
<211> 417
<212> PRT
<213> Homo sapiens

<400> 3054
Ser Gly Xaa Ser Glu His Thr Ser Xaa Met Leu Ser Leu Ser His Gln
1 5 10 15
Glu Lys Pro Glu Glu Pro Pro Thr Ser Asn Glu Cys Leu Glu Asp Ile
20 25 30
Thr Val Lys Asp Gly Leu Ser Leu Gln Phe Lys Arg Phe Arg Glu Thr
35 40 45
Val Pro Thr Trp Asp Thr Ile Arg Asp Glu Glu Asp Val Leu Asp Glu
50 55 60
Leu Leu Gln Tyr Leu Gly Val Thr Ser Pro Glu Cys Leu Gln Arg Thr
65 70 75 80
Gly Ile Ser Leu Asn Ile Pro Ala Pro Gln Pro Val Cys Ile Ser Glu
85 90 95
Lys Gln Glu Asn Asp Val Ile Asn Ala Ile Leu Lys Gln His Thr Glu
100 105 110
Glu Lys Glu Phe Val Glu Lys His Phe Asn Asp Leu Asn Met Lys Ala
115 120 125
Val Glu Gln Asp Glu Pro Ile Pro Gln Lys Pro Gln Ser Ala Phe Tyr
130 135 140
Tyr Cys Arg Leu Leu Leu Ser Ile Leu Gly Met Asn Ser Trp Asp Lys
145 150 155 160
Arg Arg Ser Phe His Leu Leu Lys Lys Asn Glu Lys Leu Leu Arg Glu
165 170 175
Leu Arg Asn Leu Asp Ser Arg Gln Cys Arg Glu Thr His Lys Ile Ala

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            180                 185                 190
Val Phe Tyr Val Ala Glu Gly Gln Glu Asp Lys His Ser Ile Leu Thr
        195                 200                 205
Asn Thr Gly Gly Ser Gln Ala Tyr Glu Asp Phe Val Ala Gly Leu Gly
    210                 215                 220
Trp Glu Val Asn Leu Thr Asn His Cys Gly Phe Met Gly Gly Leu Gln
225                 230                 235                 240
Lys Asn Lys Ser Thr Gly Leu Thr Thr Pro Tyr Phe Ala Thr Ser Thr
                245                 250                 255
Val Glu Val Ile Phe His Val Ser Thr Arg Met Pro Ser Asp Ser Asp
            260                 265                 270
Asp Ser Leu Thr Lys Lys Leu Arg His Leu Gly Asn Asp Glu Val His
        275                 280                 285
Ile Val Trp Ser Glu His Thr Arg Asp Tyr Arg Arg Gly Ile Ile Pro
    290                 295                 300
Thr Glu Phe Gly Asp Val Leu Ile Val Ile Tyr Pro Met Lys Asn His
305                 310                 315                 320
Met Phe Ser Ile Gln Ile Met Lys Lys Pro Glu Val Pro Phe Phe Gly
                325                 330                 335
Pro Leu Phe Asp Gly Ala Ile Val Asn Gly Lys Val Leu Pro Ile Met
            340                 345                 350
Val Arg Ala Thr Ala Ile Asn Ala Ser Arg Ala Leu Lys Ser Leu Ile
        355                 360                 365
Pro Leu Tyr Gln Asn Phe Tyr Glu Glu Arg Ala Arg Tyr Leu Gln Thr
    370                 375                 380
Ile Val Gln His His Leu Glu Pro Thr Thr Phe Glu Asp Phe Ala Ala
385                 390                 395                 400
Gln Val Phe Ser Pro Ala Pro Tyr His His Leu Pro Ser Asp Ala Asp
                405                 410                 415
His
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<210> 3055
<211> 905
<212> DNA
<213> Homo sapiens

<400> 3055
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ctatcgaacc ctctacatcg ggacaggagc tgacatggat gtgtgcctta caaactatgg
120
tcactgtaac tacgtgtccg ggaaacatgc ctgcatattc tacgatgaga ataccaaaca
180
ttatgagctg ttaaactaca gtgagcatgg gacaacggtg gacaatgtgc tgtattcatg
240
tgacttctcg gagaagaccc cgccaacccc cccaagcagt attgttgcca aagtgcagag
300
tgtcatcagg cgccgccggc accagaaaca ggacgaagag ccaagtgagg aggcagccat
360
gatgagttcc caggcccagg ggccgcagcg gagaccctgc aattgcaaag ccagcagctc
420
gagcttgatt gggggcagtg gggccggctg ggagggcaca gccttactgc accatggcag
480

ctacatcaag ctgggctgcc tgcagtttgt cttcagcatc actgagtttg cgaccaaaca
540
gcccaaaggc gatgccagcc tgctgcagga tggggtcttg gccgagaagc tctctctcaa
600
gccccaccag ggccctgtgc tgcgctccaa ctctgttcct taggactggc ggctaccccg
660
ccactggcct gtacacccac ccaagactcc tgcaatgcaa aaatgtacac aaaccaagcc
720
cgggtgtttt ctatactcta ccagaaaccc ttcaactaca atctttgcat gaaatgaaga
780
aaacctttg actgtttttt aaaaatcctt tttcttttct caagttctag ggggcatttg
840
cacatatatt tgtactcaac atttcatggg aaagcggcag acctgagctg aggaacagcg
900
tgggc
905

<210> 3056
<211> 195
<212> PRT
<213> Homo sapiens

<400> 3056
Met Ser Tyr Arg Thr Leu Tyr Ile Gly Thr Gly Ala Asp Met Asp Val
1 5 10 15
Cys Leu Thr Asn Tyr Gly His Cys Asn Tyr Val Ser Gly Lys His Ala
20 25 30
Cys Ile Phe Tyr Asp Glu Asn Thr Lys His Tyr Glu Leu Leu Asn Tyr
35 40 45
Ser Glu His Gly Thr Thr Val Asp Asn Val Leu Tyr Ser Cys Asp Phe
50 55 60
Ser Glu Lys Thr Pro Pro Thr Pro Pro Ser Ser Ile Val Ala Lys Val
65 70 75 80
Gln Ser Val Ile Arg Arg Arg Arg His Gln Lys Gln Asp Glu Glu Pro
85 90 95
Ser Glu Glu Ala Ala Met Met Ser Ser Gln Ala Gln Gly Pro Gln Arg
100 105 110
Arg Pro Cys Asn Cys Lys Ala Ser Ser Ser Ser Leu Ile Gly Gly Ser
115 120 125
Gly Ala Gly Trp Glu Gly Thr Ala Leu Leu His His Gly Ser Tyr Ile
130 135 140
Lys Leu Gly Cys Leu Gln Phe Val Phe Ser Ile Thr Glu Phe Ala Thr
145 150 155 160
Lys Gln Pro Lys Gly Asp Ala Ser Leu Leu Gln Asp Gly Val Leu Ala
165 170 175
Glu Lys Leu Ser Leu Lys Pro His Gln Gly Pro Val Leu Arg Ser Asn
180 185 190
Ser Val Pro
195

<210> 3057
<211> 2169
<212> DNA
<213> Homo sapiens

<400> 3057
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acgacgctgc ctcctgggcg ccatgagttc ctgttcagct tccagctgcc cccgaccctg
120
gtgacatcct tcgagggcaa acacggtagt gtccgctact gtatcaaggc caccctgcac
180
cggccctggg tcccagcacg ccgggcaagg aaggtgttca ctgtcatcga gcctgtggac
240
atcaacacgc cagccctgct ggcacctcaa gcgggggctc gggaaaaggt tgcccgatcc
300
tggtactgta accgtggcct agtctccctt tcggccaaga tcgaccgcaa gggctacacc
360
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420
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540
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1080
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1140
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1320
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1380
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1560

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1680
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1740
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1800
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1920
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1980
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2040
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2160
aaaaaaaaa
2169

<210> 3058
<211> 298
<212> PRT
<213> Homo sapiens

<400> 3058
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Ser Val Arg Tyr Cys Ile Lys Ala Thr Leu His Arg Pro Trp Val Pro
20 25 30
Ala Arg Arg Ala Arg Lys Val Phe Thr Val Ile Glu Pro Val Asp Ile
35 40 45
Asn Thr Pro Ala Leu Leu Ala Pro Gln Ala Gly Ala Arg Glu Lys Val
50 55 60
Ala Arg Ser Trp Tyr Cys Asn Arg Gly Leu Val Ser Leu Ser Ala Lys
65 70 75 80
Ile Asp Arg Lys Gly Tyr Thr Pro Gly Glu Val Ile Pro Val Phe Ala
85 90 95
Glu Ile Asp Asn Gly Ser Thr Arg Pro Val Leu Pro Arg Ala Ala Val
100 105 110
Val Gln Thr Gln Thr Phe Met Ala Arg Gly Ala Arg Lys Gln Lys Arg
115 120 125
Ala Val Val Ala Ser Leu Ala Gly Glu Pro Val Gly Pro Gly Gln Arg
130 135 140
Ala Leu Trp Gln Gly Arg Ala Leu Arg Ile Pro Pro Val Gly Pro Ser
145 150 155 160
Ile Leu His Cys Arg Val Leu His Val Asp Tyr Ala Leu Lys Val Cys
165 170 175
Val Asp Ile Pro Gly Thr Ser Lys Leu Leu Leu Glu Leu Pro Leu Val
180 185 190
Ile Gly Thr Ile Pro Leu His Pro Phe Gly Ser Arg Ser Ser Ser Val

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        195                 200                 205
Gly Ser His Ala Ser Phe Leu Leu Asp Trp Arg Leu Gly Ala Leu Pro
    210                 215                 220
Glu Arg Pro Glu Ala Pro Pro Glu Tyr Ser Glu Val Val Ala Asp Thr
225                 230                 235                 240
Glu Glu Ala Ala Leu Gly Gln Ser Pro Phe Pro Leu Pro Gln Asp Pro
                245                 250                 255
Asp Met Ser Leu Glu Gly Pro Phe Phe Ala Tyr Ile Gln Glu Phe Arg
            260                 265                 270
Tyr Arg Pro Pro Pro Leu Tyr Ser Glu Glu Asp Pro Asn Pro Leu Leu
        275                 280                 285
Gly Asp Met Arg Pro Arg Cys Met Thr Cys
    290                 295
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<210> 3059
<211> 1411
<212> DNA
<213> Homo sapiens

<400> 3059
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120
cccaaaggtc tggacccaga aatgggacgt cggtcatcag atactgaaga agaaagcaga
180
agcaagagaa aaaagaaaca ccgtagacgg tcctcctcga gcagttcttc agatagtaga
240
acatacagcc gaaagaaagg aggaaggaaa tcaagatcaa agtcaagatc ttggtccaga
300
gatcttcagc ctcgttcaca ttcttatgat agaagacgca ggcatcgatc aagcagtagc
360
tcttcttatg gctccagaag gaaacgaagt cgaagtcgtt caaggggtcg agggaaatcc
420
tatagagttc agaggtctag gtcaaaaagc agaacaagaa ggtccaggtc aagacctcgt
480
ctccgttctc atagtcgtag cagtgaaagg tccagtcaca gaagaacgcg tagtcggtct
540
cgggatagag aacgacgtaa gggcagagat aaagagaaaa gagaaaagga gaaggataaa
600
gggaaggaca aggaattaca taacatcaaa cgtggggaat ctggaaacat caaagctgga
660
ttagaacatc tgccaccagc tgaacaggcc aaagccagac tacagctggt tcttgaagct
720
gctgcaaaag ctgatgaagc attgaaagcc aaagaaagaa atgaggaaga agcaaagaga
780
agaaaggagg aagaccaagc caccctggta gaacaagtaa aaagagtaaa agaaattgaa
840
gctattgaaa gtgattcttt tgttcagcag acattcagat caagtaaaga agtcaaaaag
900
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960
gctgatccac ccagtactga aaaagaaata gatcctacca gcatccctac tgctatcaag
1020

taccaagatg acaattccct ggcccatcca aatttattta tcgagaaagc tgatgctgag
1080
gaaaaatggt tcaagagatt aattgctctc cgacaagaaa gactaatggg cagtcctgtg
1140
gcctaagtaa tatacatata gttggattgg attgtcagca gtaacattgg aaatttaggt
1200
ttttaaatcc caatattaac tttttactct taaaaagaat tttgctgatt atatataaag
1260
gtagtctcat ttcatttgtc tctcatgtag gcttgaatat ttgttaattt gaattaaatc
1320
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1380
agctaaacat aaataagtct gttaaaaaaa a
1411

<210> 3060
<211> 334
<212> PRT
<213> Homo sapiens

<400> 3060
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Lys Lys Lys His Arg Arg Arg Ser Ser Ser Ser Ser Ser Ser Asp Ser
20 25 30
Arg Thr Tyr Ser Arg Lys Lys Gly Gly Arg Lys Ser Arg Ser Lys Ser
35 40 45
Arg Ser Trp Ser Arg Asp Leu Gln Pro Arg Ser His Ser Tyr Asp Arg
50 55 60
Arg Arg Arg His Arg Ser Ser Ser Ser Ser Ser Tyr Gly Ser Arg Arg
65 70 75 80
Lys Arg Ser Arg Ser Arg Ser Arg Gly Arg Gly Lys Ser Tyr Arg Val
85 90 95
Gln Arg Ser Arg Ser Lys Ser Arg Thr Arg Arg Ser Arg Ser Arg Pro
100 105 110
Arg Leu Arg Ser His Ser Arg Ser Ser Glu Arg Ser Ser His Arg Arg
115 120 125
Thr Arg Ser Arg Ser Arg Asp Arg Glu Arg Arg Lys Gly Arg Asp Lys
130 135 140
Glu Lys Arg Glu Lys Glu Lys Asp Lys Gly Lys Asp Lys Glu Leu His
145 150 155 160
Asn Ile Lys Arg Gly Glu Ser Gly Asn Ile Lys Ala Gly Leu Glu His
165 170 175
Leu Pro Pro Ala Glu Gln Ala Lys Ala Arg Leu Gln Leu Val Leu Glu
180 185 190
Ala Ala Ala Lys Ala Asp Glu Ala Leu Lys Ala Lys Glu Arg Asn Glu
195 200 205
Glu Glu Ala Lys Arg Arg Lys Glu Glu Asp Gln Ala Thr Leu Val Glu
210 215 220
Gln Val Lys Arg Val Lys Glu Ile Glu Ala Ile Glu Ser Asp Ser Phe
225 230 235 240
Val Gln Gln Thr Phe Arg Ser Ser Lys Glu Val Lys Lys Ser Val Glu
245 250 255
Pro Ser Glu Val Lys Gln Ala Thr Ser Thr Ser Gly Pro Ala Ser Ala

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            260                 265                 270
Val Ala Asp Pro Pro Ser Thr Glu Lys Glu Ile Asp Pro Thr Ser Ile
        275                 280                 285
Pro Thr Ala Ile Lys Tyr Gln Asp Asp Asn Ser Leu Ala His Pro Asn
    290                 295                 300
Leu Phe Ile Glu Lys Ala Asp Ala Glu Glu Lys Trp Phe Lys Arg Leu
305                 310                 315                 320
Ile Ala Leu Arg Gln Glu Arg Leu Met Gly Ser Pro Val Ala
                325                 330
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<210> 3061
<211> 1554
<212> DNA
<213> Homo sapiens

<400> 3061
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caggtgagcg gcagccaggt atggcgttga cggtggatgt ggccgggcca gcgccctggg
120
gcttccgtat cacaggggge agggatttcc acacgcccat catggtgact aaggtggccg
180
agcggggcaa agccaaggac gctgacctcc ggcctggaga cataatcgtg gccatcaacg
240
gggaaagcgc ggagggcatg ctgcatgccg aggcccagag caagatccgc cagagcccct
300
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360
acagctcctt ggaagtgctg gcgactcgct tccagggctc cgtgaggaca tacactgaga
420
gtcagtcctc cttaaggtcc tcctactcca gcccaacctc cctcagcccg agggccggca
480
gcccccttctc accaccaccc tctagcagct ccctcactgg agaggcggcc atcagcgctg
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660
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720
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780
gccccccgac agtccagctc ctttcgactc ttgcaggaag ccctggaggc tgaggagaga
840
ggtggcacgc cagccttctt gcccagctca ctgagccccc agtcctccct gcccgcctcc
900
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960
aaccaggctg tgcgcatcca ggagggccgg taccgccacc ccggctgcta cacctgtgcc
1020
gactgtgggc tgaacctgaa gatgcgcggg cacttctggg tgggtgacga gctgtactgt
1080
gagaagcatg cccgccagcg ctactccgca cctgccaccc tcagctctcg ggcctgagcc
1140

cgccatgccc tcagcctgcc tcactgctgg gccagggtca tgcctatata agttggcatg
1200
gcagggacaa tggtgggcag ttgctcttac atgagctaag tttggagacc tgaggcccct
1260
ttgtcctcgc tgggtgggcc aaggtctggg acctgtcttg gactgtggga gactcaccct
1320
caccttgcca ggcctctccc ctgcaggact ggcattgcac tagtctgagg tggccactgc
1380
ctttgatcaa cctttgtgtg cgagggtcta agtagggtcg aacacagaag tgggaaggag
1440
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1554

<210> 3062
<211> 146
<212> PRT
<213> Homo sapiens

<400> 3062
Met Asp Ser Glu Gly Gly Ser Leu Leu Leu Asp Glu Asp Ser Glu Val
 1   5   10   15
Phe Lys Met Leu Gln Glu Asn Arg Glu Gly Arg Ala Ala Pro Arg Gln
            20   25   30
Ser Ser Ser Phe Arg Leu Leu Gln Glu Ala Leu Glu Ala Glu Glu Arg
        35   40   45
Gly Gly Thr Pro Ala Phe Leu Pro Ser Ser Leu Ser Pro Gln Ser Ser
    50   55   60
Leu Pro Ala Ser Arg Ala Leu Ala Thr Pro Pro Lys Leu His Thr Cys
65   70   75   80
Glu Lys Cys Ser Thr Ser Ile Ala Asn Gln Ala Val Arg Ile Gln Glu
                85   90   95
Gly Arg Tyr Arg His Pro Gly Cys Tyr Thr Cys Ala Asp Cys Gly Leu
            100   105   110
Asn Leu Lys Met Arg Gly His Phe Trp Val Gly Asp Glu Leu Tyr Cys
        115   120   125
Glu Lys His Ala Arg Gln Arg Tyr Ser Ala Pro Ala Thr Leu Ser Ser
    130   135   140
Arg Ala
145

<210> 3063
<211> 386
<212> DNA
<213> Homo sapiens

<400> 3063
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aagcgagcca tcagttctgt gtgcacctac attgtttatc agtgtagtcg gccagctcct
120
ttacactcca gggatctgca ctccatgata gtggcagctt ttcagtgtct ctgtgtctgg
180

ctgacagagc accctgatat gcttgatgaa aaggactacc ttaaggaagt actggagatt
240
gtggaactgg gtatctcagg aagtaagtcc aagaacaatg agcaagaggt caagtacaaa
300
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360
acatggtatg gaagtgaccg cacagg
386

<210> 3064
<211> 128
<212> PRT
<213> Homo sapiens

<400> 3064
Xaa Leu Glu Leu Leu Ser Gly Leu Ala Lys Val Lys Val Met Val Asp
 1   5   10   15
Ser Gly Asp Arg Lys Arg Ala Ile Ser Ser Val Cys Thr Tyr Ile Val
            20   25   30
Tyr Gln Cys Ser Arg Pro Ala Pro Leu His Ser Arg Asp Leu His Ser
        35   40   45
Met Ile Val Ala Ala Phe Gln Cys Leu Cys Val Trp Leu Thr Glu His
    50   55   60
Pro Asp Met Leu Asp Glu Lys Asp Tyr Leu Lys Glu Val Leu Glu Ile
65   70   75   80
Val Glu Leu Gly Ile Ser Gly Ser Lys Ser Lys Asn Asn Glu Gln Glu
                85   90   95
Val Lys Tyr Lys Gly Asp Lys Glu Pro Asn Pro Ala Ser Met Arg Val
            100   105   110
Lys Asp Ala Ala Glu Ala Thr Leu Thr Trp Tyr Gly Ser Asp Arg Thr
        115   120   125

<210> 3065
<211> 2104
<212> DNA
<213> Homo sapiens

<400> 3065
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120
cttgtgggcc acgagttcga gcgggtcatt gaccagcacg gctgcgaggc catcgcgcgc
180
ctcatgccca aggtcgtgcg cgtcctggag atcctggagg tgctggtcag ccgccaccac
240
gtcgcgcccg agctggacga gctgcgcctg gagctggacc gcctgcgcct ggagaggatg
300
gaccgcatcg agaaggagcg caagcaccag aaggagctgg agctggtgga ggatgtgtgg
360
cgaggggagg cgcaggacct cctctcccag atcgcccagc tgcaggagga gaacaagcag
420
ctcatgacca acctctccca caaggatgtc aacttctcag aggaggagtt ccagaagcat
480

gaaggcatgt cagagcggga gcgacaggtg atgaagaagc tgaaggaggt ggtggacaaa
540
caacgcgacg agatccgcgc caaggacagg gagctgggcc tgaaaaatga ggacgttgag
600
gctttacagc agcagcagac acggctgatg aagatcaacc atgaccttcg gcaccgggtc
660
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720
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780
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960
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1020
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1080
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1140
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1320
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1440
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1500
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1560
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1620
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1680
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1800
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1860
taatgcctag agcatgtagc aatgttcaag gcaggtgcct tggaatctgc tgtgagttat
1920
gcagtactaa ccaaacaaag ttgctaagga tgagatgttg caacatttct tgtgtgcact
1980
ttttttttcct gacatctttt tttcctttta ggattcatta agtcatatac ttagtcccct
2040
gcaaagaaga agacagatgt cccagagcag actgaaagcg gggcgtggga tcctaggcaa
2100

tgca
2104

<210> 3066
<211> 183
<212> PRT
<213> Homo sapiens

<400> 3066
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Gln Glu Met Gly Ser Leu Arg Ala Glu Leu Gly Lys Leu Arg Glu Arg
20 25 30
Leu Gln Gly Glu His Ser Gln Asn Gly Glu Glu Glu Pro Glu Thr Glu
35 40 45
Pro Val Gly Glu Glu Ser Ile Ser Asp Ala Glu Lys Val Ala Met Xaa
50 55 60
Ser Gln Gly Pro Xaa Thr Ala Pro Gly Ser Pro Cys Arg Ser Cys Gly
65 70 75 80
Thr Cys Cys Thr Arg Gly Thr Xaa Leu Lys Ser Lys Val Phe Leu Leu
85 90 95
Gln Glu Glu Leu Ala Tyr Tyr Lys Ser Glu Glu Met Glu Glu Glu Asn
100 105 110
Arg Ile Pro Gln Pro Pro Pro Ile Ala His Pro Arg Thr Ser Pro Gln
115 120 125
Pro Glu Ser Gly Ile Lys Arg Leu Phe Ser Phe Phe Ser Arg Asp Lys
130 135 140
Lys Arg Leu Ala Asn Thr Gln Arg Asn Val His Ile Gln Glu Ser Phe
145 150 155 160
Gly Gln Trp Ala Asn Thr His Arg Asp Asp Gly Tyr Thr Glu Gln Gly
165 170 175
Gln Glu Ala Leu Gln His Leu
180

<210> 3067
<211> 645
<212> DNA
<213> Homo sapiens

<400> 3067
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120
tccnnagttc tagtccatca agcacgggag ccgactgcgg gctcaccacc ctgttctcta
180
ccccgacctg acttgcagcc cccgtccaca cctcccccgc ccgttcacaa ggagcaaaaa
240
aagtcagacc cacccccacc cccaccagga aaattcaagt ccttcctccc accgcggagc
300
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360
ccggccatgc ctcgtccacc ttcgggagcc ggcgacaggg agatccccag ggatctcgcg
420

tgtgcgccct acccaccccc gggggcagga cgggggagcg agcaccgatc ggcgccgggg
480
cgtcgatgcg gaagcaagga gccggaggcg gccgctagcc gccctccgag cccagcggaa
540
gaggagccgc cgcccgtgtc cgctgaggag actccgccta gcccggcgcc gccaccgcgg
600
ggcgagtggg gatgagggga cggagcgagg acggctccca cgcgt
645

<210> 3068
<211> 204
<212> PRT
<213> Homo sapiens

<400> 3068
Xaa Ala Ala Gly Gly Gly Gly Asp Glu Ser His Thr Gln Pro Ser Gly
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Pro Pro Ala Ala Met Ser Gly Ser Pro Ala Pro Lys Ala Gly Tyr Ala
            20   25   30
Ser Pro Asn Arg Ala Gln Gly Pro Ser Xaa Val Leu Val His Gln Ala
        35   40   45
Arg Glu Pro Thr Ala Gly Ser Pro Pro Cys Ser Leu Pro Arg Pro Asp
    50   55   60
Leu Gln Pro Pro Ser Thr Pro Pro Pro Pro Val His Lys Glu Gln Lys
65   70   75   80
Lys Ser Asp Pro Pro Pro Pro Pro Pro Gly Lys Phe Lys Ser Phe Leu
                85   90   95
Pro Pro Arg Ser Pro Gly Asn Ser Ala Leu Gly Pro Arg Arg Gly Trp
            100   105   110
Gly Trp Ile Ala Ala Gly Gly Ala Pro Ala Met Pro Arg Pro Pro Ser
        115   120   125
Gly Ala Gly Asp Arg Glu Ile Pro Arg Asp Leu Ala Cys Ala Pro Tyr
    130   135   140
Pro Pro Pro Gly Ala Gly Arg Gly Ser Glu His Arg Ser Ala Pro Gly
145   150   155   160
Arg Arg Cys Gly Ser Lys Glu Pro Glu Ala Ala Ala Ser Arg Pro Pro
                165   170   175
Ser Pro Ala Glu Glu Glu Pro Pro Pro Val Ser Ala Glu Glu Thr Pro
            180   185   190
Pro Ser Pro Ala Pro Pro Pro Arg Gly Glu Trp Gly
        195   200

<210> 3069
<211> 1561
<212> DNA
<213> Homo sapiens

<400> 3069
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aacatcttta catcaacaaa cacagcagtt tgactattga aatcataagc gatttatctt
120
gaaaaggtta tatttgtagg tggatgcaag tatattggag aaatatttct atcaaaatca
180

ctggttttgt taggagtatt ttgatttttc tatttttacg ctgggaaaaa aattaaaaca
240
agtatgtcag tgttcatttt atgggatagt tggcttcact gtgtttgtca tgtttgtccg
300
aattacagct gtttatcttg caactttaag attaattaaa tgcaaatgta actctgtgaa
360
tcatgggaat acctgccaga cctcttatta ataccttcac ttaaaacccc ctgtgcctga
420
gagtcattaa tttgctaaaa gaaaagtgct aaagcagccc tttgcccaca aacaattctg
480
cgatggctgc ccaattaatc ccaaagcatt ctgatcctcc tttcaggcct cgtggccctt
540
tgaggacaca agaaggctcc gatgataacc tggcaaccta ggtagaaacc cagccaagtg
600
tgagcgtttg aagctgcagt ttggctgcca tcgtgtcggc gaaaagaaag aattcaggca
660
ccatgtcatc cagtacaaag gataaaaacg gattcaaccg gaaattcaat gtggcaccac
720
atatgggata catgagtgcg gttatacaac aggccacata tttttttga acagtctcct
780
acatgtgatg ccgaggacat gtgtaaccat cataacgtct ctaggaatct gtatttaatt
840
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1380
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1561

<210> 3070
<211> 153
<212> PRT
<213> Homo sapiens

<400> 3070
Met His Leu Lys Asp Leu Gly Leu Asn Phe His Val Ser Val Leu Gly
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Glu Thr Phe Thr Asp Val Pro Asp Ile Phe Ser Glu Ala Lys Lys Ala
20 25 30
Leu Gly Ser Ser Val Leu His Trp Gly Tyr Leu Pro Ser Lys Asp Asp
35 40 45
Tyr Phe Gln Val Leu Cys Val Ala Asp Val Val Ile Ser Thr Ala Lys
50 55 60
His Glu Phe Phe Gly Val Ala Met Leu Glu Ala Val Tyr Cys Gly Cys
65 70 75 80
Tyr Pro Leu Cys Pro Lys Asp Leu Val Tyr Pro Glu Ile Phe Pro Ala
85 90 95
Glu Tyr Leu Tyr Ser Thr Pro Glu Gln Leu Ser Lys Arg Leu Gln Asn
100 105 110
Phe Cys Lys Arg Pro Asp Ile Ile Arg Lys His Leu Tyr Lys Gly Glu
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Ile Ala Pro Phe Ser Trp Ala Ala Leu His Gly Lys Phe Arg Ser Leu
130 135 140
Leu Thr Thr Glu Pro Arg Glu Asp Leu
145 150

<210> 3071
<211> 3343
<212> DNA
<213> Homo sapiens

<400> 3071
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240
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300
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360
cagtctccag gggagctcag tgtctgtttg tccagcttct cagagttgct gtgcagctcg
420
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480
gtggccacat tttctgcaga ggaagaaccg atgctggaac gtcgttgcag gggccccctg
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600
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660
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720
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780

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1080
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1260
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1380
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1740
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1980
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2280
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2400

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2580
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2760
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2880
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2940
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3000
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3060
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3120
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3180
ttccttataa tgaatgaatt ctgctttcct ataatttcta cctattgggc cttgttctgt
3240
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3300
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3343

<210> 3072
<211> 349
<212> PRT
<213> Homo sapiens

<400> 3072
Met Leu Glu Arg Arg Cys Arg Gly Pro Leu Ala Met Gly Leu Ala Gln
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Pro Arg Leu Leu Ser Gly Pro Ser Gln Glu Ser Pro Gln Thr Leu Gly
20 25 30
Lys Glu Ser Arg Gly Leu Arg Gln Gln Gly Thr Ser Val Ala Gln Ser
35 40 45
Gly Ala Gln Ala Pro Gly Arg Ala His Arg Cys Ala His Cys Arg Arg
50 55 60
His Phe Pro Gly Trp Val Ala Leu Trp Leu His Thr Arg Arg Cys Gln
65 70 75 80
Ala Arg Leu Pro Leu Pro Cys Pro Glu Cys Gly Arg Arg Phe Arg His
85 90 95
Ala Pro Phe Leu Ala Leu His Arg Gln Val His Ala Ala Ala Thr Pro
100 105 110
Asp Leu Gly Phe Ala Cys His Leu Cys Gly Gln Ser Phe Arg Gly Trp

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        115                 120                 125
Val Ala Leu Val Leu His Leu Arg Ala His Ser Ala Ala Lys Arg Pro
    130                 135                 140
Ile Ala Cys Pro Lys Cys Glu Arg Arg Phe Trp Arg Arg Lys Gln Leu
145                 150                 155                 160
Arg Ala His Leu Arg Arg Cys His Pro Pro Ala Pro Glu Ala Arg Pro
                165                 170                 175
Phe Ile Cys Gly Asn Cys Gly Arg Ser Phe Ala Gln Trp Asp Gln Leu
            180                 185                 190
Val Ala His Lys Arg Val His Val Ala Glu Ala Leu Glu Glu Ala Ala
        195                 200                 205
Ala Lys Ala Leu Gly Pro Arg Pro Arg Gly Arg Pro Ala Val Thr Ala
    210                 215                 220
Pro Arg Pro Gly Gly Asp Ala Val Asp Arg Pro Phe Gln Cys Ala Cys
225                 230                 235                 240
Cys Gly Lys Arg Phe Arg His Lys Pro Asn Leu Ile Ala His Arg Arg
                245                 250                 255
Val His Thr Gly Glu Arg Pro His Gln Cys Pro Glu Cys Gly Lys Arg
            260                 265                 270
Phe Thr Asn Lys Pro Tyr Leu Thr Ser His Arg Arg Ile His Thr Gly
        275                 280                 285
Glu Lys Pro Tyr Pro Cys Lys Glu Cys Gly Arg Arg Phe Arg His Lys
    290                 295                 300
Pro Asn Leu Leu Ser His Ser Lys Ile His Xaa Ser Asp Pro Arg Gly
305                 310                 315                 320
Arg Pro Arg Pro Pro Pro Ala Arg Gly Ala Pro Ser Cys Gln Pro Ala
                325                 330                 335
Pro Arg Ser Pro Arg Pro Ser Pro Pro Arg Arg Tyr Leu
            340                 345
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<210> 3073
<211> 791
<212> DNA
<213> Homo sapiens

<400> 3073
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120
gccggagggg ccggggcggg ggccgcgccc ggaccgcatc tccccccacg ggggtcggtg
180
cctggggatc ctgtccgcat ccactgcaac atcacggagt cataccctgc tgtgcccccc
240
atctggtcgg tggagtctga tgaccctaac ttggctgctg tcttggagag gctggtggac
300
ataaagaaag ggaatactct gctattgcag catctgaaga ggatcatctc cgacctgtgt
360
aaactctata acctccctca gcatccagat gtggagatgc tggatcaacc cttgccagca
420
gagcagtgca cacaggaaga cgtgtcttca gaagatgaag atgaggagat gcctgaggac
480
acagaagact tagatcacta tgaaatgaaa gaggaagagc cagctgaggg caagaaatct
540

gaagatgatg gcattggaaa agaaaacttg gccatcctag agaaaattaa aaagaaccag
600
aggcaagatt acttaaatgg tgcagtgtct ggctcggtgc aggccactga ccggctgatg
660
aaggagctcc agggatatat taccgnttca cagagtttca aaggcggaaa ctatgncagt
720
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780
ggcagcgttt a
791

<210> 3074
<211> 263
<212> PRT
<213> Homo sapiens

<400> 3074
Xaa Pro Cys Leu Arg Arg Glu Leu Lys Leu Leu Glu Ser Ile Phe His
1 5 10 15
Arg Gly His Glu Arg Phe Arg Ile Ala Ser Ala Cys Leu Asp Glu Leu
20 25 30
Ser Cys Glu Phe Leu Leu Ala Gly Ala Gly Gly Ala Gly Ala Gly Ala
35 40 45
Ala Pro Gly Pro His Leu Pro Pro Arg Gly Ser Val Pro Gly Asp Pro
50 55 60
Val Arg Ile His Cys Asn Ile Thr Glu Ser Tyr Pro Ala Val Pro Pro
65 70 75 80
Ile Trp Ser Val Glu Ser Asp Asp Pro Asn Leu Ala Ala Val Leu Glu
85 90 95
Arg Leu Val Asp Ile Lys Lys Gly Asn Thr Leu Leu Leu Gln His Leu
100 105 110
Lys Arg Ile Ile Ser Asp Leu Cys Lys Leu Tyr Asn Leu Pro Gln His
115 120 125
Pro Asp Val Glu Met Leu Asp Gln Pro Leu Pro Ala Glu Gln Cys Thr
130 135 140
Gln Glu Asp Val Ser Ser Glu Asp Glu Asp Glu Glu Met Pro Glu Asp
145 150 155 160
Thr Glu Asp Leu Asp His Tyr Glu Met Lys Glu Glu Glu Pro Ala Glu
165 170 175
Gly Lys Lys Ser Glu Asp Asp Gly Ile Gly Lys Glu Asn Leu Ala Ile
180 185 190
Leu Glu Lys Ile Lys Lys Asn Gln Arg Gln Asp Tyr Leu Asn Gly Ala
195 200 205
Val Ser Gly Ser Val Gln Ala Thr Asp Arg Leu Met Lys Glu Leu Gln
210 215 220
Gly Tyr Ile Thr Xaa Ser Gln Ser Phe Lys Gly Gly Asn Tyr Xaa Ser
225 230 235 240
Ser Asn Ser Trp Asn Asp Ser Leu Tyr Gly Trp Asp Val Gln Leu Leu
245 250 255
Lys Val Asp Gln Gly Ser Val
260

<210> 3075
<211> 603

<212> DNA
<213> Homo sapiens

<400> 3075
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120
aaaaaaaaaa aagtcttggg agggggtcgg tttggccagg tccacaggtg cacagagaag
180
tctacaggcc ttgcactggc agccaagatc atcaaagtga agaacgtaaa ggaccgggag
240
gatgtgaaga atgaggtcaa catcatgaac cagctcagcc acgtaaactt gatccaactt
300
tatgatgcgt ttgagagcaa gagcagcttc actctgatca tggagtatgt ggatggaggc
360
gaactctttg accggatcac ggatgagaag taccacctca ctgagttgga tgtggtcttg
420
ttcacgaggc agatctgtga gggtgtgcat tacctgcatc agcactatat cctgcacctg
480
gacctcaagc ctgagaacat attgtgtgtc agccagacag ggcatcaaat taagatcatt
540
gactttgggc tggctagaag atacaagcct cgggagaagc taaaggtgaa ctttggtact
600
ccg
603

<210> 3076
<211> 201
<212> PRT
<213> Homo sapiens

<400> 3076
Pro Leu Gly Gly Lys Asn Phe Leu Lys Lys Met Val Gly Lys Asn Pro
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Pro Pro Pro Pro Pro Phe Phe Ser Pro Val Gly Ala Lys Lys Lys Asn
            20   25   30
Val Gly Pro Gln Lys Lys Lys Lys Lys Lys Lys Lys Val Leu Gly Gly
        35   40   45
Gly Arg Phe Gly Gln Val His Arg Cys Thr Glu Lys Ser Thr Gly Leu
    50   55   60
Ala Leu Ala Ala Lys Ile Ile Lys Val Lys Asn Val Lys Asp Arg Glu
65   70   75   80
Asp Val Lys Asn Glu Val Asn Ile Met Asn Gln Leu Ser His Val Asn
                85   90   95
Leu Ile Gln Leu Tyr Asp Ala Phe Glu Ser Lys Ser Ser Phe Thr Leu
            100   105   110
Ile Met Glu Tyr Val Asp Gly Gly Glu Leu Phe Asp Arg Ile Thr Asp
        115   120   125
Glu Lys Tyr His Leu Thr Glu Leu Asp Val Val Leu Phe Thr Arg Gln
    130   135   140
Ile Cys Glu Gly Val His Tyr Leu His Gln His Tyr Ile Leu His Leu
145   150   155   160
Asp Leu Lys Pro Glu Asn Ile Leu Cys Val Ser Gln Thr Gly His Gln

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                165                 170                 175
Ile Lys Ile Ile Asp Phe Gly Leu Ala Arg Arg Tyr Lys Pro Arg Glu
            180                 185                 190
Lys Leu Lys Val Asn Phe Gly Thr Pro
        195                 200
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<210> 3077
<211> 1377
<212> DNA
<213> Homo sapiens

<400> 3077
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acattctgaa gggaggcaag gaggcggact gagcgctccc aattggggag gatgctggtg
120
gtggaggtgg cgaacggccg ctccctggtg tggggagccg aggcggtgca ggccctccgg
180
gagcgcctgg gtgtgggggg ccgcacggta ggcgccctgc cccgcgggcc ccgccagaac
240
tcgcgcctgg gcctcccgct gctgctgatg cccgaagagg cgcggctctt ggccgagatc
300
ggcgccgtga ctctggtcag cgccccgcgt ccagactctc ggcaccacag cctggccctg
360
acatccttca agcgccagca agaggagagc ttccaggagc agagcgcctt ggcagctgag
420
gcccgggaga cccgtcgtca ggagctcctg gagaagatta cggagggcca ggctgctaag
480
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540
gctgccaaag aggatgagac cagtgatggc caggcttcgg gagagcagga ggaagctggc
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720
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780
tacagagacc tgtgggagcg aggcttcttc ctcagtgcgg ctggcaagtt cggaggtgac
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1260

tcccgagaat ggggcctggg tttgattcat ctgttttcta cagggtttaa gtctcaggag
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1377

<210> 3078
<211> 310
<212> PRT
<213> Homo sapiens

<400> 3078
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Glu Ala Val Gln Ala Leu Arg Glu Arg Leu Gly Val Gly Gly Arg Thr
20 25 30
Val Gly Ala Leu Pro Arg Gly Pro Arg Gln Asn Ser Arg Leu Gly Leu
35 40 45
Pro Leu Leu Leu Met Pro Glu Glu Ala Arg Leu Leu Ala Glu Ile Gly
50 55 60
Ala Val Thr Leu Val Ser Ala Pro Arg Pro Asp Ser Arg His His Ser
65 70 75 80
Leu Ala Leu Thr Ser Phe Lys Arg Gln Gln Glu Glu Ser Phe Gln Glu
85 90 95
Gln Ser Ala Leu Ala Ala Glu Ala Arg Glu Thr Arg Arg Gln Glu Leu
100 105 110
Leu Glu Lys Ile Thr Glu Gly Gln Ala Ala Lys Lys Gln Lys Leu Glu
115 120 125
Gln Ala Ser Gly Ala Ser Ser Ser Gln Glu Ala Gly Ser Ser Gln Ala
130 135 140
Ala Lys Glu Asp Glu Thr Ser Asp Gly Gln Ala Ser Gly Glu Gln Glu
145 150 155 160
Glu Ala Gly Pro Ser Ser Ser Gln Ala Gly Pro Ser Asn Gly Val Ala
165 170 175
Pro Leu Pro Arg Ser Ala Leu Leu Val Gln Leu Ala Thr Ala Arg Pro
180 185 190
Arg Pro Val Lys Ala Arg Pro Leu Asp Trp Arg Val Gln Ser Lys Asp
195 200 205
Trp Pro His Ala Gly Arg Pro Ala His Glu Leu Arg Tyr Ser Ile Tyr
210 215 220
Arg Asp Leu Trp Glu Arg Gly Phe Phe Leu Ser Ala Ala Gly Lys Phe
225 230 235 240
Gly Gly Asp Phe Leu Val Tyr Pro Gly Asp Pro Leu Arg Phe His Ala
245 250 255
His Tyr Ile Ala Gln Cys Trp Ala Pro Glu Asp Thr Ile Pro Leu Gln
260 265 270
Asp Leu Val Ala Ala Gly Arg Leu Gly Thr Ser Val Arg Lys Thr Leu
275 280 285
Leu Leu Cys Ser Pro Gln Pro Asp Gly Lys Val Val Tyr Thr Ser Leu
290 295 300
Gln Trp Ala Ser Leu Gln
305 310

<210> 3079
<211> 1785

<212> DNA
<213> Homo sapiens

<400> 3079
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120
tccaaggcat cagcacctga acccccctgca gaagaagaag tggcaactgg tacaacctca
180
gcctctgatg acctggaagc cctgggtaca ctgagcctgg ggaccacaga ggagaaggca
240
gcagctgagg cggctgtgcc caggaccatt ggggccgagc tgatggagct ggtgcggaga
300
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360
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420
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480
gaggtgatct ttgcagacct ggctcgccgg aaggacgacg cccagcagcg cagttgggca
540
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720
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780
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1500

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1620
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1680
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1785

<210> 3080
<211> 500
<212> PRT
<213> Homo sapiens

<400> 3080
Met Asp Thr Leu Tyr Thr Gly Ser Ser Pro Ser Glu Pro Gly Ser Ser
1 5 10 15
Cys Ser Pro Thr Pro Pro Pro Val Pro Arg Arg Gly Thr His Thr Thr
20 25 30
Val Ser Gln Val Gln Pro Pro Pro Ser Lys Ala Ser Ala Pro Glu Pro
35 40 45
Pro Ala Glu Glu Glu Val Ala Thr Gly Thr Thr Ser Ala Ser Asp Asp
50 55 60
Leu Glu Ala Leu Gly Thr Leu Ser Leu Gly Thr Thr Glu Glu Lys Ala
65 70 75 80
Ala Ala Glu Ala Ala Val Pro Arg Thr Ile Gly Ala Glu Leu Met Glu
85 90 95
Leu Val Arg Arg Asn Thr Gly Leu Ser His Glu Leu Cys Arg Val Ala
100 105 110
Ile Gly Ile Ile Val Gly His Ile Gln Ala Ser Val Pro Ala Ser Ser
115 120 125
Pro Val Met Glu Gln Val Leu Leu Ser Leu Val Glu Gly Lys Asp Leu
130 135 140
Ser Met Ala Leu Pro Ser Gly Gln Val Cys His Asp Gln Gln Arg Leu
145 150 155 160
Glu Val Ile Phe Ala Asp Leu Ala Arg Arg Lys Asp Asp Ala Gln Gln
165 170 175
Arg Ser Trp Ala Leu Tyr Glu Asp Glu Gly Val Ile Arg Cys Tyr Leu
180 185 190
Glu Glu Leu Leu His Ile Leu Thr Asp Ala Asp Pro Glu Val Cys Lys
195 200 205
Lys Met Cys Lys Arg Asn Glu Phe Glu Ser Val Leu Ala Leu Val Ala
210 215 220
Tyr Tyr Gln Met Glu His Arg Ala Ser Leu Arg Leu Leu Leu Leu Lys
225 230 235 240
Cys Phe Gly Ala Met Cys Ser Leu Asp Ala Ala Ile Ile Ser Thr Leu
245 250 255
Val Ser Ser Val Leu Pro Val Glu Leu Ala Arg Asp Met Gln Thr Asp
260 265 270
Thr Gln Asp His Gln Lys Leu Cys Tyr Ser Ala Leu Ile Leu Ala Met
275 280 285
Val Phe Ser Met Gly Glu Ala Val Pro Tyr Ala His Tyr Glu His Leu

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    290                 295                 300
Gly Thr Pro Phe Ala Gln Phe Leu Leu Asn Ile Val Glu Asp Gly Leu
305                 310                 315                 320
Pro Leu Asp Thr Thr Glu Gln Leu Pro Asp Leu Cys Val Asn Leu Leu
                325                 330                 335
Leu Ala Leu Asn Leu His Leu Pro Ala Ala Asp Gln Asn Val Ile Met
            340                 345                 350
Ala Ala Leu Ser Lys His Ala Asn Val Lys Ile Phe Ser Glu Lys Leu
        355                 360                 365
Leu Leu Leu Leu Asn Arg Gly Asp Asp Pro Val Arg Ile Phe Lys His
    370                 375                 380
Glu Pro Gln Pro Pro His Ser Val Leu Lys Phe Leu Gln Asp Val Phe
385                 390                 395                 400
Gly Ser Pro Ala Thr Ala Ala Ile Phe Tyr His Thr Asp Met Met Ala
                405                 410                 415
Leu Ile Asp Ile Thr Val Arg His Ile Ala Asp Leu Ser Pro Gly Asp
            420                 425                 430
Lys Gly Pro Phe Gly Ala Gly Gln Arg Pro Trp Pro Gly Val Pro Arg
        435                 440                 445
Leu Leu Glu Pro Gly Ser Thr Pro Ser Arg Glu Pro His Pro Val Glu
    450                 455                 460
Arg Ser Gly Val Pro Ala Leu Thr Ser Ser Trp Ala Ser Gly Cys Pro
465                 470                 475                 480
Arg Pro Leu His Pro Ala Leu Gln Leu Val Ile Asp Ser Ala Phe Gly
                485                 490                 495
Gly Arg Ser Val
            500
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<210> 3081
<211> 1902
<212> DNA
<213> Homo sapiens

<400> 3081

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ccacatggcg acgaacttgt ggacggacac ggagcccgtg cgctcccccc ggccacgagc
120
caaagcattc cgaccttcta cttccccaga ggacgcccgc aggactccgt caacgtggat
180
gccgtcatca gcaagatcga gagcaccttc gcccggttcc cccacgagag ggccaccatg
240
gatgacatgg gcctggtggc caaggcctgc ggctgccccc tctactggaa ggggccgctc
300
ttctatggcg ccggcgggga gcgcacgggc tccgtgtccg tccacaagtt cgtcgccatg
360
tggagaaaaa tcctccagaa ctgccacgac gacgcggcca agttcgtcca tctgctcatg
420
agccccggct gcaactacct ggtgcaggag gactttgtcc ccttcttgca ggacgtggtg
480
aacacgcacc cggggctgtc gttcctgaag gaggcgtccg agttccactc gcgctacatc
540
accacggtca tccagcggat cttctacgcc gtgaaccggt cctggtccgg caggatcacc
600
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tgcgccgagc tgcggaggag ctccttcctg cagaatgtgg cgctgctgga ggaggaggcg
660
gacatcaacc agctgaccga attcttctcg tacgagcatt tctacgtcat ctactgcaag
720
ttctgggagc tggacacgga ccacgacctg ctcatcgacg cggacgacct ggcgcggcac
780
aatgaccacg ccctttctac caagatgata gacaggatct tctcaggagc agtcacacga
840
ggcagaaaag tgcagaagga agggaagatc agctatgccg actttgtctg gtttttgatc
900
tctgaggaag acaaaaaaac accgaccagc atcgagtact ggttccgctg catggacctg
960
gacggggacg gcgccctgtc catgttcgag ctcgagtact tctacgagga gcagtgccga
1020
aggctggaca gcatggccat cgaggccctg cccttccagg actgcctctg ccagatgctg
1080
gacctggtca agccgaggac tgaagggaag atcacgctgc aggacctgaa gcgctgcaag
1140
ctggccaacg tcttcttcga caccttcttc aacatcgaga agtacctcga ccacgagcag
1200
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1260
gagaagtacg cggccgagga gtacgacatc ctggtggccg aggagaccgt gggagagccc
1320
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1380
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1440
tacgagtacg catgcgggga cgaggacctg gagccgctgt gacgccaccc gcgagaacgc
1500
cgccgcgggg ccgcccccca cgtgccacca ccgggccacc gcggctcgtg taaaaactgt
1560
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1620
tgattgccac tgtgggttcg tggctggacc tgcccagagc cctgtgcccg ggggacacgt
1680
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1740
gacccggcct gggttccggg gcctgcgtct gtggaaaggg tccatgtgcg cacaacggtg
1800
accggcggct cccgggcgcc tcagtcctgg acaggagcct ccaccacagg ctgtgtgaat
1860
gttttgtgta aacgtacaaa accgtttctg gcgatcacga aa
1902

<210> 3082
<211> 414
<212> PRT
<213> Homo sapiens

<400> 3082
Met Asp Asp Met Gly Leu Val Ala Lys Ala Cys Gly Cys Pro Leu Tyr
 1   5   10   15
Trp Lys Gly Pro Leu Phe Tyr Gly Ala Gly Gly Glu Arg Thr Gly Ser

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            20                  25                  30
Val Ser Val His Lys Phe Val Ala Met Trp Arg Lys Ile Leu Gln Asn
        35                  40                  45
Cys His Asp Asp Ala Ala Lys Phe Val His Leu Leu Met Ser Pro Gly
    50                  55                  60
Cys Asn Tyr Leu Val Gln Glu Asp Phe Val Pro Phe Leu Gln Asp Val
65                  70                  75                  80
Val Asn Thr His Pro Gly Leu Ser Phe Leu Lys Glu Ala Ser Glu Phe
                85                  90                  95
His Ser Arg Tyr Ile Thr Thr Val Ile Gln Arg Ile Phe Tyr Ala Val
            100                 105                 110
Asn Arg Ser Trp Ser Gly Arg Ile Thr Cys Ala Glu Leu Arg Arg Ser
        115                 120                 125
Ser Phe Leu Gln Asn Val Ala Leu Leu Glu Glu Glu Ala Asp Ile Asn
    130                 135                 140
Gln Leu Thr Glu Phe Phe Ser Tyr Glu His Phe Tyr Val Ile Tyr Cys
145                 150                 155                 160
Lys Phe Trp Glu Leu Asp Thr Asp His Asp Leu Leu Ile Asp Ala Asp
                165                 170                 175
Asp Leu Ala Arg His Asn Asp His Ala Leu Ser Thr Lys Met Ile Asp
            180                 185                 190
Arg Ile Phe Ser Gly Ala Val Thr Arg Gly Arg Lys Val Gln Lys Glu
        195                 200                 205
Gly Lys Ile Ser Tyr Ala Asp Phe Val Trp Phe Leu Ile Ser Glu Glu
    210                 215                 220
Asp Lys Lys Thr Pro Thr Ser Ile Glu Tyr Trp Phe Arg Cys Met Asp
225                 230                 235                 240
Leu Asp Gly Asp Gly Ala Leu Ser Met Phe Glu Leu Glu Tyr Phe Tyr
                245                 250                 255
Glu Glu Gln Cys Arg Arg Leu Asp Ser Met Ala Ile Glu Ala Leu Pro
            260                 265                 270
Phe Gln Asp Cys Leu Cys Gln Met Leu Asp Leu Val Lys Pro Arg Thr
        275                 280                 285
Glu Gly Lys Ile Thr Leu Gln Asp Leu Lys Arg Cys Lys Leu Ala Asn
    290                 295                 300
Val Phe Phe Asp Thr Phe Phe Asn Ile Glu Lys Tyr Leu Asp His Glu
305                 310                 315                 320
Gln Lys Glu Gln Ile Ser Leu Leu Arg Asp Gly Asp Ser Gly Gly Pro
                325                 330                 335
Glu Leu Ser Asp Trp Glu Lys Tyr Ala Ala Glu Glu Tyr Asp Ile Leu
            340                 345                 350
Val Ala Glu Glu Thr Val Gly Glu Pro Trp Glu Asp Gly Phe Glu Ala
        355                 360                 365
Glu Leu Ser Pro Val Glu Gln Lys Leu Ser Ala Leu Arg Ser Pro Leu
    370                 375                 380
Ala Gln Arg Pro Phe Phe Glu Ala Pro Ser Pro Leu Gly Ala Val Asp
385                 390                 395                 400
Leu Tyr Glu Tyr Ala Cys Gly Asp Glu Asp Leu Glu Pro Leu
                405                 410
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<210> 3083
<211> 610
<212> DNA
<213> Homo sapiens

<400> 3083
ngccggccca gctgctggga acctgtcagg ccctcgggct ccagtcacct gagctggcac
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agggggccac cctgtgaggt gtacattgcc gtcctgcaga gatccaggct gcacgcggcg
120
gactgggcag gccgggcccg ggcactggtg ggtgacagtc atacttcgtg gagcccagcg
180
agcatcccgg gcaagcacta ccaggctgtg ggtctgcacc tctggaaggt agagaagcgg
240
cgggtcaatc tgcctagggt cctgtccatg ccccccgtgg ctggcaccgc gtgccatgca
300
tacgaccggg aggtccacct gcgttgtgag ctctcaccgg gctactacct ggctgtcccc
360
agcaccttcc tgaaggacgc gccaggggag ttcctgctcc gagtcttctc taccgggcga
420
gtctccctta ggtgagagga accgcgcagt gctgctggct ctccgaggcc acaggccctt
480
ccaaggcagg atttgggcac tttccctctg tggttggcag gtgtccatgt gggaactgag
540
gccaccggga acctgctgcc agcgccctcc catgtttgtc ttcttggcag cgccatcagg
600
gcagtggcca
610

<210> 3084
<211> 144
<212> PRT
<213> Homo sapiens

<400> 3084
Xaa Arg Pro Ser Cys Trp Glu Pro Val Arg Pro Ser Gly Ser Ser His
 1   5   10   15
Leu Ser Trp His Arg Gly Pro Pro Cys Glu Val Tyr Ile Ala Val Leu
            20   25   30
Gln Arg Ser Arg Leu His Ala Ala Asp Trp Ala Gly Arg Ala Arg Ala
        35   40   45
Leu Val Gly Asp Ser His Thr Ser Trp Ser Pro Ala Ser Ile Pro Gly
    50   55   60
Lys His Tyr Gln Ala Val Gly Leu His Leu Trp Lys Val Glu Lys Arg
65   70   75   80
Arg Val Asn Leu Pro Arg Val Leu Ser Met Pro Pro Val Ala Gly Thr
                85   90   95
Ala Cys His Ala Tyr Asp Arg Glu Val His Leu Arg Cys Glu Leu Ser
            100   105   110
Pro Gly Tyr Tyr Leu Ala Val Pro Ser Thr Phe Leu Lys Asp Ala Pro
        115   120   125
Gly Glu Phe Leu Leu Arg Val Phe Ser Thr Gly Arg Val Ser Leu Arg
    130   135   140

<210> 3085
<211> 1080
<212> DNA
<213> Homo sapiens

<400> 3085
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60
cttctccaat aagaagatat tcagatattg tagtaccccg cttgttaatg gcagccattt
120
caaaagataa gaaaatggaa attaagggaa atctgttcag caacaaagat cttgaggaat
180
tatgcagaca tatcaacaac agaaaccaag cagcacagca ttctcagaag cagtctactg
240
agctcttcca gtgcatgtac ttcaaagaca aagaccctgc caccgaggag cgttgcatat
300
ctgacggagt tatttattca attagaacaa atggtgtgct tctatttata ccaaggtttg
360
ggattaaagg tgctgcttat ctaaaaaata aagatggttt agtcatctca tgtggcccag
420
atagctgttc tgaatggaaa ccaggatccc ttcaacgatt tcaaaacaaa attacctcta
480
ctacaacaga tggggaatct gttacgttcc atttgtttga ccatgtaacc gtaagaatat
540
ccatacaggc ctcacgttgc cattctgata caatcagact tgaaataatt agtaacaaac
600
catacaagat accaaataca gaacttattc atcagagttc ccccttgctg aagagtgagt
660
tagtgaaaga agtaactaaa tctgtggaag aagctcagct tgcccaagaa gtcaaagtaa
720
acatcattca ggaggaatat caagaatatc gccaaacaaa gggaaggagc ctatacacac
780
ttctagagga gatacgggac ctagctctcc tggatgtttc aaacaattat ggaatatgag
840
aggctcttac ttcactaaga gctgtcatat gtgaatgttt tacagtcttt tcaaacttaa
900
catttaatgt gtgtcactca gtgctctagt cgatcaggac tgggtagcta tttcgcatat
960
atgtanaatg ttctcagccg ggcacggtgg ctcacgcctg taaccccagc actttgggag
1020
gctgaggcgg gcggatcacg aggtcaggag attgagacca tcctggctaa cacggtgaaa
1080

<210> 3086
<211> 58
<212> PRT
<213> Homo sapiens

<400> 3086
Met Cys Val Thr Gln Cys Ser Ser Arg Ser Gly Leu Gly Ser Tyr Phe
 1   5   10   15
Ala Tyr Met Xaa Asn Val Leu Ser Arg Ala Arg Trp Leu Thr Pro Val
            20   25   30
Thr Pro Ala Leu Trp Glu Ala Glu Ala Gly Gly Ser Arg Gly Gln Glu
        35   40   45
Ile Glu Thr Ile Leu Ala Asn Thr Val Lys
    50   55

<210> 3087
<211> 2329
<212> DNA
<213> Homo sapiens

<400> 3087
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cgagagaggg agcactgtga cacggaggga gaggctgacg actttgatcc tgggaagaag
120
gtggaggtgg agccgccccc agatcggcca gtccgagcgt gccggacaca gcagccggaa
180
atggagcgca cccatattca gcaactcctg gaacacttcc tccgccagct tcagagaaaa
240
gatccccatg gatttttttgc ttttcctgtc acggatgcaa ttgctcctgg atattcaatg
300
ataataaaac atcccatgga ttttggcacc atgaaagaca aaattgtagc taatgaatac
360
aagtcagtta cggaatttaa ggcagatttc aagctgatgt gtgataatgc aatgacatac
420
aataggccag ataccgtgta ctacaagttg gcgaagaaga tccttcacgc aggctttaag
480
atgatgagca aacaggcagc tcttttgggc aatgaagata cagctgttga ggaacctgtc
540
cctgaagttg taccagtaca agtagaaact gccaagaaat ccaaaaagcc gagtagagaa
600
gttatcagct gcatgtttga gcctgaaggg aatgcctgca gcttgacgga cagtaccgca
660
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720
cggttcctcc caggcggcaa gatgggctat ctgaagagga acggggacgg gagcctgctc
780
tacagcgtgg tcaacacggc cgagccgaac gctgatgagg aggagaccca cccggtgact
840
tgagctcgct ctccagtaag ctactcccag gcttcaccac gctgggcttc aaagacgaga
900
gaagaaacaa agtcaccttt ctctccagtg ccactactgc gctttcgatg cagaataatt
960
cagtatttgg cgacttgaag tcggacgaga tggagctgct ctactcagcc tacggagatg
1020
agacaggcgt gcagtgtgcg ctgagcctgc aggagtttgt gaaggatgct gggagctaca
1080
gcaagaaagt ggtggacgac ctcctggacc agatcacagg cggagaccac tctaggacgc
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1200
gggacaccct aggagacagc agcagctctg ttctggagtt catgtcgatg aagtcctatc
1260
ccgacgtttc tgtggatatc tccatgctca gctctctggg gaaggtgaag aaggagctgg
1320
accctgacga cagccatttg aacttggatg agacgacgaa gctcctgcag gacctgcacg
1380
aagcacaggc ggagcgcggc ggctctcggc cgtcgtccaa cctcagctcc ctgtccaacg
1440

cctccgagag ggaccagcac cacctgggaa gcccttctcg cctgagtgtc ggggagcagc
1500
cagacgtcac ccacgacccc tatgagtttc ttcagtctcc agagcctgcg gcctctgcca
1560
agacctaact ctagaccacc ttcagctctt ttattttatt tttttagttt tattttgcac
1620
gtgtagagtt tttgtcatca gacaaggact ttgatcctgt ccccttttggc atgcgggaag
1680
cagccgcggg gaggtaatga attgtctgtg gtatcatgtc agcagagtct ccaagcccca
1740
cgaaccctga ggagtggagt catacgcgaa ggccatatgg ccatcgtgtc agcagagaga
1800
gtctctgtac acagccccgt gaaccctgag gagtggagtc atacacgaag ggcgtgtggc
1860
catcgtgtca gcagagagag tctctgtaca cagccccgtg aaccctgagg agtggagtca
1920
tacgcgaagg gtgtgtggcc aggctgcaga gctgcgtgcc gtttgtgtcc gagcatcacg
1980
tgtggctcca gcccttgttt ctgccagtgt agacacctct gtctgcccca ctgtcctggg
2040
gtcgctcttg ggaggcacag gcatgggtgt gtctggcctc attctgtatc agtccagtgt
2100
gttcctgtca tagtttgtgt ctcccaggca ggccatggta ggggcctcgc aggggccatt
2160
ggggagcaca gggccaggct ggggtgagga gagctcccct gttttctgtt taattgatga
2220
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2280
cgttttctaa ctgggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa
2329

<210> 3088
<211> 280
<212> PRT
<213> Homo sapiens

<400> 3088

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Lys	Lys	Arg	Lys	Arg	Glu	Arg	Glu	His	Cys	Asp	Thr	Glu	Gly	Glu	Ala
			20					25					30		
Asp	Asp	Phe	Asp	Pro	Gly	Lys	Lys	Val	Glu	Val	Glu	Pro	Pro	Pro	Asp
		35					40					45			
Arg	Pro	Val	Arg	Ala	Cys	Arg	Thr	Gln	Gln	Pro	Glu	Met	Glu	Arg	Thr
	50					55					60				
His	Ile	Gln	Gln	Leu	Leu	Glu	His	Phe	Leu	Arg	Gln	Leu	Gln	Arg	Lys
65					70					75					80
Asp	Pro	His	Gly	Phe	Phe	Ala	Phe	Pro	Val	Thr	Asp	Ala	Ile	Ala	Pro
			85					90					95		
Gly	Tyr	Ser	Met	Ile	Ile	Lys	His	Pro	Met	Asp	Phe	Gly	Thr	Met	Lys
		100					105					110			
Asp	Lys	Ile	Val	Ala	Asn	Glu	Tyr	Lys	Ser	Val	Thr	Glu	Phe	Lys	Ala
	115					120					125				
Asp	Phe	Lys	Leu	Met	Cys	Asp	Asn	Ala	Met	Thr	Tyr	Asn	Arg	Pro	Asp

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    130                 135                 140
Thr Val Tyr Tyr Lys Leu Ala Lys Lys Ile Leu His Ala Gly Phe Lys
145                 150                 155                 160
Met Met Ser Lys Gln Ala Ala Leu Leu Gly Asn Glu Asp Thr Ala Val
                165                 170                 175
Glu Glu Pro Val Pro Glu Val Val Pro Val Gln Val Glu Thr Ala Lys
            180                 185                 190
Lys Ser Lys Lys Pro Ser Arg Glu Val Ile Ser Cys Met Phe Glu Pro
        195                 200                 205
Glu Gly Asn Ala Cys Ser Leu Thr Asp Ser Thr Ala Glu Glu His Val
    210                 215                 220
Leu Ala Leu Val Glu His Ala Ala Asp Glu Ala Arg Asp Arg Ile Asn
225                 230                 235                 240
Arg Phe Leu Pro Gly Gly Lys Met Gly Tyr Leu Lys Arg Asn Gly Asp
                245                 250                 255
Gly Ser Leu Leu Tyr Ser Val Val Asn Thr Ala Glu Pro Asn Ala Asp
            260                 265                 270
Glu Glu Glu Thr His Pro Val Thr
        275                 280
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<210> 3089
<211> 722
<212> DNA
<213> Homo sapiens

<400> 3089
ncagctttgg accaagcgac catgagaggg ccagagctcg ggcccgaaac cagcatggag
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ggagacgtgc tggacacact ggaggcgctg gggtataaag gaccattgtt agaagagcaa
120
gcccttacaa aggcggcaga gggtggatta tcttcacctg aattttcaga gctctgtatt
180
tggttaggct ctcaaataaa atcattatgc aacttggaag aaagtatcac gtctgctggg
240
agagatgacc tagagagctt ccagcttgag ataagtgggt ttttaaaaga gatggcctgt
300
ccatactcgg tactcgtctc aggagacatt aaagagcgcc tcacaaagaa ggatgactgc
360
ttgaaacttc tgttgttttt aagtacagaa cttcaagctt tacaaatatt acagaacaag
420
aaacataaaa attctcaatt agataaaaat agtgaagttt atcaggaagt tcaagctatg
480
tttgatacac ttggtatacc caagtcaaca acttctgaca ttccgcatat gctaaaccaa
540
gtggaatcaa aggtgaaaga tattctctca aaggtccaga aaaatcatgt gggaaaacca
600
ctactgaaaa tggatttaaa ttcagaacag gcggaacaac tggaaagaat caatgatgct
660
ctttcctgtg aatatgagtg ccgccgacga atgttaatga aacgattaga tgtgactgta
720
ca
722

<210> 3090

<211> 240
<212> PRT
<213> Homo sapiens

<400> 3090
Xaa Ala Leu Asp Gln Ala Thr Met Arg Gly Pro Glu Leu Gly Pro Glu
1 5 10 15
Thr Ser Met Glu Gly Asp Val Leu Asp Thr Leu Glu Ala Leu Gly Tyr
20 25 30
Lys Gly Pro Leu Leu Glu Glu Gln Ala Leu Thr Lys Ala Ala Glu Gly
35 40 45
Gly Leu Ser Ser Pro Glu Phe Ser Glu Leu Cys Ile Trp Leu Gly Ser
50 55 60
Gln Ile Lys Ser Leu Cys Asn Leu Glu Glu Ser Ile Thr Ser Ala Gly
65 70 75 80
Arg Asp Asp Leu Glu Ser Phe Gln Leu Glu Ile Ser Gly Phe Leu Lys
85 90 95
Glu Met Ala Cys Pro Tyr Ser Val Leu Val Ser Gly Asp Ile Lys Glu
100 105 110
Arg Leu Thr Lys Lys Asp Asp Cys Leu Lys Leu Leu Leu Phe Leu Ser
115 120 125
Thr Glu Leu Gln Ala Leu Gln Ile Leu Gln Asn Lys Lys His Lys Asn
130 135 140
Ser Gln Leu Asp Lys Asn Ser Glu Val Tyr Gln Glu Val Gln Ala Met
145 150 155 160
Phe Asp Thr Leu Gly Ile Pro Lys Ser Thr Thr Ser Asp Ile Pro His
165 170 175
Met Leu Asn Gln Val Glu Ser Lys Val Lys Asp Ile Leu Ser Lys Val
180 185 190
Gln Lys Asn His Val Gly Lys Pro Leu Leu Lys Met Asp Leu Asn Ser
195 200 205
Glu Gln Ala Glu Gln Leu Glu Arg Ile Asn Asp Ala Leu Ser Cys Glu
210 215 220
Tyr Glu Cys Arg Arg Arg Met Leu Met Lys Arg Leu Asp Val Thr Val
225 230 235 240

<210> 3091
<211> 333
<212> DNA
<213> Homo sapiens

<400> 3091
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caccatcttg gcctggcagg ggtctgggac tgacagggag caccccaggc ccttggtacc
120
cccagggcga ccccttctgc caagtgtccc aaaatgattg ctaaatgcct ggctcccccа
180
ctctttgact ccatctcttg gttccctctt tctgctgcca gctcccccga ctcttccctg
240
gggactcctt tttgtgtccc ccttctcccc tgcccctact gccaggcaga tcccctttтc
300
ttccataccc atccctgcct ccctgctcgg ccg
333

<210> 3092
<211> 104
<212> PRT
<213> Homo sapiens

<400> 3092
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Lys Gly Asp Thr Lys Arg Ser Pro Gln Gly Arg Val Gly Gly Ala Gly
20 25 30
Ser Arg Lys Arg Glu Pro Arg Asp Gly Val Lys Glu Trp Gly Ser Gln
35 40 45
Ala Phe Ser Asn His Phe Gly Thr Leu Gly Arg Arg Gly Arg Pro Gly
50 55 60
Gly Thr Lys Gly Leu Gly Cys Ser Leu Ser Val Pro Asp Pro Cys Gln
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Ala Lys Met Val Trp Gln Arg Gly Glu Gln Leu Leu Pro Arg Ala Ser
85 90 95
Phe Pro Ser Ala Pro Phe Thr Arg
100

<210> 3093
<211> 720
<212> DNA
<213> Homo sapiens

<400> 3093
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420
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<210> 3094

<211> 179
<212> PRT
<213> Homo sapiens

<400> 3094
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Leu Asp Ile Ser Gln Leu Gln Pro Pro Leu Pro Asp Gln Val Val Ile
35 40 45
Lys Thr Gln Thr Glu Tyr Gln Leu Ser Ser Pro Asp Gln Gln Asn Phe
50 55 60
Pro Asp Leu Glu Gly Gln Arg Leu Asn Cys Ser His Pro Glu Glu Gly
65 70 75 80
Arg Arg Leu Pro Thr Ala Arg Met Ile Ala Phe Ala Met Ala Leu Leu
85 90 95
Gly Cys Val Leu Ile Met Tyr Lys Ala Ile Trp Tyr Asp Gln Phe Thr
100 105 110
Cys Pro Asp Gly Phe Leu Leu Arg His Lys Ile Cys Thr Pro Leu Thr
115 120 125
Leu Glu Met Tyr Tyr Thr Glu Met Asp Pro Glu Arg His Arg Ser Ile
130 135 140
Leu Ala Ala Ile Gly Ala Tyr Pro Leu Ser Arg Lys His Gly Thr Glu
145 150 155 160
Thr Pro Ala Ala Trp Gly Asp Gly Tyr Arg Ala Ala Lys Glu Glu Arg
165 170 175
Lys Gly Pro

<210> 3095
<211> 519
<212> DNA
<213> Homo sapiens

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420
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<210> 3096
<211> 159
<212> PRT
<213> Homo sapiens

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35 40 45
Ser Leu Ala Arg Arg Pro Asp Arg Arg Glu Arg Met Leu Ala Ser Leu
50 55 60
Trp Glu Met Glu Ile Ser Gly Arg Val Val Asp Ala Val Asp Gly Trp
65 70 75 80
Met Leu Asn Ser Ser Ala Ile Arg Asn Leu Gly Val Asp Leu Leu Pro
85 90 95
Gly Tyr Gln Asp Pro Tyr Ser Gly Arg Thr Leu Thr Lys Gly Glu Val
100 105 110
Gly Cys Phe Leu Ser His Tyr Ser Ile Trp Glu Glu Arg Ala Val Gln
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Gly Thr Leu Leu Ala Thr Gly Pro Gly Gly Leu Leu Arg Pro Ala Pro
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Ala Arg Cys Pro Tyr Pro Leu Cys Arg Gly Arg Arg Val Ala Gln
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<210> 3097
<211> 4953
<212> DNA
<213> Homo sapiens

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4953

<210> 3098
<211> 1359
<212> PRT
<213> Homo sapiens

<400> 3098
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His Gly Ser Arg Gly Gly Arg Gly Asp Arg Ala Arg Ala Gly Gly Gly
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Gly Pro Ser Arg Gly Ser Gly Gly Gly Gly Arg Gly Gly Leu Arg Ala
35 40 45
Asp Gly Arg Ala Pro Gly Leu Arg Gly Leu Gly Ala Ala Pro His Cys
50 55 60
Pro Ala Gly Leu Gly Pro Gly Ala Met Ser Gly Gly Gly Gly Gly Gly

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65                  70                  75                  80
Gly Ser Ala Pro Ser Arg Phe Ala Asp Tyr Phe Val Ile Cys Gly Leu
                85                  90                  95
Asp Thr Glu Thr Gly Leu Glu Pro Asp Glu Leu Ser Ala Leu Cys Gln
            100                 105                 110
Tyr Ile Gln Ala Ser Lys Ala Arg Asp Gly Ala Ser Pro Phe Ile Ser
        115                 120                 125
Ser Thr Thr Glu Gly Glu Asn Phe Glu Gln Thr Pro Leu Arg Arg Thr
    130                 135                 140
Phe Lys Ser Lys Val Leu Ala Arg Tyr Pro Glu Asn Val Glu Trp Asn
145                 150                 155                 160
Pro Phe Asp Gln Asp Ala Val Gly Met Leu Cys Met Pro Lys Gly Leu
                165                 170                 175
Ala Phe Lys Thr Gln Ala Asp Pro Arg Glu Pro Gln Phe His Ala Phe
            180                 185                 190
Ile Ile Thr Arg Glu Asp Gly Ser Arg Thr Phe Gly Phe Ala Leu Thr
        195                 200                 205
Phe Tyr Glu Glu Val Thr Ser Lys Gln Ile Cys Ser Ala Met Gln Thr
    210                 215                 220
Leu Tyr His Met His Asn Ala Glu Tyr Asp Val Leu His Ala Pro Pro
225                 230                 235                 240
Ala Asp Asp Arg Asp Gln Ser Ser Met Glu Asp Gly Glu Asp Thr Pro
                245                 250                 255
Val Thr Lys Leu Gln Arg Phe Asn Ser Tyr Asp Ile Ser Arg Asp Thr
            260                 265                 270
Leu Tyr Val Ser Lys Cys Ile Cys Leu Ile Thr Pro Met Ser Phe Met
        275                 280                 285
Lys Ala Cys Arg Ser Val Pro Gly Gln Leu His Gln Ala Val Thr Ser
    290                 295                 300
Pro Gln Pro Pro Pro Leu Pro Leu Glu Ser Tyr Ile Tyr Asn Val Leu
305                 310                 315                 320
Tyr Glu Val Pro Leu Pro Pro Pro Gly Arg Ser Leu Lys Phe Ser Gly
                325                 330                 335
Val Tyr Trp Pro Ile Ile Cys Gln Arg Pro Ser Thr Asn Glu Leu Pro
            340                 345                 350
Leu Phe Asp Phe Pro Val Lys Glu Val Phe Glu Leu Leu Gly Val Glu
        355                 360                 365
Asn Val Phe Gln Leu Phe Thr Cys Ala Leu Leu Glu Phe Gln Ile Leu
    370                 375                 380
Leu Tyr Ser Gln His Tyr Gln Arg Leu Met Thr Val Ala Glu Thr Ile
385                 390                 395                 400
Thr Ala Leu Met Phe Pro Phe Gln Trp Gln His Val Tyr Val Pro Ile
                405                 410                 415
Leu Pro Ala Ser Leu Leu His Phe Leu Asp Ala Pro Val Pro Tyr Leu
            420                 425                 430
Met Gly Leu His Ser Asn Gly Leu Asp Asp Arg Ser Lys Leu Glu Leu
        435                 440                 445
Pro Gln Glu Ala Asn Leu Cys Phe Val Asp Ile Asp Asn His Phe Ile
    450                 455                 460
Glu Leu Pro Glu Asp Leu Pro Gln Phe Pro Asn Lys Leu Glu Phe Val
465                 470                 475                 480
Gln Glu Val Ser Glu Ile Leu Met Ala Phe Gly Ile Pro Pro Glu Gly
                485                 490                 495
Asn Leu His Cys Ser Glu Ser Ala Ser Lys Leu Lys Arg Leu Arg Ala
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                500                 505                 510
Ser Glu Leu Val Ser Asp Lys Arg Asn Gly Asn Ile Ala Gly Ser Pro
        515                 520                 525
Leu His Ser Tyr Glu Leu Leu Lys Glu Asn Glu Thr Ile Ala Arg Leu
    530                 535                 540
Gln Ala Leu Val Lys Arg Thr Gly Val Ser Leu Glu Lys Leu Glu Val
545                 550                 555                 560
Arg Glu Asp Pro Ser Ser Asn Lys Asp Leu Lys Val Gln Cys Asp Glu
                565                 570                 575
Glu Glu Leu Arg Ile Tyr Gln Leu Asn Ile Gln Ile Arg Glu Val Phe
            580                 585                 590
Ala Asn Arg Phe Thr Gln Met Phe Ala Asp Tyr Glu Val Phe Val Ile
        595                 600                 605
Gln Pro Ser Gln Asp Lys Glu Ser Trp Phe Thr Asn Arg Glu Gln Met
    610                 615                 620
Gln Asn Phe Asp Lys Ala Ser Phe Leu Ser Asp Gln Pro Glu Pro Tyr
625                 630                 635                 640
Leu Pro Phe Leu Ser Arg Phe Leu Glu Thr Gln Met Phe Ala Phe Phe
                645                 650                 655
Ile Asp Asn Lys Ile Met Cys His Asp Asp Asp Asp Lys Asp Pro Val
            660                 665                 670
Leu Arg Val Phe Asp Ser Arg Val Asp Lys Ile Arg Leu Leu Asn Val
        675                 680                 685
Arg Thr Pro Thr Leu Arg Thr Ser Met Tyr Gln Lys Cys Thr Thr Val
    690                 695                 700
Asp Glu Ala Glu Lys Ala Ile Glu Leu Arg Leu Ala Lys Ile Asp His
705                 710                 715                 720
Thr Ala Ile His Pro His Leu Leu Asp Met Lys Ile Gly Gln Gly Lys
                725                 730                 735
Tyr Glu Pro Gly Phe Phe Pro Lys Leu Gln Ser Asp Val Leu Cys Thr
            740                 745                 750
Gly Pro Ala Ser Asn Lys Trp Thr Lys Arg Asn Ala Pro Ala Gln Trp
        755                 760                 765
Arg Arg Lys Asp Arg Gln Lys Gln His Thr Glu His Leu Arg Leu Asp
    770                 775                 780
Asn Asp Gln Arg Glu Lys Tyr Ile Gln Glu Ala Arg Thr Met Gly Ser
785                 790                 795                 800
Thr Ile Arg Gln Pro Lys Leu Ser Asn Leu Ser Pro Ser Val Ile Ala
                805                 810                 815
Gln Thr Asn Trp Lys Phe Val Glu Gly Leu Leu Lys Glu Cys Arg Asn
            820                 825                 830
Lys Thr Lys Arg Met Leu Val Glu Lys Met Gly Arg Glu Ala Val Glu
        835                 840                 845
Leu Gly His Gly Glu Val Asn Ile Thr Gly Val Glu Glu Asn Thr Leu
    850                 855                 860
Ile Ala Ser Leu Cys Asp Leu Leu Glu Arg Ile Trp Ser His Gly Leu
865                 870                 875                 880
Gln Val Lys Gln Gly Lys Ser Ala Leu Trp Ser His Leu Leu His Tyr
                885                 890                 895
Gln Asp Asn Arg Gln Arg Lys Leu Thr Ser Gly Ser Leu Ser Thr Ser
            900                 905                 910
Gly Ile Leu Leu Asp Ser Glu Arg Arg Lys Ser Asp Ala Ser Ser Leu
        915                 920                 925
Met Pro Pro Leu Arg Ile Ser Leu Ile Gln Asp Met Arg His Ile Gln
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Asn Ile Gly Glu Ile Lys Thr Asp Val Gly Lys Ala Arg Ala Trp Val
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Arg Leu Ser Met Glu Lys Lys Leu Leu Ser Arg His Leu Lys Gln Leu
                965                 970                 975
Leu Ser Asp His Glu Leu Thr Lys Lys Leu Tyr Lys Arg Tyr Ala Phe
            980                 985                 990
Leu Arg Cys Asp Asp Glu Lys Glu Gln Phe Leu Tyr His Leu Leu Ser
        995                 1000                1005
Phe Asn Ala Val Asp Tyr Phe Cys Phe Thr Asn Val Phe Thr Thr Ile
    1010                1015                1020
Leu Ile Pro Tyr His Ile Leu Ile Val Pro Ser Lys Lys Leu Gly Gly
1025                1030                1035                1040
Ser Met Phe Thr Ala Asn Pro Trp Ile Cys Ile Ser Gly Glu Leu Gly
                1045                1050                1055
Glu Thr Gln Ile Met Gln Ile Pro Arg Asn Val Leu Glu Met Thr Phe
            1060                1065                1070
Glu Cys Gln Asn Leu Gly Lys Leu Thr Thr Val Gln Ile Gly His Asp
        1075                1080                1085
Asn Ser Gly Leu Tyr Ala Lys Trp Leu Val Glu Tyr Val Met Val Arg
    1090                1095                1100
Asn Glu Ile Thr Gly His Thr Tyr Lys Phe Pro Cys Gly Arg Trp Leu
1105                1110                1115                1120
Gly Lys Gly Met Asp Asp Gly Ser Leu Glu Arg Ile Leu Val Gly Glu
                1125                1130                1135
Leu Leu Thr Ser Gln Pro Glu Val Asp Glu Arg Pro Cys Arg Thr Pro
            1140                1145                1150
Pro Leu Gln Gln Ser Pro Ser Val Ile Arg Arg Leu Val Thr Ile Ser
        1155                1160                1165
Pro Asn Asn Lys Pro Lys Leu Asn Thr Gly Gln Ile Gln Glu Ser Ile
    1170                1175                1180
Gly Glu Ala Val Asn Gly Ile Val Lys His Phe His Lys Pro Glu Lys
1185                1190                1195                1200
Glu Arg Gly Ser Leu Thr Leu Leu Leu Cys Gly Glu Cys Gly Leu Val
                1205                1210                1215
Ser Ala Leu Glu Gln Ala Phe Gln His Gly Phe Lys Ser Pro Arg Leu
            1220                1225                1230
Phe Lys Asn Val Phe Ile Trp Asp Phe Leu Glu Lys Ala Gln Thr Tyr
        1235                1240                1245
Tyr Glu Thr Leu Glu Lys Asn Glu Val Val Pro Glu Glu Asn Trp His
    1250                1255                1260
Thr Arg Ala Arg Asn Phe Cys Arg Phe Val Thr Ala Ile Asn Asn Thr
1265                1270                1275                1280
Pro Arg Asn Ile Gly Lys Asp Gly Lys Phe Gln Met Leu Val Cys Leu
                1285                1290                1295
Gly Ala Arg Asp His Leu Leu His His Trp Ile Ala Leu Leu Ala Asp
            1300                1305                1310
Cys Pro Ile Thr Ala His Met Tyr Glu Asp Val Ala Leu Ile Lys Asp
        1315                1320                1325
His Thr Leu Val Asn Ser Leu Ile Arg Val Leu Gln Thr Leu Gln Glu
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<210> 3099
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<212> DNA
<213> Homo sapiens

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120
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1001

<210> 3100
<211> 159
<212> PRT
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Phe Thr Leu Pro Phe Trp Ala Val Asn Ala Val His Gly Trp Val Leu
35 40 45
Gly Lys Ile Met Cys Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe

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Val Ser Gly Met Gln Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val
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Ala Val Thr Lys Val Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp
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Ile Ile Cys Phe Cys Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro
            100                 105                 110
Gln Leu Val Phe Tyr Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile
        115                 120                 125
Phe Pro Arg Tyr Leu Gly Thr Ser Met Lys Ala Leu Ile His Met Leu
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<211> 2623
<212> DNA
<213> Homo sapiens

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2623

<210> 3102
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<212> PRT
<213> Homo sapiens

<400> 3102
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Gln Tyr Ala Gly Pro Gly Leu Ser Leu Gly Ala Pro Gly Gly Arg Ala
35 40 45
Pro Pro Asp Asp Leu Asp Leu Phe Pro Thr Pro Asp Pro His Tyr Glu
50 55 60
Lys Lys Tyr Tyr Phe Pro Val Arg Glu Leu Glu Arg Ser Leu Arg Phe
65 70 75 80
Asp Met Lys Gly Asp Asp Val Ile Val Phe Leu His Ile Gln Lys Thr
85 90 95
Gly Gly Thr Thr Phe Gly Arg His Leu Val Gln Asn Val Arg Leu Glu
100 105 110
Val Pro Cys Asp Cys Arg Pro Gly Gln Lys Lys Cys Thr Cys Tyr Arg
115 120 125
Pro Asn Arg Arg Glu Thr Trp Leu Phe Ser Arg Phe Ser Thr Gly Trp
130 135 140
Ser Cys Gly Leu His Ala Asp Trp Thr Glu Leu Thr Asn Cys Val Pro
145 150 155 160
Gly Val Leu Asp Arg Arg Asp Ser Ala Ala Leu Arg Thr Pro Arg Lys
165 170 175
Phe Tyr Tyr Ile Thr Leu Leu Arg Asp Pro Val Ser Arg Tyr Leu Ser
180 185 190
Glu Trp Arg His Val Gln Arg Gly Ala Thr Trp Lys Thr Ser Leu His
195 200 205
Met Cys Asp Gly Arg Thr Pro Thr Pro Glu Glu Leu Pro Pro Cys Tyr
210 215 220
Glu Gly Thr Asp Trp Ser Gly Cys Thr Leu Gln Glu Phe Met Asp Cys
225 230 235 240
Pro Tyr Asn Leu Ala Asn Asn Arg Gln Val Arg Met Leu Ala Asp Leu
245 250 255
Ser Leu Val Gly Cys Tyr Asn Leu Ser Phe Ile Pro Glu Gly Lys Arg
260 265 270
Ala Gln Leu Leu Leu Glu Ser Ala Lys Lys Asn Leu Arg Gly Met Ala
275 280 285
Phe Phe Gly Leu Thr Glu Phe Gln Arg Lys Thr Gln Tyr Leu Phe Glu
290 295 300
Arg Thr Phe Asn Leu Lys Phe Ile Arg Pro Phe Met Gln Tyr Asn Ser
305 310 315 320
Thr Arg Ala Gly Gly Val Glu Val Asp Glu Asp Thr Ile Arg Arg Ile
325 330 335
Glu Glu Leu Asn Asp Leu Asp Met Gln Leu Tyr Asp Tyr Ala Lys Asp
340 345 350
Leu Phe Gln Gln Arg Tyr Gln Tyr Lys Arg Gln Leu Glu Arg Arg Glu
355 360 365
Gln Arg Leu Arg Ser Arg Glu Glu Arg Leu Leu His Arg Ala Lys Glu

370 375 380
Ala Leu Pro Arg Glu Asp Ala Asp Glu Pro Gly Arg Val Pro Thr Glu
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Asp Tyr Met Ser His Ile Ile Glu Lys Trp
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<210> 3103
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<212> DNA
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<210> 3104
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<212> PRT
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<400> 3104
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Pro Gly Gly Arg Leu Arg Thr Arg Arg Pro Ala Thr Ile Leu Ser Val
35 40 45
Ala Ala Ala Trp Gln Arg Ala Ser Leu Gly Gln Trp Xaa Arg Arg Pro
50 55 60
Val Ala Ala Leu Ala Pro Tyr Ser Asp Ser Leu Val Glu Pro Leu Val
65 70 75 80
Cys Arg Leu Gln Val Leu Phe Leu Lys Lys Ala Gly Ser Glu Arg Pro
85 90 95
Cys Glu Thr Thr Pro Gly Ala Lys Gly Asp Ser His Lys Thr Gln Val
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Leu Leu Glu His Arg Lys Val Ser Leu Gln Val Glu Glu Gly Arg Glu
115 120 125
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130 135 140

<210> 3105
<211> 4924
<212> DNA
<213> Homo sapiens

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<210> 3106
<211> 1366
<212> PRT
<213> Homo sapiens

<400> 3106
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35 40 45
Pro Ala Phe Ser Ser Asp Ser Arg Pro Phe Met Ser Ser Ala Ser Phe
50 55 60
Leu Gly Ser Gln Pro Cys Pro Asp Thr Ser Tyr Ala Pro Val Ala Thr
65 70 75 80
Ala Ser Ser Leu Pro Pro Lys Thr Cys Asp Phe Ala Gln Asp Ser Ser

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Tyr Phe Glu Asp Phe Ser Asn Ile Ser Ile Phe Ser Ser Ser Val Asp
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Ser Leu Ser Asp Ile Val Asp Thr Pro Asp Phe Leu Pro Ala Asp Ser
        115                 120                 125
Leu Asn Gln Val Ser Thr Ile Trp Asp Asp Asn Pro Ala Pro Ser Thr
    130                 135                 140
His Asp Lys Leu Phe Gln Leu Ser Arg Pro Phe Ala Gly Phe Glu Asp
145                 150                 155                 160
Phe Leu Pro Ser His Ser Thr Pro Leu Leu Val Ser Tyr Gln Glu Gln
                165                 170                 175
Ser Val Gln Ser Gln Pro Glu Glu Glu Asp Glu Ala Glu Glu Glu Glu
            180                 185                 190
Ala Glu Glu Leu Gly His Thr Glu Thr Tyr Ala Asp Tyr Val Pro Ser
        195                 200                 205
Lys Ser Lys Ile Gly Lys Gln His Pro Asp Arg Val Val Glu Thr Ser
    210                 215                 220
Thr Leu Ser Ser Val Pro Pro Pro Asp Ile Thr Tyr Thr Leu Ala Leu
225                 230                 235                 240
Pro Ser Asp Ser Gly Ala Leu Ser Ala Leu Gln Leu Glu Ala Ile Thr
                245                 250                 255
Tyr Ala Cys Gln Gln His Glu Val Leu Leu Pro Ser Gly Gln Arg Ala
            260                 265                 270
Gly Phe Leu Ile Gly Asp Gly Ala Gly Val Gly Lys Gly Arg Thr Val
        275                 280                 285
Ala Gly Val Ile Leu Glu Asn His Leu Arg Gly Arg Lys Lys Ala Leu
    290                 295                 300
Trp Phe Ser Val Ser Asn Asp Leu Lys Tyr Asp Ala Glu Arg Asp Leu
305                 310                 315                 320
Arg Asp Ile Glu Ala Thr Gly Ile Ala Val His Ala Leu Ser Lys Ile
                325                 330                 335
Lys Tyr Gly Asp Thr Thr Thr Ser Glu Gly Val Leu Phe Ala Thr Tyr
            340                 345                 350
Ser Ala Leu Ile Gly Glu Ser Gln Ala Gly Gly Gln His Arg Thr Arg
        355                 360                 365
Leu Arg Gln Ile Leu Asp Trp Cys Gly Glu Ala Phe Glu Gly Val Ile
    370                 375                 380
Val Phe Asp Glu Cys His Lys Ala Lys Asn Ala Gly Ser Thr Lys Met
385                 390                 395                 400
Gly Lys Ala Val Leu Asp Leu Gln Asn Lys Leu Pro Leu Ala Arg Val
                405                 410                 415
Val Tyr Ala Ser Ala Thr Gly Thr Ser Glu Pro Arg Asn Met Ile Tyr
            420                 425                 430
Met Ser Arg Leu Gly Ile Trp Gly Glu Gly Thr Pro Phe Arg Asn Phe
        435                 440                 445
Glu Glu Phe Leu His Ala Ile Glu Lys Arg Gly Val Gly Ala Met Glu
    450                 455                 460
Ile Val Ala Met Asp Met Lys Val Ser Gly Met Tyr Ile Ala Arg Gln
465                 470                 475                 480
Leu Ser Phe Ser Gly Val Thr Phe Arg Ile Glu Glu Ile Pro Leu Ala
                485                 490                 495
Pro Ala Phe Glu Cys Val Tyr Asn Arg Ala Ala Leu Leu Trp Ala Glu
            500                 505                 510
Ala Leu Asn Val Phe Gln Gln Ala Ala Asp Trp Ile Gly Leu Glu Ser
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    530                 535                 540
Lys Tyr Leu Cys Ile Ala Ala Lys Val Arg Arg Leu Val Glu Leu Ala
545                 550                 555                 560
Arg Glu Glu Leu Ala Arg Asp Lys Cys Val Val Ile Gly Leu Gln Ser
                565                 570                 575
Thr Gly Glu Ala Arg Thr Arg Glu Val Leu Gly Glu Asn Asp Gly His
            580                 585                 590
Leu Asn Cys Phe Val Ser Ala Ala Glu Gly Val Phe Leu Ser Leu Ile
        595                 600                 605
Gln Lys His Phe Pro Ser Thr Lys Arg Lys Arg Asp Arg Gly Ala Gly
    610                 615                 620
Ser Lys Arg Lys Arg Arg Pro Arg Gly Arg Gly Ala Lys Ala Pro Arg
625                 630                 635                 640
Leu Ala Cys Glu Thr Ala Gly Val Ile Arg Ile Ser Asp Asp Ser Ser
                645                 650                 655
Thr Glu Ser Asp Pro Gly Leu Asp Ser Asp Phe Asn Ser Ser Pro Glu
            660                 665                 670
Ser Leu Val Asp Asp Asp Val Val Ile Val Asp Ala Val Gly Leu Pro
        675                 680                 685
Ser Asp Asp Arg Gly Ser Leu Cys Leu Leu Gln Arg Asp Pro His Gly
    690                 695                 700
Pro Gly Val Leu Glu Arg Val Glu Arg Leu Lys Gln Asp Leu Leu Asp
705                 710                 715                 720
Lys Val Arg Arg Leu Gly Arg Glu Leu Pro Val Asn Thr Leu Asp Glu
                725                 730                 735
Leu Ile Asp Gln Leu Gly Gly Pro Gln Arg Val Ala Glu Met Thr Gly
            740                 745                 750
Arg Lys Gly Arg Val Val Ser Arg Pro Asp Gly Thr Val Ala Phe Glu
        755                 760                 765
Ser Arg Ala Glu Gln Gly Leu Ser Ile Asp His Val Asn Leu Arg Glu
    770                 775                 780
Lys Gln Arg Phe Met Ser Gly Glu Lys Leu Val Ala Ile Ile Ser Glu
785                 790                 795                 800
Ala Ser Ser Ser Gly Val Ser Leu Gln Ala Asp Arg Arg Val Gln Asn
                805                 810                 815
Gln Arg Arg Arg Val His Met Thr Leu Glu Leu Pro Trp Ser Ala Asp
            820                 825                 830
Arg Ala Ile Gln Gln Phe Gly Arg Thr His Arg Ser Asn Gln Val Ser
        835                 840                 845
Ala Pro Glu Tyr Val Phe Leu Ile Ser Glu Leu Ala Gly Glu Arg Arg
    850                 855                 860
Phe Ala Ser Ile Val Ala Lys Arg Leu Glu Ser Leu Gly Ala Leu Thr
865                 870                 875                 880
His Gly Asp Arg Arg Ala Thr Glu Ser Arg Asp Leu Ser Lys Tyr Asn
                885                 890                 895
Phe Glu Asn Lys Tyr Gly Thr Arg Ala Leu His Cys Val Leu Thr Thr
            900                 905                 910
Ile Leu Ser Gln Thr Glu Asn Lys Val Pro Val Pro Gln Gly Tyr Pro
        915                 920                 925
Gly Gly Val Pro Thr Phe Phe Arg Asp Met Lys Gln Gly Leu Leu Ser
    930                 935                 940
Val Gly Ile Gly Gly Arg Glu Ser Arg Asn Gly Cys Leu Asp Val Glu
```

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945                 950                 955                 960
Lys Asp Cys Ser Ile Thr Lys Phe Leu Asn Arg Ile Leu Gly Leu Glu
                965                 970                 975
Val His Lys Gln Asn Ala Leu Phe Gln Tyr Phe Ser Asp Thr Phe Asp
            980                 985                 990
His Leu Ile Glu Met Asp Lys Arg Glu Gly Lys Tyr Asp Met Gly Ile
        995                 1000                1005
Leu Asp Leu Ala Pro Gly Ile Glu Glu Ile Tyr Glu Glu Ser Gln Gln
    1010                1015                1020
Val Phe Leu Ala Pro Gly His Pro Gln Asp Gly Gln Val Val Phe Tyr
1025                1030                1035                1040
Lys Ile Ser Val Asp Arg Gly Leu Lys Trp Glu Asp Ala Phe Ala Lys
                1045                1050                1055
Ser Leu Ala Leu Thr Gly Pro Tyr Asp Gly Phe Tyr Leu Ser Tyr Lys
            1060                1065                1070
Val Arg Gly Asn Lys Pro Ser Cys Leu Leu Ala Glu Gln Asn Arg Gly
        1075                1080                1085
Gln Phe Phe Thr Val Tyr Lys Pro Asn Ile Gly Arg Gln Ser Gln Leu
    1090                1095                1100
Glu Ala Leu Asp Ser Leu Arg Arg Lys Phe His Arg Val Thr Ala Glu
1105                1110                1115                1120
Glu Ala Lys Glu Pro Trp Glu Ser Gly Tyr Ala Leu Ser Leu Thr His
                1125                1130                1135
Cys Ser His Ser Ala Trp Asn Arg His Cys Arg Leu Ala Gln Glu Gly
            1140                1145                1150
Lys Asp Cys Leu Gln Gly Leu Arg Leu Arg His His Tyr Met Leu Cys
        1155                1160                1165
Gly Ala Leu Leu Arg Val Trp Gly Arg Ile Ala Ala Val Met Ala Asp
    1170                1175                1180
Val Ser Ser Ser Ser Tyr Leu Gln Ile Val Arg Leu Lys Thr Lys Asp
1185                1190                1195                1200
Arg Lys Lys Gln Val Gly Ile Lys Ile Pro Glu Gly Cys Val Arg Arg
                1205                1210                1215
Val Leu Gln Glu Leu Arg Leu Met Asp Ala Asp Val Lys Arg Arg Gln
            1220                1225                1230
Ala Pro Ala Leu Gly Cys Pro Ala Pro Pro Ala Pro Arg Pro Leu Ala
        1235                1240                1245
Leu Pro Cys Gly Pro Gly Glu Val Leu Asp Leu Thr Tyr Ser Pro Pro
    1250                1255                1260
Ala Glu Ala Phe Pro Pro Pro Pro His Phe Ser Phe Pro Ala Pro Leu
1265                1270                1275                1280
Ser Leu Asp Ala Gly Pro Gly Val Val Pro Leu Gly Thr Pro Asp Ala
                1285                1290                1295
Gln Ala Asp Pro Ala Ala Leu Ala His Gln Gly Cys Asp Ile Asn Phe
            1300                1305                1310
Lys Glu Val Leu Glu Asp Met Leu Arg Ser Leu His Ala Gly Pro Pro
        1315                1320                1325
Ser Glu Gly Ala Leu Gly Glu Gly Ala Gly Ala Gly Gly Ala Ala Gly
    1330                1335                1340
Gly Gly Pro Glu Arg Gln Ser Val Ile Gln Phe Ser Pro Pro Phe Pro
1345                1350                1355                1360
Gly Ala Gln Ala Pro Leu
                1365
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<210> 3107
<211> 2102
<212> DNA
<213> Homo sapiens

<400> 3107
atgctgcagg agtggctggc ggctgtgggc gatgactatg ctgctgtggt ctggaggcct
60
gagggcgagc ccaggttcta cccagatgaa gagggtccca agcactggac caaagaaagg
120
caccagtttc tgatggagct gaagcaggaa gccctcacct ttgccaggaa ctgggggggcc
180
gactatatcc tgtttgcaga cacagacaac attctgacca acaatcagac tctgcggctt
240
ctcatggggc aggggcttcc agtggtggcc ccaatgctgg actcccagac ctactactcc
300
aacttctggt gtgggatcac cccccagggc tactaccgcc gcacagccga gtacttcccc
360
accaagaacc gccagcgccg gggctgcttc cgtgtcccca tggtccactc caccttcctt
420
gcatccctgc gggctgaagg ggcagaccag cttgctttct acccgccaca tcccaactac
480
acttggcctt tcgacgacat catcgtcttc gcctatgcct gccaggctgc tggggtctcc
540
gtccacgtgt gcaatgagca ccgttatggg tacatgaatg tgccggtgaa atcccaccag
600
gggctggaag acgagagggt caacttcatc cacctgatct tagaagcact agtggacggc
660
ccccgcatgc aggcctcagc tcatgtgact cggccctcta agaggcccag caagataggg
720
tttgacgagg tctttgtcat cagcctggct cgcaggcctg accgtcggga acgcatgctc
780
gcctcgctct gggagatgga gatctctggg agggtggtgg acgctgtgga tggctggatg
840
ctcaacagca gtgccatcag gaacctcggc gtagacctgc tcccgggcta ccaggaccct
900
tactcgggcc gcactctgac caagggcgag gtgggctgct tcctcagcca ttactccatc
960
tgggaagagg tggttgccag gggcctggcc cgggtcctgg tgtttgagga tgacgtgcgc
1020
tttgagagca acttcagggg gcggctggag cggctgatgg aggatgtgga ggcagagaaa
1080
ctgtcttggg acctgatcta cctcggacgg aagcaggtga accctgagaa ggagacggcc
1140
gtggaggggc tgccgggcct ggtggtggct gggtactcct actggacgct ggcctatgcc
1200
ctgcgtctgg cgggtgcccg caagctgctg gcctcacagc ctctgcgccg catgctgccc
1260
gtggacgagt tcctgcccat catgttcgac cagcacccca acgagcagta caaggcacac
1320
ttctggccac gggacctggt ggccttctcc gcccagcccc tgctcgctgc ccctacccac
1380
tatgccgggg acgccgagtg gctcagtgac acggagacat cctctccatg ggatgatgac
1440

agcggccgcc tcatcagctg gagcggctcc caaaagaccc tgcgcagccc ccgcctggac
1500
ctgactggca gcagcgggca cagcctccaa ccccagcccc gagatgagct ctaggtccag
1560
gtgatgactg caaagcagtg tccaggagca ggccactact gcccagagag cagaggagga
1620
ggttgttggc agggactgca gatcctgtca gacctggcca ccaccttggg catggccact
1680
ctgccctctg gacctgtctt tcatcgggag aaaccactca gagatggatc ccattcccta
1740
aaggtctcac agcaaaggag caggactccc aggcccctgt accctgcctg gcctgattca
1800
gggccttgtg gcccccagct tctgtttcaa gctgggcaga ccccaggatc ccttccctcc
1860
ctaaggactc agctgagggg cccctctgcc cccttctacc tccacctcag caccctcccc
1920
cagcttgatg tttgggtctc cccagcaccc tcctccctgg ccggtgcaaa gtacagggag
1980
gtaaagcagg acccttgcag acatgttgcc cagcacacag taggccctca ataaaagcca
2040
tttgcacttt aaatatatat atgtatgtat atatatgtat atatatatat atatatatat
2100
gt
2102

<210> 3108
<211> 517
<212> PRT
<213> Homo sapiens

<400> 3108
Met Leu Gln Glu Trp Leu Ala Ala Val Gly Asp Asp Tyr Ala Ala Val
 1   5   10   15
Val Trp Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp Glu Glu Gly
            20   25   30
Pro Lys His Trp Thr Lys Glu Arg His Gln Phe Leu Met Glu Leu Lys
        35   40   45
Gln Glu Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp Tyr Ile Leu
    50   55   60
Phe Ala Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr Leu Arg Leu
65   70   75   80
Leu Met Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu Asp Ser Gln
                85   90   95
Thr Tyr Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln Gly Tyr Tyr
            100   105   110
Arg Arg Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln Arg Arg Gly
        115   120   125
Cys Phe Arg Val Pro Met Val His Ser Thr Phe Leu Ala Ser Leu Arg
    130   135   140
Ala Glu Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His Pro Asn Tyr
145   150   155   160
Thr Trp Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala Cys Gln Ala
                165   170   175
Ala Gly Val Ser Val His Val Cys Asn Glu His Arg Tyr Gly Tyr Met

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            180                 185                 190
Asn Val Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu Arg Val Asn
        195                 200                 205
Phe Ile His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro Arg Met Gln
    210                 215                 220
Ala Ser Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser Lys Ile Gly
225                 230                 235                 240
Phe Asp Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro Asp Arg Arg
                245                 250                 255
Glu Arg Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser Gly Arg Val
            260                 265                 270
Val Asp Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala Ile Arg Asn
        275                 280                 285
Leu Gly Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr Ser Gly Arg
    290                 295                 300
Thr Leu Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His Tyr Ser Ile
305                 310                 315                 320
Trp Glu Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu Val Phe Glu
                325                 330                 335
Asp Asp Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu Glu Arg Leu
            340                 345                 350
Met Glu Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu Ile Tyr Leu
        355                 360                 365
Gly Arg Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val Glu Gly Leu
    370                 375                 380
Pro Gly Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu Ala Tyr Ala
385                 390                 395                 400
Leu Arg Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln Pro Leu Arg
                405                 410                 415
Arg Met Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe Asp Gln His
            420                 425                 430
Pro Asn Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala
        435                 440                 445
Phe Ser Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp
    450                 455                 460
Ala Glu Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Asp
465                 470                 475                 480
Ser Gly Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr Leu Arg Ser
                485                 490                 495
Pro Arg Leu Asp Leu Thr Gly Ser Ser Gly His Ser Leu Gln Pro Gln
            500                 505                 510
Pro Arg Asp Glu Leu
        515
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<210> 3109
<211> 959
<212> DNA
<213> Homo sapiens

<400> 3109
nnacgcgtcc ttttcaccaa gtctcctgaa cacacaaccg ggtgccactg gaagtgattc
60
gcagcgcacc tgccctttgt taatacaaca tcaccttgct ccatatccta ccaaagatcc
120

cctggaatct ggaaggatct acttcactcg atccctccac agtcagcagg acaactttat
180
tccagtctgg gggacgcctt acccgcagga gctgccaatc actgcagacg aagatgctca
240
cgtaatcttt gcagtcgcgc cgttctgcca gcgccatgta gcggccgtcc ctggtgaagg
300
tgattccctg cagactcgct cttcatcctg tgcgccatgt acaagcgagg gctggtgcag
360
gtctggtctt tagagcagcc cgaatggcac tgcaaaatag acgagggctc agccgggctg
420
gtggcctcgt gctggagccc ggacgggcgc cacattctca acaccacgga attccatctg
480
cggataaccg tctggtcctt gtgcacaaaa tccgtgtctt acatcaaata cccgaaagct
540
tgtctgcagg gaatcacctt caccagggac ggccgctaca tggcgctggc agaacggcgc
600
gactgcaaag attacgtgag catcttcgtc tgcagtgatt ggcagctcct gcggcatttt
660
gatacggaca cccaggatct cacagggatt gagtgggccc caaacggctg tgtgctggca
720
gtgtgggaca cctgcttgga gtacaagatt ctgctgtact cattggatgg ccggttgttg
780
tccacgtaca gcgctntacg agtggtcnnc ctgggcatca agtctgtggc ctggagcccc
840
agcagtcagt tcctggcagt tgggagctat gatggaaagg tgcgcatcct taatcacgtg
900
acttggaaaa tgatcacgga gtttgggcat ccctgcagcc ccataaatga ttcccaaaa
959

<210> 3110
<211> 207
<212> PRT
<213> Homo sapiens

<400> 3110
Met Tyr Lys Arg Gly Leu Val Gln Val Trp Ser Leu Glu Gln Pro Glu
1 5 10 15
Trp His Cys Lys Ile Asp Glu Gly Ser Ala Gly Leu Val Ala Ser Cys
20 25 30
Trp Ser Pro Asp Gly Arg His Ile Leu Asn Thr Thr Glu Phe His Leu
35 40 45
Arg Ile Thr Val Trp Ser Leu Cys Thr Lys Ser Val Ser Tyr Ile Lys
50 55 60
Tyr Pro Lys Ala Cys Leu Gln Gly Ile Thr Phe Thr Arg Asp Gly Arg
65 70 75 80
Tyr Met Ala Leu Ala Glu Arg Arg Asp Cys Lys Asp Tyr Val Ser Ile
85 90 95
Phe Val Cys Ser Asp Trp Gln Leu Leu Arg His Phe Asp Thr Asp Thr
100 105 110
Gln Asp Leu Thr Gly Ile Glu Trp Ala Pro Asn Gly Cys Val Leu Ala
115 120 125
Val Trp Asp Thr Cys Leu Glu Tyr Lys Ile Leu Leu Tyr Ser Leu Asp
130 135 140
Gly Arg Leu Leu Ser Thr Tyr Ser Ala Xaa Arg Val Val Xaa Leu Gly

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145                 150                 155                 160
Ile Lys Ser Val Ala Trp Ser Pro Ser Ser Gln Phe Leu Ala Val Gly
                165                 170                 175
Ser Tyr Asp Gly Lys Val Arg Ile Leu Asn His Val Thr Trp Lys Met
            180                 185                 190
Ile Thr Glu Phe Gly His Pro Cys Ser Pro Ile Asn Asp Ser Gln
        195                 200                 205
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<210> 3111
<211> 1269
<212> DNA
<213> Homo sapiens

<400> 3111
tttttttttt tttttttttt tttttttttt tttttcttta acaaaatttt tatttaataa
60
atggttaaaa tcgcagtgcc aaaaatacat tgacatttag caatttcact gaaaggaaga
120
aactacagaa tgcacggttt cagaaagcta ttttaagtta tttacaaata aagtatctaa
180
aactcaaaaa caggctctgt atgctatatc tagtttatcc cttcccgaac aaaatttctg
240
ttatttgggc aaattcttaa accatggttt aaaccgtaat ggttacaaac cacaaacaca
300
tccatccaga gactgaaacc gtttctatcc ggtcagtggc aaaactgttg aaagggcaat
360
agttgaagct gttgggtttt atatagtgtg aactctgata aatattccta ccaggactaa
420
aacacagcac gctttgcggg catggctgac tcacaaaggt tgtaacaaac aagaactact
480
cttcactcga caccatggct cagaggccac cgagaagcac gagtgactga cagctcctct
540
gcttacaaac gaatgaaacc caaagtggat gtcgttctca cagcactgaa agtgcttcag
600
gactcacact gatccaatac taactttctt ccctatttta cacatatttt tctactgtcc
660
agtggaaatc attttctgtt ttggctaaac aacaaatact agtttataac aggaatggta
720
aaatctgtga gaattctgct caatttaata caagatcact actttcttta gaatggtttc
780
tgcgtgtttc tacgtcaccc tctgtatttt tagcttccag tttcctggta aggaataagt
840
tctccttccc agtcacactc ggggtcattt acacgtttct gggatgccct tgctcgtcca
900
tggaggccag gtgcgtgcag tgactcactc tgcctcttcc ctcttctcag gaccagtccc
960
cgaaccttct gccttgcaga tcctcccgct tccgccacac tctcgcgctc ggaagcgagc
1020
tcctggatca tacagctgca aggctggccg gtccttgttt gccagtcgct cttttctggg
1080
tgctggactg tcgtcacacc tctgcgctct tcccagtctc tccatggcct cccccggagc
1140
cccgctgtcc tggctcccct tcttccctct gtcttggcca ggtcctttcc cccatctctg
1200

ctcatcctca ctccttctgg aaagccgttc aggctcgtgg tgagctctgt gcctcctgcc
1260
gtcatccac
1269

<210> 3112
<211> 151
<212> PRT
<213> Homo sapiens

<400> 3112
Met Thr Ala Gly Gly Thr Glu Leu Thr Thr Ser Leu Asn Gly Phe Pro
1 5 10 15
Glu Gly Val Arg Met Ser Arg Asp Gly Gly Lys Asp Leu Ala Lys Thr
20 25 30
Glu Gly Arg Arg Gly Ala Arg Thr Ala Gly Leu Arg Gly Arg Pro Trp
35 40 45
Arg Asp Trp Glu Glu Arg Arg Gly Val Thr Thr Val Gln His Pro Glu
50 55 60
Lys Ser Asp Trp Gln Thr Arg Thr Gly Gln Pro Cys Ser Cys Met Ile
65 70 75 80
Gln Glu Leu Ala Ser Glu Arg Glu Ser Val Ala Glu Ala Gly Gly Ser
85 90 95
Ala Arg Gln Lys Val Arg Gly Leu Val Leu Arg Arg Gly Lys Arg Gln
100 105 110
Ser Glu Ser Leu His Ala Pro Gly Leu His Gly Arg Ala Arg Ala Ser
115 120 125
Gln Lys Arg Val Asn Asp Pro Glu Cys Asp Trp Glu Gly Glu Leu Ile
130 135 140
Pro Tyr Gln Glu Thr Gly Ser
145 150

<210> 3113
<211> 631
<212> DNA
<213> Homo sapiens

<400> 3113
nacgcgttcc tgcagaacgc ctcagccgtg gtcatcttca acgtgggctc caacaccaac
60
gagaccatca ccatgcccca cgcgggtgta gaagacatcg tggccataat gattcctgag
120
ccaaaaggga aggagatagt aagcctgctg gaaagaaaca tcaccgtgac aatgtacatc
180
accatcggaa cccggaactt gcagaaatat gtgagccgca cttcggttgt gtttgtctcc
240
atctccttca ttgtcctgat gatcatttcc ctcgcatggc tcgtctttta ttacatccag
300
aggtttcgat atgcaaatgc cagggatagg aaccagcgcc gactggggga tgcagcaaag
360
aaagccatca gcaaactcca gatcaggacc atcaagaagg gtgacaagga aacagagtct
420
gattttgaca actgtgcagt ttgtattgaa gggtacaagc ccaatgacgt tgtccggatc
480

ctgccctgcc ggcatctttt ccacaagtcc tgtgttgacc cctggcttct agaccatcgt
540
acctgtccca tgtgcaagat gaacattctt aaagccctag ggatcccccc caatgccgac
600
tgcatggacg actttgccac tgacttcgag g
631

<210> 3114
<211> 210
<212> PRT
<213> Homo sapiens

<400> 3114
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Ser Asn Thr Asn Glu Thr Ile Thr Met Pro His Ala Gly Val Glu Asp
            20   25   30
Ile Val Ala Ile Met Ile Pro Glu Pro Lys Gly Lys Glu Ile Val Ser
        35   40   45
Leu Leu Glu Arg Asn Ile Thr Val Thr Met Tyr Ile Thr Ile Gly Thr
    50   55   60
Arg Asn Leu Gln Lys Tyr Val Ser Arg Thr Ser Val Val Phe Val Ser
65   70   75   80
Ile Ser Phe Ile Val Leu Met Ile Ile Ser Leu Ala Trp Leu Val Phe
                85   90   95
Tyr Tyr Ile Gln Arg Phe Arg Tyr Ala Asn Ala Arg Asp Arg Asn Gln
            100   105   110
Arg Arg Leu Gly Asp Ala Ala Lys Lys Ala Ile Ser Lys Leu Gln Ile
        115   120   125
Arg Thr Ile Lys Lys Gly Asp Lys Glu Thr Glu Ser Asp Phe Asp Asn
    130   135   140
Cys Ala Val Cys Ile Glu Gly Tyr Lys Pro Asn Asp Val Val Arg Ile
145   150   155   160
Leu Pro Cys Arg His Leu Phe His Lys Ser Cys Val Asp Pro Trp Leu
                165   170   175
Leu Asp His Arg Thr Cys Pro Met Cys Lys Met Asn Ile Leu Lys Ala
            180   185   190
Leu Gly Ile Pro Pro Asn Ala Asp Cys Met Asp Asp Phe Ala Thr Asp
        195   200   205
Phe Glu
    210

<210> 3115
<211> 1366
<212> DNA
<213> Homo sapiens

<400> 3115
ncacaaaggc accaaaccac aaaacgtcac acgtaaacat catacgtggc aaccacaagc
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caatcagttg gatatttcat tcattggtat acatatggac tgtaaggtgt ctttcaggtt
120
gcagaaaaga tggaaaaaag gacatgtgca ctctgcccca aagatgtcga atataatgtc
180

ctatactttg cacaatcaga gaatatagct gctcatgaga attgtttgct gtattcttca
240
ggacttgtgg aatgtgagga tcaggatcca cttaatcctg atagaagttt tgatgtggaa
300
tcagtaaaga aagaaatcca gagaggaagg aagttgaaat gcaaattttg tcataaaaga
360
ggagccaccg tgggatgtga tttaaaaaac tgtaacaaga attaccactt tttctgtgcc
420
aagaaggacg acgcagttcc acagtctgat ggagttcgag gaatttataa actgctttgc
480
cagcaacatg ctcaattccc gatcatcgct caaagtggta aattttcagg agtgaaaaga
540
aaaagaggaa ggaagaaacc cctctcaggc aatcatgtac agccacccga aacaatgaaa
600
tgtaatacat tcataagaca agtgaaagaa gagcatggca gacacacaga tgcaactgtg
660
aaagttcctt ttcttaagaa atgcaagnga agcaggactt cttaattact tacttgaaga
720
aatattagac aaagttcatt caattccaga aaaactcatg gatgagacta cttcagaatc
780
agactatgaa gaaatcggga gtgcactttt tgactgtaga ttgttcgaag acacatttgt
840
aaattttcaa gcagcaatag agaaaaaaat tcatgcatct caacaaaggt ggcagcagtt
900
gaaggaagag attgagctac ttcaggactt aaaacaaacc ttgtgctctt ttcaagaaaa
960
tagagatctt atgtcaagtt ctacatcaat atcatccctg tcttattagg gattaccgtt
1020
tcctaagcca agagtcatgt caaattgcaa tcaggctcaa aaccagagac caggctgtga
1080
aatccacaca tctttagaac tagtcgtctc ctcttggcct cagcagctct tccctgttct
1140
tactggttga cattttgatc actctttgca cactcttgtg ttttttgctc actgtcacat
1200
tcccagcacc tagtatgctc agtaaatgtt tgtggaataa gtgcataaaa tgttcttaac
1260
ctttgattct acttacagcc catgatagcc tcttcttaga tataataaat ttggattata
1320
ctaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa
1366

<210> 3116
<211> 191
<212> PRT
<213> Homo sapiens

<400> 3116
Met Glu Lys Arg Thr Cys Ala Leu Cys Pro Lys Asp Val Glu Tyr Asn
1 5 10 15
Val Leu Tyr Phe Ala Gln Ser Glu Asn Ile Ala Ala His Glu Asn Cys
20 25 30
Leu Leu Tyr Ser Ser Gly Leu Val Glu Cys Glu Asp Gln Asp Pro Leu
35 40 45
Asn Pro Asp Arg Ser Phe Asp Val Glu Ser Val Lys Lys Glu Ile Gln

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    50                  55                  60
Arg Gly Arg Lys Leu Lys Cys Lys Phe Cys His Lys Arg Gly Ala Thr
65                  70                  75                  80
Val Gly Cys Asp Leu Lys Asn Cys Asn Lys Asn Tyr His Phe Phe Cys
                85                  90                  95
Ala Lys Lys Asp Asp Ala Val Pro Gln Ser Asp Gly Val Arg Gly Ile
            100                 105                 110
Tyr Lys Leu Leu Cys Gln Gln His Ala Gln Phe Pro Ile Ile Ala Gln
        115                 120                 125
Ser Gly Lys Phe Ser Gly Val Lys Arg Lys Arg Gly Arg Lys Lys Pro
    130                 135                 140
Leu Ser Gly Asn His Val Gln Pro Pro Glu Thr Met Lys Cys Asn Thr
145                 150                 155                 160
Phe Ile Arg Gln Val Lys Glu Glu His Gly Arg His Thr Asp Ala Thr
                165                 170                 175
Val Lys Val Pro Phe Leu Lys Lys Cys Lys Xaa Ser Arg Thr Ser
            180                 185                 190
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<210> 3117
<211> 1373
<212> DNA
<213> Homo sapiens

<400> 3117
nnaacccaga agcaaaagag cagagctacc atgtcctctt ggagcagaca gcgaccaaaa
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agcccagggg gcattcaacc ccatgtttct agaactctgt tcctgctgct gctgttggca
120
gcctcagcct ggggggtcac cctgagcccc aaagactgcc aggtgttccg ctcagaccat
180
ggcagctcca tctcctgtca accacctgcc gaaatccccg gctacctgcc agccgacacc
240
gtgcacctgg ccgtggaatt cttcaacctg acccacctgc cagccaacct cctccagggc
300
gcctctaagc tccaagaatt gcacctctcc agcaatgggc tggaaagcct ctcgcccgaa
360
ttcctgcggc cagtgccgca gctgagggtg ctggatctaa cccgaaacgc cctgaccggg
420
ctgcccccgg gcctcttcca ggcctcagcc accctggaca ccctggtatt gaaagaaaac
480
cagctggagg tcctggaggt ctcgtggcta cacggcctga aagctctggg gcatctggac
540
ctgtctggga accgcctccg gaaactgccc cccgggctgc tggccaactt caccctcctg
600
cgcacccttg accttgggga gaaccagttg gagaccttgc cacctgacct cctgaggggt
660
ccgctgcaat tagaacggct acatctagaa ggcaacaaat tgcaagtact gggaaaagat
720
ctcctcttgc cgcagccgga cctgcgctac ctcttcctga gcggcaacaa gctggccagg
780
gtggcagccg gtgccttcca gggcctgcgg cagctggaca tgctggacct ctccaataac
840
tcactggcca gcgtgcccga ggggctctgg gcatccctag ggcagccaaa ctgggacatg
900

cgggatggct tcgacatctc cggcaacccc tggatctgtg accagaacct gagcgacctc
960
tatcgttggc ttcaggccca aaaagacaag atgttttccc agaatgacac gcgctgtgct
1020
gggcctgaag ccgtgaaggg ccagacgctc ctggcagtgg ccaagtccca gtgagaccag
1080
gggcttgggt tgagggtggg gggtctggta gaacactgca acccgcttaa caaataatcc
1140
tgcctttggc cgggtgcggg ggctcacgcc tgtaatccca gcactttggg gaggcccagg
1200
tggcggaatc acgaggtcag gagatcgaga ccatcttggc taacatggtg aaaccctgtc
1260
tctactaaaa atataaaaaa ttagccaggc gtggtggtgg gcacctgtag tcccagcaac
1320
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1373

<210> 3118
<211> 312
<212> PRT
<213> Homo sapiens

<400> 3118
Val Thr Leu Ser Pro Lys Asp Cys Gln Val Phe Arg Ser Asp His Gly
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Ser Ser Ile Ser Cys Gln Pro Pro Ala Glu Ile Pro Gly Tyr Leu Pro
20 25 30
Ala Asp Thr Val His Leu Ala Val Glu Phe Phe Asn Leu Thr His Leu
35 40 45
Pro Ala Asn Leu Leu Gln Gly Ala Ser Lys Leu Gln Glu Leu His Leu
50 55 60
Ser Ser Asn Gly Leu Glu Ser Leu Ser Pro Glu Phe Leu Arg Pro Val
65 70 75 80
Pro Gln Leu Arg Val Leu Asp Leu Thr Arg Asn Ala Leu Thr Gly Leu
85 90 95
Pro Pro Gly Leu Phe Gln Ala Ser Ala Thr Leu Asp Thr Leu Val Leu
100 105 110
Lys Glu Asn Gln Leu Glu Val Leu Glu Val Ser Trp Leu His Gly Leu
115 120 125
Lys Ala Leu Gly His Leu Asp Leu Ser Gly Asn Arg Leu Arg Lys Leu
130 135 140
Pro Pro Gly Leu Leu Ala Asn Phe Thr Leu Leu Arg Thr Leu Asp Leu
145 150 155 160
Gly Glu Asn Gln Leu Glu Thr Leu Pro Pro Asp Leu Leu Arg Gly Pro
165 170 175
Leu Gln Leu Glu Arg Leu His Leu Glu Gly Asn Lys Leu Gln Val Leu
180 185 190
Gly Lys Asp Leu Leu Leu Pro Gln Pro Asp Leu Arg Tyr Leu Phe Leu
195 200 205
Ser Gly Asn Lys Leu Ala Arg Val Ala Ala Gly Ala Phe Gln Gly Leu
210 215 220
Arg Gln Leu Asp Met Leu Asp Leu Ser Asn Asn Ser Leu Ala Ser Val
225 230 235 240
Pro Glu Gly Leu Trp Ala Ser Leu Gly Gln Pro Asn Trp Asp Met Arg

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                245                 250                 255
Asp Gly Phe Asp Ile Ser Gly Asn Pro Trp Ile Cys Asp Gln Asn Leu
            260                 265                 270
Ser Asp Leu Tyr Arg Trp Leu Gln Ala Gln Lys Asp Lys Met Phe Ser
        275                 280                 285
Gln Asn Asp Thr Arg Cys Ala Gly Pro Glu Ala Val Lys Gly Gln Thr
    290                 295                 300
Leu Leu Ala Val Ala Lys Ser Gln
305                 310
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<210> 3119
<211> 427
<212> DNA
<213> Homo sapiens

<400> 3119
gtacacatgg tgctcaacca gcagggccgg ccatcgggcg atgccttcat tcagatgaca
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tcagcagagc gagccctagc tgctgctcag cgttgccata agaaggtgat gaaggagcgc
120
tacgtggagg tggtcccctg ttccacagag gagatgagcc gagtgctgat ggggggcacc
180
ttgggccgca gtggcatgtc ccctccaccc tgcaagctgc cctgcctctc accacctacc
240
tacaccacct tccaagccac cccaacgctc attcccacgg agacggcagc tctatacccc
300
tcttcagcac tgctcccagc tgccagggtg cctgctgccc ccacccctgt tgcctactat
360
ccagggccag ccactcaact ctacctgaac tacacagcct actacccaag ccccgaagac
420
aacgcgt
427

<210> 3120
<211> 142
<212> PRT
<213> Homo sapiens

<400> 3120
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Val His Met Val Leu Asn Gln Gln Gly Arg Pro Ser Gly Asp Ala Phe
 1               5                  10                  15
Ile Gln Met Thr Ser Ala Glu Arg Ala Leu Ala Ala Ala Gln Arg Cys
            20                  25                  30
His Lys Lys Val Met Lys Glu Arg Tyr Val Glu Val Val Pro Cys Ser
        35                  40                  45
Thr Glu Glu Met Ser Arg Val Leu Met Gly Gly Thr Leu Gly Arg Ser
    50                  55                  60
Gly Met Ser Pro Pro Pro Cys Lys Leu Pro Cys Leu Ser Pro Pro Thr
65                  70                  75                  80
Tyr Thr Thr Phe Gln Ala Thr Pro Thr Leu Ile Pro Thr Glu Thr Ala
                85                  90                  95
Ala Leu Tyr Pro Ser Ser Ala Leu Leu Pro Ala Ala Arg Val Pro Ala
            100                 105                 110
Ala Pro Thr Pro Val Ala Tyr Tyr Pro Gly Pro Ala Thr Gln Leu Tyr
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        115                 120                 125
Leu Asn Tyr Thr Ala Tyr Tyr Pro Ser Pro Glu Asp Asn Ala
    130                 135                 140

<210> 3121
<211> 284
<212> DNA
<213> Homo sapiens

<400> 3121
gaattccatg gcagctggga catctgtgag ccacgtgggt tcctgggcag caccaggacc
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atctgaggat ttctcaactt ctgcagcaac ttctgcagcc agctcacacg tgaggagaaa
120
taagaggaac atgaacctgg acggggcagc ttccattgtc cctctcctgc tcctgctaat
180
gaacaaggcc tccccagagt atgaagagaa catgcacaga taccagaagg cagccaagct
240
cttccgggga agattctctt tattctggtg gacagtggta tgaa
284

<210> 3122
<211> 91
<212> PRT
<213> Homo sapiens

<400> 3122
Met Ala Ala Gly Thr Ser Val Ser His Val Gly Ser Trp Ala Ala Pro
 1               5                  10                  15
Gly Pro Ser Glu Asp Phe Ser Thr Ser Ala Ala Thr Ser Ala Ala Ser
            20                  25                  30
Ser His Val Arg Arg Asn Lys Arg Asn Met Asn Leu Asp Gly Ala Ala
        35                  40                  45
Ser Ile Val Pro Leu Leu Leu Leu Leu Met Asn Lys Ala Ser Pro Glu
    50                  55                  60
Tyr Glu Glu Asn Met His Arg Tyr Gln Lys Ala Ala Lys Leu Phe Arg
65                  70                  75                  80
Gly Arg Phe Ser Leu Phe Trp Trp Thr Val Val
                85                  90

<210> 3123
<211> 344
<212> DNA
<213> Homo sapiens

<400> 3123
aagaaagtga actgcaagcc caagaaccag gacgaacagg agattccttt ccggctccgg
60
gagattatga ggagccgcca agagatgaaa aacccgatca gtaacaagaa gaggaagaaa
120
gcagcccagg tgaccttcag aaagacattg gagaaggaag caaagggaga ggagcccgac
180
atcgcagtcc ccaagttcaa acagaggaag ggggagtccg acggggccta tatccaccgc
240
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atgcagcaag aggcccagca tgtgctgttc ctcagcaaga accaggccat ccggcagcca
300
gaggtgcagg cagctcccaa ggagaagtct gagcagaaaa aagc
344

<210> 3124
<211> 92
<212> PRT
<213> Homo sapiens

<400> 3124
Met Arg Ser Arg Gln Glu Met Lys Asn Pro Ile Ser Asn Lys Lys Arg
 1   5   10   15
Lys Lys Ala Ala Gln Val Thr Phe Arg Lys Thr Leu Glu Lys Glu Ala
            20   25   30
Lys Gly Glu Glu Pro Asp Ile Ala Val Pro Lys Phe Lys Gln Arg Lys
        35   40   45
Gly Glu Ser Asp Gly Ala Tyr Ile His Arg Met Gln Gln Glu Ala Gln
    50   55   60
His Val Leu Phe Leu Ser Lys Asn Gln Ala Ile Arg Gln Pro Glu Val
65   70   75   80
Gln Ala Ala Pro Lys Glu Lys Ser Glu Gln Lys Lys
                85   90

<210> 3125
<211> 647
<212> DNA
<213> Homo sapiens

<400> 3125
agatggagtt ttgctcttcg tgcccaggct ggagtaccat ggtgacagtg cgaagctaag
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acattaggaa ggtgctgagg aaagccatta agcatccaca gctccactgc ctaggcagat
120
ggtcagcagg cagtttagtt gtgggagtat ttccaatttg catgaatgaa acatggacaa
180
ataagataag gctggctcca gggaagtaat tcccccagtt cccctgagcc ttggatctgg
240
aaaactgcag cccatcctgg aattagggaa catcacaaaa cgtactgggg agaactcccc
300
atgtggcctc ggcccacgcc agaagccggg caaggtccca agtgccggct cgcccacaag
360
ctatggctaa gacagaaaaa caaaggaaaa aaagtcctcc ccaaacacac acataagcaa
420
aacccatctt cctgtgttct ctgccaagag agctggagca aaagagatga gtttgagact
480
ctgattcatc catcaagaca aataaactca gtctatggag gttagcaggg caatttgtga
540
agcaaacaaa agttgagttt tggaaagggg ctctgaagaa aatgaagatg acataccagg
600
aatttaactt catgacaaga agagaaagtg actcactctt gacgcgt
647

<210> 3126

<211> 116
<212> PRT
<213> Homo sapiens

<400> 3126
Met Lys Leu Asn Ser Trp Tyr Val Ile Phe Ile Phe Phe Arg Ala Pro
1 5 10 15
Phe Gln Asn Ser Thr Phe Val Cys Phe Thr Asn Cys Pro Ala Asn Leu
20 25 30
His Arg Leu Ser Leu Phe Val Leu Met Asp Glu Ser Glu Ser Gln Thr
35 40 45
His Leu Phe Cys Ser Ser Ser Leu Gly Arg Glu His Arg Lys Met Gly
50 55 60
Phe Ala Tyr Val Cys Val Trp Gly Gly Leu Phe Phe Leu Cys Phe Ser
65 70 75 80
Val Leu Ala Ile Ala Cys Gly Arg Ala Gly Thr Trp Asp Leu Ala Arg
85 90 95
Leu Leu Ala Trp Ala Glu Ala Thr Trp Gly Val Leu Pro Ser Thr Phe
100 105 110
Cys Asp Val Pro
115

<210> 3127
<211> 2218
<212> DNA
<213> Homo sapiens

<400> 3127
ncagaagtta gccaagatga acttaatgaa atcaatcagt tcttgggacc cgtggaaaaa
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ttcttcactg aagaggtgga ctcccgaaaa attgaccagg aagggaaaat cccagatgaa
120
actttggaga aattgaagag cctagggctt tttgggctgc aagtcccaga agaatatggt
180
ggcctgggct tctccaacac catgtactca agactagggg agatcatcag catggatggg
240
tccatcactg tgaccctggc agcgcaccag gctattggcc tcaaggggat catcttggct
300
ggcactgagg agcagaaagc caaatacttg cctaaactgg cgtccgggga gcacatagca
360
gccttctgcc tcacggagcc agccagtggg agcgatgcag cctcaatccg gagcagagcc
420
acactaagtg aagacaagaa gcactacatc ctcaatggct ccaaggtctg gattactaat
480
ggaggactgg ccaatatttt tactgtgttt gcaaagactg aggtcgttga ttctgatgga
540
tcagtgaaag acaagatcac agcattcata gtagaaagag actttggtgg agtcactaat
600
gggaaacccg aagataaatt aggcattcgg ggctccaaca cttgtgaagt ccattttgaa
660
aacaccaaga tacctgtgga aaacatcctt ggagaggtcg gagatgggtt taaggtggcc
720
atgaacatcc tcaacagcgg ccggttcagc atgggcagcg tcgtggctgg gctgctcaag
780

agattgattg aaatgactgc tgagtacgcc tgcacaagga aacagtttaa caagaggctc
840
agtgaatttg gattgattca ggagaaattt gcactgatgg ctcagaaggc ttacgtcatg
900
gagagtatga cctacctcac agcagggatg ctggaccaac ctggctttcc cgactgctcc
960
atcgaggcag ccatggtgaa ggtgttcagc tccgaggccg cctggcagtg tgtgagtgag
1020
gcgctgcaga tcctcggggg cttgggctac acaagggact atccgtacga gcgcatactg
1080
cgtgacaccc gcatcctcct catcttcgag ggaaccaatg agattctccg gatgtacatc
1140
gccctgacgg gtctgcagca tgccggccgc atcctgacta ccaggatcca tgagcttaaa
1200
caggccaaag tgagcacagt catggatacc gttggccgga ggcttcggga ctccctgggc
1260
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1320
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1440
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1500
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1560
ttgcagaatc tcttcagcct ctctcagctg gacaagtatg ctccagaaaa cctagatgag
1620
cagattaaga aagtgtccca gcagatcctt gagaagcgag cctatatctg tgcccaccct
1680
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1740
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1800
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1860
aggttttgac ctgcaggcag tgctctctaa caggaccatc acagcttctg aactgagccg
1920
gagagagaga atggaattgc tgacccctgg aactggcggg tattctggtc attgaggaga
1980
caccatagtg gaaactgggg cttatgctgc tgcctccagg gtgtgaggtg ggtggggacc
2040
tgtgtcaggt gtggatagcc atttctgctc aaccacacat tctctaagaa acagcttgaa
2100
agctctgtct gggtcattca tttaaactag aagcagaggc acttaaaaca tgtaccagga
2160
accatttaac aaagaatata aaatgtcaca atctgtgtac tgttaaaaaa aaaaaaaa
2218

<210> 3128
<211> 565
<212> PRT
<213> Homo sapiens

<400> 3128
Xaa Glu Val Ser Gln Asp Glu Leu Asn Glu Ile Asn Gln Phe Leu Gly
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Pro Val Glu Lys Phe Phe Thr Glu Glu Val Asp Ser Arg Lys Ile Asp
20 25 30
Gln Glu Gly Lys Ile Pro Asp Glu Thr Leu Glu Lys Leu Lys Ser Leu
35 40 45
Gly Leu Phe Gly Leu Gln Val Pro Glu Glu Tyr Gly Gly Leu Gly Phe
50 55 60
Ser Asn Thr Met Tyr Ser Arg Leu Gly Glu Ile Ile Ser Met Asp Gly
65 70 75 80
Ser Ile Thr Val Thr Leu Ala Ala His Gln Ala Ile Gly Leu Lys Gly
85 90 95
Ile Ile Leu Ala Gly Thr Glu Glu Gln Lys Ala Lys Tyr Leu Pro Lys
100 105 110
Leu Ala Ser Gly Glu His Ile Ala Ala Phe Cys Leu Thr Glu Pro Ala
115 120 125
Ser Gly Ser Asp Ala Ala Ser Ile Arg Ser Arg Ala Thr Leu Ser Glu
130 135 140
Asp Lys Lys His Tyr Ile Leu Asn Gly Ser Lys Val Trp Ile Thr Asn
145 150 155 160
Gly Gly Leu Ala Asn Ile Phe Thr Val Phe Ala Lys Thr Glu Val Val
165 170 175
Asp Ser Asp Gly Ser Val Lys Asp Lys Ile Thr Ala Phe Ile Val Glu
180 185 190
Arg Asp Phe Gly Gly Val Thr Asn Gly Lys Pro Glu Asp Lys Leu Gly
195 200 205
Ile Arg Gly Ser Asn Thr Cys Glu Val His Phe Glu Asn Thr Lys Ile
210 215 220
Pro Val Glu Asn Ile Leu Gly Glu Val Gly Asp Gly Phe Lys Val Ala
225 230 235 240
Met Asn Ile Leu Asn Ser Gly Arg Phe Ser Met Gly Ser Val Val Ala
245 250 255
Gly Leu Leu Lys Arg Leu Ile Glu Met Thr Ala Glu Tyr Ala Cys Thr
260 265 270
Arg Lys Gln Phe Asn Lys Arg Leu Ser Glu Phe Gly Leu Ile Gln Glu
275 280 285
Lys Phe Ala Leu Met Ala Gln Lys Ala Tyr Val Met Glu Ser Met Thr
290 295 300
Tyr Leu Thr Ala Gly Met Leu Asp Gln Pro Gly Phe Pro Asp Cys Ser
305 310 315 320
Ile Glu Ala Ala Met Val Lys Val Phe Ser Ser Glu Ala Ala Trp Gln
325 330 335
Cys Val Ser Glu Ala Leu Gln Ile Leu Gly Gly Leu Gly Tyr Thr Arg
340 345 350
Asp Tyr Pro Tyr Glu Arg Ile Leu Arg Asp Thr Arg Ile Leu Leu Ile
355 360 365
Phe Glu Gly Thr Asn Glu Ile Leu Arg Met Tyr Ile Ala Leu Thr Gly
370 375 380
Leu Gln His Ala Gly Arg Ile Leu Thr Thr Arg Ile His Glu Leu Lys
385 390 395 400
Gln Ala Lys Val Ser Thr Val Met Asp Thr Val Gly Arg Arg Leu Arg
405 410 415
Asp Ser Leu Gly Arg Thr Val Asp Leu Gly Leu Thr Gly Asn His Gly

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            420                 425                 430
Val Val His Pro Ser Leu Ala Asp Ser Ala Asn Lys Phe Glu Glu Asn
        435                 440                 445
Thr Tyr Cys Phe Gly Arg Thr Val Glu Thr Leu Leu Leu Arg Phe Gly
    450                 455                 460
Lys Thr Ile Met Glu Glu Gln Leu Val Leu Lys Arg Val Ala Asn Ile
465                 470                 475                 480
Leu Ile Asn Leu Tyr Gly Met Thr Ala Val Leu Ser Arg Ala Ser Arg
                485                 490                 495
Ser Ile Arg Ile Gly Leu Arg Asn His Asp His Glu Val Leu Leu Ala
            500                 505                 510
Asn Thr Phe Cys Val Glu Ala Tyr Leu Gln Asn Leu Phe Ser Leu Ser
        515                 520                 525
Gln Leu Asp Lys Tyr Ala Pro Glu Asn Leu Asp Glu Gln Ile Lys Lys
    530                 535                 540
Val Ser Gln Gln Ile Leu Glu Lys Arg Ala Tyr Ile Cys Ala His Pro
545                 550                 555                 560
Leu Asp Arg Thr Cys
                565
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<210> 3129
<211> 1964
<212> DNA
<213> Homo sapiens

<400> 3129

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nttttttttt tctcctataa catgattgcc ttttatttat tatgcaggtt gttgatttac
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120
tcagggactt ggagacagcc tttaacttct ggcaaaaaga caatttcaca aaggtgttta
180
aaaccatcct ttggtttttg atcctgagtc agagacggac atgtgcttat gaaagaaggt
240
agagtttcaa cccttaggta accttaaaag agcaggaact atgttgtgtg taagtcatgt
300
gcagtataca aacttgatat taaatgacaa attggaacaa tctttctcta ggaatgcctc
360
tctttcatag aggcatcaca gtgagtctct taaagccttg atctaggtgt gttacagatg
420
ggcttacaga gtatgaatgc acgataagaa ggaaattgga tagggagtga ggatatgaaa
480
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720
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780
atccatcaca aaagttttgc acatgctcta cggaaacttc tgctgtgggc agtgtatccc
840
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actcgtcatc tagagtctgg taaattgcca aagctggcag ttgagactcc tttagtttga
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aaaatgatat caccttccca ttttctttca taccactgtc caccagaata aagagaatct
960
tcccctggaa gagcttggct gccttctggt atctgtgcat gttctcttca tactctgggg
1020
aggccttgtt cattatcagg aggagatgaa tctgaattac gctgttgaat aacccaatca
1080
cagtcacagg gttggagcag gagcaggaga gggacaatgg aagctgcccc gtccaggttc
1140
atgttcctct tatttctcct cacgtgtgag ctggctgcag aagttgctgc agaagttgag
1200
aaatcctcag atggtcctgg tgctgcccag gaacccacgt ggctcacaga tgtcccagct
1260
gccatggaat tcattgctgc cactgaggtg gctgtcatag gcttcttcca ggatttagaa
1320
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1380
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1500
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1560
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1620
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1740
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1800
gatgacgagt gggatacact gcccacagca gaagtttccg tagagcatgt gcaaaacttt
1860
tgtgatggat tcctaagtgg aaaattgttg aaagaaaatc gtgaatcgaa aagaaagact
1920
cccaaggtgg aactctgact tctccttgga actacatatg gcca
1964

<210> 3130
<211> 273
<212> PRT
<213> Homo sapiens

<400> 3130
Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu Thr
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Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser Ser Asp
            20   25   30
Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp Val Pro Ala
        35   40   45
Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val Ile Gly Phe Phe
    50   55   60
Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu His Ser Met Val Gln

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65                  70                  75                  80
Lys Phe Pro Gly Val Ser Phe Gly Ile Ser Thr Asp Ser Glu Val Leu
                85                  90                  95
Thr His Tyr Asn Ile Thr Gly Asn Thr Ile Cys Leu Phe Arg Leu Val
            100                 105                 110
Asp Asn Glu Gln Leu Asn Leu Glu Asp Glu Asp Ile Glu Ser Ile Asp
        115                 120                 125
Ala Thr Lys Leu Ser Arg Phe Ile Glu Ile Asn Ser Leu His Met Val
    130                 135                 140
Thr Glu Tyr Asn Pro Val Thr Val Ile Gly Leu Phe Asn Ser Val Ile
145                 150                 155                 160
Gln Ile His Leu Leu Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu
                165                 170                 175
Glu Asn Met His Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys
            180                 185                 190
Ile Leu Phe Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val
        195                 200                 205
Ile Ser Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile
    210                 215                 220
Tyr Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
225                 230                 235                 240
Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly Lys
                245                 250                 255
Leu Leu Lys Glu Asn Arg Glu Ser Lys Arg Lys Thr Pro Lys Val Glu
            260                 265                 270
Leu
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<210> 3131
<211> 1544
<212> DNA
<213> Homo sapiens

<400> 3131
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caggccgccg agaccggcag ctgcgtgggg cgggggctgc gctgagcccg atactgccgg
120
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35 40 45
Ala Gln Leu Thr Lys Ser Asn Ala Pro Val His Ile Asp Val Gly Gly
50 55 60
His Met Tyr Thr Ser Ser Leu Ala Thr Leu Thr Lys Tyr Pro Glu Ser
65 70 75 80
Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu Pro Ile Val Leu Asp Ser
85 90 95
Leu Lys Gln His Tyr Phe Ile Asp Arg Asp Gly Gln Met Phe Arg Tyr
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Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu Leu Ile Pro Asp Asp Phe

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145                 150                 155                 160
Arg Phe Ser Arg Pro Cys Glu Cys Leu Val Val Arg Val Ala Pro Asp
                165                 170                 175
Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp Lys Ser Leu Ile Glu Glu
            180                 185                 190
Val Phe Pro Glu Ile Gly Asp Val Met Cys Asn Ser Val Asn Ala Gly
        195                 200                 205
Trp Asn His Asp Ser Thr His Val Ile Arg Phe Pro Leu Asn Gly Tyr
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Cys His Leu Asn Ser Val Gln Val Leu Glu Arg Leu Gln Gln Arg Gly
225                 230                 235                 240
Phe Glu Ile Val Gly Ser Cys Gly Gly Gly Val Asp Ser Ser Gln Phe
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<213> Homo sapiens

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Thr Glu Val Lys Ser Glu Glu Gly Pro Gly Trp Thr Ile Leu Arg Asp
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Asp Phe Met
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<213> Homo sapiens

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Thr His Thr Arg Glu His Arg Leu Gly Asn His Tyr Lys Cys Asp Gln
50 55 60
Cys Gly Tyr Leu Ser Lys Thr Ala Asn Lys Leu Ile Glu His Val Arg
65 70 75 80
Val His Thr Gly Ser Gly Pro Phe His Trp Asp Gln Cys Ser Tyr Ser
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Cys Lys Arg Lys Asp Asn Leu Asn Leu His Lys Lys Leu Lys His Ala
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Pro Arg Gln Thr Phe Ser Cys Glu Glu Cys Leu Phe Lys Thr Thr His
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130 135 140
Pro Glu Glu Asp Lys Lys Gly Leu Cys Pro Ala Pro Lys Glu Pro Ala
145 150 155 160
Gly Pro Gly Ala Pro Leu Leu Val Val Gly Ser Ser Arg Asn Leu Leu
165 170 175
Ser Pro Leu Ser Val Met Ser Ala Ser Gln Ala Leu Gln Thr Val Ala
180 185 190
Leu Ser Ala Ala His Gly Ser Ser Ser Glu Pro Asn Leu Ala Leu Lys
195 200 205
Ala Leu Ala Phe Asn Gly Ser Pro Leu Arg Phe Asp Lys Tyr Arg Asn
210 215 220
Ser Asp Phe Ala His Leu Ile Pro Leu Thr Met Leu Tyr Pro Lys Asn
225 230 235 240
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<212> PRT
<213> Homo sapiens

<400> 3138
Leu Ala Asp Ser Ser Pro Ser Asn Leu Gln Ile Ile Ile Lys Glu Leu
1 5 10 15
Leu Ser Met His His Gln Pro Asp Pro Ala Leu Thr Lys Glu Phe Asp

```
            20                  25                  30
Tyr Leu Pro Pro Val Asp Ser Arg Ser Ser Ser Gly Phe Val Gly Leu
        35                  40                  45
Arg Asn Gly Gly Ala Thr Cys Tyr Met Asn Ala Val Phe Gln Gln Leu
    50                  55                  60
Tyr Met Gln Pro Gly Leu Pro Glu Ser Leu Leu Ser Val Asp Asp Asp
65                  70                  75                  80
Thr Asp Asn Pro Asp Asp Ser Val Phe Tyr Gln Val Gln Ser Leu Phe
                85                  90                  95
Gly His Leu Met Glu Ser Lys Leu Gln Tyr Tyr Val Pro Glu Asn Phe
            100                 105                 110
Trp Lys Ile Phe Lys Met Trp Asn Lys Glu Leu Tyr Val Arg Glu Gln
        115                 120                 125
Gln Asp Ala Tyr Glu Phe Phe Thr Ser Leu Ile Asp Gln Met Asp Glu
    130                 135                 140
Tyr Leu Lys Lys Met Gly Arg Asp Gln Ile Phe Lys Asn Thr Phe Gln
145                 150                 155                 160
Gly Ile Tyr Ser Asp Gln Lys Ile Cys Lys Asp Cys Pro His Arg Tyr
                165                 170                 175
Glu Arg Glu Glu Ala Phe Met Ala Leu Asn Leu Gly Val Thr Ser Cys
            180                 185                 190
Gln Ser Leu Glu Ile Ser Leu Asp Gln Phe Val Arg Gly Glu Val Leu
        195                 200                 205
Glu Gly Ser Asn Ala Tyr Tyr Cys Glu Lys Cys Lys Glu Lys Arg Ile
    210                 215                 220
Thr Val Lys Arg Thr Cys Ile Lys Ser Leu Pro Ser Val Leu Val Ile
225                 230                 235                 240
His Leu Met Arg Phe Gly Phe Asp Trp Glu Ser Gly Arg Ser Ile Lys
                245                 250                 255
Tyr Asp Glu Gln Ile Arg Phe Pro Trp Met Leu Asn Met Glu Pro Tyr
            260                 265                 270
Thr Val Ser Gly Met Ala Arg Gln Asp Ser Ser Ser Glu Val Gly Glu
        275                 280                 285
Asn Gly Arg Ser Val Asp Gln Gly Gly Gly Gly Ser Pro Arg Lys Lys
    290                 295                 300
Val Ala Leu Thr Glu Asn Tyr Glu Leu Val Gly Val Ile Val His Ser
305                 310                 315                 320
Gly Gln Ala His Ala Gly His Tyr Tyr Ser Phe Ile Lys Asp Arg Arg
                325                 330                 335
Gly Cys Gly Lys Gly Lys Trp Tyr Lys Phe Asn Asp Thr Val Ile Glu
            340                 345                 350
Glu Phe Asp Leu Asn Asp Glu Thr Leu Glu Tyr Glu Cys Phe Gly Gly
        355                 360                 365
Glu Tyr Arg Pro Lys Val Tyr Asp Gln Thr Asn Pro Tyr Thr Asp Val
    370                 375                 380
Arg Arg Arg Tyr Trp Asn Ala Tyr Met Leu Phe Tyr Gln Arg Val Ser
385                 390                 395                 400
Asp Gln Asn Ser Pro Val Leu Pro Lys Lys Ser Arg Val Ser Val Val
                405                 410                 415
Arg Gln Glu Ala Glu Asp Leu Ser Leu Ser Ala Pro Ser Ser Pro Glu
            420                 425                 430
Ile Ser Pro Gln Ser Ser Pro Arg Pro His Arg Pro Asn Asn Asp Arg
        435                 440                 445
Leu Ser Ile Leu Thr Lys Leu Val Lys Lys Gly Glu Lys Lys Gly Leu
```

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    450                 455                 460
Phe Val Glu Lys Met Pro Ala Arg Ile Tyr Gln Met Val Arg Asp Glu
465                 470                 475                 480
Asn Leu Lys Phe Met Lys Asn Arg Asp Val Tyr Ser Ser Asp Tyr Phe
                485                 490                 495
Ser Phe Val Leu Ser Leu Ala Ser Leu Asn Ala Thr Lys Leu Lys His
            500                 505                 510
Pro Tyr Tyr Pro Cys Met Ala Lys Val Ser Leu Gln Leu Ala Ile Gln
        515                 520                 525
Phe Leu Phe Gln Thr Tyr Leu Arg Thr Lys Lys Lys Leu Arg Val Asp
    530                 535                 540
Thr Glu Glu Trp Ile Ala Thr Ile Glu Ala Leu Leu Ser Lys Ser Phe
545                 550                 555                 560
Asp Ala Cys Gln Trp Leu Val Glu Tyr Phe Ile Ser Ser Glu Gly Arg
565                 570                 575
Glu Leu Ile Lys Ile Phe Leu Leu Glu Cys Asn Val Arg Glu Val Arg
            580                 585                 590
Val Ala Val Ala Thr Ile Leu Glu Lys Thr Leu Asp Ser Ala Leu Phe
        595                 600                 605
Tyr Gln Asp Lys Leu Lys Ser Leu His Gln Leu Leu Glu Val Leu Leu
    610                 615                 620
Ala Leu Leu Asp Lys Asp Val Pro Glu Asn Cys Lys Asn Cys Ala Gln
625                 630                 635                 640
Tyr Phe Phe Leu Phe Asn Thr Phe Val Gln Lys Gln Gly Ile Arg Ala
                645                 650                 655
Gly Asp Leu Leu Leu Arg His Ser Ala Leu Arg His Met Ile Ser Phe
            660                 665                 670
Leu Leu Gly Ala Ser Arg Gln Asn Asn Gln Ile Arg Arg Trp Ser Ser
        675                 680                 685
Ala Gln Ala Arg Glu Phe Gly Asn Leu His Asn Thr Val Ala Leu Leu
    690                 695                 700
Val Leu His Ser Asp Val Ser Ser Gln Arg Asn Val Ala Pro Gly Ile
705                 710                 715                 720
Phe Lys Gln Arg Pro Pro Ile Ser Ile Ala Pro Ser Ser Pro Leu Leu
                725                 730                 735
Pro Leu His Glu Glu Val Glu Ala Leu Leu Phe Met Ser Glu Gly Lys
            740                 745                 750
Pro Tyr Leu Leu Glu Val Met Phe Ala Leu Arg Glu Leu Thr Gly Ser
        755                 760                 765
Leu Leu Ala Leu Ile Glu Met Val Val Tyr Cys Cys Phe Cys Asn Glu
    770                 775                 780
His Phe Ser Phe Thr Met Leu His Phe Ile Lys Asn Gln Leu Glu Thr
785                 790                 795                 800
Ala Pro Pro His Glu Leu Lys Asn Thr Phe Gln Leu Leu His Glu Ile
                805                 810                 815
Leu Val Ile Glu Asp Pro Ile Gln Ala Glu Arg Val Lys Phe Val Phe
            820                 825                 830
Glu Thr Glu Asn Gly Leu Leu Ala Leu Met His His Ser Asn His Val
        835                 840                 845
Asp Ser Ser Arg Cys Tyr Gln Cys Val Lys Phe Leu Val Thr Leu Ala
    850                 855                 860
Gln Lys Cys Pro Ala Ala Lys Glu Tyr Phe Lys Glu Asn Ser His His
865                 870                 875                 880
Trp Ser Trp Ala Val Gln Trp Leu Gln Lys Lys Met Ser Glu His Tyr
```

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                885                 890                 895
Trp Thr Pro Gln Ser Asn Val Ser Asn Glu Thr Ser Thr Gly Lys Thr
            900                 905                 910
Phe Gln Arg Thr Ile Ser Ala Gln Asp Ala Leu Ala Tyr Ala Thr Ala
        915                 920                 925
Leu Leu Asn Glu Lys Glu Gln Ser Gly Ser Ser Asn Gly Ser Glu Ser
    930                 935                 940
Ser Pro Ala Asn Glu Asn Gly Asp Arg His Leu Gln Gln Gly Ser Glu
945                 950                 955                 960
Ser Pro Met Met Ile Gly Glu Leu Arg Ser Asp Leu Asp Asp Val Asp
                965                 970                 975
Pro
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<210> 3139
<211> 503
<212> DNA
<213> Homo sapiens

<400> 3139
nggatcctct gtttaggact gacggttgct gtggactctt atttttggcg gcagctcact
60
tggccggaag gaaaggtgct ttggtacaac actgtcctga acaaaagctc caactggggg
120
acctccccgc tgctatggta cttctactca gccctgcccc gcggcctggg ctgcagcctg
180
ctcttcatcc ccttgggctt ggtagacaga aggacgcacg cgccgacggt gctggcactg
240
ggcttcatgg cactctactc cctcctgcca cacaaggagc tacgcttcat catctatgcc
300
ttccccatgc tcaacatcac ggctgccaga ggctgctcct acctgtgagt gctcttttg
360
tgacatgcat ttttatagtt tcattggaaa caggttcact gatttactgt tgggggatg
420
tatgtgtgtg tttaattttt gaaacagggt cttgctctgt cgcccagctg gagtggggct
480
tactgcaccc ctcaactcct agg
503

<210> 3140
<211> 115
<212> PRT
<213> Homo sapiens

<400> 3140
```
Xaa Ile Leu Cys Leu Gly Leu Thr Val Ala Val Asp Ser Tyr Phe Trp
 1               5                  10                  15
Arg Gln Leu Thr Trp Pro Glu Gly Lys Val Leu Trp Tyr Asn Thr Val
            20                  25                  30
Leu Asn Lys Ser Ser Asn Trp Gly Thr Ser Pro Leu Leu Trp Tyr Phe
        35                  40                  45
Tyr Ser Ala Leu Pro Arg Gly Leu Gly Cys Ser Leu Leu Phe Ile Pro
    50                  55                  60
Leu Gly Leu Val Asp Arg Arg Thr His Ala Pro Thr Val Leu Ala Leu
```

65 70 75 80
Gly Phe Met Ala Leu Tyr Ser Leu Leu Pro His Lys Glu Leu Arg Phe
85 90 95
Ile Ile Tyr Ala Phe Pro Met Leu Asn Ile Thr Ala Ala Arg Gly Cys
100 105 110
Ser Tyr Leu
115

<210> 3141
<211> 1815
<212> DNA
<213> Homo sapiens

<400> 3141
nnattcttgg atgacatccc tcagcatgtc tgagcgactg ctgagggaga aaatgatgcc
60
caggttggcg tccccggccc accggccagg agaggcctgc gctgcacacg cgcagaccga
120
gcatccgcgt caagaggcga agagagcgcg cgctccccac gtcctgcgct cctggctgcc
180
gggcattcgt ctcagccgtg actctcgcca ggccggggct ggcgcgccca cgtctgaaga
240
gcgatgcccc gggagatcat caccctgcag ctgggccagt gcggcaacca gattgggttc
300
gagttctgga aacagctgtg cgccgagcat ggtatcagcc ccgagggcat cgtggaggag
360
ttcgccaccg agggcactga ccgcaaggac gtctttttct accaggcaga cgatgagcac
420
tacatccccc gggccgtgct gctggacttg gaaccccggg tgatccactc catcctcaac
480
tccccctatg ccaagctcta caacccagag aacatctacc tgtcggaaca tggaggagga
540
gctggcaaca actgggccag cggattctcc cagggtgaga aaattcatga ggacattttt
600
gacatcatag accgggaggc agatggtagt gacagtctag agggctttgt gctgtgtcac
660
tccattgctg gggggacagg ctctggactg ggttcctacc tcttagaacg gctgaatgac
720
aggtatccta agaagctggt gcagacatac tcagtgtttc ccaaccagga cgagatgagc
780
gatgtggtgg tccagcctta caattcactc ctcacactca agaggctgac gcagaatgca
840
gactgtgtgg tggtgctgga caacacagcc ctgaaccgga ttgccacaga ccgcctgcac
900
atccagaacc catccttctc ccagatcaac cagctggtgt ctaccatcat gtcagccagc
960
accaccaccc tgcgctaccc tggctacatg aacaatgacc tcatcggcct catcgcctcg
1020
ctcattccca ccccacggct ccacttcctc atgaccggct acaccccgct cactacagac
1080
cagtcagtgg ccagcgtgag gaagaccacg gtcctggatg tcatgaggcg gctgctgcag
1140
cccaagaacg tgatggtgtc cacaggccga gaccgccaga ccaaccactg ctacatcgcc
1200

atcctcaaca tcatccaggg agaggtggac cccacccagg tccacaagag cttgcagagg
1260
atccgggaac gcaagttggc caacttcatc ccgtggggcc ccgccagcat ccaggtggcc
1320
ctgtcgagga agtctcccta cctgccctcg gcccaccggg tcagcgggct catgatggcc
1380
aaccacacca gcatctcctc gctcttcgag agaacctgtc gccagtatga caagctgcgt
1440
aagcgggagg ccttcctgga gcagttccgc aaggaggaca tgttcaagga caactttgat
1500
gagatggaca catccaggga gattgtgcag cagctcatcg atgagtacca tgcggccaca
1560
cggccagact acatctcctg gggcacccag gagcagtgag tcccccagga cagggaccct
1620
catctgcctt actggttggc ccaagccctg cctgactgac cacccctca gagcacagat
1680
cagggacctc acgcatctct ttctcatata catggactct ctgttggcct gcaaacacat
1740
ttacttctcc tcttatgaga ctatttatct ttaataaagc actggatata aaaaaaaaaa
1800
aaaaaaaaaa aaaaa
1815

<210> 3142
<211> 451
<212> PRT
<213> Homo sapiens

<400> 3142
Met Pro Arg Glu Ile Ile Thr Leu Gln Leu Gly Gln Cys Gly Asn Gln
1 5 10 15
Ile Gly Phe Glu Phe Trp Lys Gln Leu Cys Ala Glu His Gly Ile Ser
20 25 30
Pro Glu Gly Ile Val Glu Glu Phe Ala Thr Glu Gly Thr Asp Arg Lys
35 40 45
Asp Val Phe Phe Tyr Gln Ala Asp Asp Glu His Tyr Ile Pro Arg Ala
50 55 60
Val Leu Leu Asp Leu Glu Pro Arg Val Ile His Ser Ile Leu Asn Ser
65 70 75 80
Pro Tyr Ala Lys Leu Tyr Asn Pro Glu Asn Ile Tyr Leu Ser Glu His
85 90 95
Gly Gly Gly Ala Gly Asn Asn Trp Ala Ser Gly Phe Ser Gln Gly Glu
100 105 110
Lys Ile His Glu Asp Ile Phe Asp Ile Ile Asp Arg Glu Ala Asp Gly
115 120 125
Ser Asp Ser Leu Glu Gly Phe Val Leu Cys His Ser Ile Ala Gly Gly
130 135 140
Thr Gly Ser Gly Leu Gly Ser Tyr Leu Leu Glu Arg Leu Asn Asp Arg
145 150 155 160
Tyr Pro Lys Lys Leu Val Gln Thr Tyr Ser Val Phe Pro Asn Gln Asp
165 170 175
Glu Met Ser Asp Val Val Val Gln Pro Tyr Asn Ser Leu Leu Thr Leu
180 185 190
Lys Arg Leu Thr Gln Asn Ala Asp Cys Val Val Val Leu Asp Asn Thr

```
        195                 200                 205
Ala Leu Asn Arg Ile Ala Thr Asp Arg Leu His Ile Gln Asn Pro Ser
    210                 215                 220
Phe Ser Gln Ile Asn Gln Leu Val Ser Thr Ile Met Ser Ala Ser Thr
225                 230                 235                 240
Thr Thr Leu Arg Tyr Pro Gly Tyr Met Asn Asn Asp Leu Ile Gly Leu
                245                 250                 255
Ile Ala Ser Leu Ile Pro Thr Pro Arg Leu His Phe Leu Met Thr Gly
            260                 265                 270
Tyr Thr Pro Leu Thr Thr Asp Gln Ser Val Ala Ser Val Arg Lys Thr
        275                 280                 285
Thr Val Leu Asp Val Met Arg Arg Leu Leu Gln Pro Lys Asn Val Met
    290                 295                 300
Val Ser Thr Gly Arg Asp Arg Gln Thr Asn His Cys Tyr Ile Ala Ile
305                 310                 315                 320
Leu Asn Ile Ile Gln Gly Glu Val Asp Pro Thr Gln Val His Lys Ser
                325                 330                 335
Leu Gln Arg Ile Arg Glu Arg Lys Leu Ala Asn Phe Ile Pro Trp Gly
            340                 345                 350
Pro Ala Ser Ile Gln Val Ala Leu Ser Arg Lys Ser Pro Tyr Leu Pro
        355                 360                 365
Ser Ala His Arg Val Ser Gly Leu Met Met Ala Asn His Thr Ser Ile
    370                 375                 380
Ser Ser Leu Phe Glu Arg Thr Cys Arg Gln Tyr Asp Lys Leu Arg Lys
385                 390                 395                 400
Arg Glu Ala Phe Leu Glu Gln Phe Arg Lys Glu Asp Met Phe Lys Asp
                405                 410                 415
Asn Phe Asp Glu Met Asp Thr Ser Arg Glu Ile Val Gln Gln Leu Ile
            420                 425                 430
Asp Glu Tyr His Ala Ala Thr Arg Pro Asp Tyr Ile Ser Trp Gly Thr
        435                 440                 445
Gln Glu Gln
    450
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<210> 3143
<211> 356
<212> DNA
<213> Homo sapiens

<400> 3143
gctagctacc aaaaagggca ggagaaggaa gagcaacgtc tcagtgtcag gaggggccc
60
ggagacagac cctctgcggt ggagtctggg agtggtgtgg ttgctgcttg ggctgggctg
120
caggcctgag ctcctggctg gtgggaaggg gaggctgctg gtccacagtg tgggggtgct
180
tcacggttaa ccaagccatc ccccatgctg ggcgtgaggc actagcggaa ttgagagcct
240
cagaaaccca ggtgctgctg tgtgaggctg tcgcagccac gaagatgacc atgactgcaa
300
gggctgtgag gggccccctg agcgtccagc agcactaaca gataggaacc acgcgt
356

<210> 3144

<211> 81
<212> PRT
<213> Homo sapiens

<400> 3144
Met Val Ile Phe Val Ala Ala Thr Ala Ser His Ser Ser Thr Trp Val
1 5 10 15
Ser Glu Ala Leu Asn Ser Ala Ser Ala Ser Arg Pro Ala Trp Gly Met
20 25 30
Ala Trp Leu Thr Val Lys His Pro His Thr Val Asp Gln Gln Pro Pro
35 40 45
Leu Pro Thr Ser Gln Glu Leu Arg Pro Ala Ala Gln Pro Lys Gln Gln
50 55 60
Pro His His Ser Gln Thr Pro Pro Gln Arg Val Cys Leu Arg Ala Pro
65 70 75 80
Ser

<210> 3145
<211> 436
<212> DNA
<213> Homo sapiens

<400> 3145
taaaagcccg gagccgctca gctatggaga agctgcgctc caaaactcca ctcggcctcc
60
atccgaagag cccgattacc agctgctcgg gagggccaag caggaccggg ggaggccaaa
120
ctccgaggag cccgctccac ctgccctcag gagggtgttt aaaacggagg ttgccaccgt
180
ttacgcacct gccctcagtg ccagggcccc cgagcctggt ttgtcagact ctgcagccgc
240
cagccagtgg tcactctgcc cggcagatga cgagcggagg agagccacac atctcaacgg
300
gctccaggcg ccctcggaaa ctgccctggc ctgctcaccc ccgatgcagt gcctgtcccc
360
cgaatgtagt gagcagccgt cgcagactca caccccgccg gggctgggga accagctaag
420
tcccacagcg gttgct
436

<210> 3146
<211> 131
<212> PRT
<213> Homo sapiens

<400> 3146
Met Glu Lys Leu Arg Ser Lys Thr Pro Leu Gly Leu His Pro Lys Ser
1 5 10 15
Pro Ile Thr Ser Cys Ser Gly Gly Pro Ser Arg Thr Gly Gly Gly Gln
20 25 30
Thr Pro Arg Ser Pro Leu His Leu Pro Ser Gly Gly Cys Leu Lys Arg
35 40 45
Arg Leu Pro Pro Phe Thr His Leu Pro Ser Val Pro Gly Pro Pro Ser

50 55 60
Leu Val Cys Gln Thr Leu Gln Pro Pro Ala Ser Gly His Ser Ala Arg
65 70 75 80
Gln Met Thr Ser Gly Gly Glu Pro His Ile Ser Thr Gly Ser Arg Arg
85 90 95
Pro Arg Lys Leu Pro Trp Pro Ala His Pro Arg Cys Ser Ala Cys Pro
100 105 110
Pro Asn Val Val Ser Ser Arg Arg Arg Leu Thr Pro Arg Arg Gly Trp
115 120 125
Gly Thr Ser
130

<210> 3147
<211> 3106
<212> DNA
<213> Homo sapiens

<400> 3147
cacaccggct gggaggcagc cgtctgtgca gcgagcagcc ggcgcgggga ggccgcagtg
60
cacggggcgt cacagtcggc aggcagcatg gggaagggag ggaaccaggg cgaggggccc
120
gccgagcgcg aggtgtcggt gcccaccttc agctgggagg agattcagaa gcataacctg
180
cgcaccgaca ggtggctggt cattgaccgc aaggtttaca acatcaccaa atggtccatc
240
cagcacccgg ggggccagcg ggtcatcggg cactacgctg gagaagatgc aacggatgcc
300
ttccgcgcct tccaccctga cctggaattc gtgggcaagt tcttgaaacc cctgctgatt
360
ggtgaactgg ccccggagga gcccagccag gaccacggca agaactcaaa gatcactgag
420
gacttccggg ccctgaggaa gacggctgag gacatgaacc tgttcaagac caaccacgtg
480
ttcttcctcc tcctcctggc ccacatcatc gccctggaga gcattgcatg gttcactgtc
540
ttttactttg gcaatggctg gattcctacc ctcatcacgg cctttgtcct tgctacctct
600
caggcccaag ctggatggct gcaacatgat tatggccacc tgtctgtcta cagaaaaccc
660
aagtggaacc accttgtcca caaattcgtc attggccact taaagggtgc ctctgccaac
720
tggtggaatc atcgccactt ccagcaccac gccaagccta acatcttcca caaggatccc
780
gatgtgaaca tgctgcacgt gtttgttctg ggcgaatggc agcccatcga gtacggcaag
840
aagaagctga aatacctgcc ctacaatcac cagcacgaat acttcttcct gattgggccg
900
ccgctgctca tccccatgta tttccagtac cagatcatca tgaccatgat cgtccataag
960
aactgggtgg acctggcctg ggccgtcagc tactacatcc ggttcttcat cacctacatc
1020
cctttctacg gcatcctggg agccctcctt ttcctcaact tcatcaggtt cctggagagc
1080

cactggtttg tgtgggtcac acagatgaat cacatcgtca tggagattga ccaggaggcc
1140
taccgtgact ggttcagtag ccagctgaca gccacctgca acgtggagca gtccttcttc
1200
aacgactggt tcagtggaca ccttaacttc cagattgagc accacctctt ccccaccatg
1260
ccccggcaca acttacacaa gatcgccccg ctggtgaagt ctctatgtgc caagcatggc
1320
attgaatacc aggagaagcc gctactgagg gccctgctgg acatcatcag gtccctgaag
1380
aagtctggga agctgtggct ggacgcctac cttcacaaat gaagccacag cccccgggac
1440
accgtgggga aggggtgcag gtggggtgat ggccagagga atgatgggct tttgttctga
1500
ggggtgtccg agaggctggt gtatgcactg ctcacggacc ccatgttgga tctttctccc
1560
tttctcctct ccttttttctc ttcacatctc ccccatagca ccctgccctc atgggacctg
1620
ccctccctca gccgtcagcc atcagccatg gccctcccag tgcctcctag ccccttcttc
1680
caaggagcag agaggtggcc accgggggtg gctctgtcct acctccactc tctgccccta
1740
aagatgggag gagaccagcg gtccatgggt ctggcctgtg agtctccccc tgcagcctgg
1800
tcactaggca tcacccccgc tttggttctt cagatgctct tggggttcat aggggcaggt
1860
cctagtcggg cagggccccc gaccctcccg gcctggcttc actctccctg acggctgcca
1920
ttggtccacc ctttcataga gaggcctgct ttgttacaaa gctcgggtct ccctcctgca
1980
gctcggttaa gtacccgagg cctctcttaa gatgtccagg gccccaggcc cgcgggcaca
2040
gccagcccaa accttgggcc ctggaagagt cctccacccc atcactagag tgctctgacc
2100
ctgggctttc acgggcccca ttccaccgcc tccccaactt gagcctgtga ccttgggacc
2160
aaaggggggag tccctcgtct cttgtgactc agcagaggca gtggccacgt tcagggaggg
2220
gccggctggc ctggaggctc agcccaccct ccagcttttc ctcagggtgt cctgaggtcc
2280
aagattctgg agcaatctga cccttctcca aaggctctgt tatcagctgg gcagtgccag
2340
ccaatccctg gccatttggc cccaggggac gtgggccctg caggctgcag gagggcactg
2400
gagctgggag gtctcgtccc agccctcccc atctcggggc tgctgtgtgg acggcgctgc
2460
ctcaggcact ctcctgtctg aacctgccct tactgtgttt aacctgttgc tccaggatgc
2520
attctgatag gaggggggcgg cagggctggg ccttgtgaca atctgccttt caccacatgg
2580
ccttgcctcg gtggccctga ctgtcaggga gggccaggga ggcagagcgg gagggagtct
2640
caggaggagg ctgccctgag gggctgggga gggggtacct catgaggacc agggtggagc
2700

tgagaagagg aggaggtggg ggctggaggt gctggtagct gaggggacgg gcaagtgaga
2760
ggggagggag ggaagtcctg ggaggatcct gagctgctgt tgcagtctaa cccactaatc
2820
agttcttaga ttcaggggaa gggcaggcac caacaactca gaatgggggc tttcggggag
2880
ggcgcctagt ccccccagct ctaagcagcc aggagggacc tgcatctaag catctgggtt
2940
gccatggcaa tggcatgccc cccagctact gtatgccccc gacccccgca gaggcagaat
3000
gaacccatag ggagctgatc gtaatgttta tcatgttact tccccacccc tacatttttt
3060
gaaataaaat aaggaatttt attctcaaaa aaaaaaaaaa aaaaaa
3106

<210> 3148
<211> 444
<212> PRT
<213> Homo sapiens

<400> 3148
Met Gly Lys Gly Gly Asn Gln Gly Glu Gly Ala Ala Glu Arg Glu Val
1 5 10 15
Ser Val Pro Thr Phe Ser Trp Glu Glu Ile Gln Lys His Asn Leu Arg
20 25 30
Thr Asp Arg Trp Leu Val Ile Asp Arg Lys Val Tyr Asn Ile Thr Lys
35 40 45
Trp Ser Ile Gln His Pro Gly Gly Gln Arg Val Ile Gly His Tyr Ala
50 55 60
Gly Glu Asp Ala Thr Asp Ala Phe Arg Ala Phe His Pro Asp Leu Glu
65 70 75 80
Phe Val Gly Lys Phe Leu Lys Pro Leu Leu Ile Gly Glu Leu Ala Pro
85 90 95
Glu Glu Pro Ser Gln Asp His Gly Lys Asn Ser Lys Ile Thr Glu Asp
100 105 110
Phe Arg Ala Leu Arg Lys Thr Ala Glu Asp Met Asn Leu Phe Lys Thr
115 120 125
Asn His Val Phe Phe Leu Leu Leu Leu Ala His Ile Ile Ala Leu Glu
130 135 140
Ser Ile Ala Trp Phe Thr Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro
145 150 155 160
Thr Leu Ile Thr Ala Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly
165 170 175
Trp Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys
180 185 190
Trp Asn His Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala
195 200 205
Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro
210 215 220
Asn Ile Phe His Lys Asp Pro Asp Val Asn Met Leu His Val Phe Val
225 230 235 240
Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys Lys Leu Lys Tyr
245 250 255
Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe Leu Ile Gly Pro Pro

```
            260                 265                 270
Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile Met Thr Met Ile
        275                 280                 285
Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val Ser Tyr Tyr Ile
    290                 295                 300
Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly Ile Leu Gly Ala Leu
305                 310                 315                 320
Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu Ser His Trp Phe Val Trp
                325                 330                 335
Val Thr Gln Met Asn His Ile Val Met Glu Ile Asp Gln Glu Ala Tyr
            340                 345                 350
Arg Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys Asn Val Glu Gln
        355                 360                 365
Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
    370                 375                 380
His His Leu Phe Pro Thr Met Pro Arg His Asn Leu His Lys Ile Ala
385                 390                 395                 400
Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Glu
                405                 410                 415
Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys
            420                 425                 430
Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His Lys
        435                 440
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<210> 3149
<211> 1006
<212> DNA
<213> Homo sapiens

<400> 3149
ncttcgccgg cgtcccgacc cgaggccgga cccgaggcca gtcccgccgc tgccaccgaa
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gccagtgcgg ggcctgagag ggacgcgcgc cccggggccc ccgccgcggg caccatgggc
120
gctgcccact ccgcgtctga ggaggtgcgg gagctcgagg gcaagaccgg cttctcatcg
180
gatcagatcg agcagctcca tcggagattt aagcagctga gtggagatca gcctaccatt
240
cgcaaggaga acttcaacaa tgtcccggac ctggagctca accccatccg atccaaaatt
300
gttcgtgcct tcttcgacaa caggaacctg cgcaagggac ccagtggcct ggctgatgag
360
atcaatttcg aggacttcct gaccatcatg tcctacttcc ggcccatcga caccaccatg
420
gacgaggaac aggtggagct gtcccggaag gagaagctga gatttctgtt ccacatgtac
480
gactcggaca gcgacggccg catcactctg gaagaatatc gaaatgtaaa gtggtcgagg
540
agctgctgtc gggaaaccct cacatcgaga aggagtccgc tcgctccatc gccgacgggg
600
ccatgatgga ggcggccagc gtgtgcatgg ggcagatgga gcctgatcag gtgtacgagg
660
ggatcacctt cgaggacttc ctgaagatct ggcaggggat cgacattgag accaagatgc
720

acgtccgctt ccttaacatg gaaaccatgg ccctctgcca ctgacccacc gccacctccg
780
cggagaaact gcactttgca atggggccgc ctccccgcgt agctggagca gcccaggccc
840
ggcggacagc ctcttcctgc agcgccggta catagccaag gctcgtctgc gcaccttgtg
900
tcttgtaggg tatggtatgt gggacttcgc tgtttttatc tccaataaaa aaaaaaaaaa
960
ggtttgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa
1006

<210> 3150
<211> 201
<212> PRT
<213> Homo sapiens

<400> 3150
Xaa Ser Pro Ala Ser Arg Pro Glu Ala Gly Pro Glu Ala Ser Pro Ala
 1   5   10   15
Ala Ala Thr Glu Ala Ser Ala Gly Pro Glu Arg Asp Ala Arg Pro Gly
            20   25   30
Ala Pro Ala Ala Gly Thr Met Gly Ala Ala His Ser Ala Ser Glu Glu
        35   40   45
Val Arg Glu Leu Glu Gly Lys Thr Gly Phe Ser Ser Asp Gln Ile Glu
    50   55   60
Gln Leu His Arg Arg Phe Lys Gln Leu Ser Gly Asp Gln Pro Thr Ile
65   70   75   80
Arg Lys Glu Asn Phe Asn Asn Val Pro Asp Leu Glu Leu Asn Pro Ile
                85   90   95
Arg Ser Lys Ile Val Arg Ala Phe Phe Asp Asn Arg Asn Leu Arg Lys
            100   105   110
Gly Pro Ser Gly Leu Ala Asp Glu Ile Asn Phe Glu Asp Phe Leu Thr
        115   120   125
Ile Met Ser Tyr Phe Arg Pro Ile Asp Thr Thr Met Asp Glu Glu Gln
    130   135   140
Val Glu Leu Ser Arg Lys Glu Lys Leu Arg Phe Leu Phe His Met Tyr
145   150   155   160
Asp Ser Asp Ser Asp Gly Arg Ile Thr Leu Glu Glu Tyr Arg Asn Val
                165   170   175
Lys Trp Ser Arg Ser Cys Cys Arg Glu Thr Leu Thr Ser Arg Arg Ser
            180   185   190
Pro Leu Ala Pro Ser Pro Thr Gly Pro
        195   200

<210> 3151
<211> 2079
<212> DNA
<213> Homo sapiens

<400> 3151
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aggacggagc cgtggctcag gtcggcccct ccccaacacc accccgggcc tccgcccctt
120

cctgggcctc tcggtggagc agggacccga accggtgccc atccagtccg gtgccatctg
180
aagccccctt cccagaaaat gagccacaga gcaagctgac cccagcgaca cagccccca
240
gccctactat atttccgttc ctatcaaaaa atggatgact cggagacagg tttcaatctg
300
aaagtcgtcc tggtcagttt caagcagtgt ctcgatgaga aggaagaggt cttgctggac
360
ccctacattg ccagctggaa gggcctggtc aggtttctga acagcctggg caccatcttc
420
tcattcatct ccaaggacgt ggtctccaag ctgcggatca tggagcgcct caggggcggc
480
ccgcagagcg agcactaccg cagcctgcag gccatggtgg cccacgagct gagcaaccgg
540
ctggtggacc tggagggccg ctcccaccac ccggagtctg gctgccggac ggtgctgcgc
600
ctgcaccgcg ccctgcactg gctgcagctg ttcctggagg gcctgcgtac cagccccgag
660
gacgcacgca cctccgcact ctgcgccgac tcctacaacg cctcgctggc cgcctaccac
720
ccctgggtcg tgcgccgtgc cgtcaccgtg gccttctgca cgctgcccac acgcgaggtc
780
ttcctggagg ccatgaacgt ggggcccccg gagcaggccg tgcagatgct aggcgaggcc
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900
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960
gctgcggtgg ccagggccgt gagtcccgtg gcagagcctt ctgggcgctg cgggaacagg
1020
agatcctctg tcgcccctgt gagctgagct ggttaggaac cacagactgt gacagagaag
1080
gtggcgacca gcccagaaga ggcccaccct ctcggtccgg aacaagacgc ctcagccacg
1140
gctccccctc ggcctattac acgcgtgcgc agccaggcct cgccagggtg cggtgcagag
1200
cagagcaggc aggggtgggg gccgggcccg caagagcccg aaaggtcgcc acccctagc
1260
ctgtggggtg catctgcgaa ccagggtgaa gtcacaggtc ccggggtgtg gaggctccat
1320
cctttctcct ttctgccagc cgatgtgtcc tcatctcagg cccgtgcctg ggaccccgtg
1380
tctgcccagg tgggcagcct tgagcccagg ggactcagtg ccctccatgc cctggctggc
1440
agaaaccctc aacagcagtc tgggcactgt ggggctctcc ccgcctctcc tgccttgttt
1500
gcccctcagc gtgccaggca gactgggggc aggacagccg gaagctgaga ccaaggctcc
1560
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1620
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1680
cccagcccag cccaaggccc ccaggagctg ggactctgct acacccagtg aaatgctgtg
1740

tcccttctcc cccgtgcccc ttgatgcccc ctccccacag tgctcaggag acccgtgggg
1800
cacggaacag gagggtctgg accctgtggc ccagccaaag gctaccagac agccacaacc
1860
agcccagcca ccatccagtg cctggggcct ggccactggc tcttcacagt ggaccccagc
1920
acctcggggt ggcagaggga cggccccccac ggcccagcag acatgcgagc ttccagagtg
1980
caatctatgt gatgtcttcc aacgttaata aatcacacag cctcccagga gggagacgct
2040
ggggtgcaaa aaaaaagcaa aaaaaaaaaa aaaaaaaat
2079

<210> 3152
<211> 214
<212> PRT
<213> Homo sapiens

<400> 3152
Met Asp Asp Ser Glu Thr Gly Phe Asn Leu Lys Val Val Leu Val Ser
1 5 10 15
Phe Lys Gln Cys Leu Asp Glu Lys Glu Glu Val Leu Leu Asp Pro Tyr
20 25 30
Ile Ala Ser Trp Lys Gly Leu Val Arg Phe Leu Asn Ser Leu Gly Thr
35 40 45
Ile Phe Ser Phe Ile Ser Lys Asp Val Val Ser Lys Leu Arg Ile Met
50 55 60
Glu Arg Leu Arg Gly Gly Pro Gln Ser Glu His Tyr Arg Ser Leu Gln
65 70 75 80
Ala Met Val Ala His Glu Leu Ser Asn Arg Leu Val Asp Leu Glu Gly
85 90 95
Arg Ser His His Pro Glu Ser Gly Cys Arg Thr Val Leu Arg Leu His
100 105 110
Arg Ala Leu His Trp Leu Gln Leu Phe Leu Glu Gly Leu Arg Thr Ser
115 120 125
Pro Glu Asp Ala Arg Thr Ser Ala Leu Cys Ala Asp Ser Tyr Asn Ala
130 135 140
Ser Leu Ala Ala Tyr His Pro Trp Val Val Arg Arg Ala Val Thr Val
145 150 155 160
Ala Phe Cys Thr Leu Pro Thr Arg Glu Val Phe Leu Glu Ala Met Asn
165 170 175
Val Gly Pro Pro Glu Gln Ala Val Gln Met Leu Gly Glu Ala Leu Pro
180 185 190
Phe Ile Gln Arg Val Tyr Asn Val Ser Gln Lys Leu Tyr Ala Glu His
195 200 205
Ser Leu Leu Asp Leu Pro
210

<210> 3153
<211> 1498
<212> DNA
<213> Homo sapiens

<400> 3153

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taattagaaa cggagttttg gcaagggagg cagaagcggc tccttttctc cccttggccg
120
cccactcagc aaccaacaag gaggaaagcc cccgcagtgc tcggccagtg ccgcgccatc
180
gccaccaggg agcgccccgc gcgcggtcca cgtggcagag gtcgcggcct cgcggcgcgg
240
ggaggagccg cacgccacag tggcaggtcc caggccgtca ctccgagctc tcgccttccg
300
ggccgctgtc cggcgtgggc gggaggaggg gtctccggcg cgagcgcttg acccggcgcg
360
agggctgcag cagcctccgc ttcagcacag cagccactgt gtcctggctg tccgctgtgg
420
gcccccagta gatgctctcc ccgcgtcgga agtttctgtg cagccgtgtg cagagcgtgg
480
ccagggtgag cagcaccagc aggaaggtca gggccatggc agcccaggcg gcctcttcag
540
tgcgtggggt ggggccccgg gctgcccgtg gagcgctgct gcgcgagggg ccggggaagc
600
ctgacttgaa cagacacagc cccctgggct gccttgcccg ttgggcacct gagcctctgt
660
cctggagctg gcattgcctc caggcgcccc cggcagcagg gagacagtgg gcacagatgg
720
ggcattactc tccctaccag ggattcccgc catggactgc ttggccttca agctccctgg
780
ggaagcagag ggaaacctca gggctgagcg agtgggctgg ggaccaaggg cagcccgcag
840
cctccgcctc ttggcaccac tagaagaggg ctgcctgggc ccttgagatg tcacctctgt
900
gccaggggggc cgccagctcc gcaaaagcaa aggccaaaac cccgggcctg cacacaccct
960
cttcgggcac agcctccctc taccgggagt tggctcggag ggagcaggcc ctgaaaggct
1020
ttcacagtag atccatgcct tcttcttcct ctgcttcctc ctccgcctcc tcatcagcca
1080
gtgggcagcc caggctggct ctacccaggc catctccagc gccagccccc atgcagtcag
1140
caccaggggc cgatcctgcg tgaggctgaa gtcaggggtg agggaagggt tagccataca
1200
agcataggcc aggagggcaa gctggagctt cagccaggga tgggcacagg ggtggtagag
1260
gaaggtgaca tcctcagcct gccctgggct cactcgtgtg taggtcactc ttggtgacac
1320
ctgcggaggc agaggccaca ggctctcggg acaatgggct cccgcctcct ccgccggtcc
1380
agccatcacc tgtgggtcca aagcgaagag ttggggcgct ggacgcggcg aggccctgcc
1440
ctctctctcc ccaggcccag cccgccagcg gaagaactcc gcgtcccccc cggcgcgc
1498

<210> 3154
<211> 65
<212> PRT

<213> Homo sapiens

<400> 3154
Thr Asp Thr Ala Pro Trp Ala Ala Leu Pro Val Gly His Leu Ser Leu
1 5 10 15
Cys Pro Gly Ala Gly Ile Ala Ser Arg Arg Pro Arg Gln Gln Gly Asp
20 25 30
Ser Gly His Arg Trp Gly Ile Thr Leu Pro Thr Arg Asp Ser Arg His
35 40 45
Gly Leu Leu Gly Leu Gln Ala Pro Trp Gly Ser Arg Gly Lys Pro Gln
50 55 60
Gly
65

<210> 3155
<211> 551
<212> DNA
<213> Homo sapiens

<400> 3155
caattggatg taattatggt aaaaccttat aaactctgta acaatcaaga agaaaacgat
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gcagtgtctt ctgctaagaa accaaagcta gccctggaag attcggaaaa cactgcctct
120
actaactgtg actcttcttc agaaggactg gaaaaggaca cagcaacaca gagaagtgac
180
cagacttgcc tagaaccatc atgttcatgt tcttctgaaa atcaggaatg ccagactgct
240
gccagccctg gggaaattct ggaaattttg aagaaaggga aggcatttgt tttagatatt
300
gacttggatt ttttttcagt caagaatccc ttcaaaaaaa tgttcactca ggaagagtac
360
aaaatcttac aagagctgta ccaatttaag aaacctggca ccaacctaac agaggaagat
420
ttggtagata ttgttgatac tcgaattcat caattagagg atttagaagc cactttcgct
480
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540
gaatcactag t
551

<210> 3156
<211> 178
<212> PRT
<213> Homo sapiens

<400> 3156
Met Val Lys Pro Tyr Lys Leu Cys Asn Asn Gln Glu Glu Asn Asp Ala
1 5 10 15
Val Ser Ser Ala Lys Lys Pro Lys Leu Ala Leu Glu Asp Ser Glu Asn
20 25 30
Thr Ala Ser Thr Asn Cys Asp Ser Ser Ser Glu Gly Leu Glu Lys Asp
35 40 45
Thr Ala Thr Gln Arg Ser Asp Gln Thr Cys Leu Glu Pro Ser Cys Ser

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    50                  55                  60
Cys Ser Ser Glu Asn Gln Glu Cys Gln Thr Ala Ala Ser Pro Gly Glu
65                  70                  75                  80
Ile Leu Glu Ile Leu Lys Lys Gly Lys Ala Phe Val Leu Asp Ile Asp
                85                  90                  95
Leu Asp Phe Phe Ser Val Lys Asn Pro Phe Lys Lys Met Phe Thr Gln
            100                 105                 110
Glu Glu Tyr Lys Ile Leu Gln Glu Leu Tyr Gln Phe Lys Lys Pro Gly
        115                 120                 125
Thr Asn Leu Thr Glu Glu Asp Leu Val Asp Ile Val Asp Thr Arg Ile
    130                 135                 140
His Gln Leu Glu Asp Leu Glu Ala Thr Phe Ala Asp Leu Cys Asp Gly
145                 150                 155                 160
Asp Asp Glu Glu Thr Val Gln Gly Trp Ala Ser Asn Pro Gly Met Glu
                165                 170                 175
Ser Leu
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<210> 3157
<211> 903
<212> DNA
<213> Homo sapiens

<400> 3157
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gcccctggga tcctacagtg ggatgggcac ccacaaaccc caggttgcgg ccagccttac
120
tctctggtag gacttctgat ggtgggggca cctccccagg tcacagtcca ggtgcagggc
180
caggaggtcc tatcagagaa gatggagccc tccagtttcc agcccctacc tgaaactgag
240
cctccaactc cagagcctgg gcccaagaca cctcctagga ctatgcagga atcaccactg
300
ggcctgcagg tgaaagagga gtcagaggtt acagaggact cagatttcct ggagtctggg
360
cctctagctg ccacccagga gtctgtaccc accctcctgc ctgaggaggc ccagtgacca
420
ctgtgatttc agagatgtgg gaccgtgctg gaccagatct ttccccacag caagactggg
480
cctgagggtc cctcatggag ggagcacccc agggccctgt ggcatgagga agctgggggc
540
atcttctccc cagggttcgc gctgcagcta ggcagcatct ccgcaggtcc aggtagtgta
600
agccctcacc tccacgtccc ctgggacctc ggcatggctg gcctttctgg ccagatccaa
660
tcaccctccc gcgaaggtgg ctttgcgcat gcgcttctgc tccccagcga tctgaggagt
720
gaacaggacc ccacggacga ggatccctgc cggggtgtgg gccctgctct ggtcaccacc
780
cgctggcgct cccccagggg ccggagccgg ggccgcccca gcactggggg cggggtggtt
840
aggggcggcc gttgcgatgt atgtggcaag gtgttcagcc aacgcagcaa cctgctgagg
900

cac
903

<210> 3158
<211> 92
<212> PRT
<213> Homo sapiens

<400> 3158
Met Val Gly Ala Pro Pro Gln Val Thr Val Gln Val Gln Gly Gln Glu
1 5 10 15
Val Leu Ser Glu Lys Met Glu Pro Ser Ser Phe Gln Pro Leu Pro Glu
20 25 30
Thr Glu Pro Pro Thr Pro Glu Pro Gly Pro Lys Thr Pro Pro Arg Thr
35 40 45
Met Gln Glu Ser Pro Leu Gly Leu Gln Val Lys Glu Glu Ser Glu Val
50 55 60
Thr Glu Asp Ser Asp Phe Leu Glu Ser Gly Pro Leu Ala Ala Thr Gln
65 70 75 80
Glu Ser Val Pro Thr Leu Leu Pro Glu Glu Ala Gln
85 90

<210> 3159
<211> 2408
<212> DNA
<213> Homo sapiens

<400> 3159
nncgcgtact ggctgtacgg agcaggagca agaggtcgcc gccagcctcc gccgccgagc
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ctcgttcgtg tccccgcccc tcgctcctgc agctactgct cagaaacgct ggggcgccca
120
ccctggcaga ctaacgaagc agctcccttc ccaccccaac tgcaggtcta attttggacg
180
ctttgcctgc catttcttcc aggttgaggg agccgcagag gcggaggctc gcgtattcct
240
gcagtcagca cccacgtcgc ccccggacgc tcggtgctca ggcccttcgc gagcggggct
300
ctccgtctgc ggtcccttgt gaaggctctg ggcggctgca gaggccggcc gtccggtttg
360
gctcacctct cccaggaaac ttcacactgg agagccaaaa ggagtggaag agcctgtctt
420
ggagattttc ctggggaaat cctgaggtca ttcattatga agtgtaccgc gcgggagtgg
480
ctcagagtaa ccacagtgct gttcatggct agagcaattc cagccatggt ggttcccaat
540
gccactttat tggagaaact tttggaaaaa tacatggatg aggatggtga gtggtggata
600
gccaaacaac gagggaaaag ggccatcaca gacaatgaca tgcagagtat tttggacctt
660
cataataaat tacgaagtca ggtgtatcca acagcctcta atatggagta tatgacatgg
720
gatgtagagc tggaaagatc tgcagaatcc tgggctgaaa gttgcttgtg ggaacatgga
780

cctgcaagct tgcttccatc aattggacag aatttgggag cacactgggg aagatatagg
840
cccccgacgt ttcatgtaca atcgtggtat gatgaagtga aagactttag ctacccatat
900
gaacatgaat gcaacccata ttgtccattc aggtgttctg gccctgtatg tacacattat
960
acacaggtcg tgtgggcaac tagtaacaga atcggttgtg ccattaattt gtgtcataac
1020
atgaacatct gggggcagat atggcccaaa gctgtctacc tggtgtgcaa ttactcccca
1080
aagggaaact ggtggggcca tgccccttac aaacatgggc ggccctgttc tgcttgccca
1140
cctagttttg gagggggctg tagagaaaat ctgtgctaca aagaagggtc agacaggtat
1200
tatcccctc gagaagagga aacaaatgaa atagaacgac agcagtcaca agtccatgac
1260
acccatgtcc ggacaagatc agatgatagt agcagaaatg aagtcataag cgcacagcaa
1320
atgtcccaaa ttgtttcttg tgaagtaaga ttaagagatc agtgcaaagg aacaacctgc
1380
aataggtacg aatgtcctgc tggctgtttg gatagtaaag ctaaagttat tggcagtgta
1440
cattatgaaa tgcaatccag catctgtaga gctgcaattc attatggtat aatagacaat
1500
gatggtggct gggtagatat cactagacaa ggaagaaagc attatttcat caagtccaat
1560
agaaatggta ttcaaacaat tggcaaatat cagtctgcta attccttcac agtctctaaa
1620
gtaacagttc aggctgtgac ttgtgaaaca actgtggaca gctctgtcca tttcataagc
1680
ctgcttcaca ttgcccaaga gtatactgtc ctcgtaactg tatgcaagca aatccacatt
1740
atgctcgtgt aattgggact cgagtttatt ctgatctgtc cagtatctgc agagcagcag
1800
tacatgctgg gagtagttcg aaatcacggt ggttatgttg atgtaatgcc tgtggaccaa
1860
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1920
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1980
ccataaagac tattccaaat gcaatatttc tgaattttgt ataaaactgt aacattactg
2040
tacagagtac atcaactatt ttcagcccaa aaaggtgcca aatgcatata aatcttgata
2100
aacaaagtct ataaaataaa acatgggaca ttagctttgg gaaaagtaat gaaaatataa
2160
tggttttaga aatcctgtgt taaatattgc tatattttct tagcagttat ttctacagtt
2220
aattacatag tcatgattgt tctacgtttc atatattata tggtgctttg tatatgccac
2280
taataaaatg aatctaaaca ttgaatgtga atggccctca gaaaatcatc tagtgcattt
2340
aaaaataatc gactctaaaa ctgaaagaaa ccttatcaca tttttccccag ttcaatgcta
2400

tgccatta
2408

<210> 3160
<211> 431
<212> PRT
<213> Homo sapiens

<400> 3160
Met Lys Cys Thr Ala Arg Glu Trp Leu Arg Val Thr Thr Val Leu Phe
1 5 10 15
Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr Leu Leu
20 25 30
Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu Trp Trp Ile
35 40 45
Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn Asp Met Gln Ser
50 55 60
Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln Val Tyr Pro Thr Ala
65 70 75 80
Ser Asn Met Glu Tyr Met Thr Trp Asp Val Glu Leu Glu Arg Ser Ala
85 90 95
Glu Ser Trp Ala Glu Ser Cys Leu Trp Glu His Gly Pro Ala Ser Leu
100 105 110
Leu Pro Ser Ile Gly Gln Asn Leu Gly Ala His Trp Gly Arg Tyr Arg
115 120 125
Pro Pro Thr Phe His Val Gln Ser Trp Tyr Asp Glu Val Lys Asp Phe
130 135 140
Ser Tyr Pro Tyr Glu His Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys
145 150 155 160
Ser Gly Pro Val Cys Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser
165 170 175
Asn Arg Ile Gly Cys Ala Ile Asn Leu Cys His Asn Met Asn Ile Trp
180 185 190
Gly Gln Ile Trp Pro Lys Ala Val Tyr Leu Val Cys Asn Tyr Ser Pro
195 200 205
Lys Gly Asn Trp Trp Gly His Ala Pro Tyr Lys His Gly Arg Pro Cys
210 215 220
Ser Ala Cys Pro Pro Ser Phe Gly Gly Gly Cys Arg Glu Asn Leu Cys
225 230 235 240
Tyr Lys Glu Gly Ser Asp Arg Tyr Tyr Pro Pro Arg Glu Glu Glu Thr
245 250 255
Asn Glu Ile Glu Arg Gln Gln Ser Gln Val His Asp Thr His Val Arg
260 265 270
Thr Arg Ser Asp Asp Ser Ser Arg Asn Glu Val Ile Ser Ala Gln Gln
275 280 285
Met Ser Gln Ile Val Ser Cys Glu Val Arg Leu Arg Asp Gln Cys Lys
290 295 300
Gly Thr Thr Cys Asn Arg Tyr Glu Cys Pro Ala Gly Cys Leu Asp Ser
305 310 315 320
Lys Ala Lys Val Ile Gly Ser Val His Tyr Glu Met Gln Ser Ser Ile
325 330 335
Cys Arg Ala Ala Ile His Tyr Gly Ile Ile Asp Asn Asp Gly Gly Trp
340 345 350
Val Asp Ile Thr Arg Gln Gly Arg Lys His Tyr Phe Ile Lys Ser Asn

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        355                 360                 365
Arg Asn Gly Ile Gln Thr Ile Gly Lys Tyr Gln Ser Ala Asn Ser Phe
    370                 375                 380
Thr Val Ser Lys Val Thr Val Gln Ala Val Thr Cys Glu Thr Thr Val
385                 390                 395                 400
Asp Ser Ser Val His Phe Ile Ser Leu Leu His Ile Ala Gln Glu Tyr
                405                 410                 415
Thr Val Leu Val Thr Val Cys Lys Gln Ile His Ile Met Leu Val
            420                 425                 430
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<210> 3161
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 3161
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240
aacgtggtgg aggatgagat tgatcagtac ctcagcaaac aggacgggaa gatttacaga
300
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360
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1197

<210> 3162
<211> 386
<212> PRT
<213> Homo sapiens

<400> 3162
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Ile Thr Ala Ser Ser Asn Lys Ser Leu Asn Leu Leu Lys Ile Lys His
        35   40   45
Gly Asp Leu Leu Phe Leu Phe Pro Ser Ser Leu Ala Gly Pro Ser Ser
    50   55   60
Glu Met Glu Thr Ser Val Pro Pro Gly Phe Lys Val Phe Gly Ala Pro
65   70   75   80
Asn Val Val Glu Asp Glu Ile Asp Gln Tyr Leu Ser Lys Gln Asp Gly
                85   90   95
Lys Ile Tyr Arg Ser Arg Asp Pro Gln Leu Cys Arg His Gly Pro Leu
            100   105   110
Gly Lys Cys Val His Cys Val Pro Leu Glu Pro Phe Asp Glu Asp Tyr
        115   120   125
Leu Asn His Leu Glu Pro Pro Val Lys His Met Ser Phe His Ala Tyr
    130   135   140
Ile Arg Lys Leu Thr Gly Gly Ala Asp Lys Gly Lys Phe Val Ala Leu
145   150   155   160
Glu Asn Ile Ser Cys Lys Ile Lys Ser Gly Cys Glu Gly His Leu Pro
                165   170   175
Trp Pro Asn Gly Ile Cys Thr Lys Cys Gln Pro Ser Ala Ile Thr Leu
            180   185   190
Asn Arg Gln Lys Tyr Arg His Val Asp Asn Ile Met Phe Glu Asn His
        195   200   205
Thr Val Ala Asp Arg Phe Leu Asp Phe Trp Arg Lys Thr Gly Asn Gln
    210   215   220
His Phe Gly Tyr Leu Tyr Gly Arg Tyr Thr Glu His Lys Asp Ile Pro
225   230   235   240
Leu Gly Ile Arg Ala Glu Val Ala Ala Ile Tyr Glu Pro Pro Gln Ile
                245   250   255
Gly Thr Gln Asn Ser Leu Glu Leu Leu Glu Asp Pro Lys Ala Glu Val
            260   265   270
Val Asp Glu Ile Ala Ala Lys Leu Gly Leu Arg Lys Val Gly Trp Ile
        275   280   285
Phe Thr Asp Leu Val Ser Glu Asp Thr Arg Lys Gly Thr Val Arg Tyr
    290   295   300
Ser Arg Asn Lys Asp Thr Tyr Phe Leu Ser Ser Glu Glu Cys Ile Thr
305   310   315   320
Ala Gly Asp Phe Gln Asn Lys His Pro Asn Met Cys Arg Leu Ser Pro
                325   330   335
Asp Gly His Phe Gly Ser Lys Phe Val Thr Ala Val Ala Thr Gly Gly
            340   345   350
Pro Asp Asn Gln Val His Phe Glu Gly Tyr Gln Val Ser Asn Gln Cys

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Val Cys
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<210> 3163
<211> 1075
<212> DNA
<213> Homo sapiens

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180
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240
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360
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420
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480
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540
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600
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660
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720
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780
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900
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1075

<210> 3164
<211> 94
<212> PRT
<213> Homo sapiens

<400> 3164
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20 25 30
Ser Ser Val Pro Pro Arg Gln Ala Cys Ala Ser Pro Ala Ser Cys Ser
35 40 45
Ser Ser Ala Ala Xaa Ala Ser Ala Ser Thr Gly Pro Trp His Ser Gly
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Cys Gly Ser Ser Cys Gly Ser Cys Cys Cys Trp Gly Ser Pro Ser Ala
65 70 75 80
Ser Val Gly Val Gly Ala Gly Ala Ile Arg Ser Arg Thr Val
85 90

<210> 3165
<211> 2413
<212> DNA
<213> Homo sapiens

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420
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480
gtaaatattc cggattggat tgttgacctt cgccatgagt tgacccacaa gaaaatgccc
540
catataaatg actgccgcag aggctgctac tttgtcctgg attggctcca gaagacctat
600
tggtgccgcc aactggagaa cagcctgaga gagacctggg agttggagga gttcagggaa
660
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720
cagaaaccag agcctcagga tgatgggaaa agtacggagt cagatgtaaa ggccgatgga
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gagaaattta ggtatttacc taaggccatt aaggcgtgga ataacccgtc cccacgtgta
960
gaatgtgtcc tggcagagct caagggcgtt acatgcgaga acagggaggc tgtgctggat
1020

gcttttctgg atgatggctt ccttgtcccc acatttgaac agttggcagc tttgcagata
1080
gaatatgaag aaaacgtgga cttgaatgac gtcctggtgc caaagccgtt ctctcagttc
1140
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1260
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1320
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2413

<210> 3166
<211> 717
<212> PRT
<213> Homo sapiens

<400> 3166
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35 40 45
Ala Glu Trp Asp Gln Val Thr Val Tyr Leu Phe Cys Asp Asp His Lys
50 55 60
Leu Gln Arg Tyr Ala Leu Asn Arg Ile Thr Val Trp Arg Ser Arg Ser
65 70 75 80
Gly Asn Glu Leu Pro Leu Ala Val Ala Ser Thr Ala Asp Leu Ile Arg
85 90 95
Cys Lys Leu Leu Asp Val Thr Gly Gly Leu Gly Thr Asp Glu Leu Arg
100 105 110
Leu Leu Tyr Gly Met Ala Leu Val Arg Phe Val Asn Leu Ile Ser Glu
115 120 125
Arg Lys Thr Lys Phe Ala Lys Val Pro Leu Lys Cys Leu Ala Gln Glu
130 135 140
Val Asn Ile Pro Asp Trp Ile Val Asp Leu Arg His Glu Leu Thr His
145 150 155 160
Lys Lys Met Pro His Ile Asn Asp Cys Arg Arg Gly Cys Tyr Phe Val
165 170 175
Leu Asp Trp Leu Gln Lys Thr Tyr Trp Cys Arg Gln Leu Glu Asn Ser
180 185 190
Leu Arg Glu Thr Trp Glu Leu Glu Glu Phe Arg Glu Gly Ile Glu Glu
195 200 205
Glu Asp Gln Glu Glu Asp Lys Asn Ile Val Val Asp Asp Ile Thr Glu
210 215 220
Gln Lys Pro Glu Pro Gln Asp Asp Gly Lys Ser Thr Glu Ser Asp Val
225 230 235 240
Lys Ala Asp Gly Asp Ser Lys Gly Ser Glu Glu Val Asp Ser His Cys
245 250 255
Lys Lys Ala Leu Ser His Lys Glu Leu Tyr Glu Arg Ala Arg Glu Leu
260 265 270
Leu Val Ser Tyr Glu Glu Glu Gln Phe Thr Val Leu Glu Lys Phe Arg
275 280 285
Tyr Leu Pro Lys Ala Ile Lys Ala Trp Asn Asn Pro Ser Pro Arg Val
290 295 300
Glu Cys Val Leu Ala Glu Leu Lys Gly Val Thr Cys Glu Asn Arg Glu
305 310 315 320
Ala Val Leu Asp Ala Phe Leu Asp Asp Gly Phe Leu Val Pro Thr Phe
325 330 335
Glu Gln Leu Ala Ala Leu Gln Ile Glu Tyr Glu Glu Asn Val Asp Leu
340 345 350
Asn Asp Val Leu Val Pro Lys Pro Phe Ser Gln Phe Trp Gln Pro Leu
355 360 365
Leu Arg Gly Leu His Ser Gln Asn Phe Thr Gln Ala Leu Leu Glu Arg
370 375 380
Met Leu Ser Glu Leu Pro Ala Leu Gly Ile Ser Gly Ile Arg Pro Thr
385 390 395 400
Tyr Ile Leu Arg Trp Thr Val Glu Leu Ile Val Ala Asn Thr Lys Thr
405 410 415
Gly Arg Asn Ala Arg Arg Phe Ser Ala Gly Gln Trp Glu Ala Arg Arg

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            420                 425                 430
Gly Trp Arg Leu Phe Asn Cys Ser Ala Ser Leu Asp Trp Pro Arg Met
        435                 440                 445
Val Glu Ser Cys Leu Gly Ser Pro Cys Trp Ala Ser Pro Gln Leu Leu
    450                 455                 460
Arg Ile Ile Phe Lys Ala Met Gly Gln Gly Leu Pro Asp Glu Glu Gln
465                 470                 475                 480
Glu Lys Leu Leu Arg Ile Cys Ser Ile Tyr Thr Gln Ser Gly Glu Asn
                485                 490                 495
Ser Leu Val Gln Glu Gly Ser Glu Ala Ser Pro Ile Gly Lys Ser Pro
            500                 505                 510
Tyr Thr Leu Asp Ser Leu Tyr Trp Ser Val Lys Pro Ala Ser Ser Ser
        515                 520                 525
Phe Gly Ser Glu Ala Lys Ala Gln Gln Gln Glu Glu Gln Gly Ser Val
    530                 535                 540
Asn Asp Val Lys Glu Glu Glu Lys Glu Glu Lys Glu Val Leu Pro Asp
545                 550                 555                 560
Gln Val Glu Glu Glu Glu Glu Asn Asp Asp Gln Glu Glu Glu Glu Glu
                565                 570                 575
Asp Glu Asp Asp Glu Asp Asp Glu Glu Glu Asp Arg Met Glu Val Gly
            580                 585                 590
Pro Phe Ser Thr Gly Gln Glu Ser Pro Thr Ala Glu Asn Ala Arg Leu
        595                 600                 605
Leu Ala Gln Lys Arg Gly Ala Leu Gln Gly Ser Ala Trp Gln Val Ser
    610                 615                 620
Ser Glu Asp Val Arg Trp Asp Thr Phe Pro Leu Gly Arg Met Pro Gly
625                 630                 635                 640
Gln Thr Glu Asp Pro Ala Glu Leu Met Leu Glu Asn Tyr Asp Thr Met
                645                 650                 655
Tyr Leu Leu Asp Gln Pro Val Leu Glu Gln Arg Leu Glu Pro Ser Thr
            660                 665                 670
Cys Lys Thr Asp Thr Leu Gly Leu Ser Cys Gly Val Gly Ser Gly Asn
        675                 680                 685
Cys Ser Asn Ser Ser Ser Ser Asn Phe Glu Gly Leu Leu Trp Ser Gln
    690                 695                 700
Gly Gln Leu His Gly Leu Lys Thr Gly Leu Gln Leu Phe
705                 710                 715

<210> 3167
<211> 2730
<212> DNA
<213> Homo sapiens

<400> 3167
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300
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aaggttgtcc ttatcagcag atcaaaggat aaacttgacc aggtttccag tgaaataaaa
360
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420
gataaaatta aaacaggctt ggctggtctt gaaatcggca tcttagtgaa caacgtggga
480
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1140
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1200
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1260
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1320
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1380
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1920

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1980
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2040
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2100
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2160
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2220
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2280
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<210> 3168
<211> 312
<212> PRT
<213> Homo sapiens

<400> 3168
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Gly Thr Val Ala Tyr Leu Ala Leu Arg Ile Ser Tyr Ser Leu Phe Thr
20 25 30
Ala Leu Arg Val Trp Gly Val Gly Asn Glu Ala Gly Val Gly Pro Gly
35 40 45
Leu Gly Glu Trp Ala Val Val Thr Gly Ser Thr Asp Gly Ile Gly Lys
50 55 60
Ser Tyr Ala Glu Glu Leu Ala Lys His Gly Met Lys Val Val Leu Ile
65 70 75 80
Ser Arg Ser Lys Asp Lys Leu Asp Gln Val Ser Ser Glu Ile Lys Glu
85 90 95
Lys Phe Lys Val Glu Thr Arg Thr Ile Ala Val Asp Phe Ala Ser Glu
100 105 110
Asp Ile Tyr Asp Lys Ile Lys Thr Gly Leu Ala Gly Leu Glu Ile Gly
115 120 125
Ile Leu Val Asn Asn Val Gly Met Ser Tyr Glu Tyr Pro Glu Tyr Phe
130 135 140
Leu Asp Val Pro Asp Leu Asp Asn Val Ile Lys Lys Met Ile Asn Ile

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145                 150                 155                 160
Asn Ile Leu Ser Val Cys Lys Met Thr Gln Leu Val Leu Pro Gly Met
                165                 170                 175
Val Glu Arg Ser Lys Gly Ala Ile Leu Asn Ile Ser Ser Gly Ser Gly
            180                 185                 190
Met Leu Pro Val Pro Leu Leu Thr Ile Tyr Ser Ala Thr Lys Thr Phe
        195                 200                 205
Val Asp Phe Phe Ser Gln Cys Leu His Glu Glu Tyr Arg Ser Lys Gly
    210                 215                 220
Val Phe Val Gln Ser Val Leu Pro Tyr Phe Val Ala Thr Lys Leu Ala
225                 230                 235                 240
Lys Ile Arg Lys Pro Thr Leu Asp Lys Pro Ser Pro Glu Thr Phe Val
                245                 250                 255
Lys Ser Ala Ile Lys Thr Val Gly Leu Gln Ser Arg Thr Asn Gly Tyr
            260                 265                 270
Leu Ile His Ala Leu Met Gly Ser Ile Ile Ser Asn Leu Pro Ser Trp
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Ile Tyr Leu Lys Ile Val Met Asn Met Asn Lys Ser Thr Arg Ala His
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Tyr Leu Lys Lys Thr Lys Lys Asn
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<210> 3169
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<212> DNA
<213> Homo sapiens

<400> 3169

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180
aagctgctcc tctcccatgg tgccaatgtg aacgccaagg acaacgagct gtggacacct
240
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300
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360
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660
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720
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780
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1140
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1380
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2040
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2160
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2280
atttcgttcc tggaatcaac caaatcatgt tttcctcttg gatggaagtg tcaaaggcag
2340
aagggtgtgg gaggggggaca aggtcagtat ttaccaaagt gtatctgatt ttaaaaattc
2400

405 410 415
Arg Ser Ala Leu Leu Pro Thr Ile Pro Asp Thr Glu Asp Glu Ile Ser
420 425 430
Pro Asp Lys Val Ile Leu Cys Leu
435 440

<210> 3629
<211> 695
<212> DNA
<213> Homo sapiens

<400> 3629
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120
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180
tcactctcgc atctgctggt cctcgggctg tatcttgggc cacagccgga ctcacggcct
240
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360
tccctgcact cacgccggcg gctggacacc gagaagaagc accaggtcag ccgggcctag
420
gaaggtcaga gcagcgctcc gagggaggag ttgcttagat tacataacgg ggctcctcca
480
caagttgagt gactctgggc aggtttcttg acctgtttct tcttttgtat aaaatgtggg
540
tattgcccat cttagaaggt tgtgaggctc aaacaaacca aagcttataa aaagcacttt
600
agagcattat gatattaagt gaactcccat tcaggtgttg atactgggag tttagtcact
660
aaaggtgatc agtgtaggat ggagtgctgg ggccc
695

<210> 3630
<211> 139
<212> PRT
<213> Homo sapiens

<400> 3630
Thr Arg Pro Leu Ser Gly Leu Val Trp Val Ala Leu Leu Ala Leu Gly
1 5 10 15
His Ala Phe Leu Phe Thr Gly Gly Val Val Ser Ala Trp Asp Gln Val
20 25 30
Ser Tyr Phe Leu Phe Val Ile Phe Thr Ala Tyr Ala Met Leu Pro Leu
35 40 45
Gly Met Arg Asp Ala Ala Val Ala Gly Leu Ala Ser Ser Leu Ser His
50 55 60
Leu Leu Val Leu Gly Leu Tyr Leu Gly Pro Gln Pro Asp Ser Arg Pro
65 70 75 80
Ala Leu Leu Pro Gln Leu Ala Ala Asn Ala Val Leu Phe Leu Cys Gly

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                85                  90                  95
Asn Val Ala Gly Val Tyr His Lys Ala Leu Met Glu Arg Ala Leu Arg
            100                 105                 110
Ala Thr Phe Arg Glu Ala Leu Ser Ser Leu His Ser Arg Arg Arg Leu
        115                 120                 125
Asp Thr Glu Lys Lys His Gln Val Ser Arg Ala
    130                 135
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<210> 3631
<211> 864
<212> DNA
<213> Homo sapiens

<400> 3631
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agcggctaga agagaagagg tcctggaaag gctcaaaggt gtccatgaag tccaggttag
120
gctgcaaagg aatcagtccc ggctggatca tgtctgcatt tcccagatgt gctatttccc
180
ggggattggg cctggtacat gcagtatctg gagaagcgca agaatcctgt gtgccacttt
240
gtgacacccc tggacggctc tgtggacgta gacgagcacc gccggccgga ggccatcacc
300
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360
agaacctact tcaagaaaag gctacagcag cacaaggatg aggacctctc cagcctggtc
420
caggacgatg acatgctgta ttggcacaag cacggggatg gatggaagac ccccgtcccc
480
atggaggagg atcccctgct ggacacagac atgctcatgt cggaattcag cgacaccctc
540
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600
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660
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720
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780
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cccaccgccc catccctggc gcgc
864

<210> 3632
<211> 222
<212> PRT
<213> Homo sapiens

<400> 3632
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Met Gln Tyr Leu Glu Lys Arg Lys Asn Pro Val Cys His Phe Val Thr
 1               5                  10                  15
Pro Leu Asp Gly Ser Val Asp Val Asp Glu His Arg Arg Pro Glu Ala
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            20                  25                  30
Ile Thr Thr Glu Gly Lys Tyr Trp Lys Ser Arg Ile Glu Ile Val Ile
        35                  40                  45
Arg Glu Tyr His Lys Trp Arg Thr Tyr Phe Lys Lys Arg Leu Gln Gln
    50                  55                  60
His Lys Asp Glu Asp Leu Ser Ser Leu Val Gln Asp Asp Asp Met Leu
65                  70                  75                  80
Tyr Trp His Lys His Gly Asp Gly Trp Lys Thr Pro Val Pro Met Glu
                85                  90                  95
Glu Asp Pro Leu Leu Asp Thr Asp Met Leu Met Ser Glu Phe Ser Asp
            100                 105                 110
Thr Leu Phe Ser Thr Leu Ser Ser His Gln Pro Val Ala Trp Pro Asn
        115                 120                 125
Pro Arg Glu Ile Ala His Leu Gly Asn Ala Asp Met Ile Gln Pro Gly
    130                 135                 140
Leu Ile Pro Leu Gln Pro Asn Leu Asp Phe Met Asp Thr Phe Glu Pro
145                 150                 155                 160
Phe Gln Asp Leu Phe Ser Ser Ser Arg Ser Ile Phe Gly Ser Met Leu
                165                 170                 175
Pro Ala Ser Ala Ser Ala Pro Val Pro Asp Pro Asn Asn Pro Pro Ala
            180                 185                 190
Gln Glu Ser Ile Leu Pro Thr Thr Ala Leu Pro Thr Val Ser Leu Pro
        195                 200                 205
Asp Ser Leu Ile Ala Pro Pro Thr Ala Pro Ser Leu Ala Arg
    210                 215                 220
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<210> 3633
<211> 1570
<212> DNA
<213> Homo sapiens

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gcagaagggc tgaagtgaca ggatgttcat tgacctgtca gtggatctga aagttctcta
120
aggagagcct gggcaagcat tcttaggttg atgctggggc ccagagtagc agtgagcatc
180
ctgtgtgaag atggcatttc tcactgatta ttggaaaagc acaagagcca cgtgctggag
240
ccattgtcca gccttgccct ggaggagcag tgtctggctt tgtccctaga ttggtccact
300
gggaaaactg gaagggccgg ggaccagccc ttgaagatca tcagcagtga ctccacaggg
360
cagctccacc tcctgatggt gaatgagacg aggcccaggc tgcagaaagt ggcctcatgg
420
caggcacatc aattcgaggc ctggattgct gctttcaatt actggcatcc agaaattgtg
480
tattcagggg gcgacgatgg ccttctgagg ggctgggaca ccagggtacc cggcaaattt
540
ctcttcacca gcnaaaagac acaccatnng ggtgtgtgca gcatccagag cagccctcat
600
cgggagcaca tcctggccac gggaagctat gatgaacaca tcctactgtg ggacacacga
660

aacatgaagc agccgttggc agatacgcct gtgcagggtg gggtatggag aatcaagtgg
720
caccctttcc accaccacct gctcctggcc gcctgcatgc acagtggctt taagatcctc
780
aactgccaaa aggcaatgga ggagaggcag gaggcgacgg tcctgacatc tcacacattg
840
cccgactcgc tggtgtatgg agccgactgg tcctggctgc tcttccgttc tctgcagcgg
900
gccccctcgt ggtcctttcc tagcaaccta ggaaccaaga cggcagacct gaagggtgca
960
agcgagttgc caacaccctg tcatgaatgc agagaggata acgatgggga gggccatgcc
1020
agaccccaga gtggaatgaa gccactcaca gagggcatga ggaagaatgg cacctggctg
1080
caggctacag cagccaccac acgtgactgt ggcgtgaacc cagaagaagc agactcagcc
1140
ttcagcctcc tggccacctg ctccttctat gaccatgcgc tccacctctg ggagtgggag
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1260
agtgagtgcc cgggaccacc tcatcagaga tgcttactgc agccctgcag gtgcctgtgc
1320
actgatggaa tccacagtgt agtcagaaaa gctgttgact tctcttaaat cagcttccct
1380
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1440
gtttccagct tgcagatttg ttaagtttct caggcagatt ttgactttca gcctttcata
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1560
aaaaaaaaaa
1570

<210> 3634
<211> 277
<212> PRT
<213> Homo sapiens

<400> 3634
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Ala His Gln Phe Glu Ala Trp Ile Ala Ala Phe Asn Tyr Trp His Pro
20 25 30
Glu Ile Val Tyr Ser Gly Gly Asp Asp Gly Leu Leu Arg Gly Trp Asp
35 40 45
Thr Arg Val Pro Gly Lys Phe Leu Phe Thr Ser Xaa Lys Thr His His
50 55 60
Xaa Gly Val Cys Ser Ile Gln Ser Ser Pro His Arg Glu His Ile Leu
65 70 75 80
Ala Thr Gly Ser Tyr Asp Glu His Ile Leu Leu Trp Asp Thr Arg Asn
85 90 95
Met Lys Gln Pro Leu Ala Asp Thr Pro Val Gln Gly Gly Val Trp Arg
100 105 110
Ile Lys Trp His Pro Phe His His His Leu Leu Leu Ala Ala Cys Met

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        115                 120                 125
His Ser Gly Phe Lys Ile Leu Asn Cys Gln Lys Ala Met Glu Glu Arg
    130                 135                 140
Gln Glu Ala Thr Val Leu Thr Ser His Thr Leu Pro Asp Ser Leu Val
145                 150                 155                 160
Tyr Gly Ala Asp Trp Ser Trp Leu Leu Phe Arg Ser Leu Gln Arg Ala
                165                 170                 175
Pro Ser Trp Ser Phe Pro Ser Asn Leu Gly Thr Lys Thr Ala Asp Leu
            180                 185                 190
Lys Gly Ala Ser Glu Leu Pro Thr Pro Cys His Glu Cys Arg Glu Asp
        195                 200                 205
Asn Asp Gly Glu Gly His Ala Arg Pro Gln Ser Gly Met Lys Pro Leu
    210                 215                 220
Thr Glu Gly Met Arg Lys Asn Gly Thr Trp Leu Gln Ala Thr Ala Ala
225                 230                 235                 240
Thr Thr Arg Asp Cys Gly Val Asn Pro Glu Glu Ala Asp Ser Ala Phe
                245                 250                 255
Ser Leu Leu Ala Thr Cys Ser Phe Tyr Asp His Ala Leu His Leu Trp
            260                 265                 270
Glu Trp Glu Gly Asn
        275
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<210> 3635
<211> 835
<212> DNA
<213> Homo sapiens

<400> 3635
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gttggagttg gagagcagct ttctgaggga gactatgcac ggttacagca agtggatcct
120
gttttactta aagatgaacc ccagcagact gctgctcaga tgggttgtgc gccaatccag
180
cctctggcga tgcctcaagc tttgcctctg gcggcaggtc ccttgcctcc agggtccatc
240
gcaaatctta cagaactgca aggagtgata gttggacagc cagtactggg ccaagcacag
300
ttggcagggc tggggcaagg aattctgaca gaaacacaac aagggttaat ggtagccagc
360
cctgctcaga ccctcaatga cacgctggat gacatcatgg cagcagtcag tggaagagca
420
tctgcaatgt caaacactcc tacccacagt attgctgcat ccatttccca acctcagact
480
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540
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600
cacgaggaac tggtacaaac actgctagag agaggagcta gtatagagca ccgagacaag
660
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720
ttgctggaca atggtgcaga cattgaagcc cagtctgaaa gaaccaagga cacaccactc
780

tccttggctt gttctggggg aagacaggag gtggtggagc tattgttagc tcgag
835

<210> 3636
<211> 278
<212> PRT
<213> Homo sapiens

<400> 3636
Xaa Ile Gln Leu Gln Gln Gln Gln Gln Ser Cys Gln His Leu Gly
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Leu Leu Thr Pro Val Gly Val Gly Glu Gln Leu Ser Glu Gly Asp Tyr
20 25 30
Ala Arg Leu Gln Gln Val Asp Pro Val Leu Leu Lys Asp Glu Pro Gln
35 40 45
Gln Thr Ala Ala Gln Met Gly Cys Ala Pro Ile Gln Pro Leu Ala Met
50 55 60
Pro Gln Ala Leu Pro Leu Ala Ala Gly Pro Leu Pro Pro Gly Ser Ile
65 70 75 80
Ala Asn Leu Thr Glu Leu Gln Gly Val Ile Val Gly Gln Pro Val Leu
85 90 95
Gly Gln Ala Gln Leu Ala Gly Leu Gly Gln Gly Ile Leu Thr Glu Thr
100 105 110
Gln Gln Gly Leu Met Val Ala Ser Pro Ala Gln Thr Leu Asn Asp Thr
115 120 125
Leu Asp Asp Ile Met Ala Ala Val Ser Gly Arg Ala Ser Ala Met Ser
130 135 140
Asn Thr Pro Thr His Ser Ile Ala Ala Ser Ile Ser Gln Pro Gln Thr
145 150 155 160
Pro Thr Pro Ser Pro Ile Ile Ser Pro Ser Ala Met Leu Pro Ile Tyr
165 170 175
Pro Ala Ile Asp Ile Asp Ala Gln Thr Glu Ser Asn His Asp Thr Ala
180 185 190
Leu Thr Leu Ala Cys Ala Gly Gly His Glu Glu Leu Val Gln Thr Leu
195 200 205
Leu Glu Arg Gly Ala Ser Ile Glu His Arg Asp Lys Lys Gly Phe Thr
210 215 220
Pro Leu Ile Leu Ala Ala Thr Ala Gly His Val Gly Val Val Glu Ile
225 230 235 240
Leu Leu Asp Asn Gly Ala Asp Ile Glu Ala Gln Ser Glu Arg Thr Lys
245 250 255
Asp Thr Pro Leu Ser Leu Ala Cys Ser Gly Gly Arg Gln Glu Val Val
260 265 270
Glu Leu Leu Leu Ala Arg
275

<210> 3637
<211> 2128
<212> DNA
<213> Homo sapiens

<400> 3637
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120
cctgccaacc cctgctcttc caggtcgggc cccggggttc tgcggctgtt agggacagag
180
gcaaagaagg gcaggacggt ccggtttccc gtggatgttc ccgcccgaga aagacagcaa
240
gttgtgtgtg cgcccgggac gcgggaggga aggtagccgc cgcccgccag ccatggacca
300
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420
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720
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780
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1020
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1140
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1320
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1380
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1440
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1560
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1620
tgggaggttt agtggtgcat ttctcctctg ttttcttttt aatatacatt taaaatacag
1680

tattatcact ttataaaaca tacattaagc ctaataaatg gaccaataag ccaaactatc
1740
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1800
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1860
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1920
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1980
tgttttcttt tgtccattat tgtactgtgc tgtaccacat ttatttctat attcattttg
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2100
tttgatcaat aaaaaaaaaa aaaaaaaa
2128

<210> 3638
<211> 200
<212> PRT
<213> Homo sapiens

<400> 3638
Met Ala Ser Ser Leu Thr Cys Thr Gly Val Ile Trp Ala Leu Leu Ser
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Phe Leu Cys Ala Ala Thr Ser Cys Val Gly Phe Phe Met Pro Tyr Trp
20 25 30
Leu Trp Gly Ser Gln Leu Gly Lys Pro Val Ser Phe Gly Thr Phe Arg
35 40 45
Arg Cys Ser Tyr Pro Val His Asp Glu Ser Arg Gln Met Met Val Met
50 55 60
Val Glu Glu Cys Gly Arg Tyr Ala Ser Phe Gln Gly Ile Pro Ser Ala
65 70 75 80
Glu Trp Arg Ile Cys Thr Ile Val Thr Gly Leu Gly Cys Gly Leu Leu
85 90 95
Leu Leu Val Ala Leu Thr Ala Leu Met Gly Cys Cys Val Ser Asp Leu
100 105 110
Ile Ser Arg Thr Val Gly Arg Val Ala Gly Gly Ile Gln Phe Leu Gly
115 120 125
Gly Leu Leu Ile Gly Ala Gly Cys Ala Leu Tyr Pro Leu Gly Trp Asp
130 135 140
Ser Glu Glu Val Arg Gln Thr Cys Gly Tyr Thr Ser Gly Gln Phe Asp
145 150 155 160
Leu Gly Lys Cys Glu Ile Gly Trp Ala Tyr Tyr Cys Thr Gly Ala Gly
165 170 175
Ala Thr Ala Ala Met Leu Leu Cys Thr Trp Leu Ala Cys Phe Ser Gly
180 185 190
Lys Lys Gln Lys His Tyr Pro Tyr
195 200

<210> 3639
<211> 726
<212> DNA
<213> Homo sapiens

<400> 3639
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120
aagactaaca gtggttatct ctcagcggga ttataaatgt tttggttttt ttttttttt
180
tgtacatttt agtatttttt gaaatttttt taataagcgt gtattacata cagtaaacaa
240
aagcacatta atgtaggcag attatcaatg ttatgcattt cactgattgc atatctcttt
300
ttttatcaat ggtgaacatt gcaaatgatt gatacgtttt tcttaggaag tggcattgcc
360
acaaatggtt tttccaacac cagcagggcc tgagagtgtc atcaccatac actcttgccg
420
gcaataaaaa aatttcacct tttaatggat ttaaaaggga aaagttgggg tgttgggttc
480
tccagggcat ttctttcatt atgagtgaca tttttctgaa aggaacgtga tctcgttttc
540
tagccgcatg aagcatttct ccaacaagac ccactgtacc agtcctggga tctccacacc
600
tgtgccttct ccctgctctt tctaggtcct gattctcacc tctgcctgtg taataaccct
660
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720
taagat
726

<210> 3640
<211> 102
<212> PRT
<213> Homo sapiens

<400> 3640
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Ser Leu Ile Met Lys Glu Met Pro Trp Arg Thr Gln His Pro Asn Phe
20 25 30
Ser Leu Leu Asn Pro Leu Lys Gly Glu Ile Phe Leu Leu Pro Ala Arg
35 40 45
Val Tyr Gly Asp Asp Thr Leu Arg Pro Cys Trp Cys Trp Lys Asn His
50 55 60
Leu Trp Gln Cys His Phe Leu Arg Lys Thr Tyr Gln Ser Phe Ala Met
65 70 75 80
Phe Thr Ile Asp Lys Lys Arg Asp Met Gln Ser Val Lys Cys Ile Thr
85 90 95
Leu Ile Ile Cys Leu His
100

<210> 3641
<211> 455
<212> DNA
<213> Homo sapiens

<400> 3641
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60
cgcgggggcg ggcgggcggt gcggctcccg gaggcgagga aatgtcgcag agccccgagg
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gagctcgaga cgctcgcgcg ctcacctcct gggcccctgt gcgtggggaa gtcaggaaga
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300
ggaggtggcc gaagggaaga gggtggggca ggggctgctc tgcacctct agcagagcgg
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455

<210> 3642
<211> 148
<212> PRT
<213> Homo sapiens

<400> 3642
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Pro Arg Gly Arg Ala Gly Gly Ala Ala Pro Gly Gly Glu Glu Met Ser
20 25 30
Gln Ser Pro Glu Glu Ser Arg Ser Ser His Ala Ser Arg Asp Leu Ala
35 40 45
Pro Leu Glu Arg Arg Ser Gly Arg Gly Ala Arg Asp Ala Arg Ala Leu
50 55 60
Thr Ser Trp Ala Pro Val Arg Gly Glu Val Arg Lys Lys Thr Pro Ser
65 70 75 80
Glu Val Thr Val Pro Thr Arg Val Asp Ser Pro Arg Pro Asp His Ala
85 90 95
Arg Arg Trp Pro Lys Gly Arg Gly Trp Gly Arg Gly Cys Ser Ala Pro
100 105 110
Ser Ser Arg Ala Ala Ser Leu Gln Val Phe Ala Leu Ala Arg Arg Ser
115 120 125
Pro Arg Glu Gln Phe Gly Thr Val Arg Ile Gly Phe Arg Glu Pro Ala
130 135 140
Phe Lys Thr Arg
145

<210> 3643
<211> 2243
<212> DNA
<213> Homo sapiens

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120
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240
attgcccgca ttgtggagac ccaccagcca atagtggaga cctattatgg gccagggaga
300
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360
gacaagttca tcaagcaaag ggactaccac cagcagttcc ggcatgttca gaacaacctg
420
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480
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540
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1140
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1380
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1500
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1560
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1680

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1980
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2040
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2100
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2220
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2243

<210> 3644
<211> 560
<212> PRT
<213> Homo sapiens

<400> 3644
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20 25 30
Asp Met Ser Asp Arg Arg Ala Ala Val Ile Phe Ala Asp Thr Leu Thr
35 40 45
Leu Leu Phe Glu Gly Ile Ala Arg Ile Val Glu Thr His Gln Pro Ile
50 55 60
Val Glu Thr Tyr Tyr Gly Pro Gly Arg Leu Tyr Thr Leu Ile Lys Tyr
65 70 75 80
Leu Gln Val Glu Cys Asp Arg Gln Val Glu Lys Val Val Asp Lys Phe
85 90 95
Ile Lys Gln Arg Asp Tyr His Gln Gln Phe Arg His Val Gln Asn Asn
100 105 110
Leu Met Arg Asn Ser Thr Thr Glu Lys Ile Glu Pro Arg Glu Leu Asp
115 120 125
Pro Ile Leu Thr Glu Val Thr Leu Met Asn Ala Arg Ser Glu Leu Tyr
130 135 140
Leu Arg Phe Leu Lys Lys Arg Ile Ser Ser Asp Phe Glu Val Gly Asp
145 150 155 160
Ser Met Ala Ser Glu Glu Val Lys Gln Glu His Gln Lys Cys Leu Asp
165 170 175
Lys Leu Leu Asn Asn Cys Leu Leu Ser Cys Thr Met Gln Glu Leu Ile
180 185 190
Gly Leu Tyr Val Thr Met Glu Glu Tyr Phe Met Arg Glu Thr Val Asn
195 200 205
Lys Ala Val Ala Leu Asp Thr Tyr Glu Lys Gly Gln Leu Thr Ser Ser

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    210                 215                 220
Met Val Asp Asp Val Phe Tyr Ile Val Lys Lys Cys Ile Gly Arg Ala
225                 230                 235                 240
Leu Ser Ser Ser Ser Ile Asp Cys Leu Cys Ala Met Ile Asn Leu Ala
                245                 250                 255
Thr Thr Glu Leu Glu Ser Asp Phe Arg Asp Val Leu Cys Asn Lys Leu
            260                 265                 270
Arg Met Gly Phe Pro Ala Thr Thr Phe Gln Asp Ile Gln Arg Gly Val
        275                 280                 285
Thr Ser Ala Val Asn Ile Met His Ser Ser Leu Gln Gln Gly Lys Phe
    290                 295                 300
Asp Thr Lys Gly Ile Glu Ser Thr Asp Glu Ala Lys Met Ser Phe Leu
305                 310                 315                 320
Val Thr Leu Asn Asn Val Glu Val Cys Ser Glu Asn Ile Ser Thr Leu
                325                 330                 335
Lys Lys Thr Leu Glu Ser Asp Cys Thr Lys Leu Phe Ser Gln Gly Ile
            340                 345                 350
Gly Gly Glu Gln Ala Gln Ala Lys Phe Asp Ser Cys Leu Ser Asp Leu
        355                 360                 365
Ala Ala Val Ser Asn Lys Phe Arg Asp Leu Leu Gln Glu Gly Leu Thr
    370                 375                 380
Glu Leu Asn Ser Thr Ala Ile Lys Pro Gln Val Gln Pro Trp Ile Asn
385                 390                 395                 400
Ser Phe Phe Ser Val Ser His Asn Ile Glu Glu Glu Glu Phe Asn Asp
                405                 410                 415
Tyr Glu Ala Asn Asp Pro Trp Val Gln Gln Phe Ile Leu Asn Leu Glu
            420                 425                 430
Gln Gln Met Ala Glu Phe Lys Ala Ser Leu Ser Pro Val Ile Tyr Asp
        435                 440                 445
Ser Leu Thr Gly Leu Met Thr Ser Leu Val Ala Val Glu Leu Glu Lys
    450                 455                 460
Val Val Leu Lys Ser Thr Phe Asn Arg Leu Gly Gly Leu Gln Phe Asp
465                 470                 475                 480
Lys Glu Leu Arg Ser Leu Ile Ala Tyr Leu Thr Thr Val Thr Thr Trp
                485                 490                 495
Thr Ile Arg Asp Lys Phe Ala Arg Leu Ser Gln Met Ala Thr Ile Leu
            500                 505                 510
Asn Leu Glu Arg Val Thr Glu Ile Leu Asp Tyr Trp Gly Pro Asn Ser
        515                 520                 525
Gly Pro Leu Thr Trp Arg Leu Thr Pro Ala Glu Val Arg Gln Val Leu
    530                 535                 540
Ala Leu Arg Ile Asp Phe Arg Ser Glu Asp Ile Lys Arg Leu Arg Leu
545                 550                 555                 560
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<210> 3645
<211> 823
<212> DNA
<213> Homo sapiens

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120

tcgggttgat ttcctcatct tctatttgat gggctaactg ctctatggaa ggaagatctt
180
cctcctcctt ggaggctaag atttggcgta actctttcct gagatcaata aaacgatcgt
240
ggaacagggc caggcaccac ggctcggtga agtagctata gagatctgtg atcaggtttt
300
catcgtaccg agcacacagg ttgttgagga gttgctcgtg ctggccaaac aagcggatgt
360
agttggaggc ggggaagggc tccctagaaa ggcacgtgat ggtttccacc attttatact
420
tgttaatatg aattcggaag taagtcccat ttttcgcact gccggttact agttctaaac
480
cataattagg ctgggccatt tgtacctcca agggagttgg aatggcaggc ttggcaatat
540
gcagataatg gtaagaccca ggaagaatgc ccccttgaat cttggctccc ttgtacatgg
600
ggatgagccg gtcaagatta gctggtggct cggtcacagg ctcaagggtt ggatcaaaga
660
gatgtagcat agctgctgcc agctgaaagc caatttcttt ggaactgaag ttgctggtgg
720
gcccattcat ttgagtagta tctattggag aatttggtga gggagccagc agctctgatg
780
gctatgtcgt tggtgtggaa gttggtatca atcacaagtc gac
823

<210> 3646
<211> 243
<212> PRT
<213> Homo sapiens

<400> 3646

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Leu	Ala	Ala	Ala	Met	Leu	His	Leu	Phe	Asp	Pro	Thr	Leu	Glu	Pro	Val
			20					25					30		
Thr	Glu	Pro	Pro	Ala	Asn	Leu	Asp	Arg	Leu	Ile	Pro	Met	Tyr	Lys	Gly
		35					40					45			
Ala	Lys	Ile	Gln	Gly	Gly	Ile	Leu	Pro	Gly	Ser	Tyr	His	Tyr	Leu	His
	50					55					60				
Ile	Ala	Lys	Pro	Ala	Ile	Pro	Thr	Pro	Leu	Glu	Val	Gln	Met	Ala	Gln
65					70					75					80
Pro	Asn	Tyr	Gly	Leu	Glu	Leu	Val	Thr	Gly	Ser	Ala	Lys	Asn	Gly	Thr
				85					90					95	
Tyr	Phe	Arg	Ile	His	Ile	Asn	Lys	Tyr	Lys	Met	Val	Glu	Thr	Ile	Thr
			100					105					110		
Cys	Leu	Ser	Arg	Glu	Pro	Phe	Pro	Ala	Ser	Asn	Tyr	Ile	Arg	Leu	Phe
		115					120					125			
Gly	Gln	His	Glu	Gln	Leu	Leu	Asn	Asn	Leu	Cys	Ala	Arg	Tyr	Asp	Glu
	130					135					140				
Asn	Leu	Ile	Thr	Asp	Leu	Tyr	Ser	Tyr	Phe	Thr	Glu	Pro	Trp	Cys	Leu
145					150					155					160
Ala	Leu	Phe	His	Asp	Arg	Phe	Ile	Asp	Leu	Arg	Lys	Glu	Leu	Arg	Gln
				165					170					175	
Ile	Leu	Ala	Ser	Lys	Glu	Glu	Glu	Asp	Leu	Pro	Ser	Ile	Glu	Gln	Leu

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            180                 185                 190
Ala His Gln Ile Glu Asp Glu Glu Ile Asn Pro Thr Glu Lys Pro Arg
        195                 200                 205
Gln Tyr Leu Lys Arg Val Phe Glu Glu Ser Ile Tyr Lys Thr Leu Val
    210                 215                 220
Glu Arg Ser Thr Leu Asp Tyr Leu His Tyr Asn Arg Tyr His Leu Pro
225                 230                 235                 240
Met Tyr Ala
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<210> 3647
<211> 584
<212> DNA
<213> Homo sapiens

<400> 3647
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120
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180
tcttccacct gacggtcgcc gaaccccacg cggagccgcc cccccggggc tctccgggca
240
acggctccag ccacagcggc gccccaggcc caggtgaagg aggcctccct gggacccggg
300
aaggcgggag cccaccccac cgggggttgc tctgcgcccg ctgtcccttg cccgaggccc
360
gcggatccca gcgggnnggc cgtggcccgg gtcggggcgc aggtcttgct ggtacctgac
420
gccgctccga ccccgcgttc cccgcagacc ccacactggc gcgcggccac aacgtcatca
480
atgtcatcgt ccccgagagc cgagcccact tcttccagca gctgggctac gtgctggcca
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584

<210> 3648
<211> 63
<212> PRT
<213> Homo sapiens

<400> 3648
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Thr Arg Arg Ala Ser Ala Ala Pro Thr Gly Pro Phe Phe Cys Ala Thr
 1               5                  10                  15
Ala Trp Leu Trp Ala Arg Met Pro Leu Ser Ala Val Thr Ser His Cys
            20                  25                  30
Val Ser Ser Arg Trp Arg Ser Pro Thr Arg Ala Pro Thr Pro Ala Thr
        35                  40                  45
Cys Thr Thr Ile Thr Val Ala Cys Thr Asn Ala Ala Ser Ser Thr
    50                  55                  60
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<210> 3649
<211> 648

<212> DNA
<213> Homo sapiens

<400> 3649
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ggaagcatga tactgaaggc ttgtcactcc tgttttcact tccacacaga caagcatatt
120
tgctcattgt ttgctgtgct ccccttttt tttcaggttg ctatttctgc agatgtcaaa
180
gaagttctgt taactgatgg gaatgaaaag gccatcagaa atgtgcaaga catcatcaca
240
aggaatcaga aggctggtgt gtttaagacc cagaaaatat caagctgcgt tttacgatgg
300
gataatgaga cagatgtctc tcaactggaa ggacattttg acattgttat gtgtgctgac
360
tgcctgtttc tggaccagta cagagccagc cttgttgatg caataaagag attactccag
420
cccaggggga aagcgatggt atttgcccca cgccgaggga atactttaaa ccagttttgc
480
aatctagctg aaaaagctgg tttctgtatc caaagacatg aaaattatga tgaacacatt
540
tcaaacttcc actccaagtt gaaaaaggaa aacccggaca tatatgaaga aaaccttcat
600
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648

<210> 3650
<211> 189
<212> PRT
<213> Homo sapiens

<400> 3650
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His Ile Cys Ser Leu Phe Ala Val Leu Pro Phe Phe Phe Gln Val Ala
            20   25   30
Ile Ser Ala Asp Val Lys Glu Val Leu Leu Thr Asp Gly Asn Glu Lys
        35   40   45
Ala Ile Arg Asn Val Gln Asp Ile Ile Thr Arg Asn Gln Lys Ala Gly
    50   55   60
Val Phe Lys Thr Gln Lys Ile Ser Ser Cys Val Leu Arg Trp Asp Asn
65   70   75   80
Glu Thr Asp Val Ser Gln Leu Glu Gly His Phe Asp Ile Val Met Cys
                85   90   95
Ala Asp Cys Leu Phe Leu Asp Gln Tyr Arg Ala Ser Leu Val Asp Ala
            100   105   110
Ile Lys Arg Leu Leu Gln Pro Arg Gly Lys Ala Met Val Phe Ala Pro
        115   120   125
Arg Arg Gly Asn Thr Leu Asn Gln Phe Cys Asn Leu Ala Glu Lys Ala
    130   135   140
Gly Phe Cys Ile Gln Arg His Glu Asn Tyr Asp Glu His Ile Ser Asn
145   150   155   160
Phe His Ser Lys Leu Lys Lys Glu Asn Pro Asp Ile Tyr Glu Glu Asn

165 170 175
Leu His Tyr Pro Pro Leu Leu Ile Leu Thr Lys His Gly
180 185

<210> 3651
<211> 2469
<212> DNA
<213> Homo sapiens

<400> 3651
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cccaccactg gccccatggc tgccgtgcag atggatcctg agctagccaa gcgcctcttc
120
tttgaagggg ccactgtggt catcctgaac atgcccaagg gaacagagtt tgggattgac
180
tataactcct gggaggtcgg gcccaagttc cggggcgtga agatgatccc tccaggcatc
240
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360
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420
caggagctgg accagttcct ggggccttac ccatatgcca ccctgaagaa gtggatctca
480
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540
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600
cagaatctac cccgctgtgg cattgagtgc aaaagctacc aagagggcct ggcccggcta
660
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720
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780
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1080
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1140
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1320

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1380
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1620
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1980
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2280
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2469

<210> 3652
<211> 384
<212> PRT
<213> Homo sapiens

<400> 3652
Met Ala Ala Val Gln Met Asp Pro Glu Leu Ala Lys Arg Leu Phe Phe
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Glu Gly Ala Thr Val Val Ile Leu Asn Met Pro Lys Gly Thr Glu Phe
            20   25   30
Gly Ile Asp Tyr Asn Ser Trp Glu Val Gly Pro Lys Phe Arg Gly Val
        35   40   45
Lys Met Ile Pro Pro Gly Ile His Phe Leu His Tyr Ser Ser Val Asp

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    50                  55                  60
Lys Ala Asn Pro Lys Glu Val Gly Pro Arg Met Gly Phe Phe Leu Ser
65                  70                  75                  80
Leu His Gln Arg Gly Leu Thr Val Leu Arg Trp Ser Thr Leu Arg Glu
                85                  90                  95
Glu Val Asp Leu Ser Pro Ala Pro Glu Ser Glu Val Glu Ala Met Arg
            100                 105                 110
Ala Asn Leu Gln Glu Leu Asp Gln Phe Leu Gly Pro Tyr Pro Tyr Ala
        115                 120                 125
Thr Leu Lys Lys Trp Ile Ser Leu Thr Asn Phe Ile Ser Glu Ala Thr
    130                 135                 140
Val Glu Lys Leu Gln Pro Glu Asn Arg Gln Ile Cys Ala Phe Ser Asp
145                 150                 155                 160
Val Leu Pro Val Leu Ser Met Lys His Thr Lys Asp Arg Val Gly Gln
                165                 170                 175
Asn Leu Pro Arg Cys Gly Ile Glu Cys Lys Ser Tyr Gln Glu Gly Leu
            180                 185                 190
Ala Arg Leu Pro Glu Met Lys Pro Arg Ala Gly Thr Glu Ile Arg Phe
        195                 200                 205
Ser Glu Leu Pro Thr Gln Met Phe Pro Glu Gly Ala Thr Pro Ala Glu
    210                 215                 220
Ile Thr Lys His Ser Met Asp Leu Ser Tyr Ala Leu Glu Thr Val Leu
225                 230                 235                 240
Ile Lys Gln Phe Pro Ser Ser Pro Gln Asp Val Leu Gly Glu Leu Gln
                245                 250                 255
Phe Ala Phe Val Cys Phe Leu Leu Gly Asn Val Tyr Glu Ala Phe Glu
            260                 265                 270
His Trp Lys Arg Leu Leu His Leu Leu Cys Arg Ser Glu Ala Ala Met
        275                 280                 285
Met Lys His His Thr Leu Tyr Ile Asn Leu Met Ser Ile Leu Tyr His
    290                 295                 300
Gln Leu Gly Glu Ile Pro Ala Asp Phe Phe Val Asp Ile Val Ser Gln
305                 310                 315                 320
Asp Asn Phe Leu Thr Ser Thr Leu Gln Val Phe Phe Ser Ser Ala Cys
                325                 330                 335
Ser Ile Ala Val Asp Ala Thr Leu Arg Lys Lys Ala Glu Lys Phe Gln
            340                 345                 350
Ala His Leu Thr Lys Lys Phe Arg Trp Asp Phe Ala Ala Glu Pro Glu
        355                 360                 365
Asp Cys Ala Pro Val Val Val Glu Leu Pro Glu Gly Ile Glu Met Gly
    370                 375                 380
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<210> 3653
<211> 283
<212> DNA
<213> Homo sapiens

<400> 3653
ncaaagagca agggtggatg ccccaggcca gcccaggagc ttggcgccac tggaggaagt
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gcattatacc aatcagagct tcttttgctg ctgctgaaat ggaacggtgc catcaggccg
120
tcttctccac tggagatgct ccttcagctc agcaggacgc tagctcggaa ctcagactgc
180

acatttttgc ggattgggag gagggccgac gccgtggccg gatagtctct ggagctgcct
240
tttgggggtg tttgcctgtt ggcattttca gtactccacg cgt
283

<210> 3654
<211> 88
<212> PRT
<213> Homo sapiens

<400> 3654
Met Pro Gln Ala Ser Pro Gly Ala Trp Arg His Trp Arg Lys Cys Ile
1 5 10 15
Ile Pro Ile Arg Ala Ser Phe Ala Ala Ala Glu Met Glu Arg Cys His
20 25 30
Gln Ala Val Phe Ser Thr Gly Asp Ala Pro Ser Ala Gln Gln Asp Ala
35 40 45
Ser Ser Glu Leu Arg Leu His Ile Phe Ala Asp Trp Glu Glu Gly Arg
50 55 60
Arg Arg Gly Arg Ile Val Ser Gly Ala Ala Phe Trp Gly Cys Leu Pro
65 70 75 80
Val Gly Ile Phe Ser Thr Pro Arg
85

<210> 3655
<211> 3477
<212> DNA
<213> Homo sapiens

<400> 3655
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taatggaggt gctcatttca atgccacaga ggtggtggca actgtggaac gtggcatggg
120
gagtgagagg ttgctctggt gcagctggag gaagaacagg gaacctaggg ttggggagag
180
atgtatagag gaaaactccc ccaggcacac agcctccgct ctggaccaac gcaggcttca
240
gtgagtacac acaaaggaac tgatgtcaag gccctttcta tgacccttcc cattctagca
300
agacctccca ccccagtcat cttgggatct acagccacat gaaatacaga cacatcgttc
360
ccccaagtca ggccagtttt aggccattga gttatgggga aatgattaat gggatgaatg
420
aaaaacaaat aaaataaata aataaataaa tacactaaag ccttattagc caggcgtgat
480
cacatgccca acactccccc ccatcccagc actatgcaca gttcacggct catatgcaaa
540
gtggaagaca cgtgggacaa gagcaaagca caagtgacac atggtccctc tctaacacct
600
cagcacacca accctgacgc tcccatcaca gatgctgatc attcttccac ggacccccct
660
ttataataat cctcattcac atttctagtt tctgagggaa gagagaaaga gaaaggaaga
720

agtggaaagt gcggaacccc aatgagtagg gcacagaaag gagggcgagc agagacagca
780
agaggtcagg taagccaagg agcagcggag caggtcaatc agggaagttc tgggcaccct
840
ggggctcagg ggatctcagg gggtgaacta tcacagatca ggacagcaag gttccaggag
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gatgagacag aggttccacg tctccaggca agcagaggaa tcacagcaca ctgggattac
960
ggaacttgcg tccagcaaac ttagccttgc tgcccaagag cctcttcaat tctgaggagt
1020
tggttgtatt tggccagacg ctccgagcgg caggggcac cagtcttgat ctgtcctgtg
1080
cagagcccca ccacaaggtc agcaatgaat gtgtcctcag tctccccaga gcggtggctc
1140
accatcaccc cccagccatt ctcctgggcc agcttgcacg cctgaagaga ctcggtcacg
1200
gagccgatct ggttgacttt gagcaggagg cagttgcagg ccttctcgtt cacggcccgc
1260
tcaatacgtt ttgggttggt cactgtgaga tcatccccca caatctggat tcctacattg
1320
gctgtgaact tctgccaagc tccccaatca tcctggtcaa atgggtcctc aatggagacc
1380
actgggtagt ccctgacaaa gtcctggtag agtgccccca gctggtcccc agtgatgtac
1440
ctgctggggt cagtgggaga cttgaagtcc aagtcatatt tgccatcacg ataaaactcg
1500
gaggcagcaa catccatgcc gatgacaacc tggtcagtgt agccggcctt tgcgattgca
1560
gtcttcacca gctccagtgc ttctttgttc tccaggatgt taggtgcgaa tccaccttca
1620
tcacccacat tggtggcatc cttcccgtac ttctccttga tgacccccct gagtgtatgg
1680
tagacctctg cacctagtcg catggcttcc ttgaaggagc tggctcccac aggcagaatc
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1800
gctggcactg ggagtatgag gtcagggttc ccagccaagt cagcgatgtg gcggtacagg
1860
gggacccccc tctcaaaggc tgttgagcac atcaataaaa ctattgcgcc tgccctggtt
1920
agcaagaaac tgaacgtcac agaacaagag aagattgaca aactgatgat cgagatggat
1980
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2040
tgcaaagctg gtgccgttga gaaggggtc cccctgtacc gccacatcgc tgacttggct
2100
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2160
gctggcaaca agctggccat gcaggagttc atgatcctcc cagtcggtgc agcaaacttc
2220
agggaagcca tgcgcattgg agcagaggtt taccacaacc tgaagaatgt catcaaggag
2280
aaatatggga aagatgccac caatgtgggg gatgaaggcg ggtttgctcc caacatcctg
2340

gagaataaag aaggcctgga gctgctgaag actgctattg ggaaagctgg ctacactgat
2400
aaggtggtca tcggcatgga cgtagcggcc tccgagttct tcaggtctgg gaagtatgac
2460
ctggacttca agtctcccga tgaccccagc aggtacatct cgcctgacca gctggctgac
2520
ctgtacaagt ccttcatcaa ggactaccca gtggtgtcta tcgaagatcc ctttgaccag
2580
gatgactggg gagcttggca gaagttcaca gccagtgcag gaatccaggt agtgggggat
2640
gatctcacag tgaccaaccc caagaggatc gcccaggccg tgaacgagaa gtcctgcaac
2700
tgcctcctgc tcaaagtcaa ccagattggc tccgtgaccg agtctcttca ggcgtgcaag
2760
ctggcccagg ccaatggttg gggcgtcatg gtgtctcatc gttcggggga gactgaagat
2820
accttcatcg ctgacctggt tgtggggctg tgcactgggc agatcaagac tggtgcccct
2880
tgccgatctg agcgcttggc caagtacaac cagctcctca gaattgaaga ggagctgggc
2940
agcaaggcta agtttgccgg caggaacttc agaaacccct tggccaagta agctgtgggc
3000
aggcaagccc ttcggtcacc tgttggctac acagacccct cccctcgtgt cagctcaggc
3060
agctcgaggc ccccgaccaa cacttgcagg ggtccctgct agttagcgcc ccaccgccgt
3120
ggagttcgta ccgcttcctt agaacttcta cagaagccaa gctccctgga gccctgttgg
3180
cagctctagc tttgcagtcg tgtaattggc ccaagtcatt gtttttctcg cctcactttc
3240
caccaagtgt ctagagtcat gtgagcctcg tgtcatctcc ggggtggcca caggctagat
3300
ccccggtggt tttgtgctca aaataaaaag cctcagtgac ccatgaaaaa aaaaaaaaaa
3360
actcgtgccg actcgtgccg aattcggaga ncccatgtcc ggagacccca cggctggcac
3420
ttcgggcccc gtatgacctg ggacctcgcc gtcccgagac ctcctgggtc cctccgt
3477

<210> 3656
<211> 429
<212> PRT
<213> Homo sapiens

<400> 3656
Met Ala Ser Leu Lys Glu Leu Ala Pro Thr Gly Arg Ile Met Asn Ser
1 5 10 15
Cys Met Ala Ser Leu Phe Pro Ala Trp Glu Pro Pro Leu Ile Thr Leu
20 25 30
Lys Ala Gly Thr Gly Ser Met Arg Ser Gly Phe Pro Ala Lys Ser Ala
35 40 45
Met Trp Arg Tyr Arg Gly Thr Pro Phe Ser Lys Ala Val Glu His Ile
50 55 60
Asn Lys Thr Ile Ala Pro Ala Leu Val Ser Lys Lys Leu Asn Val Thr

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65                  70                  75                  80
Glu Gln Glu Lys Ile Asp Lys Leu Met Ile Glu Met Asp Gly Thr Glu
                85                  90                  95
Asn Lys Ser Lys Phe Gly Ala Asn Ala Ile Leu Gly Val Ser Leu Ala
            100                 105                 110
Val Cys Lys Ala Gly Ala Val Glu Lys Gly Val Pro Leu Tyr Arg His
        115                 120                 125
Ile Ala Asp Leu Ala Gly Asn Ser Glu Val Ile Leu Pro Val Pro Ala
    130                 135                 140
Phe Asn Val Ile Asn Gly Gly Ser His Ala Gly Asn Lys Leu Ala Met
145                 150                 155                 160
Gln Glu Phe Met Ile Leu Pro Val Gly Ala Ala Asn Phe Arg Glu Ala
                165                 170                 175
Met Arg Ile Gly Ala Glu Val Tyr His Asn Leu Lys Asn Val Ile Lys
            180                 185                 190
Glu Lys Tyr Gly Lys Asp Ala Thr Asn Val Gly Asp Glu Gly Gly Phe
        195                 200                 205
Ala Pro Asn Ile Leu Glu Asn Lys Glu Gly Leu Glu Leu Leu Lys Thr
    210                 215                 220
Ala Ile Gly Lys Ala Gly Tyr Thr Asp Lys Val Val Ile Gly Met Asp
225                 230                 235                 240
Val Ala Ala Ser Glu Phe Phe Arg Ser Gly Lys Tyr Asp Leu Asp Phe
                245                 250                 255
Lys Ser Pro Asp Asp Pro Ser Arg Tyr Ile Ser Pro Asp Gln Leu Ala
            260                 265                 270
Asp Leu Tyr Lys Ser Phe Ile Lys Asp Tyr Pro Val Val Ser Ile Glu
        275                 280                 285
Asp Pro Phe Asp Gln Asp Asp Trp Gly Ala Trp Gln Lys Phe Thr Ala
    290                 295                 300
Ser Ala Gly Ile Gln Val Val Gly Asp Asp Leu Thr Val Thr Asn Pro
305                 310                 315                 320
Lys Arg Ile Ala Gln Ala Val Asn Glu Lys Ser Cys Asn Cys Leu Leu
                325                 330                 335
Leu Lys Val Asn Gln Ile Gly Ser Val Thr Glu Ser Leu Gln Ala Cys
            340                 345                 350
Lys Leu Ala Gln Ala Asn Gly Trp Gly Val Met Val Ser His Arg Ser
        355                 360                 365
Gly Glu Thr Glu Asp Thr Phe Ile Ala Asp Leu Val Val Gly Leu Cys
    370                 375                 380
Thr Gly Gln Ile Lys Thr Gly Ala Pro Cys Arg Ser Glu Arg Leu Ala
385                 390                 395                 400
Lys Tyr Asn Gln Leu Leu Arg Ile Glu Glu Glu Leu Gly Ser Lys Ala
                405                 410                 415
Lys Phe Ala Gly Arg Asn Phe Arg Asn Pro Leu Ala Lys
            420                 425
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<210> 3657
<211> 337
<212> DNA
<213> Homo sapiens

<400> 3657
tgttacgtgt tcattttcga ctcaaggcgt acacgtgcag atgtgtcaca tgttcatttt
60

cagctcaagg cgtacacgtg caggtgtgtt acgtgttcat tttcgactca aggcgtacac
120
gtgcagatgt gtcacatgtt cattttcggc tcaaggcgta cacgtgcagg tgtgttacgt
180
gttcattttc ggctcaaggc ttacacgtgc aggtgtgcca catgttcatt ttcggctcaa
240
ggcgtacatg tgcaggtgtg ttacatgttc attgtcagct caacgcgtac acgtgcaggt
300
gtgccacatg ttcattttcg gttcaaggcg tacgcgt
337

<210> 3658
<211> 99
<212> PRT
<213> Homo sapiens

<400> 3658
Met Cys His Met Phe Ile Phe Ser Ser Arg Arg Thr Arg Ala Gly Val
 1   5   10   15
Leu Arg Val His Phe Arg Leu Lys Ala Tyr Thr Cys Arg Cys Val Thr
            20   25   30
Cys Ser Phe Ser Ala Gln Gly Val His Val Gln Val Cys Tyr Val Phe
        35   40   45
Ile Phe Gly Ser Arg Leu Thr Arg Ala Gly Val Pro His Val His Phe
    50   55   60
Arg Leu Lys Ala Tyr Met Cys Arg Cys Val Thr Cys Ser Leu Ser Ala
65   70   75   80
Gln Arg Val His Val Gln Val Cys His Met Phe Ile Phe Gly Ser Arg
                85   90   95
Arg Thr Arg

<210> 3659
<211> 1025
<212> DNA
<213> Homo sapiens

<400> 3659
naagctttta ctgctgatgg tgatcaagtt tttgcaggac gttattattc atctgaaaat
60
acaagaccta agttcctaag cagagatgtg gattctgaaa taagtgactt ggagaatgag
120
gttgaaaata agacggccca gatattaaat cttcagcaac atttatctgc ccttgaaaaa
180
gatattaaac acaatgagga acttcttaaa aggtgccaac tacattataa agaactaaag
240
atgaaaataa gaaaaaatat ttctgaaatt cgggaacttg agaacataga agaacaccag
300
tctgtagata ttgcaacttt ggaagatgaa gctcaggaaa ataaaagcaa aatgaaaatg
360
gttgaggaac atatggagca acaaaaagaa aatatggagc atcttaaaag tctgaaaata
420
gaagcagaaa ataagtatga tgcaattaaa ttcaaaatta atcaactatc ggagctagca
480

gacccactta aggatgaatt aaaccttgct gattctgaag tggataacca aaaacgaggg
540
aaacgacatt atgaaaaaaa acaaaaagaa cacttggata ccttaaataa aaagaaacga
600
gaactggata tgaaagagaa agaactagag gagaaaatgt cacaagcaag acaaatctgc
660
ccagagcgta tagaagtaga aaaatctgca tcaattctgg acaaagaaat taatcgatta
720
aggcagaaga tacaggcaga acatgctagt catggagatc gagaggaaat aatgaggcag
780
taccaagaag caagagagac ctatcttgat ctggatagta aagtgaggac tttaaaaaag
840
tttattaaat tactgggaga aatcatggag cacagattca agacatatca acaatttaga
900
aggtgtttga ctttacgatg caaattatac tttgacaact tactatctca gcgggcctat
960
tgtggaaaaa tgaattttga ccacaagaat gaaactctaa gtatatcagt tcagcctgga
1020
gaaaa
1025

<210> 3660
<211> 341
<212> PRT
<213> Homo sapiens

<400> 3660
Xaa Ala Phe Thr Ala Asp Gly Asp Gln Val Phe Ala Gly Arg Tyr Tyr
 1   5   10   15
Ser Ser Glu Asn Thr Arg Pro Lys Phe Leu Ser Arg Asp Val Asp Ser
            20   25   30
Glu Ile Ser Asp Leu Glu Asn Glu Val Glu Asn Lys Thr Ala Gln Ile
        35   40   45
Leu Asn Leu Gln Gln His Leu Ser Ala Leu Glu Lys Asp Ile Lys His
    50   55   60
Asn Glu Glu Leu Leu Lys Arg Cys Gln Leu His Tyr Lys Glu Leu Lys
65   70   75   80
Met Lys Ile Arg Lys Asn Ile Ser Glu Ile Arg Glu Leu Glu Asn Ile
                85   90   95
Glu Glu His Gln Ser Val Asp Ile Ala Thr Leu Glu Asp Glu Ala Gln
            100   105   110
Glu Asn Lys Ser Lys Met Lys Met Val Glu Glu His Met Glu Gln Gln
        115   120   125
Lys Glu Asn Met Glu His Leu Lys Ser Leu Lys Ile Glu Ala Glu Asn
    130   135   140
Lys Tyr Asp Ala Ile Lys Phe Lys Ile Asn Gln Leu Ser Glu Leu Ala
145   150   155   160
Asp Pro Leu Lys Asp Glu Leu Asn Leu Ala Asp Ser Glu Val Asp Asn
                165   170   175
Gln Lys Arg Gly Lys Arg His Tyr Glu Lys Lys Gln Lys Glu His Leu
            180   185   190
Asp Thr Leu Asn Lys Lys Lys Arg Glu Leu Asp Met Lys Glu Lys Glu
        195   200   205
Leu Glu Glu Lys Met Ser Gln Ala Arg Gln Ile Cys Pro Glu Arg Ile

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    210                 215                 220
Glu Val Glu Lys Ser Ala Ser Ile Leu Asp Lys Glu Ile Asn Arg Leu
225                 230                 235                 240
Arg Gln Lys Ile Gln Ala Glu His Ala Ser His Gly Asp Arg Glu Glu
                245                 250                 255
Ile Met Arg Gln Tyr Gln Glu Ala Arg Glu Thr Tyr Leu Asp Leu Asp
            260                 265                 270
Ser Lys Val Arg Thr Leu Lys Lys Phe Ile Lys Leu Leu Gly Glu Ile
        275                 280                 285
Met Glu His Arg Phe Lys Thr Tyr Gln Gln Phe Arg Arg Cys Leu Thr
    290                 295                 300
Leu Arg Cys Lys Leu Tyr Phe Asp Asn Leu Leu Ser Gln Arg Ala Tyr
305                 310                 315                 320
Cys Gly Lys Met Asn Phe Asp His Lys Asn Glu Thr Leu Ser Ile Ser
                325                 330                 335
Val Gln Pro Gly Glu
            340
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<210> 3661
<211> 1117
<212> DNA
<213> Homo sapiens

<400> 3661
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tgtggcaaaa gctcctcctg catctgatac ttgggtcttc tccctctttt ataaaacaat
120
ttagatccta gaatgtgcct tttcacaatg gcttcgtttc caattttcac tgttatttgg
180
caaaggggtg caacattact atttgtggag gttcccggca gagcaggttt tgcaatgtag
240
gtttcaattt tgctggtttc ttcagcaata tttgtggttt tgctcagtga tcctccagga
300
tcagcaacat agtttgactc ctccggtatt tctcccctgg tatgtgatgt agttttcttt
360
ttctccttaa tgcttttggg tctgcttgca aacctaccca ctttatctgg ctcgggctta
420
ctgtcatctt tcagggactg actgacagct gggtctgaaa aggctctgtg gttgctgctg
480
gtcatggcag caatggcatt gctgtgcatg atcaccgatg aaaactggct gctgtgtaca
540
atgaccgagg gtgcagagcc actgtagctg atcacagagg cggcattctc actgctatta
600
ctcaaagata aaacaggtac atcccctgcc cggaggtcag aactgacagc attttcagtg
660
gaagaaactg acacctcagt tgaattaaag ttattgtcaa gatccatttt caatgcctcc
720
tctccccatt tggtaccctc tgcattttgt acattggcag aagtgggtat gtcctgacat
780
gcagatgttt ccaatgggat ggctggactg ttggtcaggg tgtttacagt attttggaaa
840
ttcagcgttg gtaattcaga gctgtgtgga ttctgaacaa cataggtacc aggtgcagac
900

tcattcattt gactgttttc tcgtgcattt tcataggaag aatttcggta gctcttataa
960
ggggctctct tgcatttcat aggcagtagc ctataaagtt tatacggata gacactaggc
1020
ttcaagcctc catttgctgt ttttttactg atggaaagtc tatgatcgat ggcatggaaa
1080
gacttctgat gatttttgag tatatagtag gtcatga
1117

<210> 3662
<211> 371
<212> PRT
<213> Homo sapiens

<400> 3662
Met Thr Tyr Tyr Ile Leu Lys Asn His Gln Lys Ser Phe His Ala Ile
1 5 10 15
Asp His Arg Leu Ser Ile Ser Lys Lys Thr Ala Asn Gly Gly Leu Lys
20 25 30
Pro Ser Val Tyr Pro Tyr Lys Leu Tyr Arg Leu Leu Pro Met Lys Cys
35 40 45
Lys Arg Ala Pro Tyr Lys Ser Tyr Arg Asn Ser Ser Tyr Glu Asn Ala
50 55 60
Arg Glu Asn Ser Gln Met Asn Glu Ser Ala Pro Gly Thr Tyr Val Val
65 70 75 80
Gln Asn Pro His Ser Ser Glu Leu Pro Thr Leu Asn Phe Gln Asp Thr
85 90 95
Val Asn Thr Leu Thr Asn Ser Pro Ala Ile Pro Leu Glu Thr Ser Ala
100 105 110
Cys Gln Asp Ile Pro Thr Ser Ala Asn Val Gln Asn Ala Glu Gly Thr
115 120 125
Lys Trp Gly Glu Glu Ala Leu Lys Met Asp Leu Asp Asn Asn Phe Tyr
130 135 140
Ser Thr Glu Val Ser Val Ser Ser Thr Glu Asn Ala Val Ser Ser Asp
145 150 155 160
Leu Arg Ala Gly Asp Val Pro Val Leu Ser Leu Ser Asn Ser Ser Glu
165 170 175
Asn Ala Ala Ser Val Ile Ser Tyr Ser Gly Ser Ala Pro Ser Val Ile
180 185 190
Val His Ser Ser Gln Phe Ser Ser Val Ile Met His Ser Asn Ala Ile
195 200 205
Ala Ala Met Thr Ser Ser Asn His Arg Ala Phe Ser Asp Pro Ala Val
210 215 220
Ser Gln Ser Leu Lys Asp Asp Ser Lys Pro Glu Pro Asp Lys Val Gly
225 230 235 240
Arg Phe Ala Ser Arg Pro Lys Ser Ile Lys Glu Lys Lys Lys Thr Thr
245 250 255
Ser His Thr Arg Gly Glu Ile Pro Glu Glu Ser Asn Tyr Val Ala Asp
260 265 270
Pro Gly Gly Ser Leu Ser Lys Thr Thr Asn Ile Ala Glu Glu Thr Ser
275 280 285
Lys Ile Glu Thr Tyr Ile Ala Lys Pro Ala Leu Pro Gly Thr Ser Thr
290 295 300
Asn Ser Asn Val Ala Pro Leu Cys Gln Ile Thr Val Lys Ile Gly Asn

305 310 315 320
Glu Ala Ile Val Lys Arg His Ile Leu Gly Ser Lys Leu Phe Tyr Lys
325 330 335
Arg Gly Arg Arg Pro Lys Tyr Gln Met Gln Glu Glu Leu Leu Pro Gln
340 345 350
Gly Asn Asp Pro Glu Pro Ser Gly Asp Ser Pro Leu Gly Leu Cys Gln
355 360 365
Ser Glu Cys
370

<210> 3663
<211> 481
<212> DNA
<213> Homo sapiens

<400> 3663
gatcctgata cgttgctgga atggctgcag atgggacagg gagatgaaag ggacatgcag
60
ctaatagccc tggagcagct atgcatgctg cttttgatgt ctgacaatgt ggatcgctgt
120
tttgaaacat gtcctcctcg cactttctta ccagcccttt acaaaatttt tcttgatgaa
180
agtgctccag acaatgtatt agaggtgaca gcccgtgcca taacatacta cctggatgta
240
tctgcggaat gtacccgaag gattgttggg gtagatggag ctataaaagc actttgtaat
300
cgtttggtgg tagttgaact taacaacagg actagcagag acttagctga acagtgtgta
360
aaggtaagta ttacttattg gctcattact tatttttctc agacctctca gggatgagta
420
ttggctcatt taaacatcac ttagagactg aaaaatgtat ttactaaaaa aaaagtcgac
480
g
481

<210> 3664
<211> 138
<212> PRT
<213> Homo sapiens

<400> 3664
Asp Pro Asp Thr Leu Leu Glu Trp Leu Gln Met Gly Gln Gly Asp Glu
1 5 10 15
Arg Asp Met Gln Leu Ile Ala Leu Glu Gln Leu Cys Met Leu Leu Leu
20 25 30
Met Ser Asp Asn Val Asp Arg Cys Phe Glu Thr Cys Pro Pro Arg Thr
35 40 45
Phe Leu Pro Ala Leu Tyr Lys Ile Phe Leu Asp Glu Ser Ala Pro Asp
50 55 60
Asn Val Leu Glu Val Thr Ala Arg Ala Ile Thr Tyr Tyr Leu Asp Val
65 70 75 80
Ser Ala Glu Cys Thr Arg Arg Ile Val Gly Val Asp Gly Ala Ile Lys
85 90 95
Ala Leu Cys Asn Arg Leu Val Val Val Glu Leu Asn Asn Arg Thr Ser

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            100                 105                 110
Arg Asp Leu Ala Glu Gln Cys Val Lys Val Ser Ile Thr Tyr Trp Leu
        115                 120                 125
Ile Thr Tyr Phe Ser Gln Thr Ser Gln Gly
    130                 135
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<210> 3665
<211> 6633
<212> DNA
<213> Homo sapiens

<400> 3665
agggcgcgcc ctgacggact ggccgagccg gcggtgagag gccggcgcgt cgggagcggg
60
ccgcgcggca ccatgtcggc caaggtgcgg ctcaagaagc tggagcagct gctcctggac
120
gggccctggc gcaacgagag cgccctgagc gtggaaacgc tgctcgacgt gctcgtctgc
180
ctgtacaccg agtgcagcca ctcggccctg cgccgcgaca agtacgtggc cgagttcctc
240
gagtgggcta aaccatttac acagctggtg aaagaaatgc agcttcatcg agaagacttt
300
gaaataatta aagtaattgg aagaggtgct tttggtgagg ttgctgttgt caaaatgaag
360
aatactgaac gaatttatgc aatgaaaatc ctcaacaagt gggagatgct gaaaagagca
420
gagaccgcgt gcttccgaga ggagcgcgat gtgctggtga acggcgactg ccagtggatc
480
accgcgctgc actacgcctt tcaggacgag aaccacctgt acttagtcat ggattactat
540
gtgggtggtg atttactgac cctgctcagc aaatttgaag acaagcttcc ggaagatatg
600
gcgaggttct acattggtga aatggtgctg gccattgact ccatccatca gcttcattac
660
gtgcacagag acattaaacc tgacaatgtc cttttggacg tgaatggtca tatccgcctg
720
gctgactttg gatcatgttt gaagatgaat gatgatggca ctgtgcagtc ctccgtggcc
780
gtgggcacac ctgactacat ctcgccggag atcctgcagg cgatggagga cggcatgggc
840
aaatacgggc ctgagtgtga ctggtggtct ctgggtgtct gcatgtatga gatgctctat
900
ggagaaacgc cgttttatgc ggagtcactc gtggagacct atgggaagat catgaaccat
960
gaagagcgat tccagttccc atcccatgtc acggatgtat ctgaagaagc gaaggacctc
1020
atccagagac tgatctgcag tagagaacgc cggctggggc agaatggaat agaggatttc
1080
aaaaagcatg cgtttttga aggtctaaat tgggaaaata tacgaaacct agaagcacct
1140
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Val Ile Gly Arg Gly Ala Phe Gly Glu Val Ala Val Val Lys Met Lys
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cagagaataa aatgtggtgg agagaagtat caactctacc tgtcatcatt aaaagcttaa
1200
ttttcacggg aactgtggaa gctagc
1226

<210> 3670
<211> 385
<212> PRT
<213> Homo sapiens

<400> 3670
Met Ser Gly Leu Ser Met Ala Glu Val Leu Ala Arg Thr Asp Trp Thr
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Val Glu Asp Gly Leu Gln Lys Tyr Glu Arg Gly Leu Ile Phe Tyr Ile
20 25 30
Asn His Ser Leu Tyr Glu Asn Leu Asp Glu Glu Leu Asn Glu Glu Leu
35 40 45
Ala Ala Lys Val Val Gln Met Phe Tyr Val Ala Glu Pro Lys Gln Val
50 55 60
Pro His Ile Leu Cys Ser Pro Ser Met Lys Asn Ile Asn Pro Leu Thr
65 70 75 80
Ala Met Ser Tyr Leu Arg Lys Met Asp Thr Ser Gly Phe Ser Ser Ile
85 90 95
Leu Val Thr Leu Ser Lys Ala Ala Val Ala Leu Lys Met Gly Asp Leu
100 105 110
Asp Val Tyr Arg Asn Glu Met Lys Ser His Pro Glu Met Lys Leu Val
115 120 125
Cys Gly Phe Ile Leu Glu Pro Arg Leu Leu Ile Gln His Arg Lys Gly
130 135 140
Gln Ile Val Pro Thr Glu Leu Ala Thr His Leu Lys Glu Thr Gln Pro
145 150 155 160
Gly Leu Leu Val Ala Ser Val Leu Gly Leu Gln Lys Asn Ser Lys Ile
165 170 175
Gly Ile Glu Glu Ala Asp Ser Phe Phe Lys Val Leu Cys Gly Lys Asp
180 185 190
Glu Asp Thr Ile Pro Gln Leu Leu Ile Asp Phe Trp Glu Ala Gln Leu
195 200 205
Val Ala Cys Leu Pro Asp Val Val Leu Gln Glu Leu Phe Phe Lys Leu
210 215 220
Thr Ser Gln Tyr Ile Trp Arg Leu Ser Lys Arg Gln Pro Pro Asp Thr
225 230 235 240
Thr Pro Leu Arg Thr Ser Glu Asp Leu Ile Asn Ala Cys Ser His Tyr
245 250 255
Gly Leu Ile Tyr Pro Trp Val His Val Val Ile Ser Ser Asp Ser Leu

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            260                 265                 270
Ala Asp Lys Asn Tyr Thr Glu Asp Leu Ser Lys Leu Gln Ser Leu Ile
        275                 280                 285
Cys Gly Pro Ser Phe Asp Ile Ala Ser Ile Ile Pro Phe Leu Glu Pro
    290                 295                 300
Leu Ser Glu Asp Thr Ile Ala Gly Leu Ser Val His Val Leu Cys Arg
305                 310                 315                 320
Thr Arg Leu Lys Glu Tyr Glu Gln Cys Ile Asp Ile Leu Leu Glu Arg
                325                 330                 335
Cys Pro Glu Ala Val Ile Pro Tyr Ala Asn His Glu Leu Lys Glu Glu
            340                 345                 350
Asn Arg Thr Leu Trp Trp Lys Lys Leu Leu Pro Glu Leu Cys Gln Arg
        355                 360                 365
Ile Lys Cys Gly Gly Glu Lys Tyr Gln Leu Tyr Leu Ser Ser Leu Lys
    370                 375                 380
Ala
385
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<210> 3671
<211> 828
<212> DNA
<213> Homo sapiens

<400> 3671
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ccaatgaaat tatgtatctt tatttaatga aaatgcctgc tgcgtaccaa ggtatgtact
120
agggcatctg gggtaagtaa aaacaaacac atagagcctg cctggagaag ctcatggtct
180
gatggaaaga taagcaagaa gagttaattt ctaatcaata tgataaaaag gtcagagagc
240
agtttctgaa aaacatgttt ttgagttgag tcctgaaaga caaggagatg ttagtaaagc
300
agagaaggga gaattcattc tagaaagatc agacaatgtg tgggaagggc agagtctgaa
360
aagagcatgc cccatttgga gaagcatcaa gaagcccacg cgttagaagc accggcccca
420
tgagacaaag acacagctag agagattgac taggccatgt cggaatgtcc tcttatttta
480
tacatacata agcatataga tacatatagc caaagttacc tttttaatga tctttttac
540
ccagtgtatt ctggaggtcg aatggtcaca tatgaacatc tccgagaggt tgtgtttggc
600
aaaagtgaag atgagcatta tccccttgg aaatcagtca ttggagggat gatggctggt
660
gttattggcc agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa
720
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca tgcatttgca
780
aaaatcttag ctgaaggagg aatacgaggg ctttgggcag gctgggta
828

<210> 3672

<211> 124
<212> PRT
<213> Homo sapiens

<400> 3672
Met Ser Glu Cys Pro Leu Ile Leu Tyr Ile His Lys His Ile Asp Thr
1 5 10 15
Tyr Ser Gln Ser Tyr Leu Phe Asn Asp Leu Phe Tyr Pro Val Tyr Ser
20 25 30
Gly Gly Arg Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly
35 40 45
Lys Ser Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly
50 55 60
Met Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
65 70 75 80
Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly Lys
85 90 95
Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile Leu Ala
100 105 110
Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val
115 120

<210> 3673
<211> 1052
<212> DNA
<213> Homo sapiens

<400> 3673
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60
gttcattctg ggagcgctgc tggtggtcat tattatgcat gtataaagtc attcagtgat
120
gagcagtggt acagcttcaa tgatcaacat gtcagcagga taacacaaga ggacattaag
180
aaaacacatg gtggatcttc aggaagcaga ggatattatt ctagtgcttt cgcaagttcc
240
acaaatgcat atatgctgat ctatagactg aaggatccag ccagaaatgc aaaatttcta
300
gaagtggatg aatacccaga acatattaaa aacttggtgc agaaagagag agagttggaa
360
gaacaagaaa agagacaacg agaaattgag cgcaatacat gcaagataaa attattctgt
420
ttgcatccta caaaacaagt aatgatggaa aataaattgg aggttcataa ggataagaca
480
ttaaaggaag cagtagaaat ggcttataag atgatggatt tagaagaggt aataccccctg
540
gattgctgtc gccttgttaa atatgatgag tttcatgatt atctagaacg gtcatatgaa
600
ggagaagaag atacaccaat ggggcttcta ctaggtggcg tcaagtcaac atatatgttt
660
gatctgctgt tggagacgag aaagcctgat caggttttcc aatcttataa acctggaggg
720
gagccatttt acaccatttt tagttggtct gtacttagaa ttttcctgag aaaggttttt
780

ttttttattgt agcaatgaac ataatttaca ttttgtatat ggtcttacaa tgtagaataa
840
ttttgacagg ttgagaagta ctcagcacca gcttggaatt aagttctaga ttacttgcaa
900
agagttgtgt acataatttt aaaaacaaca aaaaacaaca aagcttctag cttacggtct
960
tcagtgggtt ttttcttctc cagtgggcgg tactgaatca ttctggatgc tgtcaatccc
1020
taaagttatc aattgctctc ttaggaagat ct
1052

<210> 3674
<211> 263
<212> PRT
<213> Homo sapiens

<400> 3674
Xaa Ile Ser Lys Ser Gly Leu Glu Lys Asn Ser Leu Ile Tyr Glu Leu
 1   5   10   15
Phe Ser Val Met Val His Ser Gly Ser Ala Ala Gly Gly His Tyr Tyr
            20   25   30
Ala Cys Ile Lys Ser Phe Ser Asp Glu Gln Trp Tyr Ser Phe Asn Asp
        35   40   45
Gln His Val Ser Arg Ile Thr Gln Glu Asp Ile Lys Lys Thr His Gly
    50   55   60
Gly Ser Ser Gly Ser Arg Gly Tyr Tyr Ser Ser Ala Phe Ala Ser Ser
65   70   75   80
Thr Asn Ala Tyr Met Leu Ile Tyr Arg Leu Lys Asp Pro Ala Arg Asn
                85   90   95
Ala Lys Phe Leu Glu Val Asp Glu Tyr Pro Glu His Ile Lys Asn Leu
            100   105   110
Val Gln Lys Glu Arg Glu Leu Glu Glu Gln Glu Lys Arg Gln Arg Glu
        115   120   125
Ile Glu Arg Asn Thr Cys Lys Ile Lys Leu Phe Cys Leu His Pro Thr
    130   135   140
Lys Gln Val Met Met Glu Asn Lys Leu Glu Val His Lys Asp Lys Thr
145   150   155   160
Leu Lys Glu Ala Val Glu Met Ala Tyr Lys Met Met Asp Leu Glu Glu
                165   170   175
Val Ile Pro Leu Asp Cys Cys Arg Leu Val Lys Tyr Asp Glu Phe His
            180   185   190
Asp Tyr Leu Glu Arg Ser Tyr Glu Gly Glu Glu Asp Thr Pro Met Gly
        195   200   205
Leu Leu Leu Gly Gly Val Lys Ser Thr Tyr Met Phe Asp Leu Leu Leu
    210   215   220
Glu Thr Arg Lys Pro Asp Gln Val Phe Gln Ser Tyr Lys Pro Gly Gly
225   230   235   240
Glu Pro Phe Tyr Thr Ile Phe Ser Trp Ser Val Leu Arg Ile Phe Leu
                245   250   255
Arg Lys Val Phe Phe Leu Leu
            260

<210> 3675
<211> 837

<212> DNA
<213> Homo sapiens

<400> 3675
nntccggaga tgtgaagaag gggggcgagc ggacaggaag atgaagggag caaagctgcc
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cgccgcggga caggcgtcta ggtgaacaag aaaatgaccg aagaaacaca cccagacgat
120
gacagctata ttgtgcgtgt caaggctgtg gttatgacca gagatgactc cagcggggga
180
tggttcccac aggaaggagg cgggatcagt cgcgtcgggg tctgtaaggt catgcacccc
240
gaaggcaatg gacgaagcgg ctttctcatc catggtgaac gacagaaaga caaactggtg
300
gtattggaat gctatgtaag aaaggacttg gtctacacca aagccaatcc aacgtttcat
360
cactggaagg tcgataatag gaagtttgga cttactttcc aaagccctgc tgatgcccga
420
gcctttgaca ggggagtaag gaaagcaatc gaagacctta tagaagaagt agaaaatgat
480
tctggcgggc ccagaaggct cctggcctac ccactgtcct cctgtaatca gaggcccagg
540
gtgtacagct gccactgaaa aggaaaggga tctgtgacct ctggagccct ggttcggttt
600
aggccttggt ctatgggtaa gtgagtagta ggcattgtgt tacatctgat cgtggcctgg
660
agggcccttg ggcagtcagt tctcatggtg ggcttgacta gagtccacag atgcaaacac
720
aaaaattctc cactgcagca catccaggta tcaaatcaga gggttaaaga agccatagac
780
agggccctgt gaagaaagaa atatcaagca aggcatgtta ataccaaatt cagatct
837

<210> 3676
<211> 154
<212> PRT
<213> Homo sapiens

<400> 3676
Met Thr Glu Glu Thr His Pro Asp Asp Asp Ser Tyr Ile Val Arg Val
 1   5   10   15
Lys Ala Val Val Met Thr Arg Asp Asp Ser Ser Gly Gly Trp Phe Pro
            20   25   30
Gln Glu Gly Gly Gly Ile Ser Arg Val Gly Val Cys Lys Val Met His
        35   40   45
Pro Glu Gly Asn Gly Arg Ser Gly Phe Leu Ile His Gly Glu Arg Gln
    50   55   60
Lys Asp Lys Leu Val Val Leu Glu Cys Tyr Val Arg Lys Asp Leu Val
65   70   75   80
Tyr Thr Lys Ala Asn Pro Thr Phe His His Trp Lys Val Asp Asn Arg
                85   90   95
Lys Phe Gly Leu Thr Phe Gln Ser Pro Ala Asp Ala Arg Ala Phe Asp
            100   105   110
Arg Gly Val Arg Lys Ala Ile Glu Asp Leu Ile Glu Glu Val Glu Asn

```
        115                 120                 125
Asp Ser Gly Gly Pro Arg Arg Leu Leu Ala Tyr Pro Leu Ser Ser Cys
    130                 135                 140
Asn Gln Arg Pro Arg Val Tyr Ser Cys His
145                 150
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<210> 3677
<211> 418
<212> DNA
<213> Homo sapiens

<400> 3677
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ttcatgccaa agctcgtcaa gaatctccta ggcgagatgc ctctgtgggt ctgccagagt
120
tgccgaaaga gcatggagga agatgaaagg cagacaggtc gagaacatgc agtggcgatc
180
tccttgtcac acacatcctg caaatcacag tcttgtggag atgactctca ttcgtcctcg
240
tcttcctcct catcatcctc atcctcgtcc tcctcttcct gccctgggaa ctcgggagac
300
tgggatccta gctcgttcct gtcggcacat aagctctcgg gcctctggaa ttccccacat
360
tccagtgggg ccatgccagg cagctctctt gggagtcctc ctaccatccc tggcgcgc
418

<210> 3678
<211> 139
<212> PRT
<213> Homo sapiens

<400> 3678

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Xaa Glu Glu Gly Pro Ser Gln Asn Gly Leu Val Leu Gln Gly Glu Lys
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Leu Pro Pro Asp Phe Met Pro Lys Leu Val Lys Asn Leu Leu Gly Glu
            20                  25                  30
Met Pro Leu Trp Val Cys Gln Ser Cys Arg Lys Ser Met Glu Glu Asp
        35                  40                  45
Glu Arg Gln Thr Gly Arg Glu His Ala Val Ala Ile Ser Leu Ser His
    50                  55                  60
Thr Ser Cys Lys Ser Gln Ser Cys Gly Asp Asp Ser His Ser Ser Ser
65                  70                  75                  80
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Cys Pro Gly
                85                  90                  95
Asn Ser Gly Asp Trp Asp Pro Ser Ser Phe Leu Ser Ala His Lys Leu
            100                 105                 110
Ser Gly Leu Trp Asn Ser Pro His Ser Ser Gly Ala Met Pro Gly Ser
        115                 120                 125
Ser Leu Gly Ser Pro Pro Thr Ile Pro Gly Ala
    130                 135
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<210> 3679
<211> 567

<212> DNA
<213> Homo sapiens

<400> 3679
cgcgtgaagg gctatgacct ggagttaagt atggcgctgg ggacatacta cccacctccc
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cgcctcaggc agctgctccc catgcttctt cagggaacaa gtatcttcac tgcccctaag
120
gagatcgcag agatcaaggc ccagctggag acagccctga agtggaggaa ctatgaggtg
180
aagctgcggc tgctgctgca cctggaggaa ctgcagatgg agcatgatat ccggcactat
240
gacctggagt cggtgcccat gacctgggac cctgtggacc agaaccccag gctgctcacg
300
ctggaggttc ctggagtgac tgagagccgc ccctcagtgc tacggggcga ccacctgttt
360
gccctttttgt cctcggagac acaccaggag gaccccatca catataaggg ctttgtgcac
420
aaggtggaat tggaccgtgt caagctgagc ttttccatga gcctcctgag ccgctttgtg
480
gatgggctga ccttcaaggt gaactttacc ttcaaccgcc agccgctgcg agtccagcac
540
cgtgcctggg agttgacagg gcgctgg
567

<210> 3680
<211> 189
<212> PRT
<213> Homo sapiens

<400> 3680
Arg Val Lys Gly Tyr Asp Leu Glu Leu Ser Met Ala Leu Gly Thr Tyr
 1   5   10   15
Tyr Pro Pro Pro Arg Leu Arg Gln Leu Leu Pro Met Leu Leu Gln Gly
            20   25   30
Thr Ser Ile Phe Thr Ala Pro Lys Glu Ile Ala Glu Ile Lys Ala Gln
        35   40   45
Leu Glu Thr Ala Leu Lys Trp Arg Asn Tyr Glu Val Lys Leu Arg Leu
    50   55   60
Leu Leu His Leu Glu Glu Leu Gln Met Glu His Asp Ile Arg His Tyr
65   70   75   80
Asp Leu Glu Ser Val Pro Met Thr Trp Asp Pro Val Asp Gln Asn Pro
                85   90   95
Arg Leu Leu Thr Leu Glu Val Pro Gly Val Thr Glu Ser Arg Pro Ser
            100   105   110
Val Leu Arg Gly Asp His Leu Phe Ala Leu Leu Ser Ser Glu Thr His
        115   120   125
Gln Glu Asp Pro Ile Thr Tyr Lys Gly Phe Val His Lys Val Glu Leu
    130   135   140
Asp Arg Val Lys Leu Ser Phe Ser Met Ser Leu Leu Ser Arg Phe Val
145   150   155   160
Asp Gly Leu Thr Phe Lys Val Asn Phe Thr Phe Asn Arg Gln Pro Leu
                165   170   175
Arg Val Gln His Arg Ala Trp Glu Leu Thr Gly Arg Trp

180 185

<210> 3681
<211> 788
<212> DNA
<213> Homo sapiens

<400> 3681
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60
ccccgcctcc acttccttcg gatgaggccc tgctgcactg tgtcctggaa ggaaagctcc
120
gagaccggga ggcagagctt cagcagctgc gggacagcct ggggctgagc atggagcagc
180
gcggcggagg tcgcctgcga ggccgctggc caggcctgag cctctgccac catggccatt
240
gtgcagactc tgccagtgcc actggagcct gctcctgaag ctgccactgc cccacaagct
300
ccagtcatgg gtagtgtgag cagccttatc tcaggccggc cctgtcccgg ggggccagct
360
cctccccgcc accacggccc tcctgggccc accttcttcc gccagcagga tggcctgcta
420
cggggtggct atgaggcaca ggagccgctg tgcccagctg tgccccctag gaaggctgtc
480
cctgtcacca gcttcaccta catcaatgag gacttccgga cagagtcacc ccccagccca
540
agcagtgatg ttgaggatgc ccgagagcag cgggcacaca atgcccacct ccgcggccca
600
ccaccaaagc tcatccctgt ctctggaaag ctggagaaga acatagagaa gatcctgatc
660
cgcccaacag ccttcaagcc agtgctgccc aaacctcgag gggctccgtc cctgcctagc
720
ttcatgggtc ctcgggccac cgggctgtct gggagccagg gcagcctgac gcagctgttt
780
gggggccc
788

<210> 3682
<211> 185
<212> PRT
<213> Homo sapiens

<400> 3682
Met Ala Ile Val Gln Thr Leu Pro Val Pro Leu Glu Pro Ala Pro Glu
1 5 10 15
Ala Ala Thr Ala Pro Gln Ala Pro Val Met Gly Ser Val Ser Ser Leu
20 25 30
Ile Ser Gly Arg Pro Cys Pro Gly Gly Pro Ala Pro Pro Arg His His
35 40 45
Gly Pro Pro Gly Pro Thr Phe Phe Arg Gln Gln Asp Gly Leu Leu Arg
50 55 60
Gly Gly Tyr Glu Ala Gln Glu Pro Leu Cys Pro Ala Val Pro Pro Arg
65 70 75 80
Lys Ala Val Pro Val Thr Ser Phe Thr Tyr Ile Asn Glu Asp Phe Arg

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                85                  90                  95
Thr Glu Ser Pro Pro Ser Pro Ser Ser Asp Val Glu Asp Ala Arg Glu
            100                 105                 110
Gln Arg Ala His Asn Ala His Leu Arg Gly Pro Pro Pro Lys Leu Ile
        115                 120                 125
Pro Val Ser Gly Lys Leu Glu Lys Asn Ile Glu Lys Ile Leu Ile Arg
    130                 135                 140
Pro Thr Ala Phe Lys Pro Val Leu Pro Lys Pro Arg Gly Ala Pro Ser
145                 150                 155                 160
Leu Pro Ser Phe Met Gly Pro Arg Ala Thr Gly Leu Ser Gly Ser Gln
                165                 170                 175
Gly Ser Leu Thr Gln Leu Phe Gly Gly
            180                 185
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<210> 3683
<211> 4421
<212> DNA
<213> Homo sapiens

<400> 3683
gcggccgctc gcgcgcagcc ccgcacctcc gcccctgcct ctgcctcctg ggccatgccc
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tgctgtttac atgccggtga ggtccccggc cgctccgaac ccctccgagc cccggctccc
120
cgagggtgaa gcccgccggc ccgcgaactg gactggtgga tctctcagac ctggggcccc
180
ggactccgat ctccgccgtc tccgccacca tcagggcggg atccggctct ggtgttttga
240
ggaggggtg tggtgtaggg aaaggaatcc cgtccctctc cacctttttt cgccttcggg
300
gcttcagact cagggaactc gctcatggct ttcttgatga agaagaagaa attcaaattc
360
caaactactt tcaccctgga ggagctgact gcggttccct tcgtgaacgg ggtcctcttc
420
tgcaaggtcc ggctgctgga tggaggggat tttgtcagct tgtcgtcaag ggaggaggta
480
caggagaact gtgtgcggtg gcgaaagagg ttcaccttcg tgtgtaagat gagtgctaac
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600
ggcgggaagg cttattccaa gctgggcttc gctgacttga acctggccga gtttgcgggc
660
tcgggctcca cggtgcgctg ctgcctgctc gagggatatg acacgaagaa cactcgccag
720
gacaactcca tccttaaggt caccattggt atgttcctgc tctctggaga tccctgcttc
780
aagacgccac catcgactgc caagtccatc tccatcccag gccaggattc ctccctgcag
840
ctgacgtgta agggtggtgg gaccagcagt gggggcagca gcaccaactc cctgactggg
900
tcccggcccc ccaaggctcg gcccactatt ctcagctcag ggctgccaga ggaacccgac
960
cagaacctgt ccagccctga ggaggtgttc cactctggcc actcccgcaa ctccagctat
1020

gccagccagc agtccaagat ctccggctac agcacagagc actcgcactc ctccagcctc
1080
tcagacctga cgcaccgccg caacacgtcc accagcagca gcgcctctgg gggccttggc
1140
atgaccgtgg agggccctga gggcagtgag cgggagcacc ggcccccgga gaagccgccg
1200
cggccacccc ggcccctgca tctgtccgat cgctctttca ggcggaagaa ggactcggtg
1260
gagagccacc cgacctgggt ggacgacacg cggatcgatg cggatgccat cgtggagaag
1320
atcgtgcaga gccaggactt cacagatggc agcaacaccg aggacagcaa cctccggctg
1380
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1500
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cagatcacct ctgcgccaca tctcatccat gcctcctcca tgcactccag tccacactcc
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1800
acccagccct ctggctgagg acatgcagca gctcctaaat gtagagatgc ctgtggctga
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1920
gcagcagggc cttgctccgt tgttcccttg ccctggtggt gggggggcca gaccgcctcc
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2040
cctgggggac ctgctggcgg cctcttcctg ggagccatga cctcagaccc cacccacact
2100
ccagatcgag acccctgcct ccccccggca aatgtcctcc cgctgccttg cagcctgcac
2160
tttgcacatg ctcaccccca gcacagtccc actggcccct cacctcccct tccctgagct
2220
ccttcccaag gactcctggt cactgcctgc tgtgcagtca gaggcccagg gtccagcagc
2280
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2340
gctgagaaag gtctgagcac cgaccgtgcc ctctgcccag ggctgggtcc tgagcagctg
2400
gttttcctgc aggaaggttg gagcaagcaa agtccttctc tgccctcagg gtcagctgcc
2460
cagactgggg cggatgccag agaggcaggt gggctgtggc tggactggtc cggagctggc
2520
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2580
aagggctcct ttaaggggtg tgctttccca gtggggagca gtctggccct gccccctact
2640

aaagcctctg ctctcagcac tttcccccaa gtccttgtaa cttgcttgaa ggtgggttct
2700
ggctgccagc cagtccctgg acaaactctc ctgccccttt taaatttcac tcattttgta
2760
taaacccagc aggctggtgt ttacttagcc ctgtagcttt tttcattttt tctttccgtc
2820
tttcttcttg agttcacggt tcaatattgc ctcctcgccc tggtgagggg aggtgctgct
2880
tttctgcccc acctgccggc tggttccagc agcgctgggg cccagctggg gggccgggat
2940
gggggcttct ctctctggga ggggtgcagg tgccctcccc aggctgggag ggttccttcc
3000
ctagctcccc atctgccccc gctggtgaga gttgggcttc ttggtcttgg aactccctgg
3060
cattgggaac agagcatttc cagcatttgt tgttgttgtt ttactcacct aacccttaga
3120
aaatgaatgt tagaaggtgc ctgccgaggc gggacagagt gtttgctcgc gctggagaag
3180
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3240
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3300
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3360
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3420
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3480
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3660
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3720
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3780
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3840
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4200
agcaaaagct ctgtcctcag ggccaagttc taaccactgc tctgtagacc ttctctgcaa
4260

tcaagtggcc tctaaggagc atgcctgagg acaaataact gtgcctcagt ttcctcacct
4320
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<210> 3684
<211> 384
<212> PRT
<213> Homo sapiens

<400> 3684
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Thr Leu Glu Glu Leu Thr Ala Val Pro Phe Val Asn Gly Val Leu Phe
20 25 30
Cys Lys Val Arg Leu Leu Asp Gly Gly Asp Phe Val Ser Leu Ser Ser
35 40 45
Arg Glu Glu Val Gln Glu Asn Cys Val Arg Trp Arg Lys Arg Phe Thr
50 55 60
Phe Val Cys Lys Met Ser Ala Asn Pro Ala Thr Gly Leu Leu Asp Pro
65 70 75 80
Cys Val Phe Arg Val Ser Val Arg Lys Glu Leu Lys Gly Gly Lys Ala
85 90 95
Tyr Ser Lys Leu Gly Phe Ala Asp Leu Asn Leu Ala Glu Phe Ala Gly
100 105 110
Ser Gly Ser Thr Val Arg Cys Cys Leu Leu Glu Gly Tyr Asp Thr Lys
115 120 125
Asn Thr Arg Gln Asp Asn Ser Ile Leu Lys Val Thr Ile Gly Met Phe
130 135 140
Leu Leu Ser Gly Asp Pro Cys Phe Lys Thr Pro Pro Ser Thr Ala Lys
145 150 155 160
Ser Ile Ser Ile Pro Gly Gln Asp Ser Ser Leu Gln Leu Thr Cys Lys
165 170 175
Gly Gly Gly Thr Ser Ser Gly Gly Ser Ser Thr Asn Ser Leu Thr Gly
180 185 190
Ser Arg Pro Pro Lys Ala Arg Pro Thr Ile Leu Ser Ser Gly Leu Pro
195 200 205
Glu Glu Pro Asp Gln Asn Leu Ser Ser Pro Glu Glu Val Phe His Ser
210 215 220
Gly His Ser Arg Asn Ser Ser Tyr Ala Ser Gln Gln Ser Lys Ile Ser
225 230 235 240
Gly Tyr Ser Thr Glu His Ser His Ser Ser Ser Leu Ser Asp Leu Thr
245 250 255
His Arg Arg Asn Thr Ser Thr Ser Ser Ser Ala Ser Gly Gly Leu Gly
260 265 270
Met Thr Val Glu Gly Pro Glu Gly Ser Glu Arg Glu His Arg Pro Pro
275 280 285
Glu Lys Pro Pro Arg Pro Pro Arg Pro Leu His Leu Ser Asp Arg Ser
290 295 300
Phe Arg Arg Lys Lys Asp Ser Val Glu Ser His Pro Thr Trp Val Asp
305 310 315 320
Asp Thr Arg Ile Asp Ala Asp Ala Ile Val Glu Lys Ile Val Gln Ser

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                325                 330                 335
Gln Asp Phe Thr Asp Gly Ser Asn Thr Glu Asp Ser Asn Leu Arg Leu
            340                 345                 350
Phe Val Ser Arg Asp Gly Ser Ala Thr Leu Ser Gly Ile Gln Leu Ala
        355                 360                 365
Thr Arg Val Ser Ser Gly Val Tyr Glu Pro Val Val Ile Glu Ser His
    370                 375                 380
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<210> 3685
<211> 1293
<212> DNA
<213> Homo sapiens

<400> 3685
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120
gtgccgtggt ctggtgggcc ccctcctgct cctctgtggc tctccccgcc gccattctga
180
tactggcgtc cccaatctcc ttgagaaacc attttctcta ctctgatgtc ttttcagaag
240
tcacatcctg ttctggggat gcacccctgc tcctccagcc ccacccaaac tgacttaaca
300
cccaccaccc ttcccaggtc agcccaaatg ccacttcccc caggaagctc tccctgatgc
360
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420
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480
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540
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600
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660
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720
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780
gacagtgggg aaggggcctg gctgacatct cgccacccgg tcagcctgta tcctccttcc
840
cccatctttc tgtgatcata aaggatccct tgagccactt gattttcaca ctgtcaatga
900
cctagagtca ccaaacacct ctcaacaagc cgtggtctcc acttgacatc tggaacaacg
960
ctcctcgggt ctgggaggac cacgcgtcga aagggaagag cagaggacgc tggctctcat
1020
ggcaggatgg tgtgtgtacg ggacgcgtct ttcgggagga tgacggcggc cttggagagc
1080
cccagaatgt cacaagcgtc catgaattcc ttcagactct ggaagctcga aacattctgc
1140
ctatctgagg ttgagatcag gatcacatca gagactccag ctctggccat tttagggtct
1200

gcaccctgac ccccatccct accccaggag ctgctgaaat gtcctcagag cttaggcgtg
1260
aagcaggggt tggtcagggg aggacagcgg ccg
1293

<210> 3686
<211> 111
<212> PRT
<213> Homo sapiens

<400> 3686
Met Gly Glu Gly Gly Tyr Arg Leu Thr Gly Trp Arg Asp Val Ser Gln
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Ala Pro Ser Pro Leu Ser Ser Gly Ala His Cys Arg Leu Leu Leu Phe
20 25 30
Pro Val Cys Cys Glu Thr Asp His Arg Pro Ala Gln Arg Ser Pro Arg
35 40 45
Arg Val Pro Cys Leu Cys Pro Pro Arg Arg Arg His Pro Pro Arg Ser
50 55 60
Phe Thr Ser Cys Thr Phe Ser Gly Ser Arg Ser His Ile His Pro Thr
65 70 75 80
Trp Arg Ser Pro His Asp Val Pro Gly Ser Val Leu Ala Pro Ala Ala
85 90 95
Ala Leu Gly Asn Arg Ile Gly Lys Arg Ser Pro Arg Val Asp Ala
100 105 110

<210> 3687
<211> 566
<212> DNA
<213> Homo sapiens

<400> 3687
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gtggccatgg tggaggtgca gctggagagt gaccacgagt acccaccagg cctgctggtg
120
gctgtgcacc tctttgcact catgngtctc cacgtgtctg ctgccccaca ttgaagctgt
180
nngagcaaca tccacaacct caactctgtc caccagtcgc cacaccagag actgcaccgc
240
tacgtggagc tggcctgggg cttctccact gccctgggca cctttctctt ccttgctgaa
300
gttgtcctgg ttggttgggt caagtttgtg cccattgggg ctcccttgga cacaccgacc
360
cccatggtgc ccacatcccg ggtgcccggg actctggcac cagtggctac ctcccttagt
420
ccagcttcca atctcccacg gtcctctgcg tctgcagcac cgtcccaggc tgagccagcc
480
tgcccacccc ggcaagcctg tggtggtggt ggggcccatg ggccaggctg gcaagcagcc
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atggcctcca cagccatcat ggtacc
566

<210> 3688

<211> 57
<212> PRT
<213> Homo sapiens

<400> 3688
Xaa Gly Ala Lys Leu Lys Ala Ser Ser Arg Thr Ser Ala Leu Leu Ser
1 5 10 15
Gly Phe Ala Met Val Ala Met Val Glu Val Gln Leu Glu Ser Asp His
20 25 30
Glu Tyr Pro Pro Gly Leu Leu Val Ala Val His Leu Phe Ala Leu Met
35 40 45
Xaa Leu His Val Ser Ala Ala Pro His
50 55

<210> 3689
<211> 1562
<212> DNA
<213> Homo sapiens

<400> 3689
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atggagacca agacgatcgt gtacgacttg gacacatcag gggggctgat ggagcaaatc
120
caagctctgc tggctccccc caagacggac gaggcagaaa agcgcagtcg gaagcctgag
180
aaggagcccc ggagaagcgg cagggccacc aaccacgaca gctgcgatag ctgcaaggaa
240
ggtggagatc tcctgtgctg cgaccactgc ccggctgcct tccacctcca gtgctgtaac
300
cctccactga gtgaagaaat gttgcctcct ggagagtgga tgtgtcaccg gtgcactgtt
360
cgccgaaaga aacgagagca gaaaaaggag ctgggtcatg tcaatggact ggtggacaaa
420
tctggcaaac ggactacatc ccccagcagt gacactgact tgttggacag atcggccagc
480
aaaactgaac taaaggccat tgcccatgcc cggatcctgg aaaggagagc cagcaggcct
540
ggcacaccca catccagcgc cagcacagag actcccacct ctgagcagaa tgatgtcgac
600
gaagacatca ttgacgtgga tgaggaacca gtagcagcgg agccagacta tgtgcagccc
660
cagctgaggc ggccctttga gctgctgatt gctgccgcca tggagcggaa ccccacccaa
720
tttcagttgc ccaatgaact gacttgtacc actgcactac caggttctag caagaggaga
780
agaaaggagg aaaccacagg gaaaaatgtt aagaagacac agcatgaatt agatcacaat
840
ggtctcgttc ccttacccgt caaagtctgc ttcacgtgta acaggagttg ccgtgtggct
900
cctctcatcc agtgtgacta ttgccctctc ctgtttcaca tggattgcct cgagccgccg
960
ctcactgcca tgcccctggg cagatggatg tgtccgaatc acatcgaaca tgtggtgctg
1020

aaccagaaga atatgacact gagcaatcgg tgccaggtgt ttgatcgttt ccaggacacc
1080
gtttcgcagc atgtcgtcaa agtggacttc ctgaaccgaa tccacaagaa gcacccccct
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aaccggcgtg tgctccagtc ggtcaaaaga agaagcttga aggttcctga tgctataaaa
1200
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1260
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1320
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1380
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1440
gatattaagc ctgttattgt gactgacagc tcagtcacca cctccctgca aacagctgac
1500
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1560
tc
1562

<210> 3690
<211> 504
<212> PRT
<213> Homo sapiens

<400> 3690
Met Trp Glu Lys Met Glu Thr Lys Thr Ile Val Tyr Asp Leu Asp Thr
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20 25 30
Thr Asp Glu Ala Glu Lys Arg Ser Arg Lys Pro Glu Lys Glu Pro Arg
35 40 45
Arg Ser Gly Arg Ala Thr Asn His Asp Ser Cys Asp Ser Cys Lys Glu
50 55 60
Gly Gly Asp Leu Leu Cys Cys Asp His Cys Pro Ala Ala Phe His Leu
65 70 75 80
Gln Cys Cys Asn Pro Pro Leu Ser Glu Glu Met Leu Pro Pro Gly Glu
85 90 95
Trp Met Cys His Arg Cys Thr Val Arg Arg Lys Lys Arg Glu Gln Lys
100 105 110
Lys Glu Leu Gly His Val Asn Gly Leu Val Asp Lys Ser Gly Lys Arg
115 120 125
Thr Thr Ser Pro Ser Ser Asp Thr Asp Leu Leu Asp Arg Ser Ala Ser
130 135 140
Lys Thr Glu Leu Lys Ala Ile Ala His Ala Arg Ile Leu Glu Arg Arg
145 150 155 160
Ala Ser Arg Pro Gly Thr Pro Thr Ser Ser Ala Ser Thr Glu Thr Pro
165 170 175
Thr Ser Glu Gln Asn Asp Val Asp Glu Asp Ile Ile Asp Val Asp Glu
180 185 190
Glu Pro Val Ala Ala Glu Pro Asp Tyr Val Gln Pro Gln Leu Arg Arg
195 200 205
Pro Phe Glu Leu Leu Ile Ala Ala Ala Met Glu Arg Asn Pro Thr Gln

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    210                 215                 220
Phe Gln Leu Pro Asn Glu Leu Thr Cys Thr Thr Ala Leu Pro Gly Ser
225                 230                 235                 240
Ser Lys Arg Arg Arg Lys Glu Glu Thr Thr Gly Lys Asn Val Lys Lys
                245                 250                 255
Thr Gln His Glu Leu Asp His Asn Gly Leu Val Pro Leu Pro Val Lys
            260                 265                 270
Val Cys Phe Thr Cys Asn Arg Ser Cys Arg Val Ala Pro Leu Ile Gln
        275                 280                 285
Cys Asp Tyr Cys Pro Leu Leu Phe His Met Asp Cys Leu Glu Pro Pro
    290                 295                 300
Leu Thr Ala Met Pro Leu Gly Arg Trp Met Cys Pro Asn His Ile Glu
305                 310                 315                 320
His Val Val Leu Asn Gln Lys Asn Met Thr Leu Ser Asn Arg Cys Gln
                325                 330                 335
Val Phe Asp Arg Phe Gln Asp Thr Val Ser Gln His Val Val Lys Val
            340                 345                 350
Asp Phe Leu Asn Arg Ile His Lys Lys His Pro Pro Asn Arg Arg Val
        355                 360                 365
Leu Gln Ser Val Lys Arg Arg Ser Leu Lys Val Pro Asp Ala Ile Lys
    370                 375                 380
Ser Gln Tyr Gln Phe Pro Pro Pro Leu Ile Ala Pro Ala Ala Ile Arg
385                 390                 395                 400
Asp Gly Glu Leu Ile Cys Asn Gly Ile Pro Glu Glu Ser Gln Met His
                405                 410                 415
Leu Leu Asn Ser Glu His Leu Ala Thr Gln Ala Glu Gln Gln Glu Trp
            420                 425                 430
Leu Cys Ser Val Val Ala Leu Gln Cys Ser Ile Leu Lys His Leu Ser
        435                 440                 445
Ala Lys Gln Met Pro Ser His Trp Asp Ser Glu Gln Thr Glu Lys Ala
    450                 455                 460
Asp Ile Lys Pro Val Ile Val Thr Asp Ser Ser Val Thr Thr Ser Leu
465                 470                 475                 480
Gln Thr Ala Asp Lys Thr Pro Thr Pro Ser His Tyr Pro Leu Ser Cys
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Pro Ser Gly Ile Ser Thr Gln Asn
            500
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<210> 3691
<211> 418
<212> DNA
<213> Homo sapiens

<400> 3691
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120
cagcctttct acgtcttaag gcagagaata gccaggataa ggtgccagct caaagctgtg
180
tgccaaccac gatgcaaaca tggtgaatgt atcgggccaa acaagtgcaa gtgtcatcct
240
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300

gaagacacct ctatcactcc caaattaaaa atattcttat ctcaaactac tttccatggc
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418

<210> 3692
<211> 94
<212> PRT
<213> Homo sapiens

<400> 3692
Xaa Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val Ser Ser
1 5 10 15
Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp
20 25 30
Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Phe Tyr Val Leu Arg Gln
35 40 45
Arg Ile Ala Arg Ile Arg Cys Gln Leu Lys Ala Val Cys Gln Pro Arg
50 55 60
Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro
65 70 75 80
Gly Tyr Ala Gly Lys Thr Cys Asn Gln Gly Arg Lys Thr Val
85 90

<210> 3693
<211> 2641
<212> DNA
<213> Homo sapiens

<400> 3693
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120
gcttccggcc gggctgtgcc ccgcgcggtc ttcgccggga tgaagcgccc ctgcgaggag
180
acgacctccg agagcgacat ggacgagacc atcgacgtgg ggagcgagaa caattactcg
240
gggcaaagta ctagctctgt gattagattg aattctccaa caacaacatc tcagattatg
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360
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gaaaaagctg aaatattgca aatgacagtg gatcatttga agatgcttca ggcaacaggg
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660
gccatgacat cctccatggc ccaccacnca tcatccgctc cacccgcatc actgggccgc
720

cgccttccac cacctgcccg cagccctgct ccagcccaac ggcctccatg cctcagagtc
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840
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900
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1080
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1320
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1980
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2280
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2340

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2460
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2520
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2640
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2641

<210> 3694
<211> 390
<212> PRT
<213> Homo sapiens

<400> 3694
Arg Pro Arg Arg Arg Glu Arg Ala Ala Arg Ala Asp Arg Ala Ala Ala
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Gly Ala Ala Pro Ala Gln Ala Arg Gly Gly Arg Arg Arg Ala Ser Gly
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Cys Cys Ala Pro Leu Gly Val Arg Ala Ser Gly Arg Ala Val Pro Arg
35 40 45
Ala Val Phe Ala Gly Met Lys Arg Pro Cys Glu Glu Thr Thr Ser Glu
50 55 60
Ser Asp Met Asp Glu Thr Ile Asp Val Gly Ser Glu Asn Asn Tyr Ser
65 70 75 80
Gly Gln Ser Thr Ser Ser Val Ile Arg Leu Asn Ser Pro Thr Thr Thr
85 90 95
Ser Gln Ile Met Ala Arg Lys Lys Arg Arg Gly Ile Ile Glu Lys Arg
100 105 110
Arg Arg Asp Arg Ile Asn Asn Ser Leu Ser Glu Leu Arg Arg Leu Val
115 120 125
Pro Thr Ala Phe Glu Lys Gln Gly Ser Ala Lys Leu Glu Lys Ala Glu
130 135 140
Ile Leu Gln Met Thr Val Asp His Leu Lys Met Leu Gln Ala Thr Gly
145 150 155 160
Gly Lys Gly Tyr Phe Asp Ala His Ala Leu Ala Met Asp Phe Met Ser
165 170 175
Ile Gly Phe Arg Glu Cys Leu Thr Glu Val Ala Arg Tyr Leu Ser Ser
180 185 190
Val Glu Gly Leu Asp Ser Ser Asp Pro Leu Arg Val Arg Leu Val Ser
195 200 205
His Leu Ser Thr Cys Ala Thr Gln Arg Glu Ala Ala Ala Met Thr Ser
210 215 220
Ser Met Ala His His Xaa Ser Ser Ala Pro Pro Ala Ser Leu Gly Arg
225 230 235 240
Arg Leu Pro Pro Pro Ala Arg Ser Pro Ala Pro Ala Gln Arg Pro Pro
245 250 255
Cys Leu Arg Val Asn Pro Leu Ser Pro Leu His Asn Phe Arg Ser Ala
260 265 270
Ser Ala His Gly Ser Ala Leu Leu Thr Ala Thr Phe Ala His Ala Asp

275 280 285
Ser Ala Leu Arg Met Pro Ser Thr Gly Ser Val Ala Pro Cys Val Pro
290 295 300
Pro Leu Ser Thr Ser Leu Leu Ser Leu Ser Ala Thr Val His Ala Ala
305 310 315 320
Ala Ala Ala Ala Thr Ala Ala Ala His Ser Phe Pro Leu Ser Phe Ala
325 330 335
Gly Ala Phe Pro Met Leu Pro Pro Asn Ala Ala Ala Ala Val Ala Ala
340 345 350
Ala Thr Ala Ile Ser Pro Pro Leu Ser Val Ser Ala Thr Ser Ser Pro
355 360 365
Gln Gln Thr Ser Ser Gly Thr Asn Asn Lys Pro Tyr Arg Pro Trp Gly
370 375 380
Thr Glu Val Gly Ala Phe
385 390

<210> 3695
<211> 1615
<212> DNA
<213> Homo sapiens

<400> 3695
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aattgctgct cagtgatgtg tgtgtgcctg ccgctggtgg agctgagact gctcatctca
120
gaaggatggg gatgcttgat ttcctggcca ggttgtccca gcacagtggg gattggccct
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240
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480
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720
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900
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960

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1440
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1615

<210> 3696
<211> 146
<212> PRT
<213> Homo sapiens

<400> 3696
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Gly Cys Gly Gln Tyr Ile Ser Tyr Arg Cys Gln Glu Lys Arg Asn Thr
            20   25   30
Tyr Phe Ala Glu Tyr Trp Tyr Gln Ala Gln Cys Cys Gln Tyr Asp Tyr
        35   40   45
Cys Asn Ser Trp Ser Ser Pro Gln Leu Gln Ser Ser Leu Pro Glu Pro
    50   55   60
His Asp Arg Pro Leu Ala Leu Pro Leu Ser Asp Ser Gln Ile Gln Trp
65   70   75   80
Phe Tyr Gln Ala Leu Asn Leu Ser Leu Pro Leu Pro Asn Phe His Ala
                85   90   95
Gly Thr Glu Pro Asp Gly Leu Asp Pro Met Val Thr Leu Ser Leu Asn
            100   105   110
Leu Gly Leu Ser Phe Ala Glu Leu Arg Arg Met Tyr Leu Phe Leu Asn
        115   120   125
Ser Ser Gly Leu Leu Val Leu Pro Gln Ala Gly Leu Leu Thr Pro His
    130   135   140
Pro Ser
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<210> 3697
<211> 550
<212> DNA
<213> Homo sapiens

<400> 3697
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120
cagcctgtgt gccaaccacg atgcaaacat ggtgagtgta tcgggccaaa caagtgcaag
180
tgtcatcctg gttatgctgg aaaaacctgt aatcaagatc taaatgagtg tggcctgaag
240
ccccggccct gtaagcacag gtgcatgaac acttacggca gctacaagtg ctactgtctc
300
aacggatata tgctcatgcc ggatggttcc tgctcaagtg ccctgacctg ctccatggca
360
aactgtcagt atggctgtga tgttgttaaa ggacaaatac ggtgccagtg cccatcccct
420
ggcctgcagc tggctcctga tgggaggacc tgtgtagatg ttgatgaatg tgctacagga
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540
tgtcataaag
550

<210> 3698
<211> 183
<212> PRT
<213> Homo sapiens

<400> 3698
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Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp
20 25 30
Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys Gln Pro Arg Cys
35 40 45
Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro Gly
50 55 60
Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu Asn Glu Cys Gly Leu Lys
65 70 75 80
Pro Arg Pro Cys Lys His Arg Cys Met Asn Thr Tyr Gly Ser Tyr Lys
85 90 95
Cys Tyr Cys Leu Asn Gly Tyr Met Leu Met Pro Asp Gly Ser Cys Ser
100 105 110
Ser Ala Leu Thr Cys Ser Met Ala Asn Cys Gln Tyr Gly Cys Asp Val
115 120 125
Val Lys Gly Gln Ile Arg Cys Gln Cys Pro Ser Pro Gly Leu Gln Leu
130 135 140
Ala Pro Asp Gly Arg Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly
145 150 155 160
Arg Ala Ser Cys Pro Lys Phe Arg Gln Cys Val Asn Thr Phe Gly Ser
165 170 175
Tyr Ile Cys Lys Cys His Lys
180

<210> 3699
<211> 510
<212> DNA
<213> Homo sapiens

<400> 3699
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120
tggcccttga tggaggggag ccgacctcgc agcagcctga gcctggccag cagcgcctcc
180
accatctcct cgctcagcag cctgagcccc aagaagccca cccgggcagt aaacaaggtc
240
cacgcctttg ggaagagagg caatgcgctc aggagggatc ccaaccttcc cgtgcacatc
300
cgaggctggc ttcataagca ggacagctcg gggctccgtc tctggaaacg ccgctggttc
360
gtcctctccg gccattgcct cttttattac aaggacagcc gcgaggagag tgtcctaggc
420
agcgtcctgc tccccagcta caatattaga ccagatgggc cgggagcccc ccgagggcgg
480
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510

<210> 3700
<211> 127
<212> PRT
<213> Homo sapiens

<400> 3700
Met Glu Gly Ser Arg Pro Arg Ser Ser Leu Ser Leu Ala Ser Ser Ala
 1   5   10   15
Ser Thr Ile Ser Ser Leu Ser Ser Leu Ser Pro Lys Lys Pro Thr Arg
            20   25   30
Ala Val Asn Lys Val His Ala Phe Gly Lys Arg Gly Asn Ala Leu Arg
        35   40   45
Arg Asp Pro Asn Leu Pro Val His Ile Arg Gly Trp Leu His Lys Gln
    50   55   60
Asp Ser Ser Gly Leu Arg Leu Trp Lys Arg Arg Trp Phe Val Leu Ser
65   70   75   80
Gly His Cys Leu Phe Tyr Tyr Lys Asp Ser Arg Glu Glu Ser Val Leu
                85   90   95
Gly Ser Val Leu Leu Pro Ser Tyr Asn Ile Arg Pro Asp Gly Pro Gly
            100   105   110
Ala Pro Arg Gly Arg Arg Phe Thr Phe Thr Ala Glu His Pro Gly
        115   120   125

<210> 3701
<211> 733
<212> DNA
<213> Homo sapiens

<400> 3701

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120
agtaatttga aggagcacaa aaagacacac acggctgata aagtcttcac ctgtgatgag
180
tgtggaaagt cttttaatat gcaaaggaag ttagtaaagc acagaattcg gcacacgggg
240
gagcggcctt acagctgctc tgcctgcggg aaatgttttg ggggatcagg tgacctccgc
300
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360
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420
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480
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600
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720
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733

<210> 3702
<211> 236
<212> PRT
<213> Homo sapiens

<400> 3702
Val Cys Ser Leu Trp Ser Val Gln Arg His Ile Ile Ile His Ser Gly
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Glu Lys Pro His Leu Cys Asp Ile Cys Gly Arg Gly Phe Ser Asn Phe
20 25 30
Ser Asn Leu Lys Glu His Lys Lys Thr His Thr Ala Asp Lys Val Phe
35 40 45
Thr Cys Asp Glu Cys Gly Lys Ser Phe Asn Met Gln Arg Lys Leu Val
50 55 60
Lys His Arg Ile Arg His Thr Gly Glu Arg Pro Tyr Ser Cys Ser Ala
65 70 75 80
Cys Gly Lys Cys Phe Gly Gly Ser Gly Asp Leu Arg Arg His Val Arg
85 90 95
Thr His Thr Gly Glu Lys Pro Tyr Thr Cys Glu Ile Cys Asn Lys Cys
100 105 110
Phe Thr Arg Ser Ala Val Leu Arg Arg His Lys Lys Met His Cys Lys
115 120 125
Ala Gly Asp Glu Ser Pro Asp Val Leu Glu Glu Leu Ser Gln Ala Ile
130 135 140
Glu Thr Ser Asp Leu Glu Lys Ser Gln Ser Ser Asp Ser Phe Ser Gln
145 150 155 160
Asp Thr Ser Val Thr Leu Met Pro Val Ser Val Lys Leu Pro Val His

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                165                 170                 175
Pro Val Glu Asn Ser Val Ala Glu Phe Asp Ser His Ser Gly Gly Ser
            180                 185                 190
Tyr Cys Lys Leu Arg Ser Met Ile Gln Pro His Gly Val Ser Asp Gln
        195                 200                 205
Glu Lys Leu Ser Leu Asp Pro Gly Lys Leu Ala Lys Pro Gln Ile His
    210                 215                 220
His Thr Gln Pro His Ala Tyr Ser Tyr Ser Asp Phe
225                 230                 235
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<210> 3703
<211> 3294
<212> DNA
<213> Homo sapiens

<400> 3703
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120
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240
cacctcctga agtccagctg tgcccctagt gtccagatga agatcaaaga gctttaccga
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420
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720
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960
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1140

tgcgcccacc tgcagagctt cgatgctgcc ctttatctac agatgaatga gaagaagcct
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2760

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3294

<210> 3704
<211> 619
<212> PRT
<213> Homo sapiens

<400> 3704
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Ala Gly Arg Asn Lys Ser Gly Arg Lys His Glu Leu Leu Ala Lys Ala
20 25 30
Leu His Leu Leu Lys Ser Ser Cys Ala Pro Ser Val Gln Met Lys Ile
35 40 45
Lys Glu Leu Tyr Arg Arg Arg Phe Pro Arg Lys Thr Leu Gly Pro Ser
50 55 60
Asp Leu Ser Leu Leu Ser Leu Pro Pro Gly Thr Ser Pro Val Gly Ser
65 70 75 80
Pro Gly Pro Leu Ala Pro Ile Pro Pro Thr Leu Leu Ala Pro Gly Thr
85 90 95
Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro Leu Pro Gln
100 105 110
Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe Tyr Glu Val
115 120 125
Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr Ser Ser Gln
130 135 140
Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro Gln Gln Val
145 150 155 160
Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala Lys Cys Asp
165 170 175
Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu Thr Ser Cys
180 185 190
Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys Val Asn Gly
195 200 205
Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys Asn Gly Ala
210 215 220
Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro Leu Ala Arg

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225                 230                 235                 240
Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp Ser Ser Glu
                245                 250                 255
Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg Gln Leu Thr
            260                 265                 270
Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile Arg Asn Pro
        275                 280                 285
Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala Asp Pro Asp
    290                 295                 300
Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met Cys Pro Leu
305                 310                 315                 320
Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr Cys Ala His
                325                 330                 335
Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn Glu Lys Lys
            340                 345                 350
Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro Tyr Glu Ser
        355                 360                 365
Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Ser Ser Cys Ser Asp
    370                 375                 380
Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys Pro Met Lys
385                 390                 395                 400
Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Pro Gly Tyr Gly Leu
                405                 410                 415
Asp Gly Leu Gln Tyr Ser Pro Val Gln Gly Gly Asp Pro Ser Glu Asn
            420                 425                 430
Lys Lys Lys Val Glu Val Ile Asp Leu Thr Ile Glu Ser Ser Ser Asp
        435                 440                 445
Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Ser Val Thr Ser Ala
    450                 455                 460
Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Val Leu Thr Ser Gly His
465                 470                 475                 480
Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr Leu Gly Gly
                485                 490                 495
Asp Phe Leu Ser Ser Leu Pro Leu His Glu Tyr Pro Pro Ala Phe Pro
            500                 505                 510
Leu Gly Ala Asp Ile Gln Gly Leu Asp Leu Phe Ser Phe Leu Gln Thr
        515                 520                 525
Glu Ser Gln His Tyr Gly Pro Ser Val Ile Thr Ser Leu Asp Glu Gln
    530                 535                 540
Asp Ala Leu Gly His Phe Phe Gln Tyr Arg Gly Thr Pro Ser His Phe
545                 550                 555                 560
Leu Gly Pro Leu Ala Pro Thr Leu Gly Ser Ser His Cys Ser Ala Thr
                565                 570                 575
Pro Ala Pro Pro Pro Gly Arg Val Ser Ser Ile Val Ala Pro Gly Gly
            580                 585                 590
Ala Leu Arg Glu Gly His Gly Gly Pro Leu Pro Ser Gly Pro Ser Leu
        595                 600                 605
Thr Gly Cys Arg Ser Asp Ile Ile Ser Leu Asp
    610                 615
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<210> 3705
<211> 1737
<212> DNA
<213> Homo sapiens

<400> 3705
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120
tggtgtctgg cctggacggg gtgtggtcat cagcatggct gaaagaccag gcgggtcccg
180
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240
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300
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360
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420
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480
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720
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840
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960
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1020
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1080
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1140
cagacagcat atccgtgtgt gtgtgtgtgt nccaggcagc acatctgcgc atgggtgtgc
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1320
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1560

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<210> 3706
<211> 191
<212> PRT
<213> Homo sapiens

<400> 3706
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Pro Thr Ala Val Gly Asp Ser Trp Ala Pro Lys Ala Gly Gly Lys Asn
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Ser Arg Gln Gly Gln Gly Thr Glu Ala Gly Met Glu Ala Gly Thr Glu
35 40 45
Ala Gly Thr Glu Ala Gly Arg Val Gly Gly Val Thr Val Glu Gln Gly
50 55 60
Lys Ser Leu Ile Asn Tyr Glu Pro His Gly Thr Arg Thr Ala Gly Phe
65 70 75 80
Thr Ala His Pro Pro Lys Ser Thr Ser Val Cys Val Cys Xaa Arg Gln
85 90 95
His Ile Cys Thr Cys Val Cys Met Cys Val Arg Lys Cys Val Pro Arg
100 105 110
Gln His Ile Cys Met Cys Ala Cys Val Cys Ile Arg Thr Ala Ile Cys
115 120 125
Thr Cys Val His Val Gln Thr Ala Tyr Leu Cys Thr Cys Val Cys Pro
130 135 140
Gly Asn Ile Cys Thr Cys Val Ser Val Glu Ala Ala Leu Ser Val Cys
145 150 155 160
Val Ser Arg Ser Ile Ser Ala Cys Val Cys Val Ser Xaa Thr Ala Tyr
165 170 175
Leu Cys Met Arg Val Cys Val Arg Thr Ala Val Cys Val Cys Val
180 185 190

<210> 3707
<211> 585
<212> DNA
<213> Homo sapiens

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240
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480
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<210> 3708
<211> 106
<212> PRT
<213> Homo sapiens

<400> 3708
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Glu Asn Ala Phe Asp Asn Ile Gln Leu Pro Tyr Met Ile Lys Thr Leu
35 40 45
Lys Lys Leu Gly Ile Glu Gly Met Tyr Leu Asn Val Ile Lys Ala Val
50 55 60
Tyr Asp Arg Pro Xaa Val Ser Ile Ile Leu Asn Gly Glu Asn Leu Gln
65 70 75 80
Glu Leu Gln Thr Phe Gly Leu Arg Ser Gly Thr Gln Gln Gly Cys Pro
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Leu Ser Pro Gln Leu Leu Asn Ile Val Leu
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<210> 3709
<211> 3768
<212> DNA
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gcagtgcttt ttgcccgttg cctagacgat cacttggttt ctctgaggat gtctggttct
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420
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480

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720
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1320
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2100

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2820
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3768

<210> 3710
<211> 70
<212> PRT
<213> Homo sapiens

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            20   25   30
Cys Asp Val Ile Leu Val Ala Gly Asp Arg Arg Ile Pro Ala His Arg
        35   40   45
Leu Val Leu Ser Ser Val Ser Asp Tyr Phe Ala Ala Met Phe Thr Asn
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Asp Val Arg Glu Ala Arg
65   70

<210> 3711
<211> 1366
<212> DNA
<213> Homo sapiens

<400> 3711
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240
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1260
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1366

<210> 3712
<211> 368
<212> PRT
<213> Homo sapiens

<400> 3712
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Leu Gly Arg Gly Phe Asn Thr Gly Val Ile Leu Leu Arg Leu Asp Arg
35 40 45
Leu Arg Gln Ala Gly Trp Glu Gln Met Trp Arg Leu Thr Ala Arg Arg
50 55 60
Glu Leu Leu Ser Leu Pro Ala Ala Ser Leu Ala Asp Gln Asp Ile Phe
65 70 75 80
Asn Ala Val Ile Lys Glu His Pro Gly Leu Val Gln Arg Leu Pro Cys
85 90 95
Val Trp Asn Val Gln Leu Ser Asp His Thr Leu Ala Glu Arg Cys Tyr
100 105 110
Ser Glu Ala Ser Asp Leu Lys Val Ile His Trp Asn Ser Pro Lys Lys
115 120 125
Leu Arg Val Lys Asn Lys His Val Glu Phe Phe Arg Asn Phe Tyr Leu
130 135 140
Thr Phe Leu Glu Tyr Asp Gly Asn Leu Leu Arg Arg Glu Leu Phe Val
145 150 155 160
Cys Pro Ser Gln Pro Pro Pro Gly Ala Glu Gln Leu Gln Gln Ala Leu
165 170 175
Ala Gln Leu Asp Glu Glu Asp Pro Cys Phe Glu Phe Arg Gln Gln Gln
180 185 190
Leu Thr Val His Arg Val His Val Thr Phe Leu Pro His Glu Pro Pro
195 200 205
Pro Pro Arg Pro His Asp Val Thr Leu Val Ala Gln Leu Ser Met Asp
210 215 220
Arg Leu Gln Met Leu Glu Ala Leu Cys Arg His Trp Pro Gly Pro Met

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225                 230                 235                 240
Ser Leu Ala Leu Tyr Leu Thr Asp Ala Glu Ala Gln Gln Phe Leu His
                245                 250                 255
Phe Val Glu Ala Ser Pro Val Leu Ala Ala Arg Gln Asp Val Ala Tyr
            260                 265                 270
His Val Val Tyr Arg Glu Gly Pro Leu Tyr Pro Val Asn Gln Leu Arg
        275                 280                 285
Asn Val Ala Leu Ala Gln Ala Leu Thr Pro Tyr Val Phe Leu Ser Asp
    290                 295                 300
Ile Asp Phe Leu Pro Ala Tyr Ser Leu Tyr Asp Tyr Leu Arg Ala Ser
305                 310                 315                 320
Ile Glu Gln Leu Gly Leu Gly Ser Arg Arg Lys Ala Ala Leu Val Val
                325                 330                 335
Pro Ala Phe Glu Thr Leu Arg Tyr Arg Phe Ser Phe Pro His Ser Lys
            340                 345                 350
Val Glu Leu Leu Ala Leu Leu Asp Ala Gly Thr Leu Tyr Thr Phe Arg
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<210> 3713
<211> 1719
<212> DNA
<213> Homo sapiens

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180
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240
gagagtccgc ctgccatgga ctcggaatat tacagcggcg accagtcaga tgatggtggt
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780
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900

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1080
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<210> 3714
<211> 488
<212> PRT
<213> Homo sapiens

<400> 3714
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20 25 30
Val Asn Glu Gln His Ser Gly Ser Asp Thr Gly Ser Val Glu Arg His
35 40 45
Ser Glu Asn Glu Thr Ser Asp Arg Glu Asp Gly Pro Pro Lys Gly His
50 55 60
His Val Thr Asp Ser Glu Asn Asp Glu Pro Leu Asn Leu Asn Ala Ser
65 70 75 80
Asp Ser Glu Ser Glu Glu Leu His Arg Gln Lys Asp Ser Asp Ser Glu
85 90 95
Ser Glu Glu Arg Ala Glu Pro Pro Ala Ser Asp Ser Glu Asn Glu Asp
100 105 110
Val Asn Gln His Gly Ser Asp Ser Glu Ser Glu Glu Thr Arg Lys Leu
115 120 125
Pro Gly Ser Asp Ser Glu Asn Glu Glu Leu Leu Asn Gly His Ala Ser
130 135 140
Asp Ser Glu Asn Glu Asp Val Gly Lys His Pro Ala Ser Asp Ser Glu

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145                 150                 155                 160
Ile Glu Glu Leu Gln Lys Ser Pro Ala Ser Asp Ser Glu Thr Glu Asp
                165                 170                 175
Ala Leu Lys Pro Gln Ile Ser Asp Ser Glu Ser Glu Glu Pro Pro Arg
            180                 185                 190
His Gln Ala Ser Asp Ser Glu Asn Glu Glu Pro Pro Lys Pro Arg Met
        195                 200                 205
Ser Asp Ser Glu Ser Glu Glu Leu Pro Lys Pro Gln Val Ser Asp Ser
    210                 215                 220
Glu Ser Glu Glu Pro Pro Arg His Gln Ala Ser Asp Ser Glu Asn Glu
225                 230                 235                 240
Glu Leu Pro Lys Pro Arg Ile Ser Asp Ser Glu Ser Glu Asp Pro Pro
                245                 250                 255
Arg His Gln Ala Ser Asp Ser Glu Asn Glu Glu Leu Pro Lys Pro Arg
            260                 265                 270
Ile Ser Asp Ser Glu Ser Glu Asp Pro Pro Arg Asn Gln Ala Ser Asp
        275                 280                 285
Ser Glu Asn Glu Glu Leu Pro Lys Pro Arg Val Ser Asp Ser Glu Ser
    290                 295                 300
Glu Gly Pro Gln Lys Gly Pro Ala Ser Asp Ser Glu Thr Glu Asp Ala
305                 310                 315                 320
Ser Arg His Lys Gln Lys Pro Glu Ser Asp Asp Asp Ser Asp Arg Glu
                325                 330                 335
Asn Lys Gly Glu Asp Thr Glu Met Gln Asn Asp Ser Phe His Ser Asp
            340                 345                 350
Ser His Met Asp Arg Lys Lys Phe His Ser Ser Asp Ser Glu Glu Glu
        355                 360                 365
Glu His Lys Lys Gln Lys Met Asp Ser Asp Glu Asp Glu Lys Glu Gly
    370                 375                 380
Glu Glu Glu Lys Val Ala Lys Arg Lys Ala Ala Val Leu Ser Asp Ser
385                 390                 395                 400
Glu Asp Glu Glu Lys Ala Ser Ala Lys Lys Ser Arg Val Val Ser Asp
                405                 410                 415
Ala Asp Asp Ser Asp Ser Asp Ala Val Ser Asp Lys Ser Gly Lys Arg
            420                 425                 430
Glu Lys Thr Ile Ala Ser Asp Ser Glu Glu Glu Ala Gly Lys Glu Leu
        435                 440                 445
Ser Asp Lys Lys Asn Glu Glu Lys Asp Leu Phe Gly Ser Asp Ser Glu
    450                 455                 460
Ser Gly Asn Glu Glu Glu Asn Leu Ile Ala Asp Ile Phe Gly Glu Ser
465                 470                 475                 480
Gly Asp Glu Glu Glu Glu Glu Phe
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<211> 288
<212> DNA
<213> Homo sapiens

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120

cacttggaga aacatcgaaa ggacaaagcc cacaaacgct atctgctaat gagcattgac
180
cagaggaaaa agatgctcaa aaacctccgt aacaccaact atgatgtctt tgagaagata
240
tgctgggggc tgggaattga gtacaccttc ccccctctgt attaccgn
288

<210> 3716
<211> 96
<212> PRT
<213> Homo sapiens

<400> 3716
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20 25 30
Gly Lys Ile Arg Ser Tyr Glu Glu His Leu Glu Lys His Arg Lys Asp
35 40 45
Lys Ala His Lys Arg Tyr Leu Leu Met Ser Ile Asp Gln Arg Lys Lys
50 55 60
Met Leu Lys Asn Leu Arg Asn Thr Asn Tyr Asp Val Phe Glu Lys Ile
65 70 75 80
Cys Trp Gly Leu Gly Ile Glu Tyr Thr Phe Pro Pro Leu Tyr Tyr Arg
85 90 95

<210> 3717
<211> 1545
<212> DNA
<213> Homo sapiens

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180
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240
tttcagatca ttattgatat ttacttattt taaagtaaag gcattacaca ctcaacattt
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360
gccagtgaaa gtaacagaga ctgttcaaaa cctgtggcta gcactaattt agacaatgaa
420
gctatgcagc aagattgtgt atttgagaat gaagaaaata cccagtctgt aggtatattg
480
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600
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660

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720
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780
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840
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900
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1140
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1260
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1320
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1380
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1440
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<210> 3718
<211> 374
<212> PRT
<213> Homo sapiens

<400> 3718
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Gly Ile Leu Leu Glu Pro Cys Ser Asp Arg Gly Asp Ser Glu Asp Gly
20 25 30
Cys Leu Glu Arg Glu Glu Tyr Leu Leu Phe Asp Ser Asp Lys Leu Ser
35 40 45
His Leu Ile Leu Asp Ser Ser Ser Lys Ile Cys Asp Leu Asn Ala Asn
50 55 60
Thr Glu Ser Glu Val Pro Gly Gly Gln Ser Val Gly Val Gln Gly Glu
65 70 75 80
Ala Ala Cys Val Ser Ile Pro His Leu Asp Leu Lys Asn Val Ser Asp
85 90 95
Gly Asp Lys Trp Glu Glu Pro Phe Pro Ala Phe Lys Ser Trp Gln Glu
100 105 110
Asp Ser Glu Ser Gly Glu Ala Gln Leu Ser Pro Gln Ala Gly Arg Met
115 120 125
Asn His His Pro Leu Glu Glu Asp Cys Pro Pro Val Leu Ser His Arg

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    130                 135                 140
Ser Leu Asp Phe Gly Gln Ser Gln Arg Phe Leu His Asp Pro Glu Lys
145                 150                 155                 160
Leu Asp Ser Ser Ser Lys Ala Leu Ser Phe Thr Arg Ile Arg Arg Ser
                165                 170                 175
Ser Phe Ser Ser Lys Asp Glu Lys Arg Glu Asp Arg Thr Pro Tyr Gln
            180                 185                 190
Leu Val Lys Lys Leu Gln Lys Lys Ile Arg Gln Phe Glu Glu Gln Phe
        195                 200                 205
Glu Arg Glu Arg Asn Ser Lys Pro Ser Tyr Ser Asp Ile Ala Ala Asn
    210                 215                 220
Pro Lys Val Leu Lys Trp Met Thr Glu Leu Thr Lys Leu Arg Lys Gln
225                 230                 235                 240
Ile Lys Asp Ala Lys His Lys Asn Ser Asp Gly Glu Phe Val Pro Gln
                245                 250                 255
Thr Arg Pro Arg Ser Asn Thr Leu Pro Lys Ser Phe Gly Ser Ser Leu
            260                 265                 270
Asp His Glu Asp Glu Glu Asn Glu Asp Glu Pro Lys Val Ile Gln Lys
        275                 280                 285
Glu Lys Lys Pro Ser Lys Glu Ala Thr Leu Glu Leu Ile Leu Lys Arg
    290                 295                 300
Leu Lys Glu Lys Arg Ile Glu Arg Cys Leu Pro Glu Asp Ile Lys Lys
305                 310                 315                 320
Met Thr Lys Asp His Leu Val Glu Glu Lys Ala Ser Leu Gln Lys Ser
                325                 330                 335
Leu Leu Tyr Tyr Glu Ser Gln His Gly Arg Pro Val Thr Lys Glu Glu
            340                 345                 350
Arg His Ile Val Lys Pro Leu Tyr Asp Arg Tyr Arg Leu Val Lys Gln
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Met Leu Thr Arg Ala Ser
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<210> 3719
<211> 422
<212> DNA
<213> Homo sapiens

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120
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180
cagcccggtt gcaaaaatgt gtgttttgat gacttcttcc ccatttccca agtcagactt
240
tgggccttac aactgataat ggtctccaca ccttcacttc tggtggtttt acatgtagcc
300
tatcatgagg gtagagagaa aaggcacaga aagaaactct atgtcagccc aggtacaatg
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nn
422

<210> 3720
<211> 122
<212> PRT
<213> Homo sapiens

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Pro Gly Ser Tyr Met Gly Gly Gln Pro Glu Pro Arg Val Gly Lys Asn
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Asn Gln Lys Lys Phe Glu Cys Asn Ser Arg Gln Pro Gly Cys Lys Asn
35 40 45
Val Cys Phe Asp Asp Phe Phe Pro Ile Ser Gln Val Arg Leu Trp Ala
50 55 60
Leu Gln Leu Ile Met Val Ser Thr Pro Ser Leu Leu Val Val Leu His
65 70 75 80
Val Ala Tyr His Glu Gly Arg Glu Lys Arg His Arg Lys Lys Leu Tyr
85 90 95
Val Ser Pro Gly Thr Met Asp Gly Gly Leu Trp Tyr Ala Tyr Leu Ile
100 105 110
Ser Leu Ile Val Lys Thr Gly Phe Glu Thr
115 120

<210> 3721
<211> 4728
<212> DNA
<213> Homo sapiens

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120
cccaccgaca tggctcgccg gcagcagaag atcagcaaac agcagctgca gacagtcaag
180
gaccggtttc aggctttcct caatggggaa acccagatca tggctgacga agccttcatg
240
aacgctgtgc agagttacta tgaggtgttc ctgaagagcg accgtgtggc ccgcatggtt
300
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360
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420
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480
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540
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600
gacaatccag atgagcaagc agcccagatc agacgagagc tggatggacg tctacaaatg
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gcagaccaaa tagccaggga acgcaaattt cccaagtttg tatccaaaga aatggaaaac
720

atgtacattg aggagctgaa gtcatctgtc aacctgctca tggccaactt ggagagcatg
780
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900
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960
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1020
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1080
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1200
acagtctcca aaaactgccc caaccaagat ctcaaaatca aacttgctgt ccgaatggat
1260
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1320
agatggaaga aaaggttttt tgtattggtg caggtcagtc agtacacgtt tgccatgtgc
1380
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1500
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1620
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2340

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4440
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4500
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4560
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4620
catcttgctt ttgccttata taaagcctac agttatggaa gtgtggaaaa ctgtggcttc
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4728

<210> 3722
<211> 1216
<212> PRT
<213> Homo sapiens

<400> 3722
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Glu Arg Lys Lys Arg Leu Gln Leu Tyr Val Phe Val Met Arg Cys Ile
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Ala Tyr Pro Phe Asn Ala Lys Gln Pro Thr Asp Met Ala Arg Arg Gln
        35   40   45
Gln Lys Ile Ser Lys Gln Gln Leu Gln Thr Val Lys Asp Arg Phe Gln
    50   55   60
Ala Phe Leu Asn Gly Glu Thr Gln Ile Met Ala Asp Glu Ala Phe Met
65   70   75   80
Asn Ala Val Gln Ser Tyr Tyr Glu Val Phe Leu Lys Ser Asp Arg Val
                85   90   95
Ala Arg Met Val Gln Ser Gly Gly Cys Ser Ala Asn Asp Ser Arg Glu
            100   105   110
Val Phe Lys Lys His Ile Glu Lys Arg Val Arg Ser Leu Pro Glu Ile
        115   120   125
Asp Gly Leu Ser Lys Glu Thr Val Leu Ser Ser Trp Met Ala Lys Phe
    130   135   140
Asp Ala Ile Tyr Arg Gly Glu Glu Asp Pro Arg Lys Gln Gln Ala Arg
145   150   155   160
Met Thr Ala Ser Ala Ala Ser Glu Leu Ile Leu Ser Lys Glu Gln Leu

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                165                 170                 175
Tyr Glu Met Phe Gln Asn Ile Leu Gly Ile Lys Lys Phe Glu His Gln
            180                 185                 190
Leu Leu Tyr Asn Ala Cys Gln Leu Asp Asn Pro Asp Glu Gln Ala Ala
        195                 200                 205
Gln Ile Arg Arg Glu Leu Asp Gly Arg Leu Gln Met Ala Asp Gln Ile
    210                 215                 220
Ala Arg Glu Arg Lys Phe Pro Lys Phe Val Ser Lys Glu Met Glu Asn
225                 230                 235                 240
Met Tyr Ile Glu Glu Leu Lys Ser Ser Val Asn Leu Leu Met Ala Asn
                245                 250                 255
Leu Glu Ser Met Pro Val Ser Lys Gly Gly Glu Phe Lys Leu Gln Lys
            260                 265                 270
Leu Lys Arg Ser His Asn Ala Ser Ile Ile Asp Met Gly Glu Glu Ser
        275                 280                 285
Glu Asn Gln Leu Ser Lys Ser Asp Val Val Leu Ser Phe Ser Leu Glu
    290                 295                 300
Val Val Ile Met Glu Val Gln Gly Leu Lys Ser Leu Ala Pro Asn Arg
305                 310                 315                 320
Ile Val Tyr Cys Thr Met Glu Val Glu Gly Gly Glu Lys Leu Gln Thr
                325                 330                 335
Asp Gln Ala Glu Ala Ser Lys Pro Thr Trp Gly Thr Gln Gly Asp Phe
            340                 345                 350
Ser Thr Thr His Ala Leu Pro Ala Val Lys Val Lys Leu Phe Thr Glu
        355                 360                 365
Ser Thr Gly Val Leu Ala Leu Glu Asp Lys Glu Leu Gly Arg Val Ile
    370                 375                 380
Leu His Pro Thr Pro Asn Ser Pro Lys Gln Ser Glu Trp His Lys Met
385                 390                 395                 400
Thr Val Ser Lys Asn Cys Pro Asn Gln Asp Leu Lys Ile Lys Leu Ala
                405                 410                 415
Val Arg Met Asp Lys Pro Gln Asn Met Lys His Ser Gly Tyr Leu Trp
            420                 425                 430
Ala Ile Gly Lys Asn Val Trp Lys Arg Trp Lys Lys Arg Phe Phe Val
        435                 440                 445
Leu Val Gln Val Ser Gln Tyr Thr Phe Ala Met Cys Ser Tyr Arg Glu
    450                 455                 460
Lys Lys Ala Glu Pro Gln Glu Leu Leu Gln Leu Asp Gly Tyr Thr Val
465                 470                 475                 480
Asp Tyr Thr Asp Pro Gln Pro Gly Leu Glu Gly Gly Arg Ala Phe Phe
                485                 490                 495
Asn Ala Val Lys Glu Gly Asp Thr Val Ile Phe Ala Ser Asp Asp Glu
            500                 505                 510
Gln Asp Arg Ile Leu Trp Val Gln Ala Met Tyr Arg Ala Thr Gly Gln
        515                 520                 525
Ser His Lys Pro Val Pro Pro Thr Gln Val Gln Lys Leu Asn Ala Lys
    530                 535                 540
Gly Gly Asn Val Pro Gln Leu Asp Ala Pro Ile Ser Gln Phe Ser Gly
545                 550                 555                 560
Leu Lys Asp Ala Asp Arg Ala Gln Lys His Gly Met Asp Glu Phe Ile
                565                 570                 575
Ser Ser Asn Pro Cys Asn Phe Asp His Ala Ser Leu Phe Glu Met Val
            580                 585                 590
Gln Arg Leu Thr Leu Asp His Arg Leu Asn Asp Ser Tyr Ser Cys Leu
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595 600 605
Gly Trp Phe Ser Pro Gly Gln Val Phe Val Leu Asp Glu Tyr Cys Ala
610 615 620
Arg Asn Gly Val Arg Gly Cys His Arg His Leu Cys Tyr Leu Arg Asp
625 630 635 640
Leu Leu Glu Arg Ala Glu Asn Gly Ala Met Ile Asp Pro Thr Leu Leu
645 650 655
His Tyr Ser Phe Ala Phe Cys Ala Ser His Val His Gly Asn Arg Pro
660 665 670
Asp Gly Ile Gly Thr Val Thr Val Glu Glu Lys Glu Arg Phe Glu Glu
675 680 685
Ile Lys Glu Arg Leu Arg Val Leu Leu Glu Asn Gln Ile Thr His Phe
690 695 700
Arg Tyr Cys Phe Pro Phe Gly Arg Pro Glu Gly Ala Leu Lys Ala Thr
705 710 715 720
Leu Ser Leu Leu Glu Arg Val Leu Met Lys Asp Ile Val Thr Pro Val
725 730 735
Pro Gln Glu Glu Val Lys Thr Val Ile Arg Lys Cys Leu Glu Gln Ala
740 745 750
Ala Leu Val Asn Tyr Ser Arg Leu Ser Glu Tyr Ala Lys Ile Glu Glu
755 760 765
Asn Gln Lys Asp Ala Glu Asn Val Gly Arg Leu Ile Thr Pro Ala Lys
770 775 780
Lys Leu Glu Asp Thr Ile Arg Leu Ala Glu Leu Val Ile Glu Val Leu
785 790 795 800
Gln Gln Asn Glu Glu His His Ala Glu Pro His Val Asp Lys Gly Glu
805 810 815
Ala Phe Ala Trp Trp Ser Asp Leu Met Val Glu His Ala Glu Thr Phe
820 825 830
Leu Ser Leu Phe Ala Val Asp Met Asp Ala Ala Leu Glu Val Gln Pro
835 840 845
Pro Asp Thr Trp Asp Ser Phe Pro Leu Phe Gln Leu Leu Asn Asp Phe
850 855 860
Leu Arg Thr Asp Tyr Asn Leu Cys Asn Gly Lys Phe His Lys His Leu
865 870 875 880
Gln Asp Leu Phe Ala Pro Leu Val Val Arg Tyr Val Asp Leu Met Glu
885 890 895
Ser Ser Ile Ala Gln Ser Ile His Arg Gly Phe Glu Arg Glu Ser Trp
900 905 910
Glu Pro Val Asn Asn Gly Ser Gly Thr Ser Glu Asp Leu Phe Trp Lys
915 920 925
Leu Asp Ala Leu Gln Thr Phe Ile Arg Asp Leu His Trp Pro Glu Glu
930 935 940
Glu Phe Gly Lys His Leu Glu Gln Arg Leu Lys Leu Met Ala Ser Asp
945 950 955 960
Met Ile Glu Ser Cys Val Lys Arg Thr Arg Ile Ala Phe Glu Val Lys
965 970 975
Leu Gln Lys Thr Ser Arg Ser Thr Asp Phe Arg Val Pro Gln Ser Ile
980 985 990
Cys Thr Met Phe Asn Val Met Val Asp Ala Lys Ala Gln Ser Thr Lys
995 1000 1005
Leu Cys Ser Met Glu Met Gly Gln Glu Phe Ala Lys Met Trp His Gln
1010 1015 1020
Tyr His Ser Lys Ile Asp Glu Leu Ile Glu Glu Thr Val Lys Glu Met

1025 1030 1035 1040
Ile Thr Leu Leu Val Ala Lys Phe Val Thr Ile Leu Glu Gly Val Leu
1045 1050 1055
Ala Lys Leu Ser Arg Tyr Asp Glu Gly Thr Leu Phe Ser Ser Phe Leu
1060 1065 1070
Ser Phe Thr Val Lys Ala Ala Ser Lys Tyr Val Asp Val Pro Lys Pro
1075 1080 1085
Gly Met Asp Val Ala Asp Ala Tyr Val Thr Phe Val Arg His Ser Gln
1090 1095 1100
Asp Val Leu Arg Asp Lys Val Asn Glu Glu Met Tyr Ile Glu Arg Leu
1105 1110 1115 1120
Phe Asp Gln Trp Tyr Asn Ser Ser Met Asn Val Ile Cys Thr Trp Leu
1125 1130 1135
Thr Asp Arg Met Asp Leu Gln Leu His Ile Tyr Gln Leu Lys Thr Leu
1140 1145 1150
Ile Arg Met Val Lys Lys Thr Tyr Arg Asp Phe Arg Leu Gln Gly Val
1155 1160 1165
Leu Asp Ser Thr Leu Asn Ser Lys Thr Tyr Glu Thr Ile Arg Asn Arg
1170 1175 1180
Leu Thr Val Glu Glu Ala Thr Ala Ser Val Ser Glu Gly Gly Gly Leu
1185 1190 1195 1200
Gln Gly Ile Ser Met Lys Asp Ser Asp Glu Glu Asp Glu Glu Asp Asp
1205 1210 1215

<210> 3723
<211> 830
<212> DNA
<213> Homo sapiens

<400> 3723
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120
aaccccaacg agaagctgaa ggtgaacttt gggaccccag agttcctgtc acctgaggtg
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660
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720

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830

<210> 3724
<211> 203
<212> PRT
<213> Homo sapiens

<400> 3724
Ile Leu Leu Met His Lys Met Arg Val Leu His Leu Asp Leu Lys Pro
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Glu Asn Ile Leu Cys Val Asn Thr Thr Gly His Leu Val Lys Ile Ile
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Asp Phe Gly Leu Ala Arg Arg Tyr Asn Pro Asn Glu Lys Leu Lys Val
35 40 45
Asn Phe Gly Thr Pro Glu Phe Leu Ser Pro Glu Val Val Asn Tyr Asp
50 55 60
Gln Ile Ser Asp Lys Thr Asp Met Trp Ser Met Gly Val Ile Thr Tyr
65 70 75 80
Met Leu Leu Ser Gly Leu Ser Pro Phe Leu Gly Asp Asp Asp Thr Glu
85 90 95
Thr Leu Asn Asn Val Leu Ser Gly Asn Trp Tyr Phe Asp Glu Glu Thr
100 105 110
Phe Glu Ala Val Ser Asp Glu Ala Lys Asp Phe Val Ser Asn Leu Ile
115 120 125
Val Lys Asp Gln Arg Ala Arg Met Asn Ala Ala Gln Cys Leu Ala His
130 135 140
Pro Trp Leu Asn Asn Leu Ala Glu Lys Ala Lys Arg Cys Asn Arg Arg
145 150 155 160
Leu Lys Ser Gln Ile Leu Leu Lys Lys Tyr Leu Met Lys Arg Arg Trp
165 170 175
Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn Arg Phe Lys Lys Ile
180 185 190
Ser Ser Ser Gly Ala Leu Met Ala Leu Gly Val
195 200

<210> 3725
<211> 1244
<212> DNA
<213> Homo sapiens

<400> 3725
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120
gaccatcttc acttttgttt tcaggccttt aaaattgtgc cctacaacac agagaccctt
180
gataaactgc taaccgaatc cctgaagaac aatatccctg caagcggact gcacctcttt
240
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300

accctgttgc attttgctgc gaagtatgga ctgaagaacc tcactgcctt gttgctcacc
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480
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900
gagaccactg ctcctggtgc tcaccagctg cctgacaacg aaccatacat ttttaaaggc
960
aagtatggca gggaatgatg tccaactggt tctttggagc ttctcaacag ggatttcctg
1020
gatgacctgg ctttttgaac cattgctcag agactatccc cttctaaatg gtcttcaccc
1080
agccctacga gacagggttc atatcctggg gccagattct ggagctagaa taggagtaat
1140
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caagacccct gatatatttt tatctcctga acccccttcac gcgt
1244

<210> 3726
<211> 325
<212> PRT
<213> Homo sapiens

<400> 3726
Xaa Ile His Val Ser Gly Lys Asp Ile Thr Arg Lys Pro Glu Ile Ser
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Gly His Val Ile Ser Ala His Gly Leu Ser Val Leu Asn Leu Arg Asp
20 25 30
Gly Arg Glu Leu Asp Phe Arg Ser Asp His Leu His Phe Cys Phe Gln
35 40 45
Ala Phe Lys Ile Val Pro Tyr Asn Thr Glu Thr Leu Asp Lys Leu Leu
50 55 60
Thr Glu Ser Leu Lys Asn Asn Ile Pro Ala Ser Gly Leu His Leu Phe
65 70 75 80
Gly Ile Asn Gln Leu Glu Glu Glu Asp Met Met Thr Asn Gln Arg Asp
85 90 95
Glu Glu Leu Pro Thr Leu Leu His Phe Ala Ala Lys Tyr Gly Leu Lys
100 105 110
Asn Leu Thr Ala Leu Leu Leu Thr Cys Pro Gly Ala Leu Gln Ala Tyr

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        115                 120                 125
Ser Val Ala Asn Lys His Gly His Tyr Pro Asn Thr Ile Ala Glu Lys
    130                 135                 140
His Gly Phe Arg Asp Leu Arg Gln Phe Ile Asp Glu Tyr Val Glu Thr
145                 150                 155                 160
Val Asp Met Leu Lys Ser His Ile Lys Glu Glu Leu Met His Gly Glu
                165                 170                 175
Glu Ala Asp Ala Val Tyr Glu Ser Met Ala His Leu Ser Thr Asp Leu
            180                 185                 190
Leu Met Lys Cys Ser Leu Asn Pro Gly Cys Asp Glu Asp Leu Tyr Glu
        195                 200                 205
Ser Met Ala Ala Phe Val Pro Ala Ala Thr Glu Asp Leu Tyr Val Glu
    210                 215                 220
Met Leu Gln Ala Ser Thr Ser Asn Pro Ile Pro Gly Asp Gly Phe Ser
225                 230                 235                 240
Arg Ala Thr Lys Asp Ser Met Ile Arg Lys Phe Leu Glu Gly Asn Ser
                245                 250                 255
Met Gly Met Thr Asn Leu Glu Arg Asp Gln Cys His Leu Gly Gln Glu
            260                 265                 270
Glu Asp Val Tyr His Thr Val Asp Asp Asp Glu Ala Phe Ser Val Asp
        275                 280                 285
Leu Ala Ser Arg Pro Pro Val Pro Val Pro Arg Pro Glu Thr Thr Ala
    290                 295                 300
Pro Gly Ala His Gln Leu Pro Asp Asn Glu Pro Tyr Ile Phe Lys Gly
305                 310                 315                 320
Lys Tyr Gly Arg Glu
                325
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<210> 3727
<211> 630
<212> DNA
<213> Homo sapiens

<400> 3727
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120
ctcgaccccg ctgagaaaca agaaacaggc tgtcctcctt tgggtctgga gtccctgcga
180
gtttcagata gccggcttga ggcatccagc agccagtcct ttggtcttgg accacaccga
240
ggacggctca acattcagtc aggcctggag gacggcgatc tatatgatgg agcctggtgt
300
gctgaggagc aggacgccga tccatggttt caggtggacg ctgggcaccc cacccgcttc
360
tcgggtgtta tcacacaggg caggaactct gtctggaggt atgactgggt cacatcatac
420
aaggtccagt tcagcaatga cagtcggacc tggtggggaa gtaggaacca cagcagtggg
480
atggacgcag tatttcctgc caattcagac ccagaaactc cagtgctgaa cctcctgccg
540
gagccccagg tggcccgctt cattcgcctg ctgccccaga cctggctcca gggaggcgcg
600

ccttgcctcc gggcagagat cctggcctgc
630

<210> 3728
<211> 210
<212> PRT
<213> Homo sapiens

<400> 3728
Arg Ile Arg Val Ile Lys Lys Lys Lys Val Ile Met Lys Lys Arg Lys
1 5 10 15
Lys Leu Thr Leu Thr Arg Pro Thr Pro Leu Val Thr Ala Gly Pro Leu
20 25 30
Val Thr Pro Thr Pro Ala Gly Thr Leu Asp Pro Ala Glu Lys Gln Glu
35 40 45
Thr Gly Cys Pro Pro Leu Gly Leu Glu Ser Leu Arg Val Ser Asp Ser
50 55 60
Arg Leu Glu Ala Ser Ser Ser Gln Ser Phe Gly Leu Gly Pro His Arg
65 70 75 80
Gly Arg Leu Asn Ile Gln Ser Gly Leu Glu Asp Gly Asp Leu Tyr Asp
85 90 95
Gly Ala Trp Cys Ala Glu Glu Gln Asp Ala Asp Pro Trp Phe Gln Val
100 105 110
Asp Ala Gly His Pro Thr Arg Phe Ser Gly Val Ile Thr Gln Gly Arg
115 120 125
Asn Ser Val Trp Arg Tyr Asp Trp Val Thr Ser Tyr Lys Val Gln Phe
130 135 140
Ser Asn Asp Ser Arg Thr Trp Trp Gly Ser Arg Asn His Ser Ser Gly
145 150 155 160
Met Asp Ala Val Phe Pro Ala Asn Ser Asp Pro Glu Thr Pro Val Leu
165 170 175
Asn Leu Leu Pro Glu Pro Gln Val Ala Arg Phe Ile Arg Leu Leu Pro
180 185 190
Gln Thr Trp Leu Gln Gly Gly Ala Pro Cys Leu Arg Ala Glu Ile Leu
195 200 205
Ala Cys
210

<210> 3729
<211> 1552
<212> DNA
<213> Homo sapiens

<400> 3729
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cctcctccgc gcctcgcggc atggagtaga aagggaccgc ggaagcccga aagcgaaggc
120
atcaagttat cagcagatgt caaaccattt gtccccagat ttgccgggct caatgtggca
180
tggttagagt cctcagaagc atgtgtcttc cccagctctg cagccacata ctatccgttt
240
gttcaggaac caccagtgac agagcagaaa atatatactg aagacatggc ctttggagct
300

tcaacttttc cacctcagta tttatcttct gagataactc ttcatccata tgcctattct
360
ccttataccc ttgactccac acagaatgtt tactcagtgc ctggctccca gtatctttat
420
aaccaaccca gttgttaccg aggttttcaa acagtgaagc atcgaaatga gaacacatgc
480
cctctcccac aagaaatgaa agctctgttt aagaagaaaa cctatgatga gaaaaaaacg
540
tatgatcagc aaaagtttga cagtgaaagg gctgatggaa ctatatcatc tgagataaaa
600
tcagctagag gttcacatca tttgtccatt tacgctgaga atagtttgaa atcagatggt
660
taccataagc gaacagacag gaaatccaga atcattgcaa aaaatgtatc tacctccaaa
720
cctgagtttg aatttaccac actggacttt cctgaactgc aaggtgcaga gaacaatatg
780
tcagagatac agaagcaacc caagtgggga cctgtccact ctgtctctac cgacatttct
840
cttctaagag aagtagtaaa accagctgca gtgttatcaa agggtgaaat agtggtgaaa
900
aataacccaa atgaatctgt aactgctaat gccgctacca attctccttc atgtacaaga
960
gagttatctt ggacaccaat gggttatgtt gttcgacaga cattatctac agaactgtca
1020
gcagccccta aaaatgttac ttctatgata aacttaaaga ccattgcttc atcagcagat
1080
cctaaaaatg ttagtatacc atcttctgaa gctttatctt cggatccttc ctacaacaaa
1140
gaaaaacaca ttattcatcc tacccaaaag tctaaagcat cacaaggtag tgaccttgaa
1200
caaaatgaag cctcaagaaa gaataagaaa aagaaagaaa aatctacatc aaaatatgaa
1260
gtcctgacag ttcaagagcc tccaaggatt gaagatgccg aggaatttcc caacctggca
1320
gttgcatctg aaagaagaga cagaatagag acaccgaaat ttcaatctaa gcagcagcca
1380
caggataatt ttaaaaataa tgtaaagaag agccagcttc cagtgcagtt ggacttgggg
1440
ggcatgctga cagccctgga gaagaagcag cactctcagc atgcaaagca gtcctccaaa
1500
ccagtggtag tctcagttgg agcagtgcca gtcctttcca aagaatgtgc ac
1552

<210> 3730
<211> 422
<212> PRT
<213> Homo sapiens

<400> 3730
Met Ala Phe Gly Ala Ser Thr Phe Pro Pro Gln Tyr Leu Ser Ser Glu
 1   5   10   15
Ile Thr Leu His Pro Tyr Ala Tyr Ser Pro Tyr Thr Leu Asp Ser Thr
            20   25   30
Gln Asn Val Tyr Ser Val Pro Gly Ser Gln Tyr Leu Tyr Asn Gln Pro

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        35                  40                  45
Ser Cys Tyr Arg Gly Phe Gln Thr Val Lys His Arg Asn Glu Asn Thr
    50                  55                  60
Cys Pro Leu Pro Gln Glu Met Lys Ala Leu Phe Lys Lys Lys Thr Tyr
65                  70                  75                  80
Asp Glu Lys Lys Thr Tyr Asp Gln Gln Lys Phe Asp Ser Glu Arg Ala
                85                  90                  95
Asp Gly Thr Ile Ser Ser Glu Ile Lys Ser Ala Arg Gly Ser His His
            100                 105                 110
Leu Ser Ile Tyr Ala Glu Asn Ser Leu Lys Ser Asp Gly Tyr His Lys
        115                 120                 125
Arg Thr Asp Arg Lys Ser Arg Ile Ile Ala Lys Asn Val Ser Thr Ser
    130                 135                 140
Lys Pro Glu Phe Glu Phe Thr Thr Leu Asp Phe Pro Glu Leu Gln Gly
145                 150                 155                 160
Ala Glu Asn Asn Met Ser Glu Ile Gln Lys Gln Pro Lys Trp Gly Pro
                165                 170                 175
Val His Ser Val Ser Thr Asp Ile Ser Leu Leu Arg Glu Val Val Lys
            180                 185                 190
Pro Ala Ala Val Leu Ser Lys Gly Glu Ile Val Val Lys Asn Asn Pro
        195                 200                 205
Asn Glu Ser Val Thr Ala Asn Ala Ala Thr Asn Ser Pro Ser Cys Thr
    210                 215                 220
Arg Glu Leu Ser Trp Thr Pro Met Gly Tyr Val Val Arg Gln Thr Leu
225                 230                 235                 240
Ser Thr Glu Leu Ser Ala Ala Pro Lys Asn Val Thr Ser Met Ile Asn
                245                 250                 255
Leu Lys Thr Ile Ala Ser Ser Ala Asp Pro Lys Asn Val Ser Ile Pro
            260                 265                 270
Ser Ser Glu Ala Leu Ser Ser Asp Pro Ser Tyr Asn Lys Glu Lys His
        275                 280                 285
Ile Ile His Pro Thr Gln Lys Ser Lys Ala Ser Gln Gly Ser Asp Leu
    290                 295                 300
Glu Gln Asn Glu Ala Ser Arg Lys Asn Lys Lys Lys Lys Glu Lys Ser
305                 310                 315                 320
Thr Ser Lys Tyr Glu Val Leu Thr Val Gln Glu Pro Pro Arg Ile Glu
                325                 330                 335
Asp Ala Glu Glu Phe Pro Asn Leu Ala Val Ala Ser Glu Arg Arg Asp
            340                 345                 350
Arg Ile Glu Thr Pro Lys Phe Gln Ser Lys Gln Gln Pro Gln Asp Asn
        355                 360                 365
Phe Lys Asn Asn Val Lys Lys Ser Gln Leu Pro Val Gln Leu Asp Leu
    370                 375                 380
Gly Gly Met Leu Thr Ala Leu Glu Lys Lys Gln His Ser Gln His Ala
385                 390                 395                 400
Lys Gln Ser Ser Lys Pro Val Val Val Ser Val Gly Ala Val Pro Val
                405                 410                 415
Leu Ser Lys Glu Cys Ala
            420
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<210> 3731
<211> 1704
<212> DNA
<213> Homo sapiens

<400> 3731
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ctgaaccagt tggactctca cgttctgctg tgcttcgagg gaatcacaga tgcttcaagc
120
tgtgcagtgc tgctcccagc atcactgttc gtcaatagtc acccaggaat agaccggcct
180
ggcatgctct gcagtttccg gatccctggt gcctggtcct gtgcctggtc cctgaatatc
240
caagcaaata actgcttcag tacaggcttg tctcggcggg tcctgttgac caacgtggtg
300
acgggacacc ggcagtcctt tgggaccaac agtgatgtct tggcccagca gtttgctctc
360
atggctcctc tgctgtttaa tggctgccgc tctggggaaa tctttgccat tgatctgcgt
420
tgtggaaatc aaggcaaggg atggaaggcc acccgcctgt ttcatgattc agcagtgacc
480
tctgtgcgga tcctccaaga tgagcaatac ctgatggctt cagacatggc tggaaagatc
540
aagctgtggg acctgaggac cacgaagtgc gtaaggcagt acgaaggcca cgtgaatgag
600
tacgcctacc tgcccctgca tgtgcacgag gaagaaggaa tcctggtggc agtgggccag
660
gactgctaca cgagaatctg gagcctccac gatgcccgcc tactgagaac catacctcc
720
ccgtaccctg cctccaaggc cgacattccc agtgtggcct tctcgtcgcg gctgggggc
780
tcccggggcg cgccggggct gctcatggct gtcgggcagg acctttactg ttactcctac
840
agctaattct gcagggcaca gcccagagcc atgtggattt gacttacggg agtaaagcgt
900
aacttttac tgcatctaat gagggtgttt taagtgacac tcagtgtaca cagatcccat
960
cctctggctg ctaggagaga agtgctgaat gttccgtgtg gagatgctca ggaaagttat
1020
ttgagttaaa ttgctggctg agagagcttg gaagtccttt tcataaaagg tacctctttc
1080
cttttcttat tgaattctta gaacttagtt aaccctccct gccttttctt aacaaaaagg
1140
acttttctaa ggactgaaga ttggcaaaaa cgaaaagctt cttcctccaa gagcccattg
1200
aagaagccca gtgatgagac ggtgagatgg tttgagtcct cggtgcctgg gtagcaggaa
1260
gaaagacctg catcctgcat ctgtacttgg ggaagccagc ggagaggacg gggaggttac
1320
ttctctaagt ttctgcagaa atattgaagg ctggagtttg gaatccttaa acttggcctt
1380
ctcaaactca gcagcagatc tccgggattc tgctgttatt atccaaaggc gttggaagga
1440
aagatggatc ttcttacatg ctagaagttt taaacggtcc ttaacatgcc tttgttcaag
1500
caccttccag aatgtaaggt tcagcagctc tggtttctat tacggtgact tgaatgtcag
1560

attcaagggc ccggcgtcaa aggaaattgg ttttgacttt ttgtaatcta ggagcgacag
1620
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1680
agaagaaaaa aaaaaaaaaa aaaa
1704

<210> 3732
<211> 281
<212> PRT
<213> Homo sapiens

<400> 3732
Tyr Val Leu Arg Asn Leu Tyr Val Pro Asn Arg Lys Val Lys Ser Leu
1 5 10 15
Cys Trp Ala Ser Leu Asn Gln Leu Asp Ser His Val Leu Leu Cys Phe
20 25 30
Glu Gly Ile Thr Asp Ala Ser Ser Cys Ala Val Leu Leu Pro Ala Ser
35 40 45
Leu Phe Val Asn Ser His Pro Gly Ile Asp Arg Pro Gly Met Leu Cys
50 55 60
Ser Phe Arg Ile Pro Gly Ala Trp Ser Cys Ala Trp Ser Leu Asn Ile
65 70 75 80
Gln Ala Asn Asn Cys Phe Ser Thr Gly Leu Ser Arg Arg Val Leu Leu
85 90 95
Thr Asn Val Val Thr Gly His Arg Gln Ser Phe Gly Thr Asn Ser Asp
100 105 110
Val Leu Ala Gln Gln Phe Ala Leu Met Ala Pro Leu Leu Phe Asn Gly
115 120 125
Cys Arg Ser Gly Glu Ile Phe Ala Ile Asp Leu Arg Cys Gly Asn Gln
130 135 140
Gly Lys Gly Trp Lys Ala Thr Arg Leu Phe His Asp Ser Ala Val Thr
145 150 155 160
Ser Val Arg Ile Leu Gln Asp Glu Gln Tyr Leu Met Ala Ser Asp Met
165 170 175
Ala Gly Lys Ile Lys Leu Trp Asp Leu Arg Thr Thr Lys Cys Val Arg
180 185 190
Gln Tyr Glu Gly His Val Asn Glu Tyr Ala Tyr Leu Pro Leu His Val
195 200 205
His Glu Glu Glu Gly Ile Leu Val Ala Val Gly Gln Asp Cys Tyr Thr
210 215 220
Arg Ile Trp Ser Leu His Asp Ala Arg Leu Leu Arg Thr Ile Pro Ser
225 230 235 240
Pro Tyr Pro Ala Ser Lys Ala Asp Ile Pro Ser Val Ala Phe Ser Ser
245 250 255
Arg Leu Gly Gly Ser Arg Gly Ala Pro Gly Leu Leu Met Ala Val Gly
260 265 270
Gln Asp Leu Tyr Cys Tyr Ser Tyr Ser
275 280

<210> 3733
<211> 515
<212> DNA
<213> Homo sapiens

<400> 3733
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cgctaccgga gagggaggag aaggggggagg ttaaagggga aggaccccgg aagtgccccc
120
tcctcagtgc gggagaggga gacgccgggg gcangtccat gcctcccgcg gcgtggttgg
180
tgcgtcccag gtgacgtcag aagcagcccg cccctgcctg gatggtgcgc cctgagtgac
240
gtcaggagca gaggccggag ctgtccatca gcaccaaagg ccgcgggcgg gctcagggca
300
tggggccgcg gttctggggc ggcccgagcc ccggctcctg cgccttcccc ttcctcaggc
360
nccagcccga gttcccggac gccgcgggac tggagtgcca gccggtgttg gacgtggagc
420
ggcgccgcca ccgcgccgac accattctct ccggcccagc agccccttc ctcgcacgac
480
ggactttccc tggaccccag tcagttggag cctct
515

<210> 3734
<211> 171
<212> PRT
<213> Homo sapiens

<400> 3734
Xaa Gly Arg Ala Val Arg Arg Val Thr Ala Gly Thr Arg Pro Gly Trp
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Val Ser Gly Ser Arg Tyr Arg Arg Gly Arg Arg Arg Gly Arg Leu Lys
            20   25   30
Gly Lys Asp Pro Gly Ser Ala Pro Ser Ser Val Arg Glu Arg Glu Thr
        35   40   45
Pro Gly Ala Xaa Pro Cys Leu Pro Arg Arg Gly Trp Cys Val Pro Gly
    50   55   60
Asp Val Arg Ser Ser Pro Pro Leu Pro Gly Trp Cys Ala Leu Ser Asp
65   70   75   80
Val Arg Ser Arg Gly Arg Ser Cys Pro Ser Ala Pro Lys Ala Ala Gly
                85   90   95
Gly Leu Arg Ala Trp Gly Arg Gly Ser Gly Ala Ala Arg Ala Pro Ala
            100   105   110
Pro Ala Pro Ser Pro Ser Ser Gly Xaa Ser Pro Ser Ser Arg Thr Pro
        115   120   125
Arg Asp Trp Ser Ala Ser Arg Cys Trp Thr Trp Ser Gly Ala Ala Thr
    130   135   140
Ala Pro Thr Pro Phe Ser Pro Ala Gln Gln Pro Pro Ser Ser His Asp
145   150   155   160
Gly Leu Ser Leu Asp Pro Ser Gln Leu Glu Pro
                165   170

<210> 3735
<211> 2512
<212> DNA
<213> Homo sapiens

<400> 3735
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tgggcatatt gaaaaactcc aaatttctca aagtctgcct gcctgcttat gtggtaggga
120
tgatcactga acccatccct gacatccgaa accagtatcc agagcacata agcaacatca
180
tctccctcct ccaggacctt gtaagtgtct tccctgccag ctctgtgcag gaaacttcca
240
tgctggtttc cctcctgcca acctctctta atgctctgag agcctctggt gttgacatag
300
aagaggaaac ggagaagaac ctggaaaagg tacagactat cattgaacat ctgcaggaaa
360
agaggcgaga gggcactttg agagtggata cctacactct agtgcagcct gaggcagaag
420
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480
atgagaggcc cttccttcgc cccaatatca tttctggaaa atacgacagc actgctatct
540
atctggatac ccacttccgg ctcctgcgag aagatttcgt cagaccttta cgggaaggta
600
ttttggaact tctccaaagc tttgaagacc agggcctgag gaagagaaag tttgatgaca
660
tccgaatcta ctttgacacc aggattatca cccccatgtg ttcatcatca ggcatagtct
720
acaaggtgca gtttgacaca aaaccactga agtttgttcg ctggcagaat tccaaacgat
780
tgctctatgg gtctttggta tgcatgtcca aggacaactt cgagacattt ctttttgcca
840
ccgtatctaa cagggagcag gaagatctct gccgaggaat tgtccagctc tgcttcaatg
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960
caactgcata ctttgaggcc tacaggcacg tcctggaagg actccaggag gtccaggagg
1020
aagatgttcc cttccagagg aatatcgtgg agtgtaactc tcatgtgaag gagccaaggt
1080
acttgctaat ggggggcaga tatgacttta cccccttaat agagaatcct tcagccactg
1140
gggaatttct aagaaatgtc gagggtttga gacatcccag aattaatgtc ttagatcctg
1200
gccagtggcc ctcaaaagaa gccctgaagc tggatgactc ccagatggaa gccttgcagt
1260
ttgctctcac aagggaactg gctattattc aaggacctcc tggaacaggc aaaacctatg
1320
tgggtctaaa aattgttcag gccctcctaa ccaacgagtc tgtttggcaa attagcctcc
1380
agaagttccc catcttggtt gtgtgttata ctaatcatgc tttggaccag tttctggaag
1440
gcatctacaa ttgtcagaag accagcattg tgcgggtggg tggaaggagc aacagtgaaa
1500
tcctgaagca gttcacccta agggagctga ggaacaagcg ggaattccgc cgcaacctcc
1560

ccatgcacct ccgaagggcc tacatgagta tcatgacaca gatgaaggag tcagagcaag
1620
agcttcatga aggagccaag accctggagt gcaccatgcg tggtgtccta cgggaacagt
1680
acctgcagaa gtacatctca ccccagcact gggaaagtct catgaatgga ccagtgcagg
1740
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1800
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1860
cagaagggga tgaggaggaa gaaggggagg aggagagttc gctgatagag atcgcagagg
1920
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1980
ggcggaagaa ggaagagagt ggagcagacc aggagttggc taaaatgctt ctggccatga
2040
ggctagacca ttgtggcact gggacagcag ctggacagga gcaagccaca ggagagtggc
2100
agacccagcg caacccagaa aaagaaaatg aaaaaaagag tgaaggatga gcttcgcaaa
2160
ctgaacacca tgcctgcagc cgaggccaac gagatcgagg atgtttggca cctggacctc
2220
agttctcgct ggcagcttta taggctctgg ctacagttgt accaggctga caccccgccc
2280
gggaagatcc tcagctatga acgccagtac cgcacatcag cagaaagaat ggccgagctg
2340
agactccagg aagacctgca cattcttaaa gatgcccagg ttgtaggaat gacaaccaca
2400
ggtgctgcca aataccgcca gatcctacag aaggtggagc cgaggattgt catagtggaa
2460
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2512

<210> 3736
<211> 155
<212> PRT
<213> Homo sapiens

<400> 3736
Thr Ile Val Ala Leu Gly Gln Gln Leu Asp Arg Ser Lys Pro Gln Glu
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Ser Gly Arg Pro Ser Ala Thr Gln Lys Lys Lys Met Lys Lys Arg Val
20 25 30
Lys Asp Glu Leu Arg Lys Leu Asn Thr Met Pro Ala Ala Glu Ala Asn
35 40 45
Glu Ile Glu Asp Val Trp His Leu Asp Leu Ser Ser Arg Trp Gln Leu
50 55 60
Tyr Arg Leu Trp Leu Gln Leu Tyr Gln Ala Asp Thr Pro Pro Gly Lys
65 70 75 80
Ile Leu Ser Tyr Glu Arg Gln Tyr Arg Thr Ser Ala Glu Arg Met Ala
85 90 95
Glu Leu Arg Leu Gln Glu Asp Leu His Ile Leu Lys Asp Ala Gln Val
100 105 110
Val Gly Met Thr Thr Thr Gly Ala Ala Lys Tyr Arg Gln Ile Leu Gln

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        115                 120                 125
Lys Val Glu Pro Arg Ile Val Ile Val Glu Glu Ala Ala Glu Val Leu
    130                 135                 140
Glu Ala His Thr Ile Ala Thr Leu Ser Lys Ala
145                 150                 155

<210> 3737
<211> 1046
<212> DNA
<213> Homo sapiens

<400> 3737
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aatgagccca aggtgacgac aagctgcccc cagcagggcc tgcaggctgt gcccgtgggc
120
atccctgctg ccagccagcg catcttcctg cacggcaacc gcatctcgca tgtgccagct
180
gccagcttcc gtgcctgccg caacctcacc atcctgtggc tgcactcgaa tgtgctggcc
240
cgaattgatg cggctgcctt cactggcctg gccctcctgg gagcactgga cctcagcgat
300
aatgcacagc tccggtctgt ggaccctgcc acattccacg gcctgggccg cctacacacg
360
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420
gccctgcagt acctctacct gcaggacaac gcgctgcagg cactgcctga tgacaccttc
480
cgcgacctgg gcaacctcac acacctcttc ctgcacggca accgcatctc cagcgtgccc
540
gagcgcgcct tccgtgggct gcacagcctc gaccgtctcc tactgcacca gaaccgcgtg
600
gcccatgtgc acccgcatgc cttccgtgac cttggccgcc tcatgacact ctatctgttt
660
gccaacaatc tatcagcgct gcccactgag gccctggccc ccctgcgtgc cctgcagtac
720
ctgaggctca acgacaaccc ctgggtgtgt gactgccggg cacgcccact ctgggcctgg
780
ctgcagaagt tccgcggctc ctcctccgag gtgccctgca gcctcccgca acgcctggct
840
ggccgtgacc tcaaacgcct agctgccaat gacctgcagg gctgcgctgt ggccaccggc
900
ccttaccatc ccatctggac cggcagggcc accgatgagg agccgctggg gcttcccaag
960
tgctgccagc cagatgccgc tgacaaggcc tcagtactgg agcctggaag accagcttcg
1020
gcaggcaatg cgctgaaggg acgcgt
1046

<210> 3738
<211> 348
<212> PRT
<213> Homo sapiens
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<400> 3738
Xaa Ala Val Ala Ala Gly Trp Gln Val Ala Ala Pro Cys Pro Gly Ala
1 5 10 15
Cys Val Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln
20 25 30
Gly Leu Gln Ala Val Pro Val Gly Ile Pro Ala Ala Ser Gln Arg Ile
35 40 45
Phe Leu His Gly Asn Arg Ile Ser His Val Pro Ala Ala Ser Phe Arg
50 55 60
Ala Cys Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Val Leu Ala
65 70 75 80
Arg Ile Asp Ala Ala Ala Phe Thr Gly Leu Ala Leu Leu Gly Ala Leu
85 90 95
Asp Leu Ser Asp Asn Ala Gln Leu Arg Ser Val Asp Pro Ala Thr Phe
100 105 110
His Gly Leu Gly Arg Leu His Thr Leu His Leu Asp Arg Cys Gly Leu
115 120 125
Gln Glu Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr
130 135 140
Leu Tyr Leu Gln Asp Asn Ala Leu Gln Ala Leu Pro Asp Asp Thr Phe
145 150 155 160
Arg Asp Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile
165 170 175
Ser Ser Val Pro Glu Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg
180 185 190
Leu Leu Leu His Gln Asn Arg Val Ala His Val His Pro His Ala Phe
195 200 205
Arg Asp Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu
210 215 220
Ser Ala Leu Pro Thr Glu Ala Leu Ala Pro Leu Arg Ala Leu Gln Tyr
225 230 235 240
Leu Arg Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro
245 250 255
Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro
260 265 270
Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala
275 280 285
Ala Asn Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro Tyr His Pro
290 295 300
Ile Trp Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu Gly Leu Pro Lys
305 310 315 320
Cys Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly
325 330 335
Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg
340 345

<210> 3739
<211> 1252
<212> DNA
<213> Homo sapiens

<400> 3739
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acacccctca gccagctgtt cttggaggtc ctgcccctgg gacttgtccg gctcatccag
120
agtgaggagg gcctggagat gctcattcaa tgagcgggag gcacctctcc cttcccgtaa
180
cttctccctt aactgggtca gctctcgttc ctgagagtga accaggactt tatattgctg
240
tatttcttct gtcggttggc caggaagccg gccagttgag ttagaaaaca tctctctttg
300
aggtttctga actgctgttt gttctctgcc aactgggggc gcaatttctc gttgatttct
360
agaatgttca tctctgcctt ctcgctggac aaagggccgg ctgataccac catgctgacg
420
tttgtggcag aagaggtgga gtcagggact tactgttgtg aaaaatgtga tcactcccca
480
cagcacttta ggatccttca ccacaaaaac aaggttcgag gtgcctcaac tcagagctga
540
aagcactgcc agtagctcag actctgataa gagtgaggta gattgtggcc agcgtgccag
600
gtaaccgtct tgatccatag gctcacattt gatcccaact ggcggctgct tcttggcatt
660
aactttggat tcccaaccag taaatcttag caagatctga gtttctccag gtatgatatt
720
attttgtttg accatcctta tcttcaaggg ctgttggatc tggcagctct tgatgtcagc
780
ccacaccatg tgaggctgct cttggtgcac cgaatgggga agtttctaca tcagggcctc
840
ggagaatcca ctggaagccc tggacagtgg gagtcagcgg caccccagt gtggaggcca
900
agagcacaca gcactgaagc tccaggacac cctcaggagg acggcaaggg acaattggct
960
ggtgagagcc cgggtcaccg ggaaccttcg cctgggtcta aacaggattt gccttcagat
1020
tgcctcagaa acgctgggtg gacttcgcgt aacttcccat tcacagggca gccggcagcc
1080
gcgccgccgc gcctcggccc agctcctggc gccgcagatc gcccgtcccg cgttcccaaa
1140
agccccgcgc tcgctcagaa gctcgggcag cctcgcgacc ctcacctacc cctcccaata
1200
tcgccgctgt ctcaaccgcc gcccagccca tagcctgcgg ccagctggat cc
1252

<210> 3740
<211> 139
<212> PRT
<213> Homo sapiens

<400> 3740
Met Gly Lys Phe Leu His Gln Gly Leu Gly Glu Ser Thr Gly Ser Pro
1 5 10 15
Gly Gln Trp Glu Ser Ala Ala Pro Pro Val Trp Arg Pro Arg Ala His
20 25 30
Ser Thr Glu Ala Pro Gly His Pro Gln Glu Asp Gly Lys Gly Gln Leu
35 40 45
Ala Gly Glu Ser Pro Gly His Arg Glu Pro Ser Pro Gly Ser Lys Gln

```
    50                  55                  60
Asp Leu Pro Ser Asp Cys Leu Arg Asn Ala Gly Trp Thr Ser Arg Asn
65                  70                  75                  80
Phe Pro Phe Thr Gly Gln Pro Ala Ala Ala Pro Pro Arg Leu Gly Pro
                85                  90                  95
Ala Pro Gly Ala Ala Asp Arg Pro Ser Arg Val Pro Lys Ser Pro Ala
            100                 105                 110
Leu Ala Gln Lys Leu Gly Gln Pro Arg Asp Pro His Leu Pro Leu Pro
        115                 120                 125
Ile Ser Pro Leu Ser Gln Pro Pro Pro Ser Pro
    130                 135
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<210> 3741
<211> 562
<212> DNA
<213> Homo sapiens

<400> 3741
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60
gtcgtgtcca ctgtggggat ccacgtcctg actaaccttg tgttcctaga aatccctcac
120
cggcagatcg gtgcctcctg aatcccaccc aaaattccca ctgggaatgt gttcctgaaa
180
gagctgccca ggcttgagaa agcctctttt cagaccaaac ttcgtattca aagctcaaaa
240
agaactgcac acaattagga cagtcataca agatgctgcc cctaatcctg ccacaatctg
300
cgagaaggga ggcggggctt ccgagggcaa agtgcccctg ggaagggatc cgcagggaac
360
agctttgaaa ggaccacagc ccccagccac gaggggagca agcacgagcc ggggagagag
420
ctctgcgctc gcacacggga ttcatctccg ccgcctctgc ccgtttccag caacacggag
480
ccaggcggaa acagtttctc cagcccattc gcctccccga ctcttcctct cacggcacgg
540
ctgggctgct ttcatcacgc gt
562

<210> 3742
<211> 138
<212> PRT
<213> Homo sapiens

<400> 3742
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Met Gly Trp Arg Asn Cys Phe Arg Leu Ala Pro Cys Cys Trp Lys Arg
 1               5                  10                  15
Ala Glu Ala Ala Glu Met Asn Pro Val Cys Glu Arg Arg Ala Leu Ser
            20                  25                  30
Pro Ala Arg Ala Cys Ser Pro Arg Gly Trp Gly Leu Trp Ser Phe Gln
        35                  40                  45
Ser Cys Ser Leu Arg Ile Pro Ser Gln Gly His Phe Ala Leu Gly Ser
    50                  55                  60
Pro Ala Ser Leu Leu Ala Asp Cys Gly Arg Ile Arg Gly Ser Ile Leu
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65 70 75 80
Tyr Asp Cys Pro Asn Cys Val Gln Phe Phe Leu Ser Phe Glu Tyr Glu
85 90 95
Val Trp Ser Glu Lys Arg Leu Ser Gln Ala Trp Ala Ala Leu Ser Gly
100 105 110
Thr His Ser Gln Trp Glu Phe Trp Val Gly Phe Arg Arg His Arg Ser
115 120 125
Ala Gly Glu Gly Phe Leu Gly Thr Gln Gly
130 135

<210> 3743
<211> 468
<212> DNA
<213> Homo sapiens

<400> 3743
nntcatgagc cttcttacaa gctccatttt ggcaaggcgc tgacaatggc ggaggctgaa
60
ggcaatgcaa gctgcacagt cagtctaggg ggtgccaata tggcagagac ccacaaagcc
120
atgatcctgc aactcaatcc cagtgagaac tgcacctgga caatagaaag accagaaaac
180
aaaagcatca gaattatctt ttcctatgtc cagcttgatc cagatggaag ctgtgaaagt
240
gaaaacatta aagtctttga cggaacctcc agcaatgggc ctctgctagg gcaagtctgc
300
agtaaaaacg actatgttcc tgtatttgaa tcatcatcca gtacattgac gtttcaaata
360
gttactgact cagcaagaat tcaaagaact gtctttgtgt tctagtagtt cttatttcct
420
aacatcttta ttccaaagtg tggcggttac ctggatccct ggaaggat
468

<210> 3744
<211> 134
<212> PRT
<213> Homo sapiens

<400> 3744
Xaa His Glu Pro Ser Tyr Lys Leu His Phe Gly Lys Ala Leu Thr Met
1 5 10 15
Ala Glu Ala Glu Gly Asn Ala Ser Cys Thr Val Ser Leu Gly Gly Ala
20 25 30
Asn Met Ala Glu Thr His Lys Ala Met Ile Leu Gln Leu Asn Pro Ser
35 40 45
Glu Asn Cys Thr Trp Thr Ile Glu Arg Pro Glu Asn Lys Ser Ile Arg
50 55 60
Ile Ile Phe Ser Tyr Val Gln Leu Asp Pro Asp Gly Ser Cys Glu Ser
65 70 75 80
Glu Asn Ile Lys Val Phe Asp Gly Thr Ser Ser Asn Gly Pro Leu Leu
85 90 95
Gly Gln Val Cys Ser Lys Asn Asp Tyr Val Pro Val Phe Glu Ser Ser
100 105 110
Ser Ser Thr Leu Thr Phe Gln Ile Val Thr Asp Ser Ala Arg Ile Gln

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        115                 120                 125
Arg Thr Val Phe Val Phe
    130

<210> 3745
<211> 345
<212> DNA
<213> Homo sapiens

<400> 3745
acgcgtcgaa agggaagagc agaggacgct ggctctcatg gcaggatggt gtgtgtacgg
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gacgctgtgg gagaggaaaa cagccacatg tgggctggct gcttggagga gacacatgag
120
ccgtgaacac gtctcccccg gccgctccct ggttccatgc gtgctcgtct tgggcaccac
180
gagaacacag ccatgcagcc cccgatcctg cagccacagc cacggcatcg cctggtcgga
240
tgcagcatct gctccggacg cctctcgctg tcggtgccag gcctgccagg ccaagccccg
300
attctcaggg gcggcaggag gtgggaggca cgtttgggcg gatcc
345

<210> 3746
<211> 102
<212> PRT
<213> Homo sapiens

<400> 3746
Met Ala Gly Trp Cys Val Tyr Gly Thr Leu Trp Glu Arg Lys Thr Ala
 1               5                  10                  15
Thr Cys Gly Leu Ala Ala Trp Arg Arg His Met Ser Arg Glu His Val
            20                  25                  30
Ser Pro Gly Arg Ser Leu Val Pro Cys Val Leu Val Leu Gly Thr Thr
        35                  40                  45
Arg Thr Gln Pro Cys Ser Pro Arg Ser Cys Ser His Ser His Gly Ile
    50                  55                  60
Ala Trp Ser Asp Ala Ala Ser Ala Pro Asp Ala Ser Arg Cys Arg Cys
65                  70                  75                  80
Gln Ala Cys Gln Ala Lys Pro Arg Phe Ser Gly Ala Ala Gly Gly Gly
                85                  90                  95
Arg His Val Trp Ala Asp
            100

<210> 3747
<211> 800
<212> DNA
<213> Homo sapiens

<400> 3747
cctaggcgag gcgctggcgc tggggtctgg ctggcgtcat gcgtgccacg ctctcctcta
60
cgcgccggac cctgggatgc tcttcggccg catcccgctg cgctacgcca tactggtgag
120
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aaggggcgc gcccggccac tttctgcctg agccccgcac cctctctggt ggtctcctct
180
ggggcgcccc tgccaatccc cgcttccccc tcccgcagat gcagatgcgc ttcgatggac
240
gcctgggctt ccccggcgga ttcgtggaca cgcaggacag aagcctagag gacgggctga
300
accgcgagct gcgcgaggag ctgggcgaag cggctgccgc tttccgcgtg gagcgcactg
360
actaccgcag ctcccacgtc ggggtcaggg ccacgcgttg tggcccactt ctatgccaag
420
cgtctgacgc tcgaggagct gttggctgtg gaggccggcg caacacgcgc caaggaccac
480
gggctggagg tgggaccagc ctgggactct gtccctttcc caatttcctc ttctcccaaa
540
gctttctctc ccccaagaaa gcatccctgg agaaaagtct ttgcccctct gaccttgccc
600
tctccccagc tttcttggtg gagttgggat cgtgatcatc tatactctga attagtactg
660
ccaacctggg ctttctgtaa aggtctttcc cacccttac caggagagat cctttctaga
720
acacactcat ccatgtctct ctgctgttcc ctattgacag tgtgatagat tatcacatta
780
tctaggtgtg gcaacctagg
800

<210> 3748
<211> 138
<212> PRT
<213> Homo sapiens

<400> 3748
Met Gln Met Arg Phe Asp Gly Arg Leu Gly Phe Pro Gly Gly Phe Val
1 5 10 15
Asp Thr Gln Asp Arg Ser Leu Glu Asp Gly Leu Asn Arg Glu Leu Arg
20 25 30
Glu Glu Leu Gly Glu Ala Ala Ala Ala Phe Arg Val Glu Arg Thr Asp
35 40 45
Tyr Arg Ser Ser His Val Gly Val Arg Ala Thr Arg Cys Gly Pro Leu
50 55 60
Leu Cys Gln Ala Ser Asp Ala Arg Gly Ala Val Gly Cys Gly Gly Arg
65 70 75 80
Arg Asn Thr Arg Gln Gly Pro Arg Ala Gly Gly Gly Thr Ser Leu Gly
85 90 95
Leu Cys Pro Phe Pro Asn Phe Leu Phe Ser Gln Ser Phe Leu Ser Pro
100 105 110
Lys Lys Ala Ser Leu Glu Lys Ser Leu Cys Pro Ser Asp Leu Ala Leu
115 120 125
Ser Pro Ala Phe Leu Val Glu Leu Gly Ser
130 135

<210> 3749
<211> 648
<212> DNA
<213> Homo sapiens

<400> 3749
cgcgcccccc gggaggatcc tgccaagtgg gtgatggaca catatccatg ggcagccagc
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ccacaacagc acgagtggcc tcccctgctg cagttacggc ctgaggatgt cggcttcgac
120
ggctactcca tgcctcggga gggatcgaca agcaagcaga tgccccccag tgatgctgaa
180
ggtgacccgc tgatgaacat gctgatgagg ctgcaggagg cagccaacta ctccagcccc
240
cagagctatg acagcgcctc caacagcaac agccatcacg atgacatctt ggactcctct
300
ttggagtcca ctctgtgaca ggggcccgga gcccagcgcc ctcctcttct cctcaccgca
360
ttccacctgc atcccccaca tcaccctgaa gatgacttcc tgagccagcc cccagccaca
420
gccttagagc tgcgggaaca ccgagacccc ccgtccttca gcctcgacct gggtgcaggc
480
atcccgggcc agctgcctgc ggaccgcttc cttccacagc gagaactgca ctaccttctg
540
ttgtacttta attattgttt tgccttgttg ctgtgacctc cctaagacac tgaagatact
600
tctcgggaaa ggatcatcgc cgttgaaatg aaaaaaaaaa aaaaaaaa
648

<210> 3750
<211> 105
<212> PRT
<213> Homo sapiens

<400> 3750
Arg Ala Pro Trp Glu Asp Pro Ala Lys Trp Val Met Asp Thr Tyr Pro
 1   5   10   15
Trp Ala Ala Ser Pro Gln Gln His Glu Trp Pro Pro Leu Leu Gln Leu
            20   25   30
Arg Pro Glu Asp Val Gly Phe Asp Gly Tyr Ser Met Pro Arg Glu Gly
        35   40   45
Ser Thr Ser Lys Gln Met Pro Pro Ser Asp Ala Glu Gly Asp Pro Leu
    50   55   60
Met Asn Met Leu Met Arg Leu Gln Glu Ala Ala Asn Tyr Ser Ser Pro
65   70   75   80
Gln Ser Tyr Asp Ser Asp Ser Asn Ser Asn Ser His His Asp Asp Ile
                85   90   95
Leu Asp Ser Ser Leu Glu Ser Thr Leu
            100   105

<210> 3751
<211> 554
<212> DNA
<213> Homo sapiens

<400> 3751
gcgcgcctgt ctgccctcgc acgtgcgctg gcagggccgc cgcctcgccc tcaccatgga
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cctggccccg ctgctgctcg cggctcggtc gccccgagcg gggccaaggg cgtttcctac
120
acgcagggcc agagtccgga gccgcggacc cgcgaggtat ttctactacg tggaccacca
180
gggccagctt ttcctggatg attccaaaat gaagaatttc atcacctgct tcaaagaccc
240
gcagttcctg gtcaccttct tctcccgcct gagacccaac cgcagcgggc gctacgaggc
300
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360
gccggtggtc ttcacgcacc tgctgaccgc ggaccacggg cctccgcgcc tctcctactg
420
cggcggtggc gaggccctgg ccgtgccctt cgagccggcg cgcctgctgc ccctggccgc
480
caacgggcgc ctgtaccacc cggcgccgga gcgtgcgggc ggcgtgggcc tgggtgcgcc
540
ttcgcccctg gccc
554

<210> 3752
<211> 66
<212> PRT
<213> Homo sapiens

<400> 3752
Ala Arg Leu Ser Ala Leu Ala Arg Ala Leu Ala Gly Pro Pro Pro Arg
 1   5   10   15
Pro His His Gly Pro Gly Pro Ala Ala Ala Arg Gly Ser Val Ala Pro
            20   25   30
Ser Gly Ala Lys Gly Val Ser Tyr Thr Gln Gly Gln Ser Pro Glu Pro
        35   40   45
Arg Thr Arg Glu Val Phe Leu Leu Arg Gly Pro Pro Gly Pro Ala Phe
    50   55   60
Pro Gly
65

<210> 3753
<211> 1426
<212> DNA
<213> Homo sapiens

<400> 3753
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gaacccactc tcctaaccca cccccgagag gcggagagaa tgtgggagca cttcagagag
120
gcctaggctc cggagatcgg gccatctggg ctctgaaagc aaattagttt tccaactcat
180
gtctggctcc ggcgttaccc agacgcctgg aaggtccttc ctgcagtctg atcaccattt
240
ttcctgctgc actgaccaat cagctccccc tggccttcaa cctcgggaat gatggattag
300
gggagtctag aaatggacga agccctagaa acgcagctga agacgagcag aggacgcttc
360

tcggctacag aatccctccc caccttggag ctcttatctc aggtggacat ggactgcagg
420
gtccacatgc gacccatcgg cctgacgtgg gtgctgcaac tgaccttggc atggatcctg
480
ctagaagcct gtggagggag ccgcccactc caagccaggt cccagcaaca ccatgggctg
540
gcagctgatc tgggcaaagg caagctgcac ctggcaggac cttgttgtcc ctcagagatg
600
gacacaacag agacatcggg ccctggaaac catccagaac gctgtggagt gccgagccct
660
gaatgcgaat ccttcctgga acacctccaa cgtgcccttc gcagtcgctt ccgcctgcgg
720
ctattggggg tacgccaggc acagccgctc tgcgaggagc tctgccaggc ctggttcgcc
780
aactgcgaag atgatatcac ctgcggcccg acttggctcc cactctcaga aaaaaggggc
840
tgtgagccca gctgccttac ctatggacag accttcgcag acgggacgga cctttgtcgc
900
tcggctctgg gccacgccct accggtggct gctcctggag cccgtcactg cttcaacatc
960
tccatctccg cggtacctcg tcccagacca ggacgacggg gccgggaagc tccctcccgg
1020
cgttcccgca gccctcgcac ctccatcctg gacgctgcgg gcagcgggag tggcagtgga
1080
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1200
ttgagatgtc tgtccctcct ccctggagct ccagagaccc acccctctcc aggttatccc
1260
agaaatgacc caactctctc acttttccct ctccccttg aataaagtcg ccagctaaaa
1320
aaaaagtcca tgtccacctg agataagagc tgttggctgg attgggggt ccacatgcga
1380
cccatcggcc tgacgtgggt gctgcaactg acctcggcat ggatcc
1426

<210> 3754
<211> 261
<212> PRT
<213> Homo sapiens

<400> 3754
Met Asp Glu Ala Leu Glu Thr Gln Leu Lys Thr Ser Arg Gly Arg Phe
1 5 10 15
Ser Ala Thr Glu Ser Leu Pro Thr Leu Glu Leu Leu Ser Gln Val Asp
20 25 30
Met Asp Cys Arg Val His Met Arg Pro Ile Gly Leu Thr Trp Val Leu
35 40 45
Gln Leu Thr Leu Ala Trp Ile Leu Leu Glu Ala Cys Gly Gly Ser Arg
50 55 60
Pro Leu Gln Ala Arg Ser Gln Gln His His Gly Leu Ala Ala Asp Leu
65 70 75 80
Gly Lys Gly Lys Leu His Leu Ala Gly Pro Cys Cys Pro Ser Glu Met

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                85                  90                  95
Asp Thr Thr Glu Thr Ser Gly Pro Gly Asn His Pro Glu Arg Cys Gly
            100                 105                 110
Val Pro Ser Pro Glu Cys Glu Ser Phe Leu Glu His Leu Gln Arg Ala
        115                 120                 125
Leu Arg Ser Arg Phe Arg Leu Arg Leu Leu Gly Val Arg Gln Ala Gln
    130                 135                 140
Pro Leu Cys Glu Glu Leu Cys Gln Ala Trp Phe Ala Asn Cys Glu Asp
145                 150                 155                 160
Asp Ile Thr Cys Gly Pro Thr Trp Leu Pro Leu Ser Glu Lys Arg Gly
                165                 170                 175
Cys Glu Pro Ser Cys Leu Thr Tyr Gly Gln Thr Phe Ala Asp Gly Thr
            180                 185                 190
Asp Leu Cys Arg Ser Ala Leu Gly His Ala Leu Pro Val Ala Ala Pro
        195                 200                 205
Gly Ala Arg His Cys Phe Asn Ile Ser Ile Ser Ala Val Pro Arg Pro
    210                 215                 220
Arg Pro Gly Arg Arg Gly Arg Glu Ala Pro Ser Arg Arg Ser Arg Ser
225                 230                 235                 240
Pro Arg Thr Ser Ile Leu Asp Ala Ala Gly Ser Gly Ser Gly Ser Gly
                245                 250                 255
Ser Gly Ser Gly Pro
            260
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<210> 3755
<211> 3149
<212> DNA
<213> Homo sapiens

<400> 3755

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gctccaagta caagtaacag ccaatcagat ttgttttccg aagagaccac cagtgacaac
120
aacaatacct cgataaccac gccaactctt agtcccagcc agcagccgct tccgacagaa
180
ctgaatgtaa cttcaccgag taaagaggag tgtgggccat gcacagacac agctcatgtc
240
tcattaatca caccaacaaa aagatcctgt ggtacagatt cacagtctga gaatgaggct
300
tcaccagtaa aacggccacg actacttgag aatacggaac ggtccgagga aaccagtcga
360
tctaaacaga agagtcgacg tcggtgcttc cagtgccaaa ccaaactgga gctggtgcag
420
caggaattgg gatcgtgtcg ctgcggttat gtgttctgta tgttacatcg cctccccgag
480
cagcacgact gcacattcga ccacatgggc cgtggccggg aggaagccat catgaaaatg
540
gtgaagctgg accggaaagt ggggcgctcc tgccagcgca tcggggaggg gtgctcctga
600
aggccaggca tggccaccac gtgacgctgt tcttagttca ctaatgttag ccttatttag
660
gacaaagtca gccagacacc ttgtactggg cacgcgtcag actgcagcca gtccgtttcc
720
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tttctttagc cagccatcct ggtactgtag tttaggggtt gatggtggtt gaaattgatt
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900
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960
tagaagctgg tgttaaagtt cccacgacgc acatggcttt gccagaaact ctgtttaatg
1020
atcggccttt cacctcttca cttatcctta gtcccagtag ccaggatacc tgatggccac
1080
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1140
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2340

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3149

<210> 3756
<211> 199
<212> PRT
<213> Homo sapiens

<400> 3756
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20 25 30
Ser Glu Glu Thr Thr Ser Asp Asn Asn Asn Thr Ser Ile Thr Thr Pro
35 40 45
Thr Leu Ser Pro Ser Gln Gln Pro Leu Pro Thr Glu Leu Asn Val Thr
50 55 60
Ser Pro Ser Lys Glu Glu Cys Gly Pro Cys Thr Asp Thr Ala His Val
65 70 75 80
Ser Leu Ile Thr Pro Thr Lys Arg Ser Cys Gly Thr Asp Ser Gln Ser
85 90 95
Glu Asn Glu Ala Ser Pro Val Lys Arg Pro Arg Leu Leu Glu Asn Thr
100 105 110
Glu Arg Ser Glu Glu Thr Ser Arg Ser Lys Gln Lys Ser Arg Arg Arg
115 120 125
Cys Phe Gln Cys Gln Thr Lys Leu Glu Leu Val Gln Gln Glu Leu Gly
130 135 140
Ser Cys Arg Cys Gly Tyr Val Phe Cys Met Leu His Arg Leu Pro Glu

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145                 150                 155                 160
Gln His Asp Cys Thr Phe Asp His Met Gly Arg Gly Arg Glu Glu Ala
                165                 170                 175
Ile Met Lys Met Val Lys Leu Asp Arg Lys Val Gly Arg Ser Cys Gln
            180                 185                 190
Arg Ile Gly Glu Gly Cys Ser
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<210> 3757
<211> 1046
<212> DNA
<213> Homo sapiens

<400> 3757
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120
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180
ctgggtgaaa aagctgcagc aaagagacaa gtcctaaatg ccgactcagt ggaacaatct
240
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300
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360
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420
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480
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540
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600
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660
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720
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780
gacatgcccg tgctgttccc tgcccgtcct gccccatgca ccatcgctgc ttctgccttc
840
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900
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1046

<210> 3758
<211> 199
<212> PRT

<213> Homo sapiens

<400> 3758

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Ala Val Asp Leu Cys Gly Arg Leu Leu Thr Ala His Gly Gln Gly Tyr
            20                  25                  30
Gly Lys Ser Gly Leu Leu Thr Ser His Thr Thr Asp Ser Leu Gln Leu
        35                  40                  45
Trp Phe Val Arg Leu Ala Leu Leu Val Lys Leu Gly Leu Phe Gln Asn
    50                  55                  60
Ala Glu Met Glu Phe Glu Pro Phe Gly Asn Leu Asp Gln Pro Asp Leu
65                  70                  75                  80
Tyr Ser Glu Tyr Tyr Pro His Val Tyr Pro Gly Arg Arg Gly Ser Met
                85                  90                  95
Val Pro Phe Ser Met Arg Ile Leu His Ala Glu Leu Gln Gln Tyr Leu
            100                 105                 110
Gly Asn Pro Gln Glu Ser Leu Asp Arg Leu His Lys Val Lys Thr Val
        115                 120                 125
Cys Ser Lys Val Gly Gly Ala Val Ile Leu Pro Cys His Gly Glu Asn
    130                 135                 140
Met Pro Ser Thr Pro Ser Pro Gln Asp Met Pro Val Leu Phe Pro Ala
145                 150                 155                 160
Arg Pro Ala Pro Cys Thr Ile Ala Ala Ser Ala Phe Arg Arg Leu Gly
                165                 170                 175
Asp Pro Gly Leu Cys Gly Leu Val Val Val Ala Leu Ala Glu Ile Phe
            180                 185                 190
Phe Arg Asp Gly Lys Ser Phe
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<210> 3759
<211> 830
<212> DNA
<213> Homo sapiens

<400> 3759

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120
agagcaaagg caggcggacg agctcctgga aaaaattgag agcatggtgc atcagaatgg
180
gaacaagcat tgtgttttca gagaaaaaga aaccctgaac attgtccttg tggggagaag
240
cgggactggg aagagtgcga ccgggaactc tatcctgggg agcctcgtct tcacctctcg
300
gctccgggcc cagccagtca ccaagaccag ccagagtggc aggaggacat gggacggaca
360
ggaggtggtg gttgtggaca cccttccttc aaccagatgc tggatgtcaa aggacccatc
420
ccggttaaaa gaggaggtca agcgctgttt gtcctgctgt gaaaaagggg acacattttt
480
gtcctggtgt tccagctggg acgattcact gaagaggaca aaacagctgt ggcgaaactg
540
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gaggccatct ttggagcaga ctttacgaaa tacgcgatta tgctgttcac ccggaaggaa
600
gacctagggg cggggaattt ggaagacttc atgaagaact cagataacaa agcccttcgg
660
cgcattttaa aaaagtgggg ggggcgagtt tgtgctttta acaacaaaga aacaggccag
720
gcccaggaaa cccaggtgaa agctctttta acaaaggtca atgatctgag aaaagaaagt
780
gggtggtccg ggtatcccca tacacaggag aacgtcagcc cttcacgcgt
830

<210> 3760
<211> 100
<212> PRT
<213> Homo sapiens

<400> 3760
Glu His Gly Ala Ser Glu Trp Glu Gln Ala Leu Cys Phe Gln Arg Lys
1 5 10 15
Arg Asn Pro Glu His Cys Pro Cys Gly Glu Lys Arg Asp Trp Glu Glu
20 25 30
Cys Asp Arg Glu Leu Tyr Pro Gly Glu Pro Arg Leu His Leu Ser Ala
35 40 45
Pro Gly Pro Ala Ser His Gln Asp Gln Pro Glu Trp Gln Glu Asp Met
50 55 60
Gly Arg Thr Gly Gly Gly Gly Cys Gly His Pro Ser Phe Asn Gln Met
65 70 75 80
Leu Asp Val Lys Gly Pro Ile Pro Val Lys Arg Gly Gly Gln Ala Leu
85 90 95
Phe Val Leu Leu
100

<210> 3761
<211> 458
<212> DNA
<213> Homo sapiens

<400> 3761
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ccgacgccgc cattaagggc gggttgcctt tcggaacgtc ctcctcctga gggcctgggg
120
aagggaggcc gcccggccgc agcgggaggt ggcccccggg gacaccccgg cgccccgagg
180
cgaggcaccc ccgaaccccg atccctgctg gcaggaccag aggtgtgagg gtgggggcgg
240
ggaagccttg ccgcgggggc aatggtcgta cgcacggagc gcacatccct ctccttcctg
300
attggccgag cgggggtgtg cgtgatgcca cgctccgccc gtcgtacgtg gggcgctcgc
360
gctgcgtgca gacgcgcttg attggttaga taaggggggcg ggggccgccg ctgttaccag
420
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458

<210> 3762
<211> 75
<212> PRT
<213> Homo sapiens

<400> 3762
Thr Arg Ala Gly Gly Thr Gln Arg Pro Gln Val Arg Thr Pro Pro Pro
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Pro Pro Thr Pro Pro Thr Pro Pro Leu Arg Ala Gly Cys Leu Ser Glu
20 25 30
Arg Pro Pro Pro Glu Gly Leu Gly Lys Gly Gly Arg Pro Ala Ala Ala
35 40 45
Gly Gly Gly Pro Pro Gly His Pro Gly Ala Pro Arg Arg Gly Thr Pro
50 55 60
Glu Pro Arg Ser Leu Leu Ala Gly Pro Glu Val
65 70 75

<210> 3763
<211> 1340
<212> DNA
<213> Homo sapiens

<400> 3763
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120
tgggcagggt cccctcccac gctcctgccg ctgtctccca cgtcccccag gtgcgcggcc
180
accatggcgt ccagcgacga ggacggcacc aacggcggcg cctcggaggc cggcgaggac
240
cgggaggctc ccggcaagcg gaggcgcctg gggttcttgg ccaccgcctg gctcaccttc
300
tacgacatcg ccatgaccgc ggggtggttg gttctagcta ttgccatggt acgtttttat
360
atggaaaagg gaacacacag agggttatat aaaagtattc agaagacact taaatttttc
420
cagacatttg ccttgcttga gatagttcac tgtttaattg gaattgtacc tacttctgtg
480
attgtgactg gggtccaagt gagctcaaga atctttatgg tgtggctcat tactcacagt
540
ataaaaccaa tccagaatga agagagtgtg gtgctttttc tggtcgcgtg gactgtgaca
600
gagatcactc gctattcctt ctacacattc agccttcttg accacttgcc atacttcatt
660
aaatgggcca gatataattt ttttatcatc ttatatcctg ttggagttgc tggtgaactt
720
cttacaatat acgctgcctt gccgtatgtg aagaaaacag gaatgttttc aataagactt
780
cctaacaaat acaatgtctc ttttgactac tattattttc ttcttataac catggcatca
840
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900

catggagagg tgattgtaga aaaggatgat taaatgatct ctgcaaacaa ggtgcttttt
960
ccagaataac caagattacc tgagtccaag ttttaataac aagaataaac aactttgtga
1020
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1140
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aatgcaaaat ttttaacaaa
1340

<210> 3764
<211> 288
<212> PRT
<213> Homo sapiens

<400> 3764
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Ala Gly Trp Ala Gly Ser Pro Pro Thr Leu Leu Pro Leu Ser Pro Thr
            20   25   30
Ser Pro Arg Cys Ala Ala Thr Met Ala Ser Ser Asp Glu Asp Gly Thr
        35   40   45
Asn Gly Gly Ala Ser Glu Ala Gly Glu Asp Arg Glu Ala Pro Gly Lys
    50   55   60
Arg Arg Arg Leu Gly Phe Leu Ala Thr Ala Trp Leu Thr Phe Tyr Asp
65   70   75   80
Ile Ala Met Thr Ala Gly Trp Leu Val Leu Ala Ile Ala Met Val Arg
                85   90   95
Phe Tyr Met Glu Lys Gly Thr His Arg Gly Leu Tyr Lys Ser Ile Gln
            100   105   110
Lys Thr Leu Lys Phe Phe Gln Thr Phe Ala Leu Leu Glu Ile Val His
        115   120   125
Cys Leu Ile Gly Ile Val Pro Thr Ser Val Ile Val Thr Gly Val Gln
    130   135   140
Val Ser Ser Arg Ile Phe Met Val Trp Leu Ile Thr His Ser Ile Lys
145   150   155   160
Pro Ile Gln Asn Glu Glu Ser Val Val Leu Phe Leu Val Ala Trp Thr
                165   170   175
Val Thr Glu Ile Thr Arg Tyr Ser Phe Tyr Thr Phe Ser Leu Leu Asp
            180   185   190
His Leu Pro Tyr Phe Ile Lys Trp Ala Arg Tyr Asn Phe Phe Ile Ile
        195   200   205
Leu Tyr Pro Val Gly Val Ala Gly Glu Leu Leu Thr Ile Tyr Ala Ala
    210   215   220
Leu Pro Tyr Val Lys Lys Thr Gly Met Phe Ser Ile Arg Leu Pro Asn
225   230   235   240
Lys Tyr Asn Val Ser Phe Asp Tyr Tyr Tyr Phe Leu Leu Ile Thr Met

245 250 255
Ala Ser Tyr Ile Pro Leu Phe Pro Gln Leu Tyr Phe His Met Leu Arg
260 265 270
Gln Arg Arg Lys Val Leu His Gly Glu Val Ile Val Glu Lys Asp Asp
275 280 285

<210> 3765
<211> 2764
<212> DNA
<213> Homo sapiens

<400> 3765
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240
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300
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420
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720
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780
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960
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1260

aacaatttca gctggcatgc atccacagag tgctttctgt gctcttgctg cagcaaatgc
1320
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1380
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1560
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1980
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2160
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2400
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2460
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2760
ttaa
2764

<210> 3766

<211> 464
<212> PRT
<213> Homo sapiens

<400> 3766
Xaa Val Ala Val Glu Arg Arg Arg Gly Ser Ser Ala Gly Phe Pro Cys
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Ser Gln Arg Ser Arg Arg Pro Ala Glu Pro Gly Arg Gly Ile Pro Asp
20 25 30
Arg Arg Arg Arg Gly Pro Ile Gly Arg Val Asn Met Asp Leu Glu Asn
35 40 45
Lys Val Lys Lys Met Gly Leu Gly His Glu Gln Gly Phe Gly Ala Pro
50 55 60
Cys Leu Lys Cys Lys Glu Lys Cys Glu Gly Phe Glu Leu His Phe Trp
65 70 75 80
Arg Lys Ile Cys Arg Asn Cys Lys Cys Gly Gln Glu Glu His Asp Val
85 90 95
Leu Leu Ser Asn Glu Glu Asp Arg Lys Val Gly Lys Leu Phe Glu Asp
100 105 110
Thr Lys Tyr Thr Thr Leu Ile Ala Lys Leu Lys Ser Asp Gly Ile Pro
115 120 125
Met Tyr Lys Arg Asn Val Met Ile Leu Thr Asn Pro Val Ala Ala Lys
130 135 140
Lys Asn Val Ser Ile Asn Thr Val Thr Tyr Glu Trp Ala Pro Pro Val
145 150 155 160
Gln Asn Gln Ala Leu Ala Arg Gln Tyr Met Gln Met Leu Pro Lys Glu
165 170 175
Lys Gln Pro Val Ala Gly Ser Glu Gly Ala Gln Tyr Arg Lys Lys Gln
180 185 190
Leu Ala Lys Gln Leu Pro Ala His Asp Gln Asp Pro Ser Lys Cys His
195 200 205
Glu Leu Ser Pro Arg Glu Val Lys Glu Met Glu Gln Phe Val Lys Lys
210 215 220
Tyr Lys Ser Glu Ala Leu Gly Val Gly Asp Val Lys Leu Pro Cys Glu
225 230 235 240
Met Asp Ala Gln Gly Pro Lys Gln Met Asn Ile Pro Gly Gly Asp Arg
245 250 255
Ser Thr Pro Ala Ala Val Gly Ala Met Glu Asp Lys Ser Ala Glu His
260 265 270
Lys Arg Thr Gln Tyr Ser Cys Tyr Cys Cys Lys Leu Ser Met Lys Glu
275 280 285
Gly Asp Pro Ala Ile Tyr Ala Glu Arg Ala Gly Tyr Asp Lys Leu Trp
290 295 300
His Pro Ala Cys Phe Val Cys Ser Thr Cys His Glu Leu Leu Val Asp
305 310 315 320
Met Ile Tyr Phe Trp Lys Asn Glu Lys Leu Tyr Cys Gly Arg His Tyr
325 330 335
Cys Asp Ser Glu Lys Pro Arg Cys Ala Gly Cys Asp Glu Leu Ile Phe
340 345 350
Ser Asn Glu Tyr Thr Gln Ala Glu Asn Gln Asn Trp His Leu Lys His
355 360 365
Phe Cys Cys Phe Asp Cys Asp Ser Ile Leu Ala Gly Glu Ile Tyr Val
370 375 380
Met Val Asn Asp Lys Pro Val Cys Lys Pro Cys Tyr Val Lys Asn His

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385                 390                 395                 400
Ala Val Val Cys Gln Gly Cys His Asn Ala Ile Asp Pro Glu Val Gln
                405                 410                 415
Arg Val Thr Tyr Asn Asn Phe Ser Trp His Ala Ser Thr Glu Cys Phe
            420                 425                 430
Leu Cys Ser Cys Cys Ser Lys Cys Leu Ile Gly Gln Lys Phe Met Pro
        435                 440                 445
Val Glu Gly Met Val Phe Cys Ser Val Glu Cys Lys Lys Arg Met Ser
    450                 455                 460
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<210> 3767
<211> 2439
<212> DNA
<213> Homo sapiens

<400> 3767
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240
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300
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420
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1140

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1320
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2280
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2439

<210> 3768
<211> 379
<212> PRT
<213> Homo sapiens

<400> 3768
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Asn Ala Asp Ser Val Glu Gln Ser Phe Val Gly Leu Lys Gln Leu Ile

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Ser Cys Arg Asn Trp Arg Ala Ala Val Asp Leu Cys Gly Arg Leu Leu
        35                  40                  45
Thr Ala His Gly Gln Gly Tyr Gly Lys Ser Gly Leu Leu Thr Ser His
    50                  55                  60
Thr Thr Asp Ser Leu Gln Leu Trp Phe Val Arg Leu Ala Leu Leu Val
65                  70                  75                  80
Lys Leu Gly Leu Phe Gln Asn Ala Glu Met Glu Phe Glu Pro Phe Gly
                85                  90                  95
Asn Leu Asp Gln Pro Asp Leu Tyr Tyr Glu Tyr Tyr Pro His Val Tyr
            100                 105                 110
Pro Gly Arg Arg Gly Ser Met Val Pro Phe Ser Met Arg Ile Leu His
        115                 120                 125
Ala Glu Leu Gln Gln Tyr Leu Gly Asn Pro Gln Glu Ser Leu Asp Arg
    130                 135                 140
Leu His Lys Val Lys Thr Val Cys Ser Lys Ile Leu Ala Asn Leu Glu
145                 150                 155                 160
Gln Gly Leu Ala Glu Asp Gly Gly Met Ser Ser Val Thr Gln Glu Gly
                165                 170                 175
Arg Gln Ala Ser Ile Arg Leu Trp Arg Ser Arg Leu Gly Arg Val Met
            180                 185                 190
Tyr Ser Met Ala Asn Cys Leu Leu Leu Met Lys Asp Tyr Val Leu Ala
        195                 200                 205
Val Glu Ala Tyr His Ser Val Ile Lys Tyr Tyr Pro Glu Gln Glu Pro
    210                 215                 220
Gln Leu Leu Ser Gly Ile Gly Arg Ile Ser Leu Gln Ile Gly Asp Ile
225                 230                 235                 240
Lys Thr Ala Glu Lys Tyr Phe Gln Asp Val Glu Lys Val Thr Gln Lys
                245                 250                 255
Leu Asp Gly Leu Gln Gly Lys Ile Met Val Leu Met Asn Ser Ala Phe
            260                 265                 270
Leu His Leu Gly Gln Asn Asn Phe Ala Glu Ala His Arg Phe Phe Thr
        275                 280                 285
Glu Ile Leu Arg Met Asp Pro Arg Asn Ala Val Ala Asn Asn Asn Ala
    290                 295                 300
Ala Val Cys Leu Leu Tyr Leu Gly Lys Leu Lys Asp Ser Leu Arg Gln
305                 310                 315                 320
Leu Glu Ala Met Val Gln Gln Asp Pro Arg His Tyr Leu His Glu Ser
                325                 330                 335
Val Leu Phe Asn Leu Thr Thr Met Tyr Glu Leu Glu Ser Ser Arg Ser
            340                 345                 350
Met Gln Lys Lys Gln Ala Leu Leu Glu Ala Val Ala Gly Lys Glu Gly
        355                 360                 365
Asp Ser Phe Asn Thr Gln Cys Leu Lys Leu Ala
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<210> 3769
<211> 1931
<212> DNA
<213> Homo sapiens

<400> 3769
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atgaagacac tgaagtttac aacatcaccc tgtgtactgg ggatgaactc actctaatgg
120
ggcaggcaga aatcctttat gcaaagacat tcaaggaaaa gtcacgactc aacacaatct
180
tcaaaaagat tgggaagctc aattccatca gcaagctggg aaaaggcaaa atgccgtgcc
240
tcatttgtat gaatcaccgg accaacgaaa gcattagcct tccattccag tgcaagggca
300
gatttagcac ccgaagtccc ctggaacttc agatgcaaga gggcgaacac accatccgca
360
acattgtgga gaaaaccagg cttcctgtga atgtgactgt gccaagccct ccaccgagaa
420
acccatacga cctccacttc atccgtgagg ggcaccgcta taagtttgtg agcatccaga
480
ccaagacggt ggtggtttgc tgtgtgctgc ggaacaacaa gatcctcccc atgcactttc
540
ctttgcactt gactgtcccc aagttcagcc tcccagaacc cctggtgaag ggagagagct
600
ggcccgaaac cctggtccca tcccgggcta ggtatctgcc aagaacagtt cgacatcgat
660
gagtattcac gggctgtccg tgatgtgaaa accgactgga atgaagaatg caagagcccc
720
aagaagggtc ggtgctctgg ccacaaccac gtgcccaatt cgctcagcta cgcccgcgat
780
gagctcaccc agtccttcca ccgactctcg gtctgtgtgt atggcaacaa tctccatggc
840
aacagtgagg tgaaccttca tggttgcagg gacctggggg gagattgggc tccctttcct
900
catgacatcc tgccctatca ggactctgga gatagtggga gcgactacct ttcccagaa
960
gctagtgaag aatcagcagg catcccggga aagtcagaac ttccctacga agagctgtgg
1020
ctggaggaag gcaagcccag ccatcagcct ctcactcgct ctctgagcga gaagaacaga
1080
tgtgatcagt ttagaggttc tgtccgatcc aaatgtgcga cttctcctct tcccatccct
1140
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cccaaatctg aagccgtcag agaagaatgc cggctcctga acgccccacc tgttccaccc
1260
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1320
cggcaacaga ctcgctctcc cagccccacc ttgtcctact attcttcagg gctacacaac
1380
atcgtcacta aaactgacac aaatccttct gaaagcactc ctgtttcctg ctatccatgt
1440
aaccgagtga aaactgattc tgtggacctg aaatccccgt ttggaagtcc ttctgctgaa
1500
gctgtgtcct ctcggctctc atggcctaac cattattcag gagcatcaga aagccagacc
1560
aggagtgact tcctgctgga tccaagcagg agttatagtt accctagaca aaagacgcca
1620
ggcacaccaa agagaaactg cccagcacct tttgattttg atggctgtga gctcctggcc
1680

agccccacta gcccagtcac tgcagaattc agtagcagcg tctctggttg tcccaagtca
1740
gccagctact ctctggagag cacagatgtg aaatctcttg cagctggtgt gacaaagcag
1800
agtacgtcat gccctgcctt acccccccagg gctccaaaac tagtggaaga gaaggtcgcc
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1920
tcaccagatc t
1931

<210> 3770
<211> 447
<212> PRT
<213> Homo sapiens

<400> 3770
Arg Glu Arg Ala Gly Pro Lys Pro Trp Ser His Pro Gly Leu Gly Ile
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Cys Gln Glu Gln Phe Asp Ile Asp Glu Tyr Ser Arg Ala Val Arg Asp
20 25 30
Val Lys Thr Asp Trp Asn Glu Glu Cys Lys Ser Pro Lys Lys Gly Arg
35 40 45
Cys Ser Gly His Asn His Val Pro Asn Ser Leu Ser Tyr Ala Arg Asp
50 55 60
Glu Leu Thr Gln Ser Phe His Arg Leu Ser Val Cys Val Tyr Gly Asn
65 70 75 80
Asn Leu His Gly Asn Ser Glu Val Asn Leu His Gly Cys Arg Asp Leu
85 90 95
Gly Gly Asp Trp Ala Pro Phe Pro His Asp Ile Leu Pro Tyr Gln Asp
100 105 110
Ser Gly Asp Ser Gly Ser Asp Tyr Leu Phe Pro Glu Ala Ser Glu Glu
115 120 125
Ser Ala Gly Ile Pro Gly Lys Ser Glu Leu Pro Tyr Glu Glu Leu Trp
130 135 140
Leu Glu Glu Gly Lys Pro Ser His Gln Pro Leu Thr Arg Ser Leu Ser
145 150 155 160
Glu Lys Asn Arg Cys Asp Gln Phe Arg Gly Ser Val Arg Ser Lys Cys
165 170 175
Ala Thr Ser Pro Leu Pro Ile Pro Gly Thr Leu Gly Ala Ala Val Lys
180 185 190
Ser Ser Asp Thr Ala Leu Pro Pro Pro Pro Val Pro Pro Lys Ser Glu
195 200 205
Ala Val Arg Glu Glu Cys Arg Leu Leu Asn Ala Pro Pro Val Pro Pro
210 215 220
Arg Ser Ala Lys Pro Leu Ser Thr Ser Pro Ser Ile Pro Pro Arg Thr
225 230 235 240
Val Lys Pro Ala Arg Gln Gln Thr Arg Ser Pro Ser Pro Thr Leu Ser
245 250 255
Tyr Tyr Ser Ser Gly Leu His Asn Ile Val Thr Lys Thr Asp Thr Asn
260 265 270
Pro Ser Glu Ser Thr Pro Val Ser Cys Tyr Pro Cys Asn Arg Val Lys
275 280 285
Thr Asp Ser Val Asp Leu Lys Ser Pro Phe Gly Ser Pro Ser Ala Glu

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    290                 295                 300
Ala Val Ser Ser Arg Leu Ser Trp Pro Asn His Tyr Ser Gly Ala Ser
305                 310                 315                 320
Glu Ser Gln Thr Arg Ser Asp Phe Leu Leu Asp Pro Ser Arg Ser Tyr
                325                 330                 335
Ser Tyr Pro Arg Gln Lys Thr Pro Gly Thr Pro Lys Arg Asn Cys Pro
            340                 345                 350
Ala Pro Phe Asp Phe Asp Gly Cys Glu Leu Leu Ala Ser Pro Thr Ser
        355                 360                 365
Pro Val Thr Ala Glu Phe Ser Ser Ser Val Ser Gly Cys Pro Lys Ser
    370                 375                 380
Ala Ser Tyr Ser Leu Glu Ser Thr Asp Val Lys Ser Leu Ala Ala Gly
385                 390                 395                 400
Val Thr Lys Gln Ser Thr Ser Cys Pro Ala Leu Pro Pro Arg Ala Pro
                405                 410                 415
Lys Leu Val Glu Glu Lys Val Ala Ser Glu Thr Ser Pro Leu Pro Leu
            420                 425                 430
Lys Ile Asp Gly Ala Glu Glu Asp Pro Lys Ser Gly Ser Pro Asp
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<210> 3771
<211> 1514
<212> DNA
<213> Homo sapiens

<400> 3771
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attcgaatag gagaccttaa acctacaagt gaaattccta agcaggttaa agtgaaaaaa
180
ctgaagaatc taaagactct ggattccaaa cctggagttt atacttcata taagccatat
240
ttaaatagag atgaagagat cataaaacaa ttacagaagg gtgtacaaca gaaacgtcct
300
tctgaggctc aaagtgttat tcttcgacgc tatttttgg aactgacaca aagtttcatc
360
attccattag aaagatatgt ggcaagcttg atgcctttgc agaaaagtat ttccccatgg
420
aagagtccac ctcaattaag acagtttctt ccagaagaat ttatgaaaac acttgagaaa
480
acaggacctc agctaacctc tagaataaaa ggcgattgga ttggacttta ccggcatttc
540
ctaaagtctc caaattttga tggctggttt aagacccgga ggaaggaaat gacccaaaaa
600
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720
gatcgagagc acttacctgt gaaacctgac actatggaaa agttacggac acacatagat
780
gccattatct tagcattgcc agaggacttg caaggcatac tgctcaaaac gggcatgaca
840

tgatatttgc caagattttc cagccaaaaa ggattatgca tcatgaagca tactgacatt
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tcaaccagac gcacaaagga gatctctcag tggcagcgga gtggaaaatt gccatgaatg
960
ctagttacag ggtagaaaga ctgtattgta taaacagacc tttttagtgc attacttttt
1020
aaagtggata tctgtggtgg ttccacttta atactgaaac accgaaaggc atttctatat
1080
ttttaatcat gttctaaagt gctcttatga gagacttgtg ggccatcagt attagtgatt
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1200
tgttaaaact caggggata taaaaataac attcacactg gctatcttct taagaacaga
1260
aagactgaac tgtcctatgg ttagaaggaa ttgatgctta tgtagtgcct tctgttgccc
1320
tacatgtttc acagttcagc tgctagtctt gaagcttttc cttagcttca ttatgatacg
1380
taattttata aggtattctg ttgagtgatc attgtttaaa aaaaaagttt cttgctaccc
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1514

<210> 3772
<211> 280
<212> PRT
<213> Homo sapiens

<400> 3772
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20 25 30
Thr Leu Gln His Trp Pro His Ile Ile Arg Ile Gly Asp Leu Lys Pro
35 40 45
Thr Ser Glu Ile Pro Lys Gln Val Lys Val Lys Lys Leu Lys Asn Leu
50 55 60
Lys Thr Leu Asp Ser Lys Pro Gly Val Tyr Thr Ser Tyr Lys Pro Tyr
65 70 75 80
Leu Asn Arg Asp Glu Glu Ile Ile Lys Gln Leu Gln Lys Gly Val Gln
85 90 95
Gln Lys Arg Pro Ser Glu Ala Gln Ser Val Ile Leu Arg Arg Tyr Phe
100 105 110
Leu Glu Leu Thr Gln Ser Phe Ile Ile Pro Leu Glu Arg Tyr Val Ala
115 120 125
Ser Leu Met Pro Leu Gln Lys Ser Ile Ser Pro Trp Lys Ser Pro Pro
130 135 140
Gln Leu Arg Gln Phe Leu Pro Glu Glu Phe Met Lys Thr Leu Glu Lys
145 150 155 160
Thr Gly Pro Gln Leu Thr Ser Arg Ile Lys Gly Asp Trp Ile Gly Leu
165 170 175
Tyr Arg His Phe Leu Lys Ser Pro Asn Phe Asp Gly Trp Phe Lys Thr

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            180                 185                 190
Arg Arg Lys Glu Met Thr Gln Lys Leu Glu Ala Leu His Leu Glu Ala
        195                 200                 205
Leu Cys Glu Glu Asp Leu Leu Leu Trp Ile Gln Lys His Thr Glu Val
    210                 215                 220
Glu Thr Val Asp Leu Val Leu Lys Leu Lys Asn Lys Leu Leu Gln Ala
225                 230                 235                 240
Asp Arg Glu His Leu Pro Val Lys Pro Asp Thr Met Glu Lys Leu Arg
                245                 250                 255
Thr His Ile Asp Ala Ile Ile Leu Ala Leu Pro Glu Asp Leu Gln Gly
            260                 265                 270
Ile Leu Leu Lys Thr Gly Met Thr
        275                 280
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<210> 3773
<211> 2664
<212> DNA
<213> Homo sapiens

<400> 3773
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120
gccgggagca tgagcgcggg ctcggagcgc ggggcggcgg caacccccgg gggtttgccc
180
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240
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300
caggtgggca gaaccgaggt ggtccggagc agcctgcatc ccgtgttctc caaggtcttc
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420
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480
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600
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720
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780
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840
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900
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1020

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1080
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1380
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1980
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2040
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2100
tgcttggggt cccttaagct ccctccgacc tcccagaagc ctccagtccc caccaggccc
2160
cactcccagt cctcctggga tcctgctggc ttgggcccgg ctctggggcc cccaaggccg
2220
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2280
gggagatcat gagggacttg gagggagctg ggagttcatc cacgggagac cctgccccga
2340
tgagaagggg cagggactgg gggctctgct ttgcgtctaa cctttgtggg ggagggccag
2400
caaggcagtc cccccacgcc cgagaaagcc tgggggaccc agacacctgt ccccacagtc
2460
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2520
ccacacccac ctaccctgtg ctttttgccg tcgggcctct gcacctgggt ccatggggtc
2580
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2640

aaagtgtcac cctatccttg taaa
2664

<210> 3774
<211> 678
<212> PRT
<213> Homo sapiens

<400> 3774
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His Phe Pro Gly Ala Ala Ala Ala Arg Leu Ala Gly Ser Gly Pro Ser
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Val Arg Pro Ala Gly Pro Pro Asn Ala Gly Ser Met Ser Ala Gly Ser
35 40 45
Glu Arg Gly Ala Ala Ala Thr Pro Gly Gly Leu Pro Ala Pro Cys Ala
50 55 60
Ser Lys Val Glu Leu Arg Leu Ser Cys Arg His Leu Leu Asp Arg Asp
65 70 75 80
Pro Leu Thr Lys Ser Asp Pro Ser Val Ala Leu Leu Gln Gln Ala Gln
85 90 95
Gly Gln Trp Val Gln Val Gly Arg Thr Glu Val Val Arg Ser Ser Leu
100 105 110
His Pro Val Phe Ser Lys Val Phe Thr Val Asp Tyr Tyr Phe Glu Glu
115 120 125
Val Gln Arg Leu Arg Phe Glu Val Tyr Asp Thr His Gly Pro Ser Gly
130 135 140
Phe Ser Cys Gln Glu Asp Asp Phe Leu Gly Gly Met Glu Cys Thr Leu
145 150 155 160
Gly Gln Pro Ala Gln Lys Trp Leu Leu Gln Val Val Met Arg Val Ser
165 170 175
Val Asp Val Leu Gly Pro Ala Gly His Cys Ala Lys His Phe Leu Cys
180 185 190
Cys Thr Glu Ser Ser His Leu Ala Arg Thr Gly Pro Ser Phe Leu Leu
195 200 205
Arg Tyr Asp Asp Leu Cys Leu Pro Trp Ala Thr Ala Gly Ala Val Arg
210 215 220
Trp Trp Thr Cys Arg Gly Gly His Thr Gln Gly Trp Gln Ile Val Ala
225 230 235 240
Gln Lys Lys Val Thr Arg Pro Leu Leu Leu Lys Phe Gly Arg Asn Ala
245 250 255
Gly Lys Ser Thr Ile Thr Val Ile Ala Glu Asp Ile Ser Gly Asn Asn
260 265 270
Gly Tyr Val Glu Leu Ser Phe Arg Ala Arg Lys Leu Asp Asp Lys Asp
275 280 285
Leu Phe Ser Lys Ser Asp Pro Phe Leu Glu Leu Tyr Arg Val Asn Asp
290 295 300
Asp Gln Gly Leu Gln Leu Val Tyr Arg Thr Glu Val Val Lys Asn Asn
305 310 315 320
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Ser Cys Asp Val His Arg Pro Leu Lys Phe Leu Val Trp Asp Tyr Asp
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Ser Ser Gly Lys His Asp Phe Ile Gly Glu Phe Thr Ser Thr Phe Gln

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Glu Met Gln Glu Gly Thr Ala Asn Pro Gly Gln Glu Met Gln Trp Asp
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Cys Ile Asn Pro Lys Tyr Arg Asp Lys Lys Lys Asn Tyr Lys Asn Ser
385                 390                 395                 400
Gly Val Val Val Leu Ala Asp Leu Lys Phe His Arg Val Tyr Ser Phe
                405                 410                 415
Leu Asp Tyr Ile Met Gly Gly Cys Gln Ile Ser Phe Thr Val Ala Ile
            420                 425                 430
Asp Phe Thr Ala Ser Asn Gly Asp Pro Arg Ser Ser Gln Ser Leu His
        435                 440                 445
Tyr Ile Ser Pro Arg Gln Pro Asn His Tyr Leu Gln Ala Leu Arg Ala
    450                 455                 460
Val Gly Gly Ile Cys Gln Asp Tyr Asp Ser Asp Lys Arg Phe Pro Ala
465                 470                 475                 480
Phe Gly Phe Gly Ala Arg Ile Pro Pro Asn Phe Glu Val Ser His Asp
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Phe Ala Ile Asn Phe Asn Pro Glu Asp Asp Glu Cys Glu Gly Ile Gln
            500                 505                 510
Gly Val Val Glu Ala Tyr Gln Asn Cys Leu Pro Arg Val Gln Leu Tyr
        515                 520                 525
Gly Pro Thr Asn Val Ala Pro Ile Ile Ser Lys Val Ala Glu Pro Ala
    530                 535                 540
Gln Arg Glu Gln Ser Thr Gly Gln Ala Thr Lys Tyr Ser Val Leu Leu
545                 550                 555                 560
Val Leu Thr Asp Gly Val Val Ser Asp Met Ala Glu Thr Arg Thr Ala
                565                 570                 575
Ile Val Arg Ala Ser Arg Leu Pro Met Ser Ile Ile Ile Val Gly Val
            580                 585                 590
Gly Asn Ala Asp Phe Ser Asp Met Arg Leu Leu Asp Gly Asp Asp Gly
        595                 600                 605
Pro Leu Arg Cys Pro Arg Gly Glu Pro Ala Leu Arg Asp Ile Val Gln
    610                 615                 620
Phe Val Pro Phe Arg Glu Leu Lys Asn Ala Ser Pro Ala Ala Leu Ala
625                 630                 635                 640
Lys Cys Val Leu Ala Glu Val Pro Lys Gln Val Val Glu Tyr Tyr Ser
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His Arg Gly Leu Pro Pro Arg Ser Leu Gly Val Pro Ala Gly Glu Ala
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Ser Pro Gly Cys Thr Pro
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<212> DNA
<213> Homo sapiens

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420
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Asp Gln Ser Lys Tyr Pro Ile Arg Glu Ser Glu Met Arg Glu Tyr Ile
50 55 60
Val Lys Glu Tyr Arg Asn Gln Phe Pro Glu Ile Leu Arg Arg Ala Ala
65 70 75 80
Ala His Leu Glu Cys Ile Phe Arg Phe Glu Leu Arg Glu Leu Asp Pro
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Glu Ala His Thr Tyr Ile Leu Leu Asn Lys Leu Gly Pro Val Pro Phe
100 105 110
Glu Gly Leu Glu Glu Ser Pro Asn Gly Pro Lys Met Gly Leu Leu Met
115 120 125
Met Ile Leu Gly Gln Ile Phe Leu Asn Gly Asn Gln Ala Lys Glu Ala
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Glu Ile Trp Glu Met Leu Trp Arg Met Gly Val Gln Arg Glu Arg Arg
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<212> PRT
<213> Homo sapiens

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Glu Lys Arg Asn Lys Ile Glu Glu Ala Pro Glu Ala Thr Pro Gln Pro
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Ser Gln Pro Gly Pro Ser Ser Pro Ile Ser Leu Ser Ala Glu Glu Glu
50 55 60
Asn Ala Glu Gly Glu Val Ser Arg Ala Asn Thr Pro Asp Ser Asp Ile
65 70 75 80
Thr Glu Lys Thr Glu Asp Ser Ser Val Pro Glu Thr Pro Asp Asn Glu
85 90 95
Arg Lys Ala Ser Ile Ser Tyr Phe Lys Asn Gln Arg Gly Ile Gln Tyr
100 105 110
Ile Asp Leu Ser Ser Asp Ser Glu Asp Val Val Ser Pro Asn Cys Ser
115 120 125
Asn Thr Val Gln Glu Lys Thr Phe Asn Lys Asp Thr Val Ile Ile Val
130 135 140
Ser Glu Pro Ser Glu Asp Glu Glu Ser Gln Gly Leu Pro Thr Met Ala
145 150 155 160
Arg Arg Asn Asp Asp Ile Ser Glu Leu Glu Asp Leu Ser Glu Leu Glu
165 170 175
Asp Leu Lys Asp Ala Lys Leu Gln Thr Leu Lys Glu Leu Phe Pro Gln
180 185 190
Arg Ser Asp Asn Asp Leu Leu Lys Leu Ile Glu Ser Thr Ser Thr Met
195 200 205
Asp Gly Ala Ile Ala Ala Ala Leu Leu Met Phe Gly Asp Ala Gly Gly
210 215 220
Gly Pro Arg Lys Arg Lys Leu Ser Ser Ser Ser Glu Pro Tyr Glu Glu
225 230 235 240
Asp Glu Phe Asn Asp Asp Gln Ser Ile Lys Lys Thr Arg Leu Asp His
245 250 255
Gly Glu Glu Ser Asn Glu Ser Ala Glu Ser Ser Ser Asn Trp Glu Lys
260 265 270
Gln Glu Ser Ile Val Leu Lys Leu Gln Lys Glu Phe Pro Asn Phe Asp
275 280 285
Lys Gln Glu Leu Arg Glu Val Leu Lys Glu His Glu Trp Met Tyr Thr
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Glu Ala Leu Glu Ser Leu Lys Val Phe Ala Glu Asp Gln Asp Met Gln
305 310 315 320
Tyr Ala Ser Gln Ser Glu Val Pro Asn Gly Lys Glu Val Ser Ser Arg
325 330 335
Ser Gln Asn Tyr Pro Lys Asn Ala Thr Lys Thr Lys Leu Lys Gln Lys
340 345 350
Phe Ser Met Lys Ala Gln Asn Gly Phe Asn Lys Lys Arg Lys Lys Asn
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Val Phe Asn Pro Lys Arg Val Val Glu Asp Ser Glu Tyr Asp Ser Gly

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    370                 375                 380
Ser Asp Val Gly Ser Ser Leu Asp Glu Asp Tyr Ser Ser Gly Glu Glu
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Val Met Glu Asp Gly Tyr Lys Gly Lys Ile Leu His Phe Leu Gln Asp
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Ala Ser Ile Gly Glu Leu Thr Leu Ile Pro Gln Cys Ser Gln Lys Lys
            420                 425                 430
Ala Gln Lys Ile Thr Glu Leu Arg Pro Phe Asn Ser Trp Glu Ala Leu
        435                 440                 445
Phe Thr Lys Met Ser Lys Thr Asn Gly Leu Ser Glu Asp Leu Ile Trp
    450                 455                 460
His Cys Lys Thr Leu Ile Gln Glu Arg Asp Val Val Ile Arg Leu Met
465                 470                 475                 480
Asn Lys Cys Glu Asp Ile Ser Asn Lys Leu Thr Lys Gln Val Thr Met
                485                 490                 495
Leu Thr Gly Asn Gly Gly Gly Trp Asn Ile Glu Gln Pro Ser Ile Leu
            500                 505                 510
Asn Gln Ser Leu Ser Leu Lys Pro Tyr Gln Lys Val Gly Leu Asn Trp
        515                 520                 525
Leu Ala Leu Val His Lys His Gly Leu Asn Gly Ile Leu Ala Asp Glu
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Met Gly Leu Gly Lys Thr Ile Gln Ala Ile Ala Phe Leu Ala Tyr Leu
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Tyr Gln Glu Gly Asn Asn Gly Pro His Leu Ile Val Val Pro Ala Ser
                565                 570                 575
Thr Ile Asp Asn Trp Leu Arg Glu Val Asn Leu Trp Cys Pro Thr Leu
            580                 585                 590
Lys Val Leu Cys Tyr Tyr Gly Ser Gln Glu Glu Arg Lys Gln Ile Arg
        595                 600                 605
Phe Asn Ile His Ser Arg Tyr Glu Asp Tyr Asn Val Ile Val Thr Thr
    610                 615                 620
Tyr Asn Cys Ala Ile Ser Ser Ser Asp Asp Arg Ser Leu Phe Arg Arg
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Leu Lys Leu Asn Tyr Ala Ile Phe Asp Glu Gly His Met Leu Lys Asn
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Met Gly Ser Ile Arg Tyr Gln His Leu Met Thr Ile Asn Ala Asn Asn
            660                 665                 670
Arg Leu Leu Leu Thr Gly Thr Pro Val Gln Asn Asn Leu Leu Glu Leu
        675                 680                 685
Met Ser Leu Leu Asn Phe Val Met Pro His Met Phe Ser Ser Ser Thr
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Ser Glu Ile Arg Arg Met Phe Ser Ser Lys Thr Lys Ser Ala Asp Glu
705                 710                 715                 720
Gln Ser Ile Tyr Glu Lys Glu Arg Ile Ala His Ala Lys Gln Ile Ile
                725                 730                 735
Lys Pro Phe Ile Leu Arg Arg Val Lys Glu Glu Val Leu Lys Gln Leu
            740                 745                 750
Pro Pro Lys Lys Asp Arg Ile Glu Leu Cys Ala Met Ser Glu Arg Gln
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Glu Gln Leu Tyr Leu Gly Leu Phe Asn Arg Leu Lys Lys Ser Ile Asn
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Asn Leu Val Thr Glu Lys Asn Thr Glu Met Cys Asn Val Met Met Gln
785                 790                 795                 800
Leu Arg Lys Met Ala Asn His Pro Leu Leu His Arg Gln Tyr Tyr Thr
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820 825 830
His Cys Glu Ala Asn Pro Asp Leu Ile Phe Glu Asp Met Glu Val Met
835 840 845
Thr Asp Phe Glu Leu His Val Leu Cys Lys Gln Tyr Arg His Ile Asn
850 855 860
Asn Phe Gln Leu Asp Met Asp Leu Ile Leu Asp Ser Gly Lys Phe Arg
865 870 875 880
Val Leu Gly Cys Ile Leu Ser Glu Leu Lys Gln Lys Gly Asp Arg Val
885 890 895
Val Leu Phe Ser Gln Phe Thr Met Met Leu Asp Ile Leu Glu Val Leu
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Leu Lys His His Gln His Arg Tyr Leu Arg Leu Asp Gly Lys Thr Gln
915 920 925
Ile Ser Glu Arg Ile His Leu Ile Asp Glu Phe Asn Thr Asp Met Asp
930 935 940
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Leu Thr Ser Ala Asn Val Val Ile Leu His Asp Ile Asp Cys Asn Pro
965 970 975
Tyr Asn Asp Lys Gln Ala Glu Asp Arg Cys His Arg Val Gly Gln Thr
980 985 990
Lys Glu Val Leu Val Ile Lys Leu Ile Ser Gln Gly Thr Ile Glu Glu
995 1000 1005
Ser Met Leu Lys Ile Asn Gln Gln Lys Leu Lys Leu Glu Gln Asp Met
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<210> 3780
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<212> PRT
<213> Homo sapiens

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Lys Arg Gln Lys Ile Gln Arg Glu Leu Met Lys Leu Glu Gln Glu Asn
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Val Val Arg Ser Lys Leu Ser Pro Ser Pro Ser Leu Arg Lys Ser Ser
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Lys Ser Pro Lys Arg Lys Ser Ser Pro Lys Ser Ser Ser Ala Ser Lys
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Lys Asp Arg Lys Thr Ser Ala Val Ser Ser Pro Leu Leu Asp Gln Gln
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His Ser Pro Ser Pro Arg Arg Lys Arg Thr Pro Ser Pro Ser Tyr Gln
225                 230                 235                 240
Arg Thr Leu Thr Pro Pro Leu Arg Arg Ser Ala Ser Pro Tyr Pro Ser
                245                 250                 255
His Ser Leu Ser Ser Pro Gln Arg Lys Gln Ser Pro Pro Arg His Arg
            260                 265                 270
Ser Pro Met Arg Glu Lys Gly Arg His Asp His Glu Arg Thr Ser Gln
        275                 280                 285
Ser His Asp Arg Arg His Glu Gly Arg Glu Asp Thr Arg Gly Lys Arg
    290                 295                 300
Asp Arg Glu Lys Asp Ser Arg Glu Glu Arg Glu Tyr Glu Gln Asp Gln
305                 310                 315                 320
Ser Ser Ser Arg Asp His Arg Asp Asp Arg Glu Pro Arg Asp Gly Arg
                325                 330                 335
Asp Arg Arg Asp Ala Arg Asp Thr Arg Asp Arg Arg Glu Leu Arg Asp
            340                 345                 350
Ser Arg Asp Met Arg Asp Ser Arg Glu Met Arg Asp Tyr Ser Arg Asp
        355                 360                 365
Thr Lys Glu Ser Arg Asp Pro Arg Asp Ser Arg Ser Thr Arg Asp Ala
    370                 375                 380
His Asp Tyr Arg Asp Arg Glu Gly Arg Asp Thr His Arg Lys Glu Asp
385                 390                 395                 400
Thr Tyr Pro Glu Glu Ser Arg Ser Tyr Gly Arg Asn His Leu Arg Glu
                405                 410                 415
Glu Ser Ser Arg Thr Glu Ile Arg Asn Glu Ser Arg Asn Glu Ser Arg
            420                 425                 430
Ser Glu Ile Arg Asn Asp Arg Met Gly Arg Ser Arg Gly Arg Val Pro
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        435                 440                 445
Glu Leu Pro Glu Lys Gly Ser Arg Gly Ser Arg Gly Ser Gln Ile Asp
    450                 455                 460
Ser His Ser Ser Asn Ser Asn Tyr His Asp Ser Trp Glu Thr Arg Ser
465                 470                 475                 480
Ser Tyr Pro Glu Arg Asp Arg Tyr Pro Glu Arg Asp Asn Arg Asp Gln
                485                 490                 495
Ala Arg Asp Ser Ser Phe Glu Arg Arg His Gly Glu Arg Asp Arg Arg
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Asp Gln Arg Glu Arg Ser Lys Thr Lys Leu Thr Asn Ser Thr Ser Gly
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Lys Glu
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<210> 3781
<211> 1364
<212> DNA
<213> Homo sapiens

<400> 3781
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240
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360
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420
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480
ccctctgact ttgtcccctg tacaactagg ttgattagga atcagccaac tgtgttccct
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1020

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1140
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1200
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1260
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1364

<210> 3782
<211> 112
<212> PRT
<213> Homo sapiens

<400> 3782
Met Asn Asp Ile Gln Asn Ser Arg Leu Asn Pro Gln Asp Leu Cys Leu
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Thr Pro Asp Pro Gly Ser Arg Asn Ser Gly Ser Ser His Leu Val Trp
20 25 30
Asp Leu Gln Asp Ser Ser Glu Leu His Pro Glu Phe Ala Lys Cys His
35 40 45
Val Pro Trp Thr Pro Arg Phe Ala Tyr Gly Val Phe Tyr Ala Asp Pro
50 55 60
Cys Thr Gly Gly Asp Ser Tyr His Pro His Glu Gln Ser Ser Pro Pro
65 70 75 80
Ile Phe Ser Lys Gln Ser Trp Ala Leu Thr Pro Leu Glu Arg Gly Arg
85 90 95
Asn Gly Ser Lys Ile Thr Ser Arg Lys Gly Gln Ser Val Leu Met Thr
100 105 110

<210> 3783
<211> 4137
<212> DNA
<213> Homo sapiens

<400> 3783
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180
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240
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300
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420

cgcccgcgcc tttcttctcg cgcctcctcc gcccgccgcc ggcgggcccg gctccccggg
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1980
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2040

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2100
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2160
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3660

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3960
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4020
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4137

<210> 3784
<211> 804
<212> PRT
<213> Homo sapiens

<400> 3784
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Ile Gln Arg Phe Glu Ser Val His Pro Asn Ile Tyr Ser Ile Tyr Glu
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Leu Leu Glu Arg Val Glu Glu Pro Val Leu Gln Asn Gln Ile Arg Glu
35 40 45
His Val Ile Ala Ile Glu Asp Ala Phe Val Asn Ser Gln Glu Trp Thr
50 55 60
Leu Ser Arg Ser Val Pro Glu Leu Lys Val Gly Ile Val Gly Asn Leu
65 70 75 80
Ala Ser Gly Lys Ser Ala Leu Val His Arg Tyr Leu Thr Gly Thr Tyr
85 90 95
Val Gln Glu Glu Ser Pro Glu Gly Gly Arg Phe Lys Lys Glu Ile Val
100 105 110
Val Asp Gly Gln Ser Tyr Leu Leu Leu Ile Arg Asp Glu Gly Gly Pro
115 120 125
Pro Glu Ala Gln Phe Ala Met Trp Val Asp Ala Val Ile Phe Val Phe
130 135 140
Ser Leu Glu Asp Glu Ile Ser Phe Gln Thr Val Tyr His Tyr Tyr Ser
145 150 155 160
Arg Met Ala Asn Tyr Arg Asn Thr Ser Glu Ile Pro Leu Val Leu Val
165 170 175
Gly Thr Gln Asp Ala Ile Ser Ser Ala Asn Pro Arg Val Ile Asp Asp
180 185 190
Ala Arg Ala Arg Lys Leu Ser Asn Asp Leu Lys Arg Cys Thr Tyr Tyr
195 200 205
Glu Thr Cys Ala Thr Tyr Gly Leu Asn Val Glu Arg Val Phe Gln Asp
210 215 220
Val Ala Gln Lys Ile Val Ala Thr Arg Lys Lys Gln Gln Leu Ser Ile
225 230 235 240
Gly Pro Cys Lys Ser Leu Pro Asn Ser Pro Ser His Ser Ser Val Cys

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                245                 250                 255
Ser Ala Gln Val Ser Ala Val His Ile Ser Gln Thr Ser Asn Gly Gly
            260                 265                 270
Gly Ser Leu Ser Asp Tyr Ser Ser Ser Val Pro Ser Thr Pro Ser Thr
        275                 280                 285
Ser Gln Lys Glu Leu Arg Ile Asp Val Pro Pro Thr Ala Asn Thr Pro
    290                 295                 300
Thr Pro Val Arg Lys Gln Ser Lys Arg Arg Ser Asn Leu Phe Thr Ser
305                 310                 315                 320
Arg Lys Gly Ser Asp Pro Asp Lys Glu Lys Lys Gly Leu Glu Ser Arg
                325                 330                 335
Ala Asp Ser Ile Gly Ser Gly Arg Ala Ile Pro Ile Lys Gln Gly Met
            340                 345                 350
Leu Leu Lys Arg Ser Gly Lys Ser Leu Asn Lys Glu Trp Lys Lys Lys
        355                 360                 365
Tyr Val Thr Leu Cys Asp Asn Gly Val Leu Thr Tyr His Pro Ser Leu
    370                 375                 380
His Asp Tyr Met Gln Asn Val His Gly Lys Glu Ile Asp Leu Leu Arg
385                 390                 395                 400
Thr Thr Val Lys Val Pro Gly Lys Arg Pro Pro Arg Ala Thr Ser Ala
                405                 410                 415
Cys Ala Pro Ile Ser Ser Pro Lys Thr Asn Gly Leu Ser Lys Asp Met
            420                 425                 430
Ser Ser Leu His Ile Ser Pro Asn Ser Asp Thr Gly Leu Gly Asp Ser
        435                 440                 445
Val Cys Ser Ser Pro Ser Ile Ser Ser Thr Thr Ser Pro Lys Leu Asp
    450                 455                 460
Pro Pro Pro Ser Pro His Ala Asn Arg Lys Lys His Arg Arg Lys Lys
465                 470                 475                 480
Ser Thr Ser Asn Phe Lys Ala Asp Gly Leu Ser Gly Thr Ala Glu Glu
                485                 490                 495
Gln Glu Glu Asn Phe Glu Phe Ile Ile Val Ser Leu Thr Gly Gln Thr
            500                 505                 510
Trp His Phe Glu Ala Thr Thr Tyr Glu Glu Arg Asp Ala Trp Val Gln
        515                 520                 525
Ala Ile Glu Ser Gln Ile Leu Ala Ser Leu Gln Ser Cys Glu Ser Ser
    530                 535                 540
Lys Asn Lys Ser Arg Leu Thr Ser Gln Ser Glu Ala Met Ala Leu Gln
545                 550                 555                 560
Ser Ile Arg Asn Met Arg Gly Asn Ser His Cys Val Asp Cys Glu Thr
                565                 570                 575
Gln Asn Pro Asn Trp Ala Ser Leu Asn Leu Gly Ala Leu Met Cys Ile
            580                 585                 590
Glu Cys Ser Gly Ile His Arg Asn Leu Gly Thr His Leu Ser Arg Val
        595                 600                 605
Arg Ser Leu Asp Leu Asp Asp Trp Pro Ile Glu Leu Ile Lys Val Met
    610                 615                 620
Ser Ser Ile Gly Asn Glu Leu Ala Asn Ser Val Trp Glu Glu Ser Ser
625                 630                 635                 640
Gln Gly Arg Thr Lys Pro Ser Val Asp Ser Thr Arg Glu Glu Lys Glu
                645                 650                 655
Arg Trp Ile Arg Ala Lys Tyr Glu Gln Lys Leu Phe Leu Ala Pro Leu
            660                 665                 670
Pro Cys Thr Glu Leu Ser Leu Gly Gln His Leu Leu Arg Ala Thr Ala
```

675 680 685
Asp Glu Asp Leu Arg Thr Ala Ile Leu Leu Leu Ala His Gly Ser Arg
690 695 700
Asp Glu Val Asn Glu Thr Cys Gly Glu Gly Asp Gly Arg Thr Ala Leu
705 710 715 720
His Leu Ala Cys Arg Lys Gly Asn Val Val Leu Ala Gln Leu Leu Ile
725 730 735
Trp Tyr Gly Val Asp Val Thr Ala Arg Asp Ala His Gly Asn Thr Ala
740 745 750
Leu Ala Tyr Ala Arg Gln Ala Ser Ser Gln Glu Cys Ile Asp Val Leu
755 760 765
Leu Gln Tyr Gly Cys Pro Asp Glu Arg Phe Val Leu Met Ala Thr Pro
770 775 780
Asn Leu Ser Arg Arg Asn Asn Asn Arg Asn Asn Ser Ser Gly Arg Val
785 790 795 800
Pro Thr Ile Ile

<210> 3785
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 3785
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120
gcaattcacc actctcccaa agccggacca cagctgggtg aggggtggga cagagagtag
180
gagcagtccc agcatgcagt gcagcagccc aaagcctcgg gcgaggcatc gcccttcatc
240
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360
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420
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480
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540
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600
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660
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720
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900

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1020
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1140
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1260
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1901

<210> 3786
<211> 168
<212> PRT
<213> Homo sapiens

<400> 3786
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Val Trp Glu Gly Gln Leu Gln Ser Leu Val Leu Ser Glu Tyr Ala Ser
20 25 30
Thr Glu Met Ser Leu His Ala Leu Tyr Met His Gln Leu His Lys Gln
35 40 45
Gln Ala Gln Ala Glu Pro Glu Arg His Val Trp His Arg Arg Glu Ser
50 55 60
Asp Glu Ser Gly Glu Ser Ala Pro Asp Glu Gly Gly Glu Gly Ala Arg
65 70 75 80
Ala Pro Gln Ser Ile Pro Arg Ser Ala Ser Tyr Pro Cys Ala Ala Pro
85 90 95
Arg Pro Gly Ala Pro Glu Thr Thr Ala Leu His Gly Gly Phe Gln Arg

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            100                 105                 110
Arg Tyr Gly Gly Ile Thr Asp Pro Gly Thr Val Pro Arg Val Pro Ser
        115                 120                 125
His Phe Ser Arg Leu Pro Leu Gly Gly Trp Ala Glu Asp Gly Gln Ser
    130                 135                 140
Ala Ser Arg His Pro Glu Pro Val Pro Glu Glu Gly Ser Glu Asp Glu
145                 150                 155                 160
Leu Pro Pro Gln Val His Lys Val
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<210> 3787
<211> 717
<212> DNA
<213> Homo sapiens

<400> 3787
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120
gtggttgtgt ctgctgtggt gttatggaca ctgctagtgt taatacagca caataagaaa
180
gtgtgaaagg ggccgggaaa ggtggcggga gcggggcggc acgtgggttc ccctcacagc
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420
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717

<210> 3788
<211> 113
<212> PRT
<213> Homo sapiens

<400> 3788
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Cys Ala Ser Ile Lys Leu Arg His Gly Ser Arg Ala Ala Pro Pro Gly
            20                  25                  30
Pro Trp Gly Ala Lys Cys Ser Trp Arg Gln Val Ala Lys Gly Glu His
        35                  40                  45
Leu Gly Gln Thr Pro Gly Phe Ser Ser Arg Leu Pro His Leu Pro Ala
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50 55 60
Ser Leu Leu Ser Trp Leu Ser Pro Ser Leu Leu Val Cys Asn Lys Gly
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Ala Ala Val Ile Thr His Glu Gln Cys Leu Ala Gln Ser Gly Arg Ser
85 90 95
Ala Val Leu Val His Met Glu Glu Pro Lys Gln Ala Pro Cys Thr Val
100 105 110
Leu

<210> 3789
<211> 4341
<212> DNA
<213> Homo sapiens

<400> 3789
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<210> 3790
<211> 1092
<212> PRT
<213> Homo sapiens

<400> 3790
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35 40 45
Glu Asp Leu His Asn Glu Lys Glu Leu Ile Lys Glu Leu Glu Gln Ser
50 55 60
Leu Ala Ser Trp Thr Gln Asn Leu Lys Glu Leu Gln Thr Met Lys Ala
65 70 75 80
Asp Leu Thr Arg His Val Leu Val Glu Asp Val Met Val Leu Lys Glu
85 90 95
Gln Ile Glu His Leu His Arg Gln Trp Glu Asp Leu Cys Leu Arg Val
100 105 110
Ala Ile Arg Lys Gln Glu Ile Glu Asp Arg Leu Asn Thr Trp Val Val
115 120 125
Phe Asn Glu Lys Asn Lys Glu Leu Cys Ala Trp Leu Val Gln Met Glu
130 135 140
Asn Lys Val Leu Gln Thr Val Asp Ile Ser Ile Glu Glu Met Ile Glu
145 150 155 160
Lys Leu Gln Lys Asp Cys Met Glu Glu Ile Asn Leu Phe Ser Glu Asn
165 170 175
Lys Leu Gln Leu Lys Gln Met Gly Asp Gln Leu Ile Lys Ala Ser Asn
180 185 190
Lys Ser Arg Ala Ala Glu Ile Asp Asp Lys Leu Asn Lys Ile Asn Asp
195 200 205
Arg Trp Gln His Leu Phe Asp Val Ile Gly Ser Arg Val Lys Lys Leu
210 215 220
Lys Glu Thr Phe Ala Phe Ile Gln Gln Leu Asp Lys Asn Met Ser Asn
225 230 235 240
Leu Arg Thr Trp Leu Ala Arg Ile Glu Ser Glu Leu Ser Lys Pro Val
245 250 255
Val Tyr Asp Val Cys Asp Asp Gln Glu Ile Gln Lys Arg Leu Ala Glu
260 265 270
Gln Gln Asp Leu Gln Arg Asp Ile Glu Gln His Ser Ala Gly Val Glu
275 280 285
Ser Val Phe Asn Ile Cys Asp Val Leu Leu His Asp Ser Asp Ala Cys
290 295 300
Ala Asn Glu Thr Glu Cys Asp Ser Ile Gln Gln Thr Thr Arg Ser Leu
305 310 315 320
Asp Arg Arg Trp Arg Asn Ile Cys Ala Met Ser Met Glu Arg Arg Met
325 330 335
Lys Ile Glu Glu Thr Trp Arg Leu Trp Gln Lys Phe Leu Asp Asp Tyr
340 345 350
Ser Arg Phe Glu Asp Trp Leu Lys Ser Ala Glu Arg Thr Ala Ala Cys
355 360 365
Pro Asn Ser Ser Glu Val Leu Tyr Thr Ser Ala Lys Glu Glu Leu Lys

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    370                 375                 380
Arg Phe Glu Ala Phe Gln Arg Gln Ile His Glu Arg Leu Thr Gln Leu
385                 390                 395                 400
Glu Leu Ile Asn Lys Gln Tyr Arg Arg Leu Ala Arg Glu Asn Arg Thr
                405                 410                 415
Asp Thr Ala Ser Arg Leu Lys Gln Met Val His Glu Gly Asn Gln Arg
            420                 425                 430
Trp Asp Asn Leu Gln Arg Arg Val Thr Ala Val Leu Arg Arg Leu Arg
        435                 440                 445
His Phe Thr Asn Gln Arg Glu Glu Phe Glu Gly Thr Arg Glu Ser Ile
    450                 455                 460
Leu Val Trp Leu Thr Glu Met Asp Leu Gln Leu Thr Asn Val Glu His
465                 470                 475                 480
Phe Ser Glu Ser Asp Ala Asp Asp Lys Met Arg Gln Leu Asn Gly Phe
                485                 490                 495
Gln Gln Glu Ile Thr Leu Asn Thr Asn Lys Ile Asp Gln Leu Ile Val
            500                 505                 510
Phe Gly Glu Gln Leu Ile Gln Lys Ser Glu Pro Leu Asp Ala Val Leu
        515                 520                 525
Ile Glu Asp Glu Leu Glu Glu Leu His Arg Tyr Cys Gln Glu Val Phe
    530                 535                 540
Gly Arg Val Ser Arg Phe His Arg Arg Leu Thr Ser Cys Thr Pro Gly
545                 550                 555                 560
Leu Glu Asp Glu Lys Glu Ala Ser Glu Asn Glu Thr Asp Met Glu Asp
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Pro Arg Glu Ile Gln Thr Asp Ser Trp Arg Lys Arg Gly Glu Ser Glu
            580                 585                 590
Glu Pro Ser Ser Pro Gln Ser Leu Cys His Leu Val Ala Pro Gly His
        595                 600                 605
Glu Arg Ser Gly Cys Glu Thr Pro Val Ser Val Asp Ser Ile Pro Leu
    610                 615                 620
Glu Trp Asp His Thr Gly Asp Val Gly Gly Ser Ser Ser His Glu Glu
625                 630                 635                 640
Asp Glu Glu Gly Pro Tyr Tyr Ser Ala Leu Ser Gly Lys Ser Ile Ser
                645                 650                 655
Asp Gly His Ser Trp His Val Pro Asp Ser Pro Ser Cys Pro Glu His
            660                 665                 670
His Tyr Lys Gln Met Glu Gly Asp Arg Asn Val Pro Pro Val Pro Pro
        675                 680                 685
Ala Ser Ser Thr Pro Tyr Lys Pro Pro Tyr Gly Lys Leu Leu Leu Pro
    690                 695                 700
Pro Gly Thr Asp Gly Gly Lys Glu Gly Pro Arg Val Leu Asn Gly Asn
705                 710                 715                 720
Pro Gln Gln Glu Asp Gly Gly Leu Ala Gly Ile Thr Glu Gln Gln Ser
                725                 730                 735
Gly Ala Phe Asp Arg Trp Glu Met Ile Gln Ala Gln Glu Leu His Asn
            740                 745                 750
Lys Leu Lys Ile Lys Gln Asn Leu Gln Gln Leu Asn Ser Asp Ile Ser
        755                 760                 765
Ala Ile Thr Thr Trp Leu Lys Lys Thr Glu Ala Glu Leu Glu Met Leu
    770                 775                 780
Lys Met Ala Lys Pro Pro Ser Asp Ile Gln Glu Ile Glu Leu Arg Val
785                 790                 795                 800
Lys Arg Leu Gln Glu Ile Leu Lys Ala Phe Asp Thr Tyr Lys Ala Leu
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805 810 815
Val Val Ser Val Asn Val Ser Ser Lys Glu Phe Leu Gln Thr Glu Ser
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Pro Glu Ser Thr Glu Leu Gln Ser Arg Leu Arg Gln Leu Ser Leu Leu
835 840 845
Trp Glu Ala Ala Gln Gly Ala Val Asp Ser Trp Arg Gly Gly Leu Arg
850 855 860
Gln Ser Leu Met Gln Cys Gln Asp Phe His Gln Leu Ser Gln Asn Leu
865 870 875 880
Leu Leu Trp Leu Ala Ser Ala Lys Asn Arg Arg Gln Lys Ala His Val
885 890 895
Thr Asp Pro Lys Ala Asp Pro Arg Ala Leu Leu Glu Cys Arg Arg Glu
900 905 910
Leu Met Gln Leu Glu Lys Glu Leu Val Glu Arg Gln Pro Gln Val Asp
915 920 925
Met Leu Gln Glu Ile Ser Asn Ser Leu Leu Ile Lys Gly His Gly Glu
930 935 940
Asp Cys Ile Glu Ala Glu Glu Lys Val His Val Ile Glu Lys Lys Leu
945 950 955 960
Lys Gln Leu Arg Glu Gln Val Ser Gln Asp Leu Met Ala Leu Gln Gly
965 970 975
Thr Gln Asn Pro Ala Ser Pro Leu Pro Ser Phe Asp Glu Val Asp Ser
980 985 990
Gly Asp Gln Pro Pro Ala Thr Ser Val Pro Ala Pro Arg Ala Lys Gln
995 1000 1005
Phe Arg Ala Val Arg Thr Thr Glu Gly Glu Glu Glu Thr Glu Ser Arg
1010 1015 1020
Val Pro Gly Ser Thr Arg Pro Gln Arg Ser Phe Leu Ser Arg Val Val
1025 1030 1035 1040
Arg Ala Ala Leu Pro Leu Gln Leu Leu Leu Leu Leu Leu Leu Leu Leu
1045 1050 1055
Ala Cys Leu Leu Pro Ser Ser Glu Glu Asp Tyr Ser Cys Thr Gln Ala
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Pro Pro Pro Thr
1090

<210> 3791
<211> 1011
<212> DNA
<213> Homo sapiens

<400> 3791
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120
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180
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1011

<210> 3792
<211> 288
<212> PRT
<213> Homo sapiens

<400> 3792
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Ala Leu Ser Met Gly Gly Lys Val Pro Val Ser Glu Gly Leu Glu His
35 40 45
Ser Asp Leu Pro Asp Gly Thr Gly Glu Phe Leu Asp Ala Trp Leu Met
50 55 60
Leu Val Glu Lys Met Val Asn Pro Thr Thr Val Leu Glu Ser Pro His
65 70 75 80
Ser Leu Pro Ala Lys Leu Pro Gly Gly Val Gln Asn Phe Pro Gln Phe
85 90 95
Ser Ala Leu Arg Phe Leu Val Val Thr Gln Lys Ala Ala Phe Thr Cys
100 105 110
Ile Lys Asn Leu Trp Asn Arg Lys Pro Leu Lys Val Tyr Gly Gly Arg
115 120 125
Met Ala Glu Ser Met Leu Ala Ile Leu Cys His Ile Leu Arg Gly Glu
130 135 140
Pro Val Ile Arg Glu Arg Leu Ser Lys Glu Lys Glu Gly Ser Arg Gly
145 150 155 160
Glu Glu Asp Thr Gly Gln Glu Glu Gly Gly Ser Arg Arg Glu Pro Gln
165 170 175
Val Asn Gln Gln Gln Leu Gln Gln Leu Met Asp Met Gly Phe Thr Arg

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            180                 185                 190
Glu His Ala Met Glu Ala Leu Leu Asn Thr Ser Thr Met Glu Gln Ala
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Thr Glu Tyr Leu Leu Thr His Pro Pro Pro Ile Met Gly Gly Val Val
    210                 215                 220
Arg Asp Leu Ser Met Ser Glu Glu Asp Gln Met Met Arg Ala Ile Ala
225                 230                 235                 240
Met Ser Leu Gly Gln Asp Ile Pro Met Asp Gln Arg Ala Glu Ser Pro
                245                 250                 255
Glu Glu Val Ala Cys Arg Lys Glu Glu Glu Glu Arg Lys Ala Arg Glu
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Lys Gln Glu Glu Glu Glu Ala Lys Cys Leu Lys Lys Val Gln Gly Cys
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<210> 3793
<211> 360
<212> DNA
<213> Homo sapiens

<400> 3793
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<210> 3794
<211> 96
<212> PRT
<213> Homo sapiens

<400> 3794
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Phe Val Pro Gly Arg Asn Asn Ser Phe Phe Phe Ser Trp Arg Gln Cys
        35                  40                  45
Phe Thr Leu Val Ala Gln Ala Gly Gly Gln Trp Arg Asp Leu Ser Ser
    50                  55                  60
Leu Gln Pro Pro Pro Phe Gly Leu Lys Arg Phe Ser Cys Leu Ser Leu
65                  70                  75                  80
Pro Ser Ser Trp Asp Tyr Arg His Ala Ser Pro Cys Thr Met Pro Asp
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<210> 3795
<211> 1341

<212> DNA
<213> Homo sapiens

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gagctgcagg cctgtgctga tgtcgtggat cgagaacgct tctgccgctg ggcgggccta
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480
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1320
cagaccactc ccttcacgcg t
1341

<210> 3796
<211> 294
<212> PRT

<213> Homo sapiens

<400> 3796
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Pro Asn Gln Leu Tyr Tyr Glu Gly Glu Leu Gln Ala Cys Ala Asp Val
35 40 45
Val Asp Arg Glu Arg Phe Cys Arg Trp Ala Gly Leu Pro Arg Gln Gly
50 55 60
Phe Pro Ile Ile Phe His Gly Val Met Gly Lys Asp Glu Arg Glu Gly
65 70 75 80
Asn Ser Pro Ser Phe Phe Asn Pro Glu Glu Ala Ala Thr Val Thr Ser
85 90 95
Tyr Leu Lys Leu Leu Leu Ala Pro Ser Ser Lys Lys Gly Lys Ala Arg
100 105 110
Leu Ser Pro Arg Ser Val Gly Val Ile Ser Pro Tyr Arg Lys Gln Val
115 120 125
Glu Lys Ile Arg Tyr Cys Ile Thr Lys Leu Asp Arg Glu Leu Arg Gly
130 135 140
Leu Asp Asp Ile Lys Asp Leu Lys Val Gly Ser Val Glu Glu Phe Gln
145 150 155 160
Gly Gln Glu Arg Ser Val Ile Leu Ile Ser Thr Val Arg Ser Ser Gln
165 170 175
Ser Phe Val Gln Leu Asp Leu Asp Phe Asn Leu Gly Phe Leu Lys Asn
180 185 190
Pro Lys Arg Phe Asn Val Ala Val Thr Arg Ala Lys Ala Leu Leu Ile
195 200 205
Ile Val Gly Asn Pro Leu Leu Leu Gly His Asp Pro Asp Trp Lys Val
210 215 220
Phe Leu Glu Phe Cys Lys Glu Asn Gly Gly Tyr Thr Gly Cys Pro Phe
225 230 235 240
Pro Ala Lys Leu Asp Leu Gln Gln Gly Gln Asn Leu Leu Gln Gly Leu
245 250 255
Ser Lys Leu Ser Pro Ser Thr Ser Gly Pro His Ser His Asp Tyr Leu
260 265 270
Pro Gln Glu Arg Glu Gly Glu Gly Gly Leu Ser Leu Gln Val Glu Pro
275 280 285
Glu Trp Arg Asn Glu Leu
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<210> 3797
<211> 1970
<212> DNA
<213> Homo sapiens

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1740
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1800

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1860
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1920
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1970

<210> 3798
<211> 473
<212> PRT
<213> Homo sapiens

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His Trp Trp Ser Glu Arg Thr His Lys Asn Leu Ser Asp Met Glu Asn
35 40 45
Glu Phe Tyr Tyr Arg Tyr Pro Ser Phe Gln Asp Val His Val Met Val
50 55 60
Phe Val Gly Phe Gly Phe Leu Met Thr Phe Leu Gln Arg Tyr Gly Phe
65 70 75 80
Ser Ala Val Gly Phe Asn Phe Leu Leu Ala Ala Phe Gly Ile Gln Trp
85 90 95
Ala Leu Leu Met Gln Gly Trp Phe His Phe Leu Gln Asp Arg Tyr Ile
100 105 110
Val Val Gly Val Glu Asn Leu Ile Asn Ala Asp Phe Cys Val Ala Ser
115 120 125
Val Cys Val Ala Phe Gly Ala Val Leu Gly Lys Val Ser Pro Ile Gln
130 135 140
Leu Leu Ile Met Thr Phe Phe Gln Val Thr Leu Phe Ala Val Asn Glu
145 150 155 160
Phe Ile Leu Leu Asn Leu Leu Lys Val Lys Asp Ala Gly Gly Ser Met
165 170 175
Thr Ile His Thr Phe Gly Ala Tyr Phe Gly Leu Thr Val Thr Arg Ile
180 185 190
Leu Tyr Arg Arg Asn Leu Glu Gln Ser Lys Glu Arg Gln Asn Ser Val
195 200 205
Tyr Gln Ser Asp Leu Phe Ala Met Ile Gly Thr Leu Phe Leu Trp Met
210 215 220
Tyr Trp Pro Ser Phe Asn Ser Ala Ile Ser Tyr His Gly Asp Ser Gln
225 230 235 240
His Arg Ala Ala Ile Asn Thr Tyr Cys Ser Leu Ala Ala Cys Val Leu
245 250 255
Thr Ser Val Ala Ile Ser Ser Ala Leu His Lys Lys Gly Lys Leu Asp
260 265 270
Met Val His Ile Gln Asn Ala Thr Leu Ala Gly Gly Val Ala Val Gly
275 280 285
Thr Ala Ala Glu Met Met Leu Met Pro Tyr Gly Ala Leu Ile Ile Gly
290 295 300
Phe Val Cys Gly Ile Ile Ser Thr Leu Gly Phe Val Tyr Leu Thr Pro
305 310 315 320
Phe Leu Glu Ser Arg Leu His Ile Gln Asp Thr Cys Gly Ile Asn Asn

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                325                 330                 335
Leu His Gly Ile Pro Gly Ile Ile Gly Gly Ile Val Gly Ala Val Thr
            340                 345                 350
Ala Ala Ser Ala Ser Leu Glu Val Tyr Gly Lys Glu Gly Leu Val His
        355                 360                 365
Ser Phe Asp Phe Gln Gly Phe Asn Gly Asp Trp Thr Ala Arg Thr Gln
    370                 375                 380
Gly Lys Phe Gln Ile Tyr Gly Leu Leu Val Thr Leu Ala Met Ala Leu
385                 390                 395                 400
Met Gly Gly Ile Ile Val Gly Leu Ile Leu Arg Leu Pro Phe Trp Gly
                405                 410                 415
Gln Pro Ser Asp Glu Asn Cys Phe Glu Asp Ala Val Tyr Trp Glu Met
            420                 425                 430
Pro Glu Gly Asn Ser Thr Val Tyr Ile Pro Glu Asp Pro Thr Phe Lys
        435                 440                 445
Pro Ser Gly Pro Ser Val Pro Ser Val Pro Met Val Ser Pro Leu Pro
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Met Ala Ser Ser Val Pro Leu Val Pro
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<210> 3799
<211> 210
<212> DNA
<213> Homo sapiens

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210

<210> 3800
<211> 70
<212> PRT
<213> Homo sapiens

<400> 3800
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            20                  25                  30
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
        35                  40                  45
Ser Ser Ser Ser Ser Ser Ser Asp Gly Arg Lys Lys Arg Gly Lys Tyr
    50                  55                  60
Lys Asp Lys Arg Arg Lys
65                  70
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<210> 3801
<211> 4070

<212> DNA
<213> Homo sapiens

<400> 3801
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120
gcccgagcag ccgccgccat ggcaatcaaa tttctggaag tcatcaagcc cttctgtgtc
180
atcctgccgg aaattcagaa gccagagagg aagattcagt ttaaggagaa agtgctgtgg
240
accgctatca ccctctttat cttcttagtg tgctgccaga ttcccctgtt tgggatcatg
300
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420
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gcctttagtc ccactaccat taacactggc agaggtactg agtttgaggg tgcagtcata
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1080
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1200
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1260
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1320
aaggagcagc agatggtgat gagaggccac cgagagacct ccatggtcca tgaactcaac
1380
cggtacatcc ccacagccgc ggcctttggt gggctgtgca tcggggccct ctcggtcctg
1440
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1500

taccagtact ttgagatctt cgttaaggag caaagcgagg ttggcagcat gggggccctg
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3960
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4070

<210> 3802
<211> 476
<212> PRT
<213> Homo sapiens

<400> 3802
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Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
35 40 45
Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp
50 55 60
Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu Leu Gly
65 70 75 80
Ile Ser Pro Ile Val Thr Ser Gly Leu Ile Met Gln Leu Leu Ala Gly
85 90 95
Ala Lys Ile Ile Glu Val Gly Asp Thr Pro Lys Asp Arg Ala Leu Phe
100 105 110
Asn Gly Ala Gln Lys Leu Phe Gly Met Ile Ile Thr Ile Gly Gln Ser

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        115                 120                 125
Ile Val Tyr Val Met Thr Gly Met Tyr Gly Asp Pro Ser Glu Met Gly
    130                 135                 140
Ala Gly Ile Cys Leu Leu Ile Ile Ile Gln Leu Phe Val Ala Gly Leu
145                 150                 155                 160
Ile Val Leu Leu Leu Asp Glu Leu Leu Gln Lys Gly Tyr Gly Leu Gly
                165                 170                 175
Ser Gly Ile Ser Leu Phe Ile Ala Thr Asn Ile Cys Glu Thr Ile Val
            180                 185                 190
Trp Lys Ala Phe Ser Pro Thr Thr Ile Asn Thr Gly Arg Gly Thr Glu
        195                 200                 205
Phe Glu Gly Ala Val Ile Ala Leu Phe His Leu Leu Ala Thr Arg Thr
    210                 215                 220
Asp Lys Val Arg Ala Leu Arg Glu Ala Phe Tyr Arg Gln Asn Leu Pro
225                 230                 235                 240
Asn Leu Met Asn Leu Ile Ala Thr Ile Phe Val Phe Ala Val Val Ile
                245                 250                 255
Tyr Phe Gln Gly Phe Arg Val Asp Leu Pro Ile Lys Ser Ala Arg Tyr
            260                 265                 270
Arg Gly Gln Tyr Asn Thr Tyr Pro Ile Lys Leu Phe Tyr Thr Ser Asn
        275                 280                 285
Ile Pro Ile Ile Leu Gln Ser Ala Leu Val Ser Asn Leu Tyr Val Ile
    290                 295                 300
Ser Gln Met Leu Ser Ala Arg Phe Ser Gly Asn Phe Leu Val Asn Leu
305                 310                 315                 320
Leu Gly Gln Trp Ser Asp Thr Ser Ser Gly Gly Pro Ala Arg Ala Tyr
                325                 330                 335
Pro Val Gly Gly Leu Cys Tyr Tyr Leu Ser Pro Pro Glu Ser Phe Gly
            340                 345                 350
Ser Val Leu Glu Asp Pro Val His Ala Val Val Tyr Ile Val Phe Met
        355                 360                 365
Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr Trp Ile Glu Val Ser Gly
    370                 375                 380
Ser Ser Ala Lys Asp Val Ala Lys Gln Leu Lys Glu Gln Gln Met Val
385                 390                 395                 400
Met Arg Gly His Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr
                405                 410                 415
Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser
            420                 425                 430
Val Leu Ala Asp Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu
        435                 440                 445
Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu
    450                 455                 460
Gln Ser Glu Val Gly Ser Met Gly Ala Leu Leu Phe
465                 470                 475
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<210> 3803
<211> 345
<212> DNA
<213> Homo sapiens

<400> 3803
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ggcaaaggat caatgagaga taaagctaag gaagaagaac taaggaagag tggggaagcc
120
aaatatgccc acttgagtga tgagcttcat gtattaattg aagtgtttgc tccacctggg
180
gaagcttatt cacgtatgag tcatgcattg gaagagatta aaaaattcct ggttcctgac
240
tacaatgatg aaattcgtca ggaacaacta cgtgaattat cttacttaaa tggctcagag
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345

<210> 3804
<211> 115
<212> PRT
<213> Homo sapiens

<400> 3804
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Met Ser Ile Leu Gly Lys Gly Ser Met Arg Asp Lys Ala Lys Glu Glu
20 25 30
Glu Leu Arg Lys Ser Gly Glu Ala Lys Tyr Ala His Leu Ser Asp Glu
35 40 45
Leu His Val Leu Ile Glu Val Phe Ala Pro Pro Gly Glu Ala Tyr Ser
50 55 60
Arg Met Ser His Ala Leu Glu Glu Ile Lys Lys Phe Leu Val Pro Asp
65 70 75 80
Tyr Asn Asp Glu Ile Arg Gln Glu Gln Leu Arg Glu Leu Ser Tyr Leu
85 90 95
Asn Gly Ser Glu Asp Ser Gly Arg Gly Arg Gly Ile Arg Gly Arg Gly
100 105 110
Ile Arg Ile
115

<210> 3805
<211> 1923
<212> DNA
<213> Homo sapiens

<400> 3805
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120
aagagcccgt tgcctaccag atgccaggcc ctgtgcttcc tcctgccttt gaggttttgg
180
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240
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360
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420

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720
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1260
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1320
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1680
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1800
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1920
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1923

<210> 3806

<211> 280
<212> PRT
<213> Homo sapiens

<400> 3806
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Pro Leu Arg Phe Trp Leu Val Ile Asn Gln Glu Gly Asn Met Val Thr
35 40 45
Ala Arg Gln Glu Pro Arg Leu Val Leu Ile Ser Leu Thr Cys Asp Gly
50 55 60
Asp Thr Leu Thr Leu Ser Ala Ala Tyr Thr Lys Asp Leu Leu Leu Pro
65 70 75 80
Ile Lys Thr Pro Thr Thr Asn Ala Val His Lys Cys Arg Val His Gly
85 90 95
Leu Glu Ile Glu Gly Arg Asp Cys Gly Glu Ala Ala Ala Gln Trp Ile
100 105 110
Thr Ser Phe Leu Lys Ser Gln Pro Tyr Arg Leu Val His Phe Glu Pro
115 120 125
His Met Arg Pro Arg Arg Pro His Gln Ile Ala Asp Leu Phe Arg Pro
130 135 140
Lys Asp Gln Ile Ala Tyr Ser Asp Thr Ser Pro Phe Leu Ile Leu Ser
145 150 155 160
Glu Ala Ser Leu Ala Asp Leu Asn Ser Arg Leu Glu Lys Lys Val Lys
165 170 175
Ala Thr Asn Phe Arg Pro Asn Ile Val Ile Ser Gly Cys Asp Val Tyr
180 185 190
Ala Glu Asp Ser Trp Asp Glu Leu Leu Ile Gly Asp Val Glu Leu Lys
195 200 205
Arg Val Met Ala Cys Ser Arg Cys Ile Leu Thr Thr Val Asp Pro Asp
210 215 220
Thr Gly Val Met Ser Arg Lys Glu Pro Leu Glu Thr Leu Lys Ser Tyr
225 230 235 240
Arg Gln Cys Asp Pro Ser Glu Arg Lys Leu Tyr Gly Lys Ser Pro Leu
245 250 255
Phe Gly Gln Tyr Phe Val Leu Glu Asn Pro Gly Thr Ile Lys Val Gly
260 265 270
Asp Pro Val Tyr Leu Leu Gly Gln
275 280

<210> 3807
<211> 372
<212> DNA
<213> Homo sapiens

<400> 3807
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120
cagggaggtc gcttcccggt gctcagctac cacccggctc ccagcggcag agggagcgcg
180

ccctccccac gctccgcccc tgggtggctg cgtcctttct gggccttttc tttttggccc
240
ggtcaattcg cggcgtagcc gctgccccaa ctcctgcccc attctggtcc cgcccctctc
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360
cccgcgaagc tt
372

<210> 3808
<211> 85
<212> PRT
<213> Homo sapiens

<400> 3808
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1 5 10 15
Arg Tyr Pro Arg Ala Val Ile Val Pro Tyr Leu Val Asp Asp Asp Ala
20 25 30
Leu Ala Arg Ser Ala Arg Phe Arg Gln Gly Gly Arg Phe Pro Val Leu
35 40 45
Ser Tyr His Pro Ala Pro Ser Gly Arg Gly Ser Ala Pro Ser Pro Arg
50 55 60
Ser Ala Pro Gly Trp Leu Arg Pro Phe Trp Ala Phe Ser Phe Trp Pro
65 70 75 80
Gly Gln Phe Ala Ala
85

<210> 3809
<211> 1221
<212> DNA
<213> Homo sapiens

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120
ataagctgtg acttttgcc cctgatgcca taagttggag ggtcctctgc tcaaaacata
180
tggtacacac ttctccttct tttcatctgg tatcatgtat catctctcag atccaataag
240
aaaacattcc cacgtccttc cctccctccc tagtaccaag gtcctcatct cagttttcat
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420
aaggaattct ccaggaaggt aggcaggcct cctacaccat cccgcagggt atacaggggc
480
actcgcacca ggcccagcac ctccagcccg tggtccttgg cgcgtgttgc gccggcctcc
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acagccaaca gctcctcgag ctcagacgct tggcatagaa gtgccacaac gcgtggccct
600

gacccgacgt gggagctgcg gtagtcagtg cgctccacgc ggaaagcggc agccgcttcg
660
cccagctcct cgcgcagctc gcggttcagc ccgtcctcta ggcttctgtc ctgcgtgtcc
720
acgaatccgc cggggaagcc caggcgtcca tcgaagcgca tctgcatcag tatggcgtag
780
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840
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960
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1020
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1080
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1221

<210> 3810
<211> 97
<212> PRT
<213> Homo sapiens

<400> 3810
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20 25 30
Phe Ser Arg Lys Val Gly Arg Pro Pro Thr Pro Ser Arg Arg Val Tyr
35 40 45
Arg Gly Thr Arg Thr Arg Pro Ser Thr Ser Ser Pro Trp Ser Leu Ala
50 55 60
Arg Val Ala Pro Ala Ser Thr Ala Asn Ser Ser Ser Ser Ser Asp Ala
65 70 75 80
Trp His Arg Ser Ala Thr Thr Arg Gly Pro Asp Pro Thr Trp Glu Leu
85 90 95
Arg

<210> 3811
<211> 296
<212> DNA
<213> Homo sapiens

<400> 3811
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cctgtcctta aggctcagaa ctgtagaccc tcaggcagac ccgttctccc ctaccagagg
120

acaccacgcc agatatctgg gcagcaggga catctgacct ggggtgcttg ctggcagcac
180
tgcctggaca gcagggcctc cttagggcca cctcccaacc cagctaggga gcgtcttaag
240
gcctgccctc cctgctgggc ttgggtggga cgctcaggga caggcccctc acgcgt
296

<210> 3812
<211> 94
<212> PRT
<213> Homo sapiens

<400> 3812
Met Gly Ala Arg Ala Arg Ser Leu Ile Val Pro Pro Thr Ala Gln Val
1 5 10 15
Pro Val Leu Lys Ala Gln Asn Cys Arg Pro Ser Gly Arg Pro Val Leu
20 25 30
Pro Tyr Gln Arg Thr Pro Arg Gln Ile Ser Gly Gln Gln Gly His Leu
35 40 45
Thr Trp Gly Ala Cys Trp Gln His Cys Leu Asp Ser Arg Ala Ser Leu
50 55 60
Gly Pro Pro Pro Asn Pro Ala Arg Glu Arg Leu Lys Ala Cys Pro Pro
65 70 75 80
Cys Trp Ala Trp Val Gly Arg Ser Gly Thr Gly Pro Ser Arg
85 90

<210> 3813
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 3813
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120
gactcactga gtgcccgccg cacactgcac accttcgatc tgcttggctt cgggcgaagc
180
tcaaggccag cattcccaag ggacccggag ggggctgagg atgagtttgt gacatcgata
240
gagacatggc gggagaccat ggggatcccc agcatgatcc tcctggggca cagtttggga
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360
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420
gcctgggtca aagccgtggc atctgtccta ggacgttcca atccattggc tgttcttcga
480
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aatcccagtg gtgagacagc attcaaagcc atgatggagt cctttggctg ggcccggcgc
660

cctatgctgg agcgaattca cttgattcga aaagatgtgc ctatcactat gatctacggg
720
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780
tatgtccgag acatggagat taagggtgcc tcccaccatg tctatgctga ccagccacac
840
atcttcaatg ctgtggtgga ggagatctgc gactcagttg attgagctgc tctctgaaga
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tcctttcctc accaactaac atgtgccagc caggcagagt cttgtactgt tcccagaaca
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1080
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1320
ttcaccccat cccataccag ttccatccag ggtctgctta actgccaaga gcaggtcctg
1380
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1419

<210> 3814
<211> 294
<212> PRT
<213> Homo sapiens

<400> 3814
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Gln Asn Asp Arg Thr Pro Leu Val Met Val His Gly Phe Gly Gly Gly
20 25 30
Val Gly Leu Trp Ile Leu Asn Met Asp Ser Leu Ser Ala Arg Arg Thr
35 40 45
Leu His Thr Phe Asp Leu Leu Gly Phe Gly Arg Ser Ser Arg Pro Ala
50 55 60
Phe Pro Arg Asp Pro Glu Gly Ala Glu Asp Glu Phe Val Thr Ser Ile
65 70 75 80
Glu Thr Trp Arg Glu Thr Met Gly Ile Pro Ser Met Ile Leu Leu Gly
85 90 95
His Ser Leu Gly Gly Phe Leu Ala Thr Ser Tyr Ser Ile Lys Tyr Pro
100 105 110
Asp Arg Val Lys His Leu Ile Leu Val Asp Pro Trp Gly Phe Pro Leu
115 120 125
Arg Pro Thr Asn Pro Ser Glu Ile Arg Ala Pro Pro Ala Trp Val Lys
130 135 140
Ala Val Ala Ser Val Leu Gly Arg Ser Asn Pro Leu Ala Val Leu Arg
145 150 155 160
Val Ala Gly Pro Trp Gly Pro Gly Leu Val Gln Arg Phe Arg Pro Asp

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                165                 170                 175
Phe Lys Arg Lys Phe Ala Asp Phe Phe Glu Asp Asp Thr Ile Ser Glu
            180                 185                 190
Tyr Ile Tyr His Cys Asn Ala Gln Asn Pro Ser Gly Glu Thr Ala Phe
        195                 200                 205
Lys Ala Met Met Glu Ser Phe Gly Trp Ala Arg Arg Pro Met Leu Glu
    210                 215                 220
Arg Ile His Leu Ile Arg Lys Asp Val Pro Ile Thr Met Ile Tyr Gly
225                 230                 235                 240
Ser Asp Thr Trp Ile Asp Thr Ser Thr Gly Lys Lys Val Lys Met Gln
                245                 250                 255
Arg Pro Asp Ser Tyr Val Arg Asp Met Glu Ile Lys Gly Ala Ser His
            260                 265                 270
His Val Tyr Ala Asp Gln Pro His Ile Phe Asn Ala Val Val Glu Glu
        275                 280                 285
Ile Cys Asp Ser Val Asp
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<210> 3815
<211> 3669
<212> DNA
<213> Homo sapiens

<400> 3815
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240
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420
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840
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900

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1260
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1380
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1440
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2460
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3669

<210> 3816
<211> 707
<212> PRT
<213> Homo sapiens

<400> 3816
Met Gly Asp Glu Arg Pro His Tyr Tyr Gly Lys His Gly Thr Pro Gln
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Lys Tyr Asp Pro Thr Phe Lys Gly Pro Ile Tyr Asn Arg Gly Cys Thr
20 25 30
Asp Ile Ile Cys Cys Val Phe Leu Leu Leu Ala Ile Val Gly Tyr Val
35 40 45
Ala Val Gly Ile Ile Ala Trp Thr His Gly Asp Pro Arg Lys Val Ile

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    50                  55                  60
Tyr Pro Thr Asp Ser Arg Gly Glu Phe Cys Gly Gln Lys Gly Thr Lys
65                  70                  75                  80
Asn Glu Asn Lys Pro Tyr Leu Phe Tyr Phe Asn Ile Val Lys Cys Ala
                85                  90                  95
Ser Pro Leu Val Leu Leu Glu Phe Gln Cys Pro Thr Pro Gln Ile Cys
            100                 105                 110
Val Glu Lys Cys Pro Asp Arg Tyr Leu Thr Tyr Leu Asn Ala Arg Ser
        115                 120                 125
Ser Arg Asp Phe Glu Tyr Tyr Lys Gln Phe Cys Val Pro Gly Phe Lys
    130                 135                 140
Asn Asn Lys Gly Val Ala Glu Val Leu Arg Asp Gly Asp Cys Pro Ala
145                 150                 155                 160
Val Leu Ile Pro Ser Lys Pro Leu Ala Arg Arg Cys Phe Pro Ala Ile
                165                 170                 175
His Ala Tyr Lys Gly Val Leu Met Val Gly Asn Glu Thr Thr Tyr Glu
            180                 185                 190
Asp Gly His Gly Ser Arg Lys Asn Ile Thr Asp Leu Val Glu Gly Ala
        195                 200                 205
Lys Lys Ala Asn Gly Val Leu Glu Ala Arg Gln Leu Ala Met Arg Ile
    210                 215                 220
Phe Glu Asp Tyr Thr Val Ser Trp Tyr Trp Ile Ile Ile Gly Leu Val
225                 230                 235                 240
Ile Ala Met Ala Met Ser Leu Leu Phe Ile Ile Leu Leu Arg Phe Leu
                245                 250                 255
Ala Gly Ile Met Val Trp Val Met Ile Ile Met Val Ile Leu Val Leu
            260                 265                 270
Gly Tyr Gly Ile Phe His Cys Tyr Met Glu Tyr Ser Arg Leu Arg Gly
        275                 280                 285
Glu Ala Gly Ser Asp Val Ser Leu Val Asp Leu Gly Phe Gln Thr Asp
    290                 295                 300
Phe Arg Val Tyr Leu His Leu Arg Gln Thr Trp Leu Ala Phe Met Ile
305                 310                 315                 320
Ile Leu Ser Ile Leu Glu Val Ile Ile Ile Leu Leu Leu Ile Phe Leu
                325                 330                 335
Arg Lys Arg Ile Leu Ile Ala Ile Ala Leu Ile Lys Glu Ala Ser Arg
            340                 345                 350
Ala Val Gly Tyr Val Met Cys Ser Leu Leu Tyr Pro Leu Val Thr Phe
        355                 360                 365
Phe Leu Leu Cys Leu Cys Ile Ala Tyr Trp Ala Ser Thr Ala Val Phe
    370                 375                 380
Leu Ser Thr Ser Asn Glu Ala Val Tyr Lys Ile Phe Asp Asp Ser Pro
385                 390                 395                 400
Cys Pro Xaa Tyr Cys Glu Asn Leu Xaa Asn Pro Glu Thr Phe Pro Ser
                405                 410                 415
Ser Asn Glu Ser Arg Gln Cys Pro Asn Ala Arg Cys Gln Phe Ala Phe
            420                 425                 430
Tyr Gly Gly Glu Ser Gly Tyr His Arg Ala Leu Leu Gly Leu Gln Ile
        435                 440                 445
Phe Asn Ala Phe Met Phe Phe Trp Leu Ala Asn Phe Val Leu Ala Leu
    450                 455                 460
Gly Gln Val Thr Leu Ala Gly Ala Phe Ala Ser Tyr Tyr Trp Ala Leu
465                 470                 475                 480
Arg Lys Pro Asp Asp Leu Pro Ala Phe Pro Leu Phe Ser Ala Phe Gly
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                485                 490                 495
Arg Ala Leu Arg Tyr His Thr Gly Ser Leu Ala Phe Gly Ala Leu Ile
            500                 505                 510
Leu Ala Ile Val Gln Ile Ile Arg Val Ile Leu Glu Tyr Leu Asp Gln
        515                 520                 525
Arg Leu Lys Ala Ala Glu Asn Lys Phe Ala Lys Cys Leu Met Thr Cys
    530                 535                 540
Leu Lys Cys Cys Phe Trp Cys Leu Glu Lys Phe Ile Lys Phe Leu Asn
545                 550                 555                 560
Arg Asn Ala Tyr Ile Met Ile Ala Ile Tyr Gly Thr Asn Phe Cys Thr
                565                 570                 575
Ser Ala Arg Asn Ala Phe Phe Leu Leu Met Arg Asn Ile Ile Arg Val
            580                 585                 590
Ala Val Leu Asp Lys Val Thr Asp Phe Leu Phe Leu Leu Gly Lys Leu
        595                 600                 605
Leu Ile Val Gly Ser Val Gly Ile Leu Ala Phe Phe Phe Phe Thr His
    610                 615                 620
Arg Ile Arg Ile Val Gln Asp Thr Ala Pro Pro Leu Asn Tyr Tyr Trp
625                 630                 635                 640
Val Pro Ile Leu Thr Val Ile Val Gly Ser Tyr Leu Ile Ala His Gly
                645                 650                 655
Phe Phe Ser Val Tyr Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe
            660                 665                 670
Leu Glu Asp Leu Glu Arg Asn Asp Gly Ser Ala Glu Arg Pro Tyr Phe
        675                 680                 685
Met Ser Ser Thr Leu Lys Lys Leu Leu Asn Lys Thr Asn Lys Lys Ala
    690                 695                 700
Ala Glu Ser
705
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<210> 3817
<211> 419
<212> DNA
<213> Homo sapiens

<400> 3817
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120
agctacgtgg aggagctggt ggagattcgc aagctgcgcc aggacatcct gctcatgaag
180
ccgtacttca tcacctgcag ggaggccatg gaggctcgtc tgctgctgca ggacctcctg
240
gacgtgcatg ccggccgcct gggctgctcg ctcaccgaga tccacacgct cttcgccaag
300
cacatcaagc tggactgcga gcggtgccag gccaagggct tcgtgtgtga gctctgcaga
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419

<210> 3818
<211> 139
<212> PRT

<213> Homo sapiens

<400> 3818

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Arg Val Val His Asn Trp Asp Phe Glu Pro Arg Lys Val Ser Arg Cys
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Ser Met Arg Tyr Leu Ala Leu Met Val Ser Arg Pro Val Leu Arg Leu
            20                  25                  30
Arg Glu Ile Asn Pro Leu Leu Phe Ser Tyr Val Glu Glu Leu Val Glu
        35                  40                  45
Ile Arg Lys Leu Arg Gln Asp Ile Leu Leu Met Lys Pro Tyr Phe Ile
    50                  55                  60
Thr Cys Arg Glu Ala Met Glu Ala Arg Leu Leu Leu Gln Asp Leu Leu
65                  70                  75                  80
Asp Val His Ala Gly Arg Leu Gly Cys Ser Leu Thr Glu Ile His Thr
                85                  90                  95
Leu Phe Ala Lys His Ile Lys Leu Asp Cys Glu Arg Cys Gln Ala Lys
            100                 105                 110
Gly Phe Val Cys Glu Leu Cys Arg Glu Gly Asp Val Leu Phe Pro Phe
        115                 120                 125
Asp Ser His Thr Ser Val Cys Ala Asp Cys Phe
    130                 135
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<210> 3819
<211> 1731
<212> DNA
<213> Homo sapiens

<400> 3819

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180
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240
cggaagttcg acggcgccgg gcgagtggct gttgagcggc gccgcgggag ttccgcaggt
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360
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420
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480
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<211> 342
<212> PRT
<213> Homo sapiens

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35 40 45
Ser Gln Val Gln Lys Leu Thr Glu Glu Asn Thr Thr Leu Arg Glu Gln
50 55 60
Val Glu Pro Thr Pro Glu Asp Glu Asp Asp Asp Ile Glu Leu Arg Gly
65 70 75 80
Ala Ala Ala Ala Ala Ala Pro Pro Pro Pro Ile Glu Glu Glu Cys Pro
85 90 95
Glu Asp Leu Pro Glu Lys Phe Asp Gly Asn Pro Asp Met Leu Ala Pro
100 105 110
Phe Met Ala Gln Cys Gln Ile Phe Met Glu Lys Ser Thr Arg Asp Phe
115 120 125
Ser Val Asp Arg Val Arg Val Cys Phe Val Thr Ser Met Met Thr Gly
130 135 140
Arg Ala Ala Arg Trp Ala Ser Ala Lys Leu Glu Arg Ser His Tyr Leu
145 150 155 160
Met His Asn Tyr Pro Ala Phe Met Met Glu Met Lys His Val Phe Glu
165 170 175
Asp Pro Gln Arg Arg Glu Val Ala Lys Arg Lys Ile Arg Arg Leu Arg
180 185 190
Gln Gly Met Gly Ser Val Ile Asp Tyr Ser Asn Ala Phe Gln Met Ile
195 200 205
Ala Gln Asp Leu Asp Trp Asn Glu Pro Ala Leu Ile Asp Gln Tyr His

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Ala Lys Ser Leu Ser Ala Leu Ile Gly Gln Cys Ile His Ile Glu Arg
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Arg Leu Ala Arg Ala Ala Ala Ala Arg Lys Pro Arg Ser Pro Pro Arg
            260                 265                 270
Ala Leu Val Leu Pro His Ile Ala Ser His His Gln Val Asp Pro Thr
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Glu Pro Val Gly Gly Ala Arg Met Arg Leu Thr Gln Glu Glu Lys Glu
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Arg Arg Arg Lys Leu Asn Leu Cys Leu Tyr Cys Gly Thr Gly Gly His
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<212> PRT
<213> Homo sapiens

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20 25 30
Thr Asp Ser Ser Arg Gly Asn Cys Arg Gly Ser Arg Pro Ala Ser Ser
35 40 45
Ile Ser Ser Phe Asp Thr Gly Asp Ile Leu Tyr Ser Pro Phe Ser Arg

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Lys Asn Ala Lys Val Cys Thr Leu Arg Ala Pro Trp Asn Val Asp Asn
                85                  90                  95
Ser Gly Ser Lys Thr Lys Phe Cys Val Asn Glu Leu Gln Asn Ser Arg
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<212> PRT
<213> Homo sapiens

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Ser Pro Ser Phe Asp Thr Pro Glu Ser Gln Ile Arg Gly Val Trp Glu
50 55 60
Glu Leu Gly Val Gly Ser Ser Gly His Leu Ser Glu Gln Glu Leu Ala
65 70 75 80
Val Val Cys Gln Ser Val Gly Leu Gln Gly Leu Glu Lys Glu Glu Leu
85 90 95
Glu Asp Leu Phe Asn Lys Leu Asp Gln Asp Gly Asp Gly Lys Val Ser
100 105 110
Leu Glu Glu Phe Gln Leu Gly Leu Phe Ser His Glu Pro Ala Leu Leu
115 120 125
Leu Glu Ser Ser Thr Arg Val Lys Pro Ser Lys Ala Trp Ser His Tyr
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Gln Val Pro Glu Glu Ser Gly Cys His Thr Thr Thr Thr Ser Ser Leu
145 150 155 160
Val Ser Leu Cys Ser Ser Leu Arg Leu Phe Ser Ser Ile Asp Asp Gly
165 170 175
Ser Gly Phe Ala Phe Pro Asp Gln Val Leu Ala Met Trp Thr Gln Glu
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Gly Ile Gln Asn Gly Arg Glu Ile Leu Gln Ser Leu Asp Phe Ser Val
195 200 205
Asp Glu Lys Val Asn Leu Leu Glu Leu Thr Trp Ala Leu Asp Asn Glu
210 215 220
Leu Met Thr Val Asp Ser Ala Val Gln Gln Ala Ala Leu Ala Cys Tyr
225 230 235 240
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245 250 255
Glu Arg Asp Lys Ala Arg Gln Asp Leu Glu Arg Ala Glu Lys Arg Asn
260 265 270
Leu Glu Phe Val Lys Glu Met Asp Asp Cys His Ser Thr Leu Glu Gln
275 280 285
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305 310 315 320
Glu Gln Ala His Arg Gln Arg Ala Ala Leu Glu Trp Asp Val Gly Arg
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<213> Homo sapiens

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5580
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5713

<210> 3830
<211> 444
<212> PRT
<213> Homo sapiens

<400> 3830
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Phe Lys Gly Phe Arg Gly Gly Leu Asp Val Thr His Gly Gln Thr Gly
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Val Glu Ser Val Tyr Thr Thr Phe Arg Asp Arg Glu Ile Met Phe His

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        35                  40                  45
Val Ser Thr Lys Leu Pro Phe Thr Asp Gly Asp Ala Gln Gln Leu Gln
    50                  55                  60
Arg Lys Arg His Ile Gly Asn Asp Ile Val Ala Ile Ile Phe Gln Glu
65                  70                  75                  80
Glu Asn Thr Pro Phe Val Pro Asp Met Ile Ala Ser Asn Phe Leu His
                85                  90                  95
Ala Tyr Ile Val Val Gln Val Glu Thr Pro Gly Thr Glu Thr Pro Ser
            100                 105                 110
Tyr Lys Val Ser Val Thr Ala Arg Glu Asp Val Pro Thr Phe Gly Pro
        115                 120                 125
Pro Leu Pro Ser Pro Pro Val Phe Gln Lys Gly Pro Glu Phe Arg Glu
    130                 135                 140
Phe Leu Leu Thr Lys Leu Thr Asn Ala Glu Asn Ala Cys Cys Lys Ser
145                 150                 155                 160
Asp Lys Phe Ala Lys Leu Glu Asp Arg Thr Arg Ala Ala Leu Leu Asp
                165                 170                 175
Asn Leu His Asp Glu Leu His Ala His Thr Gln Ala Met Leu Gly Leu
            180                 185                 190
Gly Pro Glu Glu Asp Lys Phe Glu Asn Gly Gly His Gly Gly Phe Leu
        195                 200                 205
Glu Ser Phe Lys Arg Ala Ile Arg Val Arg Ser His Ser Met Glu Thr
    210                 215                 220
Met Val Gly Gly Gln Lys Lys Ser His Ser Gly Gly Ile Pro Gly Ser
225                 230                 235                 240
Leu Ser Gly Gly Ile Ser His Asn Ser Met Glu Val Thr Lys Thr Thr
                245                 250                 255
Phe Ser Pro Pro Val Val Ala Ala Thr Val Lys Asn Gln Ser Arg Ser
            260                 265                 270
Pro Ile Lys Arg Arg Ser Gly Leu Phe Pro Arg Leu His Thr Gly Ser
        275                 280                 285
Glu Gly Gln Gly Asp Ser Arg Ala Arg Cys Asp Ser Thr Ser Ser Thr
    290                 295                 300
Pro Lys Thr Pro Asp Gly Gly His Ser Ser Gln Glu Ile Lys Ser Glu
305                 310                 315                 320
Thr Ser Ser Asn Pro Ser Ser Pro Glu Ile Cys Pro Asn Lys Glu Lys
                325                 330                 335
Pro Phe Met Lys Leu Lys Glu Asn Gly Arg Ala Ile Ser Arg Ser Ser
            340                 345                 350
Ser Ser Thr Ser Ser Val Ser Ser Thr Ala Gly Glu Gly Glu Ala Met
        355                 360                 365
Glu Glu Gly Asp Ser Gly Gly Ser Gln Pro Ser Thr Thr Ser Pro Phe
    370                 375                 380
Lys Gln Glu Val Phe Val Tyr Ser Pro Ser Pro Ser Ser Glu Ser Pro
385                 390                 395                 400
Ser Leu Gly Ala Ala Ala Thr Pro Ile Ile Met Ser Arg Ser Pro Thr
                405                 410                 415
Asp Ala Lys Ser Arg Asn Ser Pro Arg Ser Asn Leu Lys Phe Arg Phe
            420                 425                 430
Asp Lys Leu Ser His Ala Ser Ser Gly Ala Gly His
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<210> 3831
<211> 726

<212> DNA
<213> Homo sapiens

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180
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240
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360
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420
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480
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540
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600
agcgcagcca ccactcccac agttgagaat gaacagcctt ccctcgtttg ggttgacaga
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720
gctcag
726

<210> 3832
<211> 107
<212> PRT
<213> Homo sapiens

<400> 3832
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Phe Ser Pro Glu Thr Asp Pro Leu Xaa Val Ser Gln Ile Pro Ala Ser
            20   25   30
Leu Ser Ser Ala Leu Ala Cys Tyr Gly Leu Ser Phe Leu Gln Leu His
        35   40   45
Ser Thr Asn Ser His Ile Asp Arg Ile Asn Phe Ser Val Lys Met Val
    50   55   60
Ser Ser Ile Leu Gln Ile Pro Lys Leu Ser Tyr Leu Gly Leu Gly Asp
65   70   75   80
Ile Lys Asn Met Glu Gln Lys Tyr Cys Asn Leu Cys Ile Gln Leu Phe
                85   90   95
Ile Ser Phe Leu Leu Leu Thr Val Gln Thr Phe
            100   105

<210> 3833
<211> 1764

<212> DNA
<213> Homo sapiens

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120
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180
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240
atcatcgcgc gcaccaaggg gctctccatc ctcacccacg acgtgcagag ccagctcaac
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360
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420
cccgcgcagc cgggcctggt ggaccgctac cgcgtgacgc gatgccgcca cgaggtggag
480
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660
agcaccagcg cgtcggcgct gctggcctgc gtgcgcgagg tgaaggtggc gcccagtgag
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960
cacagggaga ggctgaggaa ctcggcctgc gccgtgtctg aaggctgcac cctgctatct
1020
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1080
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1140
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1200
gttaaatgct cgagaggaat cttccacaag gcagggccat gcacgcaacc tgcacacgca
1260
cttggagggc ccaggtgtct ctccaccagc ccccatgcag tagggactgg aagatatgtc
1320
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1380
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1440
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1500

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1620
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1764

<210> 3834
<211> 361
<212> PRT
<213> Homo sapiens

<400> 3834
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Pro Ala Ser Ala Gly Gly Gly Ala Ser Ser Gln Pro Arg Lys Lys Leu
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Val Ser Val Cys Asp His Cys Lys Gly Lys Met Gln Leu Val Ala Asp
35 40 45
Leu Leu Leu Leu Ser Ser Glu Ala Arg Pro Val Leu Phe Glu Gly Pro
50 55 60
Ala Ser Ser Gly Ala Gly Ala Glu Ser Phe Glu Gln Gly Arg Asp Thr
65 70 75 80
Ile Ile Ala Arg Thr Lys Gly Leu Ser Ile Leu Thr His Asp Val Gln
85 90 95
Ser Gln Leu Asn Met Gly Arg Phe Gly Glu Ala Gly Asp Ser Leu Val
100 105 110
Glu Leu Gly Asp Leu Val Val Ser Leu Thr Glu Cys Ser Ala His Ala
115 120 125
Ala Tyr Leu Ala Ala Val Ala Thr Pro Gly Ala Gln Pro Ala Gln Pro
130 135 140
Gly Leu Val Asp Arg Tyr Arg Val Thr Arg Cys Arg His Glu Val Glu
145 150 155 160
Gln Gly Cys Ala Val Leu Arg Ala Thr Pro Leu Ala Asp Met Thr Pro
165 170 175
Gln Leu Leu Leu Glu Val Ser Gln Gly Leu Ser Arg Asn Leu Lys Phe
180 185 190
Leu Thr Asp Ala Cys Ala Leu Ala Ser Asp Lys Ser Arg Asp Arg Phe
195 200 205
Ser Arg Glu Gln Phe Lys Leu Gly Val Lys Cys Met Ser Thr Ser Ala
210 215 220
Ser Ala Leu Leu Ala Cys Val Arg Glu Val Lys Val Ala Pro Ser Glu
225 230 235 240
Leu Ala Arg Ser Arg Cys Ala Leu Phe Ser Gly Pro Leu Val Gln Ala
245 250 255
Val Ser Ala Leu Val Gly Phe Ala Thr Glu Pro Gln Phe Leu Gly Arg
260 265 270
Ala Ala Ala Val Ser Ala Glu Gly Lys Ala Val Gln Thr Ala Ile Leu
275 280 285
Gly Gly Ala Met Ser Val Val Ser Ala Cys Val Leu Leu Thr Gln Cys

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    290                 295                 300
Leu Arg Asp Leu Ala Gln His Pro Asp Gly Gly Ala Lys Met Ser Asp
305                 310                 315                 320
His Arg Glu Arg Leu Arg Asn Ser Ala Cys Ala Val Ser Glu Gly Cys
                325                 330                 335
Thr Leu Leu Ser Gln Ala Leu Arg Glu Arg Ser Ser Pro Arg Thr Leu
            340                 345                 350
Pro Pro Val Asn Ser Asn Ser Val Asn
        355                 360
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<210> 3835
<211> 2366
<212> DNA
<213> Homo sapiens

<400> 3835
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180
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480
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600
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720
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1140

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1320
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2220
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2366

<210> 3836
<211> 479
<212> PRT
<213> Homo sapiens

<400> 3836
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Glu Leu Met Arg Ala Gly Leu Val Val Ser Arg Asp Gly Ala Pro Asp
20 25 30
Gly Gly Ile Glu Gln Met Gly Leu Ala Met Glu His Gly Gly Ser Tyr

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        35                  40                  45
Ala Arg Ala Gly Gly Ser Ser Arg Gly Cys Trp Tyr Tyr Leu Arg Tyr
    50                  55                  60
Phe Phe Leu Phe Val Ser Leu Ile Gln Phe Leu Ile Ile Leu Gly Leu
65                  70                  75                  80
Val Leu Phe Met Val Tyr Gly Asn Val His Val Ser Thr Glu Ser Asn
                85                  90                  95
Leu Gln Ala Thr Glu Arg Arg Ala Glu Gly Leu Tyr Ser Gln Leu Leu
            100                 105                 110
Gly Leu Thr Ala Ser Gln Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr
        115                 120                 125
Thr Arg Ala Lys Asp Ala Ile Met Gln Met Trp Leu Asn Ala Arg Arg
    130                 135                 140
Asp Leu Asp Arg Ile Asn Ala Ser Phe Arg Gln Cys Gln Gly Asp Arg
145                 150                 155                 160
Val Ile Tyr Thr Asn Asn Gln Arg Tyr Met Ala Ala Ile Ile Leu Ser
                165                 170                 175
Glu Lys Gln Cys Arg Asp Gln Phe Lys Asp Met Asn Lys Ser Cys Asp
            180                 185                 190
Ala Leu Leu Phe Met Leu Asn Gln Lys Val Lys Thr Leu Glu Val Glu
        195                 200                 205
Ile Ala Lys Glu Lys Thr Ile Cys Thr Lys Asp Lys Glu Ser Val Leu
    210                 215                 220
Leu Asn Lys Arg Val Ala Glu Glu Gln Leu Val Glu Cys Val Lys Thr
225                 230                 235                 240
Arg Glu Leu Gln His Gln Glu Arg Gln Leu Ala Lys Glu Gln Leu Gln
                245                 250                 255
Lys Val Gln Ala Leu Cys Leu Pro Leu Asp Lys Asp Lys Phe Glu Met
            260                 265                 270
Asp Leu Arg Asn Leu Trp Arg Asp Ser Ile Ile Pro Arg Ser Leu Asp
        275                 280                 285
Asn Leu Gly Tyr Asn Leu Tyr His Pro Leu Gly Ser Glu Leu Ala Ser
    290                 295                 300
Ile Arg Arg Ala Cys Asp His Met Pro Ser Leu Met Ser Ser Lys Val
305                 310                 315                 320
Glu Glu Leu Ala Arg Ser Leu Arg Ala Asp Ile Glu Arg Val Ala Arg
                325                 330                 335
Glu Asn Ser Asp Leu Gln Arg Gln Lys Leu Glu Ala Gln Gln Gly Leu
            340                 345                 350
Arg Ala Ser Gln Glu Ala Lys Gln Lys Val Glu Lys Glu Ala Gln Ala
        355                 360                 365
Arg Glu Ala Lys Leu Gln Ala Glu Cys Ser Arg Gln Thr Gln Leu Ala
    370                 375                 380
Leu Glu Glu Lys Ala Val Leu Arg Lys Glu Arg Asp Asn Leu Ala Lys
385                 390                 395                 400
Glu Leu Glu Glu Lys Lys Arg Glu Ala Glu Gln Leu Arg Met Glu Leu
                405                 410                 415
Ala Ile Arg Asn Ser Ala Leu Asp Thr Cys Ile Lys Thr Lys Ser Gln
            420                 425                 430
Pro Met Met Pro Val Ser Arg Pro Met Gly Pro Val Pro Asn Pro Gln
        435                 440                 445
Pro Ile Asp Pro Ala Ser Leu Glu Glu Phe Lys Arg Lys Ile Leu Glu
    450                 455                 460
Ser Gln Arg Pro Pro Ala Gly Ile Pro Val Ala Pro Ser Ser Gly
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465 470 475

<210> 3837
<211> 2084
<212> DNA
<213> Homo sapiens

<400> 3837
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240
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720
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1140
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1260
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1920
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1980
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2084

<210> 3838
<211> 468
<212> PRT
<213> Homo sapiens

<400> 3838
Leu His Pro Thr Asp Trp Asp Gly Lys Val Ser Glu Ile Lys Lys Lys
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Ile Lys Ser Ile Leu Pro Gly Arg Ser Cys Asp Leu Leu Gln Asp Thr
20 25 30
Ser His Leu Pro Pro Glu His Ser Asp Val Val Ile Val Gly Gly Gly
35 40 45
Val Leu Gly Leu Ser Val Ala Tyr Trp Leu Lys Lys Leu Glu Ser Arg
50 55 60
Arg Gly Ala Ile Arg Val Leu Val Val Glu Arg Asp His Thr Tyr Ser
65 70 75 80
Gln Ala Ser Thr Gly Leu Ser Val Gly Gly Ile Cys Gln Gln Phe Ser
85 90 95
Leu Pro Glu Asn Ile Gln Leu Ser Leu Phe Ser Ala Ser Phe Leu Arg
100 105 110
Asn Ile Asn Glu Tyr Leu Ala Val Val Asp Ala Pro Pro Leu Asp Leu
115 120 125
Arg Phe Asn Pro Ser Gly Tyr Leu Leu Leu Ala Ser Glu Lys Asp Ala
130 135 140
Ala Ala Met Glu Ser Asn Val Lys Val Gln Arg Gln Glu Gly Ala Lys
145 150 155 160
Val Ser Leu Met Ser Pro Asp Gln Leu Arg Asn Lys Phe Pro Trp Ile
165 170 175
Asn Thr Glu Gly Val Ala Leu Ala Ser Tyr Gly Met Glu Asp Glu Gly

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            180                 185                 190
Trp Phe Asp Pro Trp Cys Leu Leu Gln Gly Leu Arg Arg Lys Val Gln
        195                 200                 205
Ser Leu Gly Val Leu Phe Cys Gln Gly Glu Val Thr Arg Phe Val Ser
    210                 215                 220
Ser Ser Gln Arg Met Leu Thr Thr Asp Asp Lys Ala Val Val Leu Lys
225                 230                 235                 240
Arg Ile His Glu Val His Val Lys Met Asp Arg Ser Leu Glu Tyr Gln
                245                 250                 255
Pro Val Glu Cys Ala Ile Val Ile Asn Ala Ala Gly Ala Trp Ser Ala
            260                 265                 270
Gln Ile Ala Ala Leu Ala Gly Val Gly Glu Gly Pro Pro Gly Thr Leu
        275                 280                 285
Gln Gly Thr Lys Leu Pro Val Glu Pro Arg Lys Arg Tyr Val Tyr Val
    290                 295                 300
Trp His Cys Pro Gln Gly Pro Gly Leu Glu Thr Pro Leu Val Ala Asp
305                 310                 315                 320
Thr Ser Gly Ala Tyr Phe Arg Arg Glu Gly Leu Gly Ser Asn Tyr Leu
                325                 330                 335
Gly Gly Arg Ser Pro Thr Glu Gln Glu Glu Pro Asp Pro Ala Asn Leu
            340                 345                 350
Glu Val Asp His Asp Phe Phe Gln Asp Lys Val Trp Pro His Leu Ala
        355                 360                 365
Leu Arg Val Pro Ala Phe Glu Thr Leu Lys Cys Phe Val His Pro Gln
    370                 375                 380
Val Gln Ser Ala Trp Ala Gly Tyr Tyr Asp Tyr Asn Thr Phe Asp Gln
385                 390                 395                 400
Asn Gly Val Val Gly Pro His Pro Leu Val Val Asn Met Tyr Phe Ala
                405                 410                 415
Thr Gly Phe Ser Gly His Gly Leu Gln Gln Ala Pro Gly Ile Gly Arg
            420                 425                 430
Ala Val Ala Glu Met Val Leu Lys Gly Arg Phe Gln Thr Ile Asp Leu
        435                 440                 445
Ser Pro Phe Leu Phe Thr Arg Phe Tyr Leu Gly Glu Lys Ile Gln Glu
    450                 455                 460
Asn Asn Ile Ile
465
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<210> 3839
<211> 758
<212> DNA
<213> Homo sapiens

<400> 3839
nnacgcgtgc aggactctct ggaagtcacc cttcccagca aacaagagga ggaggatgag
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gaggaggagg aggaggagaa agaccagcct gccgagatgg agtaccttaa ctctcgctgt
120
gtccttttca cttatttcca gggagacatt gggtcagtag tggatgaaca cttctcaaga
180
gctttgggcc aagccatcac cctccatcca gaatctgcca tttcaaaaag caagatgggg
240
ctaacccccc tatggcgaga cagctcagct ctctcaagcc agcggaatag tttcccaact
300

tccttttgga ccagctctta ccagccccca cctgcacctt gtttgggggg agttcatcct
360
gacttccagg tcactggacc ccctggcacc ttttctgcag ctgatcccag tccttggccg
420
ggacacaacc tgcatcagac tggcccagcc cctccccctg ctgtgtctga gtcctggcct
480
tatcctttga catctcaggt gagcccatcc tacagccata tgcatgacgt gtacatgcgg
540
caccaccacc ctcatgccca catgcaccac cgccaccgcc accatcatca ccatcaccac
600
cctcctgctg gctctgccct ggatccatcc tatgggcctc tgctgatgcc ttcagtgcat
660
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720
tctgctacct cagcatgggc tggagccttt catggaac
758

<210> 3840
<211> 252
<212> PRT
<213> Homo sapiens

<400> 3840
Xaa Arg Val Gln Asp Ser Leu Glu Val Thr Leu Pro Ser Lys Gln Glu
1 5 10 15
Glu Glu Asp Glu Glu Glu Glu Glu Glu Glu Lys Asp Gln Pro Ala Glu
20 25 30
Met Glu Tyr Leu Asn Ser Arg Cys Val Leu Phe Thr Tyr Phe Gln Gly
35 40 45
Asp Ile Gly Ser Val Val Asp Glu His Phe Ser Arg Ala Leu Gly Gln
50 55 60
Ala Ile Thr Leu His Pro Glu Ser Ala Ile Ser Lys Ser Lys Met Gly
65 70 75 80
Leu Thr Pro Leu Trp Arg Asp Ser Ser Ala Leu Ser Ser Gln Arg Asn
85 90 95
Ser Phe Pro Thr Ser Phe Trp Thr Ser Ser Tyr Gln Pro Pro Pro Ala
100 105 110
Pro Cys Leu Gly Gly Val His Pro Asp Phe Gln Val Thr Gly Pro Pro
115 120 125
Gly Thr Phe Ser Ala Ala Asp Pro Ser Pro Trp Pro Gly His Asn Leu
130 135 140
His Gln Thr Gly Pro Ala Pro Pro Pro Ala Val Ser Glu Ser Trp Pro
145 150 155 160
Tyr Pro Leu Thr Ser Gln Val Ser Pro Ser Tyr Ser His Met His Asp
165 170 175
Val Tyr Met Arg His His His Pro His Ala His Met His His Arg His
180 185 190
Arg His His His His His His His Pro Pro Ala Gly Ser Ala Leu Asp
195 200 205
Pro Ser Tyr Gly Pro Leu Leu Met Pro Ser Val His Ala Ala Arg Ile
210 215 220
Pro Ala Pro Gln Cys Asp Ile Thr Lys Thr Glu Pro Thr Thr Val Thr
225 230 235 240
Ser Ala Thr Ser Ala Trp Ala Gly Ala Phe His Gly

245 250

<210> 3841
<211> 367
<212> DNA
<213> Homo sapiens

<400> 3841
ctgggaactc cccacacttc cgtgggcaac atcttggggt cattgatcgc tggctactgg
60
gtgtccacat gctggggcct gtctttcgtc gtgcctggag ccatcgtggc agccatgggg
120
atagtgtgct ttctcttcct cattgaacat ccgaacgacg tcaggtgctc ctccaccctg
180
gtgacgcact caaaaggcta tgagaatggt acaaacaggt tgagcctccc gaagccaatc
240
ttgaagagcg aaaagaacaa gcctctggac ccagagatgc agtgcctgct gctctcagat
300
gggaagggct ccatccaccc gaaccacgtc gtcattctcc ccggggacgg tgggagtggc
360
ccggccg
367

<210> 3842
<211> 122
<212> PRT
<213> Homo sapiens

<400> 3842
Leu Gly Thr Pro His Thr Ser Val Gly Asn Ile Leu Gly Ser Leu Ile
1 5 10 15
Ala Gly Tyr Trp Val Ser Thr Cys Trp Gly Leu Ser Phe Val Val Pro
20 25 30
Gly Ala Ile Val Ala Ala Met Gly Ile Val Cys Phe Leu Phe Leu Ile
35 40 45
Glu His Pro Asn Asp Val Arg Cys Ser Ser Thr Leu Val Thr His Ser
50 55 60
Lys Gly Tyr Glu Asn Gly Thr Asn Arg Leu Ser Leu Pro Lys Pro Ile
65 70 75 80
Leu Lys Ser Glu Lys Asn Lys Pro Leu Asp Pro Glu Met Gln Cys Leu
85 90 95
Leu Leu Ser Asp Gly Lys Gly Ser Ile His Pro Asn His Val Val Ile
100 105 110
Leu Pro Gly Asp Gly Gly Ser Gly Pro Ala
115 120

<210> 3843
<211> 712
<212> DNA
<213> Homo sapiens

<400> 3843
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60

ggcggcgagg ccgcgaaggg cgcggggctg gaggcccgcg gcgccatggc tcacgtcggc
120
tcccgcaagc gctcgaggag tcgcagccgg tcccggggac gggggtcgga aaagagaaag
180
aagaagagca ggaaagacac ctcgaggaac tgctcggcct ccacatccca aggtcgcaag
240
gccagcacgg cccctggggc ggaggcctca ccttctccct gcatcacaga gagaagcaag
300
cagaaggccc ggaggagaac aagatccagc tcctcctcct cttcttccag ttcttctagc
360
tcctcttctt cctcctcgtc ctcctcctct tcctccagtg atggccggaa gaagcggggg
420
aagtacaagg acaagaggag gaagaagaag aagaagagga agaagctgaa gaagaagggc
480
aaggagaagg cggaagcaca gcaggcagag catcatccgc aaggtggtgg accctgagac
540
ggggcgcacc aggcttatta agggagatgg cgaggtccta gaggaaatcg taaccaaaga
600
acgacacaga gagatcaaca agcaagccac ccgaggggac tgcctggcct tccagatgcg
660
agctgggttg cttcctgagg gccccgctgg caaggctgtg gacgacgctg gc
712

<210> 3844
<211> 143
<212> PRT
<213> Homo sapiens

<400> 3844
Met Ala His Val Gly Ser Arg Lys Arg Ser Arg Ser Arg Ser Arg Ser
 1   5   10   15
Arg Gly Arg Gly Ser Glu Lys Arg Lys Lys Lys Ser Arg Lys Asp Thr
            20   25   30
Ser Arg Asn Cys Ser Ala Ser Thr Ser Gln Gly Arg Lys Ala Ser Thr
        35   40   45
Ala Pro Gly Ala Glu Ala Ser Pro Ser Pro Cys Ile Thr Glu Arg Ser
    50   55   60
Lys Gln Lys Ala Arg Arg Arg Thr Arg Ser Ser Ser Ser Ser Ser Ser
65   70   75   80
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
                85   90   95
Ser Ser Asp Gly Arg Lys Lys Arg Gly Lys Tyr Lys Asp Lys Arg Arg
            100   105   110
Lys Lys Lys Lys Lys Arg Lys Lys Leu Lys Lys Lys Gly Lys Glu Lys
        115   120   125
Ala Glu Ala Gln Gln Ala Glu His His Pro Gln Gly Gly Gly Pro
    130   135   140

<210> 3845
<211> 2302
<212> DNA
<213> Homo sapiens

<400> 3845

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agcccggcag tacctgctgt gccccggctc aagcggggtg gagaacacgg agctcgtcaa
120
gtcacccagt gagtacctga tgatgctgat gccacccagc caggaggagg agaaagacaa
180
gcctgtggcc cccagcaacg tcctgtcgat ggcccagctg cgcacgctgc ccctggccga
240
tcagatcaag atcctgatga agaatgtgaa ggtcatgcct tttgccaact tgatgagcct
300
cctgggcccc tccatcgatt ccgtggctgt tctgcggggc atccagaagg tggcgatgtt
360
ggtccaaggg aactgggtgg tgaagagtga catcctatac cccaaggact cgtccagccc
420
tcacagcggc gtgcctgctg aggtgctctg caggggccga gacttcgtta tgtggaagtt
480
cacgcagagc cgctgggtgg ttaggaaaga ggtggcaacc gtgaccaaac tctgcgccga
540
ggatgtgaag gacttcctgg agcacatggc cgtggtgagg atcaacaaag gctgggagtt
600
cattctgcct tatgatgggg agttcatcaa gaagcacccg gatgtggtcc agcggcagca
660
catgctgtgg acgggtatcc aggccaaact ggaaaaagtc tataatcttg taaaggaaac
720
catgccaaag aagccggatg cacaatcagg gcctgccggg ctggtctgtg gggaccagcg
780
gatccaagta gccaaaacca aggcccagca gaaccacgcg ttgctggagc gggagctgca
840
gcggcggaag gagcagctgc gggtgcctgc ggtcccgccc ggtgtgcgga tcaaggagga
900
gcccgtgagc gaggagggcg aggaggacga ggagcaggag gcggaggagg agcccatgga
960
cacttccccc agcggcctcc acagcaagct ggccaacggg ctgcctctcg ggcgggctgc
1020
gggcacagac agcttcaacg ggcacccgcc ccagggctgc gccagcaccc ctgtggctcg
1080
ggaactgaag gccttcgtgg aggccacctt tcagagacag tttgtgctca cgctgagcga
1140
actcaagcgc ctcttcaatc tgcacttggc cagcctgccc cccggccaca cactcttcag
1200
cggcatctcg gaccgcatgc tacaggacac ggtgctggcc gccggttgca agcagatact
1260
ggtgcctttt ccccccccaga ctgctgcttc cccggatgag cagaaggtgt ttgccctctg
1320
ggagtctgga gacatgagtg atcagcatcg acaggttttg cttgaaattt tttccaaaaa
1380
ttaccgggta cgccgaaaca tgatccagtc tcggttgact caagagtgtg gagaagatct
1440
cagtaaacag gaggtggata aagtactaaa ggactgctgt gtaagctatg gtggcatgtg
1500
gtaccttaaa gggacagtac agtcttgaca atagtagcaa actactaacc cagcaaatct
1560
aagcccaagg aagaagggcg gaaccagaag tagggcctcg acttgcttca gacgacacag
1620

agcaagagga actgaccatc tcatgacctg tggcattgca cggtgcagtg gacagaaggg
1680
attatcctca gccagtcgca gggtcagctt aagttagtta gatcactccc agaagagacc
1740
agctgggacc ttctttgcag tacaatttga aattcctgat gtattttgct tattatttgg
1800
tttcattctc ataataaaga gagtgtatac ttacatgggc aggatgataa aaatcatggt
1860
ttaatatttt cttttgtaaa cttaatgcca acaaggtcta agttatgttt acaacatgaa
1920
gaaaacctca aagttcttaa tttttaaaat gcctagaaga caatatttag tcttggatta
1980
tctatctgct aagacctcca ccaatttcat taaaccaaat tgaattattc tattcttggg
2040
attctgtggc cacttcacct ttgacaacaa cctactttat gtagcagtct caactgttta
2100
catgaaccat agcaaaaaaa tcagaatcaa atccatctcc ttttaatgtt tgcagaaaga
2160
tgcaaacaaa accaggtaag tatggaacaa tgtgtaagtg aggttatcac actttgatgt
2220
aaaaatttct attttgtgta tttttaaaat aaatgcaaac actaaactaa aaaaaaaaaa
2280
aaaaaaaaaa aaaaaaaaaa aa
2302

<210> 3846
<211> 197
<212> PRT
<213> Homo sapiens

<400> 3846
Ser Cys Lys Gly Asn His Ala Lys Glu Ala Gly Cys Thr Ile Arg Ala
 1   5   10   15
Cys Arg Ala Gly Leu Trp Gly Pro Ala Asp Pro Ser Ser Gln Asn Gln
            20   25   30
Gly Pro Ala Glu Pro Arg Val Ala Gly Ala Gly Ala Ala Ala Ala Glu
        35   40   45
Gly Ala Ala Ala Gly Ala Cys Gly Pro Ala Arg Cys Ala Asp Gln Gly
    50   55   60
Gly Ala Arg Glu Arg Gly Gly Arg Gly Gly Arg Gly Ala Gly Gly Gly
65   70   75   80
Gly Gly Ala His Gly His Phe Pro Gln Arg Pro Pro Gln Gln Ala Gly
                85   90   95
Gln Arg Ala Ala Ser Arg Ala Gly Cys Gly His Arg Gln Leu Gln Arg
            100   105   110
Ala Pro Ala Pro Gly Leu Arg Gln His Pro Cys Gly Ser Gly Thr Glu
        115   120   125
Gly Leu Arg Gly Gly His Leu Ser Glu Thr Val Cys Ala His Ala Glu
    130   135   140
Arg Thr Gln Ala Pro Leu Gln Ser Ala Leu Gly Gln Pro Ala Pro Arg
145   150   155   160
Pro His Thr Leu Gln Arg His Leu Gly Pro His Ala Thr Gly His Gly
                165   170   175
Ala Gly Arg Arg Leu Gln Ala Asp Thr Gly Ala Phe Ser Pro Pro Asp

180 185 190
Cys Cys Phe Pro Gly
195

<210> 3847
<211> 1570
<212> DNA
<213> Homo sapiens

<400> 3847
nnccatggtg ggcttgaggg tggggctgtc ctagagcatt aaacagctgt tgggccctgg
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gctgaccccc ccaccctgca tgtgtggggg tccccacagc tcttatgttc ctcctgggcc
120
ttctggaatt cctcctcctt aggcaagcct atcacagcat cctgacccgt ggggcctctg
180
tgcagctggt gtttggcttt gaggtaaaac tggcttggga ggttgagagg acaagcccga
240
ggtgacccca catgtgcctt gaataaccca acagaccctt cctcagcacc tgctatgtgg
300
ccaacctgtg ctggccacca aggggcagtg atcagatatg gctcctgccc tccacacgct
360
cactcctagg tgactgggga gacgcacaaa gaggctagga cagaggagga gccccaacct
420
ggggctcagg agagggttcc tggaggctcg tgccggagct agctggtaat ggacaggaga
480
ggattagttc catggacaac tggaggcgtg tccctggcag agagagaatg tgttcagtga
540
cgacagctca tatttgttga gtgcgaattt cacaccaggc cctatgctga gctcctgacc
600
tgcatctctt attcagcaag acaatactgt tataaaggaa cagttaatta tgtcatttta
660
tagataagta aactgaggtt cactgagttg ccaaaagtca cagctagtaa gtggaggggc
720
taggaggacc ctgggtgtgt ctagagcctg tgattgtacc actgcacctg ctgtgcagag
780
gccttgggga gcaatgtggg tgcagcaagg gggagctatg tgtttacatc cccctcgtcc
840
ccctctccct tcagtatgcc atcctgatga cgatggtgct caccatcttc atcaagtatg
900
tgctgcactc cgtggacctc cagagtgaga acccctggga caacaaggct gtgtacatgc
960
tctacacaga gctgtttaca ggtgagaggg gcctgggcct ctcctgatct ggaccagcat
1020
cctccactct gcctcctggc cctgtgacct gctgctttct gcatcccctc ccctcaggct
1080
tcatcaaggt tctgctgtac atggccttca tgaccatcat gatcaaggtg cacaccttcc
1140
cactctttgc catccggccc atgtacctgg ccatgaggtg agcccggccc tgtcccccga
1200
tcctcctgac ctgatcccgt cccttctcct gctttcactg actgtccttt cagacagttc
1260
aagaaagctg tgacagatgc catcatgtct cgccgagcca tccgcaacat gaacaccctg
1320

tatccagatg ccaccccaga ggagctccag gcaatggaca atgtctgcat catctgccga
1380
gaagagatgg tgactggtgc caagagactg ccctgcaacc acattttcca taccaggtgg
1440
gaggggccct ggggagcctg cccagcaggg cccaggcccc agaaggcagg ccctaaggga
1500
cctgctgacc tctgcctggc cttgacccgc agctgcctgc gctcctggtt ccagcggcag
1560
cagacctgcc
1570

<210> 3848
<211> 120
<212> PRT
<213> Homo sapiens

<400> 3848
Pro Asp Pro Val Pro Ser Pro Ala Phe Thr Asp Cys Pro Phe Arg Gln
1 5 10 15
Phe Lys Lys Ala Val Thr Asp Ala Ile Met Ser Arg Arg Ala Ile Arg
20 25 30
Asn Met Asn Thr Leu Tyr Pro Asp Ala Thr Pro Glu Glu Leu Gln Ala
35 40 45
Met Asp Asn Val Cys Ile Ile Cys Arg Glu Glu Met Val Thr Gly Ala
50 55 60
Lys Arg Leu Pro Cys Asn His Ile Phe His Thr Arg Trp Glu Gly Pro
65 70 75 80
Trp Gly Ala Cys Pro Ala Gly Pro Arg Pro Gln Lys Ala Gly Pro Lys
85 90 95
Gly Pro Ala Asp Leu Cys Leu Ala Leu Thr Arg Ser Cys Leu Arg Ser
100 105 110
Trp Phe Gln Arg Gln Gln Thr Cys
115 120

<210> 3849
<211> 1139
<212> DNA
<213> Homo sapiens

<400> 3849
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ttagaattta tacagcaccc cagcacgctg ctaaacgtgg gcacacaacc accacggccc
120
gatcacgcgc agcgggaacc cggtctctga gtccgccccg tgcgttgcgt catcagagtc
180
acgccaccta atccattctc tcggtcttcg tctgctccgg tattgcaact gcctcgattg
240
gtcgatcctg ggccagcatg gcggcgccca tgtaacccgg tccgtgccgc aaagcgaacg
300
gcggccgcgg cgcgggcccc gcgggggtta gaggtcacca tgctgagggt cgcgtggagg
360
acgctgagtt tgattcggac ccgggcagtt acccaggtcc tagtacccgg gctgccgggc
420

ggtgggagcg ccaagtttcc tttcaaccag tggggcctgc agcctcgaag tctcctcctc
480
caggccgcgc gcggatatgt cgtccggaaa ccagcccagt ctaggctgga tgatgaccca
540
cctccttcta cgctgctcaa agactaccag aatgtccctg gaattgagaa ggttgatgat
600
gtcgtgaaaa gactcttgtc tttggaaatg gccaacaaga aggagatgct aaaaatcaag
660
caagaacagt ttatgaagaa gattgttgca aacccagagg acaccagatc cctggaggct
720
cgaattattg ccttgtctgt caagatccgc agttatgaag aacacttgga gaaacatcga
780
aaggacaaag cccacaaacg ctatctgcta atgagcattg accagaggaa aaagatgctc
840
aaaaacctcc gtaacaccaa ctatgatgtc tttgagaaga tatgctgggg gctgggaatt
900
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960
gctctgtgca ttcgggtttt ccaggagact caaaagctga agaagcgaag aagagcctta
1020
aaggctgcag cagcagccca aaaacaagca aagcggagga acccagacag ccctgccaaa
1080
gccataccaa agacactcaa agacagccaa taaattctgt tcaatcattt aaaaaaaaa
1139

<210> 3850
<211> 257
<212> PRT
<213> Homo sapiens

<400> 3850
Met Leu Arg Val Ala Trp Arg Thr Leu Ser Leu Ile Arg Thr Arg Ala
 1   5   10   15
Val Thr Gln Val Leu Val Pro Gly Leu Pro Gly Gly Gly Ser Ala Lys
            20   25   30
Phe Pro Phe Asn Gln Trp Gly Leu Gln Pro Arg Ser Leu Leu Leu Gln
        35   40   45
Ala Ala Arg Gly Tyr Val Val Arg Lys Pro Ala Gln Ser Arg Leu Asp
    50   55   60
Asp Asp Pro Pro Pro Ser Thr Leu Leu Lys Asp Tyr Gln Asn Val Pro
65   70   75   80
Gly Ile Glu Lys Val Asp Asp Val Val Lys Arg Leu Leu Ser Leu Glu
                85   90   95
Met Ala Asn Lys Lys Glu Met Leu Lys Ile Lys Gln Glu Gln Phe Met
            100   105   110
Lys Lys Ile Val Ala Asn Pro Glu Asp Thr Arg Ser Leu Glu Ala Arg
        115   120   125
Ile Ile Ala Leu Ser Val Lys Ile Arg Ser Tyr Glu Glu His Leu Glu
    130   135   140
Lys His Arg Lys Asp Lys Ala His Lys Arg Tyr Leu Leu Met Ser Ile
145   150   155   160
Asp Gln Arg Lys Lys Met Leu Lys Asn Leu Arg Asn Thr Asn Tyr Asp
                165   170   175
Val Phe Glu Lys Ile Cys Trp Gly Leu Gly Ile Glu Tyr Thr Phe Pro

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            180                 185                 190
Pro Leu Tyr Tyr Arg Arg Ala His Arg Arg Phe Val Thr Lys Lys Ala
        195                 200                 205
Leu Cys Ile Arg Val Phe Gln Glu Thr Gln Lys Leu Lys Lys Arg Arg
    210                 215                 220
Arg Ala Leu Lys Ala Ala Ala Ala Gln Lys Gln Ala Lys Arg Arg
225                 230                 235                 240
Asn Pro Asp Ser Pro Ala Lys Ala Ile Pro Lys Thr Leu Lys Asp Ser
                245                 250                 255
Gln
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<210> 3851
<211> 1183
<212> DNA
<213> Homo sapiens

<400> 3851
nnacgcgttt tggcctgagt tggggagggg ggcggggagg gacctgcggc ttgcggcccc
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gccccccttct ccggctcgca gccgaccggt aagcccgcct cctcccacgg ccggccctgg
120
ggccgtgtcc gccgggcaac tccagccgag gcctgggctt ctgcctgcag gtgtctgcgg
180
cgaggcccct agggtacagc ccgatttggc cccatggtgg gtttcggggc caaccggcgg
240
gctggccgcc tgccctctct cgtgctggtg gtgctgctgg tggtgatcgt cgtcctcgcc
300
ttcaactact ggagcatctc ctcccgccac gtcctgcttc aggaggaggt ggccgagctg
360
cagggccagg tccagcgcac cgaagtggcc cgcgggcggc tggaaaagcg caattcggac
420
ctcttgctgt tggtggacac gcacaagaaa cagatcgacc agaaggaggc cgactacggc
480
cgcctcagca gccggctgca ggccagagag ggcctcggga agagatgcga ggatgacaag
540
gttaaactac agaacaacat atcgtatcag atggcagaca tacatcattt aaaggagcaa
600
cttgctgagc ttcgtcagga atttcttcga caagaagacc agcttcagga ctataggaag
660
aacaatactt accttgtgaa gaggttagaa tatgaaagtt ttcagtgtgg acagcagatg
720
aaggaattga gagcacagca tgaagaaaat attaaaaagt tagcagacca gtttttagag
780
gaacaaaagc aagagaccca aaagattcaa tcaaatgatg gaaaggaatt ggatataaac
840
aatcaagtag tacctaaaaa tattccaaaa gtagctgaga atgttgcaga taagaatgaa
900
gaaccctcaa gcaatcatat tccacatggg aaagaacaaa tcaaaagagg tggtgatgca
960
gggatgcctg gaatagaaga gaatgaccta gcaaaagttg atgatcttcc ccctgcttta
1020
aggaagcctc ctatttcagt ttctcaacat gaaagtcatc aagcaatctc ccatcttcca
1080

actggacaac ctctctcccc aaatatgcct ccagattcac acataaacca caatggaaac
1140
cccggtactt caaaacagaa tccttccagt ccccttcacg cgt
1183

<210> 3852
<211> 323
<212> PRT
<213> Homo sapiens

<400> 3852
Met Val Gly Phe Gly Ala Asn Arg Arg Ala Gly Arg Leu Pro Ser Leu
1 5 10 15
Val Leu Val Val Leu Leu Val Val Ile Val Val Leu Ala Phe Asn Tyr
20 25 30
Trp Ser Ile Ser Ser Arg His Val Leu Leu Gln Glu Glu Val Ala Glu
35 40 45
Leu Gln Gly Gln Val Gln Arg Thr Glu Val Ala Arg Gly Arg Leu Glu
50 55 60
Lys Arg Asn Ser Asp Leu Leu Leu Leu Val Asp Thr His Lys Lys Gln
65 70 75 80
Ile Asp Gln Lys Glu Ala Asp Tyr Gly Arg Leu Ser Ser Arg Leu Gln
85 90 95
Ala Arg Glu Gly Leu Gly Lys Arg Cys Glu Asp Asp Lys Val Lys Leu
100 105 110
Gln Asn Asn Ile Ser Tyr Gln Met Ala Asp Ile His His Leu Lys Glu
115 120 125
Gln Leu Ala Glu Leu Arg Gln Glu Phe Leu Arg Gln Glu Asp Gln Leu
130 135 140
Gln Asp Tyr Arg Lys Asn Asn Thr Tyr Leu Val Lys Arg Leu Glu Tyr
145 150 155 160
Glu Ser Phe Gln Cys Gly Gln Gln Met Lys Glu Leu Arg Ala Gln His
165 170 175
Glu Glu Asn Ile Lys Lys Leu Ala Asp Gln Phe Leu Glu Glu Gln Lys
180 185 190
Gln Glu Thr Gln Lys Ile Gln Ser Asn Asp Gly Lys Glu Leu Asp Ile
195 200 205
Asn Asn Gln Val Val Pro Lys Asn Ile Pro Lys Val Ala Glu Asn Val
210 215 220
Ala Asp Lys Asn Glu Glu Pro Ser Ser Asn His Ile Pro His Gly Lys
225 230 235 240
Glu Gln Ile Lys Arg Gly Gly Asp Ala Gly Met Pro Gly Ile Glu Glu
245 250 255
Asn Asp Leu Ala Lys Val Asp Asp Leu Pro Pro Ala Leu Arg Lys Pro
260 265 270
Pro Ile Ser Val Ser Gln His Glu Ser His Gln Ala Ile Ser His Leu
275 280 285
Pro Thr Gly Gln Pro Leu Ser Pro Asn Met Pro Pro Asp Ser His Ile
290 295 300
Asn His Asn Gly Asn Pro Gly Thr Ser Lys Gln Asn Pro Ser Ser Pro
305 310 315 320
Leu His Ala

<210> 3853
<211> 375
<212> DNA
<213> Homo sapiens

<400> 3853
cgtacgcata tggccgatga aaataaaaat gaatatgctg cacaattaca aaactttaat
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ggagaacaac ataaacattt ttatgtagtg attcctcaga tttacaagca actacaagaa
120
atggacgaac gaaggactat taaactcagt gagtgttaca gaggatttgc tgactcagaa
180
cgcaaagtta ttcccatcat ttcaaaatgt ttggaaggaa tgattcttgc agcaaaatca
240
gttgatgaaa gaagagactc tcaaatggtg gtagactcct tcaaatctgg ttttgaacct
300
ccaggagact ttccatttga agattacagt caacatatat atagaaccat ttctgatggg
360
actatcagtg catcc
375

<210> 3854
<211> 125
<212> PRT
<213> Homo sapiens

<400> 3854
Arg Thr His Met Ala Asp Glu Asn Lys Asn Glu Tyr Ala Ala Gln Leu
 1   5   10   15
Gln Asn Phe Asn Gly Glu Gln His Lys His Phe Tyr Val Val Ile Pro
            20   25   30
Gln Ile Tyr Lys Gln Leu Gln Glu Met Asp Glu Arg Arg Thr Ile Lys
        35   40   45
Leu Ser Glu Cys Tyr Arg Gly Phe Ala Asp Ser Glu Arg Lys Val Ile
    50   55   60
Pro Ile Ile Ser Lys Cys Leu Glu Gly Met Ile Leu Ala Ala Lys Ser
65   70   75   80
Val Asp Glu Arg Arg Asp Ser Gln Met Val Val Asp Ser Phe Lys Ser
                85   90   95
Gly Phe Glu Pro Pro Gly Asp Phe Pro Phe Glu Asp Tyr Ser Gln His
            100   105   110
Ile Tyr Arg Thr Ile Ser Asp Gly Thr Ile Ser Ala Ser
        115   120   125

<210> 3855
<211> 1377
<212> DNA
<213> Homo sapiens

<400> 3855
naagctgcga ccatggcaac ctacaaccag ctctcctatg cccagaaggc caagtaccac
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ctgtgctcag caggctggct ggagaccggg cgggttgcct accccacagc cttcgcctcc
120

cagaactgtg gctctggtgt ggttgggata gtggactatg gacctagacc caacaagagt
180
gaaatgtggg atgtcttctg ctatcggatg aaagatgtga actgcacctg caaggtgggc
240
tatgtgggag atggcttctc atgcagtggg aacctgctgc aggtcctgat gtccttcccc
300
tcactcacaa acttcctgac ggaagtgctg gcctattcca acagctcagc tcgaggccgt
360
gcatttctag aacacctgac tgacctgtcc atccgcggca ccctctttgt gccacagaac
420
agtgggctgg gggagaatga gaccttgtct gggcgggaca tcgagcacca cctcgccaat
480
gtcagcatgt ttttctacaa tgaccttgtc aatggcaccn accctgcaaa cgagggtggg
540
aagcaagctg ctcatcactg ccagccagga cccactnncc aaccgacgga gaccaggttt
600
gttgatggaa gagccattct gcagtgggac atctttgcct ccaatgggat cattcatgtc
660
atttccaggc ctttaaaagc acccccctgcc cccgtgacct tgacccacac tggcttggga
720
gcagggatct tctttgccat catcctggtg actggggctg ttgccttggc tgcttactcc
780
tactttcgga taaaccggag aacaatcggc ttccagcatt ttgagtcgga agaggacatt
840
aatgttgcag ctcttggcaa gcagcagcct gagaatatct cgaacccctt gtatgagagc
900
acaacctcag ctcccccaga accttcctac gacccccttca cggactctga agaacggcag
960
cttgagggca atgacccctt gaggacactg tgagggcctg gacgggagat gccagccatc
1020
actcactgcc acctgggcca tcaactgtga attctcagca ccagttgcct tttaggaacg
1080
taaagtcctt taagcactca gaagccatac ctcatctctc tggctgatct gggggttgtt
1140
tctgtgggtg agagatgtgt tgctgtgccc acccagtaca gcttcctcct ctgacccttt
1200
ggctcttctt cctttgtact cttcagctgg cacctgctcc attctgccct acatgatggg
1260
taactgtgat ctttcttccc tgttagattg taagcctccg tctttgtatc ccagccccta
1320
gcccagtgcc tgacacagga actgtgcaca ataaaggttt atggaacaga aacaaaa
1377

<210> 3856
<211> 330
<212> PRT
<213> Homo sapiens

<400> 3856
Xaa Ala Ala Thr Met Ala Thr Tyr Asn Gln Leu Ser Tyr Ala Gln Lys
 1   5   10   15
Ala Lys Tyr His Leu Cys Ser Ala Gly Trp Leu Glu Thr Gly Arg Val
            20   25   30
Ala Tyr Pro Thr Ala Phe Ala Ser Gln Asn Cys Gly Ser Gly Val Val

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        35                  40                  45
Gly Ile Val Asp Tyr Gly Pro Arg Pro Asn Lys Ser Glu Met Trp Asp
    50                  55                  60
Val Phe Cys Tyr Arg Met Lys Asp Val Asn Cys Thr Cys Lys Val Gly
65                  70                  75                  80
Tyr Val Gly Asp Gly Phe Ser Cys Ser Gly Asn Leu Leu Gln Val Leu
                85                  90                  95
Met Ser Phe Pro Ser Leu Thr Asn Phe Leu Thr Glu Val Leu Ala Tyr
            100                 105                 110
Ser Asn Ser Ser Ala Arg Gly Arg Ala Phe Leu Glu His Leu Thr Asp
        115                 120                 125
Leu Ser Ile Arg Gly Thr Leu Phe Val Pro Gln Asn Ser Gly Leu Gly
    130                 135                 140
Glu Asn Glu Thr Leu Ser Gly Arg Asp Ile Glu His His Leu Ala Asn
145                 150                 155                 160
Val Ser Met Phe Phe Tyr Asn Asp Leu Val Asn Gly Thr Xaa Pro Ala
                165                 170                 175
Asn Glu Gly Gly Lys Gln Ala Ala His His Cys Gln Pro Gly Pro Thr
            180                 185                 190
Xaa Gln Pro Thr Glu Thr Arg Phe Val Asp Gly Arg Ala Ile Leu Gln
        195                 200                 205
Trp Asp Ile Phe Ala Ser Asn Gly Ile Ile His Val Ile Ser Arg Pro
    210                 215                 220
Leu Lys Ala Pro Pro Ala Pro Val Thr Leu Thr His Thr Gly Leu Gly
225                 230                 235                 240
Ala Gly Ile Phe Phe Ala Ile Ile Leu Val Thr Gly Ala Val Ala Leu
                245                 250                 255
Ala Ala Tyr Ser Tyr Phe Arg Ile Asn Arg Arg Thr Ile Gly Phe Gln
            260                 265                 270
His Phe Glu Ser Glu Glu Asp Ile Asn Val Ala Ala Leu Gly Lys Gln
        275                 280                 285
Gln Pro Glu Asn Ile Ser Asn Pro Leu Tyr Glu Ser Thr Thr Ser Ala
    290                 295                 300
Pro Pro Glu Pro Ser Tyr Asp Pro Phe Thr Asp Ser Glu Glu Arg Gln
305                 310                 315                 320
Leu Glu Gly Asn Asp Pro Leu Arg Thr Leu
                325                 330
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<210> 3857
<211> 797
<212> DNA
<213> Homo sapiens

<400> 3857
nngcgcgcca ccacgagaac agcntccggg gcgcggtcgt gggcgtgggc gacgagagcc
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gcgccctgcc cgacgtcatg cagggcatgg tgctcagctc catgcagcac ttcagcgagg
120
ccttccacca ggtcctgggc gagaagcata agcgcggcca cctggccgag gccgagggcc
180
acagggacac ttgcgacgaa gactcggtgg ccggcgagtc ggaccgcata gacgatggca
240
ctgttaatgg ccgcggctgc tccccgggcg agtcggcctc ggggggcctg tccaaaaagc
300

tgctgctggg cagccccagc tcgctgagcc ccttctctaa gcgcatcaag ctcgagaagg
360
agttcgacct gcccccggcc gcgatgccca acacggagaa cgtgtactcg cagtggctcg
420
ccggctacgc ggcctccagg cagctcaaag atcccttcct tagcttcgga gactccagac
480
aatcgccttt tgcctcctcg tcggagcact cctcggagaa cgggagcttg cgcttctcca
540
caccgcccgg ggagctggac ggagggatct cggggcgcag cggcacggga agtggaggga
600
gcacgcccca tattagtggt ccgggcccgg gcaggcccag ctcaaaagag ggcagacgca
660
gcgacacttg ttcttcacac acccccattc ggcgtagtac ccagagagct caagatgtgt
720
ggcagttttc ggatggaagc tcgagagccc ttaagttctg agaaaatttg aagcccccgg
780
gggtggggtg gacgcgt
797

<210> 3858
<211> 76
<212> PRT
<213> Homo sapiens

<400> 3858
Xaa Arg Ala Thr Thr Arg Thr Ala Ser Gly Ala Arg Ser Trp Ala Trp
 1   5   10   15
Ala Thr Arg Ala Ala Pro Cys Pro Thr Ser Cys Arg Ala Trp Cys Ser
            20   25   30
Ala Pro Cys Ser Thr Ser Ala Arg Pro Ser Thr Arg Ser Trp Ala Arg
        35   40   45
Ser Ile Ser Ala Ala Thr Trp Pro Arg Pro Arg Ala Thr Gly Thr Leu
    50   55   60
Ala Thr Lys Thr Arg Trp Pro Ala Ser Arg Thr Ala
65   70   75

<210> 3859
<211> 1449
<212> DNA
<213> Homo sapiens

<400> 3859
tacaagaata aaaagcaagt ggggaagtat ttctggcctc ggattacaaa ggttcacttc
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aaggagactc aatttgaact cagagtactg ggaaaagatt gtaacgaaac ctcattcttt
120
tttgaagctc ggagtaaaac tgcttgcaag cacctctgga agtgcagtgt ggaacatcat
180
acatttttta gaatgccaga aaatgaatcc aattcactgt caagaaaact cagcaagttt
240
ggatccatac gttataagca ccgctacagt ggcaggacag ctttgcaaat gagccgagat
300
ctttctattc agcttccccg gcctgatcag aatgtgacaa gaagtcgaag caagacttac
360

cctaagcgaa tagcacaaac acagccagct gaatcaaaca ccatcagtag gataactgca
420
aacatggaaa atggagaaaa tgaaggaaca attaaaatta ttgcaccttc accagtaaaa
480
agctttaaga aagcaaagaa tgaaaatagc cctgataccc aaagaagcaa atctcatgca
540
ccgtgggaag aaaatggccc ccagagtgga ctctacaatt ctcccagtga tcgcactaag
600
tcgccaaagt tcccttacac gcgtcgccga aacccctcct gtggaagtga caatgattct
660
gtacagcctg tgaggaggag gaaagcccat aacagtggtg aagattcaga tcttaagcaa
720
aggaggaggt cacgttcacg ctgtaacacc agcagtggta gtgaatcaga aaattctaat
780
agagaacacc ggaaaaagag aaacagaata cggcaggaga atgatatggt tgattcagcg
840
cctcagtggg aagctgtatt aaggagacaa aaggaaaaaa accaagccga ccccaacaac
900
aggcgatcca gacacagatc tcgttcgaga agccccgata tccaagcaaa agaagagtta
960
tggaagcaca ttcaaaaaga acttgtggat ccatccggat tgtccgaaga acaattaaaa
1020
gagattccat acactaaaat agagtgagtg cctttcagaa tcttctcacc aaagctttat
1080
tagtgcttga cacaaggtga cccaatccgc atcaggcatt ctcattcgcc acgaagttac
1140
cgccagtatc gcaggtccca gtgttcagat ggggagcgat cagttctctc ggaagtgaat
1200
tcaaaaacag atcttgtacc accacttccg gtgacccatt cttcggatgc tcagggttct
1260
ggggatgcta cagttcatca gagaagaaat gggtctaaag atagcctgat ggaagaaaaa
1320
cctcagacat ctacaaacaa cctggctgga aaacacacag caaaaacaat aaaaactata
1380
caagcttccc gcctcaagac agagacttga tcctgatgaa gggtcaaggg taggggtggg
1440
aaggttgtg
1449

<210> 3860
<211> 348
<212> PRT
<213> Homo sapiens

<400> 3860
Tyr Lys Asn Lys Lys Gln Val Gly Lys Tyr Phe Trp Pro Arg Ile Thr
1 5 10 15
Lys Val His Phe Lys Glu Thr Gln Phe Glu Leu Arg Val Leu Gly Lys
20 25 30
Asp Cys Asn Glu Thr Ser Phe Phe Phe Glu Ala Arg Ser Lys Thr Ala
35 40 45
Cys Lys His Leu Trp Lys Cys Ser Val Glu His His Thr Phe Phe Arg
50 55 60
Met Pro Glu Asn Glu Ser Asn Ser Leu Ser Arg Lys Leu Ser Lys Phe

65 70 75 80
Gly Ser Ile Arg Tyr Lys His Arg Tyr Ser Gly Arg Thr Ala Leu Gln
85 90 95
Met Ser Arg Asp Leu Ser Ile Gln Leu Pro Arg Pro Asp Gln Asn Val
100 105 110
Thr Arg Ser Arg Ser Lys Thr Tyr Pro Lys Arg Ile Ala Gln Thr Gln
115 120 125
Pro Ala Glu Ser Asn Thr Ile Ser Arg Ile Thr Ala Asn Met Glu Asn
130 135 140
Gly Glu Asn Glu Gly Thr Ile Lys Ile Ile Ala Pro Ser Pro Val Lys
145 150 155 160
Ser Phe Lys Lys Ala Lys Asn Glu Asn Ser Pro Asp Thr Gln Arg Ser
165 170 175
Lys Ser His Ala Pro Trp Glu Glu Asn Gly Pro Gln Ser Gly Leu Tyr
180 185 190
Asn Ser Pro Ser Asp Arg Thr Lys Ser Pro Lys Phe Pro Tyr Thr Arg
195 200 205
Arg Arg Asn Pro Ser Cys Gly Ser Asp Asn Asp Ser Val Gln Pro Val
210 215 220
Arg Arg Arg Lys Ala His Asn Ser Gly Glu Asp Ser Asp Leu Lys Gln
225 230 235 240
Arg Arg Arg Ser Arg Ser Arg Cys Asn Thr Ser Ser Gly Ser Glu Ser
245 250 255
Glu Asn Ser Asn Arg Glu His Arg Lys Lys Arg Asn Arg Ile Arg Gln
260 265 270
Glu Asn Asp Met Val Asp Ser Ala Pro Gln Trp Glu Ala Val Leu Arg
275 280 285
Arg Gln Lys Glu Lys Asn Gln Ala Asp Pro Asn Asn Arg Arg Ser Arg
290 295 300
His Arg Ser Arg Ser Arg Ser Pro Asp Ile Gln Ala Lys Glu Glu Leu
305 310 315 320
Trp Lys His Ile Gln Lys Glu Leu Val Asp Pro Ser Gly Leu Ser Glu
325 330 335
Glu Gln Leu Lys Glu Ile Pro Tyr Thr Lys Ile Glu
340 345

<210> 3861
<211> 748
<212> DNA
<213> Homo sapiens

<400> 3861
nagattggag tccggccgcc ccccgacagc agccgcctcc tgccttcctc gctgctaggc
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gccaccatgt cgggagacaa acttctgagc gaactcggtt ataagctggg ccgcacaatt
120
ggagagggca gctactccaa ggtgaaggtg gccacatcca agaagtacaa gggtaccgtg
180
gccatcaagg tggtggaccg gcggcgagcg cccccggact tcgtcaacaa gttcctgccg
240
cgagagctgt ccatcctgcg gggcgtgcga cacccgcaca tcgtgcacgt cttcgagttc
300
atcgaggtgt gcaacgggaa actgtacatc gtgatggaag cggccgccac cgacctgctg
360

caagccgtgc agcgcaacgg gcgcatcccc ggagttcagg cgcgcgacct ctttgcgcag
420
atcgccggcg ccgtgcgcta cctgcacgat catcacctgg tgcaccgcga cctcaagtgc
480
gaaaacgtgc tgctgagccc ggacgagcgc cgcgtcaagc tcaccgactt cggcttcggc
540
cgccaggccc atggctaccc agacctgagc accacctact gcggctcagc cgtacgcgtc
600
acccgagtca tgcatttctt gagcacctac tgtctgccag gccccagagc tcatggcgaa
660
gagacttggg cccatccctg ccgaaaacga gacaattgaa aagtcaagta aaataaaaga
720
atgacatgga aataaaaaaa aaaaaaaa
748

<210> 3862
<211> 210
<212> PRT
<213> Homo sapiens

<400> 3862
Met Ser Gly Asp Lys Leu Leu Ser Glu Leu Gly Tyr Lys Leu Gly Arg
 1   5   10   15
Thr Ile Gly Glu Gly Ser Tyr Ser Lys Val Lys Val Ala Thr Ser Lys
            20   25   30
Lys Tyr Lys Gly Thr Val Ala Ile Lys Val Val Asp Arg Arg Arg Ala
        35   40   45
Pro Pro Asp Phe Val Asn Lys Phe Leu Pro Arg Glu Leu Ser Ile Leu
    50   55   60
Arg Gly Val Arg His Pro His Ile Val His Val Phe Glu Phe Ile Glu
65   70   75   80
Val Cys Asn Gly Lys Leu Tyr Ile Val Met Glu Ala Ala Ala Thr Asp
                85   90   95
Leu Leu Gln Ala Val Gln Arg Asn Gly Arg Ile Pro Gly Val Gln Ala
            100   105   110
Arg Asp Leu Phe Ala Gln Ile Ala Gly Ala Val Arg Tyr Leu His Asp
        115   120   125
His His Leu Val His Arg Asp Leu Lys Cys Glu Asn Val Leu Leu Ser
    130   135   140
Pro Asp Glu Arg Arg Val Lys Leu Thr Asp Phe Gly Phe Gly Arg Gln
145   150   155   160
Ala His Gly Tyr Pro Asp Leu Ser Thr Thr Tyr Cys Gly Ser Ala Val
                165   170   175
Arg Val Thr Arg Val Met His Phe Leu Ser Thr Tyr Cys Leu Pro Gly
            180   185   190
Pro Arg Ala His Gly Glu Glu Thr Trp Ala His Pro Cys Arg Lys Arg
        195   200   205
Asp Asn
    210

<210> 3863
<211> 341
<212> DNA
<213> Homo sapiens

<400> 3863
acgcgtgaag ggggatccag atgctgataa cgaaggccca tcagcaggaa ctcctcacag
60
ctcactttga ggcttcctat tttctttaat cctggggtac agctcccacc tggacacttc
120
agttttgctc tcagttggga ctctgggaaa aaaactgtgt ggctgatctc cacgaggttc
180
ttctggtcga ggctccccga gaaccatctg gccatgggct ggcagccgag ttctcgcagt
240
gtccaggctg acggtacatt ccaggctagc catcctatca taatcgaatc tgagtagatt
300
tttatcaatc gcttgggaca agccattgaa ttttcggaga g
341

<210> 3864
<211> 108
<212> PRT
<213> Homo sapiens

<400> 3864
Met Ala Cys Pro Lys Arg Leu Ile Lys Ile Tyr Ser Asp Ser Ile Met
1 5 10 15
Ile Gly Trp Leu Ala Trp Asn Val Pro Ser Ala Trp Thr Leu Arg Glu
20 25 30
Leu Gly Cys Gln Pro Met Ala Arg Trp Phe Ser Gly Ser Leu Asp Gln
35 40 45
Lys Asn Leu Val Glu Ile Ser His Thr Val Phe Phe Pro Glu Ser Gln
50 55 60
Leu Arg Ala Lys Leu Lys Cys Pro Gly Gly Ser Cys Thr Pro Gly Leu
65 70 75 80
Lys Lys Ile Gly Ser Leu Lys Val Ser Cys Glu Glu Phe Leu Leu Met
85 90 95
Gly Leu Arg Tyr Gln His Leu Asp Pro Pro Ser Arg
100 105

<210> 3865
<211> 492
<212> DNA
<213> Homo sapiens

<400> 3865
nattgcaaaa caatatatga cacgtctttt accagccaca accttcaaca aaccaatatt
60
aatcaggaat tgacgataag cttactacat tttgaaatta tctgactttc ctcatgaaat
120
gagacctatg tgaagcccac ttaattttct gaaacttcac atcatgtacc ttcattgtaa
180
tattctgaca cttgtttcat gcagccatac cagtcacaac tttaaatttt tagtcagact
240
ttgctcacaa ggtttcagga taattaatac aaatggtttg ggccagccat cacacagcag
300
tctcctattt acttcactac aactacagct ttcattcttc attacattac tttttctgag
360

tagtctgggt caaatagtac aaactgaata ttccttaacc aaaatgcttg gaagtaggcc
420
gggagcagcg gctcaccccct gtaatcccag cattttggga ggccaaagca gacagatcac
480
tcaaggtcag ca
492

<210> 3866
<211> 109
<212> PRT
<213> Homo sapiens

<400> 3866
Met Tyr Leu His Cys Asn Ile Leu Thr Leu Val Ser Cys Ser His Thr
1 5 10 15
Ser His Asn Phe Lys Phe Leu Val Arg Leu Cys Ser Gln Gly Phe Arg
20 25 30
Ile Ile Asn Thr Asn Gly Leu Gly Gln Pro Ser His Ser Ser Leu Leu
35 40 45
Phe Thr Ser Leu Gln Leu Gln Leu Ser Phe Phe Ile Thr Leu Leu Phe
50 55 60
Leu Ser Ser Leu Gly Gln Ile Val Gln Thr Glu Tyr Ser Leu Thr Lys
65 70 75 80
Met Leu Gly Ser Arg Pro Gly Ala Ala Ala His Pro Cys Asn Pro Ser
85 90 95
Ile Leu Gly Gly Gln Ser Arg Gln Ile Thr Gln Gly Gln
100 105

<210> 3867
<211> 1032
<212> DNA
<213> Homo sapiens

<400> 3867
acgcgtgaag gggagctccg gaagaatctg gaggagctat tccaggtgaa gatggaacgg
60
gagcagcatc agactgagat cagggatctc caggaccagc tctcagaaat gcacgatgaa
120
ctggacagtg caaagcgatc ggaggacagg gagaagggag ctctgattga ggagctctta
180
caggcaaaac aggatcttca agatctgctg attgccaaag aggagcaaga agacctcttg
240
agaaagcgag agcgtgaact caccgccctg aagggagccc tgaaagaaga ggtttccagc
300
catgatcagg agatggacaa gctgaaggag caatatgatg ctgagttgca ggccctgagg
360
gagagtgtgg aagaagcaac caagaatgtc gaggtcttgg cgagcaggag caacacttca
420
gagcaagacc aggcggggac tgaaatgcgc gtgaagcttc tgcaggagga gaatgagaag
480
ctgcagggaa gaagcgaaga gctggagcgg agagttgctc agcttcaaag gcagatcgag
540
gacctgaaag gcgatgaagc caaggcgaag gaaacgctga agaagtacga gggagaaata
600

cgacagttag aggaggccct tgtgcacgcc agaaaggaag aaaaagaagc tgtgtcagcc
660
agaagggccc tggagaatga actggaggct gctcagggaa atctgagtca gactacccag
720
gagcagaagc agttgtctga gaagctcaaa gaggagagtg agcagaagga gcagctaaga
780
aggttgaaga acgagatgga gaatgagcgg tggcacctgg gcaaaaccat tgagaaactg
840
cagaaggaga tggcagacat tgttgaggcc tcccgtacct caaccctgga gctccagaac
900
cagctggatg agtataagga gaaaaaccgc agggagctcg cagaaatgca aagacagttg
960
aaggagaaaa cgctggaggc agaaaagtcc cgactgacag ccatgaaaat gcaggatgag
1020
atgcgtctga tg
1032

<210> 3868
<211> 344
<212> PRT
<213> Homo sapiens

<400> 3868
Thr Arg Glu Gly Glu Leu Arg Lys Asn Leu Glu Glu Leu Phe Gln Val
1 5 10 15
Lys Met Glu Arg Glu Gln His Gln Thr Glu Ile Arg Asp Leu Gln Asp
20 25 30
Gln Leu Ser Glu Met His Asp Glu Leu Asp Ser Ala Lys Arg Ser Glu
35 40 45
Asp Arg Glu Lys Gly Ala Leu Ile Glu Glu Leu Leu Gln Ala Lys Gln
50 55 60
Asp Leu Gln Asp Leu Leu Ile Ala Lys Glu Glu Gln Glu Asp Leu Leu
65 70 75 80
Arg Lys Arg Glu Arg Glu Leu Thr Ala Leu Lys Gly Ala Leu Lys Glu
85 90 95
Glu Val Ser Ser His Asp Gln Glu Met Asp Lys Leu Lys Glu Gln Tyr
100 105 110
Asp Ala Glu Leu Gln Ala Leu Arg Glu Ser Val Glu Glu Ala Thr Lys
115 120 125
Asn Val Glu Val Leu Ala Ser Arg Ser Asn Thr Ser Glu Gln Asp Gln
130 135 140
Ala Gly Thr Glu Met Arg Val Lys Leu Leu Gln Glu Glu Asn Glu Lys
145 150 155 160
Leu Gln Gly Arg Ser Glu Glu Leu Glu Arg Arg Val Ala Gln Leu Gln
165 170 175
Arg Gln Ile Glu Asp Leu Lys Gly Asp Glu Ala Lys Ala Lys Glu Thr
180 185 190
Leu Lys Lys Tyr Glu Gly Glu Ile Arg Gln Leu Glu Glu Ala Leu Val
195 200 205
His Ala Arg Lys Glu Glu Lys Glu Ala Val Ser Ala Arg Arg Ala Leu
210 215 220
Glu Asn Glu Leu Glu Ala Ala Gln Gly Asn Leu Ser Gln Thr Thr Gln
225 230 235 240
Glu Gln Lys Gln Leu Ser Glu Lys Leu Lys Glu Glu Ser Glu Gln Lys

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                245                 250                 255
Glu Gln Leu Arg Arg Leu Lys Asn Glu Met Glu Asn Glu Arg Trp His
            260                 265                 270
Leu Gly Lys Thr Ile Glu Lys Leu Gln Lys Glu Met Ala Asp Ile Val
        275                 280                 285
Glu Ala Ser Arg Thr Ser Thr Leu Glu Leu Gln Asn Gln Leu Asp Glu
    290                 295                 300
Tyr Lys Glu Lys Asn Arg Arg Glu Leu Ala Glu Met Gln Arg Gln Leu
305                 310                 315                 320
Lys Glu Lys Thr Leu Glu Ala Glu Lys Ser Arg Leu Thr Ala Met Lys
                325                 330                 335
Met Gln Asp Glu Met Arg Leu Met
            340
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<210> 3869
<211> 1226
<212> DNA
<213> Homo sapiens

<400> 3869
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60
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120
tgatgcacac acattccaga aatgcagagg tatgctgctg ccacggggta ggggtgcggg
180
aggcggcctg gcctcatggc cgcagaccgt gccccagccc gggcctggca ggtagctggc
240
cactgataaa tgccactggg atcctaggag aagctgggga ccatgcgtga ggtactgaag
300
gggaccatgg tggatggcat cctgggcact ttgtagcttg tctgagggaa aggcctctgc
360
tgccatagaa aagctggaca catgtcaccc tggggccctg acatcctaaa atgccccact
420
gactaccagt cactaggaga aaggtctccg gctatgccct tcccagtgat gcttgcccca
480
gagtgactgg tcacaggtgg gggacaggtt tgctccagaa accgtaggcc tttcttgtct
540
ggcccccctaa agaggaccca agatcaggaa aactccccag tttaaaaaaa tatctgtcca
600
tctgtatata aaatacctat tattagctgg agttgcacac atgcaggacc aggagagact
660
gcctgaggtt ctgcctggac cgaaggaggc ctcgctcaca gcacctctgt gaggggactg
720
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780
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840
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900
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960
gtgagcctgg cgcaggtcgg ctgacagcga gcttctcatc tgcctggtgg tagagcggac
1020

gctctcggca gcctgcacgg cccggctcag ggccttgttg agctcctcta ggtcgcccag
1080
gtcgagctgg atggagtgcc ggtgtctccg ggctggtggg ggagaggctg tgggcggcca
1140
cttggcagct ggttgggctg aggtaggtcc tgcaggcgca tagtacacag cggcaggtgg
1200
ataaggcatg atgggaaccg aggaga
1226

<210> 3870
<211> 100
<212> PRT
<213> Homo sapiens

<400> 3870
Met Ala Ala Glu Ala Phe Pro Ser Asp Lys Leu Gln Ser Ala Gln Asp
 1   5   10   15
Ala Ile His His Gly Pro Leu Gln Tyr Leu Thr His Gly Pro Gln Leu
            20   25   30
Leu Leu Gly Ser Gln Trp His Leu Ser Val Ala Ser Tyr Leu Pro Gly
        35   40   45
Pro Gly Trp Gly Thr Val Cys Gly His Glu Ala Arg Pro Pro Pro Ala
    50   55   60
Pro Leu Pro Arg Gly Ser Ser Ile Pro Leu His Phe Trp Asn Val Cys
65   70   75   80
Ala Ser Met Met Phe Val Tyr Leu Arg His Leu Lys Ile Tyr Phe Arg
                85   90   95
Tyr Glu Gly Lys
            100

<210> 3871
<211> 473
<212> DNA
<213> Homo sapiens

<400> 3871
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tgcctcacat ttcccagtgc ttcctctgca cccctccatt ggagtaaaaa ccacagtttg
120
tgggatggtt gagttgacag ctctgaatcc cagaaacctt aattttggct tatcttttga
180
taggctgagg gaaaatacaa agatgatcct gttgatctcc gccttgatat tgaacgtcgt
240
aaaaaacata aggagagaga tcttaaacga ggtaaatcga gagaatcagt ggattcccga
300
gactccagtc actcaaggga aaggtcagct gaaaaaacag agaaaactca taaaggatca
360
aagaaacaga agaaagacct ctgagagccg agacaagctg ggagcgaaag gagattttcc
420
cacaggaaag tcttcctttt ccattactcg agaggcacag gtcaatgtcc gga
473

<210> 3872

<211> 66
<212> PRT
<213> Homo sapiens

<400> 3872
Ala Glu Gly Lys Tyr Lys Asp Asp Pro Val Asp Leu Arg Leu Asp Ile
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Glu Arg Arg Lys Lys His Lys Glu Arg Asp Leu Lys Arg Gly Lys Ser
20 25 30
Arg Glu Ser Val Asp Ser Arg Asp Ser Ser His Ser Arg Glu Arg Ser
35 40 45
Ala Glu Lys Thr Glu Lys Thr His Lys Gly Ser Lys Lys Gln Lys Lys
50 55 60
Asp Leu
65

<210> 3873
<211> 869
<212> DNA
<213> Homo sapiens

<400> 3873
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aagtgtgcat taaactcaaa gattctgtct gtaatggaag cctatcacct gtccttcgag
120
aggaggcaga agtcgtccga ggcccctgtg cagtccccgc agcgctccgt ggactccatc
180
agccaagagt cctccacttc cagcttctcc tccatgtcag ccggctcaag gcaggaggag
240
accaagaagg actacagaga ggtagaaaaa cttttgagag cagttgctga tggagatcta
300
gaaatggtgc gttacctgtt ggaatggaca gaggaggacc tggaggatgc ggaggacact
360
gtcagtgcag cggaccccga attctgtcac ccgttgtgcc agtgccccaa gtgtgcccca
420
gctcagaaga ggctggcgaa ggttcctgcc agtgggcttg gtgtgaacgt gaccagccag
480
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540
ctgctgaagc acggggccaa cgcaggtgcc aggaacgcag accaagccgt cccgctccac
600
ctggcctgcc agcagggcca ctttcaggtg gtgaagtgtc tgttagattc gaatgcaaaa
660
cccaataaga aggacctcag tggaaacacg cccctcattt acgcctgctc cggtggccat
720
cacgagcttg tggcactgct gctacagcac ggggcctcca ttaacgctct aacaataagg
780
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840
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869

<210> 3874

<211> 289
<212> PRT
<213> Homo sapiens

<400> 3874
Asp Ile Ala Ala Glu Arg Ser Val His Arg Asp Pro Glu Gln Thr Glu
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Gly Asp Pro Leu Lys Cys Ala Leu Asn Ser Lys Ile Leu Ser Val Met
20 25 30
Glu Ala Tyr His Leu Ser Phe Glu Arg Arg Gln Lys Ser Ser Glu Ala
35 40 45
Pro Val Gln Ser Pro Gln Arg Ser Val Asp Ser Ile Ser Gln Glu Ser
50 55 60
Ser Thr Ser Ser Phe Ser Ser Met Ser Ala Gly Ser Arg Gln Glu Glu
65 70 75 80
Thr Lys Lys Asp Tyr Arg Glu Val Glu Lys Leu Leu Arg Ala Val Ala
85 90 95
Asp Gly Asp Leu Glu Met Val Arg Tyr Leu Leu Glu Trp Thr Glu Glu
100 105 110
Asp Leu Glu Asp Ala Glu Asp Thr Val Ser Ala Ala Asp Pro Glu Phe
115 120 125
Cys His Pro Leu Cys Gln Cys Pro Lys Cys Ala Pro Ala Gln Lys Arg
130 135 140
Leu Ala Lys Val Pro Ala Ser Gly Leu Gly Val Asn Val Thr Ser Gln
145 150 155 160
Asp Gly Ser Ser Pro Leu His Val Ala Ala Leu His Gly Arg Ala Asp
165 170 175
Leu Ile Arg Leu Leu Leu Lys His Gly Ala Asn Ala Gly Ala Arg Asn
180 185 190
Ala Asp Gln Ala Val Pro Leu His Leu Ala Cys Gln Gln Gly His Phe
195 200 205
Gln Val Val Lys Cys Leu Leu Asp Ser Asn Ala Lys Pro Asn Lys Lys
210 215 220
Asp Leu Ser Gly Asn Thr Pro Leu Ile Tyr Ala Cys Ser Gly Gly His
225 230 235 240Glu Leu
Val Ala Leu Leu Leu Gln His Gly Ala Ser Ile Asn Ala
245 250 255
Leu Thr Ile Arg Gly Asn Thr Ala Leu His Glu Ala Val Ile Glu Lys
260 265 270
His Val Phe Val Val Glu Leu Leu Leu Leu His Gly Ala Ser Val Arg
275 280 285
Cys

<210> 3875
<211> 2640
<212> DNA
<213> Homo sapiens

<400> 3875
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120

tcttcccgga ccagcggtgc agtcccgcca aaggaagagg agctccgggc ggcggtggag
180
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240
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300
tctgcggatg agccccagtg ccttttgcta ctccttgacg cttttggcct gctggagagc
360
cgcctggatc cctacctgcg tagcctagag ctgctggaga aatggactcg cctgggcttg
420
ctgatgggca ctggtgctca ggggctgcga gaagaagtcc acactatgtt gcgcggagtc
480
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600
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660
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720
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780
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960
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1080
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1140
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1200
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1260
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1320
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1380
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1440
gtcccggacc ctgtggatgc cgatccaggg aagtcgagct ccaagcggcg ttcatcggac
1500
atcatcagcc tgctggtcag catctacggc agcaaggacc tcttcatcaa tgagtaccgc
1560
tcgctgctgg ccgaccgcct gctgcaccag ttcagcttca gccccgagcg ggagatccgc
1620
aacgtggagc tgctgaagct gcgctttggc gaggccccaa tgcacttctg tgaagtcatg
1680
ctgaaggaca tggcggactc ccgccgcatc aatgccaaca tccgggagga ggatgagaag
1740

cggnnccagc agaggagcag ccaccgttcg gggtctacgc tgtcatcctg tccagtgagt
1800
tctggccgcc cttcaaggac gnagaagctg gaggtccccg aggatatcag ggcagccctg
1860
gaggcttact gcaagaagta tgagcagctc aaggccatgc ggaccctcag ttggaagcac
1920
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1980
accccagtac aggcggtgat cttgctgtat tttcaggacc aagccagctg gaccctggag
2040
gaactgagca aggcggtgaa aatgcccgtg gcgctgctgc ggcggcggat gtccgtgtgg
2100
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2160
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2220
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2280
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2340
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2400
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2460
aagaactgca gctgacacat cgcccgcccg cccgcccgcc cgccaggcgc tgccctgcag
2520
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2580
agcatgccca cccccacccc cgcagtgtgc agattaaagc aagtcagatc atcaaaaaaa
2640

<210> 3876
<211> 824
<212> PRT
<213> Homo sapiens

<400> 3876
Met Ala Ala Ala Val Val Val Ala Glu Gly Asp Ser Asp Ser Arg Pro
1 5 10 15
Gly Gln Glu Leu Leu Val Ala Trp Asn Thr Val Ser Thr Gly Leu Val
20 25 30
Pro Pro Ala Ala Leu Gly Leu Val Ser Ser Arg Thr Ser Gly Ala Val
35 40 45
Pro Pro Lys Glu Glu Glu Leu Arg Ala Ala Val Glu Val Leu Arg Gly
50 55 60
His Gly Leu His Ser Val Leu Glu Glu Trp Phe Val Glu Val Leu Gln
65 70 75 80
Asn Asp Leu Gln Ala Asn Ile Ser Pro Glu Phe Trp Asn Ala Ile Ser
85 90 95
Gln Cys Glu Asn Ser Ala Asp Glu Pro Gln Cys Leu Leu Leu Leu Leu
100 105 110
Asp Ala Phe Gly Leu Leu Glu Ser Arg Leu Asp Pro Tyr Leu Arg Ser
115 120 125
Leu Glu Leu Leu Glu Lys Trp Thr Arg Leu Gly Leu Leu Met Gly Thr

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    130                 135                 140
Gly Ala Gln Gly Leu Arg Glu Glu Val His Thr Met Leu Arg Gly Val
145                 150                 155                 160
Leu Phe Phe Ser Thr Pro Arg Thr Phe Gln Glu Met Ile Gln Arg Leu
                165                 170                 175
Tyr Gly Cys Phe Leu Arg Val Tyr Met Gln Ser Lys Arg Lys Gly Glu
            180                 185                 190
Gly Gly Thr Asp Pro Glu Leu Glu Gly Glu Leu Asp Ser Arg Tyr Ala
        195                 200                 205
Arg Arg Arg Tyr Tyr Arg Leu Leu Gln Ser Pro Leu Cys Ala Gly Cys
    210                 215                 220
Ser Ser Asp Lys Gln Gln Cys Trp Cys Arg Gln Ala Leu Glu Gln Phe
225                 230                 235                 240
His Gln Leu Ser Gln Val Leu His Arg Leu Ser Leu Leu Glu Arg Val
                245                 250                 255
Ser Ala Glu Ala Val Thr Thr Thr Leu His Gln Val Thr Arg Glu Arg
            260                 265                 270
Met Glu Asp Arg Cys Arg Gly Glu Tyr Glu Arg Ser Phe Leu Arg Glu
        275                 280                 285
Phe His Arg Trp Ile Glu Arg Val Val Gly Trp Leu Gly Lys Val Phe
    290                 295                 300
Leu Gln Asp Gly Pro Ala Arg Pro Ala Ser Pro Glu Ala Gly Asn Thr
305                 310                 315                 320
Leu Arg Arg Trp Arg Cys His Val Gln Arg Phe Phe Tyr Arg Ile Tyr
                325                 330                 335
Ala Ser Leu Arg Ile Glu Glu Leu Phe Ser Ile Val Arg Asp Phe Pro
            340                 345                 350
Asp Ser Arg Pro Ala Ile Glu Asp Leu Lys Tyr Cys Leu Glu Arg Thr
        355                 360                 365
Asp Gln Arg Gln Gln Leu Leu Val Ser Leu Lys Ala Ala Leu Glu Thr
    370                 375                 380
Arg Leu Leu His Pro Gly Val Asn Thr Cys Asp Ile Ile Thr Leu Tyr
385                 390                 395                 400
Ile Ser Ala Ile Lys Ala Leu Arg Val Leu Asp Pro Ser Met Val Ile
                405                 410                 415
Leu Glu Val Ala Cys Glu Pro Ile Arg Arg Tyr Leu Arg Thr Arg Glu
            420                 425                 430
Asp Thr Val Arg Gln Ile Val Ala Gly Leu Thr Gly Asp Ser Asp Gly
        435                 440                 445
Thr Gly Asp Leu Ala Val Glu Leu Ser Lys Thr Asp Pro Ala Ser Leu
    450                 455                 460
Glu Thr Gly Gln Asp Ser Glu Asp Asp Ser Gly Glu Pro Glu Asp Trp
465                 470                 475                 480
Val Pro Asp Pro Val Asp Ala Asp Pro Gly Lys Ser Ser Ser Lys Arg
                485                 490                 495
Arg Ser Ser Asp Ile Ile Ser Leu Leu Val Ser Ile Tyr Gly Ser Lys
            500                 505                 510
Asp Leu Phe Ile Asn Glu Tyr Arg Ser Leu Leu Ala Asp Arg Leu Leu
        515                 520                 525
His Gln Phe Ser Phe Ser Pro Glu Arg Glu Ile Arg Asn Val Glu Leu
    530                 535                 540
Leu Lys Leu Arg Phe Gly Glu Ala Pro Met His Phe Cys Glu Val Met
545                 550                 555                 560
Leu Lys Asp Met Ala Asp Ser Arg Arg Ile Asn Ala Asn Ile Arg Glu
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                565                 570                 575
Glu Asp Glu Lys Arg Xaa Gln Gln Arg Ser Ser His Arg Ser Gly Ser
            580                 585                 590
Thr Leu Ser Ser Cys Pro Val Ser Ser Gly Arg Pro Ser Arg Thr Xaa
        595                 600                 605
Lys Leu Glu Val Pro Glu Asp Ile Arg Ala Ala Leu Glu Ala Tyr Cys
    610                 615                 620
Lys Lys Tyr Glu Gln Leu Lys Ala Met Arg Thr Leu Ser Trp Lys His
625                 630                 635                 640
Thr Leu Gly Leu Val Thr Met Asp Val Glu Leu Ala Asp Arg Thr Leu
                645                 650                 655
Ser Val Ala Val Thr Pro Val Gln Ala Val Ile Leu Leu Tyr Phe Gln
            660                 665                 670
Asp Gln Ala Ser Trp Thr Leu Glu Glu Leu Ser Lys Ala Val Lys Met
        675                 680                 685
Pro Val Ala Leu Leu Arg Arg Arg Met Ser Val Trp Leu Gln Gln Gly
    690                 695                 700
Val Leu Arg Glu Xaa Ser Pro Pro Ala Pro Ser Leu Ser Leu Arg Arg
705                 710                 715                 720
Ser Gly Leu Arg Thr Gly Xaa Asn Met Val Leu Ile Asp Ser Asp Asp
                725                 730                 735
Glu Ser Asp Ser Gly Met Ala Ser Gln Ala Asp Gln Lys Glu Glu Glu
            740                 745                 750
Leu Leu Leu Phe Trp Thr Tyr Ile Gln Ala Met Leu Thr Asn Leu Glu
        755                 760                 765
Ser Leu Ser Leu Asp Arg Ile Tyr Asn Met Leu Arg Met Phe Val Val
    770                 775                 780
Thr Gly Pro Ala Leu Ala Glu Ile Asp Leu Gln Glu Leu Gln Gly Tyr
785                 790                 795                 800
Leu Gln Lys Lys Val Arg Asp Gln Gln Leu Val Tyr Ser Ala Gly Val
                805                 810                 815
Tyr Arg Leu Pro Lys Asn Cys Ser
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<210> 3877
<211> 1112
<212> DNA
<213> Homo sapiens

<400> 3877
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gttaatggct cattaggtga agtgactcca tgccaacatg caaagaaggc gaatggccca
120
aactatattc agcctcaaaa aagacagacc acttttgaaa gccaggatcg caaggcagtg
180
tcccctagca gttctgaaaa gagaagtaag aatcctattt ctaggccatt agaaggtaag
240
aagtccttaa gtcttagtgc aaagactcac aacataggct ttgacaaaga cagctgccat
300
agtaccacaa agacagaagc ttcacaggaa gagcggtctg attcaagcgg cctcacatct
360
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420

ctttctatta gtaattcgtc agatgtgagt gctaaagata agcatgctga agacaatgag
480
aagcgtttgg cagccttgga agcgaggcaa aaagcaaaag aagtgcagaa gaagctggtg
540
cataatgctc tggcaaattt ggatggtcat ccagaggata agccaacgca catcatcttc
600
ggttctgaca gtgaatgtga aacagaggag acatcgactc aggagcagag ccatccagga
660
gaggaatggg tgaaagagtc tatgggtaaa acatcaggga agctgtttga tagcagtgat
720
gatgaggaat ctgattctga agatgacagt aataggttca aaattaaacc tcagtttgag
780
ggcagagctg gacagaagct catggattta cagtcgcact ttggcaccga tgacagattc
840
cgcatggact ctcgatttct agaaactgac agtgaagagg aacaggaaga ggtaaatgaa
900
aagaaaactg ctgaggaaga agagcttgct gaagaaaaaa agaaagccct gaatgttgta
960
caaagtgttt tgcaaatcaa cttaagcaat tctacaaaca gaggatcagt agctgctaag
1020
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1080
aaaagagatg ataaaccaaa agaaagtaaa gc
1112

<210> 3878
<211> 370
<212> PRT
<213> Homo sapiens

<400> 3878
Xaa Asn Ser Met Lys His Glu Asp Pro Ser Ile Ile Ser Met Glu Asp
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Gly Ser Pro Tyr Val Asn Gly Ser Leu Gly Glu Val Thr Pro Cys Gln
20 25 30
His Ala Lys Lys Ala Asn Gly Pro Asn Tyr Ile Gln Pro Gln Lys Arg
35 40 45
Gln Thr Thr Phe Glu Ser Gln Asp Arg Lys Ala Val Ser Pro Ser Ser
50 55 60
Ser Glu Lys Arg Ser Lys Asn Pro Ile Ser Arg Pro Leu Glu Gly Lys
65 70 75 80
Lys Ser Leu Ser Leu Ser Ala Lys Thr His Asn Ile Gly Phe Asp Lys
85 90 95
Asp Ser Cys His Ser Thr Thr Lys Thr Glu Ala Ser Gln Glu Glu Arg
100 105 110
Ser Asp Ser Ser Gly Leu Thr Ser Leu Lys Lys Ser Pro Lys Val Ser
115 120 125
Ser Lys Asp Thr Arg Glu Ile Lys Thr Asp Phe Ser Leu Ser Ile Ser
130 135 140
Asn Ser Ser Asp Val Ser Ala Lys Asp Lys His Ala Glu Asp Asn Glu
145 150 155 160
Lys Arg Leu Ala Ala Leu Glu Ala Arg Gln Lys Ala Lys Glu Val Gln
165 170 175
Lys Lys Leu Val His Asn Ala Leu Ala Asn Leu Asp Gly His Pro Glu

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            180                 185                 190
Asp Lys Pro Thr His Ile Ile Phe Gly Ser Asp Ser Glu Cys Glu Thr
        195                 200                 205
Glu Glu Thr Ser Thr Gln Glu Gln Ser His Pro Gly Glu Glu Trp Val
    210                 215                 220
Lys Glu Ser Met Gly Lys Thr Ser Gly Lys Leu Phe Asp Ser Ser Asp
225                 230                 235                 240
Asp Glu Glu Ser Asp Ser Glu Asp Asp Ser Asn Arg Phe Lys Ile Lys
                245                 250                 255
Pro Gln Phe Glu Gly Arg Ala Gly Gln Lys Leu Met Asp Leu Gln Ser
            260                 265                 270
His Phe Gly Thr Asp Asp Arg Phe Arg Met Asp Ser Arg Phe Leu Glu
        275                 280                 285
Thr Asp Ser Glu Glu Glu Gln Glu Glu Val Asn Glu Lys Lys Thr Ala
    290                 295                 300
Glu Glu Glu Glu Leu Ala Glu Glu Lys Lys Lys Ala Leu Asn Val Val
305                 310                 315                 320
Gln Ser Val Leu Gln Ile Asn Leu Ser Asn Ser Thr Asn Arg Gly Ser
                325                 330                 335
Val Ala Ala Lys Lys Phe Lys Asp Ile Ile His Tyr Asp Pro Thr Lys
            340                 345                 350
Gln Asp His Ala Thr Tyr Glu Arg Lys Arg Asp Asp Lys Pro Lys Glu
        355                 360                 365
Ser Lys
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<210> 3879
<211> 2769
<212> DNA
<213> Homo sapiens

<400> 3879
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120
ttccaggact tccctgagca gcttaccgcc ctgccggcgc tggagaccat caacctggag
180
gagaacgaga tcgtagatgt gcccgtggag aagctggccg ccatgccagc cttgcgcagc
240
atcaacctcc gcttcaaccc actcaacgcc gaggtgcgcg tgatcgcccc gccgctcatc
300
aagtttgaca tgctcatgtc tccggaaggc gcaagagccc ccctaccttа ggccaccctc
360
ctcatgccca cccagcaagg gacagaggcc acaggcctgg aaccctggaa gggagggagg
420
cccatgggag gccaagcctg ggggctgggg gcgggtgggc caagcagcac gtggtgggtg
480
gggtgcagct ggtctggata gatagcttac agcagtagtg ggctctggaa tgcccaaggg
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600
gcagatctcc tgccctctct gagccttgtc acttgaaaaa aacaggaccc tttccctcct
660

ttgggctccc tggaggtttt taagcagtac gtgcctccaa gttacctcca gatcagcagg
720
cacaggtggg cattgccagg tattttctga gcccctgcgg gtttgaggcc ttgtttttag
780
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<212> PRT
<213> Homo sapiens

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Ala Ile Asp Leu Ser Arg Asn Gln Phe Gln Asp Phe Pro Glu Gln Leu
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Thr Ala Leu Pro Ala Leu Glu Thr Ile Asn Leu Glu Glu Asn Glu Ile
    50   55   60
Val Asp Val Pro Val Glu Lys Leu Ala Ala Met Pro Ala Leu Arg Ser
65   70   75   80
Ile Asn Leu Arg Phe Asn Pro Leu Asn Ala Glu Val Arg Val Ile Ala
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Pro Pro Leu Ile Lys Phe Asp Met Leu Met Ser Pro Glu Gly Ala Arg
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Ala Pro Leu Pro
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<211> 1393
<212> DNA
<213> Homo sapiens

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<210> 3882
<211> 277
<212> PRT
<213> Homo sapiens

<400> 3882
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Gln Met Pro Ser Leu Asn Trp Pro Glu Ala Leu Pro Pro Pro Pro Pro

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65                  70                  75                  80
Leu Thr Glu Pro Ser Ser Ser Gly Gly Trp Leu Val Thr Pro Ser Arg
                85                  90                  95
Arg Glu Thr Pro Ser Pro Thr Pro Ser Tyr Gly Gln Gln Ser Thr Ala
            100                 105                 110
Thr Leu Thr Pro Ser Pro Pro Asp Pro Pro Gln Pro Pro Thr Asp Met
        115                 120                 125
Pro His Leu His Gln Met Pro Arg Arg Val Pro Leu Gly Pro Ser Ser
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Pro Leu Ser Val Ser Gln Pro Met Leu Gly Ile Arg Glu Ala Arg Pro
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Ala Gly Leu Gly Ala Gly Pro Ala Ala Ser Pro His Leu Ser Pro Ser
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Pro Ala Pro Ser Thr Ala Ser Ser Ala Pro Gly Arg Thr Trp Gln Gly
            180                 185                 190
Asn Gly Glu Met Thr Pro Pro Leu Gln Gly Pro Arg Ala Arg Phe Arg
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Lys Lys Pro Lys Ala Leu Pro Tyr Arg Arg Glu Asn Ser Pro Gly Asp
    210                 215                 220
Leu Pro Pro Pro Pro Leu Pro Pro Pro Glu Xaa Arg Gly Glu Leu Gly
225                 230                 235                 240
Pro Arg Ala Glu Gly Ser Arg Gln His Val Leu Pro Gly Ala Gly Ala
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<212> DNA
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<210> 3884
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<212> PRT
<213> Homo sapiens

<400> 3884
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50 55 60
Asp Gly Arg Lys Lys Arg Gly Lys Tyr Lys Asp Lys Arg Arg Lys Lys
65 70 75 80
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85 90 95
Ala Gln Gln Val Glu Ala Leu Pro Gly Pro Ser Leu Asp Gln Trp His
100 105 110
Arg Ser Ala Gly Glu Glu Glu Asp Gly Pro Val Leu Thr Asp Glu Gln
115 120 125
Val Pro Asn Pro Gly His Glu Ala His Asp Gln Gly Gly Trp Asp Ala
130 135 140
Arg Gln Ser Val Ile Arg Lys Val Val Asp Pro Glu Thr Gly Arg Thr
145 150 155 160
Arg Leu Ile Lys Gly Asp Gly Glu Val Leu Glu Glu Ile Val Thr Lys
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Ile Arg Pro Gln Leu Cys Leu
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<210> 3885
<211> 1671
<212> DNA
<213> Homo sapiens

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<211> 277
<212> PRT
<213> Homo sapiens

<400> 3886
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Gln Val Leu Ala Ala Thr Tyr Asn Gln Ala Ala Gln Leu Trp Lys Val
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Gly Glu Ala Gln Ser Lys Glu Thr Leu Ser Gly His Lys Asp Lys Val
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Thr Ala Ala Lys Phe Lys Leu Thr Arg His Gln Ala Val Thr Gly Ser
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Arg Asp Arg Thr Val Lys Glu Trp Asp Leu Gly Arg Ala Tyr Cys Ser
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Arg Thr Ile Asn Val Leu Ser Tyr Cys Asn Asp Val Val Xaa Trp Gly
115 120 125
Pro Tyr His His Xaa Ser Gly His Asn Asp Gln Lys Ile Arg Phe Trp
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Asp Ser Xaa Gly Gly Pro Thr Ala Pro Arg Ser Ser Leu Xaa Gln Gly
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Arg Val Thr Ser Leu Ser Leu Ser Xaa Arg Pro Thr Xaa His Leu Leu
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180 185 190
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195 200 205
Trp Thr Lys Ala Val Phe Ser Pro Asp Arg Ser Tyr Ala Leu Ala Gly
210 215 220
Ser Cys Asp Gly Ala Leu Tyr Ile Trp Asp Val Asp Thr Gly Lys Leu
225 230 235 240
Glu Ser Arg Leu Gln Gly Pro His Cys Ala Ala Val Asn Ala Val Ala
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<210> 3887
<211> 5612
<212> DNA
<213> Homo sapiens

<400> 3887

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4320
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4380
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4440
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4500
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4560
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4620
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4680
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4740
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4800
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4860

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4920
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5040
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5100
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5160
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5280
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5340
ggtgccattt caaaatgtgg caggtgataa tcttttacca taatttgcat aaaactgtaa
5400
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5460
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5580
taaatccaaa tacttcaact ggcaaaaaaa aa
5612

<210> 3888
<211> 1230
<212> PRT
<213> Homo sapiens

<400> 3888
Met Ala Ser Ala Ser Tyr His Ile Ser Asn Leu Leu Glu Lys Met Thr
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Ser Ser Asp Lys Asp Phe Arg Phe Met Ala Thr Asn Asp Leu Met Thr
20 25 30
Glu Leu Gln Lys Asp Ser Ile Lys Leu Asp Asp Asp Ser Glu Arg Lys
35 40 45
Val Val Lys Met Ile Leu Lys Leu Leu Glu Asp Lys Asn Gly Glu Val
50 55 60
Gln Asn Leu Ala Val Lys Cys Leu Gly Pro Leu Val Ser Lys Val Lys
65 70 75 80
Glu Tyr Gln Val Glu Thr Ile Val Asp Thr Leu Cys Thr Asn Met Leu
85 90 95
Ser Asp Lys Glu Gln Leu Arg Asp Ile Ser Ser Ile Gly Leu Lys Thr
100 105 110
Val Ile Gly Glu Leu Pro Pro Ala Ser Ser Gly Ser Ala Leu Ala Ala
115 120 125
Asn Val Cys Lys Lys Ile Thr Gly Arg Leu Thr Ser Ala Ile Ala Lys
130 135 140
Gln Glu Asp Val Ser Val Gln Leu Glu Ala Leu Asp Ile Met Ala Asp
145 150 155 160
Met Leu Ser Arg Gln Gly Gly Leu Leu Val Asn Phe His Pro Ser Ile

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                165                 170                 175
Leu Thr Cys Leu Leu Pro Gln Leu Thr Ser Pro Arg Leu Ala Val Arg
            180                 185                 190
Lys Arg Thr Ile Ile Ala Leu Gly His Leu Val Met Ser Cys Gly Asn
        195                 200                 205
Ile Val Phe Val Asp Leu Ile Glu His Leu Leu Ser Glu Leu Ser Lys
    210                 215                 220
Asn Asp Ser Met Ser Thr Thr Arg Thr Tyr Ile Gln Cys Ile Ala Ala
225                 230                 235                 240
Ile Ser Arg Gln Ala Gly His Arg Ile Gly Glu Tyr Leu Glu Lys Ile
                245                 250                 255
Ile Pro Leu Val Val Lys Phe Cys Asn Val Asp Asp Asp Glu Leu Arg
            260                 265                 270
Glu Tyr Cys Ile Gln Ala Phe Glu Ser Phe Val Arg Arg Cys Pro Lys
        275                 280                 285
Glu Val Tyr Pro His Val Ser Thr Ile Ile Asn Ile Cys Leu Lys Tyr
    290                 295                 300
Leu Thr Tyr Asp Pro Asn Tyr Asn Tyr Asp Asp Glu Asp Glu Asp Glu
305                 310                 315                 320
Asn Ala Met Asp Ala Asp Gly Gly Asp Asp Asp Asp Gln Gly Ser Asp
                325                 330                 335
Asp Glu Tyr Ser Asp Asp Asp Asp Met Ser Trp Lys Val Arg Arg Ala
            340                 345                 350
Ala Ala Lys Cys Leu Asp Ala Val Val Ser Thr Arg His Glu Met Leu
        355                 360                 365
Pro Glu Phe Tyr Lys Thr Val Ser Pro Ala Leu Ile Ser Arg Phe Lys
    370                 375                 380
Glu Arg Glu Glu Asn Val Lys Ala Asp Val Phe His Ala Tyr Leu Ser
385                 390                 395                 400
Leu Leu Lys Gln Thr Arg Pro Val Gln Ser Trp Leu Cys Asp Pro Asp
                405                 410                 415
Ala Met Glu Gln Gly Glu Thr Pro Leu Thr Met Leu Gln Ser Gln Val
            420                 425                 430
Pro Asn Ile Val Lys Ala Leu His Lys Gln Met Lys Glu Lys Ser Val
        435                 440                 445
Lys Thr Arg Gln Cys Cys Phe Asn Met Leu Thr Glu Leu Val Asn Val
    450                 455                 460
Leu Pro Gly Ala Leu Thr Gln His Ile Pro Val Leu Val Pro Gly Ile
465                 470                 475                 480
Ile Phe Ser Leu Asn Asp Lys Ser Ser Ser Ser Asn Leu Lys Ile Asp
                485                 490                 495
Ala Leu Ser Cys Leu Tyr Val Ile Leu Cys Asn His Ser Pro Gln Val
            500                 505                 510
Phe His Pro His Val Gln Ala Leu Val Pro Pro Val Val Ala Cys Val
        515                 520                 525
Gly Asp Pro Phe Tyr Lys Ile Thr Ser Glu Ala Leu Leu Val Thr Gln
    530                 535                 540
Gln Leu Val Lys Val Ile Arg Pro Leu Asp Gln Pro Ser Ser Phe Asp
545                 550                 555                 560
Ala Thr Pro Tyr Ile Lys Asp Leu Phe Thr Cys Thr Ile Lys Arg Leu
                565                 570                 575
Lys Ala Ala Asp Ile Asp Gln Glu Val Lys Glu Arg Ala Ile Ser Cys
            580                 585                 590
Met Gly Gln Ile Ile Cys Asn Leu Gly Asp Asn Leu Gly Ser Asp Leu
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595 600 605
Pro Asn Thr Leu Gln Ile Phe Leu Glu Arg Leu Lys Asn Glu Ile Thr
610 615 620
Arg Leu Thr Thr Val Lys Ala Leu Thr Leu Ile Ala Gly Ser Pro Leu
625 630 635 640
Lys Ile Asp Leu Arg Pro Val Leu Gly Glu Gly Val Pro Ile Leu Ala
645 650 655
Ser Phe Leu Arg Lys Asn Gln Arg Ala Leu Lys Leu Gly Thr Leu Ser
660 665 670
Ala Leu Asp Ile Leu Ile Lys Asn Tyr Ser Asp Ser Leu Thr Ala Ala
675 680 685
Met Ile Asp Ala Val Leu Asp Glu Leu Pro Pro Leu Ile Ser Glu Ser
690 695 700
Asp Met His Val Ser Gln Met Ala Ile Ser Phe Leu Thr Thr Leu Ala
705 710 715 720
Lys Val Tyr Pro Ser Ser Leu Ser Lys Ile Ser Gly Ser Ile Leu Asn
725 730 735
Glu Leu Ile Gly Leu Val Arg Ser Pro Leu Leu Gln Gly Gly Ala Leu
740 745 750
Ser Ala Met Leu Asp Phe Phe Gln Ala Leu Val Val Thr Gly Thr Asn
755 760 765
Asn Leu Gly Tyr Met Asp Leu Leu Arg Met Leu Thr Gly Pro Val Tyr
770 775 780
Ser Gln Ser Thr Ala Leu Thr His Lys Gln Ser Tyr Tyr Ser Ile Ala
785 790 795 800
Lys Cys Val Ala Ala Leu Thr Arg Ala Cys Pro Lys Glu Gly Pro Ala
805 810 815
Val Val Gly Gln Phe Ile Gln Asp Val Lys Asn Ser Arg Ser Thr Asp
820 825 830
Ser Ile Arg Leu Leu Ala Leu Leu Ser Leu Gly Glu Val Gly His His
835 840 845
Ile Asp Leu Ser Gly Gln Leu Glu Leu Lys Ser Val Ile Leu Glu Ala
850 855 860
Phe Ser Ser Pro Ser Glu Glu Val Lys Ser Ala Ala Ser Tyr Ala Leu
865 870 875 880
Gly Ser Ile Ser Val Gly Asn Leu Pro Glu Tyr Leu Pro Phe Val Leu
885 890 895
Gln Glu Ile Thr Ser Gln Pro Lys Arg Gln Tyr Leu Leu Leu His Ser
900 905 910
Leu Lys Glu Ile Ile Ser Ser Ala Ser Val Val Gly Leu Lys Pro Tyr
915 920 925
Val Glu Asn Ile Trp Ala Leu Leu Leu Lys His Cys Glu Cys Ala Glu
930 935 940
Glu Gly Thr Arg Asn Val Val Ala Glu Cys Leu Gly Lys Leu Thr Leu
945 950 955 960
Ile Asp Pro Glu Thr Leu Leu Pro Arg Leu Lys Gly Tyr Leu Ile Ser
965 970 975
Gly Ser Ser Tyr Ala Arg Ser Ser Val Val Thr Ala Val Lys Phe Thr
980 985 990
Ile Ser Asp His Pro Gln Pro Ile Asp Pro Leu Leu Lys Asn Cys Ile
995 1000 1005
Gly Asp Phe Leu Lys Thr Leu Glu Asp Pro Asp Leu Asn Val Arg Arg
1010 1015 1020
Val Ala Leu Val Thr Phe Asn Ser Ala Ala His Asn Lys Pro Ser Leu

1025 1030 1035 1040
Ile Arg Asp Leu Leu Asp Thr Val Leu Pro His Leu Tyr Asn Glu Thr
1045 1050 1055
Lys Val Arg Lys Glu Leu Ile Arg Glu Val Glu Met Gly Pro Phe Lys
1060 1065 1070
His Thr Val Asp Asp Gly Leu Asp Ile Arg Lys Ala Ala Phe Glu Cys
1075 1080 1085
Met Tyr Thr Leu Leu Asp Ser Cys Leu Asp Arg Leu Asp Ile Phe Glu
1090 1095 1100
Phe Leu Asn His Val Glu Asp Gly Leu Lys Asp His Tyr Asp Ile Lys
1105 1110 1115 1120
Met Leu Thr Phe Leu Met Leu Val Arg Leu Ser Thr Leu Cys Pro Ser
1125 1130 1135
Ala Val Leu Gln Arg Leu Asp Arg Leu Val Glu Pro Leu Arg Ala Thr
1140 1145 1150
Cys Thr Thr Lys Val Lys Ala Asn Ser Val Lys Gln Glu Phe Glu Lys
1155 1160 1165
Gln Asp Glu Leu Lys Arg Ser Ala Met Arg Ala Val Ala Ala Leu Leu
1170 1175 1180
Thr Ile Pro Glu Ala Glu Lys Ser Pro Leu Met Ser Glu Phe Gln Ser
1185 1190 1195 1200
Gln Ile Ser Ser Asn Pro Glu Leu Ala Ala Ile Phe Glu Ser Ile Gln
1205 1210 1215
Lys Asp Ser Ser Ser Thr Asn Leu Glu Ser Met Asp Thr Ser
1220 1225 1230

<210> 3889
<211> 556
<212> DNA
<213> Homo sapiens

<400> 3889
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ccagtcctga cggatgagca ggtcccgaat ccaggccatg aagcccatga ccaaggagga
120
tgggatgccc ggcagagcat catccgcaag gtggtggacc ctgagacggg gcgcaccagg
180
cttattaagg gagatggcga ggtcctagag gaaatcgtaa ccaaagaacg acacagagag
240
atcaacaagc aagccacccg aggggactgc ctggccttcc agatgcgagc tgggttgctt
300
ccctgagggc ccccgctggc caaggcctgt ggacgacgct ggcggcccag cctgggcagg
360
tttcagggtg ccagtgggaa gcctgatggg tgctggtggc ctttcccccg tggattggtc
420
tctggcccag cccagtctct tctcaggggc aggggggtgga ggttggggtc accggcctgc
480
ttggcacccc catctgaaag agcagcactt ctcagctatt aaaggccccc tggatagaca
540
aaaaaaaaaa aaaaaa
556

<210> 3890

<211> 101
<212> PRT
<213> Homo sapiens

<400> 3890
Ala Leu Pro Gly Pro Ser Leu Asp Gln Trp His Arg Ser Ala Gly Glu
1 5 10 15
Glu Glu Asp Gly Pro Val Leu Thr Asp Glu Gln Val Pro Asn Pro Gly
20 25 30
His Glu Ala His Asp Gln Gly Gly Trp Asp Ala Arg Gln Ser Ile Ile
35 40 45
Arg Lys Val Val Asp Pro Glu Thr Gly Arg Thr Arg Leu Ile Lys Gly
50 55 60
Asp Gly Glu Val Leu Glu Glu Ile Val Thr Lys Glu Arg His Arg Glu
65 70 75 80
Ile Asn Lys Gln Ala Thr Arg Gly Asp Cys Leu Ala Phe Gln Met Arg
85 90 95
Ala Gly Leu Leu Pro
100

<210> 3891
<211> 1687
<212> DNA
<213> Homo sapiens

<400> 3891
ncctaggcta cacagaccgt gtggtgcgag ctttccgctg ggaggagcta ggtgagggtc
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ctgaacatct ggccgtatcc acaacaagaa tgtctccact cacctaattg gcaacatcaa
120
acaggccacg gcactgagag tagtggctct ggcctctttg ccctgtgcac cctggatggg
180
acactgaagc tcatggaaga aatggaagaa gcagacaagc tgctgtggtc agtgcaggtg
240
gatcaccagc tctttgccct ggagaaactg gatgtcaccg gcaacgggca tgaggaggta
300
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360
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420
cgcaacagcc cctgcctcgt atatgtcact ttcaaccaga agatctatgt gtactgggag
480
gtgcagctgg agcggatgga gtctaccaat ctggtgaaac tgctggagac caagccgagt
540
accacagcct gctgcaggag ctgggcgtgg atcctgacga cctccctgtg actcgtgccc
600
tgcttcacca aacgctctac catccagacc agccaccaca gtgtgctccc tcaagcctcc
660
aggatcccac ctagctgtac ttgcctcata gctggtgaag gattcttctg aacccccacc
720
ctacccccta aaggtatctg tggtattggc aggataggga atatgcatta cagaaatgca
780
ggatttgact ctgggcatga aagatggcag cagccctagg gtgaccgtga actatagacc
840

tcgcagtctt ttcggtgaaa gaagagacaa gttgaccctc tgcccatttc cttatggacc
900
tcacccatca tgccagcagg gtcataggac ctggccttgt tccaaatcat ctgggacatg
960
acccactccc cactgtcact gtgttgaaaa cagagacttg tttgtgtggc cccaacaccc
1020
ataaggaaac caggctttag gcccagggga gcagtggagg taagggctcc accccatctt
1080
aagctctgtc ttccgtggca caattccaag ttcttgacgt tagtaattgt taaaggaatg
1140
gcaaactgtt ttgttttgaa ggatctttct acagtctggt cttacccatg ttcctagcaa
1200
ccctgagatg attttcttcc atttaccaaa gcagccgggt cagtgctttc tcacgttgcc
1260
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1320
cccccataaa acagcttatt gtctccaaga caatagacat ttaaaatgtg atgcgggttt
1380
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1440
tctctatgct ctaaatcggt gtttttcaaa ctgtggttgc agtcctttgg tggattatgg
1500
ccagcatttt ttaaataggt agaatagaat aaagtaaaat agaaaatagc agagtacatt
1560
gctctcagtg taggtaagta ttgttttgtt agtcatatgt gcatgtgtgt actgagtgcc
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1680
caaattc
1687

<210> 3892
<211> 179
<212> PRT
<213> Homo sapiens

<400> 3892
Val Arg Val Leu Asn Ile Trp Pro Tyr Pro Gln Gln Glu Cys Leu His
1 5 10 15
Ser Pro Asn Trp Gln His Gln Thr Gly His Gly Thr Glu Ser Ser Gly
20 25 30
Ser Gly Leu Phe Ala Leu Cys Thr Leu Asp Gly Thr Leu Lys Leu Met
35 40 45
Glu Glu Met Glu Glu Ala Asp Lys Leu Leu Trp Ser Val Gln Val Asp
50 55 60
His Gln Leu Phe Ala Leu Glu Lys Leu Asp Val Thr Gly Asn Gly His
65 70 75 80
Glu Glu Val Val Ala Cys Ala Trp Asp Gly Gln Thr Tyr Ile Ile Asp
85 90 95
His Asn Arg Thr Val Val Arg Phe Gln Val Asp Glu Asn Ile Arg Ala
100 105 110
Phe Cys Ala Gly Leu Tyr Ala Cys Lys Glu Gly Arg Asn Ser Pro Cys
115 120 125
Leu Val Tyr Val Thr Phe Asn Gln Lys Ile Tyr Val Tyr Trp Glu Val

130 135 140
Gln Leu Glu Arg Met Glu Ser Thr Asn Leu Val Lys Leu Leu Glu Thr
145 150 155 160
Lys Pro Ser Thr Thr Ala Cys Cys Arg Ser Trp Ala Trp Ile Leu Thr
165 170 175
Thr Ser Leu

<210> 3893
<211> 1591
<212> DNA
<213> Homo sapiens

<400> 3893
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120
aagagtaaag aaaattgtgt tgtggataac atcaaagtgt gcagtaatga cactgggagt
180
ggaaaattca agtgtgtttg catcactatg agagtgcctc ggaacccaac tatcggagat
240
aaatttgcca gtcgccatgg gcagaagggc attttaagca gattgtggcc ggctgaggac
300
atgcctttta ctgagagtgg gatggtccca gacattctgt tcaatcccca tggttttcca
360
tcccgcatga ccattgggat gttaattgag agtatggccg ggaagtctgc agctttgcat
420
ggtctctgcc atgatgctac acccttcatc ttctcagagg agaactcggc cttagaatac
480
tttggtgaga tgttaaaggc tgctggctac aatttctatg gcaccgagag gttatatagt
540
ggcatcagtg ggctagaact ggaagcagac atcttcatag gagtggttta ttatcagcgc
600
ttacgccata tggtctcaga caaatttcaa gtaaggacaa ctggagcccg agacagagtc
660
accaaccagc ctattggggg aagaaatgtc cagggtggaa tccgttttgg ggagatggaa
720
cgggatgcgc ttttagctca tggtacatct tttctccttc atgaccgcct cttcaactgc
780
tcagatcggt cggtagccca tgtgtgtgtg aagtgtggca gtttactctc tccactgttg
840
gagaagccac ccccttcttg gtctgccatg cgcaacagaa aatacaactg tactctgtgt
900
agtcgcagtg acactatcga tactgtttct gtgccttatg tttttcggta ttttgtagct
960
gaactggcag ctatgaacat caaagtgaaa ctggatgttg tttaacttga tgttgacctt
1020
ttggattaag aggactatca gattaaagca aaatgtaatt ttaattcaat gaagatatca
1080
ttaccaggtt actcttgaga tttttcaacg gtgttagaac tctcaaccaa gacctgaaaa
1140
ccaagtatgc aaggtttctg aatctctctg gtagattaac tattgacaat gattttctgt
1200

tatctttgtt caaaaagttc atgtcttctc aaaatatgaa atattgataa atggaagagc
1260
atacggtgac aagtctcctt tccaacccca ggttccctac accctgctct cagcaggcag
1320
tgagtgtcac acacctgtta atccatcttg agcaggacag tactatacaa atagaatgca
1380
agctgtaatg taattttata ttttcttata gccacgttga agtaaaaaca aacaggtaca
1440
gtgtttttta ccagctttat agaagtacag ttgttacata tttaatgaat acaatttgat
1500
gggtctgact atatgcacac acctttgata ccatcaccac aatcagggta ataaacatac
1560
ctgtcatctc caaaaaaaaa aaaaaaaaaa a
1591

<210> 3894
<211> 334
<212> PRT
<213> Homo sapiens

<400> 3894
Arg Val Leu Gln Lys Leu Asp Asp Asp Gly Leu Pro Phe Ile Gly Ala
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Lys Leu Gln Tyr Gly Asp Pro Tyr Tyr Ser Tyr Leu Asn Leu Asn Thr
20 25 30
Gly Glu Ser Phe Val Met Tyr Tyr Lys Ser Lys Glu Asn Cys Val Val
35 40 45
Asp Asn Ile Lys Val Cys Ser Asn Asp Thr Gly Ser Gly Lys Phe Lys
50 55 60
Cys Val Cys Ile Thr Met Arg Val Pro Arg Asn Pro Thr Ile Gly Asp
65 70 75 80
Lys Phe Ala Ser Arg His Gly Gln Lys Gly Ile Leu Ser Arg Leu Trp
85 90 95
Pro Ala Glu Asp Met Pro Phe Thr Glu Ser Gly Met Val Pro Asp Ile
100 105 110
Leu Phe Asn Pro His Gly Phe Pro Ser Arg Met Thr Ile Gly Met Leu
115 120 125
Ile Glu Ser Met Ala Gly Lys Ser Ala Ala Leu His Gly Leu Cys His
130 135 140
Asp Ala Thr Pro Phe Ile Phe Ser Glu Glu Asn Ser Ala Leu Glu Tyr
145 150 155 160
Phe Gly Glu Met Leu Lys Ala Ala Gly Tyr Asn Phe Tyr Gly Thr Glu
165 170 175
Arg Leu Tyr Ser Gly Ile Ser Gly Leu Glu Leu Glu Ala Asp Ile Phe
180 185 190
Ile Gly Val Val Tyr Tyr Gln Arg Leu Arg His Met Val Ser Asp Lys
195 200 205
Phe Gln Val Arg Thr Thr Gly Ala Arg Asp Arg Val Thr Asn Gln Pro
210 215 220
Ile Gly Gly Arg Asn Val Gln Gly Gly Ile Arg Phe Gly Glu Met Glu
225 230 235 240
Arg Asp Ala Leu Leu Ala His Gly Thr Ser Phe Leu Leu His Asp Arg
245 250 255
Leu Phe Asn Cys Ser Asp Arg Ser Val Ala His Val Cys Val Lys Cys

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            260                 265                 270
Gly Ser Leu Leu Ser Pro Leu Leu Glu Lys Pro Pro Pro Ser Trp Ser
        275                 280                 285
Ala Met Arg Asn Arg Lys Tyr Asn Cys Thr Leu Cys Ser Arg Ser Asp
    290                 295                 300
Thr Ile Asp Thr Val Ser Val Pro Tyr Val Phe Arg Tyr Phe Val Ala
305                 310                 315                 320
Glu Leu Ala Ala Met Asn Ile Lys Val Lys Leu Asp Val Val
                325                 330
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<210> 3895
<211> 1227
<212> DNA
<213> Homo sapiens

<400> 3895

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aaagaagcca agcgcttcga aatcgctagg tctcaacctg aagacacccc tgaaaacaca
120
gtgaggaggc aagagcagcc cagcattgag agtacatctc cgatttcaag aactgatgaa
180
attagaaaaa acacctacag aacattggat agcctggagc agaccattaa acagctcgaa
240
aatacaatca gtgaaatgag tcccaaagcc ctagttgata cctcatgttc ttccaacaga
300
gattctgttg caagttcatc ccacatagcc caagaggcct ctccccgacc cttgctagtt
360
ccggatgaag gtcccactgc cctagagccc cctacgtcga taccttcagc ttcacgtaag
420
ggctccagcg gggccccaca gacgagcagg atgcctgtcc ccatgagtgc caagaacaga
480
cccggaaccc tggacaaacc cggcaagcag tccaaactgc aggatccccg ccaatatcgt
540
caggctaatg gaagtgctaa gaaatctggt ggggacttta agcctacttc cccctcctta
600
cctgcttcta agattccagc cctttctccc agctctggga aaagcagttc tctgccctct
660
tctagtggtg acagctctaa cctccctaat ccacctgcta ctaaaccatc gattgcttct
720
aaccctctca gcccccaaac aggaccacct gctcactctg cctccctcat ccctttctgtc
780
tctaatggct ctttgaagtt tcagagcctc actcatacag gtaaaggtca ccatctttca
840
ttctcaccgc agagtcaaaa tggccgagca ccccctcctt tgtcattttc ctcctcccct
900
ccttctcctg cctcctccgt ctcactgaat caaggtgcca agggcaccag gaccatccat
960
actcccagcc tcaccagcta caaggcacag aatggaagtt caagcaaagc caccccatcc
1020
acagcaaaag aaacctctta aaggtcaaat cctattaggc acaagtcgga gttacattta
1080
aaaaaaatta acagtctaca acaactgttt tcacaagaga atgtaacata ttgctgtatc
1140
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gtttgaggct taatgctaaa tatgtgctaa atactggatt aatagatttc agtaaagctc
1200
gttcaaaaaa aaaaaaaaaa aaaaaaa
1227

<210> 3896
<211> 346
<212> PRT
<213> Homo sapiens

<400> 3896
Lys Thr Leu Arg Val Val Val Tyr Glu Glu Glu Glu Glu Asp Gly Thr
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Leu Lys Gln His Lys Glu Ala Lys Arg Phe Glu Ile Ala Arg Ser Gln
20 25 30
Pro Glu Asp Thr Pro Glu Asn Thr Val Arg Arg Gln Glu Gln Pro Ser
35 40 45
Ile Glu Ser Thr Ser Pro Ile Ser Arg Thr Asp Glu Ile Arg Lys Asn
50 55 60
Thr Tyr Arg Thr Leu Asp Ser Leu Glu Gln Thr Ile Lys Gln Leu Glu
65 70 75 80
Asn Thr Ile Ser Glu Met Ser Pro Lys Ala Leu Val Asp Thr Ser Cys
85 90 95
Ser Ser Asn Arg Asp Ser Val Ala Ser Ser Ser His Ile Ala Gln Glu
100 105 110
Ala Ser Pro Arg Pro Leu Leu Val Pro Asp Glu Gly Pro Thr Ala Leu
115 120 125
Glu Pro Pro Thr Ser Ile Pro Ser Ala Ser Arg Lys Gly Ser Ser Gly
130 135 140
Ala Pro Gln Thr Ser Arg Met Pro Val Pro Met Ser Ala Lys Asn Arg
145 150 155 160
Pro Gly Thr Leu Asp Lys Pro Gly Lys Gln Ser Lys Leu Gln Asp Pro
165 170 175
Arg Gln Tyr Arg Gln Ala Asn Gly Ser Ala Lys Lys Ser Gly Gly Asp
180 185 190
Phe Lys Pro Thr Ser Pro Ser Leu Pro Ala Ser Lys Ile Pro Ala Leu
195 200 205
Ser Pro Ser Ser Gly Lys Ser Ser Ser Leu Pro Ser Ser Ser Gly Asp
210 215 220
Ser Ser Asn Leu Pro Asn Pro Pro Ala Thr Lys Pro Ser Ile Ala Ser
225 230 235 240
Asn Pro Leu Ser Pro Gln Thr Gly Pro Pro Ala His Ser Ala Ser Leu
245 250 255
Ile Pro Ser Val Ser Asn Gly Ser Leu Lys Phe Gln Ser Leu Thr His
260 265 270
Thr Gly Lys Gly His His Leu Ser Phe Ser Pro Gln Ser Gln Asn Gly
275 280 285
Arg Ala Pro Pro Pro Leu Ser Phe Ser Ser Ser Pro Pro Ser Pro Ala
290 295 300
Ser Ser Val Ser Leu Asn Gln Gly Ala Lys Gly Thr Arg Thr Ile His
305 310 315 320
Thr Pro Ser Leu Thr Ser Tyr Lys Ala Gln Asn Gly Ser Ser Ser Lys
325 330 335
Ala Thr Pro Ser Thr Ala Lys Glu Thr Ser

340 345

<210> 3897
<211> 366
<212> DNA
<213> Homo sapiens

<400> 3897
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agctcagcca gcaccgggtg atggcaggga ggcctgggct tctgcactgg cttctggcct
120
cttctgggca cccacgcttt gtccatgaat ggaaagcaat gctgacggct gcccaatgtg
180
tccaggacgt ttctgaaact cctgttcctc tccccgtccc tctctctgtc ccactgtcca
240
cctcagtgac ctcctctctt cgtggctctc accccacact ctgccactgc cacattttcc
300
tctgcgccca gcctctgcct ccacctgaaa ctttcctgga aatctcaaaa tgtaattcca
360
ggtccc
366

<210> 3898
<211> 111
<212> PRT
<213> Homo sapiens

<400> 3898
Met Glu Glu Ala Leu His Ser His Leu Gln Leu Ser Gln His Arg Val
1 5 10 15
Met Ala Gly Arg Pro Gly Leu Leu His Trp Leu Leu Ala Ser Ser Gly
20 25 30
His Pro Arg Phe Val His Glu Trp Lys Ala Met Leu Thr Ala Ala Gln
35 40 45
Cys Val Gln Asp Val Ser Glu Thr Pro Val Pro Leu Pro Val Pro Leu
50 55 60
Ser Val Pro Leu Ser Thr Ser Val Thr Ser Ser Leu Arg Gly Ser His
65 70 75 80
Pro Thr Leu Cys His Cys His Ile Phe Leu Cys Ala Gln Pro Leu Pro
85 90 95
Pro Pro Glu Thr Phe Leu Glu Ile Ser Lys Cys Asn Ser Arg Ser
100 105 110

<210> 3899
<211> 1092
<212> DNA
<213> Homo sapiens

<400> 3899
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60
cgagaggtga gggtgccccc gcctcacctg cagaggggcc gttccgggct cgaacccggc
120

accttccgga aaatggcggc tgccaggccc agcctgggcc gagtcctccc aggatcctct
180
gtcctgttcc tgtgtgacat gcaggagaag ttccgccaca acatcgccta cttcccacag
240
atcgtctcag tggctgcccg catgctcaag gtggcccggc tgcttgaggt gccagtcatg
300
ctgacggagc agtacccaca aggcctgggc cccacggtgc ccgagctggg gactngaggg
360
ccttcggccg ctggccaaga cctgcttcag catggtgcct gcctgcagca ggagctggac
420
agtcggcccc agctgcgctc tgtgctgctc tgtggcattg aggcacaggc ctgcatcttg
480
aacacgaccc tggacctcct agaccggggg ctgcaggtcc atgtggtggt ggacgcctgc
540
tcctcacgca gccaggtgga ccggctggtg gctctggccc gcatgagaca gagtggtgcc
600
ttcctctcca ccagcgaagg gctcattctg cagcttgtgg gcgatgccgt ccacccccag
660
ttcaaggaga tccagaaact catcaaggag cccgccccag acagcggact gctgggcctc
720
ttccaaggcc agaactccct cctccactga actccaaccc tgccttgagg gaagaccacc
780
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tgcgatccac caggagtgcc gccccccttgt ggggggggggc agggtgctgc cttcccattg
900
gacagctgct cccggaaatg caaatgagac tcctggaaac tgggtgggaa ttggctgagc
960
caagatggag gcggggctcg gccccgggcc acttcacggg gcgggaaggg gaggggaaga
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agagtctcag actgtgggac acggactcgc agaataaaca tatatgtggc tgtgaaaaaa
1080
aaaaaaaaaa aa
1092

<210> 3900
<211> 249
<212> PRT
<213> Homo sapiens

<400> 3900
Xaa Asn Gly Asn Gln Pro Trp Glu Ala Arg Lys Arg Pro Gln Arg Trp
 1   5   10   15
Pro Ser Glu Arg Arg Glu Val Arg Val Pro Pro Pro His Leu Gln Arg
            20   25   30
Gly Arg Ser Gly Leu Glu Pro Gly Thr Phe Arg Lys Met Ala Ala Ala
        35   40   45
Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser Val Leu Phe Leu
    50   55   60
Cys Asp Met Gln Glu Lys Phe Arg His Asn Ile Ala Tyr Phe Pro Gln
65   70   75   80
Ile Val Ser Val Ala Ala Arg Met Leu Lys Val Ala Arg Leu Leu Glu
                85   90   95
Val Pro Val Met Leu Thr Glu Gln Tyr Pro Gln Gly Leu Gly Pro Thr

```
            100                 105                 110
Val Pro Glu Leu Gly Thr Xaa Gly Pro Ser Ala Ala Gly Gln Asp Leu
        115                 120                 125
Leu Gln His Gly Ala Cys Leu Gln Gln Glu Leu Asp Ser Arg Pro Gln
    130                 135                 140
Leu Arg Ser Val Leu Leu Cys Gly Ile Glu Ala Gln Ala Cys Ile Leu
145                 150                 155                 160
Asn Thr Thr Leu Asp Leu Leu Asp Arg Gly Leu Gln Val His Val Val
                165                 170                 175
Val Asp Ala Cys Ser Ser Arg Ser Gln Val Asp Arg Leu Val Ala Leu
            180                 185                 190
Ala Arg Met Arg Gln Ser Gly Ala Phe Leu Ser Thr Ser Glu Gly Leu
        195                 200                 205
Ile Leu Gln Leu Val Gly Asp Ala Val His Pro Gln Phe Lys Glu Ile
    210                 215                 220
Gln Lys Leu Ile Lys Glu Pro Ala Pro Asp Ser Gly Leu Leu Gly Leu
225                 230                 235                 240
Phe Gln Gly Gln Asn Ser Leu Leu His
                245
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<210> 3901
<211> 1287
<212> DNA
<213> Homo sapiens

<400> 3901

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120
ttcttcctgc aggtgtacca caccttcctc aggattgcag agaccagggt aggtgacgcc
180
gtcctggggc tggtctgcat gctgctgctg ctggtgctga agctgatgcg ggaccacgtg
240
cctcccgtcc accccgagat gccccctggt gtgcggctca gccgtgggct ggtctgggct
300
gccacgacag ctcgcaacgc cctggtggtc tccttcgcag ccctggttgc gtactccttc
360
gaggtgactg gataccagcc tttcatccta acaggggaga cagctgaggg gctccctcca
420
gtccggatcc cgcccttctc agtgaccaca gccaacggga cgatctcctt caccgagatg
480
gtgcaggaca tgggagccgg gctggccgtg gtgcccctga tgggcctcct ggagagcatt
540
gcggtggcca aagccttcgc atctcagaat aattaccgca tcgatgccaa ccaggagctg
600
ctggccatcg gtctcaccaa catgttgggc tccctcgtct cctcctaccc ggtcacaggc
660
agctttggac ggacagccgt gaacgctcag tcgggggtgt gcaccccggc ggggggcctg
720
gtgacgggag tgctggtgct gctgtctctg gactacctga cctcactgtt ctactacatc
780
cccaagtctg ccctggctgc cgtcatcatc atggccgtgg ccccgctgtt cgacaccaag
840
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atcttcagga cgctctggcg tgttaagagg ctggacctgc tgcccctgtg cgtgaccttc
900
ctgctgtgct tctgggaggt gcagtacggc atcctggccg gggccctggt gtctctgctc
960
atgctcctgc actctgcagc caggcctgag accaaggtgt cagaggggcc ggttctggtc
1020
ctgcagccgg ccagcggcct gtccttccct gtcctctgcc ccccactccc tgctgttcag
1080
gaccccaaga ccctgtcccc gacgctctcc agtccacaag gatgcaggca tctctgagtg
1140
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1260
gggagctaag ggcctgtgag tcctagt
1287

<210> 3902
<211> 312
<212> PRT
<213> Homo sapiens

<400> 3902
Met Leu Leu Leu Leu Val Leu Lys Leu Met Arg Asp His Val Pro Pro
1 5 10 15
Val His Pro Glu Met Pro Pro Gly Val Arg Leu Ser Arg Gly Leu Val
20 25 30
Trp Ala Ala Thr Thr Ala Arg Asn Ala Leu Val Val Ser Phe Ala Ala
35 40 45
Leu Val Ala Tyr Ser Phe Glu Val Thr Gly Tyr Gln Pro Phe Ile Leu
50 55 60
Thr Gly Glu Thr Ala Glu Gly Leu Pro Pro Val Arg Ile Pro Pro Phe
65 70 75 80
Ser Val Thr Thr Ala Asn Gly Thr Ile Ser Phe Thr Glu Met Val Gln
85 90 95
Asp Met Gly Ala Gly Leu Ala Val Val Pro Leu Met Gly Leu Leu Glu
100 105 110
Ser Ile Ala Val Ala Lys Ala Phe Ala Ser Gln Asn Asn Tyr Arg Ile
115 120 125
Asp Ala Asn Gln Glu Leu Leu Ala Ile Gly Leu Thr Asn Met Leu Gly
130 135 140
Ser Leu Val Ser Ser Tyr Pro Val Thr Gly Ser Phe Gly Arg Thr Ala
145 150 155 160
Val Asn Ala Gln Ser Gly Val Cys Thr Pro Ala Gly Gly Leu Val Thr
165 170 175
Gly Val Leu Val Leu Leu Ser Leu Asp Tyr Leu Thr Ser Leu Phe Tyr
180 185 190
Tyr Ile Pro Lys Ser Ala Leu Ala Ala Val Ile Ile Met Ala Val Ala
195 200 205
Pro Leu Phe Asp Thr Lys Ile Phe Arg Thr Leu Trp Arg Val Lys Arg
210 215 220
Leu Asp Leu Leu Pro Leu Cys Val Thr Phe Leu Leu Cys Phe Trp Glu
225 230 235 240
Val Gln Tyr Gly Ile Leu Ala Gly Ala Leu Val Ser Leu Leu Met Leu

```
                245                 250                 255
Leu His Ser Ala Ala Arg Pro Glu Thr Lys Val Ser Glu Gly Pro Val
            260                 265                 270
Leu Val Leu Gln Pro Ala Ser Gly Leu Ser Phe Pro Val Leu Cys Pro
        275                 280                 285
Pro Leu Pro Ala Val Gln Asp Pro Lys Thr Leu Ser Pro Thr Leu Ser
    290                 295                 300
Ser Pro Gln Gly Cys Arg His Leu
305                 310
```

<210> 3903
<211> 598
<212> DNA
<213> Homo sapiens

<400> 3903
gcgcgccggg gagcgcgcgt ggtgctggcc tgccgcagcc aggagcgcgg ggaggcggct
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gccttcgacc tccgccagga gagtgggaac aatgaggtca tcttcatggc cttggacttg
120
gccagtctgg cctcggtgcg ggcctttgcc actgcctttc tgagctctga gccacggttg
180
gacatcctca tccacaatgc cggtatcagt tcctgtggcc ggacccgtga ggcgtttaac
240
ctgctgcttc gggtgaacca tatcggtccc tttctgctga cacatctgct gctgccttgc
300
ctgaaggcat gtgcccctag ccgcgtggtg gtggtagcct cagctgccca ctgtcgggga
360
cgtcttgact tcaaacgcct ggaccgccca gtggtgctgg cggcaggagc tgcggcatat
420
gctgacacta agctggctaa tgtactgttt gcccgggagc tcgccaacca gcttgaggcc
480
actggcgtca cctgctatgc agcccaccca gggcctgtga actcggagct gttcctgcgc
540
catgttcctg gatggctgcg cccacttttg cgcccattgg cttggctggt gccccggg
598

<210> 3904
<211> 199
<212> PRT
<213> Homo sapiens

<400> 3904
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Ala Arg Arg Gly Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg
 1               5                  10                  15
Gly Glu Ala Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu
            20                  25                  30
Val Ile Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala
        35                  40                  45
Phe Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile
    50                  55                  60
His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe Asn
65                  70                  75                  80
Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr His Leu
```

```
                85                  90                  95
Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val Val Val Val
            100                 105                 110
Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe Lys Arg Leu Asp
        115                 120                 125
Arg Pro Val Val Leu Ala Ala Gly Ala Ala Ala Tyr Ala Asp Thr Lys
    130                 135                 140
Leu Ala Asn Val Leu Phe Ala Arg Glu Leu Ala Asn Gln Leu Glu Ala
145                 150                 155                 160
Thr Gly Val Thr Cys Tyr Ala Ala His Pro Gly Pro Val Asn Ser Glu
                165                 170                 175
Leu Phe Leu Arg His Val Pro Gly Trp Leu Arg Pro Leu Leu Arg Pro
            180                 185                 190
Leu Ala Trp Leu Val Pro Arg
        195
```

<210> 3905
<211> 370
<212> DNA
<213> Homo sapiens

<400> 3905
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tcggagatgg cggtgacctt cgacaaggtg tacgtgaaca tcgggggcga cttcgatgtg
120
gccaccggcc agtttcgctg ccgcgtgccc ggcgcctact tcttctcctt cacggctggc
180
aaggccccgc acaagagccc gtcggtgatg ctggtgcgaa accgcgacga ggtgcaggcg
240
ctggccttcg acgagcagcg gcggccaggc gcgcggcgcg cagccagcca gagcgccatg
300
ctgcagctcg actacggcga cacagtgtgg ctgcggctgc atggcgcccc gcagtacgcg
360
ctaggcgcgc
370

<210> 3906
<211> 123
<212> PRT
<213> Homo sapiens

<400> 3906

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Gly Ser Ser Glu Leu Arg Ser Ala Phe Ser Ala Ala Arg Thr Thr Pro
 1               5                  10                  15
Leu Glu Gly Thr Ser Glu Met Ala Val Thr Phe Asp Lys Val Tyr Val
            20                  25                  30
Asn Ile Gly Gly Asp Phe Asp Val Ala Thr Gly Gln Phe Arg Cys Arg
        35                  40                  45
Val Pro Gly Ala Tyr Phe Phe Ser Phe Thr Ala Gly Lys Ala Pro His
    50                  55                  60
Lys Ser Pro Ser Val Met Leu Val Arg Asn Arg Asp Glu Val Gln Ala
65                  70                  75                  80
Leu Ala Phe Asp Glu Gln Arg Arg Pro Gly Ala Arg Arg Ala Ala Ser
```

85 90 95
Gln Ser Ala Met Leu Gln Leu Asp Tyr Gly Asp Thr Val Trp Leu Arg
100 105 110
Leu His Gly Ala Pro Gln Tyr Ala Leu Gly Ala
115 120

<210> 3907
<211> 4474
<212> DNA
<213> Homo sapiens

<400> 3907
gcgcgccgga accggaaccg acctgcgccg gaaccggaac ggagagcggg ttgccagggc
60
ccgaagaggg ctggctgcgg cggtctcgct cggctgtccg ttccttgctg gagaatttgg
120
ccacaaagag ctgccaagat agctgggcca ggaagaaagc gccgcagccc tgacccagac
180
gctgttgccg accccggggc actctggctg tcgaccaagc ggctcaagat gtctggcggg
240
gccagtgcca caggcccaag gagagggccc ccaggactgg aggacaccac tagtaagaag
300
aagcagaagg atcgagcaaa ccaggagagc aaggatggag atcctaggaa agagacaggg
360
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420
gcctcccatg cagctgggat cacaggctca cgccaccgta cccggctgtt ctttccttca
480
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540
cctcatgatc tcttggctac tcccactcca gagttgttgc tcgattggag gcagagtgca
600
gaagaggtga ttgtcaagct tcgtgtggga gtaggtcccc tgcagctgga ggatgtagat
660
gctgctttca cagatacaga ctgtgtggtg cggtttgcag gtggtcagca gtggggtggt
720
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ccagccatgg tccggagcag aaaccctggg aaagatgact gtgccaagga ggagatggca
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1260

accttccgtt ggcaggtgaa gctcaggaat ctgattgagc cagagcagtg caccttctgt
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4380
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4474

<210> 3908
<211> 1373
<212> PRT
<213> Homo sapiens

<400> 3908
Ala Gly Cys Gly Gly Leu Ala Arg Leu Ser Val Pro Cys Trp Arg Ile
1 5 10 15
Trp Pro Gln Arg Ala Ala Lys Ile Ala Gly Pro Gly Arg Lys Arg Arg
20 25 30
Ser Pro Asp Pro Asp Ala Val Ala Asp Pro Gly Ala Leu Trp Leu Ser
35 40 45
Thr Lys Arg Leu Lys Met Ser Gly Gly Ala Ser Ala Thr Gly Pro Arg
50 55 60
Arg Gly Pro Pro Gly Leu Glu Asp Thr Thr Ser Lys Lys Lys Gln Lys
65 70 75 80
Asp Arg Ala Asn Gln Glu Ser Lys Asp Gly Asp Pro Arg Lys Glu Thr
85 90 95
Gly Ser Arg Tyr Val Ala Gln Ala Gly Leu Glu Pro Leu Ala Ser Gly
100 105 110
Asp Pro Ser Ala Ser Ala Ser His Ala Ala Gly Ile Thr Gly Ser Arg
115 120 125
His Arg Thr Arg Leu Phe Phe Pro Ser Ser Ser Gly Ser Ala Ser Thr
130 135 140
Pro Gln Glu Glu Gln Thr Lys Glu Gly Ala Cys Glu Asp Pro His Asp
145 150 155 160
Leu Leu Ala Thr Pro Thr Pro Glu Leu Leu Leu Asp Trp Arg Gln Ser
165 170 175
Ala Glu Glu Val Ile Val Lys Leu Arg Val Gly Val Gly Pro Leu Gln
180 185 190
Leu Glu Asp Val Asp Ala Ala Phe Thr Asp Thr Asp Cys Val Val Arg
195 200 205
Phe Ala Gly Gly Gln Gln Trp Gly Gly Val Phe Tyr Ala Glu Ile Lys
210 215 220
Ser Ser Cys Ala Lys Val Gln Thr Arg Lys Gly Ser Leu Leu His Leu
225 230 235 240
Thr Leu Pro Lys Lys Val Pro Met Leu Thr Trp Pro Ser Leu Leu Val
245 250 255
Glu Ala Asp Glu Gln Leu Cys Ile Pro Pro Leu Asn Ser Gln Thr Cys
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Leu Leu Gly Ser Glu Glu Asn Leu Ala Pro Leu Ala Gly Glu Lys Ala
275 280 285
Val Pro Pro Gly Asn Asp Pro Val Ser Pro Ala Met Val Arg Ser Arg
290 295 300
Asn Pro Gly Lys Asp Asp Cys Ala Lys Glu Glu Met Ala Val Ala Ala
305 310 315 320
Asp Ala Ala Thr Leu Val Asp Gly Lys Glu Pro Glu Ser Met Val Asn
325 330 335
Leu Ala Phe Val Lys Asn Asp Ser Tyr Glu Lys Gly Pro Asp Ser Val
340 345 350
Val Val His Val Tyr Val Lys Glu Ile Cys Arg Asp Thr Ser Arg Val
355 360 365
Leu Phe Arg Glu Gln Asp Phe Thr Leu Ile Phe Gln Thr Arg Asp Gly

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Asn Phe Leu Arg Leu His Pro Gly Cys Gly Pro His Thr Thr Phe Arg
385                 390                 395                 400
Trp Gln Val Lys Leu Arg Asn Leu Ile Glu Pro Glu Gln Cys Thr Phe
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Cys Phe Thr Ala Ser Arg Ile Asp Ile Cys Leu Arg Lys Arg Gln Ser
            420                 425                 430
Gln Arg Trp Gly Gly Leu Glu Ala Pro Ala Ala Arg Val Gly Gly Ala
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Lys Val Ala Val Pro Thr Gly Pro Thr Pro Leu Asp Ser Thr Pro Pro
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Gly Gly Ala Pro His Pro Leu Thr Gly Gln Glu Glu Ala Arg Ala Val
465                 470                 475                 480
Glu Lys Asp Lys Ser Lys Ala Arg Ser Glu Asp Thr Gly Leu Asp Ser
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Val Ala Thr Arg Thr Pro Met Glu His Val Thr Pro Lys Pro Glu Thr
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His Leu Ala Ser Pro Lys Pro Thr Cys Met Val Pro Pro Met Pro His
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Ser Pro Val Ser Gly Asp Ser Val Glu Glu Glu Glu Glu Glu Glu Lys
    530                 535                 540
Lys Val Cys Leu Pro Gly Phe Thr Gly Leu Val Asn Leu Gly Asn Thr
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Cys Phe Met Asn Ser Val Ile Gln Ser Leu Ser Asn Thr Arg Glu Leu
                565                 570                 575
Arg Asp Phe Phe His Asp Arg Ser Phe Glu Ala Glu Ile Asn Tyr Asn
            580                 585                 590
Asn Pro Leu Gly Thr Gly Gly Arg Leu Ala Ile Gly Phe Ala Val Leu
        595                 600                 605
Leu Arg Ala Leu Trp Lys Gly Thr His His Ala Phe Gln Pro Ser Lys
    610                 615                 620
Leu Lys Ala Ile Val Ala Ser Lys Ala Ser Gln Phe Thr Gly Tyr Ala
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Gln His Asp Ala Gln Glu Phe Met Ala Phe Leu Leu Asp Gly Leu His
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Glu Asp Leu Asn Arg Ile Gln Asn Lys Pro Tyr Thr Glu Thr Val Asp
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Ser Asp Gly Arg Pro Asp Glu Val Val Ala Glu Glu Ala Trp Gln Arg
        675                 680                 685
His Lys Met Arg Asn Asp Ser Phe Ile Val Asp Leu Phe Gln Gly Gln
    690                 695                 700
Tyr Lys Ser Lys Leu Val Cys Pro Val Cys Ala Lys Val Ser Ile Thr
705                 710                 715                 720
Phe Asp Pro Phe Leu Tyr Leu Pro Val Pro Leu Pro Gln Lys Gln Lys
                725                 730                 735
Val Leu Pro Val Phe Tyr Phe Ala Arg Glu Pro His Ser Lys Pro Ile
            740                 745                 750
Lys Phe Leu Val Ser Val Ser Lys Glu Asn Ser Thr Ala Ser Glu Val
        755                 760                 765
Leu Asp Ser Leu Ser Gln Ser Val His Val Lys Pro Glu Asn Leu Arg
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Leu Ala Glu Val Ile Lys Asn Arg Phe His Arg Val Phe Leu Pro Ser
785                 790                 795                 800
His Ser Leu Asp Thr Val Ser Pro Ser Asp Thr Leu Leu Cys Phe Glu
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Cys Gln Arg Lys Gln Gln Ser Glu Asp Glu Lys Leu Lys Arg Cys Thr
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Arg Cys Tyr Arg Val Gly Tyr Cys Asn Gln Leu Cys Gln Lys Thr His
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Trp Pro Asp His Lys Gly Leu Cys Arg Pro Glu Asn Ile Gly Tyr Pro
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Phe Leu Val Ser Val Pro Ala Ser Arg Leu Thr Tyr Ala Arg Leu Ala
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Gln Leu Leu Glu Gly Tyr Ala Arg Tyr Ser Val Ser Val Phe Gln Pro
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Pro Phe Gln Pro Gly Arg Met Ala Leu Glu Ser Gln Ser Pro Gly Cys
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Thr Thr Leu Leu Ser Thr Gly Ser Leu Glu Ala Gly Asp Ser Glu Arg
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Asp Pro Ile Gln Pro Pro Glu Leu Gln Leu Val Thr Pro Met Ala Glu
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Gly Asp Thr Gly Leu Pro Arg Val Trp Ala Ala Pro Asp Arg Gly Pro
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Val Pro Ser Thr Ser Gly Ile Ser Ser Glu Met Leu Ala Ser Gly Pro
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Ile Glu Val Gly Ser Leu Pro Ala Gly Glu Arg Val Ser Arg Pro Glu
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Ala Ala Val Pro Gly Tyr Gln His Pro Ser Glu Ala Met Asn Ala His
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Thr Pro Gln Phe Phe Ile Tyr Lys Ile Asp Ser Ser Asn Arg Glu Gln
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Arg Leu Glu Asp Lys Gly Asp Thr Pro Leu Glu Leu Gly Asp Asp Cys
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Ser Leu Ala Leu Val Trp Arg Asn Asn Glu Arg Leu Gln Glu Phe Val
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Leu Val Ala Ser Lys Glu Leu Glu Cys Ala Glu Asp Pro Gly Ser Ala
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Gly Glu Ala Ala Arg Ala Gly His Phe Thr Leu Asp Gln Cys Leu Asn
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Leu Phe Thr Arg Pro Glu Val Leu Ala Pro Glu Glu Ala Trp Tyr Cys
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Pro Gln Cys Lys Gln His Arg Glu Ala Ser Lys Gln Leu Leu Leu Trp
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Arg Leu Pro Asn Val Leu Ile Val Gln Leu Lys Arg Phe Ser Phe Arg
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Ser Phe Ile Trp Arg Asp Lys Ile Asn Asp Leu Val Glu Phe Pro Val
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Arg Asn Leu Asp Leu Ser Lys Phe Cys Ile Gly Gln Lys Glu Glu Gln
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Leu Pro Ser Tyr Asp Leu Tyr Ala Val Ile Asn His Tyr Gly Gly Met
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Ile Gly Gly His Tyr Thr Ala Cys Ala Arg Leu Pro Asn Asp Arg Ser
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Ser Gln Arg Ser Asp Val Gly Trp Arg Leu Phe Asp Asp Ser Thr Val
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His Ser Glu His His Pro Asp Leu Gly Pro Ala Ala Glu Ala Ala Ala
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Ser Gln Ala Ser Arg Ile Trp Gln Glu Leu Glu Ala Glu Glu Glu Pro
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Val Pro Glu Gly Ser Gly Pro Leu Gly Pro Trp Gly Pro Gln Asp Trp
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Val Gly Pro Leu Pro Arg Gly Pro Thr Thr Pro Asp Glu Gly Cys Leu
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Arg Tyr Phe Val Leu Gly Thr Val Ala Ala Leu Val Ala Leu Val Leu
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<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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35 40 45
Glu Ile Tyr Ser Glu Asn Ser Val Ser Ile Arg Glu Tyr Gly Thr Ile
50 55 60
Asp Asp Val Asp Ile Asp Leu His Ile Asn Ile Ser Phe Leu Asp Glu
65 70 75 80
Glu Val Ser Thr Ala Trp Lys Val Leu Arg Thr Glu Pro Ile Val Leu
85 90 95
Arg Leu Arg Phe Ser Leu Ser Gln Tyr Leu Asp Gly Pro Glu Pro Ser
100 105 110
Ile Glu Val Phe Gln Pro Ser Asn Lys Glu Gly Phe Gly Leu Gly Leu
115 120 125
Gln Leu Lys Lys Ile Leu Gly Met Phe Thr Ser Gln Gln Trp Lys His
130 135 140
Leu Ser Asn Asp Phe Leu Lys Thr Gln Gln Glu Lys Arg His Ser Trp
145 150 155 160
Phe Lys Ala Ser Gly Thr Ile Lys Lys Phe Arg Ala Gly Leu Ser Ile
165 170 175
Phe Ser Pro Ile Pro Lys Ser Pro Ser Phe Pro Ile Ile Gln Asp Ser
180 185 190
Met Leu Lys Gly Lys Leu Gly Val Pro Glu Leu Arg Val Gly Arg Leu
195 200 205
Met Asn Arg Ser Ile Ser Cys Thr Met Asn Asn Pro Lys Val Glu Val
210 215 220
Phe Gly Tyr Pro Pro Ser Pro Gln Val Ser Gly His Cys Lys Asn Ile
225 230 235 240
Pro Thr Leu Glu Tyr Gly Phe Leu Val Gln Ile Met Lys Tyr Ala Glu
245 250 255
Gln Arg Ile Pro Thr Leu Asn Glu Tyr Cys Val Val Cys Asp Glu Gln
260 265 270
His Val Phe Gln Asn Gly Ser Met Leu Lys Pro Ala Val Cys Thr Arg
275 280 285
Glu Leu Cys Val Phe Ser Phe Tyr Thr Leu Gly Val Met Ser Gly Ala
290 295 300
Ala Glu Glu Val Ala Thr Gly Ala Glu Val Val Asp Leu Leu Val Ala

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Met Cys Arg Ala Ala Leu Glu Ser Pro Arg Lys Ser Ile Ile Phe Glu
                325                 330                 335
Pro Tyr Pro Ser Val Val Asp Pro Thr Asp Pro Lys Thr Leu Ala Phe
            340                 345                 350
Asn Pro Lys Lys Lys Asn Tyr Glu Arg Leu Gln Lys Ala Leu Asp Ser
        355                 360                 365
Val Met Ser Ile Arg Glu Met Thr Gln Gly Ser Tyr Leu Glu Ile Lys
    370                 375                 380
Lys Gln Met Asp Lys Leu Asp Pro Leu Ala His Pro Leu Leu Gln Trp
385                 390                 395                 400
Ile Ile Ser Ser Asn Arg Ser His Ile Val Lys Leu Pro Leu Ser Arg
                405                 410                 415
Gln Leu Lys Phe Met His Thr Ser His Gln Phe Leu Leu Leu Ser Ser
            420                 425                 430
Pro Pro Ala Lys Glu Ala Arg Phe Arg Thr Ala Lys Lys Leu Tyr Gly
        435                 440                 445
Ser Thr Phe Ala Phe His Gly Ser His Ile Glu Asn Trp His Ser Ile
    450                 455                 460
Leu Arg Asn Gly Leu Val Asn Ala Ser Tyr Thr Lys Leu Gln Glu Trp
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<212> DNA
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35 40 45
Leu Thr Ser Glu Val His Met Arg Asp Pro Asn Asn Gln Leu His Val
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Ile Lys Asn Leu Lys Ile Ala Val Ser Asn Ile Val Thr Gln Pro Pro
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Gln Pro Gly Ala Ile Arg Lys Leu Leu Asn Asp Val Val Ser Gly Ser
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Gln Pro Ala Glu Gly Leu Val Ala Asn Val Ile Thr Ala Gly Asp Tyr
100 105 110
Asp Leu Asn Ile Ser Ala Thr Thr Pro Trp Phe Glu Ser Tyr Arg Glu
115 120 125
Thr Phe Leu Gln Ser Met Pro Ala Ser Asp His Glu Phe Leu Asn His
130 135 140
Tyr Leu Ala Cys Met Leu Val Ala Ser Ser Ser Glu Ala Glu Pro Val
145 150 155 160
Glu Gln Phe Ser Lys Leu Ser Gln Glu Gln His Arg Ile Gln His Asn
165 170 175
Ser Asp Tyr Ser Tyr Pro Lys Trp Phe Ile Pro Asn Thr Leu Lys Tyr
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Tyr Val Leu Leu His Asp Val Ser Ala Gly Asp Glu Gln Arg Ala Glu
195 200 205
Ser Ile Tyr Glu Glu Met Lys Gln Lys Tyr Gly Thr Gln Gly Cys Tyr

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Ile Pro Asp Pro Trp Ser Gln Tyr Leu Gln Lys Asn Ser Ile Gln Asn
                245                 250                 255
Gln Glu Ser Tyr Glu Asp Gly Pro Cys Thr Ile Thr Ser Asn Lys Asn
            260                 265                 270
Ser Asp Asn Asn Leu Leu Ser Leu Asp Gly Leu Asp Asn Glu Val Lys
        275                 280                 285
Asp Gly Leu Pro Asn Asn Phe Arg Ala His Pro Leu Gln Leu Glu Gln
    290                 295                 300
Ser Ser Asp Pro Ser Asn Ser Ile Asp Gly Pro Asp His Leu Arg Ser
305                 310                 315                 320
Ala Ser Ser Leu His Glu Thr Lys Lys Gly Asn Thr Gly Ile Ile His
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Gly Ala Cys Leu Thr Leu Thr Asp His Asp Arg Ile Arg Gln Phe Ile
            340                 345                 350
Gln Lys Phe Thr Phe Arg Gly Leu Leu Pro His Ile Glu Lys Thr Ile
        355                 360                 365
Arg Gln Leu Asn Asp Gln Leu Ile Ser Arg Lys Gly Leu Ser Arg Ser
    370                 375                 380
Leu Phe Ser Ala Thr Lys Lys Trp Phe Ser Gly Ser Lys Val Pro Glu
385                 390                 395                 400
Lys Ser Ile Asn Asp Leu Lys Asn Thr Ser Gly Leu Leu Tyr Pro Pro
                405                 410                 415
Glu Ala Pro Glu Leu Gln Ile Arg Lys Met Ala Asp Leu Cys Phe Leu
            420                 425                 430
Val Gln His Tyr Asp Leu Ala Tyr Ser Cys Tyr His Thr Ala Lys Lys
        435                 440                 445
Asp Phe Leu Asn Asp Gln Ala Met Leu Tyr Ala Ala Gly Ala Leu Glu
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Pro Ala His Tyr Met Asp Thr Ala Ile Gln Thr Tyr Arg Asp Ile Cys
                485                 490                 495
Lys Asn Met Val Leu Ala Glu Arg Cys Val Leu Leu Ser Ala Glu Leu
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Leu Lys Ser Gln Ser Lys Tyr Ser Glu Ala Ala Ala Leu Leu Ile Arg
        515                 520                 525
Leu Thr Ser Glu Asp Ser Asp Leu Arg Ser Ala Leu Leu Leu Glu Gln
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Ala Ala His Cys Phe Ile Asn Met Lys Ser Pro Met Val Arg Lys Tyr
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Ala Phe His Met Ile Leu Ala Gly His Arg Phe Ser Lys Ala Gly Gln
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Lys Lys His Ala Leu Arg Cys Tyr Cys Gln Ala Met Gln Val Tyr Lys
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Gly Lys Gly Trp Ser Leu Ala Glu Asp His Ile Asn Phe Thr Ile Gly
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Arg Gln Ser Tyr Thr Leu Arg Gln Leu Asp Asn Ala Val Ser Ala Phe
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Ala Phe Leu Arg Glu Tyr Leu Tyr Val Tyr Lys Asn Val Ser Gln Leu
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Glu Lys Gln Ala Ala Thr His Val Ser Leu Asp Gln Glu Tyr Asp Ser
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705                 710                 715                 720
Val Asn Lys Gly Val Ile Pro Ser Asn Phe His Pro Thr Gln Tyr Cys
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Leu Asn Ser Tyr Ser Asp Asn Ser Arg Phe Pro Leu Ala Val Val Glu
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Glu Pro Ile Thr Val Glu Val Ala Phe Arg Asn Pro Leu Lys Val Leu
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Pro Glu Met Ile Gly Ala Glu Val Ile Ser Glu Phe Leu Ile Asn Gly
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Gln Gly Pro Arg Leu Asn Asn Thr Lys Glu Glu Lys Thr Ser Val Lys
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Tyr Gly Pro Asp Arg Arg Leu Asp Pro Ile Ile Thr Glu Glu Met Pro
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Glu Ile Arg Lys Ala Tyr Val Glu Phe Val Asn Val Ser Lys Cys Pro
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Leu Thr Gly Leu Lys Val Val Ser Lys Arg Pro Glu Phe Phe Thr Phe
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Gly Gly Asn Thr Ala Val Leu Thr Pro Leu Ser Pro Ser Ala Ser Glu
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Thr Ala Leu Ile Ser Ser Ala Ser Ser Val Asp Phe Gly Ile Gly Thr
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Gly Ser Gln Pro Glu Val Ile Pro Val Pro Leu Pro Asp Thr Val Leu
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Glu Glu Gly Val His Glu Ile Asn Phe Leu Phe Tyr Tyr Glu Ser Val
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His Ile Val Gln Val Ser Ser Ser Ser Lys His Trp Lys Leu Gln Lys
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Val Glu Asp Ser Lys Gln Leu Ile Leu Glu Gly Gln His His Val Ile
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Val Ser Ser Arg Pro Ser Val Glu Gln Leu Ser Ser Leu Ile Lys Thr
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Ser Leu His Tyr Pro Glu Ser Phe Asn His Pro Phe His Gln Lys Ser
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Asp Val Asp Val Ile Val Asp Leu Arg His Lys Thr Thr Ser Pro Glu
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Ala Leu Glu Ile His Gly Ser Phe Thr Trp Leu Gly Gln Thr Gln Tyr
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Lys Leu Gln Leu Lys Ser Gln Glu Ile His Ser Leu Gln Leu Lys Ala
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Cys Phe Val His Thr Gly Val Tyr Asn Leu Gly Thr Pro Arg Val Phe
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Ala Lys Leu Ser Asp Gln Val Thr Val Phe Glu Thr Ser Gln Gln Asn
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Leu Glu Lys Arg Gln Glu Gly Arg Ser Ser Thr Gln Thr Leu Glu Asp
50 55 60
Ser Trp Arg Tyr Glu Glu Thr Ser Glu Asn Glu Ala Val Ala Glu Glu
65 70 75 80
Glu Glu Glu Glu Val Glu Glu Glu Gly Glu Glu Asp Val Phe Thr Glu
85 90 95
Lys Ala Ser Pro Asp Met Asp Gly Tyr Pro Ala Leu Lys Val Asp Lys
100 105 110
Glu Thr Asn Thr Glu Thr Pro Ala Pro Ser Pro Thr Val Val Arg Pro
115 120 125
Lys Asp Arg Arg Val Gly Thr Pro Ser Gln Gly Pro Phe Leu Arg Gly
130 135 140
Ser Thr Ile Ile Arg Ser Lys Thr Phe Ser Pro Gly Pro Gln Ser Gln
145 150 155 160
Tyr Val Cys Arg Leu Asn Arg Ser Asp Ser Asp Ser Ser Thr Leu Ser
165 170 175
Lys Lys Pro Pro Phe Val Arg Asn Ser Leu Glu Arg Arg Ser Val Arg
180 185 190
Met Lys Arg Pro Ser Pro Pro Pro Gln Pro Ser Ser Val Lys Ser Leu
195 200 205
Arg Ser Glu Arg Leu Ile Arg Thr Ser Leu Asp Leu Glu Leu Asp Leu
210 215 220
Gln Ala Thr Arg Thr Trp His Ser Gln Leu Thr Gln Glu Ile Ser Val
225 230 235 240
Leu Lys Glu Leu Lys Glu Gln Leu Glu Gln Ala Lys Ser His Gly Glu
245 250 255
Lys Glu Leu Pro Gln Trp Leu Arg Glu Asp Glu Arg Phe Arg Leu Leu
260 265 270
Leu Arg Met Leu Glu Lys Arg Gln Met Asp Arg Ala Glu His Lys Gly
275 280 285
Glu Leu Gln Thr Asp Lys Met Met Arg Ala Ala Ala Lys Asp Val His
290 295 300
Arg Leu Arg Gly Gln Ser Cys Lys Glu Pro Pro Glu Val Gln Ser Phe
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35 40 45
Met Glu Glu Val Leu Leu Leu Gly Leu Lys Asp Lys Glu Gly Tyr Thr
50 55 60
Ser Phe Trp Asn Asp Cys Ile Ser Ser Gly Leu Arg Gly Gly Ile Leu
65 70 75 80
Ile Glu Leu Ala Met Arg Gly Arg Ile Tyr Leu Glu Pro Pro Thr Met
85 90 95
Arg Lys Lys Arg Leu Leu Asp Arg Lys Val Leu Leu Lys Ser Asp Ser
100 105 110
Pro Thr Gly Asp Val Leu Leu Asp Glu Thr Leu Lys His Ile Lys Ala
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1278

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<211> 426
<212> PRT
<213> Homo sapiens

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Leu Thr Gln Glu Arg Asp Tyr Leu Gln Ala Gln His Pro Pro Ser Pro
35 40 45
Ile Lys Ser Ser Ser Ala Asp Ser Thr Pro Ser Pro Thr Ser Ser Leu
50 55 60
Ser Ser Glu Asp Lys Gln His Leu Ala Val Glu Leu Ala Asp Thr Lys
65 70 75 80
Ala Arg Leu Arg Arg Val Arg Gln Glu Leu Glu Asp Lys Thr Glu Gln
85 90 95
Leu Val Asp Thr Arg His Glu Val Asp Gln Leu Val Leu Glu Leu Gln
100 105 110
Lys Val Lys Gln Glu Asn Ile Gln Leu Ala Ala Asp Ala Arg Ser Ala
115 120 125
Arg Ala Tyr Arg Asp Glu Leu Asp Ser Leu Arg Glu Lys Ala Asn Arg
130 135 140
Val Glu Arg Leu Glu Leu Glu Leu Thr Arg Cys Lys Glu Lys Leu His
145 150 155 160
Asp Val Asp Phe Tyr Lys Ala Arg Met Glu Glu Leu Arg Glu Asp Asn
165 170 175
Ile Ile Leu Ile Glu Thr Lys Ala Met Leu Glu Glu Gln Leu Thr Ala
180 185 190
Ala Arg Ala Arg Gly Asp Lys Val His Glu Leu Glu Lys Glu Asn Leu
195 200 205
Gln Leu Lys Ser Lys Leu His Asp Leu Glu Leu Asp Arg Asp Thr Asp
210 215 220
Lys Lys Arg Ile Glu Glu Leu Leu Glu Glu Asn Met Val Leu Glu Ile
225 230 235 240
Ala Gln Lys Gln Ser Met Asn Glu Ser Ala His Leu Gly Trp Glu Leu
245 250 255
Glu Gln Leu Ser Lys Asn Ala Asp Leu Ser Asp Ala Ser Arg Lys Ser
260 265 270
Phe Val Phe Glu Leu Asn Glu Cys Ala Ser Ser Arg Ile Leu Lys Leu
275 280 285
Glu Lys Glu Asn Gln Ser Leu Gln Ser Thr Ile Gln Gly Leu Arg Asp
290 295 300
Ala Ser Leu Val Leu Glu Glu Ser Gly Leu Lys Cys Gly Glu Leu Glu
305 310 315 320
Lys Glu Asn His Gln Leu Ser Lys Lys Ile Glu Lys Leu Gln Thr Gln
325 330 335
Leu Glu Arg Glu Lys Gln Ser Asn Gln Asp Leu Glu Thr Leu Ser Glu
340 345 350
Glu Leu Ile Arg Glu Lys Glu Gln Leu Gln Ser Asp Met Glu Thr Leu
355 360 365
Lys Ala Asp Lys Ala Arg Gln Ile Lys Asp Leu Glu Gln Glu Lys Asp

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    370                 375                 380
His Leu Asn Arg Ala Met Trp Ser Leu Arg Glu Arg Ser Gln Val Ser
385                 390                 395                 400
Ser Glu Ala Arg Met Lys Asp Val Glu Lys Glu Asn Lys Ala Leu His
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Gln Thr Val Thr Glu Ala Asn Gly Lys Leu
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<211> 413
<212> DNA
<213> Homo sapiens

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413

<210> 3922
<211> 126
<212> PRT
<213> Homo sapiens

<400> 3922
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Leu Leu Ala Ser Leu Val Thr Phe Ile His Ala Gly Pro Cys Phe Leu
        35                  40                  45
Asp Ser Val Gly Pro Ile Pro Ala Pro Arg Gly Asp Gly Cys Cys Arg
    50                  55                  60
Asp Val Gln Ala Val Glu Gly Ser Arg Glu Trp Ala Trp Arg Ser Ala
65                  70                  75                  80
Ser Leu Ala Pro Leu Leu Asp Ala Phe Leu Gln Pro Leu Glu Leu Arg
                85                  90                  95
Gln Cys Ser Val Arg Met Ile Ile Gly Phe Pro Pro Gln Phe Leu Ala
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His Ser Phe Val Ala Leu Val Thr Ala Phe Cys Asp Asn Ile
        115                 120                 125
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<210> 3923
<211> 820

<212> DNA
<213> Homo sapiens

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120
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240
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480
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720
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820

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<211> 250
<212> PRT
<213> Homo sapiens

<400> 3924
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            20   25   30
Ser Glu Tyr Thr Gly Pro Thr Ser Ala Asp Leu Asp His Phe Pro Ser
        35   40   45
Val Ser Gln Thr Lys Ala Glu Gln Asp Ser Asp Asn Lys Ser Ser Thr
    50   55   60
Glu Ile Pro Leu Glu Thr Cys Cys Ser Ser Glu Leu Lys Gly Gly Gly
65   70   75   80
Ser Gly Thr Ser Leu Glu Arg Glu Gln Phe Glu Gly Leu Gly Ser Thr
                85   90   95
Pro Asp Ala Lys Leu Asp Lys Thr Cys Ile Ser Arg Ala Met Lys Ile
            100   105   110
Thr Thr Val Asn Ser Val Leu Pro Gln Asn Ser Val Leu Gly Gly Val

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        115                 120                 125
Leu Lys Thr Lys Gln Gln Leu Lys Thr Leu Asn His Phe Asp Leu Thr
    130                 135                 140
Asn Gly Val Leu Val Glu Ser Leu Ser Glu Glu Pro Leu Pro Ser Leu
145                 150                 155                 160
Arg Arg Gly Arg Lys Arg His Cys Lys Thr Lys His Leu Glu Gln Asn
                165                 170                 175
Gly Ser Leu Lys Lys Leu Arg Gln Thr Ser Gly Glu Val Gly Leu Ala
            180                 185                 190
Pro Thr Asp Pro Val Leu Arg Glu Met Glu Gln Lys Leu Gln Gln Glu
        195                 200                 205
Glu Glu Asp Arg Gln Leu Ala Leu Gln Leu Gln Arg Met Phe Asp Asn
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Glu Arg Arg Thr Val Ser Arg Arg Lys Gly Ser Val Asp Gln Tyr Leu
225                 230                 235                 240
Leu Arg Ser Ser Asn Met Ala Gly Gly Arg
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<210> 3925
<211> 3296
<212> DNA
<213> Homo sapiens

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120
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300
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420
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3296

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<211> 683
<212> PRT
<213> Homo sapiens

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Thr Arg Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser
35 40 45
Val Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn
50 55 60
Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu Val
65 70 75 80
Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu Gly Tyr
85 90 95
Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys Gln Val Ser
100 105 110
Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His Lys Gly Tyr Lys
115 120 125
Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala Gln Asn Arg Pro Glu
130 135 140
Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Ala Val
145 150 155 160
Pro Leu Tyr Asp Thr Leu Gly Pro Glu Ala Ile Val His Ile Val Asn

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                165                 170                 175
Lys Ala Asp Ile Ala Met Val Ile Cys Asp Thr Pro Gln Lys Ala Leu
            180                 185                 190
Val Leu Ile Gly Asn Val Glu Lys Gly Phe Thr Pro Ser Leu Lys Val
        195                 200                 205
Ile Ile Leu Met Asp Pro Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu
    210                 215                 220
Lys Ser Gly Ile Glu Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Asp
225                 230                 235                 240
Lys Glu His Phe Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser
                245                 250                 255
Val Ile Cys Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met
            260                 265                 270
Ile Thr His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys
        275                 280                 285
Val Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr
    290                 295                 300
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val Tyr
305                 310                 315                 320
Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu
                325                 330                 335
Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro Ala Val Pro
            340                 345                 350
Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn Glu Ala Lys Thr
        355                 360                 365
Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val Ser Ser Lys Phe Lys
    370                 375                 380
Glu Leu Gln Lys Gly Ile Ile Arg His Asp Ser Phe Trp Asp Lys Leu
385                 390                 395                 400
Ile Phe Ala Lys Ile Gln Asp Ser Leu Gly Gly Arg Val Arg Val Ile
                405                 410                 415
Val Thr Gly Ala Ala Pro Ile Ser Thr Pro Val Leu Thr Phe Phe Arg
            420                 425                 430
Ala Ala Met Gly Cys Trp Val Phe Glu Ala Tyr Gly Gln Thr Glu Cys
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Thr Gly Gly Cys Thr Phe Thr Leu Pro Gly Asp Trp Thr Ser Gly His
    450                 455                 460
Val Gly Val Pro Leu Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala
465                 470                 475                 480
Asp Met Asn Tyr Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys
                485                 490                 495
Gly Thr Asn Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln
            500                 505                 510
Glu Ala Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg
        515                 520                 525
Trp Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile
    530                 535                 540
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu Asn
545                 550                 555                 560
Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His Gly Glu
                565                 570                 575
Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp Thr Asp Val
            580                 585                 590
Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly Ser Phe Glu Glu
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595 600 605
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Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr Phe Glu Gln Val Lys Ala
625 630 635 640
Ile Phe Leu His Pro Glu Pro Phe Ser Ile Glu Asn Gly Leu Leu Thr
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Pro Thr Leu Lys Ala Lys Arg Gly Glu Leu Ser Lys Tyr Phe Arg Thr
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Gln Ile Asp Ser Leu Tyr Glu His Ile Gln Asp
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<210> 3927
<211> 3197
<212> DNA
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<212> PRT
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35 40 45
Pro Met Pro Arg Leu Pro Ser Leu Trp Pro Leu Ser Leu Pro Leu Arg
50 55 60
Ser Leu Ser Ser Pro His Arg Val Gln Gly Leu Gly Pro Pro Arg Arg
65 70 75 80
Leu Lys Ser Gln Leu Leu Pro Arg Phe Phe Trp Arg Arg Gln Gln Glu
85 90 95
Pro Leu Ser Ser Phe Pro Gly Arg Asn Glu Gly Gly Ser Glu Met Glu
100 105 110
Ile Leu Gly Val Cys Pro Val Ser Pro Gly Ala Leu Ser Tyr Met Glu
115 120 125
Ser Pro Thr Gly Phe Trp Arg Pro Arg Glu Ala Ser Ser Leu Glu Leu
130 135 140
Ala Lys Gly Ile Ser Lys Arg Arg His Phe Leu Pro Ala Pro Ala Leu
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Cys Pro Asn Pro Arg Ser Ser Glu Ala Phe Pro Gly Ala Val Cys Val
165 170 175
Thr Leu Ala Ile
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<211> 470
<212> DNA
<213> Homo sapiens

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470

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<211> 115
<212> PRT
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20 25 30
Gln Ser Glu Asn Glu Ala Ser Pro Val Lys Arg Pro Arg Leu Leu Glu
35 40 45
Asn Thr Glu Arg Ser Glu Glu Thr Ser Arg Ser Lys Gln Lys Ser Arg
50 55 60
Arg Arg Cys Phe Gln Cys Gln Thr Lys Leu Glu Leu Val Gln Gln Glu
65 70 75 80
Leu Gly Ser Cys Arg Cys Gly Tyr Val Phe Cys Met Leu His Arg Leu
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Pro Glu Gln His Asp Cys Thr Phe Asp His Met Gly Val Ala Gly Arg
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Ser His His
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<212> DNA
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180

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240
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420
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<212> PRT
<213> Homo sapiens

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Cys His Tyr Trp Lys Ser Ser Ser Ile Glu Glu Arg Gly Tyr Trp Gly
35 40 45
Ser Gly Ser Ala Ile Met Ala Pro Ala Pro Phe Arg Ser Gln Ser Thr
50 55 60
Arg Ser Ser Ile Glu Asp Asp Phe Asn Tyr Gly Ser Ser Val Ala Ser
65 70 75 80
Ala Thr Val His Ile Arg Met Ala Phe Leu Arg Lys Val Tyr Ser Ile
85 90 95
Leu Ser Leu Gln Val Leu Leu Thr Thr Val Thr Ser Thr Val Phe Leu
100 105 110
Tyr Phe Glu Ser Val Arg Thr Phe Val His Glu Ser Pro Ala Leu Ile
115 120 125
Leu Leu Phe Ala Leu Gly Ser Leu Gly Leu Ile Phe Ala Leu Thr Leu
130 135 140
Asn Arg His Lys Tyr Pro Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr
145 150 155 160
Leu Leu Glu Ala Leu Thr Val Ala Val Val Val Thr Phe Tyr Asp Val
165 170 175
Tyr Ile Ile Leu Gln Ala Phe Ile Leu Thr Thr Thr Val Phe Phe Gly
180 185 190
Leu Thr Val Tyr Thr Leu Gln Ser Lys Lys Asp Phe Ser Lys Phe Gly
195 200 205
Ala Gly Leu Phe Ala Leu Leu Trp Ile Leu Cys Leu Ser Gly Phe Leu
210 215 220
Lys Phe Phe Phe Tyr Ser Glu Ile Met Glu Leu Val Leu Ala Ala Ala
225 230 235 240
Gly Ala Leu Leu Phe Cys Gly Phe Ile Ile Tyr Asp Thr His Ser Leu
245 250 255
Met His Lys Leu Ser Pro Glu Glu Tyr Val Leu Ala Ala Ile Ser Leu
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<210> 3933
<211> 4082

<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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35 40 45
Ser Ser Ser Asn Lys Ser Pro Ser Ser Ala Trp Ser Ser Ser Ser Trp
50 55 60
His Gly Arg Ile Lys Gly Gly Met Lys Gly Phe Gln Ser Phe Met Val
65 70 75 80
Ser Asp Ser Asn Met Ser Phe Val Glu Phe Val Glu Leu Phe Lys Ser
85 90 95
Phe Ser Val Arg Ser Arg Lys Asp Leu Lys Asp Leu Phe Asp Xaa Leu

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Cys Ser Ala Leu Gln Pro Xaa Leu Ala Pro Ser Gln Pro His Ser Thr
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Pro Thr
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<210> 3935
<211> 1103
<212> DNA
<213> Homo sapiens

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<210> 3936
<211> 265
<212> PRT

<213> Homo sapiens

<400> 3936

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Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr
    50                  55                  60
Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala
65                  70                  75                  80
Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser
                85                  90                  95
Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg
            100                 105                 110
Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly
        115                 120                 125
Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg
    130                 135                 140
Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp
145                 150                 155                 160
Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys
                165                 170                 175
Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Lys
            180                 185                 190
Gln Pro Trp Leu Cys Leu Ala Trp Gly Gly Gly Gln Ala Val Asp Ile
        195                 200                 205
Ala Val Trp Leu Leu Gly Met Val Gly Gly Thr Gly Ile Trp Ala Glu
    210                 215                 220
Gly Gly Gly Asp Ser Leu Ser Arg Glu Gly Gly Trp Gly Gly Arg Ile
225                 230                 235                 240
Gly Gly Phe Pro Arg Thr Gly Gly Arg Leu Pro Gly Ala Ser Tyr Gln
                245                 250                 255
Pro Arg Arg Gln Lys Cys Pro Val Pro
            260                 265
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<210> 3937
<211> 744
<212> DNA
<213> Homo sapiens

<400> 3937

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caaggtccgg cgcccacgga ggcaagtccg gtctcacggt gacctcccgc cggcgccgcc
120
ttcgccgcca accatccagt tcttcctcca ggccacgttc tccttgcgga aaatgctgat
180
ctcagtcgca atgctgggcg caggggctgg cgtgggctac gcgctcctcg ttatcgtgac
240
cccgggagag cggcggaagc aggaaatgct aaaggagatg ccactgcagg acccaaggag
300
```

cagggaggag gcggccagga cccagcagct attgctggcc actctgcagg aggcagcgac
360
cacgcaggag aacgtggcct gngaggaaga actggatggt tggcggcgaa ggcggcgcca
420
gcgggaggtc accgtgagac cggacttgcc tccgtgggcg ccggaccttg gcttgggcgc
480
aggaatccga ggcagccttt ctccttcgtg ggcccagcgg agagtccgga ccgagatacc
540
atgccaggac tctccggggt cctgtgagct gccgtcgggt gagcacgttt cccccaaacc
600
ctggactgac tgctttaagg tccgcaaggc gggccagggc cgagacgcga gtcggatgtg
660
gtgaactgaa agaaccaata aaatcatgtt cctccaccca gaatgagccc tgcagtcgac
720
acctaccaat gcttagagac gcgt
744

<210> 3938
<211> 154
<212> PRT
<213> Homo sapiens

<400> 3938
Pro Pro Ala Gly Ala Ala Phe Ala Ala Asn His Pro Val Leu Pro Pro
1 5 10 15
Gly His Val Leu Leu Ala Glu Asn Ala Asp Leu Ser Arg Asn Ala Gly
20 25 30
Arg Arg Gly Trp Arg Gly Leu Arg Ala Pro Arg Tyr Arg Asp Pro Gly
35 40 45
Arg Ala Ala Glu Ala Gly Asn Ala Lys Gly Asp Ala Thr Ala Gly Pro
50 55 60
Lys Glu Gln Gly Gly Gly Gly Gln Asp Pro Ala Ala Ile Ala Gly His
65 70 75 80
Ser Ala Gly Gly Ser Asp His Ala Gly Glu Arg Gly Leu Xaa Gly Arg
85 90 95
Thr Gly Trp Leu Ala Ala Lys Ala Ala Pro Ala Gly Gly His Arg Glu
100 105 110
Thr Gly Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg Arg Asn
115 120 125
Pro Arg Gln Pro Phe Ser Phe Val Gly Pro Ala Glu Ser Pro Asp Arg
130 135 140
Asp Thr Met Pro Gly Leu Ser Gly Val Leu
145 150

<210> 3939
<211> 490
<212> DNA
<213> Homo sapiens

<400> 3939
nnttgcaacg tgagagggcg ctcaagagat tcaggaaagg aaagacagac agacagacag
60
acgggaaagg tgagatggaa acacacagaa gatgagagag acagacagtg ggaggcagag
120

ctgaagactg tgaaagaaag ggcaacagac agcgagggag gaagagacag gctggagccc
180
ttcttgtaaa cgcaggtgac ctggtgcacg gctgatggtg gttaaatcgg aactccaggt
240
gataaccact gtctcctgga gcctgtgggt cggcctcctg ctctgctgca agggccctgc
300
tggctggcgg ggggcggtcc cggagcctcg acccttcacg ttttcactcc gtttctgttc
360
taaggaaccc acggtgcgga ggtgtcagga ggaaggtagc agcgtcttga ctttccaccg
420
tctgaccctc cctggagtgc tggggcctgt tcggggccgg ccaggttcag gctccacaga
480
cctcacgcgt
490

<210> 3940
<211> 62
<212> PRT
<213> Homo sapiens

<400> 3940
Xaa Cys Asn Val Arg Gly Arg Ser Arg Asp Ser Gly Lys Glu Arg Gln
 1   5   10   15
Thr Asp Arg Gln Thr Gly Lys Val Arg Trp Lys His Thr Glu Asp Glu
            20   25   30
Arg Asp Arg Gln Trp Glu Ala Glu Leu Lys Thr Val Lys Glu Arg Ala
        35   40   45
Thr Asp Ser Glu Gly Gly Arg Asp Arg Leu Glu Pro Phe Leu
    50   55   60

<210> 3941
<211> 2077
<212> DNA
<213> Homo sapiens

<400> 3941
nnttttttttt ttttttttca agatggcagc tttaatcaca ttggccaagg gcctaggttc
60
cctctgttca ggcccactta gccacacacc caccctggcc atatccagaa cacttctacc
120
aggtgggccc tgccctgtgg ccactgatgt gggaacctga ggtcacatca gtctgtggac
180
tcctgggtta ggtgaccctt ctgccttgag gtctgctgga cacctgggca tgggatccag
240
tagtcctgag ctcactcttt tggccatctc cagctgctcc taggggacgt ggctcaggcc
300
cgctcctggg gcaggggggtt ggcggtggca tgaggtgggt tggggaggag gacgtgtctc
360
cacattgcag ctggcttcct cctgggctga acctccttgt gctttgagac tgacaggaag
420
agcagagttg cttcaggtag aggctcggcc caggcccttg gggcaggata acagcagaga
480
actcaggtgc ctcctggcac agacaggagg acagatggca caggtgagca tccacacact
540

ccattgccac aggggtatg gcatggccca tgacccatca aagcttccag gtcgggatac
600
aggagagggc ctcagaagag ggggaccaag ccctaggccc catacttccc agaaggagcc
660
ccaggcctgc aggggcatct gaaaggatgg agtcctggcc cagctgggcc tcaggggaca
720
gggagtcccc ctcaagagag gctgcggctg acaaggggct ggagcccaca aggaggctgt
780
ggagcccgct cccagagcac tccgagttca gacacacttc caccagctct cctaggctcc
840
ccagcttctg tgtcaggtac aggtgggaca gacatgtctt cagctaacgc ccactccgct
900
ctatgagggt cttggtgtgg ctgccacccc ctcgggggcc cacaggggtg gcggtgctgt
960
tggcatatgt gtcataactg ttgtctgaac atacggagag cacatcggag acctctacac
1020
catcgctgat ctctgagaaa ataagcttct ccttcatgat gctgacgtcc cggctggtcc
1080
ggcgcaccgc agcactcagc atgatctgct cagggttgta gctccgtatg ccacccaggc
1140
gccacctgat caagtgatag ttctggagca cgaagatgcc cacgatgagg gtgaaggaga
1200
ccaggtcggc agtgacccac atgagacagt actcgtccgg gggcatgatc cagaggggg
1260
aaggcacctg ggacagggtg tgggagttgt cagaggtgac ggatgggacc cccgcacacc
1320
acagcaggga gaagagccac ggtgcgttga ctgtgtagag gttcacactc aggttccagg
1380
acgcgtagtc cctgagctcc tggcgggaca cctgagtgta gcgcaggttc agccgctgga
1440
tgtggcctct ccgcaggctg gcgactgcct ccttggagcc tgatgtctgt tggaagccgg
1500
gagccacctt ccgcaccagg ggcctctgcc tgctaggcag ccacatgacc tggtgctggg
1560
ggaagccgga gtgcagcacg gcctccagag tcacgttgat aaaactgctg ctcaacctgc
1620
gtgacccgcc ccgggagcac ccctaccgca gcagttttat caacgtgact ctggaggccg
1680
tgctgcactc cggcttcccc cagctccagg tgctctagga ggagtaggta ctcttacgca
1740
tcgtgcagaa gagaagtctg aggctgcctc tcttctgcct gcaggtcatg tggctgccta
1800
gcaggcagag gcccctggtg cggaaggtgg ctcccggctt ccaacagaca tcaggctcca
1860
aggaggcagt cgccagcctg cggagaggcc acatccagcg gctgaacctg cgctacactc
1920
aggtgtcccg ccagcgtcca ggtgcctgcc ctgccctggg ctcctccagg agagggtggg
1980
actgagtctc taacagtcct gccaccacca ccccccaaca cacacacaca cacacacaca
2040
ctgtcgggca gagggatggg cacacagagg tatcagg
2077

<210> 3942

<211> 89
<212> PRT
<213> Homo sapiens

<400> 3942
Ala Pro Tyr Phe Pro Glu Gly Ala Pro Gly Leu Gln Gly His Leu Lys
1 5 10 15
Gly Trp Ser Pro Gly Pro Ala Gly Pro Gln Gly Thr Gly Ser Pro Pro
20 25 30
Gln Glu Arg Leu Arg Leu Thr Arg Gly Trp Ser Pro Gln Gly Gly Cys
35 40 45
Gly Ala Arg Ser Gln Ser Thr Pro Ser Ser Asp Thr Leu Pro Pro Ala
50 55 60
Leu Leu Gly Ser Pro Ala Ser Val Ser Gly Thr Gly Gly Thr Asp Met
65 70 75 80
Ser Ser Ala Asn Ala His Ser Ala Leu
85

<210> 3943
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 3943
tctagacaaa aatccgcttc agaaataggc tgcgggcggc cggctaggag gcttggcccc
60
accccgggac ccccgccgtc cccgggccgg ccggcggtgg gcacgatgag ccaggtgctg
120
gggaagccgc agccgcagga cgaggacgac gcggaggagg aggaggagga ggatgagctg
180
gtggggctag cggactacgg agacgggccc gactcctccg acgccgatcc ggacagcggc
240
acagaggagg gagttctgga cttcagtgac cccttcagca ctgaagtgaa gccgagaatc
300
ctgctcatgg gcctgaggag aagcggcaag tcgtctattc agaaagttgt ctttcacaaa
360
atgtctccca acgaaactct gttcttggag agcactaata agatatgccg ggaagatgtt
420
tccaacagct cctttgtcaa ttttcagatt tgggacttcc caggacagat tgacttttt
480
gaccctacat ttgactatga gatgatcttc cggggaacag gagcattgat atttgtcatt
540
gacgcacagg atgactacat ggaggcttta acaagacttc acattactgt ttctaaagcc
600
tacaaagtta acccagacat gaattttgag gtttttattc ataaagttga tggtctgtct
660
gatgatcaca aaatagaaac acagagggac attcatcaaa gggccaatga tgaccttgca
720
gatgctggat tagaaaaaat tcacctcagc ttttatctga caagcatata tgatcattca
780
atatttgaag cttttagcaa agttgttcag aaactgattc cacaactccc aactctggag
840
aatttgctga acatctttat ctcaaattct ggaattgaaa aggcatttct atttgatgtg
900

gtcagtaaaa tttatattgc aactgatagt actccggtgg atatgcaaac ctatgagctc
960
tgctgtgata tgatagatgt ggttattgac atctcttgta tttatggtct caaagaagat
1020
ggagcaggaa ccccctatga caaggaatcc acagccatca taaagcttaa taatacaacc
1080
gtgctttatt taaaagaggt gacaaagttc ctggctctcg tttgctttgt cagagaggaa
1140
agctttgaaa gaaaagggct aattgactat aattttcatt gcttccggaa ggccattcat
1200
gaagtttttg aggtgagaat gaaagtagta aaatctcgaa aggttcagaa tcggctgcag
1260
aagaaaaaga gagccacccc taatgggacc cctagagtgc tgctgtaggt gaggtttcag
1320
gaatgtcttt tgaaatcaga ccttatccat gaggctgctg cgccatgttg cactaaagga
1380
agaggaagaa ggagattggg acacatacca ttgatttgtt gttaaaaaaa aaaaattcct
1440
gcaacctct tgatcttctc ttttataaat aaagtaagca ctttgaagca aaaaaaaaaa
1500
aaaaaaaaaa aaaaaaaaaa aaaa
1524

<210> 3944
<211> 435
<212> PRT
<213> Homo sapiens

<400> 3944
Ser Arg Gln Lys Ser Ala Ser Glu Ile Gly Cys Gly Arg Pro Ala Arg
1 5 10 15
Arg Leu Gly Pro Thr Pro Gly Pro Pro Pro Ser Pro Gly Arg Pro Ala
20 25 30
Val Gly Thr Met Ser Gln Val Leu Gly Lys Pro Gln Pro Gln Asp Glu
35 40 45
Asp Asp Ala Glu Glu Glu Glu Glu Glu Asp Glu Leu Val Gly Leu Ala
50 55 60
Asp Tyr Gly Asp Gly Pro Asp Ser Ser Asp Ala Asp Pro Asp Ser Gly
65 70 75 80
Thr Glu Glu Gly Val Leu Asp Phe Ser Asp Pro Phe Ser Thr Glu Val
85 90 95
Lys Pro Arg Ile Leu Leu Met Gly Leu Arg Arg Ser Gly Lys Ser Ser
100 105 110
Ile Gln Lys Val Val Phe His Lys Met Ser Pro Asn Glu Thr Leu Phe
115 120 125
Leu Glu Ser Thr Asn Lys Ile Cys Arg Glu Asp Val Ser Asn Ser Ser
130 135 140
Phe Val Asn Phe Gln Ile Trp Asp Phe Pro Gly Gln Ile Asp Phe Phe
145 150 155 160
Asp Pro Thr Phe Asp Tyr Glu Met Ile Phe Arg Gly Thr Gly Ala Leu
165 170 175
Ile Phe Val Ile Asp Ala Gln Asp Asp Tyr Met Glu Ala Leu Thr Arg
180 185 190
Leu His Ile Thr Val Ser Lys Ala Tyr Lys Val Asn Pro Asp Met Asn

```
        195                 200                 205
Phe Glu Val Phe Ile His Lys Val Asp Gly Leu Ser Asp Asp His Lys
    210                 215                 220
Ile Glu Thr Gln Arg Asp Ile His Gln Arg Ala Asn Asp Asp Leu Ala
225                 230                 235                 240
Asp Ala Gly Leu Glu Lys Ile His Leu Ser Phe Tyr Leu Thr Ser Ile
                245                 250                 255
Tyr Asp His Ser Ile Phe Glu Ala Phe Ser Lys Val Val Gln Lys Leu
            260                 265                 270
Ile Pro Gln Leu Pro Thr Leu Glu Asn Leu Leu Asn Ile Phe Ile Ser
        275                 280                 285
Asn Ser Gly Ile Glu Lys Ala Phe Leu Phe Asp Val Val Ser Lys Ile
    290                 295                 300
Tyr Ile Ala Thr Asp Ser Thr Pro Val Asp Met Gln Thr Tyr Glu Leu
305                 310                 315                 320
Cys Cys Asp Met Ile Asp Val Val Ile Asp Ile Ser Cys Ile Tyr Gly
                325                 330                 335
Leu Lys Glu Asp Gly Ala Gly Thr Pro Tyr Asp Lys Glu Ser Thr Ala
            340                 345                 350
Ile Ile Lys Leu Asn Asn Thr Thr Val Leu Tyr Leu Lys Glu Val Thr
        355                 360                 365
Lys Phe Leu Ala Leu Val Cys Phe Val Arg Glu Glu Ser Phe Glu Arg
    370                 375                 380
Lys Gly Leu Ile Asp Tyr Asn Phe His Cys Phe Arg Lys Ala Ile His
385                 390                 395                 400
Glu Val Phe Glu Val Arg Met Lys Val Val Lys Ser Arg Lys Val Gln
                405                 410                 415
Asn Arg Leu Gln Lys Lys Lys Arg Ala Thr Pro Asn Gly Thr Pro Arg
            420                 425                 430
Val Leu Leu
        435
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<210> 3945
<211> 696
<212> DNA
<213> Homo sapiens

<400> 3945
cggccggctg taaacctgcc actaggaccc ggtcggtgag atctagcctc ttgacctgag
60
agccgagagt ggatcgctgg gctgggctaa cggcgacgga gagcgcgccc tcgctgactc
120
cgggcgcgcc cagcagtagc accgcccgcg cccgcccctg gacacttgta agtttcgatt
180
tccgatttcc gcggaaccga gtcccgcgcc gcggcagagc cagcacagcc agcgcgccat
240
ggcggacccg gaggtgtgct gcttcatcac caaaatcctg tgcgcccacg ggggccgcat
300
ggccctggac gcgctgctcc aggagatcgc gctgtctgag ccgcagctct gtgaggtgct
360
gcaggtggcc gggcccgacc gctttgtggt gttggagacc ggcggcgagg ccgggatcac
420
ccgatcggtg gtggccacca ctcgagcccg ggtctgccgt cgcaagtact gccagagacc
480

ctgcgataac ctgcatctct gcaaactcaa cttgctgggc cggtgcaact attcgcagtc
540
cgagcggaat ttatgcaaat attctcatga ggttctctca gaagagaact tcaaagtcct
600
gaaaaatcac gaactctctg gactgaacaa agaggaatta gcagtgctcc tcctccaaag
660
tgatcctttt tttatgcccg agccctatgc agtctc
696

<210> 3946
<211> 165
<212> PRT
<213> Homo sapiens

<400> 3946
Met Gln Val Ile Ala Gly Ser Leu Ala Val Leu Ala Thr Ala Asp Pro
1 5 10 15
Gly Ser Ser Gly Gly His His Arg Ser Gly Asp Pro Gly Leu Ala Ala
20 25 30
Gly Leu Gln His His Lys Ala Val Gly Pro Gly His Leu Gln His Leu
35 40 45
Thr Glu Leu Arg Leu Arg Gln Arg Asp Leu Leu Glu Gln Arg Val Gln
50 55 60
Gly His Ala Ala Pro Val Gly Ala Gln Asp Phe Gly Asp Glu Ala Ala
65 70 75 80
His Leu Arg Val Arg His Gly Ala Leu Ala Val Leu Ala Leu Pro Arg
85 90 95
Arg Gly Thr Arg Phe Arg Gly Asn Arg Lys Ser Lys Leu Thr Ser Val
100 105 110
Gln Gly Arg Ala Arg Ala Val Leu Leu Leu Gly Ala Pro Gly Val Ser
115 120 125
Glu Gly Ala Leu Ser Val Ala Val Ser Pro Ala Gln Arg Ser Thr Leu
130 135 140
Gly Ser Gln Val Lys Arg Leu Asp Leu Thr Asp Arg Val Leu Val Ala
145 150 155 160
Gly Leu Gln Pro Ala
165

<210> 3947
<211> 400
<212> DNA
<213> Homo sapiens

<400> 3947
nnggagaagc aggccattct cttggcgctg atcgaggagc ggggccgctt ctgcaccttc
60
atcaccttcc tgcagcctgt ggtgaatgga gagctgacca tgctgggaga gatcacccac
120
ctgcagggca tcatcgacga cttggtggtg ctgacagcag aaccccacaa actgcctccc
180
gccagcgagc aggtaatcaa agacctaaag ggctcggact acagctggtc ctaccagacc
240
ccaccctcat cacccagcag ctccagctcc cggaagtcca gcatgtgcag tgcccccagc
300

agcagtagca gtgccaaggg tggcggaagc cccatggcct gggggtgccc aaacatactc
360
acccagttcc acctgtcgct accgcagcct ggcgcagcca
400

<210> 3948
<211> 133
<212> PRT
<213> Homo sapiens

<400> 3948
Xaa Glu Lys Gln Ala Ile Leu Leu Ala Leu Ile Glu Glu Arg Gly Arg
 1   5   10   15
Phe Cys Thr Phe Ile Thr Phe Leu Gln Pro Val Val Asn Gly Glu Leu
            20   25   30
Thr Met Leu Gly Glu Ile Thr His Leu Gln Gly Ile Ile Asp Asp Leu
        35   40   45
Val Val Leu Thr Ala Glu Pro His Lys Leu Pro Pro Ala Ser Glu Gln
    50   55   60
Val Ile Lys Asp Leu Lys Gly Ser Asp Tyr Ser Trp Ser Tyr Gln Thr
65   70   75   80
Pro Pro Ser Ser Pro Ser Ser Ser Ser Ser Arg Lys Ser Ser Met Cys
                85   90   95
Ser Ala Pro Ser Ser Ser Ser Ser Ala Lys Gly Gly Gly Ser Pro Met
            100   105   110
Ala Trp Gly Cys Pro Asn Ile Leu Thr Gln Phe His Leu Ser Leu Pro
        115   120   125
Gln Pro Gly Ala Ala
    130

<210> 3949
<211> 1462
<212> DNA
<213> Homo sapiens

<400> 3949
ctcgagaact ccagccttgg aagaaaggcc acaggctgag tttcttattt ttatggcttt
60
tacccagaga gcaagacaca ggtctgcatt gtgcagcaca gctaaagttc ctttagaaaa
120
ccaccatctt tctggctgca agagtcaggg gtcagaatgg ggggcagcca ccactgctga
180
aaagagttgg gggaggaacc cctgaaagga gagccagaaa tgggggagct ccaaactctt
240
tgtgtcagct ctgtccaaat ctctaactga cttgtgaact aaaaagaaag gtttctacca
300
tcagcagact gtcacccata gacatttaca cagtattttg gtttggagtt cttcctaata
360
gtcacttcac agaaaaatat ataggtgctg ttttgccctg gaagccagac agatcagaat
420
attgggtaag atagctgggt cagctgtcct tggatggatc ccaaacacta tgctcctttc
480
caggcctgag aatcgccgaa cactgtccaa cacaatgtga tcacccaaca tatcacatgc
540

atcactgagc tgcaccaccc ttttcttcct cattgctttc aagagctcat acttatagtg
600
ctccacttct tttgcggtgc tgacaagcac agcaacatcc tttggagaat agcccctatc
660
aaagaagcgc ctgcacgtgt ctgccacaca ggtcattatt tgctccacag tcaagtattt
720
cttaattcgt aaggttccct gaacaccctg ggaccattcg gcttcaggaa atacctcgag
780
gcacccagtg gggatattaa ttggaggatt ttctataatt agttgcattt ctttttgtaa
840
gtactcggct atttcatctg cattgcgaac tattctggtg agctcttctc ttggatattg
900
gtctgagaga ggagggaggc cactgtgacc caagtggctg gtctgaaagt aatccagaaa
960
gatccagaga actcctggac aatccttttc tctctgagtg atgctttttg ccttcccata
1020
ccagtcccca tcttcagtac ggaaattctg agcttcgtca atgacgatgt gttgaatgtg
1080
ttcaaatttt tctcttagga aagtttcccg ggtctctgct cggcagatat ttctatcact
1140
gataaagttc ctcagaggct ggttttcaca aacgtagaga attctgtgtg cctcacagtg
1200
aaacacattc ctgatcttct ccatgatttt catggccatg atgttcttcc ctgagccagg
1260
taagccgtgg acaaacaact ctctgttctt gcggaggctt ctggagaata tctcatactg
1320
ctgggctgtg agcagattta aaacctcaca gccgagctgg tcactcaaga gagacctgaa
1380
gccgagtaag acaatcacga gggactgcag cagggcttcc atgtgctggg tgcctgcaag
1440
gctataggac gcagggtaat cc
1462

<210> 3950
<211> 351
<212> PRT
<213> Homo sapiens

<400> 3950
Met Glu Ala Leu Leu Gln Ser Leu Val Ile Val Leu Leu Gly Phe Arg
1 5 10 15
Ser Leu Leu Ser Asp Gln Leu Gly Cys Glu Val Leu Asn Leu Leu Thr
20 25 30
Ala Gln Gln Tyr Glu Ile Phe Ser Arg Ser Leu Arg Lys Asn Arg Glu
35 40 45
Leu Phe Val His Gly Leu Pro Gly Ser Gly Lys Asn Ile Met Ala Met
50 55 60
Lys Ile Met Glu Lys Ile Arg Asn Val Phe His Cys Glu Ala His Arg
65 70 75 80
Ile Leu Tyr Val Cys Glu Asn Gln Pro Leu Arg Asn Phe Ile Ser Asp
85 90 95
Arg Asn Ile Cys Arg Ala Glu Thr Arg Glu Thr Phe Leu Arg Glu Lys
100 105 110
Phe Glu His Ile Gln His Ile Val Ile Asp Glu Ala Gln Asn Phe Arg

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        115                 120                 125
Thr Glu Asp Gly Asp Trp Tyr Gly Lys Ala Lys Ser Ile Thr Gln Arg
    130                 135                 140
Glu Lys Asp Cys Pro Gly Val Leu Trp Ile Phe Leu Asp Tyr Phe Gln
145                 150                 155                 160
Thr Ser His Leu Gly His Ser Gly Leu Pro Pro Leu Ser Asp Gln Tyr
                165                 170                 175
Pro Arg Glu Glu Leu Thr Arg Ile Val Arg Asn Ala Asp Glu Ile Ala
            180                 185                 190
Glu Tyr Leu Gln Lys Glu Met Gln Leu Ile Ile Glu Asn Pro Pro Ile
        195                 200                 205
Asn Ile Pro Thr Gly Cys Leu Glu Val Phe Pro Glu Ala Glu Trp Ser
    210                 215                 220
Gln Gly Val Gln Gly Thr Leu Arg Ile Lys Lys Tyr Leu Thr Val Glu
225                 230                 235                 240
Gln Ile Met Thr Cys Val Ala Asp Thr Cys Arg Arg Phe Phe Asp Arg
                245                 250                 255
Gly Tyr Ser Pro Lys Asp Val Ala Val Leu Val Ser Thr Ala Lys Glu
            260                 265                 270
Val Glu His Tyr Lys Tyr Glu Leu Leu Lys Ala Met Arg Lys Lys Arg
        275                 280                 285
Val Val Gln Leu Ser Asp Ala Cys Asp Met Leu Gly Asp His Ile Val
    290                 295                 300
Leu Asp Ser Val Arg Arg Phe Ser Gly Leu Glu Arg Ser Ile Val Phe
305                 310                 315                 320
Gly Ile His Pro Arg Thr Ala Asp Pro Ala Ile Leu Pro Asn Ile Leu
                325                 330                 335
Ile Cys Leu Ala Ser Arg Ala Lys Gln His Leu Tyr Ile Phe Leu
            340                 345                 350
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<210> 3951
<211> 1012
<212> DNA
<213> Homo sapiens

<400> 3951
ctggttcgag actccaatcc tgtttcgaat tgctgcttgc tgcccttggg ctggggataa
60
tggaagttct ttcccttccc aactctttcc agacccaagc actctgggac tcactccata
120
gtccaggagt tccaggttcc ggattatgtt ccatggcagc agtccaagca ggaaaccaag
180
ccatctactc tgcctccagt ccaacaagcc aacagccttc atacaagcaa aatgaagact
240
ttgactaggg tccaaccagt gtttcacttc aagcccacta cggtggtgac aagctgccag
300
ccgaagaatc caagagaact acatagaagg cggaagttgg accctgggaa gatgcatgcc
360
aaaatctggt taatgaagac ctcgctcagg agcgggaggg ccgctctgcg agagctccga
420
agccgtgaga acttcctcag caagctcaac cgggagctga tcgagaccat ccaggagatg
480
gagaacagca cgaccctgca cgtgcgggcc ctgctgcagc agcaggacac cctggcgacc
540

atcatcgaca tcttggagta ctcaaacaag aagaggctgc agcaattgaa atctgagctt
600
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660
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<213> Homo sapiens

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Lys Thr Ser Leu Arg Ser Gly Arg Ala Ala Leu Arg Glu Leu Arg Ser
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Arg Glu Asn Phe Leu Ser Lys Leu Asn Arg Glu Leu Ile Glu Thr Ile
65   70   75   80
Gln Glu Met Glu Asn Ser Thr Thr Leu His Val Arg Ala Leu Leu Gln
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Gln Gln Asp Thr Leu Ala Thr Ile Ile Asp Ile Leu Glu Tyr Ser Asn
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Lys Lys Arg Leu Gln Gln Leu Lys Ser Glu Leu Gln Glu Trp Glu Glu
        115   120   125
Lys Lys Lys Cys Lys Met Ser Tyr Leu Glu Gln Gln Ala Glu Gln Leu
    130   135   140
Asn Ala Lys Ile Glu Lys Thr Gln Glu Glu Val Asn Phe Leu Ser Thr
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Tyr Met Asp His Glu Tyr Ser Ile Lys Ser Val Gln Ile Ser Thr Leu
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Met Arg His Cys Ser Arg Leu Arg Thr Ala Ser Arg
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<212> DNA
<213> Homo sapiens

<400> 3953

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<212> PRT
<213> Homo sapiens

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Leu Tyr Pro Phe Phe Gly Val Leu Arg Ser Asn Glu Val Ala Ala Glu
65                  70                  75                  80
Tyr Phe Lys Asn Thr Thr Leu Leu Leu Val Gly Val Ile Cys Val Ala
                85                  90                  95
Ala Ala Val Glu Lys Trp Asn Leu His Lys Arg Ile Ala Leu Arg Met
            100                 105                 110
Val Leu Met Ala Gly Ala Lys Pro Gly Met Leu Leu Leu Cys Phe Met
        115                 120                 125
Cys Cys Thr Thr Leu Leu Ser Met Trp Leu Ser Asn Thr Ser Thr Thr
    130                 135                 140
Ala Met Val Met Pro Ile Val Glu Ala Val Leu Gln Glu Leu Val Ser
145                 150                 155                 160
Ala Glu Asp Glu Gln Leu Val Ala Gly Asn Ser Asn Thr Glu Glu Ala
                165                 170                 175
Glu Pro Ile Ser Leu Asp Val Lys Asn Ser Gln Pro Ser Leu Glu Leu
            180                 185                 190
Ile Phe Val Asn Glu Asp Arg Ser Asn Ala Asp Leu Thr Thr Leu Met
        195                 200                 205
His Asn Glu Asn Leu Asn Gly Val Pro Ser Ile Thr Asn Pro Ile Lys
    210                 215                 220
Thr Ala Asn Gln His Gln Gly Lys Lys Gln His Pro Ser Gln Glu Lys
225                 230                 235                 240
Pro Gln Val Leu Thr Pro Ser Pro Arg Lys Gln Lys Leu Asn Arg Lys
                245                 250                 255
Tyr Arg Ser His His Asp Gln Met Ile Cys Lys Cys Leu Ser Leu Ser
            260                 265                 270
Ile Ser Tyr Ser Ala Thr Ile Gly Gly Leu Thr Thr Ile Ile Gly Thr
        275                 280                 285
Ser Thr Ser Leu Ile Phe Leu Glu His Phe Asn Asn Gln Tyr Pro Ala
    290                 295                 300
Ala Glu Val Val Asn Phe Gly Thr Trp Phe Leu Phe Ser Phe Pro Ile
305                 310                 315                 320
Ser Leu Ile Met Leu Val Val Ser Trp Phe Trp Met His Trp Leu Phe
                325                 330                 335
Leu Gly Cys Asn Phe Lys Glu Thr Cys Ser Leu Ser Lys Lys Lys Lys
            340                 345                 350
Thr Lys Arg Glu Gln Leu Ser Glu Lys Arg Ile Gln Glu Glu Tyr Glu
        355                 360                 365
Lys Leu Gly Asp Ile Ser Tyr Pro Glu Met Val Thr Gly Phe Phe Phe
    370                 375                 380
Ile Leu Met Thr Val Leu Trp Phe Thr Arg Glu Pro Gly Phe Val Pro
385                 390                 395                 400
Gly Trp Asp Ser Phe Phe Glu Lys Lys Gly Tyr Arg Thr Asp Ala Thr
                405                 410                 415
Val Ser Val Phe Leu Gly Phe Leu Leu Phe Leu Ile Pro Ala Lys Lys
            420                 425                 430
Pro Cys Phe Gly Lys Lys Asn Asp Gly Glu Asn Gln Glu His Ser Leu
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Gly Thr Glu Pro Ile Ile Thr Trp Lys Asp Phe Gln Lys Thr Met Pro
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Trp Glu Ile Val Ile Leu Val Gly Gly Gly Tyr Ala Leu Ala Ser Gly
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Ser Lys Ser Ser Gly Leu Ser Thr Trp Ile Gly Asn Gln Met Leu Ser
                485                 490                 495
Leu Ser Ser Leu Pro Pro Trp Ala Val Thr Leu Leu Ala Cys Ile Leu
            500                 505                 510
Val Ser Ile Val Thr Glu Phe Val Ser Asn Pro Ala Thr Ile Thr Ile
        515                 520                 525
Phe Leu Pro Ile Leu Cys Ser Leu Ser Glu Thr Met His Ile Asn Pro
    530                 535                 540
Leu Tyr Thr Leu Ile Pro Val Thr Met Cys Ile Ser Phe Ala Val Met
545                 550                 555                 560
Leu Pro Val Gly Asn Pro Pro Asn Ala Ile Val Phe Ser Tyr Gly His
                565                 570                 575
Cys Gln Ile Lys Asp Met Val Lys Ala Gly Leu Gly Val Asn Val Ile
            580                 585                 590
Gly Leu Val Ile Val Met Val Ala Ile Asn Thr Trp Gly Val Ser Leu
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Phe His Leu Asp Thr Tyr Pro Ala Trp Ala Arg Val Ser Asn Ile Thr
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<212> DNA
<213> Homo sapiens

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<211> 174
<212> PRT
<213> Homo sapiens

<400> 3956
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35 40 45
Lys Glu Val Ser Ser Ser Glu Asn Pro Ser Ser His Ser Lys Val Arg
50 55 60
Ser Val Ile Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln
65 70 75 80
Leu Arg His Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln
85 90 95
Arg Cys Ile Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser
100 105 110
Asn Ile Glu Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile
115 120 125
Asn Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp
130 135 140
Phe Ser Ser Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val
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Asp Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His
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<210> 3957
<211> 3891
<212> DNA
<213> Homo sapiens

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<210> 3958

<211> 440
<212> PRT
<213> Homo sapiens

<400> 3958
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Thr Glu Pro Ala Gln Ala Gln Lys Cys Tyr Arg Asp Leu Ala Leu Val
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Ser Arg Asp Gly Met Asn Ile Val Leu Asn Lys Ile Asn Gln Ile Leu
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Met Glu Lys Tyr Leu Lys Leu Gln Asp Thr Cys Arg Thr Gln Leu Val
65 70 75 80
Trp Leu Val Arg Glu Leu Val Lys Ser Gly Val Leu Gly Ala Asp Gly
85 90 95
Val Cys Met Thr Phe Met Lys Gln Ile Ala Gly Gly Asp Val Thr Ala
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Lys Asn Ile Trp Leu Ala Glu Ser Val Leu Asp Ile Leu Thr Glu Gln
115 120 125
Arg Glu Trp Val Leu Lys Ser Ser Ile Leu Ile Ala Met Ala Val Tyr
130 135 140
Thr Tyr Leu Arg Leu Ile Val Asp His His Gly Thr Ala Gln Leu Gln
145 150 155 160
Ala Leu Arg Gln Lys Glu Val Asp Phe Cys Ile Ser Leu Leu Arg Glu
165 170 175
Arg Phe Met Glu Cys Leu Met Ile Gly Arg Asp Leu Val Arg Leu Leu
180 185 190
Gln Asn Val Ala Arg Ile Pro Glu Phe Glu Leu Leu Trp Lys Asp Ile
195 200 205
Ile His Asn Pro Gln Ala Leu Ser Pro Gln Phe Thr Gly Ile Leu Gln
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225 230 235 240
Pro Asp Met Glu Thr Lys Leu Leu Phe Met Thr Ser Arg Val Arg Phe
245 250 255
Gly Gln Gln Lys Arg Tyr Gln Asp Trp Phe Gln Arg Gln Tyr Leu Ser
260 265 270
Thr Pro Asp Ser Gln Ser Leu Arg Cys Asp Leu Ile Arg Tyr Ile Cys
275 280 285
Gly Val Val His Pro Ser Asn Glu Val Leu Ser Ser Asp Ile Leu Pro
290 295 300
Arg Trp Ala Ile Ile Gly Trp Leu Leu Thr Thr Cys Thr Ser Asn Val
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Ala Ala Ser Asn Ala Lys Leu Ala Leu Phe Tyr Asp Trp Leu Phe Phe
325 330 335
Ser Pro Asp Lys Asp Ser Ile Met Asn Ile Glu Pro Ala Ile Leu Val
340 345 350
Met His His Ser Met Lys Pro His Pro Ala Ile Thr Ala Thr Leu Leu
355 360 365
Asp Phe Met Cys Arg Ile Ile Pro Asn Phe Tyr Pro Pro Leu Glu Gly
370 375 380
His Val Arg Gln Gly Val Phe Ser Ser Leu Asn His Ile Val Glu Lys

385 390 395 400
Arg Val Leu Ala Cys Lys Lys Tyr Trp Leu Tyr Leu Arg Leu Leu Gly
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<210> 3959
<211> 752
<212> DNA
<213> Homo sapiens

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660
ggggtctgag tgtacttggt ttcctctaaa gcaacgttct gcggttggct gcgtgcgatc
720
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752

<210> 3960
<211> 94
<212> PRT
<213> Homo sapiens

<400> 3960
Pro Leu Gly Arg Pro Gly Ala His Arg Ala Phe Ile Trp Leu Tyr Lys
1 5 10 15
Gly Pro Asn Ser Pro Leu Asp Phe Leu Phe Ser Phe Gln Asn Ala Val
20 25 30
Ser Lys Tyr Gly Ser Gln Phe Gln Gly Asn Ser Gln His Asp Ala Leu
35 40 45
Glu Phe Leu Leu Trp Leu Leu Asp Arg Val His Glu Asp Leu Glu Gly

50 55 60
Ser Ser Arg Trp Ala Arg Cys Arg Arg Ser Phe Arg Leu Lys Pro Leu
65 70 75 80
Lys Pro Leu Arg Thr Ala Cys His His Gln Leu Ser Phe Leu
85 90

<210> 3961
<211> 2505
<212> DNA
<213> Homo sapiens

<400> 3961
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tacccgggcg ctttatagtc ccgccgcctc ctcctccacc tcctcctcct cctcctctcc
120
tcctggggca gaggaggttg tggcggtggc tggagaaagc ggcggcggag gatggaggaa
180
ggaggcggcg gcgtacggag tctggtcccg ggcgggccgg tgttactggt cctctgcggc
240
ctcctggagg cgtccggcgg cggccgagcc cttcctcaac tcagcgatga catccctttc
300
cgagtcaact ggcccggcac cgagttctct ctgcccacaa ctggagtttt atataaagaa
360
gataattatg tcatcatgac aactgcacat aaagaaaaat ataaatgcat acttcccctt
420
gtgacaagtg gggatgagga agaagaaaag gattataaag gccctaatcc aagagagctt
480
ttggagccac tatttaaaca aagcagttgt tcctacagaa ttgagtctta ttggacttac
540
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600
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660
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720
cagatgacac catactatcc tgtgggaatg ggaaatggta caccttgtag tttgaaacag
780
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840
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900
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960
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1020
ctaagggtgc cttttaggag aaataaagag gaagatttgc agtcaactaa agaagagaga
1080
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1140
acccacatat ccaaattgac agatgaccaa ctcataaaag agtttcttag tggttcttac
1200
tgctttcgtg ggggtgtcgg ttggtggaaa tatgaattct gctatggcaa acatgtacat
1260

caataccatg aggacaagga tagtgggaaa acctctgtgg ttgtcgggac atggaaccaa
1320
gaagagcata ttgaatgggc taagaagaat actgctagag cttatcatct tcaagacgat
1380
ggtacccaga cagtcaggat ggtgtcacat ttttatggaa atggagatat ttgtgatata
1440
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1500
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1560
ccagtgatct gtaaaatctt agatacagca gatgaaaatg gacttctttc tctccccaac
1620
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1680
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1800
ggcagacatt tgtctcgctt tttttcattt ttgttgtgtc ttataaactg actgtttttc
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1920
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1980
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2040
taaatgagag accatgtaaa atatgtaaat tctagtacct gaaatccttt caacagattt
2100
ttatatagca actgctctct gcaagtagtt aaactagaaa ctgggcacat ggtagaggct
2160
cacatgggag ttgtcctcac ccttgttaat ctcaagaaac tcttatttat aataggttgc
2220
ttctctctca gaacttttat ctattacttt tttcttctta tgagtatgtt tactctcaga
2280
gtatctatct gatgtagaca gttggtgatg cttctgagac tcagaatggt ttactctaac
2340
aaaacactgt gctgtctatc ccttgtactt gcctactgta atatggattt cacttctgaa
2400
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2460
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2505

<210> 3962
<211> 306
<212> PRT
<213> Homo sapiens

<400> 3962
Thr Lys Asn Ile Glu Gly Gln Met Thr Pro Tyr Tyr Pro Val Gly Met
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Gly Asn Gly Thr Pro Cys Ser Leu Lys Gln Asn Arg Pro Arg Ser Ser
20 25 30
Thr Val Met Tyr Ile Cys His Pro Glu Ser Lys His Glu Ile Leu Ser

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        35                  40                  45
Val Ala Glu Val Thr Thr Cys Glu Tyr Glu Val Val Ile Leu Thr Pro
    50                  55                  60
Leu Leu Cys Ser His Pro Lys Tyr Arg Phe Arg Ala Ser Pro Val Asn
65                  70                  75                  80
Asp Ile Phe Cys Gln Ser Leu Pro Gly Ser Pro Phe Lys Pro Leu Thr
                85                  90                  95
Leu Arg Gln Leu Glu Gln Gln Glu Glu Ile Leu Arg Val Pro Phe Arg
            100                 105                 110
Arg Asn Lys Glu Glu Asp Leu Gln Ser Thr Lys Glu Glu Arg Phe Pro
        115                 120                 125
Ala Ile His Lys Ser Ile Ala Ile Gly Ser Gln Pro Val Leu Thr Val
    130                 135                 140
Gly Thr Thr His Ile Ser Lys Leu Thr Asp Asp Gln Leu Ile Lys Glu
145                 150                 155                 160
Phe Leu Ser Gly Ser Tyr Cys Phe Arg Gly Gly Val Gly Trp Trp Lys
                165                 170                 175
Tyr Glu Phe Cys Tyr Gly Lys His Val His Gln Tyr His Glu Asp Lys
            180                 185                 190
Asp Ser Gly Lys Thr Ser Val Val Val Gly Thr Trp Asn Gln Glu Glu
        195                 200                 205
His Ile Glu Trp Ala Lys Lys Asn Thr Ala Arg Ala Tyr His Leu Gln
    210                 215                 220
Asp Asp Gly Thr Gln Thr Val Arg Met Val Ser His Phe Tyr Gly Asn
225                 230                 235                 240
Gly Asp Ile Cys Asp Ile Thr Asp Lys Pro Arg Gln Val Thr Val Lys
                245                 250                 255
Leu Lys Cys Lys Glu Ser Asp Ser Pro His Ala Val Thr Val Tyr Met
            260                 265                 270
Leu Glu Pro His Ser Cys Gln Tyr Ile Leu Gly Val Glu Ser Pro Val
        275                 280                 285
Ile Cys Lys Ile Leu Asp Thr Ala Asp Glu Asn Gly Leu Leu Ser Leu
    290                 295                 300
Pro Asn
305
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<210> 3963
<211> 1513
<212> DNA
<213> Homo sapiens

<400> 3963
cttaaggtgt attaatccgt cactataccc agataaacag agatggccat ggcatctttt
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ctactctttt attttacaaa gggaatgatg aaaggtggaa acaaacaaga agaagcgtgg
120
ataaatccat ttgttaaaca gttttcaaac atcagttttt cgagagactc accagaggaa
180
aatgtacaaa gcaataagat ggacctttct ggaggaatgt tacaagacaa acgaatggag
240
atagataaac atagcctaaa tattggtgat tacaatcgaa cggtcgggaa aggccctggt
300
tctcggcctc agatttccaa agagtcttcc atggagcgca atccttattt tgataagaat
360

ggcaatccca gtatgtttgg tgttggaaac acagcagcac aaccccgggg catgcagcag
420
cctccagcac aacctcttag ttcatctcag cctaatctcc gtgctcaagt gcctcctcca
480
ttactctccc ctcaggttcc agtttcattg ctgaagtatg caccaaacaa cggtggcctg
540
aatccactct ttggccctca acaggtagcc atgctgaacc agctatccca gctaaaccag
600
ctttctcaga tctcccagtt acagcgattg ttagcgcagc agcaaagggc gcagagtcag
660
agaagcgtgc cttctgggaa ccggccgcag caagaccagc agggtcgacc tcttagtgtg
720
cagcagcaaa tgatgcaaca atctcgtcaa cttgatccaa acctgttggt gaagcagcag
780
actccaccat ctcagcagca gccactccat cagccagcca tgaagtcttt ccttgacaat
840
gtcatgcccc acactacacc tgagctgcaa aaagggccat caccaataaa tgctttcagc
900
aacttcccta taggcttgaa ctcaaacttg aatgtaaata tggatatgaa cagtattaaa
960
gagccacagt caagactaag gaagtggacg acagtggaca gcatttctgt gaacacatct
1020
ttggatcaaa actccagcaa acatggtgct atttcaagtg gtttcaggct ggaagagtct
1080
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1140
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1200
ccagaatttc gtcctggtga gccatggaaa ggttatccaa acattgaccc tgaaactgac
1260
ccttacgtca ctcctggcag tgtcataaac aatcttccaa ttaatactgt gcgggaagtt
1320
gaccacctca gggacaggaa cagtggtacg taggggtgc aaatcaattt ctgagtgaca
1380
cttaacacag tttaagaatg gctcatgtag taaccagcta ctctgggcga ctgagcccag
1440
ggtactctgg gatcacttga gcccaggagc ttgagcaagc ctgggcaaca tagttgtggg
1500
accctgtctc ttt
1513

<210> 3964
<211> 436
<212> PRT
<213> Homo sapiens

<400> 3964
Met Ala Met Ala Ser Phe Leu Leu Phe Tyr Phe Thr Lys Gly Met Met
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Lys Gly Gly Asn Lys Gln Glu Glu Ala Trp Ile Asn Pro Phe Val Lys
            20   25   30
Gln Phe Ser Asn Ile Ser Phe Ser Arg Asp Ser Pro Glu Glu Asn Val
        35   40   45
Gln Ser Asn Lys Met Asp Leu Ser Gly Gly Met Leu Gln Asp Lys Arg

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    50                  55                  60
Met Glu Ile Asp Lys His Ser Leu Asn Ile Gly Asp Tyr Asn Arg Thr
65                  70                  75                  80
Val Gly Lys Gly Pro Gly Ser Arg Pro Gln Ile Ser Lys Glu Ser Ser
                85                  90                  95
Met Glu Arg Asn Pro Tyr Phe Asp Lys Asn Gly Asn Pro Ser Met Phe
            100                 105                 110
Gly Val Gly Asn Thr Ala Ala Gln Pro Arg Gly Met Gln Gln Pro Pro
        115                 120                 125
Ala Gln Pro Leu Ser Ser Ser Gln Pro Asn Leu Arg Ala Gln Val Pro
    130                 135                 140
Pro Pro Leu Leu Ser Pro Gln Val Pro Val Ser Leu Leu Lys Tyr Ala
145                 150                 155                 160
Pro Asn Asn Gly Gly Leu Asn Pro Leu Phe Gly Pro Gln Gln Val Ala
                165                 170                 175
Met Leu Asn Gln Leu Ser Gln Leu Asn Gln Leu Ser Gln Ile Ser Gln
            180                 185                 190
Leu Gln Arg Leu Leu Ala Gln Gln Gln Arg Ala Gln Ser Gln Arg Ser
        195                 200                 205
Val Pro Ser Gly Asn Arg Pro Gln Gln Asp Gln Gln Gly Arg Pro Leu
    210                 215                 220
Ser Val Gln Gln Gln Met Met Gln Gln Ser Arg Gln Leu Asp Pro Asn
225                 230                 235                 240
Leu Leu Val Lys Gln Gln Thr Pro Pro Ser Gln Gln Gln Pro Leu His
                245                 250                 255
Gln Pro Ala Met Lys Ser Phe Leu Asp Asn Val Met Pro His Thr Thr
            260                 265                 270
Pro Glu Leu Gln Lys Gly Pro Ser Pro Ile Asn Ala Phe Ser Asn Phe
        275                 280                 285
Pro Ile Gly Leu Asn Ser Asn Leu Asn Val Asn Met Asp Met Asn Ser
    290                 295                 300
Ile Lys Glu Pro Gln Ser Arg Leu Arg Lys Trp Thr Thr Val Asp Ser
305                 310                 315                 320
Ile Ser Val Asn Thr Ser Leu Asp Gln Asn Ser Ser Lys His Gly Ala
                325                 330                 335
Ile Ser Ser Gly Phe Arg Leu Glu Glu Ser Pro Phe Val Pro Tyr Asp
            340                 345                 350
Phe Met Asn Ser Ser Thr Ser Pro Ala Ser Pro Pro Gly Ser Ile Gly
        355                 360                 365
Asp Gly Trp Pro Arg Ala Lys Ser Pro Asn Gly Ser Ser Ser Val Asn
    370                 375                 380
Trp Pro Pro Glu Phe Arg Pro Gly Glu Pro Trp Lys Gly Tyr Pro Asn
385                 390                 395                 400
Ile Asp Pro Glu Thr Asp Pro Tyr Val Thr Pro Gly Ser Val Ile Asn
                405                 410                 415
Asn Leu Pro Ile Asn Thr Val Arg Glu Val Asp His Leu Arg Asp Arg
            420                 425                 430
Asn Ser Gly Thr
        435
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<210> 3965
<211> 2850
<212> DNA
<213> Homo sapiens

<400> 3965
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gcgaggggtg ttgacgccag gaaggttcca tcttggttaa gggcaggagt cccttacgga
120
cttgtctgag gaaagacagg aaagcgccag catctccacc ttccccggaa gcctcccttt
180
gccaggcaga aagggtttcc catggggccg cccctggcgc cgcgcccggc ccacgtaccc
240
ggggaggccg ggccccggag gacgagggaa agcaggccgg gcgccgtgag cttcgcggac
300
gtggccgtgt acttctctcc cgaggagtgg gaatgcctgc ggccagcgca gagggccctg
360
taccgggacg tgatgcggga gaccttcggc cacctgggcg cgctgggtga ggccgggccc
420
tccggccggg acccccagtc cgtcggattt tcagttccca aacccgcttt tatctcgtgg
480
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540
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600
gaaaggctga agaagtgtcc aaaacaaaaa gaggtggcgc atgaagtggc tgtcaaggag
660
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720
tggctcaagg acactctgac ccgaagactg ccccactctt gcccagactg tggccgcaac
780
ttcagctacc cttccctcct ggccagccac cagcgggtcc actccgggga gcggcccttc
840
tcctgcggcc agtgtcaggc gcgtttctcc cagcgcaggt acctgctcca gcatcagttc
900
atccacaccg gcgagaagcc ctacccctgc cccgactgcg ggcgccgctt ccgccagagg
960
ggttccctgg ctatccacag gcgggctcac accggggaga agccttacgc gtgctcagac
1020
tgcaagagtc gcttcactta cccctacctg ctggccatcc accagcgcaa gcacacgggc
1080
gagaagccct acagctgccc cgattgcagc ctccgtttcg cctacacctc cctgctggcc
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1200
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1260
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1320
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1440
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1560

tattgcgggc acagaggggt aagtgaagct tcgggccctt acatctttct tgaaggcaag
1620
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1680
gctttattta agggcaagtg ggacgatgag gccagagaaa tggcgccgcc cccagccccg
1740
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1860
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1920
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1980
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2040
aacaggaagg aagaggaacc ggaggaagtc ccaagagcca aagggcctag aaaggctcct
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2160
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2220
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2280
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2400
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2460
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2520
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2700
agtgcctgta aagattcgaa tagattagac ttgccaccca tctccccagt cttttgttta
2760
acaaaaaaaa aaaaaaaaaa aaaaaaaaag aagagagtga gaccctggac tcatttcaaa
2820
gtgttatctg aagatcaggt gcaacagaga
2850

<210> 3966
<211> 782
<212> PRT
<213> Homo sapiens

<400> 3966
Met Gly Pro Pro Leu Ala Pro Arg Pro Ala His Val Pro Gly Glu Ala
1 5 10 15
Gly Pro Arg Arg Thr Arg Glu Ser Arg Pro Gly Ala Val Ser Phe Ala

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            20                  25                  30
Asp Val Ala Val Tyr Phe Ser Pro Glu Glu Trp Glu Cys Leu Arg Pro
        35                  40                  45
Ala Gln Arg Ala Leu Tyr Arg Asp Val Met Arg Glu Thr Phe Gly His
    50                  55                  60
Leu Gly Ala Leu Gly Glu Ala Gly Pro Ser Gly Arg Asp Pro Gln Ser
65                  70                  75                  80
Val Gly Phe Ser Val Pro Lys Pro Ala Phe Ile Ser Trp Val Glu Gly
                85                  90                  95
Glu Val Glu Ala Trp Ser Pro Glu Ala Gln Asp Pro Asp Gly Glu Ser
            100                 105                 110
Ser Ala Ala Phe Ser Arg Gly Gln Gly Gln Glu Ala Gly Ser Arg Asp
        115                 120                 125
Gly Asn Glu Glu Lys Glu Arg Leu Lys Lys Cys Pro Lys Gln Lys Glu
    130                 135                 140
Val Ala His Glu Val Ala Val Lys Glu Trp Trp Pro Ser Val Ala Cys
145                 150                 155                 160
Pro Glu Phe Cys Asn Pro Arg Gln Ser Pro Met Asn Pro Trp Leu Lys
                165                 170                 175
Asp Thr Leu Thr Arg Arg Leu Pro His Ser Cys Pro Asp Cys Gly Arg
            180                 185                 190
Asn Phe Ser Tyr Pro Ser Leu Leu Ala Ser His Gln Arg Val His Ser
        195                 200                 205
Gly Glu Arg Pro Phe Ser Cys Gly Gln Cys Gln Ala Arg Phe Ser Gln
    210                 215                 220
Arg Arg Tyr Leu Leu Gln His Gln Phe Ile His Thr Gly Glu Lys Pro
225                 230                 235                 240
Tyr Pro Cys Pro Asp Cys Gly Arg Arg Phe Arg Gln Arg Gly Ser Leu
                245                 250                 255
Ala Ile His Arg Arg Ala His Thr Gly Glu Lys Pro Tyr Ala Cys Ser
            260                 265                 270
Asp Cys Lys Ser Arg Phe Thr Tyr Pro Tyr Leu Leu Ala Ile His Gln
        275                 280                 285
Arg Lys His Thr Gly Glu Lys Pro Tyr Ser Cys Pro Asp Cys Ser Leu
    290                 295                 300
Arg Phe Ala Tyr Thr Ser Leu Leu Ala Ile His Arg Arg Ile His Thr
305                 310                 315                 320
Gly Glu Lys Pro Tyr Pro Cys Pro Asp Cys Gly Arg Arg Phe Thr Tyr
                325                 330                 335
Ser Ser Leu Leu Leu Ser His Arg Arg Ile His Ser Asp Ser Arg Pro
            340                 345                 350
Phe Pro Cys Val Glu Cys Gly Lys Gly Phe Lys Arg Lys Thr Ala Leu
        355                 360                 365
Glu Ala His Arg Trp Ile His Arg Ser Cys Ser Glu Arg Arg Ala Trp
    370                 375                 380
Gln Gln Ala Val Val Gly Arg Ser Glu Pro Ile Pro Val Leu Gly Gly
385                 390                 395                 400
Lys Asp Pro Pro Val His Phe Arg His Phe Pro Asp Ile Phe Gln Glu
                405                 410                 415
Phe Cys Gln Gln Arg Leu Gln Asp Arg Gly Val Pro Ser Asn Ala Pro
            420                 425                 430
Pro Val Pro Gly Gln Ser Pro Arg Ser Phe Phe Arg Asp Arg Arg Gln
        435                 440                 445
Ser Ser Ala Val Ala Tyr Cys Gly His Arg Gly Val Ser Glu Ala Ser
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    450                 455                 460
Gly Pro Tyr Ile Phe Leu Glu Gly Lys Lys Pro Leu Leu Tyr Phe Pro
465                 470                 475                 480
Asp Thr Pro Pro Pro Pro Leu Glu Lys Ala Ala Glu Ala Ala Leu Phe
                485                 490                 495
Lys Gly Lys Trp Asp Asp Glu Ala Arg Glu Met Ala Pro Pro Pro Ala
            500                 505                 510
Pro Leu Leu Ala Pro Arg Pro Gly Glu Thr Arg Pro Gly Cys Arg Lys
        515                 520                 525
Pro Gly Thr Val Ser Phe Ala Asp Val Ala Val Tyr Phe Ser Pro Glu
    530                 535                 540
Glu Trp Gly Cys Leu Arg Pro Ala Gln Arg Ala Leu Tyr Arg Asp Val
545                 550                 555                 560
Met Gln Glu Thr Tyr Gly His Leu Gly Ala Leu Gly Phe Pro Gly Pro
                565                 570                 575
Lys Pro Ala Leu Ile Ser Trp Met Glu Gln Glu Ser Glu Ala Trp Ser
            580                 585                 590
Pro Ala Ala Gln Asp Pro Glu Lys Gly Glu Arg Leu Gly Gly Ala Arg
        595                 600                 605
Arg Gly Asp Val Pro Asn Arg Lys Glu Glu Glu Pro Glu Glu Val Pro
    610                 615                 620
Arg Ala Lys Gly Pro Arg Lys Ala Pro Val Lys Glu Ser Pro Glu Val
625                 630                 635                 640
Leu Val Glu Arg Asn Pro Asp Pro Ala Ile Ser Val Ala Pro Ala Arg
                645                 650                 655
Ala Gln Pro Pro Lys Asn Ala Ala Trp Asp Pro Thr Thr Gly Ala Gln
            660                 665                 670
Pro Pro Ala Pro Ile Pro Ser Met Asp Ala Gln Ala Gly Gln Arg Arg
        675                 680                 685
His Val Cys Thr Asp Cys Gly Arg Arg Phe Thr Tyr Pro Ser Leu Leu
    690                 695                 700
Val Ser His Arg Arg Met His Ser Gly Glu Arg Pro Phe Pro Cys Pro
705                 710                 715                 720
Glu Cys Gly Met Arg Phe Lys Arg Lys Phe Ala Val Glu Ala His Gln
                725                 730                 735
Trp Ile His Arg Ser Cys Ser Gly Gly Arg Arg Gly Arg Arg Pro Gly
            740                 745                 750
Ile Arg Ala Val Pro Arg Ala Pro Val Arg Gly Asp Arg Asp Pro Pro
        755                 760                 765
Val Leu Phe Arg His Tyr Pro Asp Ile Phe Glu Glu Cys Gly
    770                 775                 780
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<210> 3967
<211> 892
<212> DNA
<213> Homo sapiens

<400> 3967
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atcctgcccc gtggccgcgg ccgtctcgta ggggacaccg tggtgtttaa ggatggccag
120
tactggatcc gaggccggac ctcagtggac atcatcaaga ctggaggcta caaggtcagc
180

gccctggagg tggagtggca cctgctggcc caccccagca tcacagatgt ggctgtgatt
240
ggagttccgg atatgacatg gggccagcgg gtcactgctg tggtgaccct ccgagaagga
300
cactcactgt cccacaggga gctcaaagag tgggccagaa atgtcctggc cccgtacgcg
360
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420
aagaaggcgc tcatcaggca cttccacccc tcatgacccg gcagactggg actgcgggtc
480
tggtggggag cagcagacgt ccccttcaca ccgagaacca cgggggcccg tccaagacct
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tgaaatcacc atgtggggtc cccagcctcg ggccagttgt tgcagctcaa ggagaccgtc
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720
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780
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840
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892

<210> 3968
<211> 151
<212> PRT
<213> Homo sapiens

<400> 3968
Xaa Pro Ala Arg Pro Arg Arg Ala Arg Gly Gly Gly Arg Gly Arg Val
 1   5   10   15
Val Ala Arg Gln Ile Leu Pro Arg Gly Arg Gly Arg Leu Val Gly Asp
            20   25   30
Thr Val Val Phe Lys Asp Gly Gln Tyr Trp Ile Arg Gly Arg Thr Ser
        35   40   45
Val Asp Ile Ile Lys Thr Gly Gly Tyr Lys Val Ser Ala Leu Glu Val
    50   55   60
Glu Trp His Leu Leu Ala His Pro Ser Ile Thr Asp Val Ala Val Ile
65   70   75   80
Gly Val Pro Asp Met Thr Trp Gly Gln Arg Val Thr Ala Val Val Thr
                85   90   95
Leu Arg Glu Gly His Ser Leu Ser His Arg Glu Leu Lys Glu Trp Ala
            100   105   110
Arg Asn Val Leu Ala Pro Tyr Ala Val Pro Ser Glu Leu Val Leu Val
        115   120   125
Glu Glu Ile Pro Arg Asn Gln Met Gly Lys Ile Asp Lys Lys Ala Leu
    130   135   140
Ile Arg His Phe His Pro Ser
145   150

<210> 3969
<211> 915

<212> DNA
<213> Homo sapiens

<400> 3969
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120
ggattgcaac tcggggaggg atggagcacg cgtcgtcgcc tgggaaacgg gtcgacccgc
180
ggaaggcgag cgggtgggac ttccggagca gttaatggtg gggaaacttt ctagtggatg
240
tgggaggagg cgggacttcc tgcagcaaat tggggctgtg cgccgctcaa gcccgtttac
300
ctgctcccca ggccggcacc caggatgggc gaggtggagg ccccgggccg cttgtggctc
360
gagagccccc ctgggggagc gccccccatc ttcctgccct cggacgggca agccctggtc
420
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480
ctggtcgcag atcctgagac ccggacagtg gcagtgaaac aggtatcagt gcctctgcaa
540
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600
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660
tgggaggccg aggcgggcgg atcgcttgaa cccaggagtt cgagaccagc ctgagcgaca
720
tggtgaaacc tgtctctcta aaaaattagc gggaatggtg gcgcgtcctt gtagttccta
780
atcgggaggc tgaagcggga ggatcccttg agcccagtag gtcaagggtg tagtgagcag
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900
aagaaaaaat atggc
915

<210> 3970
<211> 89
<212> PRT
<213> Homo sapiens

<400> 3970
Met Gly Glu Val Glu Ala Pro Gly Arg Leu Trp Leu Glu Ser Pro Pro
 1   5   10   15
Gly Gly Ala Pro Pro Ile Phe Leu Pro Ser Asp Gly Gln Ala Leu Val
            20   25   30
Leu Gly Arg Gly Pro Leu Thr Gln Val Thr Asp Arg Lys Cys Ser Arg
        35   40   45
Thr Gln Val Glu Leu Val Ala Asp Pro Glu Thr Arg Thr Val Ala Val
    50   55   60
Lys Gln Val Ser Val Pro Leu Gln Gly Pro Ala Arg Pro Gly Asp Gly
65   70   75   80
Ile Trp Gly Gly Ile Ala Ser Arg Gln

85

<210> 3971
<211> 433
<212> DNA
<213> Homo sapiens

<400> 3971
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120
ctggggaacg ggtaatcaga gaaaccctca ctcatagggt ggtgcccttt atgcagagac
180
ttaaaggaag gagggaggtc ccctgacaga gagaatggta agtgcaaagg tcctgggtgg
240
gcttgtgttg aggaagagca aggccagtgt ggctggaaca gagtgagtga aggggagaga
300
gttgtaagca atgagcttag acaggaaatg gggtctggtt cacatgggaa atggtaggac
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attgtccgaa cttgggcttt tactccgggt gaaatgggca ctcctataga tgctcccgtc
420
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433

<210> 3972
<211> 120
<212> PRT
<213> Homo sapiens

<400> 3972
Met Ser Tyr His Phe Pro Cys Glu Pro Asp Pro Ile Ser Cys Leu Ser
 1   5   10   15
Ser Leu Leu Thr Thr Leu Ser Pro Ser Leu Thr Leu Phe Gln Pro His
            20   25   30
Trp Pro Cys Ser Ser Ser Thr Gln Ala His Pro Gly Pro Leu His Leu
        35   40   45
Pro Phe Ser Leu Ser Gly Asp Leu Pro Pro Ser Phe Lys Ser Leu His
    50   55   60
Lys Gly His His Pro Met Ser Glu Gly Phe Ser Asp Tyr Pro Phe Pro
65   70   75   80
Ser Arg Ala Leu Pro Ser Met Leu His Phe Phe Pro Arg Ala Leu Asn
                85   90   95
Thr Thr Tyr Leu Ser Phe Ile Phe Ser Leu Ser Phe Phe Cys Leu Leu
            100   105   110
Pro Leu Glu His His Gln Ser Arg
        115   120

<210> 3973
<211> 984
<212> DNA
<213> Homo sapiens

<400> 3973

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120
tgctccacct acttgcagtc cagatattac agggcccctg agatcatcct tggtttacca
180
ttttgtgagg caattgacat gtggtccctg ggctgtgtta ttgcagaatt gttcctgggt
240
tggccgttat atccaggagc ttcggagtat gatcagattc ggtatatttc acaaacacag
300
ggtttgcctg ctgaatattt attaagcgcc gggacaaaga caactaggtt tttcaaccgt
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gacacggact caccatatcc tttgtggaga ctgaagacac cagatgacca tgaagcagag
420
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480
caggtgaaca tgacgacaga tttggaaggg agcgacatgt tggtagaaaa ggctgaccgg
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600
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660
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780
accaacctga ccatgacctt taacaaccag ctgaccactg tccacaacca gccctcagcg
840
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984

<210> 3974
<211> 328
<212> PRT
<213> Homo sapiens

<400> 3974
Leu Gly Leu Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu Val
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Asp Pro Ser Arg Gln Pro Tyr Arg Val Lys Val Ile Asp Phe Gly Ser
20 25 30
Ala Ser His Val Ser Lys Ala Val Cys Ser Thr Tyr Leu Gln Ser Arg
35 40 45
Tyr Tyr Arg Ala Pro Glu Ile Ile Leu Gly Leu Pro Phe Cys Glu Ala
50 55 60
Ile Asp Met Trp Ser Leu Gly Cys Val Ile Ala Glu Leu Phe Leu Gly
65 70 75 80
Trp Pro Leu Tyr Pro Gly Ala Ser Glu Tyr Asp Gln Ile Arg Tyr Ile
85 90 95
Ser Gln Thr Gln Gly Leu Pro Ala Glu Tyr Leu Leu Ser Ala Gly Thr

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            100                 105                 110
Lys Thr Thr Arg Phe Phe Asn Arg Asp Thr Asp Ser Pro Tyr Pro Leu
        115                 120                 125
Trp Arg Leu Lys Thr Pro Asp Asp His Glu Ala Glu Thr Gly Ile Lys
    130                 135                 140
Ser Lys Glu Ala Arg Lys Tyr Ile Phe Asn Cys Leu Asp Asp Met Ala
145                 150                 155                 160
Gln Val Asn Met Thr Thr Asp Leu Glu Gly Ser Asp Met Leu Val Glu
                165                 170                 175
Lys Ala Asp Arg Arg Glu Phe Ile Asp Leu Leu Lys Lys Met Leu Thr
            180                 185                 190
Ile Asp Ala Asp Lys Arg Ile Thr Pro Ile Glu Thr Leu Asn His Pro
        195                 200                 205
Phe Val Thr Met Thr His Leu Leu Asp Phe Pro His Ser Thr His Val
    210                 215                 220
Lys Ser Cys Phe Gln Asn Met Glu Ile Cys Lys Arg Arg Val Asn Met
225                 230                 235                 240
Tyr Asp Thr Val Asn Gln Ser Lys Thr Pro Phe Ile Thr His Val Ala
                245                 250                 255
Pro Ser Thr Ser Thr Asn Leu Thr Met Thr Phe Asn Asn Gln Leu Thr
            260                 265                 270
Thr Val His Asn Gln Pro Ser Ala Ala Ser Met Ala Ala Ala Ala Gln
        275                 280                 285
Arg Ser Met Pro Leu Gln Thr Gly Thr Ala Gln Ile Cys Ala Arg Pro
    290                 295                 300
Asp Pro Phe Gln Gln Ala Leu Ile Val Cys Pro Pro Gly Leu Gln Ala
305                 310                 315                 320
Leu Gln Ala Ser Pro Phe Thr Arg
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<210> 3975
<211> 593
<212> DNA
<213> Homo sapiens

<400> 3975

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120
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180
agtcaggatt tggatgcccc cagtgcagtc ctgaggccgc cgccccccat cctactatcc
240
tgcttctgag gcgtctcgga atcataggcc tcccgtggaa ggggagcagc aggcgaggtc
300
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360
accaccaggg tacccagatc ccaggcggct cagccaggcc cagagcccca agagctgggc
420
tgttctctcc aactgggatc tggggtaggg gctgctcccc caagtccctg ggggactgtc
480
tgggacatcc aggccctgtc ttcttgtctt aaccactcac aacagagaac acgatgttct
540
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593

<210> 3976
<211> 101
<212> PRT
<213> Homo sapiens

<400> 3976
Met Gly Phe Ser Leu Leu Glu Gly Pro Ala Ser Leu Gln Pro Pro His
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Arg Glu Ser Leu Pro Leu His Ser Leu Pro Arg Asp Gly Ser Trp Gly
            20   25   30
Leu Lys Gly Ala Trp Ala Ser Ala Ser Leu Gln Ala Ala Ser Asn Ser
        35   40   45
Gln Ser Gly Phe Gly Cys Pro Gln Cys Ser Pro Glu Ala Ala Ala Pro
    50   55   60
His Pro Thr Ile Leu Leu Leu Arg Arg Leu Gly Ile Ile Gly Leu Pro
65   70   75   80
Trp Lys Gly Ser Ser Arg Arg Gly Leu Arg Glu Pro His Arg Cys Pro
                85   90   95
Leu Ala Cys Gln Thr
            100

<210> 3977
<211> 2668
<212> DNA
<213> Homo sapiens

<400> 3977
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120
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240
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300
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420
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480
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720

atcctggaaa cagtctacaa acacagctgt ggggggttgc ctcctgttcg aagtgcactg
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2340

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2520
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2668

<210> 3978
<211> 667
<212> PRT
<213> Homo sapiens

<400> 3978
Met Ile His Glu Leu Leu Leu Ala Leu Ser Gly Tyr Pro Gly Ser Ile
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Phe Thr Trp Asn Lys Arg Ser Gly Leu Gln Val Ser Gln Asp Phe Pro
20 25 30
Phe Leu His Pro Ser Glu Thr Ser Val Leu Asn Arg Leu Cys Arg Leu
35 40 45
Gly Thr Asp Tyr Ile Arg Phe Thr Glu Phe Ile Glu Gln Tyr Thr Gly
50 55 60
His Val Gln Gln Gln Asp His His Pro Ser Gln Gln Gly Gln Gly Gly
65 70 75 80
Leu His Gly Ile Tyr Leu Arg Ala Phe Cys Thr Gly Leu Asp Ser Val
85 90 95
Leu Gln Pro Tyr Arg Gln Ala Leu Leu Asp Leu Glu Gln Glu Phe Leu
100 105 110
Gly Asp Pro His Leu Ser Ile Ser His Val Asn Tyr Phe Leu Asp Gln
115 120 125
Phe Gln Leu Leu Phe Pro Ser Val Met Val Val Val Glu Gln Ile Lys
130 135 140
Ser Gln Lys Ile His Gly Cys Gln Ile Leu Glu Thr Val Tyr Lys His
145 150 155 160
Ser Cys Gly Gly Leu Pro Pro Val Arg Ser Ala Leu Glu Lys Ile Leu
165 170 175
Ala Val Cys His Gly Val Met Tyr Lys Gln Leu Ser Ala Trp Met Leu
180 185 190
His Gly Leu Leu Leu Asp Gln His Glu Glu Phe Phe Ile Lys Gln Gly
195 200 205
Pro Ser Ser Gly Asn Val Ser Ala Gln Pro Glu Glu Asp Glu Glu Asp
210 215 220
Leu Gly Ile Gly Gly Leu Thr Gly Lys Gln Leu Arg Glu Leu Gln Asp
225 230 235 240
Leu Arg Leu Ile Glu Glu Glu Asn Met Leu Ala Pro Ser Leu Lys Gln
245 250 255
Phe Ser Leu Arg Val Glu Ile Leu Pro Ser Tyr Ile Pro Val Arg Val
260 265 270
Ala Glu Lys Ile Leu Phe Val Gly Glu Ser Val Gln Met Phe Glu Asn

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        275                 280                 285
Gln Asn Val Asn Leu Thr Arg Lys Gly Ser Ile Leu Lys Asn Gln Glu
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Asp Thr Phe Ala Ala Glu Leu His Arg Leu Lys Gln Gln Pro Leu Phe
305                 310                 315                 320
Ser Leu Val Asp Phe Glu Gln Val Val Asp Arg Ile Arg Ser Thr Val
                325                 330                 335
Ala Glu His Leu Trp Lys Leu Met Val Glu Glu Ser Asp Leu Leu Gly
            340                 345                 350
Gln Leu Lys Ile Ile Lys Asp Phe Tyr Leu Leu Gly Arg Gly Glu Leu
        355                 360                 365
Phe Gln Ala Phe Ile Asp Thr Ala Gln His Met Leu Lys Thr Pro Pro
    370                 375                 380
Thr Ala Val Thr Glu His Asp Val Asn Val Ala Phe Gln Gln Ser Ala
385                 390                 395                 400
His Lys Val Leu Leu Asp Asp Asp Asn Leu Leu Pro Leu Leu His Leu
                405                 410                 415
Thr Ile Glu Tyr His Xaa Glu Arg Ser Thr Lys Met Leu Leu Arg Xaa
            420                 425                 430
Arg Glu Gly Pro Ser Arg Glu Thr Ser Pro Arg Glu Ala Pro Ala Ser
        435                 440                 445
Gly Trp Ala Ala Leu Gly Leu Ser Tyr Lys Val Gln Trp Pro Leu His
    450                 455                 460
Ile Leu Phe Thr Pro Ala Val Leu Glu Lys Tyr Asn Val Val Phe Lys
465                 470                 475                 480
Tyr Leu Leu Ser Val Arg Arg Val Gln Ala Glu Leu Gln His Cys Trp
                485                 490                 495
Ala Leu Gln Met Gln Arg Lys His Leu Lys Ser Asn Gln Thr Asp Ala
            500                 505                 510
Ile Lys Trp Arg Leu Arg Asn His Met Ala Phe Leu Val Asp Asn Leu
        515                 520                 525
Gln Tyr Tyr Leu Gln Val Asp Val Leu Glu Ser Gln Phe Ser Gln Leu
    530                 535                 540
Leu His Gln Ile Asn Ser Thr Arg Asp Phe Glu Ser Ile Arg Leu Ala
545                 550                 555                 560
His Asp His Phe Leu Ser Asn Leu Leu Ala Gln Ser Phe Ile Leu Leu
                565                 570                 575
Lys Pro Val Phe His Cys Leu Asn Glu Ile Leu Asp Leu Cys His Ser
            580                 585                 590
Phe Cys Ser Leu Val Ser Gln Asn Leu Gly Pro Leu Asp Glu Arg Gly
        595                 600                 605
Ala Ala Gln Leu Ser Ile Leu Val Lys Gly Phe Ser Arg Gln Ser Ser
    610                 615                 620
Leu Leu Phe Lys Ile Leu Ser Ser Val Arg Asn His Gln Ile Asn Ser
625                 630                 635                 640
Asp Leu Ala Gln Leu Leu Leu Arg Leu Asp Tyr Asn Lys Tyr Tyr Thr
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Gln Ala Gly Gly Thr Leu Gly Ser Phe Gly Met
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<210> 3979
<211> 2746
<212> DNA
<213> Homo sapiens

<400> 3979
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120
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180
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240
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1560

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1920
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<211> 478
<212> PRT
<213> Homo sapiens

<400> 3980
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Leu Glu Gly Asp Lys Gln Leu Ile Arg Glu Thr Ser Thr His Gln Leu

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Asn Ser Glu Arg Tyr Val His Thr Phe Lys Asp Leu Ser Asn Phe Ser
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Gly Ala Ile Asn Val Thr Tyr Arg Tyr Leu Ala Ala Thr Pro Leu Gln
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Arg Lys Arg Tyr Leu Thr Ile Gly Leu Ser Ser Val Lys Arg Lys Lys
            100                 105                 110
Gly Asn Tyr Leu Leu Glu Thr Ile Lys Ser Ile Phe Glu Gln Ser Ser
        115                 120                 125
Tyr Glu Glu Leu Lys Glu Ile Ser Val Val Val His Leu Ala Asp Phe
    130                 135                 140
Asn Ser Ser Trp Arg Asp Ala Met Val Gln Asp Ile Thr Gln Lys Phe
145                 150                 155                 160
Ala His His Ile Ile Ala Gly Arg Leu Met Val Ile His Ala Pro Glu
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Glu Tyr Tyr Pro Ile Leu Asp Gly Leu Lys Arg Asn Tyr Asn Asp Pro
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Glu Asp Arg Val Lys Phe Arg Ser Lys Gln Asn Val Asp Tyr Ala Phe
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Glu Asn Tyr Glu Ala Ser Lys Ala Tyr Ser Ser Val Asp Glu Tyr Phe
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Trp Gly Lys Pro Pro Ser Thr Gly Asp Val Phe Val Ile Val Phe Glu
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Arg Gln Asn Asp Ile Leu His His Gly Ala Leu Asp Val Gly Glu Asn
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Val Met Pro Ser Lys Gln Arg Arg Gln Cys Ser Ser Tyr Leu Arg Leu
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Gly Glu Phe Lys Asn Gly Asn Phe Glu Met Ser Gly Val Asn Gln Lys
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Ile Pro Phe Asp Ile His Cys Met Arg Ile Tyr Val Thr Lys Thr Gln
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<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

<400> 3982

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Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser Lys Lys Lys Tyr
        35                  40                  45
Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His Asp Ile Asp Phe
    50                  55                  60
Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn Lys Tyr Thr Glu
65                  70                  75                  80
Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser
                85                  90                  95
Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser
            100                 105                 110
Arg Asn Pro Thr Phe Met Gly Leu Ala Leu His Cys Ile Ala Ser Val
        115                 120                 125
Gly Ser Arg Glu Met Ala Glu Ala Phe Ala Gly Glu Ile Pro Lys Val
    130                 135                 140
Leu Val Ala Gly Asp Thr Met Asp Ser Val Lys Gln Ser Ala Ala Leu
145                 150                 155                 160
Cys Leu Leu Arg Leu Tyr Arg Thr Ser Pro Asp Leu Val Pro Met Gly
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Asp Trp Thr Ser Arg Val Val His Leu Leu Asn Asp Gln His Leu Gly
            180                 185                 190
Val Val Thr Ala Ala Thr Ser Leu Ile Thr Thr Leu Ala Gln Lys Asn
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Pro Glu Glu Phe Lys Thr Ser Val Ser Leu Ala Val Ser Arg Leu Ser
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Arg Ile Val Thr Ser Ala Ser Thr Asp Leu Gln Asp Tyr Thr Tyr Tyr
225                 230                 235                 240
Phe Val Pro Ala Pro Trp Leu Ser Val Lys Leu Leu Arg Leu Leu Gln
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Cys Tyr Pro Pro Pro Asp Pro Ala Val Arg Gly Arg Leu Thr Glu Cys
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Leu Glu Thr Ile Leu Asn Lys Ala Gln Glu Pro Pro Lys Ser Lys Lys
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Leu Ile Ile His His Asp Ser Glu Pro Asn Leu Leu Val Arg Ala Cys
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Asn Gln Leu Gly Gln Phe Leu Gln His Arg Glu Thr Asn Leu Arg Tyr
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Leu Ala Leu Glu Ser Met Cys Thr Leu Ala Ser Ser Glu Phe Ser His
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Glu Ala Val Lys Thr His Ile Asp Thr Val Ile Asn Ala Leu Lys Thr
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Glu Arg Asp Val Ser Val Arg Gln Arg Ala Ala Asp Leu Leu Tyr Ala
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Met Cys Asp Arg Ser Asn Ala Lys Gln Ile Val Ser Glu Met Leu Ser
385                 390                 395                 400
Tyr Leu Glu Thr Ala Asp Tyr Ser Ile Arg Glu Glu Ile Val Leu Lys
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Val Ala Ile Leu Ala Glu Lys Tyr Ala Val Asp Tyr Thr Trp Tyr Val
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Glu Val Trp Tyr Arg Val Ile Gln Ile Val Ile Asn Arg Asp Asp Val
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Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala Leu Gln Ala Pro Ala
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Cys His Glu Asn Met Val Lys Val Gly Gly Tyr Ile Leu Gly Glu Phe
                485                 490                 495
Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser Pro Pro Val Gln Phe
            500                 505                 510
Ser Leu Leu His Ser Lys Phe His Leu Cys Ser Val Ala Thr Arg Ala
        515                 520                 525
Leu Leu Leu Ser Thr Tyr Ile Lys Phe Val Asn Leu Phe Pro Glu Val
    530                 535                 540
Lys Pro Thr Ile Gln Asp Val Leu Arg Ser Asp Ser Gln Leu Arg Asn
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Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu Tyr Leu Arg Leu Ser
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Thr Val Ala Ser Thr Asp Ile Leu Ala Thr Val Leu Glu Glu Met Pro
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Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala Lys Leu Lys Lys Lys
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Lys Gly Pro Ser Thr Val Thr Asp Leu Glu Asp Thr Lys Arg Asp Arg
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Ser Val Asp Val Asn Gly Gly Pro Glu Pro Ala Pro Ala Ser Thr Ser
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Ala Val Ser Thr Pro Ser Pro Ser Ala Asp Leu Leu Gly Leu Gly Ala
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Ala Pro Pro Ala Pro Ala Gly Pro Pro Pro Ser Ser Gly Gly Ser Gly
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Leu Leu Val Asp Val Phe Ser Asp Ser Ala Ser Val Val Ala Pro Leu
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Ala Pro Gly Ser Glu Asp Asn Phe Ala Arg Phe Val Cys Lys Asn Asn
    690                 695                 700
Gly Val Leu Phe Glu Asn Gln Leu Leu Gln Ile Gly Leu Lys Ser Glu
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Phe Arg Gln Asn Leu Gly Arg Met Phe Ile Phe Tyr Gly Asn Lys Thr
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Ser Thr Gln Phe Leu Asn Phe Thr Pro Thr Leu Ile Cys Ser Asp Asp
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Glu Gly Gly Ala Gln Val Gln Gln Val Val Asn Ile Glu Cys Val Ser
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His Pro Met Asp Thr Glu Val Thr Lys Ala Lys Ile Ile Gly Phe Gly
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Leu Glu Pro Asn Leu Gln Ala Gln Met Tyr Arg Leu Thr Leu Arg Thr
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<212> DNA
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2300

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<212> PRT
<213> Homo sapiens

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Ile Ser Glu Lys Val Leu Thr Lys Glu Val Glu Leu Asp Arg Leu Arg

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Val Ala Gln Gln Glu Asn His His Leu Asn Leu Asp Leu Lys Glu Ala
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Lys Ser Trp Gln Glu Glu Gln Ser Ala Gln Ala Gln Arg Leu Lys Asp
            100                 105                 110
Lys Val Ala Gln Met Lys Asp Thr Leu Gly Gln Ala Gln Gln Arg Val
        115                 120                 125
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Ala Ala Ser Ser Gln Gln Lys Ala Thr Leu Leu Gly Glu Glu Leu Ala
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Arg Leu Glu Val Ala Glu Val Asn Gly Arg Leu Ala Glu Leu Gly Leu
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His Leu Lys Glu Glu Lys Cys Gln Trp Ser Lys Glu Arg Ala Gly Leu
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Leu Gln Ser Val Glu Ala Glu Lys Asp Lys Ile Leu Lys Leu Ser Ala
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Glu Ile Leu Arg Leu Glu Lys Ala Val Gln Glu Glu Lys Thr Gln Asn
225                 230                 235                 240
Gln Val Phe Lys Thr Glu Leu Ala Arg Glu Lys Asp Ser Ser Leu Val
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Gln Leu Ser Glu Ser Lys Arg Glu Leu Thr Glu Leu Arg Ser Ala Leu
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Arg Val Leu Gln Lys Glu Lys Glu Gln Leu Gln Glu Glu Lys Gln Glu
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Leu Leu Glu Tyr Met Arg Lys Leu Glu Ala Arg Leu Glu Lys Val Ala
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Asp Glu Lys Trp Asn Glu Asp Ala Thr Thr Glu Asp Glu Glu Ala Ala
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Val Gly Leu Ser Cys Pro Ala Ala Leu Thr Asp Ser Glu Asp Glu Ser
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Pro Glu Asp Met Arg Leu Pro Pro Tyr Gly Leu Cys Glu Arg Gly Asp
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Pro Gly Ser Ser Pro Ala Gly Pro Arg Glu Ala Ser Pro Leu Val Val
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Ile Ser Gln Pro Ala Pro Ile Ser Pro His Leu Ser Gly Pro Ala Glu
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Asp Ser Ser Ser Asp Ser Glu Ala Glu Asp Glu Lys Ser Val Leu Met
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Ala Ala Val Gln Ser Gly Gly Glu Glu Ala Asn Leu Leu Leu Pro Glu
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Leu Ser Glu Thr Ser Thr Gly Gly Pro Ala Thr Pro Thr Trp Lys Glu
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Cys Pro Ile Cys Lys Glu Arg Phe Pro Ala Glu Ser Asp Lys Asp Ala
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<210> 3985
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<213> Homo sapiens

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35 40 45
Ser Ser Cys Phe Cys Cys Cys Cys Cys Cys Cys Cys Cys Cys Cys Cys
50 55 60
Cys Cys Trp Met Arg Leu Arg Ser Glu Arg Leu Ser Ser Ala Leu Ala
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<211> 1817
<212> PRT
<213> Homo sapiens

<400> 3988
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Leu Gln Glu Thr Gln Gln Leu Leu Gln Met Gln Gln Lys Tyr Leu Glu
35 40 45
Glu Gln Ile Gly Ala His Arg Lys Ser Lys Lys Ala Leu Ser Ala Lys

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Gln Arg Thr Ala Lys Lys Ala Gly Arg Glu Phe Pro Glu Glu Asp Ala
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Glu Gln Leu Lys His Val Thr Glu Gln Gln Ser Met Val Gln Lys Gln
                85                  90                  95
Leu Glu Gln Ile Arg Lys Gln Gln Lys Glu His Ala Glu Leu Ile Glu
            100                 105                 110
Asp Tyr Arg Ile Lys Gln Gln Gln Gln Cys Ala Met Ala Pro Pro Thr
        115                 120                 125
Met Met Pro Ser Val Gln Pro Gln Pro Pro Leu Ile Pro Gly Ala Thr
    130                 135                 140
Pro Pro Thr Met Ser Gln Pro Thr Phe Pro Met Val Pro Gln Gln Leu
145                 150                 155                 160
Gln His Gln Gln His Thr Thr Val Ile Ser Gly His Thr Ser Pro Val
                165                 170                 175
Arg Met Pro Ser Leu Pro Gly Trp Gln Pro Asn Ser Ala Pro Ala His
            180                 185                 190
Leu Pro Leu Asn Pro Pro Arg Ile Gln Pro Pro Ile Ala Gln Leu Pro
        195                 200                 205
Ile Lys Thr Cys Thr Pro Ala Pro Gly Thr Val Ser Asn Ala Asn Pro
    210                 215                 220
Gln Ser Gly Pro Pro Pro Arg Val Glu Phe Asp Asp Asn Asn Pro Phe
225                 230                 235                 240
Ser Glu Ser Phe Gln Glu Arg Glu Arg Lys Glu Arg Leu Arg Glu Gln
                245                 250                 255
Gln Glu Arg Gln Arg Ile Gln Leu Met Gln Glu Val Asp Arg Gln Arg
            260                 265                 270
Ala Leu Gln Gln Arg Met Glu Met Glu Gln His Gly Met Val Gly Ser
        275                 280                 285
Glu Ile Ser Ser Ser Arg Thr Ser Val Ser Gln Ile Pro Phe Tyr Ser
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Ser Asp Leu Pro Cys Asp Phe Met Gln Pro Leu Gly Pro Leu Gln Gln
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Ser Pro Gln His Gln Gln Gln Met Gly Gln Val Leu Gln Gln Gln Asn
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Ile Gln Gln Gly Ser Ile Asn Ser Pro Ser Thr Gln Thr Phe Met Gln
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Thr Asn Glu Arg Arg Gln Val Gly Pro Pro Ser Phe Val Pro Asp Ser
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Pro Ser Ile Pro Val Gly Ser Pro Asn Phe Ser Ser Val Lys Gln Gly
    370                 375                 380
His Gly Asn Leu Ser Gly Thr Ser Phe Gln Gln Ser Pro Val Arg Pro
385                 390                 395                 400
Ser Phe Thr Pro Ala Leu Pro Ala Ala Pro Pro Val Ala Asn Ser Ser
                405                 410                 415
Leu Pro Cys Gly Gln Asp Ser Thr Ile Thr His Gly His Ser Tyr Pro
            420                 425                 430
Gly Ser Thr Gln Ser Leu Ile Gln Leu Tyr Ser Asp Ile Ile Pro Glu
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Glu Lys Lys Lys Lys Lys Arg Thr Arg Lys Lys Lys Arg Asp Asp Asp
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Ala Glu Ser Thr Lys Ala Pro Ser Thr Pro His Ser Asp Ile Thr Ala
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Pro Pro Thr Pro Gly Ile Ser Glu Thr Thr Ser Thr Pro Ala Val Ser
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Leu Glu Asn Lys Leu Pro Asn Ser Asp Phe Ser Gln Ala Thr Pro Asn
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Gln Gln Thr Tyr Ala Asn Ser Glu Val Asp Lys Leu Ser Met Glu Thr
545                 550                 555                 560
Pro Ala Lys Thr Glu Glu Ile Lys Leu Glu Lys Ala Glu Thr Glu Ser
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Cys Pro Gly Gln Glu Glu Pro Lys Leu Glu Glu Gln Asn Gly Ser Lys
            580                 585                 590
Val Glu Gly Asn Ala Val Ala Cys Pro Val Ser Ser Ala Gln Ser Pro
        595                 600                 605
Pro His Ser Ala Gly Ala Pro Ala Ala Lys Gly Asp Ser Gly Asn Glu
    610                 615                 620
Leu Leu Lys His Leu Leu Lys Asn Lys Lys Ser Ser Ser Leu Leu Asn
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Gln Lys Pro Glu Gly Ser Ile Cys Ser Glu Asp Asp Cys Thr Lys Asp
                645                 650                 655
Asn Lys Leu Val Glu Lys Gln Asn Pro Ala Glu Gly Leu Gln Thr Leu
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Gly Ala Gln Met Gln Gly Gly Phe Gly Cys Gly Asn Gln Leu Pro Lys
        675                 680                 685
Thr Asp Gly Gly Ser Glu Thr Lys Lys Gln Arg Ser Lys Arg Thr Gln
    690                 695                 700
Arg Thr Gly Glu Lys Ala Ala Pro Arg Ser Lys Lys Arg Lys Lys Asp
705                 710                 715                 720
Glu Glu Glu Lys Gln Ala Met Tyr Ser Ser Thr Asp Thr Phe Thr His
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Leu Lys Gln Val Arg Gln Leu Ser Leu Leu Pro Leu Met Glu Pro Ile
            740                 745                 750
Ile Gly Val Asn Phe Ala His Phe Leu Pro Tyr Gly Ser Gly Gln Phe
        755                 760                 765
Asn Ser Gly Asn Arg Leu Leu Gly Thr Phe Gly Ser Ala Thr Leu Glu
    770                 775                 780
Gly Val Ser Asp Tyr Tyr Ser Gln Leu Ile Tyr Lys Gln Asn Asn Leu
785                 790                 795                 800
Ser Asn Pro Pro Thr Pro Pro Ala Ser Leu Pro Pro Thr Pro Pro Pro
                805                 810                 815
Met Ala Cys Gln Lys Met Ala Asn Gly Phe Ala Thr Thr Glu Glu Leu
            820                 825                 830
Ala Gly Lys Ala Gly Val Leu Val Ser His Glu Val Thr Lys Thr Leu
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Gly Pro Lys Pro Phe Gln Leu Pro Phe Arg Pro Gln Asp Asp Leu Leu
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Ala Arg Ala Leu Ala Gln Gly Pro Lys Thr Val Asp Val Pro Ala Ser
865                 870                 875                 880
Leu Pro Thr Pro Pro His Asn Asn Gln Glu Glu Leu Arg Ile Gln Asp
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His Cys Gly Asp Arg Asp Thr Pro Asp Ser Phe Val Pro Ser Ser Ser
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Pro Glu Ser Val Val Gly Val Glu Val Ser Arg Tyr Pro Asp Leu Ser
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Leu Val Lys Glu Glu Pro Pro Glu Pro Val Pro Ser Pro Ile Ile Pro
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Ile Leu Pro Ser Thr Ala Gly Lys Ser Ser Glu Ser Arg Arg Asn Asp
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Ile Lys Thr Glu Pro Gly Thr Leu Tyr Phe Ala Ser Pro Phe Gly Pro
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Ser Pro Asn Gly Pro Arg Ser Gly Leu Ile Ser Val Ala Ile Thr Leu
            980                 985                 990
His Pro Thr Ala Ala Glu Asn Ile Ser Ser Val Val Ala Ala Phe Ser
        995                 1000                1005
Asp Leu Leu His Val Arg Ile Pro Asn Ser Tyr Glu Val Ser Ser Ala
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Pro Asp Val Pro Ser Met Gly Leu Val Ser Ser His Arg Ile Asn Pro
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Gly Leu Glu Tyr Arg Gln His Leu Leu Leu Arg Gly Pro Pro Pro Gly
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Ser Ala Asn Pro Pro Arg Leu Val Ser Ser Tyr Arg Leu Lys Gln Pro
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Asn Val Pro Phe Pro Pro Thr Ser Asn Gly Leu Ser Gly Tyr Lys Asp
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Ser Ser His Gly Ile Ala Glu Ser Ala Ala Leu Arg Pro Gln Trp Cys
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Cys His Cys Lys Val Val Ile Leu Gly Ser Gly Val Arg Lys Ser Phe
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Lys Asp Leu Thr Leu Leu Asn Lys Asp Ser Arg Glu Ser Thr Lys Arg
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Ser Leu Pro Gln Ser Pro Met Arg Glu Thr Pro Ser Lys Ala Phe His
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Gln Tyr Ser Asn Asn Ile Ser Thr Leu Asp Val His Cys Leu Pro Gln
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Leu Pro Glu Lys Ala Ser Pro Pro Ala Ser Pro Pro Ile Ala Phe Pro
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Pro Ala Phe Glu Ala Ala Gln Val Glu Ala Lys Pro Asp Glu Leu Lys
            1220                1225                1230
Val Thr Val Lys Leu Lys Pro Arg Leu Arg Ala Val His Gly Gly Phe
        1235                1240                1245
Glu Asp Cys Arg Pro Leu Asn Lys Lys Trp Arg Gly Met Lys Trp Lys
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Lys Trp Ser Ile His Ile Val Ile Pro Lys Gly Thr Phe Lys Pro Pro
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Cys Glu Asp Glu Ile Asp Glu Phe Leu Lys Lys Leu Gly Thr Ser Leu
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Lys Pro Asp Pro Val Pro Lys Asp Tyr Arg Lys Cys Cys Phe Cys His
            1300                1305                1310
Glu Glu Gly Asp Gly Leu Thr Asp Gly Pro Ala Arg Leu Leu Asn Leu
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Asp Leu Asp Leu Trp Val His Leu Asn Cys Ala Leu Trp Ser Thr Glu
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Val Tyr Glu Thr Gln Ala Gly Ala Leu Ile Asn Val Glu Leu Ala Leu
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Ser Ser Gln Tyr Arg Lys Met Lys Thr Glu Trp Lys Ser Asn Val Tyr
1665 1670 1675 1680
Leu Ala Arg Ser Arg Ile Gln Gly Leu Gly Leu Tyr Ala Ala Arg Asp
1685 1690 1695
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Asn Glu Val Ala Asn Arg Lys Glu Lys Leu Tyr Glu Ser Gln Asn Arg
1715 1720 1725
Gly Val Tyr Met Phe Arg Met Asp Asn Asp His Val Ile Asp Ala Thr
1730 1735 1740
Leu Thr Gly Gly Pro Ala Arg Tyr Ile Asn His Ser Cys Ala Pro Asn
1745 1750 1755 1760
Cys Val Ala Glu Val Val Thr Phe Glu Arg Gly His Lys Ile Ile Ile
1765 1770 1775
Ser Ser Ser Arg Arg Ile Gln Lys Gly Glu Glu Leu Cys Tyr Asp Tyr

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<212> DNA
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<211> 955
<212> PRT
<213> Homo sapiens

<400> 3990
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35 40 45
Ser Arg Ser Arg Ser Tyr Ser Pro Ala His Asn Arg Glu Arg Asn His
50 55 60
Pro Arg Val Tyr Gln Asn Arg Asp Phe Arg Gly His Asn Arg Gly Tyr
65 70 75 80
Arg Arg Pro Tyr Tyr Phe Arg Gly Arg Asn Arg Gly Phe Tyr Pro Trp
85 90 95
Gly Gln Tyr Asn Arg Gly Gly Tyr Gly Asn Tyr Arg Ser Asn Trp Gln
100 105 110
Asn Tyr Arg Gln Ala Tyr Ser Pro Arg Arg Gly Arg Ser Arg Ser Arg
115 120 125
Ser Pro Lys Arg Arg Ser Pro Ser Pro Arg Ser Arg Ser His Ser Arg
130 135 140
Asn Ser Asp Lys Ser Ser Ser Asp Arg Ser Arg Arg Ser Ser Ser Ser
145 150 155 160
Arg Ser Ser Ser Asn His Ser Arg Val Glu Ser Ser Lys Arg Lys Ser
165 170 175
Ala Lys Glu Lys Lys Ser Ser Ser Lys Asp Ser Arg Pro Ser Gln Ala
180 185 190
Ala Gly Asp Asn Gln Gly Asp Glu Val Lys Glu Gln Thr Phe Ser Gly
195 200 205
Gly Thr Ser Gln Asp Thr Lys Ala Ser Glu Ser Ser Lys Pro Trp Pro
210 215 220
Asp Ala Thr Tyr Gly Thr Gly Ser Ala Ser Arg Ala Ser Ala Val Ser
225 230 235 240
Glu Leu Ser Pro Arg Glu Arg Ser Pro Ala Leu Lys Ser Pro Leu Gln
245 250 255
Ser Val Val Val Arg Arg Arg Ser Pro Arg Pro Ser Pro Val Pro Lys
260 265 270
Pro Ser Pro Pro Leu Ser Ser Thr Ser Gln Met Gly Ser Thr Leu Pro
275 280 285
Ser Gly Ala Gly Tyr Gln Ser Gly Thr His Gln Gly Gln Phe Asp His
290 295 300
Gly Ser Gly Ser Leu Ser Pro Ser Lys Lys Ser Pro Val Gly Lys Ser
305 310 315 320
Pro Pro Ser Thr Gly Ser Thr Tyr Gly Ser Ser Gln Lys Glu Glu Ser
325 330 335
Ala Ala Ser Gly Gly Ala Ala Tyr Thr Lys Arg Tyr Leu Glu Glu Gln
340 345 350
Lys Thr Glu Asn Gly Lys Asp Lys Glu Gln Lys Gln Thr Asn Thr Asp

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        355                 360                 365
Lys Glu Lys Ile Lys Glu Lys Gly Ser Phe Ser Asp Thr Gly Leu Gly
    370                 375                 380
Asp Gly Lys Met Lys Ser Asp Ser Phe Ala Pro Lys Thr Asp Ser Glu
385                 390                 395                 400
Lys Pro Phe Arg Gly Ser Gln Ser Pro Lys Arg Tyr Lys Leu Arg Asp
                405                 410                 415
Asp Phe Glu Lys Lys Met Ala Asp Phe His Lys Glu Glu Met Asp Asp
            420                 425                 430
Gln Asp Lys Asp Lys Ala Lys Gly Arg Lys Glu Ser Glu Phe Asp Asp
        435                 440                 445
Glu Pro Lys Phe Met Ser Lys Val Ile Gly Ala Asn Lys Asn Gln Glu
    450                 455                 460
Glu Glu Lys Ser Gly Lys Trp Glu Gly Leu Val Tyr Ala Pro Pro Gly
465                 470                 475                 480
Lys Glu Lys Gln Arg Lys Thr Glu Glu Leu Glu Glu Glu Ser Phe Pro
                485                 490                 495
Glu Arg Ser Lys Lys Glu Asp Arg Gly Lys Arg Ser Glu Gly Gly His
            500                 505                 510
Arg Gly Phe Val Pro Glu Lys Asn Phe Arg Val Thr Ala Tyr Lys Ala
        515                 520                 525
Val Gln Glu Lys Ser Ser Ser Pro Pro Pro Arg Lys Thr Ser Glu Ser
    530                 535                 540
Arg Asp Lys Leu Gly Ala Lys Gly Asp Phe Pro Thr Gly Lys Ser Ser
545                 550                 555                 560
Phe Ser Ile Thr Arg Glu Ala Gln Val Asn Val Arg Met Asp Ser Phe
                565                 570                 575
Asp Glu Asp Leu Ala Arg Pro Ser Gly Leu Leu Ala Gln Glu Arg Lys
            580                 585                 590
Leu Cys Arg Asp Leu Val His Ser Asn Lys Lys Glu Gln Glu Phe Arg
        595                 600                 605
Ser Ile Phe Gln His Ile Gln Ser Ala Gln Ser Gln Arg Ser Pro Ser
    610                 615                 620
Glu Leu Phe Ala Gln His Ile Val Thr Ile Val His His Val Lys Glu
625                 630                 635                 640
His His Phe Gly Ser Ser Gly Met Thr Leu His Glu Arg Phe Thr Lys
                645                 650                 655
Tyr Leu Lys Arg Gly Thr Glu Gln Glu Ala Ala Lys Asn Lys Lys Ser
            660                 665                 670
Pro Glu Ile His Arg Arg Ile Asp Ile Ser Pro Ser Thr Phe Arg Lys
        675                 680                 685
His Gly Leu Ala His Asp Glu Met Lys Ser Pro Arg Glu Pro Gly Tyr
    690                 695                 700
Lys Ala Glu Gly Lys Tyr Lys Asp Asp Pro Val Asp Leu Arg Leu Asp
705                 710                 715                 720
Ile Glu Arg Arg Lys Lys His Lys Glu Arg Asp Leu Lys Arg Gly Lys
                725                 730                 735
Ser Arg Glu Ser Val Asp Ser Arg Asp Ser Ser His Ser Arg Glu Arg
            740                 745                 750
Ser Ala Glu Lys Thr Glu Lys Thr His Lys Gly Ser Lys Lys Gln Lys
        755                 760                 765
Lys His Arg Arg Ala Arg Asp Arg Ser Arg Ser Ser Ser Ser Ser Ser
    770                 775                 780
Gln Ser Ser His Ser Tyr Lys Ala Glu Glu Tyr Thr Glu Glu Thr Glu
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785                 790                 795                 800
Glu Arg Glu Glu Ser Thr Thr Gly Phe Asp Lys Ser Arg Leu Gly Thr
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Lys Asp Phe Val Gly Pro Ser Glu Arg Gly Gly Gly Arg Ala Arg Gly
            820                 825                 830
Thr Phe Gln Phe Arg Ala Arg Gly Arg Gly Trp Gly Arg Gly Asn Tyr
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Ser Gly Asn Asn Asn Asn Asn Ser Asn Asn Asp Phe Gln Lys Arg Asn
    850                 855                 860
Arg Glu Glu Glu Trp Asp Pro Glu Tyr Thr Pro Lys Ser Lys Lys Tyr
865                 870                 875                 880
Tyr Leu His Asp Asp Arg Glu Gly Glu Gly Ser Asp Lys Trp Val Ser
                885                 890                 895
Arg Gly Arg Gly Arg Gly Ala Phe Pro Arg Gly Arg Gly Arg Phe Met
            900                 905                 910
Phe Arg Lys Ser Ser Thr Ser Pro Lys Trp Ala His Asp Lys Phe Ser
        915                 920                 925
Gly Glu Glu Gly Glu Ile Glu Asp Asp Glu Ser Gly Thr Glu Asn Arg
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<211> 381
<212> DNA
<213> Homo sapiens

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240
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<210> 3992
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<212> PRT
<213> Homo sapiens

<400> 3992
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Pro Phe Glu Pro Ala Pro Tyr Gln Gln Gly Met Tyr Tyr Thr Pro Pro
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Pro Gln Cys Val Ser Arg Phe Val Arg Pro Pro Pro Ser Ala Pro Glu
    50                  55                  60
Pro Ala Pro Pro Tyr Leu Asp His Tyr Pro Pro Tyr Leu Gln Glu Arg
65                  70                  75                  80
Val Val Asn Ser Gln Tyr Gly Thr Gln Pro Gln Gln Tyr Pro Pro Ile
                85                  90                  95
Tyr Pro Ser His Tyr Asp Gly Arg Arg Val Tyr Pro Ala Pro Ser Tyr
            100                 105                 110
Thr Arg Glu Glu Ile Phe Arg Glu Ser Pro Ile Pro Ile Glu Ile
        115                 120                 125
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<212> DNA
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394

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<212> PRT
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<400> 3994
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Thr Glu Gly Ala Asn Ile Asn Lys Pro Asp Cys Glu Gly Glu Thr Pro
        35                  40                  45
Ile His Lys Ala Ala Arg Ser Gly Ser Leu Glu Cys Ile Ser Ala Leu
    50                  55                  60
Val Ala Asn Gly Ala His Val Glu
65                  70
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<212> DNA
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<210> 3996
<211> 235
<212> PRT
<213> Homo sapiens

<400> 3996
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35 40 45
Gly Ser Asn Pro Thr Pro Pro Ala Ser Val Met Gly Ser Pro Pro Ser
50 55 60
Ser Leu Gln Glu Ala Gln Arg Gly Arg Ala Ala Ser His Ser Arg Ala
65 70 75 80
Leu Thr Leu Pro Ser Ala Leu His Phe Ala Ser Ser Leu Leu Leu Thr
85 90 95
Arg Ala Gly Ala Asn Val His Glu Ala Cys Thr Phe Asp Asp Thr Ser
100 105 110
Glu Gly Ala Val His Tyr Phe Tyr Asp Glu Ser Glv Val Arg Arg Ser
115 120 125
Tyr Thr Phe Gly Leu Ala Gly Gly Gly Tyr Glu Asn Pro Val Gly Gln
130 135 140
Gln Gly Glu Gln Thr Ala Asn Gly Ala Trp Asp Arg His Ser His Ser
145 150 155 160
Ser Ser Phe His Ser Ala Asp Val Pro Glu Ala Thr Gly Gly Leu Asn
165 170 175
Leu Leu Gln Pro Arg Pro Val Val Leu Gln Gly Met Gln Val Arg Arg

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            180                 185                 190
Val Pro Leu Glu Ile Pro Glu Phe Asp Leu Leu Asp Gln Asp Ser Leu
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His Glu Ser Gln Glu Gln Thr Leu Met Glu Glu Ala Pro Pro Arg Ala
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Gln His Ser Tyr Lys Tyr Leu Gly Phe Gly Glu
225                 230                 235

<210> 3997
<211> 7484
<212> DNA
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His Asp Arg Phe Glu Glu Ser Ala Lys Ala Tyr His Glu Leu Leu Glu
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Ala Ser Leu Leu Arg Glu Ala Val Ser Ser Gly Asp Glu Lys Glu Gly
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Leu Lys His Pro Gly Leu Ile Leu Lys Tyr Ser Thr Tyr Lys Asn Leu
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Ala Gln Leu Ala Ala Gln Arg Glu Asp Leu Glu Thr Ala Met Glu Phe
            100                 105                 110
Tyr Leu Glu Ala Val Met Leu Asp Ser Thr Asp Val Asn Leu Trp Tyr
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Lys Ile Gly His Val Ala Leu Arg Leu Ile Arg Ile Pro Leu Ala Arg
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His Ala Phe Glu Glu Gly Leu Arg Cys Asn Pro Asp His Trp Pro Cys
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Cys Leu Tyr Phe Ile Cys Lys Ala Leu Glu Lys Asp Cys Arg Tyr Ser
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Lys Gly Leu Val Leu Lys Glu Lys Ile Phe Glu Glu Gln Pro Cys Leu
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Arg Lys Asp Ser Leu Arg Met Phe Leu Lys Cys Asp Met Ser Ile His
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Asp Val Ser Val Ser Ala Ala Glu Thr Gln Ala Ile Val Asp Glu Ala
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Pro Asp Leu Lys Leu Val Gln Pro Ile Pro Phe Phe Thr Trp Lys Cys
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Leu Gly Glu Ser Leu Leu Ala Met Tyr Asn His Leu Thr Thr Cys Glu
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Pro Pro Arg Pro Ser Leu Gly Lys Arg Ile Asp Leu Ser Asp Tyr Gln
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Asp Pro Ser Gln Pro Leu Glu Ser Ser Met Val Val Thr Pro Val Asn
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Val Ile Gln Pro Ser Thr Val Ser Thr Asn Pro Ala Val Ala Val Ala
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Glu Pro Val Val Ser Tyr Thr Ser Val Ala Thr Thr Ser Phe Pro Leu
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His Ser Pro Gly Leu Leu Glu Thr Gly Ala Pro Val Gly Asp Ile Ser
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Gly Gly Asp Lys Ser Lys Lys Gly Val Lys Arg Lys Lys Ile Ser Glu
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Ser Val Tyr His Ser Trp Arg Arg His Ser Thr Ser Leu Pro Asn Pro
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Ser Leu Ser Cys Met Glu Leu Gln Leu Asp Gln Trp Leu Leu Thr Lys
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Gly Arg Ser Ser Ala Val Ser Pro Arg Asn Cys Pro Ala Gly Met Val
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Asn Gly Arg Phe Gly Pro Asp Phe Pro Gly Thr His Cys Leu Gly Asp
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Leu Leu Gln Leu Ser Phe Ala Ser Ser Gln Arg Asp Leu Phe Glu Asp
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Gly Trp Leu Glu Phe Val Val Arg Val Tyr Trp Leu Lys Ala Arg Phe
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Cys Thr Glu Met Leu Gln Ser Ser Thr Ala Ile Gln Val Glu Ala Gly
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Ala Glu Arg Arg Asp Ile Val Ile Arg Leu Pro Asn Leu His Asn Asp
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Ser Val Val Ser Leu Glu Glu Ile Asp Lys Asn Leu Lys Ser Leu Glu
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Tyr Lys Ala Val Val His Leu Leu Arg Pro Thr Leu Cys Thr Ser Gly
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Phe Asp Arg Ala Lys His Leu Glu Phe Met Thr Ser Ile Pro Glu Arg
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Pro Ala Gln Leu Leu Leu Leu Gln Asp Ser Leu Leu Arg Leu Lys Asp
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Leu Arg Phe Tyr Val Arg Val Leu Gln Lys Glu Leu Ala Ala Ser Thr
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480
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780
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1080
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1140

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1500
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1560
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1680
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1740
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1800
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2280
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2340
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2400
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2546

<210> 4000
<211> 606
<212> PRT
<213> Homo sapiens

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Glu Glu Leu Cys Thr Pro Pro Asp Pro Gly Ala Ala Phe Val Val Val
35 40 45
Glu Cys Pro Asp Glu Ser Phe Ile Gln Pro Ile Cys Glu Asn Ala Thr
50 55 60
Phe Gln Arg Tyr Gln Gly Lys Ala Asp Ala Pro Val Ala Leu Val Val
65 70 75 80
His Met Ala Pro Ala Ser Val Leu Val Asp Ser Arg Tyr Gln Gln Trp
85 90 95
Met Glu Arg Phe Gly Pro Asp Thr Gln His Leu Val Leu Asn Glu Asn
100 105 110
Cys Ala Ser Val His Asn Leu Arg Ser His Lys Ile Gln Thr Gln Leu
115 120 125
Asn Leu Ile His Pro Asp Ile Phe Pro Leu Leu Thr Ser Phe Arg Cys
130 135 140
Lys Lys Glu Gly Pro Thr Leu Ser Val Pro Met Val Gln Gly Glu Cys
145 150 155 160
Leu Leu Lys Tyr Gln Leu Arg Pro Arg Arg Glu Trp Gln Arg Asp Ala
165 170 175
Ile Ile Thr Cys Asn Pro Glu Glu Phe Ile Val Glu Ala Leu Gln Leu
180 185 190
Pro Asn Phe Gln Gln Ser Val Gln Glu Tyr Arg Arg Ser Ala Gln Asp
195 200 205
Gly Pro Ala Pro Ala Glu Lys Arg Ser Gln Tyr Pro Glu Ile Ile Phe
210 215 220
Leu Gly Thr Gly Ser Ala Ile Pro Met Lys Ile Arg Asn Val Ser Ala
225 230 235 240
Thr Leu Val Asn Ile Ser Pro Asp Thr Ser Leu Leu Leu Asp Cys Gly
245 250 255
Glu Gly Thr Phe Gly Gln Leu Cys Arg His Tyr Gly Asp Gln Val Asp
260 265 270
Arg Val Leu Gly Thr Leu Ala Ala Val Phe Val Ser His Leu His Ala
275 280 285
Asp His His Thr Gly Leu Pro Ser Ile Leu Leu Gln Arg Glu Arg Ala
290 295 300
Leu Ala Ser Leu Gly Lys Pro Leu His Pro Leu Leu Val Val Ala Pro
305 310 315 320
Asn Gln Leu Lys Ala Trp Leu Gln Gln Tyr His Asn Gln Cys Gln Glu
325 330 335
Val Leu His His Ile Ser Met Ile Pro Ala Lys Cys Leu Gln Glu Gly
340 345 350
Ala Glu Ile Ser Ser Pro Ala Val Glu Arg Leu Ile Ser Ser Leu Leu
355 360 365
Arg Thr Cys Asp Leu Glu Glu Phe Gln Thr Cys Leu Val Arg His Cys
370 375 380
Lys His Ala Phe Gly Cys Ala Leu Val His Thr Ser Gly Trp Lys Val
385 390 395 400
Val Tyr Ser Gly Asp Thr Met Pro Cys Glu Ala Leu Val Arg Met Gly
405 410 415
Lys Asp Ala Thr Leu Leu Ile His Glu Ala Thr Leu Glu Asp Gly Leu

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            420                 425                 430
Glu Glu Glu Ala Val Glu Lys Thr His Ser Thr Thr Ser Gln Ala Ile
        435                 440                 445
Ser Val Gly Met Arg Met Asn Ala Glu Phe Ile Met Leu Asn His Phe
    450                 455                 460
Ser Gln Arg Tyr Ala Lys Val Pro Leu Phe Ser Pro Asn Phe Ser Glu
465                 470                 475                 480
Lys Val Gly Val Ala Phe Asp His Met Lys Val Cys Phe Gly Asp Phe
                485                 490                 495
Pro Thr Met Pro Lys Leu Ile Pro Pro Thr Glu Ser Pro Val Cys Trp
            500                 505                 510
Arg His Arg Gly Asp Gly Gly Ala Gln Gly Glu Ala Gly Ala Ala Ala
        515                 520                 525
Gly Ala Gly Gly Pro Pro Val Gln Gly Ala Gly Arg Arg Pro Gly Gly
    530                 535                 540
Trp Gly Ala Ser Ala Glu Ala Gly Pro His Arg Gly Ala Thr Gly Gln
545                 550                 555                 560
Glu Gly Gln Ser Pro Val Lys Ile Trp Glu Thr Leu Asn Ser Glu Gly
                565                 570                 575
Cys Val Ser Ser Ala Pro Arg Thr His Pro Tyr Leu Pro Ser Leu Leu
            580                 585                 590
Val Glu Ala Glu Glu His Gly Pro Pro Gly Gly Ser Ser Gly
        595                 600                 605
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<210> 4001
<211> 1251
<212> DNA
<213> Homo sapiens

<400> 4001
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cagagctctc cagagttcaa gggctccctg gcctccctct cagacagctt gggggtgtct
120
gtcatggcca ccgaccagga ctcctactcc accagcagca cggaggagga gctggagcag
180
ttcagcagcc ccagcgtgaa gaagaagccc tccatgatcc tgggcaaggc tcggcaccgg
240
ctgagctttg ccagtttcag cagcatgttc cacgctttcc tctccaacaa ccgcaagctg
300
tacaagaagg tggtggagct ggcgcaggac aagggctcgt actttggcag cctggtgcag
360
gactacaagg tgtacagcct ggagatgatg gcgcgccaga cctccagcac ggagatgctg
420
caggagattc gcaccatgat gacccagctc aagagctacc tgctgcagag caccgagctc
480
aaggccctgg tggaccccgc cctgcactcc gaggaggagc tcgaagcaat tgtagagtct
540
gccttgtaca aatgtgtcct gaagcccctg aaggaagcca tcaactcatg cctgcatcag
600
atccacagca aggatggttc gctgcagcag ctcaaggaga accagttagt gatcctggcc
660
accaccacca ctgacctagg tgtgaccacc agcgtgccgg aggtgcccat gatggagaag
720

atcctgcaga agttcaccag catgcacaag gcctactcac ctgagaagaa gatctccatc
780
ctgctcaaga cctgcaaact catctacgac tccatggccc tcggcaaccc agggaagccc
840
tatggggcgg atgacttcct gcctgtgctc atgtatgtgc tggcccgcag caacctcacg
900
gagatgcttc tcaatgtgga gtacatgatg gagctcatgg accccgccct gcagctgggg
960
gagggttcct actatctgac caccacctac ggggccctgg agcacatcaa gagctacgac
1020
aagatcacgg tgacccggca gctgagtgtg gaggtgcagg actccatcca ccgctgggag
1080
cgccggcgta ctctcaacaa ggcccgggcc tcccgctcct ccgtacagga cttcatctgc
1140
gtgtcgtacc tggagcccga gcagcaggcg cggacgctgg cgtcgcgggc ggacacccag
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gcccaggcgc tgtgcgcgca gtgcgcggag aagttcgcgg tggagcggcc g
1251

<210> 4002
<211> 417
<212> PRT
<213> Homo sapiens

<400> 4002
Glu Ser Pro Ala Ser Gln Ala Gly Thr Gln His Pro Pro Ala Gln Pro
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Thr Ala His Ser Gln Ser Ser Pro Glu Phe Lys Gly Ser Leu Ala Ser
            20   25   30
Leu Ser Asp Ser Leu Gly Val Ser Val Met Ala Thr Asp Gln Asp Ser
        35   40   45
Tyr Ser Thr Ser Ser Thr Glu Glu Glu Leu Glu Gln Phe Ser Ser Pro
    50   55   60
Ser Val Lys Lys Lys Pro Ser Met Ile Leu Gly Lys Ala Arg His Arg
65   70   75   80
Leu Ser Phe Ala Ser Phe Ser Ser Met Phe His Ala Phe Leu Ser Asn
                85   90   95
Asn Arg Lys Leu Tyr Lys Lys Val Val Glu Leu Ala Gln Asp Lys Gly
            100   105   110
Ser Tyr Phe Gly Ser Leu Val Gln Asp Tyr Lys Val Tyr Ser Leu Glu
        115   120   125
Met Met Ala Arg Gln Thr Ser Ser Thr Glu Met Leu Gln Glu Ile Arg
    130   135   140
Thr Met Met Thr Gln Leu Lys Ser Tyr Leu Leu Gln Ser Thr Glu Leu
145   150   155   160
Lys Ala Leu Val Asp Pro Ala Leu His Ser Glu Glu Glu Leu Glu Ala
                165   170   175
Ile Val Glu Ser Ala Leu Tyr Lys Cys Val Leu Lys Pro Leu Lys Glu
            180   185   190
Ala Ile Asn Ser Cys Leu His Gln Ile His Ser Lys Asp Gly Ser Leu
        195   200   205
Gln Gln Leu Lys Glu Asn Gln Leu Val Ile Leu Ala Thr Thr Thr Thr
    210   215   220
Asp Leu Gly Val Thr Thr Ser Val Pro Glu Val Pro Met Met Glu Lys

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225                 230                 235                 240
Ile Leu Gln Lys Phe Thr Ser Met His Lys Ala Tyr Ser Pro Glu Lys
                245                 250                 255
Lys Ile Ser Ile Leu Leu Lys Thr Cys Lys Leu Ile Tyr Asp Ser Met
            260                 265                 270
Ala Leu Gly Asn Pro Gly Lys Pro Tyr Gly Ala Asp Asp Phe Leu Pro
        275                 280                 285
Val Leu Met Tyr Val Leu Ala Arg Ser Asn Leu Thr Glu Met Leu Leu
    290                 295                 300
Asn Val Glu Tyr Met Met Glu Leu Met Asp Pro Ala Leu Gln Leu Gly
305                 310                 315                 320
Glu Gly Ser Tyr Tyr Leu Thr Thr Thr Tyr Gly Ala Leu Glu His Ile
                325                 330                 335
Lys Ser Tyr Asp Lys Ile Thr Val Thr Arg Gln Leu Ser Val Glu Val
            340                 345                 350
Gln Asp Ser Ile His Arg Trp Glu Arg Arg Arg Thr Leu Asn Lys Ala
        355                 360                 365
Arg Ala Ser Arg Ser Ser Val Gln Asp Phe Ile Cys Val Ser Tyr Leu
    370                 375                 380
Glu Pro Glu Gln Gln Ala Arg Thr Leu Ala Ser Arg Ala Asp Thr Gln
385                 390                 395                 400
Ala Gln Ala Leu Cys Ala Gln Cys Ala Glu Lys Phe Ala Val Glu Arg
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<210> 4003
<211> 581
<212> DNA
<213> Homo sapiens

<400> 4003
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120
cgagcaaaag atgtgataat accagcaaag ccacctgtca gctttttctc cttgaggtct
180
ccagtccttg acctcttcca ggggcagctg gattatgcag agtacgttcg acgggattca
240
gaggtggtac tgctcttctt ctatgcccct tggtgtggac agtccatcgc tgccagggca
300
gaaattgagc aagcagcaag tcggctttca gatcaggtgt tgtttgtggc aattaactgt
360
tggtggaacc aggggaaatg cagaaaacag aaacacttct tttattttcc tgtaatatat
420
ctgtatcatc ggagttttgg accaatcgaa tacaaaggcc cccatgagtg ctgtttacat
480
tgagaagttt gtccgccggg tgatgaaacc acttctctac atcccatctc aatcagaatt
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actagatttt ctctcaaact acgagcctgg agtactcgcg a
581

<210> 4004

<211> 160
<212> PRT
<213> Homo sapiens

<400> 4004
Xaa Arg Leu Arg Arg Gly Leu Arg Gly Ala Phe Leu Met Ala Arg Gln
1 5 10 15
Arg Pro Glu Leu Leu Cys Gly Ala Val Ala Leu Gly Cys Ala Leu Leu
20 25 30
Leu Ala Leu Lys Phe Thr Cys Ser Arg Ala Lys Asp Val Ile Ile Pro
35 40 45
Ala Lys Pro Pro Val Ser Phe Phe Ser Leu Arg Ser Pro Val Leu Asp
50 55 60
Leu Phe Gln Gly Gln Leu Asp Tyr Ala Glu Tyr Val Arg Arg Asp Ser
65 70 75 80
Glu Val Val Leu Leu Phe Phe Tyr Ala Pro Trp Cys Gly Gln Ser Ile
85 90 95
Ala Ala Arg Ala Glu Ile Glu Gln Ala Ala Ser Arg Leu Ser Asp Gln
100 105 110
Val Leu Phe Val Ala Ile Asn Cys Trp Trp Asn Gln Gly Lys Cys Arg
115 120 125
Lys Gln Lys His Phe Phe Tyr Phe Pro Val Ile Tyr Leu Tyr His Arg
130 135 140
Ser Phe Gly Pro Ile Glu Tyr Lys Gly Pro His Glu Cys Cys Leu His
145 150 155 160

<210> 4005
<211> 666
<212> DNA
<213> Homo sapiens

<400> 4005
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cttcatgaag taatcacaaa tgaacacgtg gtagctatga tgaaagcagc catcagtgag
120
acggaagata tgccaatgtt tgagcctaaa atgacacgct ctaaactgaa ggaagtagtg
180
gaaaaaggaa tggtaattcc aacatggaat atttcaccaa ttaagaaggc caatgaaatt
240
aagcctcctc agtttgtgga tatccacctt gaagaagatg attcctcaga tgaagaatac
300
cagccggatg atgaagaaga agatgaaact gctgaagaga gcttattgga aagtgatgtt
360
gaaagcactg cttcatctcc acgtggggca aagaaatcca gattgaggca gtcttctgag
420
atgactgaaa cagatgagga gagtggcata ttatcagagg ctgagaaagt caccacacca
480
gccatcaggc acatcagtgc tgaggtagtg cccatggggc ccccgccccc tccaaagccg
540
aaacagacca gagatagtac tttcatggag aagttacatg cggtagatga ggagctggct
600
tccagtccag tctgcatgga ttctttccag cccatggatg acagtctcat tgcatttcga
660

acgcgt
666

<210> 4006
<211> 222
<212> PRT
<213> Homo sapiens

<400> 4006
Gly Thr Leu Glu Asp Gly Ala Lys Gln His Asn Leu Thr Ala Val Asn
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Val Arg Asn Ile Leu His Glu Val Ile Thr Asn Glu His Val Val Ala
20 25 30
Met Met Lys Ala Ala Ile Ser Glu Thr Glu Asp Met Pro Met Phe Glu
35 40 45
Pro Lys Met Thr Arg Ser Lys Leu Lys Glu Val Val Glu Lys Gly Met
50 55 60
Val Ile Pro Thr Trp Asn Ile Ser Pro Ile Lys Lys Ala Asn Glu Ile
65 70 75 80
Lys Pro Pro Gln Phe Val Asp Ile His Leu Glu Glu Asp Asp Ser Ser
85 90 95
Asp Glu Glu Tyr Gln Pro Asp Asp Glu Glu Glu Asp Glu Thr Ala Glu
100 105 110
Glu Ser Leu Leu Glu Ser Asp Val Glu Ser Thr Ala Ser Ser Pro Arg
115 120 125
Gly Ala Lys Lys Ser Arg Leu Arg Gln Ser Ser Glu Met Thr Glu Thr
130 135 140
Asp Glu Glu Ser Gly Ile Leu Ser Glu Ala Glu Lys Val Thr Thr Pro
145 150 155 160
Ala Ile Arg His Ile Ser Ala Glu Val Val Pro Met Gly Pro Pro Pro
165 170 175
Pro Pro Lys Pro Lys Gln Thr Arg Asp Ser Thr Phe Met Glu Lys Leu
180 185 190
His Ala Val Asp Glu Glu Leu Ala Ser Ser Pro Val Cys Met Asp Ser
195 200 205
Phe Gln Pro Met Asp Asp Ser Leu Ile Ala Phe Arg Thr Arg
210 215 220

<210> 4007
<211> 2313
<212> DNA
<213> Homo sapiens

<400> 4007
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120
aattgggacc ggaaaacgtt gtcgctcatc ctatgacgcg aaagtaaccg agactatcag
180
gatccggaga cggaaatgtc cgaaggccgc agtacttgac cctgtatttt gggagtcgaa
240
cggagaatgg aaactgaaag tggaaatcag gaaaaggtaa tggaagaaga aagcactgaa
300

aagaaaaaag aagttgaaaa aaagaaacgg tcacgagtta aacaggtgct tgcagatatt
360
gctaagcaag tggacttctg gtttggggat gcaaatcttc acaaggatag atttcttcga
420
gaacagatag aaaaatctag agatggatat gttgatatat cactacttgt gtcttttaac
480
aaaatgaaaa aattgactac tgatgggaag ttaattgcca gagcattgag aagttcagct
540
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600
ccaaaggatg aggatgaacg cacagtgtat gtggagttac ttcccaaaaa tgttaatcac
660
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720
tataagtcta ctggagatcc aaagggattt gcgtttgtgg aatttgaaac aaaagaacaa
780
gcagcaaaag caattgagtt tcttaacaac ccaccagaag aagcaccaag aaaacctggc
840
atatttccta aaacagtgaa aaataagccc attccagcct taagagttgt ggaagagaag
900
aaaaagaaaa agaagaagaa aggccgaatg aaaaaggaag acaatatcca agccaaagaa
960
gaaaacatgg acacaagcaa caccagcatc agtaaaatga aaagatccag acccacatct
1020
gagggctctg acattgagtc cactgaaccc caaaagcagt gctcaaagaa aaagaaaaaa
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agctctgaag atgcagaatc cctagctccc cgatcaaaag taaagaaaat tattcagaaa
1200
gacatcatta aggaagcatc agaagcttcc aaggaaaata gagatataga aatctctact
1260
gaagaggaaa aggatactgg agatctaaaa gatagctctc tcttgaaaac aaaaaggaaa
1320
cataagaaaa aacataaaga gagacataaa atgggagaag aagttatacc attaagagtg
1380
ctatcaaaga gcgaatggat ggatttgaaa aaagagtatt tagcgctaca aaaagctagc
1440
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1500
agtggagtac ctcaaaacac tggaatgaaa aatgaaaaaa cagccaacag ggaagagtgt
1560
cgcacccagg agaaagttaa tgcaacagga ccacagttcg tgagtggagt gattgtgaag
1620
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1680
tcagaagttc tttatgttga tttgctagaa ggggatacag aatgccatgc tagatttaaa
1740
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1800
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1920

accaaagctg aaaagattag actggcaaag actcaacaag cgagtaaaca tataagattt
1980
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2040
tgttcttggg agattcactt ttattatggt agcactgcat aattaatgtg tttttaatta
2100
aaagaaatat ctttgttcct taacttgtaa ataagacttt tttctagaga caaatatgat
2160
gtataccaca atttttctta aacattttat ttgttgaaat tatcttagat gtcagtgtca
2220
ggtgatttag taaataaatg tgttttgaac attaaaaaaa aaaaaaaaaa aaaaaaaaaa
2280
aaaaaaaaaa aaagaaaaaa aaaaaaaaaa aaa
2313

<210> 4008
<211> 290
<212> PRT
<213> Homo sapiens

<400> 4008
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20 25 30
Ser Glu Ala Ser Lys Glu Asn Arg Asp Ile Glu Ile Ser Thr Glu Glu
35 40 45
Glu Lys Asp Thr Gly Asp Leu Lys Asp Ser Ser Leu Leu Lys Thr Lys
50 55 60
Arg Lys His Lys Lys Lys His Lys Glu Arg His Lys Met Gly Glu Glu
65 70 75 80
Val Ile Pro Leu Arg Val Leu Ser Lys Ser Glu Trp Met Asp Leu Lys
85 90 95
Lys Glu Tyr Leu Ala Leu Gln Lys Ala Ser Met Ala Ser Leu Lys Lys
100 105 110
Thr Ile Ser Gln Ile Lys Ser Glu Ser Glu Met Glu Thr Asp Ser Gly
115 120 125
Val Pro Gln Asn Thr Gly Met Lys Asn Glu Lys Thr Ala Asn Arg Glu
130 135 140
Glu Cys Arg Thr Gln Glu Lys Val Asn Ala Thr Gly Pro Gln Phe Val
145 150 155 160
Ser Gly Val Ile Val Lys Ile Ile Ser Thr Glu Pro Leu Pro Gly Arg
165 170 175
Lys Gln Val Arg Asp Thr Leu Ala Ala Ile Ser Glu Val Leu Tyr Val
180 185 190
Asp Leu Leu Glu Gly Asp Thr Glu Cys His Ala Arg Phe Lys Thr Pro
195 200 205
Glu Asp Ala Gln Ala Val Ile Asn Ala Tyr Thr Glu Ile Asn Lys Lys
210 215 220
His Cys Trp Lys Leu Glu Ile Leu Ser Gly Asp His Glu Gln Arg Tyr
225 230 235 240
Trp Gln Lys Ile Leu Val Asp Arg Gln Ala Lys Leu Asn Gln Pro Arg
245 250 255
Glu Lys Lys Arg Gly Thr Glu Lys Leu Ile Thr Lys Ala Glu Lys Ile

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Arg Leu Ala Lys Thr Gln Gln Ala Ser Lys His Ile Arg Phe Ser Glu
        275                 280                 285
Tyr Asp
    290

<210> 4009
<211> 675
<212> DNA
<213> Homo sapiens

<400> 4009
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ccagcatcat cacccagtat acaagatggt ggtctaatgc aagcctctgt acccggtcct
120
tcagaagaac cagtagttta taatccaaca acagctgcct tcatctgtga ctcacttgtg
180
aatgaaaaaa ccataggcag tcctcctaat gagttttact gttctgaaaa cacttctgtc
240
cctaacgaat ctaacaagat tcttgttaat aaagatgtac ctcagaaacc aggaggtgaa
300
accacacctt cagtaactga cttactaaat tatttttgg ctccagagat tcttactggt
360
gataaccaat attattgtga aaactgtgcc tctctgcaaa atgctgagaa aactatgcaa
420
atcacggagg aacctgaata ccttattctt actctcctga gattttcata tgatcagaag
480
tatcatgtga gaaggaaaat tttagacaat gtatcactgc cactggtttt ggagttgcca
540
gttaaaagaa ttacttcttt ctcttcattg tcagaaagtt ggtctgtaga tgttgacttc
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660
tgcacaaaat tggtg
675

<210> 4010
<211> 225
<212> PRT
<213> Homo sapiens

<400> 4010
Xaa Asp Leu Ser Leu Ala Phe Cys Pro Ser Ser Ser Leu Glu Asn Met
 1               5                  10                  15
Ser Val Gln Asp Pro Ala Ser Ser Pro Ser Ile Gln Asp Gly Gly Leu
            20                  25                  30
Met Gln Ala Ser Val Pro Gly Pro Ser Glu Glu Pro Val Val Tyr Asn
        35                  40                  45
Pro Thr Thr Ala Ala Phe Ile Cys Asp Ser Leu Val Asn Glu Lys Thr
    50                  55                  60
Ile Gly Ser Pro Pro Asn Glu Phe Tyr Cys Ser Glu Asn Thr Ser Val
65                  70                  75                  80
Pro Asn Glu Ser Asn Lys Ile Leu Val Asn Lys Asp Val Pro Gln Lys
```

```
                85                  90                  95
Pro Gly Gly Glu Thr Thr Pro Ser Val Thr Asp Leu Leu Asn Tyr Phe
            100                 105                 110
Leu Ala Pro Glu Ile Leu Thr Gly Asp Asn Gln Tyr Tyr Cys Glu Asn
        115                 120                 125
Cys Ala Ser Leu Gln Asn Ala Glu Lys Thr Met Gln Ile Thr Glu Glu
    130                 135                 140
Pro Glu Tyr Leu Ile Leu Thr Leu Leu Arg Phe Ser Tyr Asp Gln Lys
145                 150                 155                 160
Tyr His Val Arg Arg Lys Ile Leu Asp Asn Val Ser Leu Pro Leu Val
                165                 170                 175
Leu Glu Leu Pro Val Lys Arg Ile Thr Ser Phe Ser Ser Leu Ser Glu
            180                 185                 190
Ser Trp Ser Val Asp Val Asp Phe Thr Asp Leu Ser Glu Asn Leu Ala
        195                 200                 205
Lys Lys Leu Lys Pro Ser Gly Thr Asp Glu Ala Ser Cys Thr Lys Leu
    210                 215                 220
Val
225
```

<210> 4011
<211> 1371
<212> DNA
<213> Homo sapiens

<400> 4011
ctgcaggacg tggttccgac agtcaagatg gcgggagcag ctacccaggc ttccctggag
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tcggccccac ggatcatgcg gctggtggcc gaatgcagcc gctccagggc ccgggcaggc
120
gagctgtggc tgccgcatgg gacagtggcc actcctgtgt tcatgccagt gggcacgcag
180
gccaccatga agggcatcac gaccgaacag ctggacgctc tgggttgccg catctgcctg
240
ggcaatacct accatctggg tctaaggccg ggacccgagc tgatccagaa agccaacggt
300
ctccacggct tcatgaattg gcctcataat ctgctaacgc tttgcggtgg ggtttccctt
360
gacagcggcg gtttccagat ggtgtcgctg gtgtctctgt ccgaggtgac ggaggagggc
420
gtccgcttcc gctcccccta cgacggcaat gagaccctgc tgagcccgga gaaatccgtg
480
cagatccaga atgcgctggg ctcggacatc atcatgcagc tggacgacgt ggttagcagt
540
actgtgactg ggccacgtgt ggaggaggcc atgtacaggt caatccgctg gctggaccgg
600
tgcattgcag cccatcagcg gccggacaag cagaacctct tcgccattat ccagggtggg
660
ctggacgcag atctccgggc cacctgcctt gaagagatga ccaagcgaga cgtgcctggc
720
ttcgccatcg ggggcctgag cgggggtgag agcaagtcgc agttctggcg gatggtggcg
780
ctgagcacct ctcggctgcc gaaggacaag ccccgatatc tgatgggggt tggctatgcc
840

actgatctgg tagtctgcgt ggctcttgga tgtgacatgt tcgactgcgt cttccccaca
900
cggacagcgc gctttggctc tgccctggtg cccactggga acctgcagtt gaggaagaag
960
gtgtttgaga aggacttcgg ccccatagac ccggagtgca cctgccccac gtgccaaaag
1020
cacagccgcg ccttcctgca cgcactgctg cacagtgaca acacggccgc gctgcaccac
1080
ctcacggtcc acaacatcgc ctaccagctg cagctcatga gcgccgtccg caccagcatc
1140
gtggagaagc gcttcccgga cttcgtgcgg gacttcatgg gcgccatgta cggggatccc
1200
accctctgtc ccacctgggc cactgacgct ctggcctctg tgggaatcac actgggctga
1260
cctggcattg ggagagggag ggaggaagga agggagggag gggctggaag atactgaagg
1320
attccttttt gaaaggtttt ttttattgta aaaaaaaaaa aaaaaaaaaa a
1371

<210> 4012
<211> 419
<212> PRT
<213> Homo sapiens

<400> 4012
Leu Gln Asp Val Val Pro Thr Val Lys Met Ala Gly Ala Ala Thr Gln
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Ala Ser Leu Glu Ser Ala Pro Arg Ile Met Arg Leu Val Ala Glu Cys
20 25 30
Ser Arg Ser Arg Ala Arg Ala Gly Glu Leu Trp Leu Pro His Gly Thr
35 40 45
Val Ala Thr Pro Val Phe Met Pro Val Gly Thr Gln Ala Thr Met Lys
50 55 60
Gly Ile Thr Thr Glu Gln Leu Asp Ala Leu Gly Cys Arg Ile Cys Leu
65 70 75 80
Gly Asn Thr Tyr His Leu Gly Leu Arg Pro Gly Pro Glu Leu Ile Gln
85 90 95
Lys Ala Asn Gly Leu His Gly Phe Met Asn Trp Pro His Asn Leu Leu
100 105 110
Thr Leu Cys Gly Gly Val Ser Leu Asp Ser Gly Gly Phe Gln Met Val
115 120 125
Ser Leu Val Ser Leu Ser Glu Val Thr Glu Glu Gly Val Arg Phe Arg
130 135 140
Ser Pro Tyr Asp Gly Asn Glu Thr Leu Leu Ser Pro Glu Lys Ser Val
145 150 155 160
Gln Ile Gln Asn Ala Leu Gly Ser Asp Ile Ile Met Gln Leu Asp Asp
165 170 175
Val Val Ser Ser Thr Val Thr Gly Pro Arg Val Glu Glu Ala Met Tyr
180 185 190
Arg Ser Ile Arg Trp Leu Asp Arg Cys Ile Ala Ala His Gln Arg Pro
195 200 205
Asp Lys Gln Asn Leu Phe Ala Ile Ile Gln Gly Gly Leu Asp Ala Asp
210 215 220
Leu Arg Ala Thr Cys Leu Glu Glu Met Thr Lys Arg Asp Val Pro Gly

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225                 230                 235                 240
Phe Ala Ile Gly Gly Leu Ser Gly Gly Glu Ser Lys Ser Gln Phe Trp
                245                 250                 255
Arg Met Val Ala Leu Ser Thr Ser Arg Leu Pro Lys Asp Lys Pro Arg
            260                 265                 270
Tyr Leu Met Gly Val Gly Tyr Ala Thr Asp Leu Val Val Cys Val Ala
        275                 280                 285
Leu Gly Cys Asp Met Phe Asp Cys Val Phe Pro Thr Arg Thr Ala Arg
    290                 295                 300
Phe Gly Ser Ala Leu Val Pro Thr Gly Asn Leu Gln Leu Arg Lys Lys
305                 310                 315                 320
Val Phe Glu Lys Asp Phe Gly Pro Ile Asp Pro Glu Cys Thr Cys Pro
                325                 330                 335
Thr Cys Gln Lys His Ser Arg Ala Phe Leu His Ala Leu Leu His Ser
            340                 345                 350
Asp Asn Thr Ala Ala Leu His His Leu Thr Val His Asn Ile Ala Tyr
        355                 360                 365
Gln Leu Gln Leu Met Ser Ala Val Arg Thr Ser Ile Val Glu Lys Arg
    370                 375                 380
Phe Pro Asp Phe Val Arg Asp Phe Met Gly Ala Met Tyr Gly Asp Pro
385                 390                 395                 400
Thr Leu Cys Pro Thr Trp Ala Thr Asp Ala Leu Ala Ser Val Gly Ile
                405                 410                 415
Thr Leu Gly
```

<210> 4013
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 4013

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cccttcagga ggaacaccac gtggcaccgg gtgcccactc ctgccctgca gcccctctct
120
agagcttccc ccatccccgg cacgcccgac cggctgccgt gccaacagct gctccagcag
180
gcccaggctg ccattcctcg aagcacctcc ttcgaccgga agctgcccga tggcacgaga
240
agctcaccca gcaaccagtc atcctccagc gaccctggac ccggcgggag cggaccctgg
300
agaccacaag tgggctacga cgggtgccag tcccctctac tgctcgaaca ccagggctca
360
ggcccctttgg aatgtgacgg agccagggag agggaagaca ccatggaagc aagcaggcac
420
ccggaaacca aatggcatgg cccaccttcc aaagtcctgg gttcctataa agaaagagct
480
ctgcagaaag atggaagttg caaagattcc cccaataagc tttctcacat tggggataaa
540
agttgctcca gtcactccag cagcaacacg ctctccagca acacctccag caacagtgac
600
gacaagcact ttgggtctgg cgacctgatg gaccccgaat tactggggct gacctacatc
660
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aaaggggcct ccaccgacag tggcatcgac acggcccccc gcatgcctgc caccatcctc
720
ggccctgtgc acctggcagg cagcaggtcc ctgatccaca gccgggccga gcagtgggct
780
gatgctgccg acgtctctgg gcctgacgac gagccagcca agttatattc tgtgcatggc
840
tacgcgtcca ccatctccgc cggcagtgct gcggaaggca gcatgggcga tctcagtgag
900
atatcctctc attccagtgg ttctcaccat tcaggaagcc cttcagctca ctgttcaaaa
960
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1020
gttcccgggt ccatgtccaa gccctaccac agacaagggg cagtgaacaa atatgtcatc
1080
ggctggaaga aatcggaggg cagcccaccg cccgaggagc ctgaagtgac tgaatgtccc
1140
gggatgtata gtgagttgga tgtcatgtcc acagcaactc agcatcagac agtggtggga
1200
gatgctgttg cagagactca acatgttctg tctaaagaag attttctgaa attgatgctt
1260
cctgacagcc ccttagtgga ggaggggcga agaaagtttt cgttctatgg gaacctgtct
1320
ccaaggaggt cgctttaccg cacgctgtct gacgagagca tctgcagcaa caggaggggg
1380
tcctcctttg gcagttcccg gagttccgtg cttgaccag
1419

<210> 4014
<211> 473
<212> PRT
<213> Homo sapiens

<400> 4014
Xaa Ile Pro Met Val Glu Tyr Lys Leu Asp Ser Glu Gly Thr Pro Cys
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Glu Tyr Lys Thr Pro Phe Arg Arg Asn Thr Thr Trp His Arg Val Pro
20 25 30
Thr Pro Ala Leu Gln Pro Leu Ser Arg Ala Ser Pro Ile Pro Gly Thr
35 40 45
Pro Asp Arg Leu Pro Cys Gln Gln Leu Leu Gln Gln Ala Gln Ala Ala
50 55 60
Ile Pro Arg Ser Thr Ser Phe Asp Arg Lys Leu Pro Asp Gly Thr Arg
65 70 75 80
Ser Ser Pro Ser Asn Gln Ser Ser Ser Ser Asp Pro Gly Pro Gly Gly
85 90 95
Ser Gly Pro Trp Arg Pro Gln Val Gly Tyr Asp Gly Cys Gln Ser Pro
100 105 110
Leu Leu Leu Glu His Gln Gly Ser Gly Pro Leu Glu Cys Asp Gly Ala
115 120 125
Arg Glu Arg Glu Asp Thr Met Glu Ala Ser Arg His Pro Glu Thr Lys
130 135 140
Trp His Gly Pro Pro Ser Lys Val Leu Gly Ser Tyr Lys Glu Arg Ala
145 150 155 160
Leu Gln Lys Asp Gly Ser Cys Lys Asp Ser Pro Asn Lys Leu Ser His

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                165                 170                 175
Ile Gly Asp Lys Ser Cys Ser Ser His Ser Ser Ser Asn Thr Leu Ser
            180                 185                 190
Ser Asn Thr Ser Ser Asn Ser Asp Asp Lys His Phe Gly Ser Gly Asp
        195                 200                 205
Leu Met Asp Pro Glu Leu Leu Gly Leu Thr Tyr Ile Lys Gly Ala Ser
    210                 215                 220
Thr Asp Ser Gly Ile Asp Thr Ala Pro Cys Met Pro Ala Thr Ile Leu
225                 230                 235                 240
Gly Pro Val His Leu Ala Gly Ser Arg Ser Leu Ile His Ser Arg Ala
                245                 250                 255
Glu Gln Trp Ala Asp Ala Ala Asp Val Ser Gly Pro Asp Asp Glu Pro
            260                 265                 270
Ala Lys Leu Tyr Ser Val His Gly Tyr Ala Ser Thr Ile Ser Ala Gly
        275                 280                 285
Ser Ala Ala Glu Gly Ser Met Gly Asp Leu Ser Glu Ile Ser Ser His
    290                 295                 300
Ser Ser Gly Ser His His Ser Gly Ser Pro Ser Ala His Cys Ser Lys
305                 310                 315                 320
Ser Ser Gly Ser Leu Asp Ser Ser Lys Val Tyr Ile Val Ser His Ser
                325                 330                 335
Ser Gly Gln Gln Val Pro Gly Ser Met Ser Lys Pro Tyr His Arg Gln
            340                 345                 350
Gly Ala Val Asn Lys Tyr Val Ile Gly Trp Lys Lys Ser Glu Gly Ser
        355                 360                 365
Pro Pro Pro Glu Glu Pro Glu Val Thr Glu Cys Pro Gly Met Tyr Ser
    370                 375                 380
Glu Leu Asp Val Met Ser Thr Ala Thr Gln His Gln Thr Val Val Gly
385                 390                 395                 400
Asp Ala Val Ala Glu Thr Gln His Val Leu Ser Lys Glu Asp Phe Leu
                405                 410                 415
Lys Leu Met Leu Pro Asp Ser Pro Leu Val Glu Glu Gly Arg Arg Lys
            420                 425                 430
Phe Ser Phe Tyr Gly Asn Leu Ser Pro Arg Arg Ser Leu Tyr Arg Thr
        435                 440                 445
Leu Ser Asp Glu Ser Ile Cys Ser Asn Arg Arg Gly Ser Ser Phe Gly
    450                 455                 460
Ser Ser Arg Ser Ser Val Leu Asp Gln
465                 470
```

<210> 4015
<211> 823
<212> DNA
<213> Homo sapiens

<400> 4015
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120
atagtgctgc agggcggcgg cctggagtct cccaccaagc ccaaggggcg gcccaagaag
180
aactcaattc caacgagcga gcagcttact gagcaggagc gcgccaagga tgcagagaaa
240

cccgcggagg tgccgggcga gcccagcgac aggagccgcg aggactgagg gcggtatacg
300
gtgcggggcc tgggatgccc gcgccacccg cagccccctc actcggcgga aacccgcgag
360
ccggcccttc cgcgtccaag aagtttactt cctaagcctt ttattatgat cttgaatgcg
420
gacaattggg gccaaacgag gaaggacaca gacccaaaag ccagacccag gtcccagcgc
480
gcttctgggc tctaacctgg gagactcgca tccagcccgg cggaagctac agtctctacc
540
ctgagctccg tggcgcagag cgctccacgc gtattcacgc cccgctcctc gcctgcaccc
600
ccgccccgtc tggggcctgc cctcccggcc ggggagcctc caggcacaca cccgcttctg
660
gacgtcgggg acccagcggt tgggctcagc cacaacggcc tgagattgcc ccggggcaac
720
ccgtcggcat gcctggaggc cgggtccccg atgtcgctgg ggcccctacc ccctcgtgcg
780
aagacggtga ctttttttcc aataaaatat tttatgacac aaa
823

<210> 4016
<211> 95
<212> PRT
<213> Homo sapiens

<400> 4016
Arg Phe Glu Lys Gln Lys Tyr Leu Ser Thr Pro Asp Arg Ile Asp Leu
1 5 10 15
Ala Glu Ser Leu Gly Leu Ser Gln Leu Gln Val Lys Thr Trp Tyr Gln
20 25 30
Asn Arg Arg Met Lys Trp Lys Lys Ile Val Leu Gln Gly Gly Gly Leu
35 40 45
Glu Ser Pro Thr Lys Pro Lys Gly Arg Pro Lys Lys Asn Ser Ile Pro
50 55 60
Thr Ser Glu Gln Leu Thr Glu Gln Glu Arg Ala Lys Asp Ala Glu Lys
65 70 75 80
Pro Ala Glu Val Pro Gly Glu Pro Ser Asp Arg Ser Arg Glu Asp
85 90 95

<210> 4017
<211> 1521
<212> DNA
<213> Homo sapiens

<400> 4017
nnactagggg attaccatga tgcagtagca gccatgctgc cctttcttgc tggccacgct
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gggcaccgcc gccctcaata gcagcaaccc gaagactatt gctacagtgc ccggatccgc
120
agcaccgtcc tacagggcct gccctttggg ggcgtcccca ccgtgctggc cttggacttc
180
acgtgcttcc tcgccctgct gttcttattc tccatcctcc ggaaggtggc ctgggactat
240

gggcggctgg ccttggtgac agatgcagac aggcttcggc ggcaggagag ggaccgagtg
300
gaacaggaat atgtggcttc agctatgcac ggggacagcc atgaccggta tgagcgtctc
360
acctttgtct ccagctccgt tgactttgac caaagggaca atggtttctg ttcctggctg
420
acagccatct tcaggataaa ggacgatgag atccgggaca agtgtggggg cgacgctgtg
480
cactacctgt cctttcagcg gcacatcatc gggctgctgg tggttgtggg cgtcctctcc
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tccttcgcct tcctgtatct gctgctcacc gtctacagca tgcgtagaca cacctccaag
720
atgcgctaca aggaggatga tctggtgaag cggaccctct tcatcaatgg aatctccaaa
780
tatgcagagt cagaaaagat caagaagcat tttgaggaag cctaccccaa ctgcacagtt
840
ctcgaagccc gcccgtgtta caacgtggct cgcctaatgt tcctcgatgc agagaggaag
900
aaggccgagc ggggaaagct gtacttcaca aacctccaga gcaaggagaa cgtgcctacc
960
atgatcaacc ccaagccctg tggccacttc tgctgctgtg tggtgcgagg ctgtgagcag
1020
gtggaggcca ttgagtacta cacaaagctg gagcagaagc tgaaggaaga ctacaagcgg
1080
gagaagggga aggtgaatga gaagcctctt ggcatggcct ttgtcacctt ccacaatgag
1140
actatcaccg ccatcatcct gaaggacttc aacgtgtgta aatgccaggg ctgcacctgc
1200
cgtggggagc cacgcccctc atcctgcagc gagtcccttc acatccccaa ctggaccggg
1260
tcctatgccc ctgaccctca gaacatctac tgggagcacc tctccatccg aggcttcatc
1320
tggtggctgc gctgcctggt catcaatgtc gtcctcttca tcctcctctt cttcctcacc
1380
actccagcca tcatcatcac caccatggac aagttcaacg tcaccaagcc tgtggagtac
1440
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1500
ctccttccca ccattggcta c
1521

<210> 4018
<211> 480
<212> PRT
<213> Homo sapiens

<400> 4018
Gln Gln Pro Glu Asp Tyr Cys Tyr Ser Ala Arg Ile Arg Ser Thr Val
1 5 10 15
Leu Gln Gly Leu Pro Phe Gly Gly Val Pro Thr Val Leu Ala Leu Asp

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            20                  25                  30
Phe Thr Cys Phe Leu Ala Leu Leu Phe Leu Phe Ser Ile Leu Arg Lys
        35                  40                  45
Val Ala Trp Asp Tyr Gly Arg Leu Ala Leu Val Thr Asp Ala Asp Arg
    50                  55                  60
Leu Arg Arg Gln Glu Arg Asp Arg Val Glu Gln Glu Tyr Val Ala Ser
65                  70                  75                  80
Ala Met His Gly Asp Ser His Asp Arg Tyr Glu Arg Leu Thr Phe Val
                85                  90                  95
Ser Ser Ser Val Asp Phe Asp Gln Arg Asp Asn Gly Phe Cys Ser Trp
            100                 105                 110
Leu Thr Ala Ile Phe Arg Ile Lys Asp Asp Glu Ile Arg Asp Lys Cys
        115                 120                 125
Gly Gly Asp Ala Val His Tyr Leu Ser Phe Gln Arg His Ile Ile Gly
    130                 135                 140
Leu Leu Val Val Val Gly Val Leu Ser Val Gly Ile Val Leu Pro Val
145                 150                 155                 160
Asn Phe Ser Gly Asp Leu Leu Glu Asn Asn Ala Tyr Ser Phe Gly Arg
                165                 170                 175
Thr Thr Ile Ala Asn Leu Lys Ser Gly Asn Asn Leu Leu Trp Leu His
            180                 185                 190
Thr Ser Phe Ala Phe Leu Tyr Leu Leu Leu Thr Val Tyr Ser Met Arg
        195                 200                 205
Arg His Thr Ser Lys Met Arg Tyr Lys Glu Asp Asp Leu Val Lys Arg
    210                 215                 220
Thr Leu Phe Ile Asn Gly Ile Ser Lys Tyr Ala Glu Ser Glu Lys Ile
225                 230                 235                 240
Lys Lys His Phe Glu Glu Ala Tyr Pro Asn Cys Thr Val Leu Glu Ala
                245                 250                 255
Arg Pro Cys Tyr Asn Val Ala Arg Leu Met Phe Leu Asp Ala Glu Arg
            260                 265                 270
Lys Lys Ala Glu Arg Gly Lys Leu Tyr Phe Thr Asn Leu Gln Ser Lys
        275                 280                 285
Glu Asn Val Pro Thr Met Ile Asn Pro Lys Pro Cys Gly His Phe Cys
    290                 295                 300
Cys Cys Val Val Arg Gly Cys Glu Gln Val Glu Ala Ile Glu Tyr Tyr
305                 310                 315                 320
Thr Lys Leu Glu Gln Lys Leu Lys Glu Asp Tyr Lys Arg Glu Lys Gly
                325                 330                 335
Lys Val Asn Glu Lys Pro Leu Gly Met Ala Phe Val Thr Phe His Asn
            340                 345                 350
Glu Thr Ile Thr Ala Ile Ile Leu Lys Asp Phe Asn Val Cys Lys Cys
        355                 360                 365
Gln Gly Cys Thr Cys Arg Gly Glu Pro Arg Pro Ser Ser Cys Ser Glu
    370                 375                 380
Ser Leu His Ile Pro Asn Trp Thr Gly Ser Tyr Ala Pro Asp Pro Gln
385                 390                 395                 400
Asn Ile Tyr Trp Glu His Leu Ser Ile Arg Gly Phe Ile Trp Trp Leu
                405                 410                 415
Arg Cys Leu Val Ile Asn Val Val Leu Phe Ile Leu Leu Phe Phe Leu
            420                 425                 430
Thr Thr Pro Ala Ile Ile Ile Thr Thr Met Asp Lys Phe Asn Val Thr
        435                 440                 445
Lys Pro Val Glu Tyr Leu Asn Asn Pro Ile Ile Thr Gln Phe Phe Pro
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450 455 460
Thr Leu Leu Leu Trp Cys Phe Ser Ala Leu Leu Pro Thr Ile Gly Tyr
465 470 475 480

<210> 4019
<211> 2408
<212> DNA
<213> Homo sapiens

<400> 4019
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120
ctgaaccacc gctgtgtatc tgctgtccag cgctgtgatg gggttgatgc ctgtggcgat
180
ggctctgatg aagcaggttg cagctcagac cccttccctg gcctgacccc aagacccgtc
240
ccctccctgc cttgcaatgt caccttggag gacttctatg gggtcttctc ctctcctgga
300
tatacacacc tagcctcagt ctcccacccc cagtcctgcc attggctgct ggacccccat
360
gatggccggc ggctggccgt gcgcttcaca gccccggact tgggctttgg agatgcagtg
420
catgtgtatg acggccctgg gccccctgag agctcccgac tactgcgtag tctcacccac
480
ttcagcaatg gcaaggctgt cactgtggag acactgtctg gccaggctgt tgtgtcctac
540
cacacagttg cttggagcaa tggtcgtggc ttcaatgcca cctaccatgt gcggggctat
600
tgcttgcctt gggacagacc ctgtggctta ggctctggcc tgggagctgg cgaaggccta
660
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840
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1020
ggcagcctag tgtgcggcct gctcctggtc atcgccctgg gctgcacctg caagctctat
1080
gccattcgca cccaggagta cagcatcttt gccccctct cccggatgga ggctgagatt
1140
gtgcagcagc aggcaccccc ttcctacggg cagctcattg cccagggtgc catcccacct
1200
gtagaagact ttcctacaga gaatcctaat gataactcag tgctgggcaa cctgcgttct
1260
ctgctacaga tcttacgcca ggatatgact ccaggaggtg gcccaggtgc ccgccgtcgt
1320

cagcggggcc gcttgatgcg acgcctggta cgccgtctcc gccgctgggg cttgctccct
1380
cgaaccaaca ccccggctcg ggcctctgag gccagatccc aggtcacacc ttctgctgct
1440
ccccttgagg ccctagatgg tggcacaggt ccagcccgtg agggcggggc agtgggtggg
1500
caagatgggg agcaggcacc cccactgccc atcaaggctc ccctcccatc tgctagcacg
1560
tctccagccc ccactactgt ccctgaagcc ccagggccac tgccctcact gcccctagag
1620
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1680
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1800
gatgagccac tgcttacctg aggggacctg ggggctctac tgaggcctct cccctggggg
1860
ctctactcat agtggcacaa ccttttagag gtgggtcagc ctccctcca ccacttcctt
1920
ccctgtccct ggatttcagg gacttggtgg gcctcccgtt gaccctatgt agctgctata
1980
aagttaagtg tccctcaggc agggagaggg ctcacagagt ctcctctgta cgtggccatg
2040
gccagacacc ccagtccctt caccaccacc tgctccccac gccaccacca tttgggtggc
2100
tgtttttaaa aagtaaagtt cttagaggat cataggtctg gacactccat ccttgccaaa
2160
cctctaccca aaagtggcct taagcaccgg aatgccaatt aactagagac cctccagccc
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aagacctccc acagcccagt gtgccaggac gtgctgaaat tcatcagtca gtggtgtgga
5040
gggctcccca gcaccagctt ttcctttcag tagttggtag agctgaggaa gagttagggc
5100
ctctccctca ttaaagtttt ataaataaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
5160
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa
5193

<210> 4024
<211> 1690
<212> PRT
<213> Homo sapiens

<400> 4024
Xaa Arg Val Lys Gly Met Ala Phe Ser Pro Asp Ser Thr Lys Ile Ala

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 1               5                  10                  15
Ile Gly Gln Thr Asp Asn Ile Ile Tyr Val Tyr Lys Ile Gly Glu Asp
            20                  25                  30
Trp Gly Asp Lys Lys Val Ile Cys Asn Lys Phe Ile Gln Thr Ser Ala
        35                  40                  45
Val Thr Cys Leu Gln Trp Pro Ala Glu Tyr Ile Ile Val Phe Gly Leu
    50                  55                  60
Ala Glu Gly Lys Val Arg Leu Ala Asn Thr Lys Thr Asn Lys Ser Ser
65                  70                  75                  80
Thr Ile Tyr Gly Thr Glu Ser Tyr Val Val Ser Leu Thr Thr Asn Cys
                85                  90                  95
Ser Gly Lys Gly Ile Leu Ser Gly His Ala Asp Gly Thr Ile Val Arg
            100                 105                 110
Tyr Phe Phe Asp Asp Glu Gly Ser Gly Glu Ser Gln Gly Lys Leu Val
        115                 120                 125
Asn His Pro Cys Pro Pro Tyr Ala Leu Ala Trp Ala Thr Asn Ser Ile
    130                 135                 140
Val Ala Ala Gly Cys Asp Arg Lys Ile Val Ala Tyr Gly Lys Glu Gly
145                 150                 155                 160
His Met Leu Gln Thr Phe Asp Tyr Ser Arg Asp Pro Gln Glu Arg Glu
                165                 170                 175
Phe Thr Thr Ala Val Ser Ser Pro Gly Gly Gln Ser Val Val Leu Gly
            180                 185                 190
Ser Tyr Asp Arg Leu Arg Val Phe Asn Trp Ile Pro Arg Arg Ser Ile
        195                 200                 205
Trp Glu Glu Ala Lys Pro Lys Glu Ile Thr Asn Leu Tyr Thr Ile Thr
    210                 215                 220
Ala Leu Ala Trp Lys Arg Asp Gly Ser Arg Leu Cys Val Gly Thr Leu
225                 230                 235                 240
Cys Gly Gly Val Glu Gln Phe Asp Cys Cys Leu Arg Arg Ser Ile Tyr
                245                 250                 255
Lys Asn Lys Phe Glu Leu Thr Tyr Val Gly Pro Ser Gln Val Ile Val
            260                 265                 270
Lys Asn Leu Ser Ser Gly Thr Arg Val Val Leu Lys Ser His Tyr Gly
        275                 280                 285
Tyr Glu Val Glu Glu Val Lys Ile Leu Gly Lys Glu Arg Tyr Leu Val
    290                 295                 300
Ala His Thr Ser Glu Thr Leu Leu Leu Gly Asp Leu Asn Thr Asn Arg
305                 310                 315                 320
Leu Ser Glu Ile Ala Trp Gln Gly Ser Gly Gly Asn Glu Lys Tyr Phe
                325                 330                 335
Phe Glu Asn Glu Asn Val Cys Met Ile Phe Asn Ala Gly Glu Leu Thr
            340                 345                 350
Leu Val Glu Tyr Gly Asn Asn Asp Thr Leu Gly Ser Val Arg Thr Glu
        355                 360                 365
Phe Met Asn Pro His Leu Ile Ser Val Arg Ile Asn Glu Arg Cys Gln
    370                 375                 380
Arg Gly Thr Glu Asp Asn Lys Lys Leu Ala Tyr Leu Ile Asp Ile Lys
385                 390                 395                 400
Thr Ile Ala Ile Val Asp Leu Ile Gly Gly Tyr Asn Ile Gly Thr Val
                405                 410                 415
Ser His Glu Ser Arg Val Asp Trp Leu Glu Leu Asn Glu Thr Gly His
            420                 425                 430
Lys Leu Leu Phe Arg Asp Arg Lys Leu Arg Leu His Leu Tyr Asp Ile
```

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        435                 440                 445
Glu Ser Cys Ser Lys Thr Met Ile Leu Asn Phe Cys Ser Tyr Met Gln
    450                 455                 460
Trp Val Pro Gly Ser Asp Val Leu Val Ala Gln Asn Arg Asn Ser Leu
465                 470                 475                 480
Cys Val Trp Tyr Asn Ile Glu Ala Pro Glu Arg Val Thr Met Phe Thr
                485                 490                 495
Ile Arg Gly Asp Val Ile Gly Leu Glu Arg Gly Gly Gly Lys Thr Glu
            500                 505                 510
Val Met Val Met Glu Gly Val Thr Thr Val Ala Tyr Thr Leu Asp Glu
        515                 520                 525
Gly Leu Ile Glu Phe Gly Thr Ala Ile Asp Asp Gly Asn Tyr Ile Arg
    530                 535                 540
Ala Thr Ala Phe Leu Glu Thr Leu Glu Met Thr Pro Glu Thr Glu Ala
545                 550                 555                 560
Met Trp Lys Thr Leu Ser Lys Leu Ala Leu Glu Ala Arg Gln Leu His
                565                 570                 575
Ile Ala Glu Arg Cys Phe Ser Ala Leu Gly Gln Val Ala Lys Ala Arg
            580                 585                 590
Phe Leu His Glu Thr Asn Glu Ile Ala Asp Gln Val Ser Arg Glu Tyr
        595                 600                 605
Gly Gly Glu Gly Thr Asp Phe Tyr Gln Val Arg Ala Arg Leu Ala Met
    610                 615                 620
Leu Glu Lys Asn Tyr Lys Leu Ala Glu Met Ile Phe Leu Glu Gln Asn
625                 630                 635                 640
Ala Val Glu Glu Ala Met Gly Met Tyr Gln Glu Leu His Arg Trp Asp
                645                 650                 655
Glu Cys Ile Ala Val Ala Glu Ala Lys Gly His Pro Ala Leu Glu Lys
            660                 665                 670
Leu Arg Arg Ser Tyr Tyr Gln Trp Leu Met Asp Thr Gln Gln Glu Glu
        675                 680                 685
Arg Ala Gly Glu Leu Gln Glu Ser Gln Gly Asp Gly Leu Ala Ala Ile
    690                 695                 700
Ser Leu Tyr Leu Lys Ala Gly Leu Pro Ala Lys Ala Ala Arg Leu Val
705                 710                 715                 720
Leu Thr Arg Glu Glu Leu Leu Ala Asn Thr Glu Leu Val Glu His Ile
                725                 730                 735
Thr Ala Ala Leu Ile Lys Gly Glu Leu Tyr Glu Arg Ala Gly Asp Leu
            740                 745                 750
Phe Glu Lys Ile His Asn Pro Gln Lys Ala Leu Glu Cys Tyr Arg Lys
        755                 760                 765
Gly Asn Ala Phe Met Lys Ala Val Glu Leu Ala Arg Leu Ala Phe Pro
    770                 775                 780
Val Glu Val Val Lys Leu Glu Glu Ala Trp Gly Asp His Leu Val Gln
785                 790                 795                 800
Gln Lys Gln Leu Asp Ala Ala Ile Asn His Tyr Ile Glu Ala Arg Cys
                805                 810                 815
Ser Ile Lys Ala Ile Glu Ala Ala Leu Gly Ala Arg Gln Trp Lys Lys
            820                 825                 830
Ala Ile Tyr Ile Leu Asp Leu Gln Asp Arg Asn Thr Ala Ser Lys Tyr
        835                 840                 845
Tyr Pro Leu Val Ala Gln His Tyr Ala Ser Leu Gln Glu Tyr Glu Ile
    850                 855                 860
Ala Glu Glu Leu Tyr Thr Lys Gly Asp Arg Thr Lys Asp Ala Ile Asp
```

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865                 870                 875                 880
Met Tyr Thr Gln Ala Gly Arg Trp Glu Gln Ala His Lys Leu Ala Met
                885                 890                 895
Lys Cys Met Arg Pro Glu Asp Val Ser Val Leu Tyr Ile Thr Gln Ala
            900                 905                 910
Gln Glu Met Glu Lys Gln Gly Lys Tyr Arg Glu Ala Glu Arg Leu Tyr
        915                 920                 925
Val Thr Val Gln Glu Pro Asp Leu Ala Ile Thr Met Tyr Lys Lys His
    930                 935                 940
Lys Leu Tyr Asp Asp Met Ile Arg Leu Val Gly Lys His His Pro Asp
945                 950                 955                 960
Leu Leu Ser Asp Thr His Leu His Leu Gly Lys Glu Leu Glu Ala Glu
                965                 970                 975
Gly Arg Leu Gln Glu Ala Glu Tyr His Tyr Leu Glu Ala Gln Glu Trp
            980                 985                 990
Lys Ala Thr Val Asn Met Tyr Arg Ala Ser Gly Leu Trp Glu Glu Ala
        995                 1000                1005
Tyr Arg Val Ala Arg Thr Gln Gly Gly Ala Asn Ala His Lys His Val
    1010                1015                1020
Ala Tyr Leu Trp Ala Lys Ser Leu Gly Gly Glu Ala Ala Val Arg Leu
1025                1030                1035                1040
Leu Asn Lys Leu Gly Leu Leu Glu Ala Ala Val Asp His Ala Ala Asp
                1045                1050                1055
Asn Cys Ser Phe Glu Phe Ala Phe Glu Leu Ser Arg Leu Ala Leu Lys
            1060                1065                1070
His Lys Thr Pro Glu Val His Leu Lys Tyr Ala Met Phe Leu Glu Asp
        1075                1080                1085
Glu Gly Lys Phe Glu Glu Ala Glu Ala Glu Phe Ile Arg Ala Gly Lys
    1090                1095                1100
Pro Lys Glu Ala Val Leu Met Phe Val His Asn Gln Asp Trp Glu Ala
1105                1110                1115                1120
Ala Gln Arg Val Ala Glu Ala His Asp Pro Asp Ser Val Ala Glu Val
                1125                1130                1135
Leu Val Gly Gln Ala Arg Gly Ala Leu Glu Glu Lys Asp Phe Gln Lys
            1140                1145                1150
Ala Glu Gly Leu Leu Leu Arg Ala Gln Arg Pro Gly Leu Ala Leu Asn
        1155                1160                1165
Tyr Tyr Lys Glu Ala Gly Leu Trp Ser Asp Ala Leu Arg Ile Cys Lys
    1170                1175                1180
Asp Tyr Val Pro Ser Gln Leu Glu Ala Leu Gln Glu Glu Tyr Glu Arg
1185                1190                1195                1200
Glu Ala Thr Lys Lys Gly Ala Arg Gly Val Glu Gly Phe Val Glu Gln
                1205                1210                1215
Ala Arg His Trp Glu Gln Ala Gly Glu Tyr Ser Arg Ala Val Asp Cys
            1220                1225                1230
Tyr Leu Lys Val Arg Asp Ser Gly Asn Ser Gly Leu Ala Glu Lys Cys
        1235                1240                1245
Trp Met Lys Ala Ala Glu Leu Ser Ile Lys Phe Leu Pro Pro Gln Arg
    1250                1255                1260
Asn Met Glu Val Val Leu Ala Val Gly Pro Gln Leu Ile Gly Ile Gly
1265                1270                1275                1280
Lys His Ser Ala Ala Ala Glu Leu Tyr Leu Asn Leu Asp Leu Val Lys
                1285                1290                1295
Glu Ala Ile Asp Ala Phe Ile Glu Gly Glu Glu Trp Asn Lys Ala Lys
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            1300                1305                1310
Arg Val Ala Lys Glu Leu Asp Pro Arg Tyr Glu Asp Tyr Val Asp Gln
        1315                1320                1325
His Tyr Lys Glu Phe Leu Lys Asn Gln Gly Lys Val Asp Ser Leu Val
    1330                1335                1340
Gly Val Asp Val Ile Ala Ala Leu Asp Leu Tyr Val Glu Gln Gly Gln
1345                1350                1355                1360
Trp Asp Lys Cys Ile Glu Thr Ala Thr Lys Gln Asn Tyr Lys Ile Leu
                1365                1370                1375
His Lys Tyr Val Ala Leu Tyr Ala Thr His Leu Ile Arg Glu Gly Ser
            1380                1385                1390
Ser Ala Gln Ala Leu Ala Leu Tyr Val Gln His Gly Ala Pro Ala Asn
        1395                1400                1405
Pro Gln Asn Phe Asn Ile Tyr Lys Arg Ile Phe Thr Asp Met Val Ser
    1410                1415                1420
Ser Pro Gly Thr Asn Cys Ala Glu Ala Tyr His Ser Trp Ala Asp Leu
1425                1430                1435                1440
Arg Asp Val Leu Phe Asn Leu Ala Val Leu Ser Pro Ser Ser Ser Val
                1445                1450                1455
Lys Thr Trp Lys Ser Ser Glu Ala Asn Ser Pro Ala His Glu Glu Phe
            1460                1465                1470
Lys Thr Met Leu Leu Ile Ala His Tyr Tyr Ala Thr Arg Ser Ala Ala
        1475                1480                1485
Gln Ser Val Lys Gln Leu Glu Thr Val Ala Ala Arg Leu Ser Val Ser
    1490                1495                1500
Leu Leu Arg His Thr Gln Leu Leu Pro Val Asp Lys Ala Phe Tyr Glu
1505                1510                1515                1520
Ala Gly Ile Ala Ala Lys Ala Val Gly Trp Asp Asn Met Ala Phe Ile
                1525                1530                1535
Phe Leu Asn Arg Phe Leu Asp Leu Thr Asp Ala Ile Glu Glu Gly Thr
            1540                1545                1550
Leu Asp Gly Leu Asp His Ser Asp Phe Gln Asp Thr Asp Ile Pro Phe
        1555                1560                1565
Glu Val Pro Leu Pro Ala Lys Gln His Val Pro Glu Ala Glu Arg Glu
    1570                1575                1580
Glu Val Arg Asp Trp Val Leu Thr Val Ser Met Asp Gln Arg Leu Glu
1585                1590                1595                1600
Gln Val Leu Pro Arg Asp Glu Arg Gly Ala Tyr Glu Ala Ser Leu Val
                1605                1610                1615
Ala Ala Ser Thr Gly Val Arg Ala Leu Pro Cys Leu Ile Thr Gly Tyr
            1620                1625                1630
Pro Ile Leu Arg Asn Lys Ile Glu Phe Lys Arg Pro Gly Lys Ala Ala
        1635                1640                1645
Asn Lys Asp Asn Trp Asn Lys Phe Leu Met Ala Ile Lys Thr Ser His
    1650                1655                1660
Ser Pro Val Cys Gln Asp Val Leu Lys Phe Ile Ser Gln Trp Cys Gly
1665                1670                1675                1680
Gly Leu Pro Ser Thr Ser Phe Ser Phe Gln
                1685                1690
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<210> 4025
<211> 908
<212> DNA
<213> Homo sapiens

<400> 4025
ttaagaactc acactggann gaaaccctat gaatgcaatc actgtgggaa agcatttagt
60
gatccctcat cccttagact gcatttgaga attcacactg gagaaaaacc ctatgaatgt
120
aaccagtgtt ttcacgtttt ccgcaccagt tgtaacctta aaagccacaa gaggattcac
180
acgggggaga atcaccatga atgtaatcag tgtggaaaag ctttcagcac aaggtcctct
240
ctcactgggc acaattgcat tcatacaggg gagaaacctt atgaatgtaa ggaatgtggg
300
aaaaccttta tgtataattc atcccttatt caacatctga gaactcatac tggagagaaa
360
ccctatgaat gtaaggagtg tgggaaagcc tttaggcaac attcacacct tgtcacacac
420
cagaaaatcc atactggaga gaagccctat cagtgcactg aatgtgggaa agccttcagg
480
cggcgttcac tccttattca acatcggaga attcatagtg gtgagaagcc ctatgaatgt
540
aaggaatgtg ggaagctctt catttggcgc acagctttcc tcaaacatca gagcctgcat
600
gctggagaga aacttgaaga atgtgagaaa nnaccttcag caaggatgag gagcttaggg
660
gagnagcaga aaattcacca agaagagaaa gcttattggt gtaatcagtg tggtagggct
720
ttccagggca gctcagacct catcggacat caggtaactc atacaggaga gaaaccatat
780
gaatgtaaag aatgtggana aactttcaat cagagctcag accttctgag acatcataga
840
attcacagtg gagaaaaacc ttatgtatgc aacaaatgtg ggaaatcttt taggggcagc
900
tcagatct
908

<210> 4026
<211> 302
<212> PRT
<213> Homo sapiens

<400> 4026
Leu Arg Thr His Thr Gly Xaa Lys Pro Tyr Glu Cys Asn His Cys Gly
1 5 10 15
Lys Ala Phe Ser Asp Pro Ser Ser Leu Arg Leu His Leu Arg Ile His
20 25 30
Thr Gly Glu Lys Pro Tyr Glu Cys Asn Gln Cys Phe His Val Phe Arg
35 40 45
Thr Ser Cys Asn Leu Lys Ser His Lys Arg Ile His Thr Gly Glu Asn
50 55 60
His His Glu Cys Asn Gln Cys Gly Lys Ala Phe Ser Thr Arg Ser Ser
65 70 75 80
Leu Thr Gly His Asn Cys Ile His Thr Gly Glu Lys Pro Tyr Glu Cys
85 90 95
Lys Glu Cys Gly Lys Thr Phe Met Tyr Asn Ser Ser Leu Ile Gln His

```
            100                 105                 110
Leu Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly
        115                 120                 125
Lys Ala Phe Arg Gln His Ser His Leu Val Thr His Gln Lys Ile His
    130                 135                 140
Thr Gly Glu Lys Pro Tyr Gln Cys Thr Glu Cys Gly Lys Ala Phe Arg
145                 150                 155                 160
Arg Arg Ser Leu Leu Ile Gln His Arg Arg Ile His Ser Gly Glu Lys
                165                 170                 175
Pro Tyr Glu Cys Lys Glu Cys Gly Lys Leu Phe Ile Trp Arg Thr Ala
            180                 185                 190
Phe Leu Lys His Gln Ser Leu His Ala Gly Glu Lys Leu Glu Glu Cys
        195                 200                 205
Glu Lys Xaa Pro Ser Ala Arg Met Arg Ser Leu Gly Glu Xaa Gln Lys
    210                 215                 220
Ile His Gln Glu Glu Lys Ala Tyr Trp Cys Asn Gln Cys Gly Arg Ala
225                 230                 235                 240
Phe Gln Gly Ser Ser Asp Leu Ile Gly His Gln Val Thr His Thr Gly
                245                 250                 255
Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Xaa Thr Phe Asn Gln Ser
            260                 265                 270
Ser Asp Leu Leu Arg His His Arg Ile His Ser Gly Glu Lys Pro Tyr
        275                 280                 285
Val Cys Asn Lys Cys Gly Lys Ser Phe Arg Gly Ser Ser Asp
    290                 295                 300
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<210> 4027
<211> 941
<212> DNA
<213> Homo sapiens

<400> 4027
gcgcgccagg gaacctatat ctgtgaaatc cgcctcaaag gggagagcca ggtgttcaag
60
aaggcggtgg tactgcatgt gcttccagag gagcccaaag agctcatggt ccatgtgggt
120
ggattgattc agatgggatg tgttttccag agcacagaag tgaaacacgt gaccaaggta
180
gaatggatat tttcaggacg gcgcgcaaag gaggagattg tatttcgtta ctaccacaaa
240
ctcaggatgt ctgcggagta ctcccagagc tggggccact tccagaatcg tgtgaacctg
300
gtgggggaca ttttccgcaa tgacggttcc atcatgcttc aaggagtgag ggagtcagat
360
ggaggaaact acacctgcag tatccaccta gggaacctgg tgttcaagaa aaccattgtg
420
ctgcatgtca gcccggaaga gcctcgaaca ctggtgaccc cggcagccct gaggcctctg
480
gtcttgggtg gtaatcagtt ggtgatcatt gtgggaattg tctgtgccac aatcctgctg
540
ctccctgttc tgatattgat cgtgaagaag acctgtggaa ataagagttc agtgaattct
600
acagtcttgg tgaagaacac gaagaagact aatccagaga tgaaagaaaa accctgccat
660

tttgaaagat gtgaagggga ggtgaacaca cgcttcagcc taaaacacta agtagatgca
720
ggcctgggcc gttctcatac ccccgggaac catatcttac ccattgtatg tcgcagcttg
780
caggccagtg cttggcacag agcagggact caggaagcct ttgtcactaa agtaagagcc
840
tctgcggagt acagtgcatg gggtcggctg ggacaccccc aggcagcaga tcctggtatt
900
gggctgagga aagagcactg cgcttggagt cagtaagatc t
941

<210> 4028
<211> 236
<212> PRT
<213> Homo sapiens

<400> 4028
Ala Arg Gln Gly Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser
1 5 10 15
Gln Val Phe Lys Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro
20 25 30
Lys Glu Leu Met Val His Val Gly Gly Leu Ile Gln Met Gly Cys Val
35 40 45
Phe Gln Ser Thr Glu Val Lys His Val Thr Lys Val Glu Trp Ile Phe
50 55 60
Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe Arg Tyr Tyr His Lys
65 70 75 80
Leu Arg Met Ser Ala Glu Tyr Ser Gln Ser Trp Gly His Phe Gln Asn
85 90 95
Arg Val Asn Leu Val Gly Asp Ile Phe Arg Asn Asp Gly Ser Ile Met
100 105 110
Leu Gln Gly Val Arg Glu Ser Asp Gly Gly Asn Tyr Thr Cys Ser Ile
115 120 125
His Leu Gly Asn Leu Val Phe Lys Lys Thr Ile Val Leu His Val Ser
130 135 140
Pro Glu Glu Pro Arg Thr Leu Val Thr Pro Ala Ala Leu Arg Pro Leu
145 150 155 160
Val Leu Gly Gly Asn Gln Leu Val Ile Ile Val Gly Ile Val Cys Ala
165 170 175
Thr Ile Leu Leu Leu Pro Val Leu Ile Leu Ile Val Lys Lys Thr Cys
180 185 190
Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu Val Lys Asn Thr Lys
195 200 205
Lys Thr Asn Pro Glu Met Lys Glu Lys Pro Cys His Phe Glu Arg Cys
210 215 220
Glu Gly Glu Val Asn Thr Arg Phe Ser Leu Lys His
225 230 235

<210> 4029
<211> 909
<212> DNA
<213> Homo sapiens

<400> 4029

cggccgcctg ttttgggtgg cgctggacct gctggacctg ctggacatgc aggccagcct
60
gtgggagccg ccgcgctccg ggctgccgct gtgggccgag ggcctcacct tcttctactg
120
ctacatgctg ctgctggtgc tgccgtgcgt ggcgctcagc gaggtcagca tgcagggcga
180
gcacatagcg ccgcagaaga tgatgctgta cccggtgctc agtctcgcca ccgtcaatgt
240
ggtgggccgt gctggcgcgc gccgccaaca tggcgctgtt ccgggacagc cgtgtctcgg
300
ccatcttcgt cggcaaaaac gtggtggcgc tcgccaccaa ggcctgcacc tnntcctgga
360
gtaccgccgc caggtgcgcg acttcccnng ccgcctgcgc tatcactgga gctgcagccg
420
ccacccccgc agcgcaactc ggtgccgccg ccgccgccgc cgctgcacgg cccgcctggg
480
ncgcccccac atgtcctcgc ccacgcgtga ccccctggac acgtgacagg gcccgcgcgg
540
cccccgacac gcccctgggg cgcagagaca ccgggttggc ttggggcgcg cggtttgcat
600
gggatggggt gggggcgggc tcccctaggg acaggtgcct cgagtgcccg tgcctggggt
660
cccgcggccg cttcttcatc tcaggaatct ctcggaccgc ggatcctcag cccccgctcc
720
accagcccgc cccagcgcgt gggtctgttt gggaggcctg ggccggagca gagcagaggt
780
gatccggccc ctgcctgctg ggccgcccgg gttggaaggg agggcagtgt gggcggagat
840
ctgctccttc ggtgggggcc tctggctcag atttggggcc aaggaggcct ctgtcatttt
900
aaagactcg
909

<210> 4030
<211> 169
<212> PRT
<213> Homo sapiens

<400> 4030
Arg Pro Pro Val Leu Gly Gly Ala Gly Pro Ala Gly Pro Ala Gly His
1 5 10 15
Ala Gly Gln Pro Val Gly Ala Ala Ala Leu Arg Ala Ala Ala Val Gly
20 25 30
Arg Gly Pro His Leu Leu Leu Leu Leu His Ala Ala Ala Gly Ala Ala
35 40 45
Val Arg Gly Ala Gln Arg Gly Gln His Ala Gly Arg Ala His Ser Ala
50 55 60
Ala Glu Asp Asp Ala Val Pro Gly Ala Gln Ser Arg His Arg Gln Cys
65 70 75 80
Gly Gly Pro Cys Trp Arg Ala Pro Pro Thr Trp Arg Cys Ser Gly Thr
85 90 95
Ala Val Ser Arg Pro Ser Ser Ser Ala Lys Thr Trp Trp Arg Ser Pro
100 105 110
Pro Arg Pro Ala Pro Xaa Pro Gly Val Pro Pro Pro Gly Ala Arg Leu

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        115                 120                 125
Pro Xaa Pro Pro Ala Leu Ser Leu Glu Leu Gln Pro Pro Pro Pro Gln
    130                 135                 140
Arg Asn Ser Val Pro Pro Pro Pro Pro Pro Leu His Gly Pro Pro Gly
145                 150                 155                 160
Xaa Pro Pro His Val Leu Ala His Ala
                165
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<210> 4031
<211> 1406
<212> DNA
<213> Homo sapiens

<400> 4031
naagctgaga acgcatcttt agctaaactt cgcattgaac gagaaagtgc cttggaaaaa
60
ctcaggaaag aaattgcagg cttcgaacaa cagaaagcaa aagaattagc tcgaatagaa
120
gagtttaaaa aggaggagat gaggaagcta caaaaggaac gtaaagtttt tgaaaagtat
180
actacagctg caagaacttt tccagataaa aaggaacgtg aagaaataca gactttaaaa
240
cagcaaatag cagatttacg ggaagatttg aaaagaaagg agaccaaatg gtcaagtaca
300
cacagccgtc tcagaagcca gatacaaatg ttagtcagag agaacacaga cctccgggaa
360
gaaataaaag tgatggaaag attccgactg gatgcctgga agagagcaga agccatagag
420
agcagcctcg aggtggagaa gaaggacaag cttgcgaaca catctgttcg atttcaaaac
480
agtcagattt cttcaggaac ccaggtagaa aaatacaaga aaaattatct tccaatgcaa
540
ggcaatccac ctcgaagatc caagtctgca cctcctcgtg atttaggcaa tttggataag
600
ggacaggctg cctctcccag ggagccactt gaaccactga acttcccaga tcctgaatat
660
aaagaggagg aggaagacca agacatacag ggagaaatca gtcatcctga tggaaaggtg
720
gaaaaggttt ataagaatgg gtgccgtgtt atactgtttc ccaatggaac tcgaaaggaa
780
gtgagtgcag atgggaagac catcactgtc actttcttta atggtgacgt gaagcaggtc
840
atgccagacc aaagagtgat ctactactat gcagctgccc agaccactca cacgacatac
900
ccggagggac tggaagtctt acatttctca agtggacaaa tagaaaaaca ttacccagat
960
ggaagaaaag aaatcacgtt tcctgaccag actgttaaaa acttatttcc tgatggacaa
1020
gaagaaagca ttttcccaga tggtacaatt gtcagagtac aacgtgatgg caacaaactc
1080
atagagttta ataatggcca aagagaacta catactgccc agttcaagag acgggaatac
1140
ccagatggca ctgttaaaac cgtatatgca aacggtcatc aagaaacgaa gtacagatcc
1200

ggtcggataa gagttaagga caaggagggt aatgtgctaa tggacacgga gctgtgacga
1260
tcctcatgtg atcatgaagt aacagtaact gacttttttat gttaaaaaat gtacatttac
1320
tgtggattct gtttaattta ttgtgtatgt gtggggaaaa gattggattc taaaataaaa
1380
gtttaccctg tggcaaaaaa aaaaaa
1406

<210> 4032
<211> 418
<212> PRT
<213> Homo sapiens

<400> 4032
Xaa Ala Glu Asn Ala Ser Leu Ala Lys Leu Arg Ile Glu Arg Glu Ser
1 5 10 15
Ala Leu Glu Lys Leu Arg Lys Glu Ile Ala Gly Phe Glu Gln Gln Lys
20 25 30
Ala Lys Glu Leu Ala Arg Ile Glu Glu Phe Lys Lys Glu Glu Met Arg
35 40 45
Lys Leu Gln Lys Glu Arg Lys Val Phe Glu Lys Tyr Thr Thr Ala Ala
50 55 60
Arg Thr Phe Pro Asp Lys Lys Glu Arg Glu Glu Ile Gln Thr Leu Lys
65 70 75 80
Gln Gln Ile Ala Asp Leu Arg Glu Asp Leu Lys Arg Lys Glu Thr Lys
85 90 95
Trp Ser Ser Thr His Ser Arg Leu Arg Ser Gln Ile Gln Met Leu Val
100 105 110
Arg Glu Asn Thr Asp Leu Arg Glu Glu Ile Lys Val Met Glu Arg Phe
115 120 125
Arg Leu Asp Ala Trp Lys Arg Ala Glu Ala Ile Glu Ser Ser Leu Glu
130 135 140
Val Glu Lys Lys Asp Lys Leu Ala Asn Thr Ser Val Arg Phe Gln Asn
145 150 155 160
Ser Gln Ile Ser Ser Gly Thr Gln Val Glu Lys Tyr Lys Lys Asn Tyr
165 170 175
Leu Pro Met Gln Gly Asn Pro Pro Arg Arg Ser Lys Ser Ala Pro Pro
180 185 190
Arg Asp Leu Gly Asn Leu Asp Lys Gly Gln Ala Ala Ser Pro Arg Glu
195 200 205
Pro Leu Glu Pro Leu Asn Phe Pro Asp Pro Glu Tyr Lys Glu Glu Glu
210 215 220
Glu Asp Gln Asp Ile Gln Gly Glu Ile Ser His Pro Asp Gly Lys Val
225 230 235 240
Glu Lys Val Tyr Lys Asn Gly Cys Arg Val Ile Leu Phe Pro Asn Gly
245 250 255
Thr Arg Lys Glu Val Ser Ala Asp Gly Lys Thr Ile Thr Val Thr Phe
260 265 270
Phe Asn Gly Asp Val Lys Gln Val Met Pro Asp Gln Arg Val Ile Tyr
275 280 285
Tyr Tyr Ala Ala Ala Gln Thr Thr His Thr Thr Tyr Pro Glu Gly Leu
290 295 300
Glu Val Leu His Phe Ser Ser Gly Gln Ile Glu Lys His Tyr Pro Asp

305 310 315 320
Gly Arg Lys Glu Ile Thr Phe Pro Asp Gln Thr Val Lys Asn Leu Phe
325 330 335
Pro Asp Gly Gln Glu Glu Ser Ile Phe Pro Asp Gly Thr Ile Val Arg
340 345 350
Val Gln Arg Asp Gly Asn Lys Leu Ile Glu Phe Asn Asn Gly Gln Arg
355 360 365
Glu Leu His Thr Ala Gln Phe Lys Arg Arg Glu Tyr Pro Asp Gly Thr
370 375 380
Val Lys Thr Val Tyr Ala Asn Gly His Gln Glu Thr Lys Tyr Arg Ser
385 390 395 400
Gly Arg Ile Arg Val Lys Asp Lys Glu Gly Asn Val Leu Met Asp Thr
405 410 415
Glu Leu

<210> 4033
<211> 487
<212> DNA
<213> Homo sapiens

<400> 4033
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gggttttgat gggatagcag acaggtggat tgcagagctc cggaaagacc cagccgggtg
120
tcaagaagag ccctcctagt ttggcctcta actggctgtg cgaccccagg caggtcactt
180
gtcctctctg ggaagcagct gaataatgaa cactgggatt ttcccaggct ggcttctcac
240
tgcagagcag aggaaaagca ttctgggggc ctgctatgga gggtcattta tccagtttac
300
aacttccacg gccggccctc aatggcttcc tttctctccc acaagagcgc tgggccaagc
360
cagctctgca ccagttggac gccttccaag aaaaactcag gctccggggg ctgcttgtca
420
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480
ccagtcc
487

<210> 4034
<211> 94
<212> PRT
<213> Homo sapiens

<400> 4034
Met Asn Thr Gly Ile Phe Pro Gly Trp Leu Leu Thr Ala Glu Gln Arg
1 5 10 15
Lys Ser Ile Leu Gly Ala Cys Tyr Gly Gly Ser Phe Ile Gln Phe Thr
20 25 30
Thr Ser Thr Ala Gly Pro Gln Trp Leu Pro Phe Ser Pro Thr Arg Ala
35 40 45
Leu Gly Gln Ala Ser Ser Ala Pro Val Gly Arg Leu Pro Arg Lys Thr

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    50                  55                  60
Gln Ala Pro Gly Ala Ala Cys Gln Asp Gln Thr Gly Gly Leu Ala Pro
65                  70                  75                  80
Pro Pro Ala Met Cys Gly Glu Arg Ala Ser Pro Ser Gln Ser
                85                  90
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<210> 4035
<211> 343
<212> DNA
<213> Homo sapiens

<400> 4035
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aatgttctgg aatcctatgt gagggacaaa cattcagacc ccagcagcaa tgttctggaa
120
tcctatggga gggacaaact ctcagaaaat agcaagagta ttttggaatc ctatctgagg
180
tataaacact cagaacctca tagcagtgtt caggaatcct atgtgaggga caaacattca
240
gaccacagca ggagcattct agaatcctat ttgaggaaca aacattcaga caatcgtagc
300
agtgttctgg aatccttttt ttttttgaag ctttcaatct ctt
343

<210> 4036
<211> 114
<212> PRT
<213> Homo sapiens

<400> 4036
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Xaa Leu Asn Ser Ser Val Met Glu Phe His Val Arg His Lys His Ser
 1               5                  10                  15
Asp Asn Pro Ser Asn Val Leu Glu Ser Tyr Val Arg Asp Lys His Ser
            20                  25                  30
Asp Pro Ser Ser Asn Val Leu Glu Ser Tyr Gly Arg Asp Lys Leu Ser
        35                  40                  45
Glu Asn Ser Lys Ser Ile Leu Glu Ser Tyr Leu Arg Tyr Lys His Ser
    50                  55                  60
Glu Pro His Ser Ser Val Gln Glu Ser Tyr Val Arg Asp Lys His Ser
65                  70                  75                  80
Asp His Ser Arg Ser Ile Leu Glu Ser Tyr Leu Arg Asn Lys His Ser
                85                  90                  95
Asp Asn Arg Ser Ser Val Leu Glu Ser Phe Phe Phe Leu Lys Leu Ser
            100                 105                 110
Ile Ser
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<210> 4037
<211> 741
<212> DNA
<213> Homo sapiens

<400> 4037

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120
ggaggagaag gggttggtct tgctgtctca gggcggcaga ggcagaagag aatctgagca
180
tacgtggacc tgtagccagg tgggcataga taaaaggaaa tattgtttgc cagtccctgc
240
tggaatgatg cctttacaca tctgtctgat ctgattgctc cactgttttc tgacttctct
300
tccctttcca gggttctagc ctgttcatct agccccatga tggctgtgga catcgagtac
360
agatacaact gcatggctcc ttccttgcgc caagagaggt ttgcctttaa gatctcacca
420
aagcccagca aaccactgag gccttgtatt cagctgagca gcaagaatga agccagtgga
480
atggtggccc cggctgtcca ggagaagaag gtgaaaaagc gggtgtcctt cgcagacaac
540
caggggctgg ccctgacaat ggtcaaagtg ttctcggaat tcgatgaccc gctagatatg
600
ccattcaaca tcaccgagct cctagacaac attgtgagct tgacgacagc agagagcgag
660
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720
caggccgacc acgtctgcct t
741

<210> 4038
<211> 134
<212> PRT
<213> Homo sapiens

<400> 4038
Met Ala Val Asp Ile Glu Tyr Arg Tyr Asn Cys Met Ala Pro Ser Leu
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Arg Gln Glu Arg Phe Ala Phe Lys Ile Ser Pro Lys Pro Ser Lys Pro
20 25 30
Leu Arg Pro Cys Ile Gln Leu Ser Ser Lys Asn Glu Ala Ser Gly Met
35 40 45
Val Ala Pro Ala Val Gln Glu Lys Lys Val Lys Lys Arg Val Ser Phe
50 55 60
Ala Asp Asn Gln Gly Leu Ala Leu Thr Met Val Lys Val Phe Ser Glu
65 70 75 80
Phe Asp Asp Pro Leu Asp Met Pro Phe Asn Ile Thr Glu Leu Leu Asp
85 90 95
Asn Ile Val Ser Leu Thr Thr Ala Glu Ser Glu Ser Phe Val Leu Asp
100 105 110
Phe Ser Gln Pro Ser Ala Asp Tyr Leu Asp Phe Arg Asn Arg Leu Gln
115 120 125
Ala Asp His Val Cys Leu
130

<210> 4039
<211> 1503

<212> DNA
<213> Homo sapiens

<400> 4039
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gctgcgcgcg tcggagaggc tcctggggaa actcccacgg cccagggact ttcgaaagca
120
gagcgaggag ccctcgcacg cgctagtctg cgagtgagcg ctcagcccgg cacctgttcc
180
tccagcgccg ccgccttccc acccctcgga cccgcgccgc tcgcggcgcc cgcccgttcc
240
tgcgatgaat ccggccctag gcaaccagac ggacgtggcg ggccttcctg gccaacagca
300
gcgaggcgct ggagcgagcc gtgcgctgct gcacccaggc gtccgtggtg accgacgacg
360
gcttcgcgga gggaggcccg gacgagcgta gcctgtacat aatgcgcgtg gtgcagatcg
420
cggtcatgtg cgtgctctca ctcaccgtgg tcttcggcat cttcttcctc ggctgcaatc
480
tgctcatcaa gtccgagggc atgatcaact tcctcgtgaa ggaccggagg ccgtctaagg
540
aggtggaggc ggtggtcgtg gggccctact gacccgccct ctgcccccgc ggcaaccgct
600
cccacgcctg cccactttgc tagcccggct gtgcccctca ctatcagaga ctgggcgaag
660
caaacctgtc ggagtcaatt atttctctcg acttcggcct ttcggaaaga agcgaccggt
720
ttctccctcg ccctctgaaa gtcctcatgc ctggcagtcg gaggagagcg cccagactct
780
gaactcagca gaaagtggca agaagagggc gattagggcg cagaactttg gaagctgcta
840
cttacttgga atgcggggag accgacggtg cgaaggccct tctccacccg caggtgggcc
900
aagctctggg ggcaggtgga gagggcgggc aggggagaga cccagcggca ctgatcgcct
960
tgtgaccgga agagtgacct gttaaaagcc acgcagcaga ctcatggggt ctcacaaatc
1020
cgtgtccggg tgcgctccca ctcttctcct gctccccccc tgcccctgga ggggaggggc
1080
gataaatacc tttgattgta acgtgccgtt ttaagaggtt ttgtgtttgt ttgcttgaat
1140
acaaatgttt gataagtctt tttctgcccc agtggcctgt ttgcctgcct gaggagttac
1200
agttttgtca ttgtggaaga aggggtgggg ggaggggggag cctgcgaatt tgaacggggt
1260
gagttgtttc ttttagtgca tttcccactg ggtcttttgg gaggcgtcta gcgttcctgc
1320
tggccctggg acaaagaccc agaatagaac tcgtagctcg tgactgcacg gtttacgcca
1380
caaaagtgct cttgacatcc gtgacaccgt tttgactttt tgtttttttc ttatttaaca
1440
tttccttaat aaatgcaaca tttaagcgtt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
1500

aaa
1503

<210> 4040
<211> 100
<212> PRT
<213> Homo sapiens

<400> 4040
Lys Ser Leu Ala Ala Ala Arg Val Gly Glu Ala Pro Gly Glu Thr Pro
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Thr Ala Gln Gly Leu Ser Lys Ala Glu Arg Gly Ala Leu Ala Arg Ala
20 25 30
Ser Leu Arg Val Ser Ala Gln Pro Gly Thr Cys Ser Ser Ser Ala Ala
35 40 45
Ala Phe Pro Pro Leu Gly Pro Ala Pro Leu Ala Ala Pro Ala Arg Ser
50 55 60
Cys Asp Glu Ser Gly Pro Arg Gln Pro Asp Gly Arg Gly Gly Pro Ser
65 70 75 80
Trp Pro Thr Ala Ala Arg Arg Trp Ser Glu Pro Cys Ala Ala Ala Pro
85 90 95
Arg Arg Pro Trp
100

<210> 4041
<211> 573
<212> DNA
<213> Homo sapiens

<400> 4041
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ggtgagattc cagctgaatt aagggcggcg gccactgacc accggcagga gctaattgaa
120
tgtgttgcca attcagatga acagcttggt gagatgtttc tggaagaaaa aatcccctcg
180
atttctgatt taaagctagc aattcgaaga gctactctga aaagatcatt tactcctgta
240
tttttgggaa gcgccttgaa gaacaaagga gttcagcctc ttttagatgc tgttttagaa
300
tacctcccaa atccatctga agtccagaac tatgctattc tcaataaaga ggatgactca
360
aaagagaaaa ccaaaatcct aatgaactcc agtagagaca attcccaccc atttgtaggc
420
ctggctttta aactggaggt aggtcgattt ggacaattaa cttatgttcg cagttatcag
480
ggagagctaa agaagggtga caccatctat aacacaagga caagaaagaa agtacggttg
540
caacggctgg ctcgcatgca tgccgacatg atg
573

<210> 4042
<211> 191
<212> PRT

<213> Homo sapiens

<400> 4042
Asp Leu Ile Glu Glu Arg Ala Ile Tyr Phe Asp Gly Asp Phe Gly Gln
1 5 10 15
Ile Val Arg Tyr Gly Glu Ile Pro Ala Glu Leu Arg Ala Ala Ala Thr
20 25 30
Asp His Arg Gln Glu Leu Ile Glu Cys Val Ala Asn Ser Asp Glu Gln
35 40 45
Leu Gly Glu Met Phe Leu Glu Glu Lys Ile Pro Ser Ile Ser Asp Leu
50 55 60
Lys Leu Ala Ile Arg Arg Ala Thr Leu Lys Arg Ser Phe Thr Pro Val
65 70 75 80
Phe Leu Gly Ser Ala Leu Lys Asn Lys Gly Val Gln Pro Leu Leu Asp
85 90 95
Ala Val Leu Glu Tyr Leu Pro Asn Pro Ser Glu Val Gln Asn Tyr Ala
100 105 110
Ile Leu Asn Lys Glu Asp Asp Ser Lys Glu Lys Thr Lys Ile Leu Met
115 120 125
Asn Ser Ser Arg Asp Asn Ser His Pro Phe Val Gly Leu Ala Phe Lys
130 135 140
Leu Glu Val Gly Arg Phe Gly Gln Leu Thr Tyr Val Arg Ser Tyr Gln
145 150 155 160
Gly Glu Leu Lys Lys Gly Asp Thr Ile Tyr Asn Thr Arg Thr Arg Lys
165 170 175
Lys Val Arg Leu Gln Arg Leu Ala Arg Met His Ala Asp Met Met
180 185 190

<210> 4043
<211> 744
<212> DNA
<213> Homo sapiens

<400> 4043
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120
ctcccaaaaa aagacccaaa agttaaaggt gtccaatcag cagctgtaca agcttttctt
180
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240
ctagtgaaaa agcgaattga gctcaaacat gacaagaaag caagagctat ggccaagagg
300
acaaaggata atttccatgg ttacaatggg attcctattg aggaaaagtc aaagaagagg
360
caggcaacag aaagccatac cagccaagga accgaccgag agtatgaaat ggaagaagag
420
aatgaattcc tcgagtacaa tcacgcagag tcagagcagg agtatgagga agagcaagaa
480
cctcccaaag ttgaaagcaa accaaaggtc tcccttaaag gtgccccacc acccatgaac
540
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600

gtgaagaaat cagaagagcg acctatgacc gcagaagaac ttagggagcg agaattcctt
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720
aaaaaggcac ctctcggacg gaag
744

<210> 4044
<211> 219
<212> PRT
<213> Homo sapiens

<400> 4044
Met Cys Arg Lys Gly Ile Val Gly Gln Trp Gly Leu Pro Lys Lys Asp
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Pro Lys Val Lys Gly Val Gln Ser Ala Ala Val Gln Ala Phe Leu Lys
20 25 30
Arg Lys Glu Glu Glu Leu Arg Arg Lys Ala Leu Glu Glu Lys Arg Arg
35 40 45
Lys Glu Glu Leu Val Lys Lys Arg Ile Glu Leu Lys His Asp Lys Lys
50 55 60
Ala Arg Ala Met Ala Lys Arg Thr Lys Asp Asn Phe His Gly Tyr Asn
65 70 75 80
Gly Ile Pro Ile Glu Glu Lys Ser Lys Lys Arg Gln Ala Thr Glu Ser
85 90 95
His Thr Ser Gln Gly Thr Asp Arg Glu Tyr Glu Met Glu Glu Glu Asn
100 105 110
Glu Phe Leu Glu Tyr Asn His Ala Glu Ser Glu Gln Glu Tyr Glu Glu
115 120 125
Glu Gln Glu Pro Pro Lys Val Glu Ser Lys Pro Lys Val Ser Leu Lys
130 135 140
Gly Ala Pro Pro Pro Met Asn Phe Thr Asp Leu Leu Arg Leu Ala Glu
145 150 155 160
Lys Lys Gln Phe Glu Pro Val Glu Ile Lys Val Val Lys Lys Ser Glu
165 170 175
Glu Arg Pro Met Thr Ala Glu Glu Leu Arg Glu Arg Glu Phe Leu Glu
180 185 190
Arg Lys His Arg Arg Lys Lys Leu Glu Thr Asp Gly Lys Leu Pro Pro
195 200 205
Thr Val Ser Lys Lys Ala Pro Leu Gly Arg Lys
210 215

<210> 4045
<211> 2217
<212> DNA
<213> Homo sapiens

<400> 4045
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tcttcaagga catgatgtgg aagtcttgac ttgagtaact tcaatagcac taacaacagg
120
aattgaaaaa aacttagaat tttaaagctg agaaagagtt atcgctgtga tgattttgtg
180

gttaatgaca ccaagctggg actggtacag aaagtcagag aacacttaca gaacttggaa
240
aactcagctt tcacagctga caggcataag aaaagaaaac ttttggaaaa ctcaacacta
300
aacagcaagt tattaaaagt aaatggaagc accactgcca tttgtgccac aggccttcgg
360
aatttgggga acacatgttt catgaatgcc atccttcagt cactcagtaa cattgagcag
420
ttttgctgtt atttcaaaga actgcccgcc gtggagttaa ggaatgggaa aacagcagga
480
aggcggacat accacaccag gagccaaggg gataacaatg tgtctttggt agaagagttt
540
agaaagacac tctgtgcttt atggcaaggc agccagactg catttagccc agagtcctta
600
ttttatgttg tttggaagat tatgccaaac tttaggggct atcaacagca ggacgcccat
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gaattcnatg cgctaccttt tggaccacct acacttggan acttcagggc ggtttcaacg
720
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840
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1020
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1080
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1140
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1200
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1320
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1380
aaggctaaca tccttttcta cgtggaacac caggccaaag ctggatcgga taaactttaa
1440
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1500
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1560
tttgtcaatg gtagtgactt actgaacatg ggcaccaact aattttgttg ttgttctacc
1620
agaaaacctc agcagatgtt ttgatttgct gctttagttg taataattca atttttatag
1680
gtagttgtaa gaacttagtc ttatttgact tttttatttt atgttaatgt tttcagttct
1740
cactttgagg cacatttaca tcaatgcttt tgttcctctc acatgctgaa agcaagatgt
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1860
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1920
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1980
agaccaggta attactgctt gtctctcaag gctgctgtct ttatcagcac taactaaata
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2100
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2160
tgtaatgttt aaaaaaaatg ctgtgactcc ctgacatggt ataggtgtta ccagtga
2217

<210> 4046
<211> 437
<212> PRT
<213> Homo sapiens

<400> 4046
Lys Lys Leu Arg Ile Leu Lys Leu Arg Lys Ser Tyr Arg Cys Asp Asp
1 5 10 15
Phe Val Val Asn Asp Thr Lys Leu Gly Leu Val Gln Lys Val Arg Glu
20 25 30
His Leu Gln Asn Leu Glu Asn Ser Ala Phe Thr Ala Asp Arg His Lys
35 40 45
Lys Arg Lys Leu Leu Glu Asn Ser Thr Leu Asn Ser Lys Leu Leu Lys
50 55 60
Val Asn Gly Ser Thr Thr Ala Ile Cys Ala Thr Gly Leu Arg Asn Leu
65 70 75 80
Gly Asn Thr Cys Phe Met Asn Ala Ile Leu Gln Ser Leu Ser Asn Ile
85 90 95
Glu Gln Phe Cys Cys Tyr Phe Lys Glu Leu Pro Ala Val Glu Leu Arg
100 105 110
Asn Gly Lys Thr Ala Gly Arg Arg Thr Tyr His Thr Arg Ser Gln Gly
115 120 125
Asp Asn Asn Val Ser Leu Val Glu Glu Phe Arg Lys Thr Leu Cys Ala
130 135 140
Leu Trp Gln Gly Ser Gln Thr Ala Phe Ser Pro Glu Ser Leu Phe Tyr
145 150 155 160
Val Val Trp Lys Ile Met Pro Asn Phe Arg Gly Tyr Gln Gln Gln Asp
165 170 175
Ala His Glu Phe Xaa Ala Leu Pro Phe Gly Pro Pro Thr Leu Gly Xaa
180 185 190
Phe Arg Ala Val Ser Thr Val Phe Pro Ala Gln Gln Phe Cys Arg Arg
195 200 205
Ile Leu Leu Cys Leu Gln Val Xaa Lys Cys Cys Ile Asn Gly Ala Ser
210 215 220
Thr Val Val Thr Ala Ile Phe Gly Gly Ile Leu Gln Asn Glu Val Asn
225 230 235 240
Cys Leu Ile Cys Gly Thr Glu Ser Arg Lys Phe Asp Pro Phe Leu Asp
245 250 255
Leu Ser Leu Asp Ile Pro Ser Gln Phe Arg Ser Lys Arg Ser Lys Asn

260 265 270
Gln Glu Asn Gly Pro Val Cys Ser Leu Arg Asp Cys Leu Arg Ser Phe
275 280 285
Thr Asp Leu Glu Glu Leu Asp Glu Thr Glu Leu Tyr Met Cys His Lys
290 295 300
Cys Lys Xaa Lys Gln Lys Ser Thr Lys Lys Phe Trp Ile Gln Lys Leu
305 310 315 320
Pro Lys Val Leu Cys Leu His Leu Lys Arg Phe His Trp Thr Ala Tyr
325 330 335
Leu Arg Asn Lys Val Asp Thr Tyr Val Glu Phe Pro Leu Arg Gly Leu
340 345 350
Asp Met Lys Cys Tyr Leu Leu Asp Pro Glu Asn Ser Gly Pro Glu Ser
355 360 365
Cys Leu Tyr Asp Leu Ala Ala Val Val Val His His Gly Ser Gly Val
370 375 380
Gly Ser Gly His Tyr Thr Ala Tyr Ala Thr His Glu Gly Arg Trp Phe
385 390 395 400
His Phe Asn Asp Ser Thr Val Thr Leu Thr Asp Glu Glu Thr Val Val
405 410 415
Lys Ala Lys Ala Asn Ile Leu Phe Tyr Val Glu His Gln Ala Lys Ala
420 425 430
Gly Ser Asp Lys Leu
435

<210> 4047
<211> 809
<212> DNA
<213> Homo sapiens

<400> 4047
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aacttttccc ctgttactgt gaagaagagt atcatgggtc catttaatct ttgattactg
120
cctaaaagca ttcattgccc cagtagttct taattgtctt ggaaatcatt ctcttgcaaa
180
cttcacattt ccatatcata ctttacttta cgctattact tcatgggctc ctgggcattt
240
ggtctgtttg tgtttctcct ttcctctttg aacaaagtca ggaaaaatgt gtcagtagga
300
gaaaggagga gctgaaggga gtaaataatt caagatcact tctgtcattt gtagtggctg
360
agggctagaa agatattctt cggtgaagaa actcccaaca ggttccatca gactgataca
420
acttcagggg ggccaccctc tgcagatggc agtgaatttg cacctgtttg tggtacaggc
480
actaccacag catctttgat gtctgtgttt acattacatg agaagttctt ctccagtttt
540
ttggcagtgt ctgggcaatt ttgtacaaag atcacacggt tgtaggcctt cagcctgcgc
600
cacaactgaa catagacttt acactgtacg tacatgaaga caagacctcc tgtgaagcca
660
atggctacca caaccagttt tgtccaaaat ggccattcaa ggacaccttt gaaatgaaaa
720

agagaaaatg ttatcaccaa gttgtcctca gtggatttgg tcatttttt ttcctatgac
780
ccttcaaagg cccgtgcttg ccttctaga
809

<210> 4048
<211> 118
<212> PRT
<213> Homo sapiens

<400> 4048
Met Thr Lys Ser Thr Glu Asp Asn Leu Val Ile Thr Phe Ser Leu Phe
1 5 10 15
His Phe Lys Gly Val Leu Glu Trp Pro Phe Trp Thr Lys Leu Val Val
20 25 30
Val Ala Ile Gly Phe Thr Gly Gly Leu Val Phe Met Tyr Val Gln Cys
35 40 45
Lys Val Tyr Val Gln Leu Trp Arg Arg Leu Lys Ala Tyr Asn Arg Val
50 55 60
Ile Phe Val Gln Asn Cys Pro Asp Thr Ala Lys Lys Leu Glu Lys Asn
65 70 75 80
Phe Ser Cys Asn Val Asn Thr Asp Ile Lys Asp Ala Val Val Val Pro
85 90 95
Val Pro Gln Thr Gly Ala Asn Ser Leu Pro Ser Ala Glu Gly Gly Pro
100 105 110
Pro Glu Val Val Ser Val
115

<210> 4049
<211> 1211
<212> DNA
<213> Homo sapiens

<400> 4049
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ttgtaccagc ctgatgaacg tgggccctgc ttcgcctttg agggccataa gctcattgcc
120
cactggttta gaggctacct tatcattgtc tcccgtgacc ggaaggtttc tcccaagtca
180
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Ser Asn Gln Val Ser Thr Ile Val Ser Leu Leu Ser Thr Leu Cys Arg
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Gly Ser Pro Val Val Thr His Asp Leu Leu Arg Ser Glu Leu Pro Asp
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Ser Ile Glu Ser Ala Leu Gln Gly Asp Glu Arg Cys Val Leu Asp Thr
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Gly Ala Phe Glu Val Asn Phe Met Asp Asp Val Gly Gln Thr Leu Leu
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225 230 235 240
Glu Arg Gly Ala Asp Val Asn Arg Gly Gln Arg Ser Ser Ser Leu His
245 250 255
Tyr Ala Ala Cys Phe Gly Arg Pro Gln Val Ala Lys Thr Leu Leu Arg
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His Gly Ala Asn Pro Asp Leu Arg Asp Glu Asp Gly Lys Thr Pro Leu
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Asp Lys Ala Arg Glu Arg Gly His Ser Glu Val Val Ala Ile Leu Gln
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Ser Pro Gly Asp Trp Met Cys Pro Val Asn Lys Gly Asp Asp Lys Lys

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Lys Lys Asp Thr Asn Lys Asp Glu Glu Glu Cys Asn Glu Pro Lys Gly
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Asp Pro Glu Met Ala Pro Ile Tyr Leu Lys Arg Leu Leu Pro Val Phe
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Ala Gln Thr Phe Gln Gln Thr Met Leu Pro Ser Ile Arg Lys Ala Ser
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Leu Ala Leu Ile Arg Lys Met Ile His Phe Cys Ser Glu Ala Leu Leu
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Lys Glu Val Cys Asp Ser Asp Val Gly His Asn Leu Pro Thr Ile Leu
385                 390                 395                 400
Val Glu Ile Thr Ala Thr Val Leu Asp Gln Glu Asp Asp Asp Asp Gly
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His Leu Leu Ala Leu Gln Ile Ile Arg Asp Leu Val Asp Lys Gly Gly
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Asp Ile Phe Leu Asp Gln Leu Ala Arg Leu Gly Val Ile Ser Lys Val
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Ser Thr Leu Ala Gly Pro Ser Ser Asp Asp Glu Asn Glu Glu Glu Ser
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Lys Pro Glu Lys Glu Asp Glu Pro Gln Glu Asp Ala Lys Glu Leu Gln
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Gln Gly Lys Pro Tyr His Trp Arg Asp Trp Ser Ile Ile Arg Gly Arg
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Asp Cys Leu Tyr Ile Trp Ser Asp Ala Ala Ala Leu Glu Leu Ser Asn
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Gly Ser Asn Gly Trp Phe Arg Phe Ile Leu Asp Gly Lys Leu Ala Thr
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Met Tyr Ser Ser Gly Ser Pro Glu Gly Gly Ser Asp Ser Ser Glu Ser
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Arg Ser Glu Phe Leu Glu Lys Leu Gln Arg Ala Arg Gly Gln Val Lys
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Pro Ser Thr Ser Ser Gln Pro Ile Leu Ser Ala Pro Gly Pro Thr Lys
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Leu Thr Val Gly Asn Trp Ser Leu Thr Cys Leu Lys Glu Gly Glu Ile
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Ala Ile His Asn Ser Asp Gly Gln Gln Ala Thr Ile Leu Lys Glu Asp
        595                 600                 605
Leu Pro Gly Phe Val Phe Glu Ser Asn Arg Gly Thr Lys His Ser Phe
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Thr Ala Glu Thr Ser Leu Gly Ser Glu Phe Val Thr Gly Trp Thr Gly
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Lys Arg Gly Arg Lys Leu Lys Ser Lys Leu Glu Lys Thr Lys Xaa Lys
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Val Arg Thr Met Ala Arg Asp Leu Tyr Asp Asp His Phe Lys Ala Val
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Glu Ser Met Pro Arg Gly Val Val Val Thr Leu Arg Asn Ile Ala Thr
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Gln Leu Glu Ser Ser Trp Glu Leu His Thr Asn Arg Gln Cys Ile Glu
    690                 695                 700
Ser Glu Asn Thr Trp Arg Asp Leu Met Lys Thr Ala Leu Glu Asn Leu
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Ile Val Leu Leu Lys Asp Glu Asn Thr Ile Ser Pro Tyr Glu Met Cys
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Ser Ser Gly Leu Val Gln Ala Leu Leu Thr Val Leu Asn Asn Ser Met
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Asp Leu Asp Met Lys Gln Asp Cys Ser Gln Leu Val Glu Arg Ile Asn
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Val Phe Lys Thr Ala Phe Ser Glu Asn Glu Asp Asp Glu Ser Arg Pro
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Ala Val Ala Leu Ile Arg Lys Leu Ile Ala Val Leu Glu Ser Ile Glu
785                 790                 795                 800
Arg Leu Pro Leu His Leu Tyr Asp Thr Pro Gly Ser Thr Tyr Asn Leu
                805                 810                 815
Gln Ile Leu Thr Arg Arg Leu Arg Phe Arg Leu Glu Arg Ala Pro Gly
            820                 825                 830
Glu Thr Ala Leu Ile Asp Arg Thr Gly Arg Met Leu Lys Met Glu Pro
        835                 840                 845
Leu Ala Thr Val Glu Ser Leu Glu Gln Tyr Leu Leu Lys Met Val Ala
    850                 855                 860
Lys Gln Trp Tyr Asp Phe Asp Arg Ser Ser Phe Val Phe Val Arg Lys
865                 870                 875                 880
Leu Arg Glu Gly Gln Asn Phe Ile Phe Arg His Gln His Asp Phe Asp
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Glu Asn Gly Ile Ile Tyr Trp Ile Gly Thr Asn Ala Lys Thr Ala Tyr
            900                 905                 910
Glu Trp Val Asn Pro Ala Ala Tyr Gly Leu Val Val Val Thr Ser Ser
        915                 920                 925
Glu Gly Arg Asn Leu Pro Tyr Gly Arg Leu Glu Asp Ile Leu Ser Arg
    930                 935                 940
Asp Asn Ser Ala Leu Asn Cys His Ser Asn Asp Asp Lys Asn Ala Trp
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Phe Ala Ile Asp Leu Gly Leu Trp Val Ile Pro Ser Ala Tyr Thr Leu
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Arg His Ala Arg Gly Tyr Gly Arg Ser Ala Leu Arg Asn Trp Val Phe
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Gln Val Ser Lys Asp Gly Gln Asn Trp Thr Ser Leu Tyr Thr His Val
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Asp Asp Cys Ser Leu Asn Glu Pro Gly Ser Thr Ala Thr Trp Pro Leu
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Asp Pro Pro Lys Asp Glu Lys Gln Gly Trp Arg His Val Arg Ile Lys
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Gln Met Gly Lys Asn Ala Ser Gly Gln Thr His Tyr Leu Ser Leu Ser
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Gly Phe Glu Leu Tyr Gly Thr Val Asn Gly Val Cys Glu Asp Gln Leu
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Gly Lys Ala Ala Lys Glu Ala Glu Ala Asn Leu Arg Arg Gln Arg Arg
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Leu Val Arg Ser Gln Val Leu Lys Tyr Met Val Pro Gly Ala Arg Val
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Ile Arg Gly Leu Asp Trp Lys Trp Arg Asp Gln Asp Gly Ser Pro Gln
1105                1110                1115                1120
Gly Glu Gly Thr Val Thr Gly Glu Leu His Asn Gly Trp Ile Asp Val
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Thr Trp Asp Ala Gly Gly Ser Asn Ser Tyr Arg Met Gly Ala Glu Gly
            1140                1145                1150
Lys Phe Asp Leu Lys Leu Ala Pro Gly Tyr Asp Pro Asp Thr Val Ala
        1155                1160                1165
Ser Pro Lys Pro Val Ser Ser Thr Val Ser Gly Thr Thr Gln Ser Trp
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Ser Ser Leu Val Lys Asn Asn Cys Pro Asp Lys Thr Ser Ala Ala Ala
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Gly Ser Ser Ser Arg Lys Gly Ser Ser Ser Ser Val Cys Ser Val Ala
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Ser Ser Ser Asp Ile Ser Leu Gly Ser Thr Lys Thr Glu Arg Arg Ser
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Glu Ile Val Met Glu His Ser Ile Val Ser Gly Ala Asp Val His Glu
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Pro Ile Val Val Leu Ser Ser Ala Glu Asn Val Pro Gln Thr Glu Val
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Gly Ser Ser Ser Ser Ala Ser Thr Ser Thr Leu Thr Ala Glu Thr Gly
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Ser Glu Asn Ala Glu Arg Lys Leu Gly Pro Asp Ser Ser Val Arg Thr
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Pro Gly Glu Ser Ser Ala Ile Ser Met Gly Ile Val Ser Val Ser Ser
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Pro Asp Val Ser Ser Val Ser Glu Leu Thr Asn Lys Glu Ala Ala Ser
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Leu Leu Ala Ala Gly Ala Pro Met Ser Ser Ser Ala Ser Val Pro Asn
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Leu Ser Ser Arg Glu Thr Ser Ser Leu Glu Ser Phe Val Arg Arg Val
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Ala Asn Ile Ala Arg Thr Asn Ala Thr Asn Asn Met Asn Leu Ser Arg
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Ser Ser Ser Asp Asn Asn Thr Asn Thr Leu Gly Arg Asn Val Met Ser
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Thr Ala Thr Ser Pro Leu Met Gly Ala Gln Ser Phe Pro Asn Leu Thr
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Thr Pro Gly Thr Thr Ser Thr Val Thr Met Ser Thr Ser Ser Val Thr
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Ser Ser Ser Asn Val Ala Thr Ala Thr Thr Val Leu Ser Val Gly Gln
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Ser Leu Ser Asn Thr Leu Thr Thr Ser Leu Thr Ser Thr Ser Ser Glu
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Ser Asp Thr Gly Gln Glu Ala Glu Tyr Ser Leu Tyr Asp Phe Leu Asp
        1475                1480                1485
Ser Cys Arg Ala Ser Thr Leu Leu Ala Glu Leu Asp Asp Asp Glu Asp
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Gln Arg Arg Ala Gly Ser Arg Ser Asp Val Thr His His Ala Val Thr
            1540                1545                1550
Ser Gln Leu Pro Gln Val Pro Ala Gly Ala Gly Ser Arg Pro Ile Gly
        1555                1560                1565
Glu Gln Glu Glu Glu Glu Tyr Glu Thr Lys Gly Gly Arg Arg Arg Thr
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Trp Asp Asp Asp Tyr Val Leu Lys Arg Gln Phe Ser Ala Leu Val Pro
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Ala Phe Asp Pro Arg Pro Gly Arg Thr Asn Val Gln Gln Thr Thr Asp
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Val Glu Cys Thr Pro Ser Pro Arg Leu Ala Leu Thr Leu Lys Val Thr
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Ser Thr Ile Phe Tyr Tyr Val Gln Lys Leu Leu Gln Leu Ser Cys Asn
1665                1670                1675                1680
Gly Asn Val Lys Ser Asp Lys Leu Arg Arg Ile Trp Glu Pro Thr Tyr
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Thr Ile Met Tyr Arg Glu Met Lys Asp Ser Asp Lys Glu Lys Glu Asn
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Ser Ile Arg Lys Asn Arg Asn Cys Ser Gln Leu Ile Ala Ala Tyr Lys
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Ser Thr Leu Gln Ser Ser Asp Ile Leu Asn Leu Thr Lys Glu Gln Pro
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Pro Asp Glu Phe Thr Ser Lys Lys Ile Thr Thr Lys Ile Leu Gln Gln
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Ile Glu Glu Pro Leu Ala Leu Ala Ser Gly Ala Leu Pro Asp Trp Cys
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Glu Gln Leu Thr Ser Lys Cys Pro Phe Leu Ile Pro Phe Glu Thr Arg
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Gln Leu Tyr Phe Thr Cys Thr Ser Phe Gly Ala Ser Arg Ala Ile Val
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Trp Leu Gln Asn Arg Arg Glu Ala Thr Val Glu Arg Thr Arg Thr Thr
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Lys His Glu Arg Val Lys Val Pro Arg Gly Glu Ser Leu Met Glu Trp
        1955                1960                1965
Ala Glu Asn Val Met Gln Ile His Ala Asp Arg Lys Ser Val Leu Glu
    1970                1975                1980
Val Glu Phe Leu Gly Glu Glu Gly Thr Gly Leu Gly Pro Thr Leu Glu
1985                1990                1995                2000
Phe Tyr Ala Leu Val Ala Ala Glu Phe Gln Arg Thr Asp Leu Gly Ala
                2005                2010                2015
Trp Leu Cys Asp Asp Asn Phe Pro Asp Asp Glu Ser Arg His Val Asp
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Gln Asp Asn Arg Leu Val Asp Leu Pro Ile Ser Lys Pro Phe Phe Lys
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Glu Ser Arg Gly Asp Arg Asp Leu His Cys Thr Glu Ser Gln Ser Glu
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Ala Ser Thr Glu Glu Gly His Asp Ser Leu Ser Val Gly Ser Phe Glu
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Glu Asp Ser Lys Ser Glu Phe Ile Leu Asp Pro Pro Lys Pro Lys Pro
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Pro Ala Trp Leu Asn Gly Ile Leu Thr Trp Glu Asp Phe Glu Leu Val
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Asn Pro His Arg Ala Arg Phe Leu Lys Glu Ile Lys Asp Leu Ala Ile
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Lys Arg Arg Gln Ile Leu Ser Asn Lys Gly Leu Ser Glu Asp Glu Lys
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Asn Thr Lys Leu Gln Glu Leu Val Leu Lys Asn Pro Ser Gly Ser Gly
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Pro Pro Leu Ser Ile Glu Asp Leu Gly Leu Asn Phe Gln Phe Cys Pro
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Ser Ser Arg Ile Tyr Gly Phe Thr Ala Val Asp Leu Lys Pro Ser Gly
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Phe Arg Asp Gly Phe Asn Lys Val Phe Pro Met Glu Lys Leu Ser Ser
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Phe Ser His Glu Glu Val Gln Met Ile Leu Cys Gly Asn Gln Ser Pro
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Ser Trp Ala Ala Glu Asp Ile Ile Asn Tyr Thr Glu Pro Lys Leu Gly
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Tyr Thr Arg Asp Ser Pro Gly Phe Leu Arg Phe Val Arg Val Leu Cys
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Gly Met Ser Ser Asp Glu Arg Lys Ala Phe Leu Gln Phe Thr Thr Gly
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Cys Ser Thr Leu Pro Pro Gly Gly Leu Ala Asn Leu His Pro Arg Leu
    2370                2375                2380
Thr Val Val Arg Lys Val Asp Ala Thr Asp Ala Ser Tyr Pro Ser Val
2385                2390                2395                2400
Asn Thr Cys Val His Tyr Leu Lys Leu Pro Glu Tyr Ser Ser Glu Glu
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Pro Glu Leu Gln Arg Arg Leu Asp Asp Trp Thr Ala Asn Pro Arg Ile
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Gly Asp Val Ile Gln Lys Leu Ala Pro Phe Leu Lys Met Tyr Ser Glu
65 70 75 80
Tyr Val Lys Asn Phe Glu Arg Ala Ala Glu Leu Leu Ala Thr Trp Thr
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Asp Lys Ser Pro Leu Phe Gln Glu Val Leu Thr Arg Ile Gln Val Arg
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Leu Gly Glu Gly Trp Ser Gln His Cys His Ser Gln His Ala Val Ala
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3994

<210> 4060
<211> 714
<212> PRT
<213> Homo sapiens

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Pro Thr Arg Ala Gly Asn Ser Thr Pro Arg Met Gln Phe Val Ser Thr
35 40 45
Arg Pro Gln Pro Gln Gln Leu Gly Ile Gln Gly Leu Gly Leu Asp Ser
50 55 60
Gly Ser Trp Ser Trp Ala Gln Ala Leu Pro Pro Glu Glu Val Cys His
65 70 75 80
Gln Glu Pro Ala Leu Arg Gly Glu Met Ala Glu Gly Met Pro Pro Met
85 90 95
Gln Ala Gln Glu Trp Asp Met Asp Ala Arg Arg Pro Met Pro Phe Gln
100 105 110
Phe Pro Pro Phe Pro Asp Arg Ala Pro Val Phe Pro Asp Arg Met Met
115 120 125
Arg Glu Pro Gln Leu Pro Thr Ala Glu Ile Ser Leu Trp Thr Val Val
130 135 140
Ala Ala Ile Gln Ala Met Glu Arg Lys Ile Glu Ser Gln Ala Ala His

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Leu Leu Ser Leu Glu Gly Gln Thr Gly Met Ala Glu Lys Lys Leu Ala
                165                 170                 175
Asp Cys Glu Lys Thr Ala Val Glu Phe Gly Asn Gln Leu Glu Gly Lys
            180                 185                 190
Trp Ala Val Leu Gly Thr Leu Leu Gln Glu Tyr Gly Leu Leu Gln Arg
        195                 200                 205
Arg Leu Glu Asn Val Glu Asn Leu Leu Arg Asn Arg Asn Phe Trp Val
    210                 215                 220
Leu Arg Leu Pro Pro Gly Ser Lys Gly Glu Ala Pro Lys Val Pro Val
225                 230                 235                 240
Thr Phe Val Asp Ile Ala Val Tyr Phe Ser Glu Asp Glu Trp Lys Asn
                245                 250                 255
Leu Asp Glu Trp Gln Lys Glu Leu Tyr Asn Asn Leu Val Lys Glu Asn
            260                 265                 270
Tyr Lys Thr Leu Met Ser Leu Asp Ala Glu Gly Ser Val Pro Lys Pro
        275                 280                 285
Asp Ala Pro Val Gln Ala Glu Pro Arg Glu Glu Pro Cys Val Trp Glu
    290                 295                 300
Gln Arg His Pro Glu Glu Arg Glu Ile Pro Met Asp Pro Glu Ala Gly
305                 310                 315                 320
Ala Glu Pro Leu Val Pro Ala Gln Asp Ala Ser Ser Gln Val Lys Arg
                325                 330                 335
Glu Asp Thr Leu Cys Val Arg Gly Gln Arg Gly Leu Glu Glu Arg Ala
            340                 345                 350
Ile Pro Thr Glu Ser Ile Thr Val Asp Ser Pro Ile Ser Ala Gln Asp
        355                 360                 365
Leu Leu Ser Arg Ile Lys Gln Glu Glu His Gln Cys Val Trp Asp Gln
    370                 375                 380
Gln Asp Leu Ala Asp Arg Asp Ile Pro Thr Asp Pro Asn Ser Glu Ser
385                 390                 395                 400
Leu Ile Ser Ala His Asp Ile Leu Ser Trp Ile Lys Gln Glu Glu Gln
                405                 410                 415
Pro Tyr Pro Trp Gly Pro Arg Asp Ser Met Asp Gly Glu Leu Gly Leu
            420                 425                 430
Asp Ser Gly Pro Ser Asp Ser Leu Leu Met Val Lys Asn Pro Pro Pro
        435                 440                 445
Ala Pro Pro Gln Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Leu
    450                 455                 460
Gln Ser Gln Pro Gln Pro Gln Ser Leu Pro Pro Ile Ala Val Ala Glu
465                 470                 475                 480
Asn Pro Gly Gly Pro Pro Ser Arg Gly Leu Leu Asp Asp Gly Phe Gln
                485                 490                 495
Val Leu Pro Gly Glu Arg Gly Ser Gly Glu Ala Pro Pro Gly Gly Asp
            500                 505                 510
Arg Ser Thr Gly Gly Gly Gly Gly Asp Gly Gly Gly Gly Gly Gly Gly
        515                 520                 525
Ala Glu Ala Gly Thr Gly Ala Gly Gly Gly Cys Gly Ser Cys Cys Pro
    530                 535                 540
Gly Gly Leu Arg Arg Ser Leu Leu Leu His Gly Ala Arg Ser Lys Pro
545                 550                 555                 560
Tyr Ser Cys Pro Glu Cys Gly Lys Ser Phe Gly Val Arg Lys Ser Leu
                565                 570                 575
Ile Ile His His Arg Ser His Thr Lys Glu Arg Pro Tyr Glu Cys Ala
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            580                 585                 590
Glu Cys Glu Lys Ser Phe Asn Cys His Ser Gly Leu Ile Arg His Gln
        595                 600                 605
Met Thr His Arg Gly Glu Arg Pro Tyr Lys Cys Ser Glu Cys Glu Lys
    610                 615                 620
Thr Tyr Ser Arg Lys Glu His Leu Gln Asn His Gln Arg Leu His Thr
625                 630                 635                 640
Gly Glu Arg Pro Phe Gln Cys Ala Leu Cys Gly Lys Ser Phe Ile Arg
                645                 650                 655
Lys Gln Asn Leu Leu Lys His Gln Arg Ile His Thr Gly Glu Arg Pro
            660                 665                 670
Tyr Thr Cys Gly Glu Cys Gly Lys Ser Phe Arg Tyr Lys Glu Ser Leu
        675                 680                 685
Lys Asp His Leu Arg Val His Ser Gly Gly Pro Gly Pro Gly Ala Pro
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Arg Gln Leu Pro Pro Pro Pro Glu Arg Asp
705                 710
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<210> 4061
<211> 519
<212> DNA
<213> Homo sapiens

<400> 4061
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120
gcttgcagct ataatacctc tggtggtcaa gagtgtcaag tgtgcaacgg tactgtcaga
180
cattttgcgc agatgcactc tgaccactcc tggcatggtg ggacttcatg ggaggaggaa
240
ctctggtaag ctcatgtcac tggacaaagc ccccttgagg caactcttgg atgccacgat
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cggggcctac atcaacacaa cgcactcacg gctcacacac atcagtcctc ggcactatag
360
tgagtttata gagttcctca gcaaagcccg agagaccttc ttaatggcgc atgatggaca
420
cattcagttt acacagttta ttgacaacct gaaacaaatc tacaaaggca aaaagaaact
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519

<210> 4062
<211> 165
<212> PRT
<213> Homo sapiens

<400> 4062
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Asn Asp Val Leu Trp Ala Cys Ala Leu Ser His Ser Leu Gly Lys Asn
            20                  25                  30
Glu Leu Ala Ala Ile Ile Pro Leu Val Val Lys Ser Val Lys Cys Ala
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        35                  40                  45
Thr Val Leu Ser Asp Ile Leu Arg Arg Cys Thr Leu Thr Thr Pro Gly
    50                  55                  60
Met Val Gly Leu His Gly Arg Arg Asn Ser Gly Lys Leu Met Ser Leu
65                  70                  75                  80
Asp Lys Ala Pro Leu Arg Gln Leu Leu Asp Ala Thr Ile Gly Ala Tyr
                85                  90                  95
Ile Asn Thr Thr His Ser Arg Leu Thr His Ile Ser Pro Arg His Tyr
            100                 105                 110
Ser Glu Phe Ile Glu Phe Leu Ser Lys Ala Arg Glu Thr Phe Leu Met
        115                 120                 125
Ala His Asp Gly His Ile Gln Phe Thr Gln Phe Ile Asp Asn Leu Lys
    130                 135                 140
Gln Ile Tyr Lys Gly Lys Lys Lys Leu Met Met Leu Val Arg Arg Glu
145                 150                 155                 160
Val Trp Leu Ile Asp
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<210> 4063
<211> 4137
<212> DNA
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120
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180
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240
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300
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360
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420
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480
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960
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1080
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4137

<210> 4064
<211> 818
<212> PRT
<213> Homo sapiens

<400> 4064
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20 25 30
Met Cys Cys Pro Ser Arg Ser Ser Ile Leu Thr Gly Lys Tyr Val His
35 40 45
Asn His Asn Thr Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp
50 55 60
Gln Ala Gln His Glu Ser Arg Thr Phe Ala Val Tyr Leu Asn Ser Thr
65 70 75 80
Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly
85 90 95
Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp Val Gly Leu Leu Lys Asn
100 105 110
Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg Asn Gly Val Lys Glu Lys
115 120 125
His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu Thr Asp Leu Ile Thr Asn
130 135 140
Asp Ser Val Ser Phe Phe Arg Thr Ser Lys Lys Met Tyr Pro His Arg
145 150 155 160
Pro Val Leu Met Val Ile Ser His Ala Ala Pro His Gly Pro Glu Asp
165 170 175
Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro Asn Ala Ser Gln His Ile
180 185 190
Thr Pro Ser Tyr Asn Tyr Ala Pro Asp Pro Asp Lys His Trp Ile Met
195 200 205
Arg Tyr Thr Gly Pro Met Lys Pro Ile His Met Glu Phe Thr Asn Met
210 215 220
Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser Val Asp Asp Ser Met
225 230 235 240
Glu Thr Ile Tyr Asn Met Leu Val Glu Thr Gly Glu Leu Asp Asn Thr
245 250 255
Tyr Ile Val Tyr Thr Ala Asp His Gly Tyr His Ile Gly Gln Phe Gly
260 265 270
Leu Val Lys Gly Lys Ser Met Pro Tyr Glu Phe Asp Ile Arg Val Pro
275 280 285
Phe Tyr Val Arg Gly Pro Asn Val Glu Ala Gly Cys Leu Asn Pro His
290 295 300
Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile Leu Asp Ile Ala Gly
305 310 315 320
Leu Asp Ile Pro Ala Asp Met Asp Gly Lys Ser Ile Leu Lys Leu Leu
325 330 335
Asp Thr Glu Arg Pro Val Asn Arg Phe His Leu Lys Lys Lys Met Arg
340 345 350
Val Trp Arg Asp Ser Phe Leu Val Glu Arg Gly Lys Leu Leu His Lys
355 360 365
Arg Asp Asn Asp Lys Val Asp Ala Gln Glu Glu Asn Phe Leu Pro Lys

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    370                 375                 380
Tyr Gln Arg Val Lys Asp Leu Cys Gln Arg Ala Glu Tyr Gln Thr Ala
385                 390                 395                 400
Cys Glu Gln Leu Gly Gln Lys Trp Gln Cys Val Glu Asp Ala Thr Gly
                405                 410                 415
Lys Leu Lys Leu His Lys Cys Lys Gly Pro Met Arg Leu Gly Gly Ser
            420                 425                 430
Arg Ala Leu Ser Asn Leu Val Pro Lys Tyr Tyr Gly Gln Gly Ser Glu
        435                 440                 445
Ala Cys Thr Cys Asp Ser Gly Asp Tyr Lys Leu Ser Leu Ala Gly Arg
    450                 455                 460
Arg Lys Lys Xaa Leu Gln Glu Glu Xaa Tyr Lys Ala Ser Tyr Val Arg
465                 470                 475                 480
Asn Arg Ser Ile Arg Ser Val Ala Ile Glu Val Asp Gly Arg Val Tyr
                485                 490                 495
His Val Gly Leu Gly Asp Ala Ala Gln Pro Arg Asn Leu Thr Lys Arg
            500                 505                 510
His Trp Pro Gly Ala Pro Glu Asp Gln Asp Asp Lys Asp Gly Gly Asp
        515                 520                 525
Xaa Ser Val Ala Leu Glu Ala Phe Pro Thr Thr Gln Pro Pro Thr Xaa
    530                 535                 540
Ile Lys Val Thr His Arg Cys Tyr Ile Leu Glu Asn Asp Thr Val Gln
545                 550                 555                 560
Cys Asp Leu Asp Leu Tyr Lys Ser Leu Gln Ala Trp Lys Asp His Lys
                565                 570                 575
Leu His Ile Asp His Glu Ile Glu Thr Leu Gln Asn Lys Ile Lys Asn
            580                 585                 590
Leu Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg Pro Glu Glu Cys
        595                 600                 605
Asp Cys His Lys Ile Ser Tyr His Thr Gln His Lys Gly Arg Leu Lys
    610                 615                 620
His Arg Gly Ser Ser Leu His Pro Phe Arg Lys Gly Leu Gln Glu Lys
625                 630                 635                 640
Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys Lys Lys Leu Arg
                645                 650                 655
Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys Ser Met Pro Gly
            660                 665                 670
Leu Thr Cys Phe Thr His Asp Asn Gln His Trp Gln Thr Ala Pro Phe
        675                 680                 685
Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr Ser Ala Asn Asn Asn Thr
    690                 695                 700
Tyr Trp Cys Met Arg Thr Ile Asn Glu Thr His Asn Phe Leu Phe Cys
705                 710                 715                 720
Glu Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Leu Asn Thr Asp Pro
                725                 730                 735
Tyr Gln Leu Met Asn Ala Val Asn Thr Leu Asp Arg Asp Val Leu Asn
            740                 745                 750
Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys Lys Gly Tyr Lys
        755                 760                 765
Gln Cys Asn Pro Arg Thr Arg Asn Met Asp Leu Gly Leu Lys Asp Gly
    770                 775                 780
Gly Ser Tyr Glu Gln Tyr Arg Gln Phe Gln Arg Arg Lys Trp Pro Glu
785                 790                 795                 800
Met Lys Arg Pro Ser Ser Lys Ser Leu Gly Gln Leu Trp Glu Gly Trp
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805 810 815
Glu Gly

<210> 4065
<211> 696
<212> DNA
<213> Homo sapiens

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120
cttgtaaatg aagtgaattt cccattgcta ctaaactgct ttggacaacc tggtacaaag
180
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240
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300
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480
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696

<210> 4066
<211> 210
<212> PRT
<213> Homo sapiens

<400> 4066
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Phe Pro Leu Leu Leu Asn Cys Phe Gly Gln Pro Gly Thr Lys Trp Ile
35 40 45
Pro Phe Ser Tyr Thr Tyr Arg Arg Pro Leu Arg Thr His Tyr Gly Tyr
50 55 60
Ile Asn Val Lys Thr Gln Glu Pro Leu Gln Leu Asp Cys Asp Leu Cys
65 70 75 80
Ala Ile Val Ser Asn Ser Gly Gln Met Val Gly Gln Lys Val Gly Asn
85 90 95
Glu Ile Asp Arg Ser Ser Cys Ile Trp Arg Met Asn Asn Ala Pro Thr

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            100                 105                 110
Lys Gly Tyr Glu Glu Asp Val Gly Arg Met Thr Met Ile Arg Val Val
        115                 120                 125
Ser His Thr Ser Val Pro Leu Leu Leu Lys Asn Pro Asp Tyr Phe Phe
    130                 135                 140
Lys Glu Ala Asn Thr Thr Ile Tyr Val Ile Trp Gly Pro Phe Arg Asn
145                 150                 155                 160
Met Arg Lys Asp Gly Asn Gly Ile Val Tyr Asn Met Leu Lys Lys Thr
                165                 170                 175
Val Gly Ile Tyr Pro Asn Ala Gln Ile Tyr Val Thr Thr Glu Lys Arg
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Met Ser Tyr Cys Asp Gly Val Leu Arg Arg Lys Xaa Gly Lys Asp Ser
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Thr Glu
    210
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<210> 4067
<211> 1800
<212> DNA
<213> Homo sapiens

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180
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900
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1140
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<210> 4068
<211> 521
<212> PRT
<213> Homo sapiens

<400> 4068
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Phe Lys Arg Asp Arg Pro Pro Cys Ser Pro Ser Arg Val Leu His Leu
            20   25   30
Arg Lys Ile Pro Cys Asp Val Thr Glu Ala Glu Ile Ile Ser Leu Gly
        35   40   45
Leu Pro Phe Gly Lys Val Thr Asn Leu Leu Met Leu Lys Gly Lys Ser
    50   55   60
Gln Ala Phe Leu Glu Met Ala Ser Glu Glu Ala Ala Val Thr Met Val
65   70   75   80
Asn Tyr Tyr Thr Pro Ile Thr Pro His Leu Arg Ser Gln Pro Val Tyr
                85   90   95
Ile Gln Tyr Ser Asn His Arg Glu Leu Lys Thr Asp Asn Leu Pro Asn
            100   105   110
Gln Ala Arg Ala Gln Ala Ala Leu Gln Ala Val Ser Ala Val Gln Ser
        115   120   125
Gly Ser Leu Ala Leu Ser Gly Gly Pro Ser Asn Glu Gly Thr Val Leu
    130   135   140
Pro Gly Gln Ser Pro Val Leu Arg Ile Ile Ile Glu Asn Leu Phe Tyr

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145                 150                 155                 160
Pro Val Thr Leu Glu Val Leu His Gln Ile Phe Ser Lys Phe Gly Thr
                165                 170                 175
Val Leu Lys Ile Ile Thr Phe Thr Lys Asn Asn Gln Phe Gln Ala Leu
            180                 185                 190
Leu Gln Tyr Ala Asp Pro Val Asn Ala His Tyr Ala Lys Met Ala Leu
        195                 200                 205
Asp Gly Gln Asn Ile Tyr Asn Ala Cys Cys Thr Leu Arg Ile Asp Phe
    210                 215                 220
Ser Lys Leu Thr Ser Leu Asn Val Lys Tyr Asn Asn Asp Lys Ser Arg
225                 230                 235                 240
Asp Phe Thr Arg Leu Asp Leu Pro Thr Gly Asp Gly Gln Pro Ser Leu
                245                 250                 255
Glu Pro Pro Met Ala Ala Ala Phe Gly Ala Pro Gly Ile Ile Ser Ser
            260                 265                 270
Pro Tyr Ala Gly Ala Ala Gly Phe Ala Pro Ala Ile Gly Phe Pro Gln
        275                 280                 285
Ala Thr Gly Leu Ser Val Pro Ala Val Pro Gly Ala Leu Gly Pro Leu
    290                 295                 300
Thr Ile Thr Ser Ser Ala Val Thr Gly Arg Met Ala Ile Pro Gly Ala
305                 310                 315                 320
Ser Gly Ile Pro Gly Asn Ser Val Leu Leu Val Thr Asn Leu Asn Pro
                325                 330                 335
Asp Leu Ile Thr Pro His Gly Leu Phe Ile Leu Phe Gly Val Tyr Gly
            340                 345                 350
Asp Val His Arg Val Lys Ile Met Phe Asn Lys Lys Glu Asn Ala Leu
        355                 360                 365
Val Gln Met Ala Asp Ala Asn Gln Ala Gln Leu Ala Met Asn His Leu
    370                 375                 380
Ser Gly Gln Arg Leu Tyr Gly Lys Val Leu Arg Ala Thr Leu Ser Lys
385                 390                 395                 400
His Gln Ala Val Gln Leu Pro Arg Glu Gly Gln Glu Asp Gln Gly Leu
                405                 410                 415
Thr Lys Asp Phe Ser Asn Ser Pro Leu His Arg Phe Lys Lys Pro Gly
            420                 425                 430
Ser Lys Asn Phe Gln Asn Ile Phe Pro Pro Ser Ala Thr Leu His Leu
        435                 440                 445
Ser Asn Ile Pro Pro Ser Val Thr Val Asp Asp Leu Lys Asn Leu Phe
    450                 455                 460
Ile Glu Ala Gly Cys Ser Val Lys Ala Phe Lys Phe Phe Gln Lys Asp
465                 470                 475                 480
Arg Lys Met Ala Leu Ile Gln Leu Gly Ser Val Glu Glu Ala Ile Gln
                485                 490                 495
Ala Leu Ile Glu Leu His Asn His Asp Leu Gly Glu Asn His His Leu
            500                 505                 510
Arg Val Ser Phe Ser Lys Ser Thr Ile
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<210> 4069
<211> 714
<212> DNA
<213> Homo sapiens

<400> 4069

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180
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240
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300
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420
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480
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540
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agtgtatcat gtgattatgc tttaccggta taagagattc tgttgtgatt atttgaatag
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714

<210> 4070
<211> 113
<212> PRT
<213> Homo sapiens

<400> 4070
Met Ser Tyr Pro Ala Lys Val Thr Leu Leu Gly Ser Val Ile Phe Thr
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Phe Gln His Thr Gln His Leu Ala Ile Ser Lys His Asn Leu Met Phe
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Leu Tyr Thr Ile Phe Ile Val Ala Thr Lys Ile Thr Met Met Thr Thr
35 40 45
Gln Thr Ser Thr Met Thr Phe Ala Pro Phe Glu Asp Thr Leu Ser Trp
50 55 60
Met Leu Phe Gly Trp Gln Gln Pro Phe Ser Ser Cys Glu Lys Lys Ser
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Glu Ala Lys Ser Pro Ser Asn Gly Val Gly Ser Leu Ala Ser Lys Pro
85 90 95
Val Asp Val Ala Ser Asp Asn Val Lys Lys Lys His Thr Lys Lys Asn
100 105 110
Glu

<210> 4071
<211> 601
<212> DNA
<213> Homo sapiens

<400> 4071

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120
catccacgat tgcctgtagt tcctgcaggc actgcccctc cagctggaga cgtgcatcac
180
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240
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300
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480
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c
601

<210> 4072
<211> 175
<212> PRT
<213> Homo sapiens

<400> 4072
Met Val His Arg Arg Gly Trp Pro Ser Cys Leu Ala Arg Gly Gly Arg
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Cys Ala Leu Val Pro Arg Leu Val Arg Met Lys Val Phe His Leu Ser
20 25 30
Leu Ser Gln Ser Val Val Leu Arg His His Trp Ile Leu Pro Phe Val
35 40 45
Gln Ala Leu Lys Ala Arg Met Thr Ser Phe His Arg Phe Phe Phe Thr
50 55 60
Ala Asn Gln Val Lys Ile Tyr Thr Asn Gln Glu Lys Thr Arg Thr Phe
65 70 75 80
Ile Gly Leu Glu Val Thr Ser Gly His Ala Gln Phe Leu Asp Leu Val
85 90 95
Ser Glu Val Asp Arg Val Met Glu Glu Phe Asn Leu Thr Thr Phe Tyr
100 105 110
Gln Asp Pro Ser Phe His Leu Ser Leu Ala Trp Cys Val Gly Asp Ala
115 120 125
Arg Leu Gln Leu Glu Gly Gln Cys Leu Gln Glu Leu Gln Ala Ile Val
130 135 140
Asp Gly Phe Glu Asp Ala Glu Val Leu Leu Arg Val His Thr Glu Gln
145 150 155 160
Val Arg Cys Lys Ser Gly Asn Lys Phe Phe Ser Met Pro Leu Lys
165 170 175

<210> 4073
<211> 1864

<212> DNA
<213> Homo sapiens

<400> 4073
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120
gccccccggct acctcccctg gaggcacaga gggcgggggc cttggcgaat ggctttcttg
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240
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420
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1620
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1680
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attg
1864

<210> 4074
<211> 456
<212> PRT
<213> Homo sapiens

<400> 4074
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Asn Pro Val Asp Ala Ile Tyr Gln Pro Ser Pro Leu Glu Pro Val Ile
35 40 45
Ser Thr Met Pro Ser Gln Thr Val Leu Pro Pro Glu Pro Val Gln Leu
50 55 60
Cys Lys Ser Glu Gln Arg Pro Ser Ser Leu Pro Val Gly Pro Val Leu
65 70 75 80
Ala Thr Leu Gly His His Gln Thr Pro Thr Pro Asn Ser Thr Gly Ser
85 90 95
Gly His Ser Pro Pro Ser Ser Ser Leu Thr Ser Pro Ser His Val Asn
100 105 110
Leu Ser Pro Asn Thr Val Pro Glu Phe Ser Tyr Ser Ser Ser Glu Asp
115 120 125
Glu Phe Tyr Asp Ala Asp Glu Phe His Gln Ser Gly Ser Ser Pro Lys
130 135 140
Arg Leu Ile Asp Ser Ser Gly Ser Ala Ser Val Leu Thr His Ser Ser
145 150 155 160
Ser Gly Asn Ser Leu Lys Arg Pro Asp Thr Thr Glu Ser Leu Asn Ser
165 170 175
Ser Leu Ser Asn Gly Thr Ser Asp Ala Asp Leu Phe Asp Ser His Asp
180 185 190
Asp Arg Asp Asp Asp Ala Glu Ala Gly Ser Val Glu Glu His Lys Ser
195 200 205
Val Ile Met His Leu Leu Ser Gln Val Arg Leu Gly Met Asp Leu Thr
210 215 220
Lys Val Val Leu Pro Thr Phe Ile Leu Glu Arg Arg Ser Leu Leu Glu
225 230 235 240
Met Tyr Ala Asp Phe Phe Ala His Pro Asp Leu Phe Val Ser Ile Ser
245 250 255
Asp Gln Lys Asp Pro Lys Asp Arg Met Val Gln Val Val Lys Trp Tyr

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            260                 265                 270
Leu Ser Ala Phe His Ala Gly Arg Lys Gly Ser Val Ala Lys Lys Pro
        275                 280                 285
Tyr Asn Pro Ile Leu Gly Glu Ile Phe Gln Cys His Trp Thr Leu Pro
    290                 295                 300
Asn Asp Thr Glu Glu Asn Thr Glu Leu Val Ser Glu Gly Pro Val Pro
305                 310                 315                 320
Trp Val Ser Lys Asn Ser Val Thr Phe Val Ala Glu Gln Val Ser His
                325                 330                 335
His Pro Pro Ile Ser Ala Phe Tyr Ala Glu Cys Phe Asn Lys Lys Ile
            340                 345                 350
Gln Phe Asn Ala His Ile Trp Thr Lys Ser Lys Phe Leu Gly Met Ser
        355                 360                 365
Ile Gly Val His Asn Ile Gly Gln Gly Cys Val Ser Cys Leu Asp Tyr
    370                 375                 380
Asp Glu His Tyr Ile Leu Thr Phe Pro Asn Gly Tyr Gly Arg Ser Ile
385                 390                 395                 400
Leu Thr Val Pro Trp Val Glu Leu Gly Gly Glu Cys Asn Ile Asn Cys
                405                 410                 415
Ser Lys Thr Gly Tyr Ser Ala Asn Ile Ile Phe His Thr Lys Pro Phe
            420                 425                 430
Tyr Gly Gly Lys Lys His Arg Ile Thr Ala Glu Ile Phe Ser Pro Asn
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Asp Lys Lys Ser Phe Cys Ser Ile
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<210> 4075
<211> 2492
<212> DNA
<213> Homo sapiens

<400> 4075
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420
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540
aatagtaaga ccagcaatac cctagagaag gatttagatc tgttggcctc tgttccatcc
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660

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2280

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2460
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2492

<210> 4076
<211> 410
<212> PRT
<213> Homo sapiens

<400> 4076
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Ala Gly Ile His Arg Asn Leu Gly Val His Ile Ser Arg Val Lys Ser
35 40 45
Val Asn Leu Asp Gln Trp Thr Gln Glu Gln Ile Gln Cys Met Gln Glu
50 55 60
Met Gly Asn Gly Lys Ala Asn Arg Leu Tyr Glu Ala Tyr Leu Pro Glu
65 70 75 80
Thr Phe Arg Arg Pro Gln Ile Asp Pro Ala Val Glu Gly Phe Ile Arg
85 90 95
Asp Lys Tyr Glu Lys Lys Lys Tyr Met Asp Arg Ser Leu Asp Ile Asn
100 105 110
Ala Phe Arg Lys Glu Lys Asp Asp Lys Trp Lys Arg Gly Ser Glu Pro
115 120 125
Val Pro Glu Lys Lys Leu Glu Pro Val Val Phe Glu Lys Val Lys Met
130 135 140
Pro Gln Lys Lys Glu Asp Pro Gln Leu Pro Arg Lys Ser Ser Pro Lys
145 150 155 160
Ser Thr Ala Pro Val Met Asp Leu Leu Gly Leu Asp Ala Pro Val Ala
165 170 175
Cys Ser Ile Ala Asn Ser Lys Thr Ser Asn Thr Leu Glu Lys Asp Leu
180 185 190
Asp Leu Leu Ala Ser Val Pro Ser Pro Ser Ser Ser Gly Ser Arg Lys
195 200 205
Val Val Gly Ser Met Pro Thr Ala Gly Ser Ala Gly Ser Val Pro Glu
210 215 220
Asn Leu Asn Leu Phe Pro Glu Pro Gly Ser Lys Ser Glu Glu Ile Gly
225 230 235 240
Lys Lys Gln Leu Ser Lys Asp Ser Ile Leu Ser Leu Tyr Gly Ser Gln
245 250 255
Thr Pro Gln Met Pro Thr Gln Ala Met Phe Met Ala Pro Ala Gln Met
260 265 270
Ala Tyr Pro Thr Ala Tyr Pro Ser Phe Pro Gly Val Thr Pro Pro Asn
275 280 285
Ser Ile Met Gly Ser Met Met Pro Pro Pro Val Gly Met Val Ala Gln
290 295 300
Pro Gly Ala Ser Gly Met Val Ala Pro Met Ala Met Pro Ala Gly Tyr

305 310 315 320
Met Gly Gly Met Gln Ala Ser Met Met Gly Val Pro Asn Gly Met Met
325 330 335
Thr Thr Gln Gln Ala Gly Tyr Met Ala Gly Met Ala Ala Met Pro Gln
340 345 350
Thr Val Tyr Gly Val Gln Pro Ala Gln Gln Leu Gln Trp Asn Leu Thr
355 360 365
Gln Met Thr Gln Gln Met Ala Gly Met Asn Phe Tyr Gly Ala Asn Gly
370 375 380
Met Met Asn Tyr Gly Gln Ser Met Ser Gly Gly Asn Gly Gln Ala Ala
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Asn Gln Thr Leu Ser Pro Gln Met Trp Lys
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<210> 4077
<211> 684
<212> DNA
<213> Homo sapiens

<400> 4077
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<210> 4078
<211> 194
<212> PRT
<213> Homo sapiens

<400> 4078
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Ser Met Arg Tyr Leu Ala Leu Met Val Ser Arg Pro Val Leu Arg Leu

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Arg Glu Ile Asn Pro Leu Leu Phe Ser Tyr Val Glu Glu Leu Val Glu
        35                  40                  45
Ile Arg Lys Leu Arg Gln Asp Ile Leu Leu Met Lys Pro Tyr Phe Ile
    50                  55                  60
Thr Cys Arg Glu Ala Met Glu Ala Arg Leu Leu Leu Gln Leu Gln Asp
65                  70                  75                  80
Arg Gln His Phe Val Glu Asn Asp Glu Met Tyr Ser Val Gln Asp Leu
                85                  90                  95
Leu Asp Val His Ala Gly Arg Leu Gly Cys Ser Leu Thr Glu Ile His
            100                 105                 110
Thr Leu Phe Ala Lys His Ile Lys Leu Asp Cys Glu Arg Cys Gln Ala
        115                 120                 125
Lys Gly Phe Val Cys Glu Leu Cys Arg Glu Gly Asp Val Leu Phe Pro
    130                 135                 140
Phe Asp Ser His Thr Ser Val Cys Ala Asp Cys Ser Ala Val Phe His
145                 150                 155                 160
Arg Asp Cys Tyr Tyr Asp Asn Ser Thr Thr Cys Pro Lys Cys Ala Arg
                165                 170                 175
Leu Ser Leu Arg Lys Gln Ser Leu Phe Gln Glu Pro Gly Pro Asp Val
            180                 185                 190
Glu Ala
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<210> 4079
<211> 783
<212> DNA
<213> Homo sapiens

<400> 4079

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nta
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<210> 4080
<211> 101
<212> PRT
<213> Homo sapiens

<400> 4080
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20 25 30
Leu Thr Pro Ser Val Cys Leu Pro Ser Lys Leu His Cys Pro Asn Arg
35 40 45
Glu Ala Leu His Ala Gln Pro Gly Glu Gln Gly Trp Met Gly Leu Lys
50 55 60
Arg Ala Gln Pro Ser Pro Glu Arg Thr Leu His Ser Asn Leu Pro Gln
65 70 75 80
Ser Trp Gly Lys His Glu Gly Cys Pro Ser Thr Glu Val Asn Pro Gly
85 90 95
His Ala Arg Thr Lys
100

<210> 4081
<211> 645
<212> DNA
<213> Homo sapiens

<400> 4081
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180
gaggatgaag tttttgctgg agttaccaca caccaggaac tctttccaca cagcctgctg
240
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300
caatgccaga tgggtaagca aactatgggc tttccacttc tcacttatca agaccgatcg
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420
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<210> 4082
<211> 215
<212> PRT
<213> Homo sapiens

<400> 4082
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Val Arg Pro Val Gln Asn Leu Ala Leu Gly Lys Glu Glu Leu Ile Gly
35 40 45
Thr Met Glu Gln Ile Phe Met Asn Val Ala Ile Phe Glu Asp Glu Val
50 55 60
Phe Ala Gly Val Thr Thr His Gln Glu Leu Phe Pro His Ser Leu Leu
65 70 75 80
Ser Val Ile Ala Asn Phe Ile Pro Phe Ser Asp His Asn Gln Ser Pro
85 90 95
Arg Asn Met Tyr Gln Cys Gln Met Gly Lys Gln Thr Met Gly Phe Pro
100 105 110
Leu Leu Thr Tyr Gln Asp Arg Ser Asp Asn Lys Leu Tyr Arg Leu Gln
115 120 125
Thr Pro Gln Ser Pro Leu Val Arg Pro Ser Met Tyr Asp Tyr Tyr Asp
130 135 140
Met Asp Asn Tyr Pro Ile Gly Thr Asn Ala Ile Val Ala Val Ile Ser
145 150 155 160
Tyr Thr Gly Tyr Asp Met Glu Asp Ala Met Ile Val Asn Lys Ala Ser
165 170 175
Trp Glu Arg Gly Phe Ala His Gly Ser Val Tyr Lys Ser Glu Phe Ile
180 185 190
Asp Leu Ser Glu Lys Ile Lys Gln Gly Asp Ser Ser Leu Val Phe Gly
195 200 205
Ile Lys Pro Gly Asp Pro Arg
210 215

<210> 4083
<211> 2983
<212> DNA
<213> Homo sapiens

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480
gttaatatct ctaaatctaa aggcaggcag caggtttctc tgagaacaca tgcaacctca
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720
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780
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1080
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1320
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1380
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2760
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2880
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2983

<210> 4084
<211> 362
<212> PRT
<213> Homo sapiens

<400> 4084
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20 25 30
Val Tyr Gly Leu Asn Phe Ala Ser Lys Glu Glu Ala Thr Thr Phe Ser
35 40 45
Asn Ala Met Leu Phe Ala Leu Asn Ile Met Asn Ser Gln Glu Gly Gly
50 55 60
Pro Ser Ser Gln Arg Gln Val Gln Asn Gly Pro Ser Pro Asp Glu Met
65 70 75 80
Asp Ile Gln Arg Arg Gln Val Met Glu Gln His Gln Gln Gln Arg Gln
85 90 95
Glu Ser Leu Glu Arg Arg Thr Ser Ala Thr Gly Pro Ile Leu Pro Pro

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            100                 105                 110
Gly His Pro Ser Ser Ala Ala Ser Ala Pro Val Ser Cys Ser Gly Pro
        115                 120                 125
Pro Pro Pro Pro Pro Pro Pro Val Pro Pro Pro Pro Thr Gly Ala Thr
    130                 135                 140
Pro Pro Pro Pro Pro Pro Leu Pro Ala Gly Gly Ala Gln Gly Ser Ser
145                 150                 155                 160
His Asp Glu Ser Ser Met Ser Gly Leu Ala Ala Ala Ile Ala Gly Ala
                165                 170                 175
Lys Leu Arg Arg Val Gln Arg Pro Glu Asp Ala Ser Gly Gly Ser Ser
            180                 185                 190
Pro Ser Gly Thr Ser Lys Ser Asp Ala Asn Arg Ala Ser Ser Gly Gly
        195                 200                 205
Gly Gly Gly Gly Leu Met Glu Glu Met Asn Lys Leu Leu Ala Lys Arg
    210                 215                 220
Arg Lys Ala Ala Ser Gln Ser Asp Lys Pro Ala Glu Lys Lys Glu Asp
225                 230                 235                 240
Glu Ser Gln Met Glu Asp Pro Ser Thr Ser Pro Ser Pro Gly Thr Arg
                245                 250                 255
Ala Ala Ser Gln Pro Pro Asn Ser Ser Glu Ala Gly Arg Lys Pro Trp
            260                 265                 270
Glu Arg Ser Asn Ser Val Glu Lys Pro Val Ser Ser Ile Leu Ser Arg
        275                 280                 285
Thr Pro Ser Val Ala Lys Ser Pro Glu Ala Lys Ser Pro Leu Gln Ser
    290                 295                 300
Gln Pro His Ser Arg Met Lys Pro Ala Gly Ser Val Asn Asp Met Ala
305                 310                 315                 320
Leu Asp Ala Phe Asp Leu Asp Arg Met Lys Gln Glu Ile Leu Glu Glu
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Val Val Arg Glu Leu His Lys Val Lys Glu Glu Ile Ile Asp Ala Ile
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Arg Gln Glu Leu Ser Gly Ile Ser Thr Thr
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<210> 4085
<211> 2673
<212> DNA
<213> Homo sapiens

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840
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900
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1980
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2673

<210> 4086
<211> 789
<212> PRT
<213> Homo sapiens

<400> 4086

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Val Lys Arg Val Thr Ala Asn Asn Leu Glu Thr Phe Ile Phe Ile Leu
            20                  25                  30
Phe Leu Leu Val Phe Ala Ile Ala Ala Ala Ala Tyr Val Trp Ile Glu
        35                  40                  45
Gly Thr Lys Asp Pro Ser Arg Asn Arg Tyr Lys Leu Phe Leu Glu Cys
    50                  55                  60
Thr Leu Ile Leu Thr Ser Val Val Pro Pro Glu Leu Pro Ile Glu Leu
65                  70                  75                  80
Ser Leu Ala Val Asn Thr Ser Leu Ile Ala Leu Ala Lys Leu Tyr Met
                85                  90                  95
Tyr Cys Thr Glu Pro Phe Arg Ile Pro Phe Ala Gly Lys Val Glu Val
            100                 105                 110
Cys Cys Phe Asp Lys Thr Gly Thr Leu Thr Ser Asp Ser Leu Val Val
        115                 120                 125
Arg Gly Val Ala Gly Leu Arg Asp Gly Lys Glu Val Thr Pro Val Ser
    130                 135                 140
Ser Ile Pro Val Glu Thr His Arg Ala Leu Ala Ser Cys His Ser Leu
145                 150                 155                 160
Met Gln Leu Asp Asp Gly Thr Leu Val Gly Asp Pro Leu Glu Lys Ala
                165                 170                 175
Met Leu Thr Ala Val Asp Trp Thr Leu Thr Lys Asp Glu Lys Val Phe
            180                 185                 190
Pro Arg Ser Ile Lys Thr Gln Gly Leu Lys Ile His Gln Arg Phe His
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        195                 200                 205
Phe Ala Ser Ala Leu Lys Arg Met Ser Val Leu Ala Ser Tyr Glu Lys
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Leu Gly Ser Thr Asp Leu Cys Tyr Ile Ala Ala Val Lys Gly Ala Pro
225                 230                 235                 240
Glu Thr Leu His Ser Met Phe Ser Gln Cys Pro Pro Asp Tyr His His
                245                 250                 255
Ile His Thr Glu Ile Ser Arg Glu Gly Ala Arg Val Leu Ala Leu Gly
            260                 265                 270
Tyr Lys Glu Leu Gly His Leu Thr His Gln Gln Ala Arg Glu Val Lys
        275                 280                 285
Arg Glu Ala Leu Glu Cys Ser Leu Lys Phe Val Gly Phe Ile Val Val
    290                 295                 300
Ser Cys Pro Leu Lys Ala Asp Ser Lys Ala Val Ile Arg Glu Ile Gln
305                 310                 315                 320
Asn Ala Ser His Arg Val Val Met Ile Thr Gly Asp Asn Pro Leu Thr
                325                 330                 335
Ala Cys His Val Ala Gln Glu Leu His Phe Ile Glu Lys Ala His Thr
            340                 345                 350
Leu Ile Leu Gln Pro Pro Ser Glu Lys Gly Arg Gln Cys Glu Trp Arg
        355                 360                 365
Ser Ile Asp Gly Ser Ile Val Leu Pro Leu Xaa Pro Gly Ala Pro Gln
    370                 375                 380
Arg His Trp Pro Trp Ser Thr His Xaa Cys Leu Thr Gly Asp Gly Leu
385                 390                 395                 400
Ala His Leu Gln Ala Thr Asp Pro Gln Gln Leu Leu Arg Leu Ile Pro
                405                 410                 415
His Val Gln Val Phe Ala Arg Val Ala Pro Lys Gln Lys Glu Phe Val
            420                 425                 430
Ile Thr Ser Leu Lys Glu Leu Gly Tyr Val Thr Leu Met Cys Gly Asp
        435                 440                 445
Gly Thr Asn Asp Val Gly Ala Leu Lys His Ala Asp Val Gly Val Ala
    450                 455                 460
Leu Leu Ala Asn Ala Pro Glu Arg Val Val Glu Arg Arg Arg Arg Pro
465                 470                 475                 480
Arg Asp Ser Pro Thr Leu Ser Asn Ser Gly Ile Arg Ala Thr Ser Arg
                485                 490                 495
Thr Ala Lys Gln Arg Ser Gly Leu Pro Pro Ser Glu Glu Gln Pro Thr
            500                 505                 510
Ser Gln Arg Asp Arg Leu Ser Gln Val Leu Arg Asp Leu Glu Asp Glu
        515                 520                 525
Ser Thr Pro Ile Val Lys Leu Gly Asp Ala Ser Ile Ala Ala Pro Phe
    530                 535                 540
Thr Ser Lys Leu Ser Ser Ile Gln Cys Ile Cys His Val Ile Lys Gln
545                 550                 555                 560
Gly Arg Cys Thr Leu Val Thr Thr Leu Gln Met Phe Lys Ile Leu Ala
                565                 570                 575
Leu Asn Ala Leu Ile Leu Ala Tyr Ser Gln Ser Val Leu Tyr Leu Glu
            580                 585                 590
Gly Val Lys Phe Ser Asp Phe Gln Ala Thr Leu Gln Gly Leu Leu Leu
        595                 600                 605
Ala Gly Cys Phe Leu Phe Ile Ser Arg Ser Lys Pro Leu Lys Thr Leu
    610                 615                 620
Ser Arg Glu Arg Pro Leu Pro Asn Ile Phe Asn Leu Tyr Thr Ile Leu
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625 630 635 640
Thr Val Met Leu Gln Phe Phe Val His Phe Leu Ser Leu Val Tyr Leu
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Tyr Arg Glu Ala Gln Ala Arg Ser Pro Xaa Arg Xaa Gln Glu Gln Phe
660 665 670
Val Asp Leu Tyr Lys Glu Phe Glu Pro Ser Leu Val Asn Ser Thr Val
675 680 685
Tyr Ile Met Ala Met Ala Met Gln Met Ala Thr Phe Ala Ile Asn Tyr
690 695 700
Lys Gly Pro Pro Phe Met Glu Ser Leu Pro Glu Asn Lys Pro Leu Val
705 710 715 720
Trp Ser Leu Ala Val Ser Leu Leu Ala Ile Ile Gly Leu Leu Leu Gly
725 730 735
Ser Ser Pro Asp Phe Asn Ser Gln Phe Gly Leu Val Asp Ile Pro Val
740 745 750
Glu Phe Lys Leu Val Ile Ala Gln Val Leu Leu Leu Asp Phe Cys Leu
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770 775 780
Leu Lys Val Pro Ser
785

<210> 4087
<211> 959
<212> DNA
<213> Homo sapiens

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480
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660
ctggaggcac aaaggaaggc tctggctgaa caatcagaga taattcaggc tcagcttgtc
720
aatcggaaac agaaattaga gtctgtggaa ctttctagcc aatcagaaat tcaacactta
780

agcagtaaac tggagcgggc taatgacact atctgtgcca atgagttgga aatagagcgc
840
ctcaccatga gggtcaatga cttggttgga accagtatga ctgtcctaca ggagcagcag
900
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959

<210> 4088
<211> 319
<212> PRT
<213> Homo sapiens

<400> 4088
Arg Gly Ser Leu Glu Lys Ala Leu Phe Gln Leu Leu Lys Val Trp Gly
1 5 10 15
Gln Trp Ala Glu Gln Thr Arg Arg Leu Gln Arg Leu Asp Val Ser Leu
20 25 30
Ala Val Ala Arg Val Arg Ser Ala Gly Pro Ser Cys Gln Asn Lys Gly
35 40 45
Asp Leu Val Met Glu Ala Leu Leu Glu Gly Ile Gln Asn Arg Gly His
50 55 60
Gly Gly Gly Phe Leu Thr Ser Cys Glu Ala Glu Leu Gln Glu Leu Met
65 70 75 80
Lys Gln Ile Asp Ile Met Val Ala His Lys Lys Ser Glu Trp Glu Gly
85 90 95
Arg Thr His Ala Leu Glu Thr Cys Leu Lys Ile Arg Glu Gln Glu Leu
100 105 110
Lys Ser Leu Arg Ser Gln Leu Asp Val Thr His Lys Glu Val Gly Met
115 120 125
Leu His Gln Gln Val Glu Glu His Glu Lys Ile Lys Gln Glu Met Thr
130 135 140
Met Glu Tyr Lys Gln Glu Leu Lys Lys Leu His Glu Glu Leu Cys Ile
145 150 155 160
Leu Lys Arg Ser Tyr Glu Lys Leu Gln Lys Lys Gln Met Arg Glu Phe
165 170 175
Arg Gly Asn Thr Lys Asn His Arg Glu Asp Arg Ser Glu Ile Glu Arg
180 185 190
Leu Thr Ala Lys Ile Glu Glu Phe Arg Gln Lys Ser Leu Asp Trp Glu
195 200 205
Lys Gln Arg Leu Ile Tyr Gln Gln Gln Val Ser Ser Leu Glu Ala Gln
210 215 220
Arg Lys Ala Leu Ala Glu Gln Ser Glu Ile Ile Gln Ala Gln Leu Val
225 230 235 240
Asn Arg Lys Gln Lys Leu Glu Ser Val Glu Leu Ser Ser Gln Ser Glu
245 250 255
Ile Gln His Leu Ser Ser Lys Leu Glu Arg Ala Asn Asp Thr Ile Cys
260 265 270
Ala Asn Glu Leu Glu Ile Glu Arg Leu Thr Met Arg Val Asn Asp Leu
275 280 285
Val Gly Thr Ser Met Thr Val Leu Gln Glu Gln Gln Gln Lys Glu Glu
290 295 300
Lys Leu Arg Glu Ser Glu Lys Leu Leu Glu Ala Leu Gln Glu Lys
305 310 315

<210> 4089
<211> 511
<212> DNA
<213> Homo sapiens

<400> 4089
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120
aaccctgtgg ggctggcccc tacacagttt ttaaggggta cagggaaggg aagaaacagg
180
caccatgtgg ggcaggggtt ctgcttctat catatttcca ttttgttgtt ttaggagatc
240
cttccaactc tcactaacat tattttccag agaacaaaag aaaaactatg ctctccaaga
300
acatgtttcc tttgtaattt ttctgtcctc aaacttttc tggagagatg agtcatttga
360
cctgacattg agaataggct tgaagccctt tgagaggaca aaggagatag agtcagcatt
420
cctatctcca tgctctgaag atccaagtca cttggttact gctccctggg ctgtctattt
480
tcactgttta tggaagatag agtacacctg t
511

<210> 4090
<211> 109
<212> PRT
<213> Homo sapiens

<400> 4090
Met Trp Gly Arg Gly Ser Ala Ser Ile Ile Phe Pro Phe Cys Cys Phe
 1   5   10   15
Arg Arg Ser Phe Gln Leu Ser Leu Thr Leu Phe Ser Arg Glu Gln Lys
            20   25   30
Lys Asn Tyr Ala Leu Gln Glu His Val Ser Phe Val Ile Phe Leu Ser
        35   40   45
Ser Asn Phe Phe Trp Arg Asp Glu Ser Phe Asp Leu Thr Leu Arg Ile
    50   55   60
Gly Leu Lys Pro Phe Glu Arg Thr Lys Glu Ile Glu Ser Ala Phe Leu
65   70   75   80
Ser Pro Cys Ser Glu Asp Pro Ser His Leu Val Thr Ala Pro Trp Ala
                85   90   95
Val Tyr Phe His Cys Leu Trp Lys Ile Glu Tyr Thr Cys
            100   105

<210> 4091
<211> 1526
<212> DNA
<213> Homo sapiens

<400> 4091
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gtgcccagcg gctccggacg tgctacgggg tgcgagcgcg ggggagttcg gggcgcacga
120
caaggaaggg cccccgggag ctctatatgg aggaaggagc ccagaatggt gtgcaccagg
180
aagaccaaaa ctttggtgtc cacttgcgtg atcctgagcg gcatgactaa catcatctgc
240
ctgctctacg tgggctgggt caccaactac atcgccagcg tgtatgtgcg ggggcaggag
300
ccggcgcccg acaagaagct ggaggaagac aaaggggaca ctctgaagat tattgagcgg
360
ctggaccacc tggagaatgt catcaagcag cacattcaag gctataggag aaatttctcc
420
cttctgaatg tgtccaacta actctgttca cctgagaaat catattcccc agctctgggt
480
atccctgaat aaccacagga gaacagttcc aggccctgat aagtcagcta ttgcaagggg
540
gacctggctg gaagatatga aggaaaaata tcattcttga actaataagt tgagagatca
600
cagccttcag gggaccagaa gggaaggctg aacagagaag ggcaatttca cgttcgccat
660
gtccatattt ctatcgtcat gagccatctc accttacagg cagggaagtt ttgagcttag
720
agaatgggat gcgtcaagaa aaccgtggct cccccagctc tgttcctgga ttcagtgcct
780
gttgtttcat cctgtgtaga ctggagtcag ggtctacaca gttggaattc tatggaacca
840
agatgctgtg tggcagatgg atgtggactc caactgtgac aatccagaag gccttgggga
900
cttgtttcat gaacagctcc ctgtaggatc tctgttgggg tgggggattc taggggcatc
960
tccgcagttt tcttctgaaa acaaaacgaa tacaagttgg gcaggtgcaa caactgtgca
1020
tgcagtcccc tcccagggct ggctagcagt attgttgggt accgtaagca cttagcattg
1080
ttaagtgagc ataagtaaca agatgcaaca gcctctggcc aagttttgaa gattttgttt
1140
taaagtatgc ttttagatgt tgacattcat gattattaaa aggaacaaaa ctcaatttgg
1200
ggtctcaaga gccacaattc tagacttcta ggatgtcagg agccatgctc ttaagcttct
1260
caccctgctg ttttaatgag attaatgatt attttccact gagcacctac ctgtgatgtt
1320
cataaaaaag tgaaataaat gactcacatg gagatttgga aggatatcac tgtggaaagt
1380
agatgttaac agcctctaga aatatgataa ttatcagcta tttgagatgc agtcactgta
1440
atgtgataac aagatgtgtt gtgcaggtag aaagcatgga gagaaatggc acaaagtaga
1500
gttataagaa aaaaaaaaaa aaaaaa
1526

<210> 4092
<211> 146
<212> PRT

<213> Homo sapiens

<400> 4092
His Gly Gly Tyr Thr Gly Ser Gly Pro Gly Phe Gly Glu Pro Arg Asp
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Ser Gly Ala Glu Val Pro Ser Gly Ser Gly Arg Ala Thr Gly Cys Glu
20 25 30
Arg Gly Gly Val Arg Gly Ala Arg Gln Gly Arg Ala Pro Gly Ser Ser
35 40 45
Ile Trp Arg Lys Glu Pro Arg Met Val Cys Thr Arg Lys Thr Lys Thr
50 55 60
Leu Val Ser Thr Cys Val Ile Leu Ser Gly Met Thr Asn Ile Ile Cys
65 70 75 80
Leu Leu Tyr Val Gly Trp Val Thr Asn Tyr Ile Ala Ser Val Tyr Val
85 90 95
Arg Gly Gln Glu Pro Ala Pro Asp Lys Lys Leu Glu Glu Asp Lys Gly
100 105 110
Asp Thr Leu Lys Ile Ile Glu Arg Leu Asp His Leu Glu Asn Val Ile
115 120 125
Lys Gln His Ile Gln Gly Tyr Arg Arg Asn Phe Ser Leu Leu Asn Val
130 135 140
Ser Asn
145

<210> 4093
<211> 1519
<212> DNA
<213> Homo sapiens

<400> 4093
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ggcaggggggc ggtgtgcagc ggaaccatgc acataggcgc ccacgccgac tacccctccc
120
gaggaaaaga ggccggggcg cgctgggggg tgagagcatg agggaggccg gggggggctg
180
cttggagcgc tgctagggag cggtgccgcc gcacacccgc ctgggcgcgg cggagggcgg
240
ggagcgggca ggtcgcgcct cggcgcagcg accgccggga gctgttctga tttccgacgc
300
gcacctaggg gcccggagca gcccccgccc cggcgcgccg ccgacatggg caacgcaggg
360
agcatggatt cgcagcagac cgatttcagg gcgcacaacg tgcctttgaa gctgccgatg
420
ccagagccag gtgaactgga ggagcgattt gccatcgtgc tgaacgctat gaacctacct
480
cctgacaaag ccaggttact gcggcagtat gataatgaga aaaaatggga actgatttgt
540
gatcaggaac gattccaggt gaagaatcct ccccatacat acattcaaaa gctcaaaggc
600
tatctggatc cagctgtaac caggaagaaa ttcagacggc gtgttcaaga atctacacaa
660
gtgctaagag aactggaaat ttctttaaga actaaccaca ttggatgggt cagagaattt
720

ctgaatgaag aaaacaaagg tcttgatgtt ctagtggaat atctctcatt tgcacagtac
780
gcggtaactt ttgactttga aagtgtggag agtactgtgg agagctcggt ggacaaatca
840
aagccctgga gtaggtccat cgaggacctg cacagaggga gcaacctgcc ctcacctgtg
900
ggcaacagtg tctcccgctc tggaagacat tctgcactgc gatataatac attgccaagc
960
agaagaactc tgaaaaattc aagattagtg agtaagaaag atgatgtgca tgtctgtatc
1020
atgtgtttac gtgccatcat gaattatcag tatggtttca acatggtcat gtctcatcca
1080
cacgctgtca atgagattgc actaagcctg aacaacaaga atcccagaac aaaagccctt
1140
gtcttagaac tgttggcagc cgtttgtctt gtcagaggcg ggcatgaaat cattttatca
1200
gcatttgata actttaaaga ggtttgtgga gaaaaacagc gctttgagaa gttgatggaa
1260
catttcagga atgaagacaa taacatagat tttatggtgg cttctatgca gtttattaat
1320
attgtagtcc attcagtaga agatatgaat ttcagagttc acctgcagta tgaatttacc
1380
aaattaggcc tggacgaata cttggacaag ctgaaacaca ctgagagtga caagcttcaa
1440
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1500
gaaactaaga atgctgcag
1519

<210> 4094
<211> 391
<212> PRT
<213> Homo sapiens

<400> 4094
Met Gly Asn Ala Gly Ser Met Asp Ser Gln Gln Thr Asp Phe Arg Ala
1 5 10 15
His Asn Val Pro Leu Lys Leu Pro Met Pro Glu Pro Gly Glu Leu Glu
20 25 30
Glu Arg Phe Ala Ile Val Leu Asn Ala Met Asn Leu Pro Pro Asp Lys
35 40 45
Ala Arg Leu Leu Arg Gln Tyr Asp Asn Glu Lys Lys Trp Glu Leu Ile
50 55 60
Cys Asp Gln Glu Arg Phe Gln Val Lys Asn Pro Pro His Thr Tyr Ile
65 70 75 80
Gln Lys Leu Lys Gly Tyr Leu Asp Pro Ala Val Thr Arg Lys Lys Phe
85 90 95
Arg Arg Arg Val Gln Glu Ser Thr Gln Val Leu Arg Glu Leu Glu Ile
100 105 110
Ser Leu Arg Thr Asn His Ile Gly Trp Val Arg Glu Phe Leu Asn Glu
115 120 125
Glu Asn Lys Gly Leu Asp Val Leu Val Glu Tyr Leu Ser Phe Ala Gln
130 135 140
Tyr Ala Val Thr Phe Asp Phe Glu Ser Val Glu Ser Thr Val Glu Ser

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145                 150                 155                 160
Ser Val Asp Lys Ser Lys Pro Trp Ser Arg Ser Ile Glu Asp Leu His
                165                 170                 175
Arg Gly Ser Asn Leu Pro Ser Pro Val Gly Asn Ser Val Ser Arg Ser
            180                 185                 190
Gly Arg His Ser Ala Leu Arg Tyr Asn Thr Leu Pro Ser Arg Arg Thr
        195                 200                 205
Leu Lys Asn Ser Arg Leu Val Ser Lys Lys Asp Asp Val His Val Cys
    210                 215                 220
Ile Met Cys Leu Arg Ala Ile Met Asn Tyr Gln Tyr Gly Phe Asn Met
225                 230                 235                 240
Val Met Ser His Pro His Ala Val Asn Glu Ile Ala Leu Ser Leu Asn
                245                 250                 255
Asn Lys Asn Pro Arg Thr Lys Ala Leu Val Leu Glu Leu Leu Ala Ala
            260                 265                 270
Val Cys Leu Val Arg Gly Gly His Glu Ile Ile Leu Ser Ala Phe Asp
        275                 280                 285
Asn Phe Lys Glu Val Cys Gly Glu Lys Gln Arg Phe Glu Lys Leu Met
    290                 295                 300
Glu His Phe Arg Asn Glu Asp Asn Asn Ile Asp Phe Met Val Ala Ser
305                 310                 315                 320
Met Gln Phe Ile Asn Ile Val Val His Ser Val Glu Asp Met Asn Phe
                325                 330                 335
Arg Val His Leu Gln Tyr Glu Phe Thr Lys Leu Gly Leu Asp Glu Tyr
            340                 345                 350
Leu Asp Lys Leu Lys His Thr Glu Ser Asp Lys Leu Gln Val Gln Ile
        355                 360                 365
Gln Ala Tyr Leu Asp Asn Val Phe Asp Val Gly Ala Leu Leu Glu Asp
    370                 375                 380
Ala Glu Thr Lys Asn Ala Ala
385                 390
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<210> 4095
<211> 253
<212> DNA
<213> Homo sapiens

<400> 4095
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agggtcagat agtgggggggt gggttcagct ccactgtcca ggtgaggaaa ctgaggctga
120
agagagatca agtagcatcc ccagcgaaat ctgaggcctc tggaggcgcc tgtgcacgtg
180
tgtctggaag tgtgtgtcca ggcagcatat ctgcatgtgt gtgcctgtcc agacagcata
240
tctgtgcacg cgt
253

<210> 4096
<211> 83
<212> PRT
<213> Homo sapiens

<400> 4096
Met Gly Gly Gly Glu Gln Ala Ser Ala Gly Arg Val Pro Lys Arg Gln
1 5 10 15
Pro Arg Glu Gln Gly Gln Ile Val Gly Gly Gly Phe Ser Ser Thr Val
20 25 30
Gln Val Arg Lys Leu Arg Leu Lys Arg Asp Gln Val Ala Ser Pro Ala
35 40 45
Lys Ser Glu Ala Ser Gly Gly Ala Cys Ala Arg Val Ser Gly Ser Val
50 55 60
Cys Pro Gly Ser Ile Ser Ala Cys Val Cys Leu Ser Arg Gln His Ile
65 70 75 80
Cys Ala Arg

<210> 4097
<211> 1385
<212> DNA
<213> Homo sapiens

<400> 4097
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60
ctgggacgcg tgccgcgcac tggcacggca ggggcgcgag ccaggctgca cgattcactg
120
cgtgctgtcc tcacttgttc tacaatgagt gccaaatctg ctatcagcaa ggaaattttt
180
gcacctcttg atgaaaggat gctgggagct gtccaagtca agaggaggac aaagaaaaag
240
attcctttct tggcaactgg aggtcaaggc gaatatttaa cttatatctg cctgtcagtg
300
acaaacaaga aacccacaca ggcgtccatc acaaaggtca aacagtttga aggctccaca
360
tcatttgttc ggagatcaca gtggatgctc gagcagcttc gccaggttaa tggtatcgat
420
cctaatgggg attcggcaga gtttgatttg ttgtttgaaa atgcttttga ccagtgggta
480
gccagcacag cgtcagaaaa atgcaccttc ttccagatcc tccaccatac ctgccagagg
540
tacctcacgg acaggaagcc agagtttatt aactgccaat ccaaaattat gggaggaaac
600
agcatcctcc attcagctgc tgacagcgtg accagcgcag tgcagaaggc aagccaggcc
660
ttgaatgagc gtggagagcg attaggccga gcagaggaga agacagaaga cctgaagaac
720
agcgcccagc agtttgcaga aactgcgcac aagcttgcca tgaagcacaa atgttgagaa
780
actgcctatc ctggtgactc ttcttaagag aaactgaaga gtttgttcag cagtttttac
840
aagaattcgg gacctccgct tgcttctttt tttccaatat ttggacactt agagtggttt
900
ttgttttttc ttttcagatg ttaatgtgaa agaaagggtg ttgcattttt acatttccct
960
aatgatcttg ctaataaatg ctacaatagc atcagcttca ttttgggttt ttgcctcctc
1020

ccactgtgtg tatgtgtgta tatgtatgtt ttgaatatgt tttctttatt aaaaaatatt
1080
ttttgtagtt tgaatatgaa atttggacca aatgataaac tgcgctgagt ctaaactggc
1140
aacatgtatt tttttctctg atattaagca ggaaggcatt ttaatgtggt gacatcagat
1200
gttatttttc ctagatgaaa ataaaagtca agcagtgatt agtttcactc actgtcctag
1260
ctacacttaa tttgaagatt aaaattctac attgtggaaa acaattgaat ttattgggaa
1320
aaacagcagt cttagatttt gctccttgca tagtaatctt ttgcatgaac catcaccagc
1380
gttca
1385

<210> 4098
<211> 258
<212> PRT
<213> Homo sapiens

<400> 4098
Ser Gly Ala Arg Ser Pro Glu Pro Arg Ala Gly Gln Pro Pro Gly Glu
1 5 10 15
Glu Pro Arg Ala Leu Gly Arg Val Pro Arg Thr Gly Thr Ala Gly Ala
20 25 30
Arg Ala Arg Leu His Asp Ser Leu Arg Ala Val Leu Thr Cys Ser Thr
35 40 45
Met Ser Ala Lys Ser Ala Ile Ser Lys Glu Ile Phe Ala Pro Leu Asp
50 55 60
Glu Arg Met Leu Gly Ala Val Gln Val Lys Arg Arg Thr Lys Lys Lys
65 70 75 80
Ile Pro Phe Leu Ala Thr Gly Gly Gln Gly Glu Tyr Leu Thr Tyr Ile
85 90 95
Cys Leu Ser Val Thr Asn Lys Lys Pro Thr Gln Ala Ser Ile Thr Lys
100 105 110
Val Lys Gln Phe Glu Gly Ser Thr Ser Phe Val Arg Arg Ser Gln Trp
115 120 125
Met Leu Glu Gln Leu Arg Gln Val Asn Gly Ile Asp Pro Asn Gly Asp
130 135 140
Ser Ala Glu Phe Asp Leu Leu Phe Glu Asn Ala Phe Asp Gln Trp Val
145 150 155 160
Ala Ser Thr Ala Ser Glu Lys Cys Thr Phe Phe Gln Ile Leu His His
165 170 175
Thr Cys Gln Arg Tyr Leu Thr Asp Arg Lys Pro Glu Phe Ile Asn Cys
180 185 190
Gln Ser Lys Ile Met Gly Gly Asn Ser Ile Leu His Ser Ala Ala Asp
195 200 205
Ser Val Thr Ser Ala Val Gln Lys Ala Ser Gln Ala Leu Asn Glu Arg
210 215 220
Gly Glu Arg Leu Gly Arg Ala Glu Glu Lys Thr Glu Asp Leu Lys Asn
225 230 235 240
Ser Ala Gln Gln Phe Ala Glu Thr Ala His Lys Leu Ala Met Lys His
245 250 255
Lys Cys

<210> 4099
<211> 511
<212> DNA
<213> Homo sapiens

<400> 4099
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attagggaaa ggttttctgt gaaattacct tctgattgta gccacatgaa acacatcaac
120
ttaaacaata aaaaattgta taatggaatt ggatcagggg gttcccaaaa ccccccttcac
180
tgaggtttgg caattcactg agaaggactc acaggactca gcagatagtc atacttgggg
240
ctttgattta ttacatttaa tacagcaaaa agacacaaag caacatttga gaaaggaaaa
300
ggtgcatgtg tcaaagtctg gaggaagcca ggcacaagct acaggagtca tctcctgtgt
360
agctagcagg atatgcttaa ttccccccagc ctcaaatttt gacgacacat gtgcaatgtt
420
gtctaccttta ccagagtttc attagaggct cagcacccat gttttcgatg gaggctagtc
480
acataggcaa cctctcctct ccctcacgcg t
511

<210> 4100
<211> 100
<212> PRT
<213> Homo sapiens

<400> 4100
Met Glu Leu Asp Gln Gly Val Pro Lys Thr Pro Phe Thr Glu Val Trp
 1   5   10   15
Gln Phe Thr Glu Lys Asp Ser Gln Asp Ser Ala Asp Ser His Thr Trp
            20   25   30
Gly Phe Asp Leu Leu His Leu Ile Gln Gln Lys Asp Thr Lys Gln His
        35   40   45
Leu Arg Lys Glu Lys Val His Val Ser Lys Ser Gly Gly Ser Gln Ala
    50   55   60
Gln Ala Thr Gly Val Ile Ser Cys Val Ala Ser Arg Ile Cys Leu Ile
65   70   75   80
Pro Pro Ala Ser Asn Phe Asp Asp Thr Cys Ala Met Leu Ser Thr Leu
                85   90   95
Pro Glu Phe His
            100

<210> 4101
<211> 536
<212> DNA
<213> Homo sapiens

<400> 4101

tttttttttt tttttttttt tttttttttt tttttgagga accccagaaa tgtgtttatt
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120
ccaggaaaga tggcacacgg cagacgacga caggaaggac acctgctccc cacccttccc
180
gggaccccgc catgtgcaaa attcgagctg gggtctgcag ctgcttggag agacccaggg
240
cctcttgctc cacagcctgc aaggtctgag caggcaacgg ccctggggcg gtgaggcccc
300
cgcctggtca ctccccgcgc cccccatgca ggcagtggag gggaggacac gcaggaggac
360
cagacgctaa aggtgtaaac gggcagccgt ggcactcctc acctctcaat aaataagata
420
aataactaaa taaataaaca actaaataaa gacatgaagg aatggatgca gagacgtgaa
480
cggatggcgc aggacgtccc tggtgggggc cacggtcccc ttaaggcatg tgggag
536

<210> 4102
<211> 106
<212> PRT
<213> Homo sapiens

<400> 4102
Met Cys Leu Leu Ser Trp Thr Arg Ile Ala Val Trp Gly Pro Ser Ala
1 5 10 15
Arg Val Cys Thr Arg Tyr Lys Ile Gln Glu Arg Trp His Thr Ala Asp
20 25 30
Asp Asp Arg Lys Asp Thr Cys Ser Pro Pro Phe Pro Gly Pro Arg His
35 40 45
Val Gln Asn Ser Ser Trp Gly Leu Gln Leu Leu Gly Glu Thr Gln Gly
50 55 60
Leu Leu Leu His Ser Leu Gln Gly Leu Ser Arg Gln Arg Pro Trp Gly
65 70 75 80
Gly Glu Ala Pro Ala Trp Ser Leu Pro Ala Pro Pro Met Gln Ala Val
85 90 95
Glu Gly Arg Thr Arg Arg Arg Thr Arg Arg
100 105

<210> 4103
<211> 3040
<212> DNA
<213> Homo sapiens

<400> 4103
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cgcgcccaga agatggacgg ggagtccgag gaggagcagg agtccgtgga caccggggag
120
gaggaggaag gcggtgacga gtctgacctg agttcggaat ccagcattaa gaagaaatct
180
caagaggaaa ggaaagaccg acagtccctg gataagccag ccaggaaaag gaggcggaga
240

agtagaaaga agcccagcgg tgccctcggt tctgagtcgt ataagtcatc tgcaggaagc
300
gctgagcaga cggcaccagg agacagcaca gggtacatgg aagtttctct ggactccctg
360
gatctccgag tcaaaggaat tctgtcttca caagcagaag ggttggccaa cggtccagat
420
gtgctggaga cagacggcct ccaggaagtg cctctctgca gctgccggat ggaaacaccg
480
aagagtcgag agatcaccac actggccaac aaccagtgca tggctacaga gagcgtggac
540
catgaattgg gccggtgcac aaacagcgtg gtcaagtatg agctgatgcg cccctccaac
600
aaggccccgc tcctcgtgct gtgtgaagac caccggggcc gcatggtgaa gcaccagtgc
660
tgtcctggct gtggctactt ctgcacagcg ggtaatttta tggagtgtca gcccgagagc
720
agcatctctc accgtttcca caaagactgt gcctctcgag tcaataacgc cagctattgt
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840
acctcgaccg tgacaccagt ccccgggcag gagaagggct cggccnctgg aggcagggcc
900cgggcagtgc tnngccgggc caccactctc ggaggacgac aagctgcagg 960
gtgcagcctc ccacgntgcc cgagggcttt gatccaacgg gacctgctgg gcttgggagg
1020
ccaactcccg gcctttccca gggaccaggg aaggaaacct tggagagcgc tctcatcgcc
1080
ctcgactcgg aaaaacccaa gaagcttcgc ttccacccaa agcagctgta cttctccgcc
1140
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1920

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1980
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2160
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2280
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2820
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2880
caaccgaaag ggtccttcgg ggctgcgccg ccggcttcct ggaggggtcg gaggtgaggc
2940
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3040

<210> 4104
<211> 978
<212> PRT
<213> Homo sapiens

<400> 4104
Xaa Ala Ala Phe Pro Thr Glu Asp Ser Arg Thr Ser Lys Glu Ser Met
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Ser Glu Ala Asp Arg Ala Gln Lys Met Asp Gly Glu Ser Glu Glu Glu
20 25 30
Gln Glu Ser Val Asp Thr Gly Glu Glu Glu Glu Gly Gly Asp Glu Ser
35 40 45
Asp Leu Ser Ser Glu Ser Ser Ile Lys Lys Lys Ser Gln Glu Glu Arg
50 55 60
Lys Asp Arg Gln Ser Leu Asp Lys Pro Ala Arg Lys Arg Arg Arg Arg

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65                  70                  75                  80
Ser Arg Lys Lys Pro Ser Gly Ala Leu Gly Ser Glu Ser Tyr Lys Ser
                85                  90                  95
Ser Ala Gly Ser Ala Glu Gln Thr Ala Pro Gly Asp Ser Thr Gly Tyr
            100                 105                 110
Met Glu Val Ser Leu Asp Ser Leu Asp Leu Arg Val Lys Gly Ile Leu
        115                 120                 125
Ser Ser Gln Ala Glu Gly Leu Ala Asn Gly Pro Asp Val Leu Glu Thr
    130                 135                 140
Asp Gly Leu Gln Glu Val Pro Leu Cys Ser Cys Arg Met Glu Thr Pro
145                 150                 155                 160
Lys Ser Arg Glu Ile Thr Thr Leu Ala Asn Asn Gln Cys Met Ala Thr
                165                 170                 175
Glu Ser Val Asp His Glu Leu Gly Arg Cys Thr Asn Ser Val Val Lys
            180                 185                 190
Tyr Glu Leu Met Arg Pro Ser Asn Lys Ala Pro Leu Leu Val Leu Cys
        195                 200                 205
Glu Asp His Arg Gly Arg Met Val Lys His Gln Cys Cys Pro Gly Cys
    210                 215                 220
Gly Tyr Phe Cys Thr Ala Gly Asn Phe Met Glu Cys Gln Pro Glu Ser
225                 230                 235                 240
Ser Ile Ser His Arg Phe His Lys Asp Cys Ala Ser Arg Val Asn Asn
                245                 250                 255
Ala Ser Tyr Cys Pro His Cys Gly Glu Glu Ser Ser Lys Ala Lys Glu
            260                 265                 270
Val Thr Ile Ala Lys Ala Asp Thr Thr Ser Thr Val Thr Pro Val Pro
        275                 280                 285
Gly Gln Glu Lys Gly Ser Ala Xaa Gly Gly Arg Ala Asp Thr Thr Thr
    290                 295                 300
Gly Ser Ala Xaa Pro Gly His His Ser Arg Arg Thr Thr Ser Cys Arg
305                 310                 315                 320
Val Gln Pro Pro Thr Xaa Pro Glu Gly Phe Asp Pro Thr Gly Pro Ala
                325                 330                 335
Gly Leu Gly Arg Pro Thr Pro Gly Leu Ser Gln Gly Pro Gly Lys Glu
            340                 345                 350
Thr Leu Glu Ser Ala Leu Ile Ala Leu Asp Ser Glu Lys Pro Lys Lys
        355                 360                 365
Leu Arg Phe His Pro Lys Gln Leu Tyr Phe Ser Ala Arg Gln Gly Glu
    370                 375                 380
Leu Gln Lys Val Leu Leu Met Leu Val Asp Gly Ile Asp Pro Asn Phe
385                 390                 395                 400
Lys Met Glu His Gln Asn Lys Arg Ser Pro Leu His Ala Ala Ala Glu
                405                 410                 415
Ala Gly His Val Asp Ile Cys His Met Leu Val Gln Ala Gly Ala Asn
            420                 425                 430
Ile Asp Thr Cys Ser Glu Asp Gln Arg Thr Pro Leu Met Glu Ala Ala
        435                 440                 445
Glu Asn Asn His Leu Glu Ala Val Lys Tyr Leu Ile Lys Ala Gly Ala
    450                 455                 460
Leu Val Asp Pro Lys Asp Ala Glu Gly Ser Thr Cys Leu His Leu Ala
465                 470                 475                 480
Ala Lys Lys Gly His Tyr Glu Val Val Gln Tyr Leu Leu Ser Asn Gly
                485                 490                 495
Arg Met Asp Val Asn Cys Gln Asp Asp Gly Gly Trp Thr Pro Met Ile
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            500                 505                 510
Trp Ala Thr Glu Tyr Lys His Val Asp Leu Val Lys Leu Leu Leu Ser
        515                 520                 525
Lys Gly Ser Asp Ile Asn Ile Arg Asp Asn Glu Glu Asn Ile Cys Leu
    530                 535                 540
His Trp Ala Ala Phe Ser Gly Cys Val Asp Ile Ala Glu Ile Leu Leu
545                 550                 555                 560
Ala Ala Lys Cys Asp Leu His Ala Val Asn Ile His Gly Asp Ser Pro
                565                 570                 575
Leu His Ile Ala Ala Arg Glu Asn Arg Tyr Asp Cys Val Val Leu Phe
            580                 585                 590
Leu Ser Arg Asp Ser Asp Val Thr Leu Lys Asn Lys Glu Gly Glu Thr
        595                 600                 605
Pro Leu Gln Cys Ala Ser Leu Asn Ser Gln Val Trp Ser Ala Leu Gln
    610                 615                 620
Met Ser Lys Ala Leu Gln Asp Ser Ala Pro Asp Arg Pro Ser Pro Val
625                 630                 635                 640
Glu Arg Ile Val Ser Arg Asp Ile Ala Arg Gly Tyr Glu Arg Ile Pro
                645                 650                 655
Ile Pro Cys Val Asn Ala Val Asp Ser Glu Pro Cys Pro Ser Asn Tyr
            660                 665                 670
Lys Tyr Val Ser Gln Asn Cys Val Thr Ser Pro Met Asn Ile Asp Arg
        675                 680                 685
Asn Ile Thr His Leu Gln Tyr Cys Val Cys Ile Asp Asp Cys Ser Ser
    690                 695                 700
Ser Asn Cys Met Cys Gly Gln Leu Ser Met Arg Cys Trp Tyr Asp Lys
705                 710                 715                 720
Asp Gly Arg Leu Leu Pro Glu Phe Asn Met Ala Glu Pro Pro Leu Ile
                725                 730                 735
Phe Glu Cys Asn His Ala Cys Ser Cys Trp Arg Asn Cys Arg Asn Arg
            740                 745                 750
Val Val Gln Asn Gly Leu Arg Ala Arg Leu Gln Leu Tyr Arg Thr Arg
        755                 760                 765
Asp Met Gly Trp Gly Val Arg Ser Leu Gln Asp Ile Pro Pro Gly Thr
    770                 775                 780
Phe Val Cys Glu Tyr Val Gly Glu Leu Ile Ser Asp Ser Glu Ala Asp
785                 790                 795                 800
Val Arg Glu Glu Asp Ser Tyr Leu Phe Asp Leu Asp Asn Lys Asp Gly
                805                 810                 815
Glu Val Tyr Cys Ile Asp Ala Arg Phe Tyr Gly Asn Val Ser Arg Phe
            820                 825                 830
Ile Asn His His Cys Glu Pro Asn Leu Val Pro Val Arg Val Phe Met
        835                 840                 845
Ala His Gln Asp Leu Arg Phe Pro Arg Ile Ala Phe Phe Ser Thr Arg
    850                 855                 860
Leu Ile Glu Ala Gly Glu Gln Leu Gly Phe Asp Tyr Gly Glu Arg Phe
865                 870                 875                 880
Trp Asp Ile Lys Gly Lys Leu Phe Ser Cys Arg Cys Gly Ser Pro Lys
                885                 890                 895
Cys Arg His Ser Ser Ala Ala Leu Ala Gln Arg Gln Ala Ser Ala Ala
            900                 905                 910
Gln Glu Ala Gln Glu Asp Gly Leu Pro Asp Thr Ser Ser Ala Ala Ala
        915                 920                 925
Ala Thr Pro Tyr Glu Thr Pro Pro Ala Ser Gly Ala Leu Gly Ser Gln
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930 935 940
Gly Pro Pro Arg Arg Arg Leu Glu Asp Glu Glu Glu Arg Phe Arg Thr
945 950 955 960
Gln Pro Lys Gly Ser Phe Gly Ala Ala Pro Pro Ala Ser Trp Arg Gly
965 970 975
Arg Arg

<210> 4105
<211> 775
<212> DNA
<213> Homo sapiens

<400> 4105
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tcaggtcgtg ggggacggga ccgcttcacc gctgagtcct acacagttct gggggacacg
120
ctgatcgacg gcggggagca ttactgggag gtgcgctacg agccggacag caaggcgttc
180
ggcgtgggcg tggcctaccg cagcctgggc cgcttcgagc aactgggcaa gacggccgcc
240
tcctggtgcc tgcactcaac aattggctgc aggtcagctt cacggaagca cgccaacaag
300
gtcaaggtgc tggacgcccc cgtgcccgac tgcctgggtg tgcactgtga cttccaccaa
360
ggcctcctgt ccttctacaa tgcccgcacc aaacaagtgc tgcacacttt caagaccagg
420
ttcacacagc cgctgctgcc tgctttcacg gtatggtgtg gcagcttcca ggtgacgaca
480
ggcctgcagg tccccagtgc tgtgcgctgc ctgcaaaagc gaggcagtgc taccagcagc
540
tccaacacca gcctcaccta ggcccccagg cacccaccca gctggggtgt ttttgggggа
600
gtcgccgcca agcccaggct gctggagcca ggcaccctcc tctgtcactt gctgcttgga
660
gccttaactc cagatggggg ggtcaccaag agggagtggg caccctggcg ggccctctcc
720
ccacctcacc tcttaataaa ggtcagacac tggccaggca aaaaaaaaaa aaata
775

<210> 4106
<211> 186
<212> PRT
<213> Homo sapiens

<400> 4106
Xaa Arg Ala Ser Pro Ile Asn Ser Pro Ala Arg Gly Thr Pro Ser Pro
1 5 10 15
Lys Arg Met Pro Ser Gly Arg Gly Gly Arg Asp Arg Phe Thr Ala Glu
20 25 30
Ser Tyr Thr Val Leu Gly Asp Thr Leu Ile Asp Gly Gly Glu His Tyr
35 40 45
Trp Glu Val Arg Tyr Glu Pro Asp Ser Lys Ala Phe Gly Val Gly Val

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    50                  55                  60
Ala Tyr Arg Ser Leu Gly Arg Phe Glu Gln Leu Gly Lys Thr Ala Ala
65                  70                  75                  80
Ser Trp Cys Leu His Ser Thr Ile Gly Cys Arg Ser Ala Ser Arg Lys
                85                  90                  95
His Ala Asn Lys Val Lys Val Leu Asp Ala Pro Val Pro Asp Cys Leu
            100                 105                 110
Gly Val His Cys Asp Phe His Gln Gly Leu Leu Ser Phe Tyr Asn Ala
        115                 120                 125
Arg Thr Lys Gln Val Leu His Thr Phe Lys Thr Arg Phe Thr Gln Pro
    130                 135                 140
Leu Leu Pro Ala Phe Thr Val Trp Cys Gly Ser Phe Gln Val Thr Thr
145                 150                 155                 160
Gly Leu Gln Val Pro Ser Ala Val Arg Cys Leu Gln Lys Arg Gly Ser
                165                 170                 175
Ala Thr Ser Ser Ser Asn Thr Ser Leu Thr
            180                 185
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<210> 4107
<211> 1442
<212> DNA
<213> Homo sapiens

<400> 4107
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120
cgcgtcactg tcgggtcggc gagccacggg ggccgccgca gcaccatggc gaccaccgtc
180
agcactcagc gcgggccggt gtacatcggt gagctcccgc aggacttcct ccgcatcacg
240
cccacacagc agcagcggca ggtccagctg gacgcccagg cgcccagcag ctgcagtacg
300
gaggcgcagg gcaccgtggg ccgactgaac atcacggtgg tacaggcaaa gttggccaag
360
aattacggca tgacccgcat ggacccctac tgccgactgc gcctgggcta cgcggtgtac
420
gagacgccca cggcacacaa tggcgccaag aatccccgct ggaataaggt catccactgc
480
acggtgcccc caggcgtgga ctctttctat ctcgagatct tcgatgagag agccttctcc
540
atggacgacc gcattgcctg gacccacatc accatcccgg agtccctgag gcagggcaag
600
gtggaggaca agtggtacag cctgagcggg aggcaggggg acgacaagga gggcatgatc
660
aacctcgtca tgtcctacgc gctgcttcca gctgccatgg tgatgccacc ccagcccgtg
720
gtcctgatgc caacagtgta ccagcagggc gttggctatg tgcccatcac agggatgccc
780
gctgtctgta gccccggcat ggtgcccgtg gccctgcccc cggccgccgt gaacgcccag
840
ccccgctgta gcgaggagga cctgaaagcc atccaggaca tgttccccaa catggaccag
900

gaggtgatcc gctccgtgct ggaagcccag cgagggaaca aggatgccgc catcaactcc
960
ctgctgcaga tgggggagga gccatagagc ctctgcctcg atgccgtttt gcccccgctc
1020
tttggacacg ccgacccggc gctccccaag gaatgctgtc ccaacaagat tcccgtgaaa
1080
gagcacccgt gtcgcccccc cccgtggact tctgtgccgc cccgtccaca cctgttcttg
1140
ggtgcatgtg ggttttcggt tcctggcggt ccaggacggg gcgggggctc ccctcccatc
1200
tcgtgctggg aggtctcagc gcgctctcct gtccctggga cgtgcgtctc tccttctcat
1260
gccgttctgg aaaatgctct tgctgtagag agcagctgct tctgccaggg tgttggaggt
1320
ggtggagcgc cttccgattc cattcatggc attttgtgat gtgatgtaat tggaatagag
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1440
aa
1442

<210> 4108
<211> 273
<212> PRT
<213> Homo sapiens

<400> 4108
Met Ala Thr Thr Val Ser Thr Gln Arg Gly Pro Val Tyr Ile Gly Glu
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Leu Pro Gln Asp Phe Leu Arg Ile Thr Pro Thr Gln Gln Gln Arg Gln
20 25 30
Val Gln Leu Asp Ala Gln Ala Pro Ser Ser Cys Ser Thr Glu Ala Gln
35 40 45
Gly Thr Val Gly Arg Leu Asn Ile Thr Val Val Gln Ala Lys Leu Ala
50 55 60
Lys Asn Tyr Gly Met Thr Arg Met Asp Pro Tyr Cys Arg Leu Arg Leu
65 70 75 80
Gly Tyr Ala Val Tyr Glu Thr Pro Thr Ala His Asn Gly Ala Lys Asn
85 90 95
Pro Arg Trp Asn Lys Val Ile His Cys Thr Val Pro Pro Gly Val Asp
100 105 110
Ser Phe Tyr Leu Glu Ile Phe Asp Glu Arg Ala Phe Ser Met Asp Asp
115 120 125
Arg Ile Ala Trp Thr His Ile Thr Ile Pro Glu Ser Leu Arg Gln Gly
130 135 140
Lys Val Glu Asp Lys Trp Tyr Ser Leu Ser Gly Arg Gln Gly Asp Asp
145 150 155 160
Lys Glu Gly Met Ile Asn Leu Val Met Ser Tyr Ala Leu Leu Pro Ala
165 170 175
Ala Met Val Met Pro Pro Gln Pro Val Val Leu Met Pro Thr Val Tyr
180 185 190
Gln Gln Gly Val Gly Tyr Val Pro Ile Thr Gly Met Pro Ala Val Cys
195 200 205
Ser Pro Gly Met Val Pro Val Ala Leu Pro Pro Ala Ala Val Asn Ala

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    210                 215                 220
Gln Pro Arg Cys Ser Glu Glu Asp Leu Lys Ala Ile Gln Asp Met Phe
225                 230                 235                 240
Pro Asn Met Asp Gln Glu Val Ile Arg Ser Val Leu Glu Ala Gln Arg
                245                 250                 255
Gly Asn Lys Asp Ala Ala Ile Asn Ser Leu Leu Gln Met Gly Glu Glu
            260                 265                 270
Pro
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<210> 4109
<211> 1637
<212> DNA
<213> Homo sapiens

<400> 4109
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120
ctgcgtgctg gtgaagaagg cagccacagt cggaagtcgc tgtgcagaag cagagaggag
180
ctgcgggggа aggtccggga gctggccagc gccgtccgga acgccaaata cttggtcgtc
240
tacacaggcg cgggaatcag cacggcagcg tctatcccag actaccgggg ccctaatgga
300
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360
ccaaccctca cccacatgag catcacccgt ctgcatgagc agaagctggt gcagcatgtg
420
gtgtctcaga actgtgacgg gctccacctg aggagtgggc tgccgcgcac ggccatctcc
480
gagctccacg ggaacatgta cattgaagtc tgtacctcct gcgttcccaa cagggagtac
540
gtgcgggtgt tcgatgtgac ggagcgcact gccctccaca gacaccagac aggccggacc
600
tgccacaagt gtgggaccca gctgcgggac accattgtgc actttgggga gaggggacg
660
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720
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780
aagccccctg ccggcggccg actttacatc gtgaacctgc agtggacccc gaaggatgac
840
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1080
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1140

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1380
cggaactcgg gttatttcag ccccggcctg cagagtggaa gcgcccagcg gcctttcctc
1440
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gaactttata gaatcctctc tgtactggat gtgcggcaga ggggtggctc cgagcctcgg
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1620
aaaaaaaaaa aaaaaaa
1637

<210> 4110
<211> 375
<212> PRT
<213> Homo sapiens

<400> 4110
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Met Ala Glu Leu Gly Leu Glu Ile Pro Ala Tyr Ser Arg Trp Gln Asp
            20   25   30
Pro Ile Phe Ser Leu Ala Thr Pro Leu Arg Ala Gly Glu Glu Gly Ser
        35   40   45
His Ser Arg Lys Ser Leu Cys Arg Ser Arg Glu Glu Leu Arg Gly Lys
    50   55   60
Val Arg Glu Leu Ala Ser Ala Val Arg Asn Ala Lys Tyr Leu Val Val
65   70   75   80
Tyr Thr Gly Ala Gly Ile Ser Thr Ala Ala Ser Ile Pro Asp Tyr Arg
                85   90   95
Gly Pro Asn Gly Val Trp Thr Leu Leu Gln Lys Gly Arg Ser Val Ser
            100   105   110
Ala Ala Asp Leu Ser Glu Ala Glu Pro Thr Leu Thr His Met Ser Ile
        115   120   125
Thr Arg Leu His Glu Gln Lys Leu Val Gln His Val Val Ser Gln Asn
    130   135   140
Cys Asp Gly Leu His Leu Arg Ser Gly Leu Pro Arg Thr Ala Ile Ser
145   150   155   160
Glu Leu His Gly Asn Met Tyr Ile Glu Val Cys Thr Ser Cys Val Pro
                165   170   175
Asn Arg Glu Tyr Val Arg Val Phe Asp Val Thr Glu Arg Thr Ala Leu
            180   185   190
His Arg His Gln Thr Gly Arg Thr Cys His Lys Cys Gly Thr Gln Leu
        195   200   205
Arg Asp Thr Ile Val His Phe Gly Glu Arg Gly Thr Leu Gly Gln Pro
    210   215   220
Leu Asn Trp Glu Ala Ala Thr Glu Ala Ala Ser Arg Ala Asp Thr Ile

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225                 230                 235                 240
Leu Cys Leu Gly Ser Ser Leu Lys Val Leu Lys Lys Tyr Pro Arg Leu
                245                 250                 255
Trp Cys Met Thr Lys Pro Pro Ala Gly Gly Arg Leu Tyr Ile Val Asn
            260                 265                 270
Leu Gln Trp Thr Pro Lys Asp Asp Trp Ala Ala Leu Lys Leu His Gly
        275                 280                 285
Lys Cys Asp Asp Val Met Arg Leu Leu Met Ala Glu Leu Gly Leu Glu
    290                 295                 300
Ile Pro Ala Tyr Ser Arg Trp Gln Asp Pro Ile Phe Ser Leu Ala Thr
305                 310                 315                 320
Pro Leu Arg Ala Gly Glu Glu Gly Ser His Ser Arg Lys Ser Leu Cys
                325                 330                 335
Arg Ser Arg Glu Glu Ala Pro Pro Gly Asp Arg Gly Ala Pro Leu Ser
            340                 345                 350
Ser Ala Pro Ile Leu Gly Gly Trp Phe Gly Arg Gly Cys Thr Lys Arg
        355                 360                 365
Thr Lys Arg Lys Lys Val Thr
    370                 375
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<210> 4111
<211> 2599
<212> DNA
<213> Homo sapiens

<400> 4111
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120
gtctctgcaa tggcggctct agactccctg tcgctcttca ctagcctcgg cctgagcgag
180
cagaaggccc gcgagacgct caagaactcg gctctgagcg cgcagctgcg cgaggccgct
240
actcaggctc agcagaccct gggttccacc attgacaaag ctaccgggat cctgttatat
300
ggcttggcct cccgactcag ggatacccgg cgtctctcct tccttgtaag ctacatagcc
360
agtaagaaga tccacactga gccccagcta agcgctgccc ttgagtatgt gcggagtcac
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480
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540
ctggtggaac gttaccattt caacatgggg ctgctgatgg gagaggctcg ggctgtgctg
600
aagtgggcag atggcaaaat gatcaagaat gaagtggaca tgcaggtcct ccaccttctg
660
ggccccaagt tggaggctga tctggagaag aagttcaagg tggcaaaagc tcggctagaa
720
gaaacagacc ggaggacggc aaaggatgtg gtggagaatg gcgagactgc tgaccagacc
780
ctgtctctga tggagcagct ccgggggggag gcccttaagt tccacaagcc tggtgagaac
840

tacaagaccc caggctatgt ggtcactcca cacaccatga atctactaaa gcagcacctg
900
gagattactg gtgggcaggt acgtacccgg ttcccgccag aacccaatgg aatcctgcat
960
attggacatg ccaaagccat caatttcaac tttggctatg ccaaggccaa caatggcatc
1020
tgtttttctgc gttttgatga caccaaccct gagaaggagg aagcaaagtt cttcacggcc
1080
atctgtgaca tggtagcctg gctaggctac acaccttaca aagtcacata tgcgtctgac
1140
tattttgacc agctatatgc gtgggctgtg gagctcatcc gcaggggtct ggcttatgtg
1200
tgccaccagc gaggagagga gctcaaaggc cataatactc tgccttcacc ctggagagac
1260
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1320
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1380
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2400
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2460

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2580
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2599

<210> 4112
<211> 775
<212> PRT
<213> Homo sapiens

<400> 4112
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Leu Arg Glu Ala Ala Thr Gln Ala Gln Gln Thr Leu Gly Ser Thr Ile
35 40 45
Asp Lys Ala Thr Gly Ile Leu Leu Tyr Gly Leu Ala Ser Arg Leu Arg
50 55 60
Asp Thr Arg Arg Leu Ser Phe Leu Val Ser Tyr Ile Ala Ser Lys Lys
65 70 75 80
Ile His Thr Glu Pro Gln Leu Ser Ala Ala Leu Glu Tyr Val Arg Ser
85 90 95
His Pro Leu Asp Pro Ile Asp Thr Val Asp Phe Glu Arg Glu Cys Gly
100 105 110
Val Gly Val Ile Val Thr Pro Glu Gln Ile Glu Glu Ala Val Glu Ala
115 120 125
Ala Ile Asn Arg His Arg Pro Gln Leu Leu Val Glu Arg Tyr His Phe
130 135 140
Asn Met Gly Leu Leu Met Gly Glu Ala Arg Ala Val Leu Lys Trp Ala
145 150 155 160
Asp Gly Lys Met Ile Lys Asn Glu Val Asp Met Gln Val Leu His Leu
165 170 175
Leu Gly Pro Lys Leu Glu Ala Asp Leu Glu Lys Lys Phe Lys Val Ala
180 185 190
Lys Ala Arg Leu Glu Glu Thr Asp Arg Arg Thr Ala Lys Asp Val Val
195 200 205
Glu Asn Gly Glu Thr Ala Asp Gln Thr Leu Ser Leu Met Glu Gln Leu
210 215 220
Arg Gly Glu Ala Leu Lys Phe His Lys Pro Gly Glu Asn Tyr Lys Thr
225 230 235 240
Pro Gly Tyr Val Val Thr Pro His Thr Met Asn Leu Leu Lys Gln His
245 250 255
Leu Glu Ile Thr Gly Gly Gln Val Arg Thr Arg Phe Pro Pro Glu Pro
260 265 270
Asn Gly Ile Leu His Ile Gly His Ala Lys Ala Ile Asn Phe Asn Phe
275 280 285
Gly Tyr Ala Lys Ala Asn Asn Gly Ile Cys Phe Leu Arg Phe Asp Asp
290 295 300
Thr Asn Pro Glu Lys Glu Glu Ala Lys Phe Phe Thr Ala Ile Cys Asp
305 310 315 320
Met Val Ala Trp Leu Gly Tyr Thr Pro Tyr Lys Val Thr Tyr Ala Ser

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                325                 330                 335
Asp Tyr Phe Asp Gln Leu Tyr Ala Trp Ala Val Glu Leu Ile Arg Arg
            340                 345                 350
Gly Leu Ala Tyr Val Cys His Gln Arg Gly Glu Glu Leu Lys Gly His
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Asn Thr Leu Pro Ser Pro Trp Arg Asp Arg Pro Met Glu Glu Ser Leu
    370                 375                 380
Leu Leu Phe Glu Ala Met Arg Lys Gly Lys Phe Ser Glu Gly Glu Ala
385                 390                 395                 400
Thr Leu Arg Met Lys Leu Val Met Glu Asp Gly Lys Met Asp Pro Val
                405                 410                 415
Ala Tyr Arg Val Lys Tyr Thr Pro His His Arg Thr Gly Asp Lys Trp
            420                 425                 430
Cys Ile Tyr Pro Thr Tyr Asp Tyr Thr His Cys Leu Cys Asp Ser Ile
        435                 440                 445
Glu His Ile Thr His Ser Leu Cys Thr Lys Glu Phe Gln Ala Arg Arg
    450                 455                 460
Ser Ser Tyr Phe Trp Leu Cys Asn Ala Leu Asp Val Tyr Cys Pro Val
465                 470                 475                 480
Gln Trp Glu Tyr Gly Arg Leu Asn Leu His Tyr Ala Val Val Ser Lys
                485                 490                 495
Arg Lys Ile Leu Gln Leu Val Ala Thr Gly Ala Val Arg Asp Trp Asp
            500                 505                 510
Asp Pro Arg Leu Phe Thr Leu Thr Ala Leu Arg Arg Arg Gly Phe Pro
        515                 520                 525
Pro Glu Ala Ile Asn Asn Phe Cys Ala Arg Val Gly Val Thr Val Ala
    530                 535                 540
Gln Thr Thr Met Glu Pro His Leu Leu Glu Ala Cys Val Arg Asp Val
545                 550                 555                 560
Leu Asn Asp Thr Ala Pro Arg Ala Met Ala Val Leu Glu Ser Leu Arg
                565                 570                 575
Val Ile Ile Thr Asn Phe Pro Ala Ala Lys Ser Leu Asp Ile Gln Val
            580                 585                 590
Pro Asn Phe Pro Ala Asp Glu Thr Lys Gly Phe His Gln Val Pro Phe
        595                 600                 605
Ala Pro Ile Val Phe Ile Glu Arg Thr Asp Phe Lys Glu Glu Pro Glu
    610                 615                 620
Pro Gly Phe Lys Arg Leu Ala Trp Gly Gln Pro Val Gly Leu Arg His
625                 630                 635                 640
Thr Gly Tyr Val Ile Glu Leu Gln His Val Val Lys Gly Pro Ser Gly
                645                 650                 655
Cys Val Glu Ser Leu Glu Val Thr Cys Arg Arg Ala Asp Ala Gly Glu
            660                 665                 670
Lys Pro Lys Ala Phe Ile His Trp Val Ser Gln Pro Leu Met Cys Glu
        675                 680                 685
Val Arg Leu Tyr Glu Arg Leu Phe Gln His Lys Asn Pro Glu Asp Pro
    690                 695                 700
Thr Glu Val Pro Gly Gly Phe Leu Ser Asp Leu Asn Leu Ala Ser Leu
705                 710                 715                 720
His Val Val Asp Ala Ala Leu Val Asp Cys Ser Val Ala Leu Ala Lys
                725                 730                 735
Pro Phe Asp Lys Phe Gln Phe Glu Arg Leu Gly Tyr Phe Ser Val Asp
            740                 745                 750
Pro Asp Ser His Gln Gly Lys Leu Val Phe Asn Arg Thr Val Thr Leu
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755 760 765
Lys Glu Asp Pro Gly Lys Val
770 775

<210> 4113
<211> 1894
<212> DNA
<213> Homo sapiens

<400> 4113
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120
taagagggag gcgtggacgc gaaggacacg tctgccacat cccagtcagt taatggatca
180
ccccaagcgg aacaaccttc attggaatct acaagcaaag aagccttctt tagcagagtg
240
gaaacatttt cttctttgaa atgggcgggt aagccctttg agctgtctcc actcgtctgt
300
gcaaaatatg gctgggtcac agtggaatgt gatatgctca agtgctctag ctgtcaagct
360
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420
gagctgaaga aagccttgtg tactgcccat gagaagttct gtttctggcc agacagccca
480
tccccagacc gatttgggat gttgcccctg gatgagcctg ctattcttgt tagtgaattc
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600
gacttgaaaa ctatgtgctt gacagaagac aagatcagtc ttctcctaca cttgcttgaa
660
gatgaacttg atcaccgaac tgatgagaga aaaactacaa tcaaattagg ctcagacatc
720
caagtccacg tcactgcctg tattctctct gtgtgtggct gggcgtgtag ttcctctttg
780
gaatccatgc agctctccct gatagcatgt tcgcaatgta tgaggaaggt ggggctctgg
840
ggcttccagc agattgaatc gtccatgact gacctggatg catcctttgg cctgaccagc
900
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960
cggaggatga tgacccggag ccaggatgcc actttctccc caggctcaga gcaggctgaa
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aagagccctg gtcccattgt ctctcgaact cggagctggg actcttccag tcctgttgac
1080
cgtcctgagc cagaggctgc tagccccacc accagaactc gcccagtgac ccgaagcatg
1140
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1260
tctcagcata gagactggtg cccttgggtg aatatcacac ttggcaaaga aagcagggag
1320

aatggtggaa ctgaaccaga tgccagcgcc ccagcagagc caggctggaa agcagtgctg
1380
accatcctct tggcgcacaa acagtctagc cagccagctg aaacggactc catgagtctc
1440
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1500
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1620
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1680
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1740
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1800
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1860
aaatatttgc taagaaaaaa aaaaaaaaaa aaaa
1894

<210> 4114
<211> 389
<212> PRT
<213> Homo sapiens

<400> 4114
Met Leu Lys Cys Ser Ser Cys Gln Ala Phe Leu Cys Ala Ser Leu Gln
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Pro Ala Phe Asp Phe Asp Arg Tyr Lys Gln Arg Cys Ala Glu Leu Lys
            20   25   30
Lys Ala Leu Cys Thr Ala His Glu Lys Phe Cys Phe Trp Pro Asp Ser
        35   40   45
Pro Ser Pro Asp Arg Phe Gly Met Leu Pro Leu Asp Glu Pro Ala Ile
    50   55   60
Leu Val Ser Glu Phe Leu Asp Arg Phe Gln Ser Leu Cys His Leu Asp
65   70   75   80
Leu Gln Leu Pro Ser Leu Arg Pro Glu Asp Leu Lys Thr Met Cys Leu
                85   90   95
Thr Glu Asp Lys Ile Ser Leu Leu Leu His Leu Leu Glu Asp Glu Leu
            100   105   110
Asp His Arg Thr Asp Glu Arg Lys Thr Thr Ile Lys Leu Gly Ser Asp
        115   120   125
Ile Gln Val His Val Thr Ala Cys Ile Leu Ser Val Cys Gly Trp Ala
    130   135   140
Cys Ser Ser Ser Leu Glu Ser Met Gln Leu Ser Leu Ile Ala Cys Ser
145   150   155   160
Gln Cys Met Arg Lys Val Gly Leu Trp Gly Phe Gln Gln Ile Glu Ser
                165   170   175
Ser Met Thr Asp Leu Asp Ala Ser Phe Gly Leu Thr Ser Ser Pro Ile
            180   185   190
Pro Gly Leu Glu Gly Arg Pro Glu Arg Leu Pro Leu Val Pro Glu Ser
        195   200   205
Pro Arg Arg Met Met Thr Arg Ser Gln Asp Ala Thr Phe Ser Pro Gly

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    210                 215                 220
Ser Glu Gln Ala Glu Lys Ser Pro Gly Pro Ile Val Ser Arg Thr Arg
225                 230                 235                 240
Ser Trp Asp Ser Ser Ser Pro Val Asp Arg Pro Glu Pro Glu Ala Ala
                245                 250                 255
Ser Pro Thr Thr Arg Thr Arg Pro Val Thr Arg Ser Met Gly Thr Gly
            260                 265                 270
Asp Thr Pro Gly Leu Glu Val Pro Ser Ser Xaa Ser Ala Glu Ser Gln
        275                 280                 285
Ala Ser Ser Leu Cys Ser Ser Ser Ser Ser Asp Thr Ser Ser Arg Ser
    290                 295                 300
Phe Phe Asp Pro Thr Ser Gln His Arg Asp Trp Cys Pro Trp Val Asn
305                 310                 315                 320
Ile Thr Leu Gly Lys Glu Ser Arg Glu Asn Gly Gly Thr Glu Pro Asp
                325                 330                 335
Ala Ser Ala Pro Ala Glu Pro Gly Trp Lys Ala Val Leu Thr Ile Leu
            340                 345                 350
Leu Ala His Lys Gln Ser Ser Gln Pro Ala Glu Thr Asp Ser Met Ser
        355                 360                 365
Leu Ser Glu Lys Ser Arg Lys Val Phe Arg Ile Phe Arg Gln Trp Glu
    370                 375                 380
Ser Leu Cys Ser Cys
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<210> 4115
<211> 1056
<212> DNA
<213> Homo sapiens

<400> 4115

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120
accaaatatt gtacagagtg tgccagtagg cttttgcaac tggactgaaa atacctgcct
180
tttctctcca caggggaaag tggaagttga agctgggaaa gaaggtatga agtttgaagc
240
gagcgccttc tcatactatg gcgtgatggc cctgacagcc tctccaggtg aaaataagtc
300
ccctcctcgc ccatgtggct tgaatcactc agactctctc agtcgaagcg accggattga
360
cgccgtcaca ccaacactgg ggagcagcaa taaccagctc aattcttcgc tcctccaagt
420
ctacatcccc gattactcgg tgcgagccct ttcggatctg cagtttgtta agatctcaag
480
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540
cagtgaaaac actaaaatcg aattgactct tacggagctg catgacgggt tgccagacga
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gacagccaac ctgctcaacg aacagaactg tgtgacgcac agtaaggcca accacagcct
660
gcacaacgaa ggcgccatct aggccgcgct ggctgcaccc gcccaggccc gcacccgccc
720
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agtcccgagg gcccggccct gtctgcccat gacttcactg gtgtgagctt gtccgccatg
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840
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900
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960
ccttttatca ttattcacac tcctctgccc tcgatttgca tgaagttgaa aattgttgcg
1020
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1056

<210> 4116
<211> 151
<212> PRT
<213> Homo sapiens

<400> 4116
Met Lys Phe Glu Ala Ser Ala Phe Ser Tyr Tyr Gly Val Met Ala Leu
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Thr Ala Ser Pro Gly Glu Asn Lys Ser Pro Pro Arg Pro Cys Gly Leu
20 25 30
Asn His Ser Asp Ser Leu Ser Arg Ser Asp Arg Ile Asp Ala Val Thr
35 40 45
Pro Thr Leu Gly Ser Ser Asn Asn Gln Leu Asn Ser Ser Leu Leu Gln
50 55 60
Val Tyr Ile Pro Asp Tyr Ser Val Arg Ala Leu Ser Asp Leu Gln Phe
65 70 75 80
Val Lys Ile Ser Arg Gln Gln Tyr Gln Asn Ala Leu Met Ala Ser Arg
85 90 95
Met Asp Lys Thr Pro Gln Ser Ser Asp Ser Glu Asn Thr Lys Ile Glu
100 105 110
Leu Thr Leu Thr Glu Leu His Asp Gly Leu Pro Asp Glu Thr Ala Asn
115 120 125
Leu Leu Asn Glu Gln Asn Cys Val Thr His Ser Lys Ala Asn His Ser
130 135 140
Leu His Asn Glu Gly Ala Ile
145 150

<210> 4117
<211> 973
<212> DNA
<213> Homo sapiens

<400> 4117
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120
tgggtctcct gggcaccact cagagctctg tgcctgtggg tccaacaagt ccagagctgt
180
tggcactggt gcttcccggc tctggggcag tccgggggct gcaagtggaa acccaggggc
240

cctgcctggc tggggactaa gcagtgtcca gagtgggggc agggagaaca gagggcttga
300
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360
caggcacagc ctgctgtaca agcacacgac tggcctgggt gtgggcgttg gcctcagcca
420
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480
tcaccgtcac cgggagaagc taccccgccc ccttcttcag ggatctccgc agtgaagcct
540
cctctaagga gtcctaggac tctcccttta gagttgggga caggggggtg tgtttgtgct
600
ggcctgggtc caaatactcc agggtgtcag ctccatcccc ctgctgtcct ctgtccccag
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gggctgggaa gacaccaacg gctgtgaaca aactcgctga tttcttcacc aagacggtga
720
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780
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840
tattcacacc tcagagtgac catccgagct cctggtgact ggaaaaaaga aatgggtcac
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960
tcccttcacg cgt
973

<210> 4118
<211> 128
<212> PRT
<213> Homo sapiens

<400> 4118
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His Leu Gly Pro Gln Ala Gln Pro Ala Val Gln Ala His Asp Trp Pro
            20   25   30
Gly Cys Gly Arg Trp Pro Gln Pro Pro Gly Gly Ile Leu Glu Trp Glu
        35   40   45
Arg Cys Val Gly Cys Pro Arg Pro Ala Arg Pro Ala Ser Pro Ser Pro
    50   55   60
Gly Glu Ala Thr Pro Pro Pro Ser Ser Gly Ile Ser Ala Val Lys Pro
65   70   75   80
Pro Leu Arg Ser Pro Arg Thr Leu Pro Leu Glu Leu Gly Thr Gly Gly
                85   90   95
Cys Val Cys Ala Gly Leu Gly Pro Asn Thr Pro Gly Cys Gln Leu His
            100   105   110
Pro Pro Ala Val Leu Cys Pro Gln Gly Leu Gly Arg His Gln Arg Leu
        115   120   125

<210> 4119
<211> 649
<212> DNA
<213> Homo sapiens

<400> 4119
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120
accaattttc tgaactacaa aaatgatcga accataaaaa tcaggaacac ctctggttcc
180
agtcagacta aagatcagag gatccctggt cgtccagcct tccaacatcc ctgaccttct
240
gaagtctaag atctctagct gggatgtgct tcttctcctt tcttcttact gtaacacctc
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360
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420
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480
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540
agggcagctt ccgtagctgt aggctctcct ctggttactg cccacagcct tcactaattg
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gtgttcaatt cctactttga aaaatgaagt ttttcaaata gcaactagt
649

<210> 4120
<211> 100
<212> PRT
<213> Homo sapiens

<400> 4120
His Leu Phe Leu Gln Ser Ser Gly Leu Ser Thr Trp Ile Gly Asn Gln
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Met Leu Ser Leu Ser Ser Leu Pro Pro Trp Ala Val Thr Leu Leu Ala
20 25 30
Cys Ile Leu Val Ser Ile Val Thr Glu Phe Val Ser Asn Pro Ala Thr
35 40 45
Ile Thr Ile Phe Leu Pro Ile Leu Cys Ser Leu Val Ser Asn Ala Glu
50 55 60
Leu Pro Asp Ile Gln Thr Gly Cys Pro Arg Gly Leu Glu Trp Gln Ala
65 70 75 80
Trp Leu Arg Ala Ala Ser Val Ala Val Gly Ser Pro Leu Val Thr Ala
85 90 95
His Ser Leu His
100

<210> 4121
<211> 2490
<212> DNA
<213> Homo sapiens

<400> 4121
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ctgggcctca tcgaggaaaa acaggcggag agccggcggg cggtctcggc ctgtcaggag
120
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540
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cttggcaaat ggaagaactt gagtgagagt tcagtctgca gtcctgtgct cacagacatc
1680

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1860
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1920
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<211> 494
<212> PRT
<213> Homo sapiens

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35 40 45
Ser Lys Pro Gly Pro Asp Pro Leu Asp Thr Arg Arg Leu Gln Gly Phe
50 55 60
Arg Leu Glu Glu Tyr Leu Ile Gly Gln Ser Ile Gly Lys Gly Cys Ser
65 70 75 80
Ala Ala Val Tyr Glu Ala Thr Met Pro Thr Leu Pro Gln Asn Leu Glu
85 90 95
Val Thr Lys Ser Thr Gly Leu Leu Pro Gly Arg Gly Pro Gly Thr Ser
100 105 110
Ala Pro Gly Glu Gly Gln Glu Arg Ala Pro Gly Ala Pro Ala Phe Pro
115 120 125
Leu Ala Ile Lys Met Met Trp Asn Ile Ser Ala Gly Ser Ser Ser Glu
130 135 140
Ala Ile Leu Asn Thr Met Ser Gln Glu Leu Val Pro Ala Ser Arg Val

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145                 150                 155                 160
Ala Leu Ala Gly Glu Tyr Gly Ala Val Thr Tyr Arg Lys Ser Lys Arg
                165                 170                 175
Gly Pro Lys Gln Leu Ala Pro His Pro Asn Ile Ile Arg Val Leu Arg
            180                 185                 190
Ala Phe Thr Ser Ser Val Pro Leu Leu Pro Gly Ala Leu Val Asp Tyr
        195                 200                 205
Pro Asp Val Leu Pro Ser Arg Leu His Pro Glu Gly Leu Gly His Gly
    210                 215                 220
Arg Thr Leu Phe Leu Val Met Lys Asn Tyr Pro Cys Thr Leu Arg Gln
225                 230                 235                 240
Tyr Leu Cys Val Asn Thr Pro Ser Pro Arg Leu Ala Ala Met Met Leu
                245                 250                 255
Leu Gln Leu Leu Glu Gly Val Asp His Leu Val Gln Gln Gly Ile Ala
            260                 265                 270
His Arg Asp Leu Lys Ser Asp Asn Ile Leu Val Glu Leu Asp Pro Asp
        275                 280                 285
Gly Cys Pro Trp Leu Val Ile Ala Asp Phe Gly Cys Cys Leu Ala Asp
    290                 295                 300
Glu Ser Ile Gly Leu Gln Leu Pro Phe Ser Ser Trp Tyr Val Asp Arg
305                 310                 315                 320
Gly Gly Asn Gly Cys Leu Met Ala Pro Glu Val Ser Thr Ala Arg Pro
                325                 330                 335
Gly Pro Arg Ala Val Ile Asp Tyr Ser Lys Ala Asp Ala Trp Ala Val
            340                 345                 350
Gly Ala Ile Ala Tyr Glu Ile Phe Gly Leu Val Asn Pro Phe Tyr Gly
        355                 360                 365
Gln Gly Lys Ala His Leu Glu Ser Arg Ser Tyr Gln Glu Ala Gln Leu
    370                 375                 380
Pro Ala Leu Pro Glu Ser Val Pro Pro Asp Val Arg Gln Leu Val Arg
385                 390                 395                 400
Ala Leu Leu Gln Arg Glu Ala Ser Lys Arg Pro Ser Ala Arg Val Ala
                405                 410                 415
Ala Asn Val Leu His Leu Ser Leu Trp Gly Glu His Ile Leu Ala Leu
            420                 425                 430
Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp Leu Leu Gln Gln Ser
        435                 440                 445
Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu Lys Cys Cys Val Glu
    450                 455                 460
Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu Glu Cys Glu Thr Leu
465                 470                 475                 480
Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg Ala Ala Leu
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<210> 4123
<211> 1095
<212> DNA
<213> Homo sapiens

<400> 4123
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120

ggtccccgtc gcggcaggcg cggtgcagcg ggaaacggag cgagagcagc tcctcgctgg
180
agaagcccgc ctctacgccc gcgctccgct cggcagcctg tgggacgccg ccgcagcgct
240
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360
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720
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<210> 4124
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<212> PRT
<213> Homo sapiens

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Gly Asp Leu Ala Thr Leu Cys Ser Leu Leu Gln Gln Thr Pro His Ala
35 40 45
His Leu Ala Ser Glu Asp Ser Phe Tyr Gly Trp Thr Pro Val His Trp
50 55 60
Ala Ala His Phe Gly Lys Leu Glu Cys Leu Val Gln Leu Val Arg Ala
65 70 75 80
Gly Ala Thr Leu Asn Val Ser Thr Thr Arg Tyr Ala Gln Thr Pro Ala
85 90 95
His Ile Ala Ala Phe Gly Gly His Pro Gln Cys Leu Val Trp Leu Ile

100 105 110
Gln Ala Gly Ala Asn Ile Asn Lys Pro Asp Cys Glu Gly Glu Thr Pro
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Ile His Lys Ala Ala Arg Ser Gly Ser Leu Glu Cys Ile Ser Ala Leu
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Val Ala Asn Gly Ala His Val Asp Ser Gln His
145 150 155

<210> 4125
<211> 4711
<212> DNA
<213> Homo sapiens

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ctcaaaagag tccagattca acaggctgcc aataaaggag caagatggct aggggttgaa
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<211> 820
<212> PRT
<213> Homo sapiens

<400> 4126
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Ala Leu Ala Ser Glu Gln Gly Ala Ser Cys Ser Val Arg Ala Pro Glu
35 40 45
Arg Lys Leu Arg Met Lys Leu Leu Trp Gln Ala Lys Met Ser Ser Ile
50 55 60
Gln Asp Trp Gly Glu Glu Val Glu Glu Gly Ala Val Tyr His Val Thr
65 70 75 80
Leu Lys Arg Val Gln Ile Gln Gln Ala Ala Asn Lys Gly Ala Arg Trp
85 90 95
Leu Gly Val Glu Gly Asp Gln Leu Pro Pro Gly His Thr Val Ser Gln
100 105 110
Tyr Glu Thr Cys Lys Ile Arg Thr Ile Lys Ala Gly Thr Leu Glu Lys
115 120 125
Leu Val Glu Asn Leu Leu Thr Ala Phe Gly Asp Asn Asp Phe Thr Tyr
130 135 140
Ile Ser Ile Phe Leu Ser Thr Tyr Arg Gly Phe Ala Ser Thr Lys Glu
145 150 155 160
Val Leu Glu Leu Leu Leu Asp Arg Tyr Gly Asn Leu Thr Ser Pro Asn
165 170 175
Cys Glu Glu Asp Gly Ser Gln Ser Ser Ser Glu Ser Lys Met Val Ile
180 185 190
Arg Asn Ala Ile Ala Ser Ile Leu Arg Ala Trp Leu Asp Gln Cys Ala
195 200 205
Glu Asp Phe Arg Glu Pro Pro His Phe Pro Cys Leu Gln Lys Leu Leu
210 215 220
Asp Tyr Leu Thr Arg Met Met Pro Gly Ser Asp Pro Glu Arg Arg Ala
225 230 235 240
Gln Asn Leu Leu Glu Gln Phe Gln Lys Gln Glu Val Glu Thr Asp Asn
245 250 255
Gly Leu Pro Asn Thr Ile Ser Phe Ser Leu Glu Glu Glu Glu Glu Leu
260 265 270
Glu Gly Gly Glu Ser Ala Glu Phe Thr Cys Phe Ser Glu Asp Leu Val
275 280 285
Ala Glu Gln Leu Thr Tyr Met Asp Ala Gln Leu Phe Lys Lys Val Val

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    290                 295                 300
Pro His His Cys Leu Gly Cys Ile Trp Ser Arg Arg Asp Lys Lys Glu
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Asn Lys His Leu Ala Pro Thr Ile Arg Ala Thr Ile Ser Gln Phe Asn
                325                 330                 335
Thr Leu Thr Lys Cys Val Val Ser Thr Ile Leu Gly Gly Lys Glu Leu
            340                 345                 350
Lys Thr Gln Gln Arg Ala Lys Ile Ile Glu Lys Trp Ile Asn Ile Ala
        355                 360                 365
His Glu Cys Arg Leu Leu Lys Asn Phe Ser Ser Leu Arg Ala Ile Val
    370                 375                 380
Ser Ala Leu Gln Ser Asn Ser Ile Tyr Arg Leu Lys Lys Thr Trp Ala
385                 390                 395                 400
Ala Val Pro Arg Asp Arg Met Leu Met Phe Glu Glu Leu Ser Asp Ile
                405                 410                 415
Phe Ser Asp His Asn Asn His Leu Thr Ser Arg Glu Leu Leu Met Lys
            420                 425                 430
Glu Gly Thr Ser Lys Phe Ala Asn Leu Asp Ser Ser Val Lys Glu Asn
        435                 440                 445
Gln Lys Arg Thr Gln Arg Arg Leu Gln Leu Gln Lys Asp Met Gly Val
    450                 455                 460
Met Gln Gly Thr Val Pro Tyr Leu Gly Thr Phe Leu Thr Asp Leu Thr
465                 470                 475                 480
Met Leu Asp Thr Ala Leu Gln Asp Tyr Ile Glu Gly Gly Leu Ile Asn
                485                 490                 495
Phe Glu Lys Arg Arg Arg Glu Phe Glu Val Ile Ala Gln Ile Lys Leu
            500                 505                 510
Leu Gln Ser Ala Cys Asn Ser Tyr Cys Met Thr Pro Asp Gln Lys Phe
        515                 520                 525
Ile Gln Trp Phe Gln Arg Gln Gln Leu Leu Thr Glu Glu Glu Ser Tyr
    530                 535                 540
Ala Leu Ser Cys Glu Ile Glu Ala Ala Ala Gly Ala Ser Thr Thr Ser
545                 550                 555                 560
Pro Lys Pro Arg Lys Ser Met Val Lys Arg Leu Ser Leu Leu Phe Leu
                565                 570                 575
Gly Ser Asp Met Ile Thr Ser Pro Thr Pro Thr Lys Glu Gln Pro Lys
            580                 585                 590
Ser Thr Ala Ser Gly Ser Ser Gly Glu Ser Met Asp Ser Val Ser Val
        595                 600                 605
Ser Ser Cys Glu Ser Asn His Ser Glu Ala Glu Glu Gly Ser Ile Thr
    610                 615                 620
Pro Met Asp Thr Pro Asp Glu Pro Gln Lys Lys Leu Ser Glu Ser Ser
625                 630                 635                 640
Ser Ser Cys Ser Ser Ile His Ser Met Asp Thr Asn Ser Ser Gly Met
                645                 650                 655
Ser Ser Leu Ile Asn Pro Leu Ser Ser Pro Pro Ser Cys Asn Asn Asn
            660                 665                 670
Pro Lys Ile His Lys Arg Ser Val Ser Val Thr Ser Ile Thr Ser Thr
        675                 680                 685
Val Leu Pro Pro Val Tyr Asn Gln Gln Asn Glu Asp Thr Cys Ile Ile
    690                 695                 700
Arg Ile Ser Val Glu Asp Asn Asn Gly Asn Met Tyr Lys Ser Ile Met
705                 710                 715                 720
Leu Thr Ser Gln Asp Lys Thr Pro Ala Val Ile Gln Arg Ala Met Leu
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Lys His Asn Leu Asp Ser Asp Pro Ala Glu Glu Tyr Glu Leu Val Gln
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Val Ile Ser Glu Asp Lys Glu Leu Val Ile Pro Asp Ser Ala Asn Val
        755                 760                 765
Phe Tyr Ala Met Asn Ser Gln Val Asn Phe Asp Phe Ile Leu Arg Lys
    770                 775                 780
Lys Asn Ser Met Glu Glu Gln Val Lys Leu Arg Ser Arg Thr Ser Leu
785                 790                 795                 800
Thr Leu Pro Arg Thr Ala Lys Arg Gly Cys Trp Ser Asn Arg His Ser
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Lys Ile Thr Leu
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<212> DNA
<213> Homo sapiens

<400> 4127
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ctggggcctc cagcctggga ctgctgtgat ggggtatcac ggtgatggtc ccattaaact
2160
tccactctgc aaacctgaaa aaaaaaaaa
2189

<210> 4128
<211> 445
<212> PRT
<213> Homo sapiens

<400> 4128
Pro Cys Phe Leu Pro Ser Ala Thr Ser Lys Leu Ser Gly Ala Val Glu
1 5 10 15
Gln Trp Leu Ser Ala Ala Glu Arg Leu Tyr Gly Pro Tyr Met Trp Gly
20 25 30
Arg Tyr Asp Ile Val Phe Leu Pro Pro Ser Phe Pro Ile Val Ala Met
35 40 45
Glu Asn Pro Cys Leu Thr Phe Ile Ile Ser Ser Ile Leu Glu Ser Asp

```
    50                  55                  60
Glu Phe Leu Val Ile Asp Val Ile His Glu Val Ala His Ser Trp Phe
65                  70                  75                  80
Gly Asn Ala Val Thr Asn Ala Thr Trp Glu Glu Met Trp Leu Ser Glu
                85                  90                  95
Gly Leu Ala Thr Tyr Ala Gln Arg Arg Ile Thr Thr Glu Thr Tyr Gly
            100                 105                 110
Ala Ala Phe Thr Cys Leu Glu Thr Ala Phe Arg Leu Asp Ala Leu His
        115                 120                 125
Arg Gln Met Lys Leu Leu Gly Glu Asp Ser Pro Val Ser Lys Leu Gln
    130                 135                 140
Val Lys Leu Glu Pro Gly Val Asn Pro Ser His Leu Met Asn Leu Phe
145                 150                 155                 160
Thr Tyr Glu Lys Gly Tyr Cys Phe Val Tyr Tyr Leu Ser Gln Leu Cys
                165                 170                 175
Gly Asp Pro Gln Arg Phe Asp Asp Phe Leu Arg Ala Tyr Val Glu Lys
            180                 185                 190
Tyr Lys Phe Thr Ser Val Val Ala Gln Asp Leu Leu Asp Ser Phe Leu
        195                 200                 205
Ser Phe Phe Pro Glu Leu Lys Glu Gln Ser Val Asp Cys Arg Ala Gly
    210                 215                 220
Leu Glu Phe Glu Arg Trp Leu Asn Ala Thr Gly Pro Pro Leu Ala Glu
225                 230                 235                 240
Pro Asp Leu Ser Gln Gly Ser Ser Leu Thr Arg Pro Val Glu Ala Leu
                245                 250                 255
Phe Gln Leu Trp Thr Ala Glu Pro Leu Asp Gln Ala Ala Ala Ser Ala
            260                 265                 270
Ser Ala Ile Asp Ile Ser Lys Trp Arg Thr Phe Gln Thr Ala Leu Phe
        275                 280                 285
Leu Asp Arg Leu Leu Asp Gly Ser Pro Leu Pro Gln Glu Val Val Met
    290                 295                 300
Ser Leu Ser Lys Cys Tyr Ser Ser Leu Leu Asp Ser Met Asn Ala Glu
305                 310                 315                 320
Ile Arg Ile Arg Trp Leu Gln Ile Val Val Arg Asn Asp Tyr Tyr Pro
                325                 330                 335
Asp Leu His Arg Val Arg Arg Phe Leu Glu Ser Gln Met Ser Arg Met
            340                 345                 350
Tyr Thr Ile Pro Leu Tyr Glu Asp Leu Cys Thr Gly Ala Leu Lys Ser
        355                 360                 365
Phe Ala Leu Glu Val Phe Tyr Gln Thr Gln Gly Arg Leu His Pro Asn
    370                 375                 380
Leu Arg Arg Ala Ile Gln Gln Ile Leu Ser Gln Gly Leu Gly Ser Ser
385                 390                 395                 400
Thr Glu Pro Ala Ser Glu Pro Ser Thr Glu Leu Gly Lys Ala Glu Ala
                405                 410                 415
Asp Thr Asp Ser Asp Ala Gln Ala Leu Leu Leu Gly Asp Glu Ala Pro
            420                 425                 430
Ser Ser Ala Ile Ser Leu Arg Asp Val Asn Val Ser Ala
        435                 440                 445
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<210> 4129
<211> 1749
<212> DNA
<213> Homo sapiens

<400> 4129
ctgggaccag ctctgctcct tgcaccccgc tccctgcctg gacacaggct cactcgctgc
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cttcttctgg gggaaaccag cttcttgcca gccacagctg ctgcctccgc cactggccac
120
cgcccctgtc ctgggagtcc cttggcccaa acacccacct gacttagtgg ctcctctgca
180
ggaaaggggg ctgccccctg cgttcctcca tccaatcatg agctggtgcc catcaccact
240
gagaatgcac cagagaatgt agtggaccag ggagcaggag cctcccgggg tggaaacaca
300
cggaaaagcc tcgaggacaa cggctccacc agggtcaccc cgagtgtcca gccccacctc
360
cagcccatca gaaacatgag tgtgagccgg accatggagg acagctgtga gctggacctg
420
gtgtacgtca cagagaggat catcgctgtc tccttcccca gcacagccaa tgaggagaac
480
ttccggagca acctccgtga ggtggcgcag atgctcaagt ccaaacatgg aggcaactac
540
ctgctgttca acctctctga gcggagacct gacatcacga agctccatgc caaggtactg
600
gaatttggct ggcccgacct ccacacccca gccctggaga agatctgcag catctgtaag
660
gccatggaca catggctcaa tgcagaccct cacaatgtcg ttgttctaca caacaaggga
720
aaccgaggca ggataggagt tgtcatcgcg gcttacatgc actacagcaa catttctgcc
780
agtgcggacc aggctctgga ccggtttgca atgaagcggt tctatgagga taagattgtg
840
cccattggcc agccatccca aagaaggtac gtgcattact tcagtggcct gctctccggc
900
tccatcaaaa tgaacaacaa gcccttgttt ctgcaccacg tgatcatgca cggcatcccc
960
aactttgagt ctaaaggagg atgtcggcca tttctccgca tctaccaggc catgcaacct
1020
gtgtacacat ctggcatcta caacatccca ggagacagcc agactagcgt ctgcatcacc
1080
atcgagccag gactgctctt gaagggagac atcttgctga agtgctacca caagaagttc
1140
cgaagcccag cccgagacgt catcttccgt gtgcagttcc acacctgtgc catccatgcc
1200
tgggggggttg tctttgggaa ggaggacctt gatgatgctt tcaaagatga tcgatttcca
1260
gagtatggca aagtggagtt tgtatttttct tatgggccag agaaaattca aggcatggag
1320
cacctggaga acgggccgag cgtgtctgtg gactataaca cctccgaccc cctcatccgc
1380
tgggactcct acgacaactt cagtgggcat cgagatgacg gcatggagga ggtggtggga
1440
cacacgcagg ggccactaga tgggagcctg tatgctaagg tgaagaagaa agactccctg
1500
cacggcagca ccggggctgt taatgccaca cgtcctacac tgtcggccac ccccaaccac
1560

gtggaacaca cgctttctgt gagcagcgac tcgggcaact ccacagcctc caccaagacc
1620
gacaagaccg acgagcctgt ccccggggcc tccagtgccc atgctgcccg cactgtgacc
1680
atcctggttt ggcaattcat cgtccaggat gtctgtctcc cgctcagatg ctaacgcccc
1740
accattgac
1749

<210> 4130
<211> 523
<212> PRT
<213> Homo sapiens

<400> 4130
Leu Ser Gly Ser Ser Ala Gly Lys Gly Ala Ala Pro Cys Val Pro Pro
1 5 10 15
Ser Asn His Glu Leu Val Pro Ile Thr Thr Glu Asn Ala Pro Glu Asn
20 25 30
Val Val Asp Gln Gly Ala Gly Ala Ser Arg Gly Gly Asn Thr Arg Lys
35 40 45
Ser Leu Glu Asp Asn Gly Ser Thr Arg Val Thr Pro Ser Val Gln Pro
50 55 60
His Leu Gln Pro Ile Arg Asn Met Ser Val Ser Arg Thr Met Glu Asp
65 70 75 80
Ser Cys Glu Leu Asp Leu Val Tyr Val Thr Glu Arg Ile Ile Ala Val
85 90 95
Ser Phe Pro Ser Thr Ala Asn Glu Glu Asn Phe Arg Ser Asn Leu Arg
100 105 110
Glu Val Ala Gln Met Leu Lys Ser Lys His Gly Gly Asn Tyr Leu Leu
115 120 125
Phe Asn Leu Ser Glu Arg Arg Pro Asp Ile Thr Lys Leu His Ala Lys
130 135 140
Val Leu Glu Phe Gly Trp Pro Asp Leu His Thr Pro Ala Leu Glu Lys
145 150 155 160
Ile Cys Ser Ile Cys Lys Ala Met Asp Thr Trp Leu Asn Ala Asp Pro
165 170 175
His Asn Val Val Val Leu His Asn Lys Gly Asn Arg Gly Arg Ile Gly
180 185 190
Val Val Ile Ala Ala Tyr Met His Tyr Ser Asn Ile Ser Ala Ser Ala
195 200 205
Asp Gln Ala Leu Asp Arg Phe Ala Met Lys Arg Phe Tyr Glu Asp Lys
210 215 220
Ile Val Pro Ile Gly Gln Pro Ser Gln Arg Arg Tyr Val His Tyr Phe
225 230 235 240
Ser Gly Leu Leu Ser Gly Ser Ile Lys Met Asn Asn Lys Pro Leu Phe
245 250 255
Leu His His Val Ile Met His Gly Ile Pro Asn Phe Glu Ser Lys Gly
260 265 270
Gly Cys Arg Pro Phe Leu Arg Ile Tyr Gln Ala Met Gln Pro Val Tyr
275 280 285
Thr Ser Gly Ile Tyr Asn Ile Pro Gly Asp Ser Gln Thr Ser Val Cys
290 295 300
Ile Thr Ile Glu Pro Gly Leu Leu Leu Lys Gly Asp Ile Leu Leu Lys

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305                 310                 315                 320
Cys Tyr His Lys Lys Phe Arg Ser Pro Ala Arg Asp Val Ile Phe Arg
                325                 330                 335
Val Gln Phe His Thr Cys Ala Ile His Ala Trp Gly Val Val Phe Gly
            340                 345                 350
Lys Glu Asp Leu Asp Asp Ala Phe Lys Asp Asp Arg Phe Pro Glu Tyr
        355                 360                 365
Gly Lys Val Glu Phe Val Phe Ser Tyr Gly Pro Glu Lys Ile Gln Gly
    370                 375                 380
Met Glu His Leu Glu Asn Gly Pro Ser Val Ser Val Asp Tyr Asn Thr
385                 390                 395                 400
Ser Asp Pro Leu Ile Arg Trp Asp Ser Tyr Asp Asn Phe Ser Gly His
                405                 410                 415
Arg Asp Asp Gly Met Glu Glu Val Val Gly His Thr Gln Gly Pro Leu
            420                 425                 430
Asp Gly Ser Leu Tyr Ala Lys Val Lys Lys Lys Asp Ser Leu His Gly
        435                 440                 445
Ser Thr Gly Ala Val Asn Ala Thr Arg Pro Thr Leu Ser Ala Thr Pro
    450                 455                 460
Asn His Val Glu His Thr Leu Ser Val Ser Ser Asp Ser Gly Asn Ser
465                 470                 475                 480
Thr Ala Ser Thr Lys Thr Asp Lys Thr Asp Glu Pro Val Pro Gly Ala
                485                 490                 495
Ser Ser Ala His Ala Ala Arg Thr Val Thr Ile Leu Val Trp Gln Phe
            500                 505                 510
Ile Val Gln Asp Val Cys Leu Pro Leu Arg Cys
        515                 520
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<210> 4131
<211> 608
<212> DNA
<213> Homo sapiens

<400> 4131
cggccggcgc gggcgcggcg ggccgggcag gggcgagggg cgccgggtct tgccccagaa
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gctgcgggca catccacgcc tgaaatgcgg cgctcagtcc tggtcaggaa cccaggccac
120
aaaggcctga gacccgttta tgaagagctc gactctgact ccgaggacct agaccccaat
180
cctgaagatc tggacccggt ttctgaagac ccagagcctg atcctgaaga cctcaacact
240
gtcccggaag acgtggaccc cagctatgaa gatctggagc ccgtctcgga ggatctggac
300
cccgacgccg aagctccggg ctcggaaccc caagatcccg accccatgtc ttcgagtttc
360
gacctcgatc cagatgtgat tggccccgta cccctgattc tcgatcctaa cagcgacacc
420
ctcagccccg gcgatccaaa agtggacccc nnatctcctc tggcctcact gcgagccccc
480
aggtcttggc caccagcccc gcggtgctcc ccgcccccgc cagcccgccc cggcccttct
540
cctgcccgga ttgcggcgaa gccttccgcc gcagctccgg gctgagccag catcgccgca
600

cgcacagc
608

<210> 4132
<211> 194
<212> PRT
<213> Homo sapiens

<400> 4132
Arg Pro Ala Arg Ala Arg Arg Ala Gly Gln Gly Arg Gly Ala Pro Gly
1 5 10 15
Leu Ala Pro Glu Ala Ala Gly Thr Ser Thr Pro Glu Met Arg Arg Ser
20 25 30
Val Leu Val Arg Asn Pro Gly His Lys Gly Leu Arg Pro Val Tyr Glu
35 40 45
Glu Leu Asp Ser Asp Ser Glu Asp Leu Asp Pro Asn Pro Glu Asp Leu
50 55 60
Asp Pro Val Ser Glu Asp Pro Glu Pro Asp Pro Glu Asp Leu Asn Thr
65 70 75 80
Val Pro Glu Asp Val Asp Pro Ser Tyr Glu Asp Leu Glu Pro Val Ser
85 90 95
Glu Asp Leu Asp Pro Asp Ala Glu Ala Pro Gly Ser Glu Pro Gln Asp
100 105 110
Pro Asp Pro Met Ser Ser Ser Phe Asp Leu Asp Pro Asp Val Ile Gly
115 120 125
Pro Val Pro Leu Ile Leu Asp Pro Asn Ser Asp Thr Leu Ser Pro Gly
130 135 140
Asp Pro Lys Val Asp Pro Xaa Ser Pro Leu Ala Ser Leu Arg Ala Pro
145 150 155 160
Arg Ser Trp Pro Pro Ala Pro Arg Cys Ser Pro Pro Pro Pro Ala Arg
165 170 175
Pro Gly Pro Ser Pro Ala Arg Ile Ala Ala Lys Pro Ser Ala Ala Ala
180 185 190
Pro Gly

<210> 4133
<211> 1646
<212> DNA
<213> Homo sapiens

<400> 4133
ttttttttt ttttttttt ttttttttt ttttttttt ttaacgagtc tcaaattttt
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attttgatgg caaaaatcac acagggaaga acaaaaatta tccatgacaa actaggagtg
120
gaaatgggct gggagacaca gaaaatgggt gcccacagtt cctgggatcc ctcctggaat
180
cctgggtttc cctcctagga ccctgcaagg taccctacgt gcctcctgga acccccccc
240
accccggagg tcccaaggaa cccagtttga gaaccaaggc tttaggccaa ggacttcctt
300
gcacaagaag gtgcagatgt acagggatgg ttcagacagt ggcctcaacc tcaatggctt
360

catcctcctc ctccagcagg ctgtaggaag catggctctg gcaaggccgc tgcaggggt
420
gggccaacag tttcgccatg cagttgtgca actccagggc tggcccagcc agtgccacct
480
catacttgta gctggtaccc ttggtatcca ggctgcccat gaaggcaaac atatccttcc
540
aactcatctc ctcctccttc tcctcagtgc cattgtggat gtaaacaacg tcaaagaaga
600
aatatgggca ctggaacatt ttcttcatgg gctccgtcaa ggagaactgg ggctggcaag
660
gtggacggct gtagacaagg atggtgcgga ccacatatgg cgggggaatc gtctgcacgt
720
tctctgtgac cggaagctca gttttctgct ggatgaggct gaaaagtcct tccagattga
780
aggtggaaca ggaggccgtc tccagatcat agaggcagct acagagctcg cgggggtcgg
840
aggtcaggcc agacagccag gccgtgtcat cgttcaccac caccagtgca aactcgtggc
900
ttttgtcgat cttgtgtttt gtccgcacga acatctcaat catcttctgg gagacattga
960
gggcgttggt tttggagccg ttgaacgact ccagctttgg cagtgacatt tcctctgaca
1020
ggtccaggca gataatcact ttctctggac agttgaccct tggtgtccga atttggacct
1080
caggggctgg cgggggcacc tgccaggact tagggccggc tcctgaagtg ttgaggctcc
1140
catcatcagc actggcggcc tcaccctcac cctcgctgcg gctgcccacg ctggcctgtg
1200
cccctactgc ccggtcctca gccccttcag gattggagcg agtgcggggc cgaggctctg
1260
ccgagtgctc ctcttcctcc tcctcctctt cagtggggct gctgggctct gccacttcca
1320
tggctcctgt gtggcttcgg ctcaccgtag cctgaacctc cttctaaatc agccgccgac
1380
tcactaggaa gccgccatct ttacagccgg aagttgtacg gcgcagcccc gacgcctcct
1440
gggaaatgta gttcagcggg ctgcagaaca agcagagaca gaaactggtt gaggctagaa
1500
agaacttgga aactgatagg ctgaaactgg gttgggggtg gggtttggag tgagagctgc
1560
ctggagctgg gtgcggcggg acctggaatg tgattggcta cactggagca aagtatgaaa
1620
tgtgattgga ttaaaaaaat tagtga
1646

<210> 4134
<211> 329
<212> PRT
<213> Homo sapiens

<400> 4134
Met Glu Val Ala Glu Pro Ser Ser Pro Thr Glu Glu Glu Glu Glu Glu
 1   5   10   15
Glu Glu His Ser Ala Glu Pro Arg Pro Arg Thr Arg Ser Asn Pro Glu

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            20                  25                  30
Gly Ala Glu Asp Arg Ala Val Gly Ala Gln Ala Ser Val Gly Ser Arg
        35                  40                  45
Ser Glu Gly Glu Gly Glu Ala Ala Ser Ala Asp Asp Gly Ser Leu Asn
    50                  55                  60
Thr Ser Gly Ala Gly Pro Lys Ser Trp Gln Val Pro Pro Pro Ala Pro
65                  70                  75                  80
Glu Val Gln Ile Arg Thr Pro Arg Val Asn Cys Pro Glu Lys Val Ile
                85                  90                  95
Ile Cys Leu Asp Leu Ser Glu Glu Met Ser Leu Pro Lys Leu Glu Ser
            100                 105                 110
Phe Asn Gly Ser Lys Thr Asn Ala Leu Asn Val Ser Gln Lys Met Ile
        115                 120                 125
Glu Met Phe Val Arg Thr Lys His Lys Ile Asp Lys Ser His Glu Phe
    130                 135                 140
Ala Leu Val Val Val Asn Asp Asp Thr Ala Trp Leu Ser Gly Leu Thr
145                 150                 155                 160
Ser Asp Pro Arg Glu Leu Cys Ser Cys Leu Tyr Asp Leu Glu Thr Ala
                165                 170                 175
Ser Cys Ser Thr Phe Asn Leu Glu Gly Leu Phe Ser Leu Ile Gln Gln
            180                 185                 190
Lys Thr Glu Leu Pro Val Thr Glu Asn Val Gln Thr Ile Pro Pro Pro
        195                 200                 205
Tyr Val Val Arg Thr Ile Leu Val Tyr Ser Arg Pro Pro Cys Gln Pro
    210                 215                 220
Gln Phe Ser Leu Thr Glu Pro Met Lys Lys Met Phe Gln Cys Pro Tyr
225                 230                 235                 240
Phe Phe Phe Asp Val Val Tyr Ile His Asn Gly Thr Glu Glu Lys Glu
                245                 250                 255
Glu Glu Met Ser Trp Lys Asp Met Phe Ala Phe Met Gly Ser Leu Asp
            260                 265                 270
Thr Lys Gly Thr Ser Tyr Lys Tyr Glu Val Ala Leu Ala Gly Pro Ala
        275                 280                 285
Leu Glu Leu His Asn Cys Met Ala Lys Leu Leu Ala His Pro Leu Gln
    290                 295                 300
Arg Pro Cys Gln Ser His Ala Ser Tyr Ser Leu Leu Glu Glu Glu Asp
305                 310                 315                 320
Glu Ala Ile Glu Val Glu Ala Thr Val
                325
```

<210> 4135
<211> 388
<212> DNA
<213> Homo sapiens

<400> 4135
acgcgtggtg gccctggaca tgtacctcac tcagcaacgc atctccgacc cagtgatgga
60
gggtctgcga tcagccgtac gctatgacaa aacctatttc gacaagatcg tggccagcct
120
tctgccattg ctggaaaaac tgaccacagg ccggattgca gagctgctat ctcccgacta
180
catggatctt gaggacccac gaccaatctt tgactggatg cagatcatcc gcaaacgggc
240

agtggtctat gtcggcctgg acgctttatc tgatacagag gtagctgcag cggtgggcaa
300
ctcgatgttc agcgacctgg tgtcagttgc gggtcacatc tataagtttg gcatcgatga
360
tggcttgccc ggggccaccg gcggcaag
388

<210> 4136
<211> 123
<212> PRT
<213> Homo sapiens

<400> 4136
Met Tyr Leu Thr Gln Gln Arg Ile Ser Asp Pro Val Met Glu Gly Leu
 1   5   10   15
Arg Ser Ala Val Arg Tyr Asp Lys Thr Tyr Phe Asp Lys Ile Val Ala
            20   25   30
Ser Leu Leu Pro Leu Leu Glu Lys Leu Thr Thr Gly Arg Ile Ala Glu
        35   40   45
Leu Leu Ser Pro Asp Tyr Met Asp Leu Glu Asp Pro Arg Pro Ile Phe
    50   55   60
Asp Trp Met Gln Ile Ile Arg Lys Arg Ala Val Val Tyr Val Gly Leu
65   70   75   80
Asp Ala Leu Ser Asp Thr Glu Val Ala Ala Ala Val Gly Asn Ser Met
                85   90   95
Phe Ser Asp Leu Val Ser Val Ala Gly His Ile Tyr Lys Phe Gly Ile
            100   105   110
Asp Asp Gly Leu Pro Gly Ala Thr Gly Gly Lys
        115   120

<210> 4137
<211> 2255
<212> DNA
<213> Homo sapiens

<400> 4137
cggacctccc gcgcgccccg cacccgaccg gctcagccgc cggcagcgta acacgcccta
60
cgctcgcttg ctcgccggcc tcagggcagg caggcgggcg cgggagaccc cgccggggcc
120
gagacttggg gcgggcgacg aggaccaggt tacggcctcc tcgccatgtc ctcggcctgc
180
gacgcgggcg accactaccc cctgcacctc ctagtctgga aaaacgacta ccggcagctc
240
gagaaggagc tgcagggcca gaatgtggag gctgtggacc cacgaggtcg aacattattg
300
catcttgctg tttccttggg acatttggaa tctgctcgag tcttactccg acataaagca
360
gatgtgacaa aagaaaatcg ccagggatgg acagttttac atgaggctgt gagcactggc
420
gatcctgaga tggtgtacac agttctccaa catcgagact accacaacac atccatggcc
480
cttgagggag ttcctgagct gctccaaaaa attctcgagg ctccggattt ctatgtgcag
540

atgaaatggg aattcaccag ctgggtgccc ttggtttcta gaatatgccc aaatgatgtc
600
tgtcgcatct ggaaaagtgg tgccaaactg cgcgtcgata tcacattgct gggatttgaa
660
aacatgagct ggataagagg gaggcgtagt tttatattta agggagaaga caactgggcg
720
gagttaatgg aagtcaacca tgatgacaaa gtggtcacca ccgaacgctt cgacctttcc
780
caagaaatgg agcgcctcac tctggacttg atgaagccaa aaagcaggga agttgagcgg
840
cggctcacaa gccctgtcat taacaccagc ctcgatacta aaaatattgc ttttgaaaga
900
actaaatccg gattctgggg ctggaggaca gataaagcag aagttgttaa tggttacgaa
960
gcaaaggttt acacagtaaa caatgtgaat gtgatcacca aaatacgcac agaacatctg
1020
accgaggagg aaaaaaagag atataaagca gacaggaacc cgctggaatc tttgctggga
1080
actgtggaac accaatttgg tgcacaaggg gacctcacca cggaatgtgc tactgcaaac
1140
aaccccacag ccatcacgcc tgatgagtac ttcaatgaag agtttgatct gnaaagacag
1200
ggacattggn aaggccgaaa gagctgacga ttagaacaca gaagtttaaa gcaatgttgt
1260
ggatgtgtga agagtttccc ctctctctgg tggagcaggt cattcccatc attgacctaa
1320
tggctcgaac gagtgctcat tttgcaagac tgagagattt catcaaattg gaattcccac
1380
ctggatttcc tgtcaaaata gaaattccct tgtttcatgt cttaaatgca cggattacat
1440
ttggaaatgt taatggctgt agcactgccg aagaatctgt atctcaaaat gtggaaggga
1500
cccaggctga ttcagcttcc cacatcacaa actttgaggt tgatcaatct gtgtttgaaa
1560
ttcccgaatc ttactatgtt caagacaatg gcagaaatgt gcatttgcaa gatgaagatt
1620
acgagataat gcagtttgcc atccagcaaa gtctgctgga gtccagcagg agccaggaac
1680
tttcaggacc agcttcgaat ggagggatca gccagacaaa cacctatgac gcccagtatg
1740
agagggccat ccaggagagc ctcctcacca gcacagaagg cctgtgcccc agcgccctga
1800
gcgagacaag ccgttttgat aatgacttgc agctagccat ggagctctct gccaaagagc
1860
tggaggaatg ggagctccgg ctccaggagg aagaggctga gctccagcaa gtcttacagc
1920
tgtcactcac tgacaaatag acctttcagc ctgtgagcct ctgcacaaag cagaggctgt
1980
gggctgtcac agatgctgtg tcaaccaggg ccctagggct aagggcctgc accttgcgtg
2040
catgcagcag gcaacaactg ccccttcttt atgcagaggt gcagaaccag ggactcctgg
2100
gcccatccag gctgctccct ggggtggaga agggaccagg gattgcaggc cccatctcca
2160

ggctaagggg aggagagcat catcactttc cattagctgt attggcttgc aggtcacatt
2220
tttactgcca gcattagaca aaaccccaat ccccg
2255

<210> 4138
<211> 353
<212> PRT
<213> Homo sapiens

<400> 4138
Met Ser Ser Ala Cys Asp Ala Gly Asp His Tyr Pro Leu His Leu Leu
1 5 10 15
Val Trp Lys Asn Asp Tyr Arg Gln Leu Glu Lys Glu Leu Gln Gly Gln
20 25 30
Asn Val Glu Ala Val Asp Pro Arg Gly Arg Thr Leu Leu His Leu Ala
35 40 45
Val Ser Leu Gly His Leu Glu Ser Ala Arg Val Leu Leu Arg His Lys
50 55 60
Ala Asp Val Thr Lys Glu Asn Arg Gln Gly Trp Thr Val Leu His Glu
65 70 75 80
Ala Val Ser Thr Gly Asp Pro Glu Met Val Tyr Thr Val Leu Gln His
85 90 95
Arg Asp Tyr His Asn Thr Ser Met Ala Leu Glu Gly Val Pro Glu Leu
100 105 110
Leu Gln Lys Ile Leu Glu Ala Pro Asp Phe Tyr Val Gln Met Lys Trp
115 120 125
Glu Phe Thr Ser Trp Val Pro Leu Val Ser Arg Ile Cys Pro Asn Asp
130 135 140
Val Cys Arg Ile Trp Lys Ser Gly Ala Lys Leu Arg Val Asp Ile Thr
145 150 155 160
Leu Leu Gly Phe Glu Asn Met Ser Trp Ile Arg Gly Arg Arg Ser Phe
165 170 175
Ile Phe Lys Gly Glu Asp Asn Trp Ala Glu Leu Met Glu Val Asn His
180 185 190
Asp Asp Lys Val Val Thr Thr Glu Arg Phe Asp Leu Ser Gln Glu Met
195 200 205
Glu Arg Leu Thr Leu Asp Leu Met Lys Pro Lys Ser Arg Glu Val Glu
210 215 220
Arg Arg Leu Thr Ser Pro Val Ile Asn Thr Ser Leu Asp Thr Lys Asn
225 230 235 240
Ile Ala Phe Glu Arg Thr Lys Ser Gly Phe Trp Gly Trp Arg Thr Asp
245 250 255
Lys Ala Glu Val Val Asn Gly Tyr Glu Ala Lys Val Tyr Thr Val Asn
260 265 270
Asn Val Asn Val Ile Thr Lys Ile Arg Thr Glu His Leu Thr Glu Glu
275 280 285
Glu Lys Lys Arg Tyr Lys Ala Asp Arg Asn Pro Leu Glu Ser Leu Leu
290 295 300
Gly Thr Val Glu His Gln Phe Gly Ala Gln Gly Asp Leu Thr Thr Glu
305 310 315 320
Cys Ala Thr Ala Asn Asn Pro Thr Ala Ile Thr Pro Asp Glu Tyr Phe
325 330 335
Asn Glu Glu Phe Asp Leu Xaa Arg Gln Gly His Trp Xaa Gly Arg Lys

340 345 350
Ser

<210> 4139
<211> 431
<212> DNA
<213> Homo sapiens

<400> 4139
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ggtaagtgtc ctgttcctgt gcgcgtgccc tgagccccgc ctgggtccta ggccacccac
180
cgacactgcc ccccacacag ccgggaagtc cacctttctc aagaagcacc tcgtgtcggc
240
cggatatgtc cacgtgaaca gggtatgacc aggcttttgc cgccccaaat ctattataaa
300
gttcccatct ccacctctca actggtttgg ggcggctttc ctccatcatt gcctccccgt
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420
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431

<210> 4140
<211> 50
<212> PRT
<213> Homo sapiens

<400> 4140
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Val Val Ala Val Gly Phe Pro Gly Gly Lys Cys Pro Val Pro Val Arg
35 40 45
Val Pro
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<210> 4141
<211> 1182
<212> DNA
<213> Homo sapiens

<400> 4141
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120
cgaaggagga gccggacact tgtctcccgt ctccgagctg ctccccaccc ctggaggaga
180

gaccccccccc tcggctcggc gccttctgcg tctcccggct ggtggggaag cctctgcgcc
240
gccggcacca tgagtgaaca gagtatctgt caggcaagag ctgctgtgat ggtttatgat
300
gatgccaata agaagtgggt gccagctggt ggctcaactg gattcagcag agttcatatc
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gtcgtgataa actgtgccat tcctaaaggg ttgaagtaca atcaagctac acagaccttc
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aatgtcttcg caagtgccat gatgcatgcc ttagaagtgt taaattcaca ggaaacaggg
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ccaacattgc ctagacaaaa ctcacaacta cctgctcaag ttcaaaatgg cccatcccaa
660
gaagaattgg aaattcaaag aagacaacta caagaacagc aacggcaaaa ggagctggag
720
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780
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960
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1080
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1140
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1182

<210> 4142
<211> 311
<212> PRT
<213> Homo sapiens

<400> 4142
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20 25 30
Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg Val
35 40 45
Val Gly Arg Lys Ile Gln Asp His Gln Val Val Ile Asn Cys Ala Ile
50 55 60
Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln Trp
65 70 75 80
Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu Asp
85 90 95
Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu Asn

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            100                 105                 110
Ser Gln Glu Thr Gly Pro Thr Leu Pro Arg Gln Asn Ser Gln Leu Pro
        115                 120                 125
Ala Gln Val Gln Asn Gly Pro Ser Gln Glu Glu Leu Glu Ile Gln Arg
    130                 135                 140
Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu Leu Glu Arg Glu Arg
145                 150                 155                 160
Leu Glu Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu
                165                 170                 175
Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu Glu
            180                 185                 190
Arg Glu Arg Gln Glu Arg Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu
        195                 200                 205
Arg Leu Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu Arg Leu Asp Arg
    210                 215                 220
Glu Arg Glu Arg Gln Glu Arg Glu Arg Leu Glu Arg Leu Glu Arg Glu
225                 230                 235                 240
Arg Gln Glu Arg Glu Arg Gln Glu Gln Leu Glu Arg Glu Gln Leu Glu
                245                 250                 255
Trp Glu Arg Glu Arg Arg Ile Ser Ser Ala Ala Ala Pro Ala Ser Val
            260                 265                 270
Glu Thr Pro Leu Asn Ser Val Leu Gly Asp Ser Ser Ala Ser Glu Pro
        275                 280                 285
Gly Leu Gln Ala Ala Ser Gln Pro Ala Glu Thr Pro Ser Gln Gln Gly
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Ile Val Leu Gly Pro Leu Ala
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<210> 4143
<211> 1773
<212> DNA
<213> Homo sapiens

<400> 4143
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cgttagtaga cactgagcag agaagcttga agaacgggga tcctctcctg tgggcagggg
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240
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300
caggccggga agaaattcct ttcctttggg aagaaccacc aacgctcagt ccaagctcac
360
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420
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480
aaaaaaaaaa aggccacata tcccagttct cagagaaatc ctggattact aaacatcccc
540
tgcctgtggc acctggaatg ggtgacttgt caaaatctcc ctcaagacgt tttgtgcgtt
600
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tgccgtggga gggaatggtg gggagtcagg gtggctgggg ggcactaggc cacttcacca
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720
tgccctggca gtgcgcaccc tgtgggcacc aagcagggag tgaagaccct cagaacacag
780
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1773

<210> 4144
<211> 231
<212> PRT
<213> Homo sapiens

<400> 4144
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20 25 30
Gly Asp Glu Glu Glu Phe Phe Glu Ile Arg Thr Glu Trp Ser Asp Arg
35 40 45
Ser Val Leu Tyr Leu His Arg Ser Leu Ala Asp Leu Gly Arg Leu Trp

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    50                  55                  60
Gln Arg Leu Arg Asp Ala Phe Pro Glu Asp Arg Ser Glu Leu Ala Gln
65                  70                  75                  80
Gly Pro Leu Arg Gln Gly Leu Val Ala Ile Lys Glu Ala His Asp Ile
                85                  90                  95
Glu Thr Arg Leu Asn Glu Val Glu Lys Leu Leu Lys Thr Ile Ile Ser
            100                 105                 110
Met Pro Cys Lys Tyr Ser Arg Ser Glu Val Val Leu Thr Phe Phe Glu
        115                 120                 125
Arg Ser Pro Leu Asp Gln Val Leu Lys Asn Asp Asn Val His Lys Ile
    130                 135                 140
Gln Pro Ser Phe Gln Ser Pro Val Lys Ile Ser Glu Ile Met Arg Ser
145                 150                 155                 160
Asn Gly Phe Cys Leu Ala Asn Thr Glu Thr Ile Val Ile Asp His Ser
                165                 170                 175
Ile Pro Asn Gly Arg Asp Gln Gln Leu Gly Val Asp Pro Thr Glu His
            180                 185                 190
Leu Phe Glu Asn Gly Ser Glu Phe Pro Ser Glu Leu Glu Asp Gly Asp
        195                 200                 205
Asp Pro Ala Ala Tyr Val Thr Asn Leu Ser Tyr Tyr His Leu Val Pro
    210                 215                 220
Phe Glu Thr Asp Ile Trp Asp
225                 230
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<210> 4145
<211> 400
<212> DNA
<213> Homo sapiens

<400> 4145
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240
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300
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<210> 4146
<211> 133
<212> PRT
<213> Homo sapiens

<400> 4146
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Trp Ser Gly Pro Ser Pro Glu Gly Pro Val Pro Leu Thr Gly Glu Glu
        35                  40                  45
Leu Asp Leu Arg Leu Ile Arg Thr Lys Gly Gly Val Asp Ala Ala Leu
    50                  55                  60
Glu Tyr Ala Lys Thr Trp Ser Arg Tyr Ala Lys Glu Leu Leu Ala Trp
65                  70                  75                  80
Thr Glu Lys Arg Ala Ser Tyr Glu Leu Glu Phe Ala Lys Ser Thr Met
                85                  90                  95
Lys Ile Ala Glu Ala Gly Lys Val Ser Ile Gln Gln Gln Ser His Met
            100                 105                 110
Pro Leu Gln Tyr Ile Tyr Thr Leu Phe Leu Glu His Asp Leu Ser Leu
        115                 120                 125
Gly Thr Leu Ala Met
    130
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<210> 4147
<211> 4892
<212> DNA
<213> Homo sapiens

<400> 4147

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240
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420
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660
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780
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960
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<210> 4148
<211> 697
<212> PRT
<213> Homo sapiens

<400> 4148
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35 40 45
Glu Gln His Leu Phe Asp Val Asn Asn Ser Gly Gly Gln Ser Ser Glu
50 55 60
Asp Ser Glu Ser Gly Thr Leu Ser Ala Ser Ser Ala Thr Ser Ala Arg
65 70 75 80
Gln Arg Arg Arg Gln Ser Lys Glu Gln Asp Glu Val Arg His Gly Arg
85 90 95
Asp Lys Gly Leu Ile Asn Lys Glu Asn Thr Pro Ser Gly Phe Asn His
100 105 110
Leu Asp Asp Cys Ile Leu Asn Thr Gln Glu Val Glu Lys Val His Lys
115 120 125
Asn Thr Phe Gly Cys Ala Gly Glu Arg Ser Lys Pro Lys Arg Gln Lys
130 135 140
Ser Ser Thr Lys Leu Ser Glu Leu His Asp Asn Gln Asp Gly Leu Val
145 150 155 160
Asn Met Glu Ser Leu Asn Ser Thr Arg Ser His Glu Arg Thr Gly Pro
165 170 175
Asp Asp Phe Glu Trp Met Ser Asp Glu Arg Lys Gly Asn Glu Lys Asp

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                180                 185                 190
Gly Gly His Thr Gln His Phe Glu Ser Pro Thr Met Lys Ile Gln Glu
        195                 200                 205
His Pro Ser Leu Ser Asp Thr Lys Gln Gln Arg Asn Gln Asp Ala Gly
    210                 215                 220
Asp Gln Glu Glu Ser Phe Val Ser Glu Val Pro Gln Ser Asp Leu Thr
225                 230                 235                 240
Ala Leu Cys Asp Glu Lys Asn Trp Glu Glu Pro Ile Pro Ala Phe Ser
                245                 250                 255
Ser Trp Gln Arg Glu Asn Ser Asp Ser Asp Glu Ala His Leu Ser Pro
            260                 265                 270
Gln Ala Gly Arg Leu Ile Arg Gln Leu Leu Asp Glu Asp Ser Asp Pro
        275                 280                 285
Met Leu Ser Pro Arg Phe Tyr Ala Tyr Gly Gln Ser Arg Gln Tyr Leu
    290                 295                 300
Asp Asp Thr Glu Val Pro Pro Ser Pro Pro Asn Ser His Ser Phe Met
305                 310                 315                 320
Arg Arg Arg Ser Ser Ser Leu Gly Ser Tyr Asp Asp Glu Gln Glu Asp
                325                 330                 335
Leu Thr Pro Ala Gln Leu Thr Arg Arg Ile Gln Ser Leu Lys Lys Lys
            340                 345                 350
Ile Arg Lys Phe Glu Asp Arg Phe Glu Glu Glu Lys Lys Tyr Arg Pro
        355                 360                 365
Ser His Ser Asp Lys Ala Ala Asn Pro Glu Val Leu Lys Trp Thr Asn
    370                 375                 380
Asp Leu Ala Lys Phe Arg Arg Gln Leu Lys Glu Ser Lys Leu Lys Ile
385                 390                 395                 400
Ser Glu Glu Asp Leu Thr Pro Arg Met Arg Gln Arg Ser Asn Thr Leu
                405                 410                 415
Pro Lys Ser Phe Gly Ser Gln Leu Glu Lys Glu Asp Glu Lys Lys Gln
            420                 425                 430
Glu Leu Val Asp Lys Ala Ile Lys Pro Ser Val Glu Ala Thr Leu Glu
        435                 440                 445
Ser Ile Gln Arg Lys Leu Gln Glu Lys Arg Ala Glu Ser Ser Arg Pro
    450                 455                 460
Glu Asp Ile Lys Asp Met Thr Lys Asp Gln Ile Ala Asn Glu Lys Val
465                 470                 475                 480
Ala Leu Gln Lys Ala Leu Leu Tyr Tyr Glu Ser Ile His Gly Arg Pro
                485                 490                 495
Val Thr Lys Asn Glu Arg Gln Val Met Lys Pro Leu Tyr Asp Arg Tyr
            500                 505                 510
Arg Leu Val Lys Gln Ile Leu Ser Arg Ala Asn Thr Ile Pro Ile Ile
        515                 520                 525
Gly Ser Pro Ser Ser Lys Arg Arg Ser Pro Leu Leu Gln Pro Ile Ile
    530                 535                 540
Glu Gly Glu Thr Ala Ser Phe Phe Lys Glu Ile Lys Glu Glu Glu Glu
545                 550                 555                 560
Gly Ser Glu Asp Asp Ser Asn Val Lys Pro Asp Phe Met Val Thr Leu
                565                 570                 575
Lys Thr Asp Phe Ser Ala Arg Cys Phe Leu Asp Gln Phe Glu Asp Asp
            580                 585                 590
Ala Asp Gly Phe Ile Ser Pro Met Asp Asp Lys Ile Pro Ser Lys Cys
        595                 600                 605
Ser Gln Asp Thr Gly Leu Ser Asn Leu His Ala Ala Ser Ile Pro Glu
```

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    610                 615                 620
Leu Leu Glu His Leu Gln Glu Met Arg Glu Glu Lys Lys Arg Ile Arg
625                 630                 635                 640
Lys Lys Leu Arg Asp Phe Glu Asp Asn Phe Phe Arg Gln Asn Gly Arg
                645                 650                 655
Asn Val Gln Lys Glu Asp Arg Thr Pro Met Ala Glu Glu Tyr Ser Glu
            660                 665                 670
Tyr Lys His Ile Lys Ala Lys Leu Arg Leu Leu Glu Val Leu Ile Ser
        675                 680                 685
Lys Arg Asp Thr Asp Ser Lys Ser Met
    690                 695
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<210> 4149
<211> 1396
<212> DNA
<213> Homo sapiens

<400> 4149
nacaggggaa ataccgcggc gccggtagtt gctgtggttt ccgttctgag ctcgcagctt
60
aggagctgaa gatcgcggac ttagcgttgc cgcgtccgag tccggccatc agtggctgca
120
gatccggagg ccaggagctc aaccaccctt cttcggaaca gggccggcct gctgctgtgc
180
cctcgacgct cggtgcctgt atctactccg gggcctaggt cggctccggg ggcggcttag
240
gagaaggccg ccggcgagat gttcaaaaac acgttccaga gcggcttcct ctccatcctc
300
tacagcatcg gcagcaagcc tctgcaaatc tgggacaaaa aggtacggaa tggccacatc
360
aaaagaatca ctgataatga catccagtcc ctggtgctag agattgaagg gacaaatgta
420
agcaccacat atatcacatg ccctgcagac cccaagaaga cgctgggaat taaacttcct
480
ttccttgtca tgattatcaa aaacctgaag aagtatttta ccttcgaagt gcaggtacta
540
gatgacaaga atgtgcgtcg tcgctttcgg gcaagtaact accagagcac cacccgggtc
600
aaacccttca tctgcaccat gcccatgcgg ctggatgacg gctggaacca gattcagttc
660
aacttgctag acttcacacg gcgagcatac ggcaccaatt acatcgagac cctcagagtg
720
cagatccatg caaattgtcg catccgacgg gtttacttct cagacagact ctactcagaa
780
gatgagctgc cggcagagtt caaactgtat ctcccagttc agaacaaggc aaagcaataa
840
ctggaattgt gactcgaggg atagacccct ggatgtgact cttcttttta aaaggaaact
900
atgtggagga cgatgcaaaa acatatttat cttagtttgc tctgctgtag ttctgttatt
960
tatacttggt gttgcttgtc atggacaccg gtgaacatgc cgtaactctg tgactgcatt
1020
gtaagtgcag tgggggtaag cagtcctgtg agtggcgcat gaacgctgga gcttattccg
1080

ccgcctgccc cagtgtgggg ggagatacct ttaccatgaa cttacagaat taaagatggc
1140
ccataaggaa ttccagacca atatttcttc ctgcggttta ttctatgttt tatatattat
1200
ctaaatatat gtatatgctg tgtcatactc ataatctgga aatgaataaa gtgatatatt
1260
cctggtttgt aaaaaaaaaa aaaaaatttg ctataaaatg agaagtctca ctgatagagg
1320
ttctttattg ctcatttttt aaaaaatgga ctcttgaaat ctgttaaaat aaaattgtac
1380
atttggaaaa aaaaaa
1396

<210> 4150
<211> 193
<212> PRT
<213> Homo sapiens

<400> 4150
Met Phe Lys Asn Thr Phe Gln Ser Gly Phe Leu Ser Ile Leu Tyr Ser
1 5 10 15
Ile Gly Ser Lys Pro Leu Gln Ile Trp Asp Lys Lys Val Arg Asn Gly
20 25 30
His Ile Lys Arg Ile Thr Asp Asn Asp Ile Gln Ser Leu Val Leu Glu
35 40 45
Ile Glu Gly Thr Asn Val Ser Thr Thr Tyr Ile Thr Cys Pro Ala Asp
50 55 60
Pro Lys Lys Thr Leu Gly Ile Lys Leu Pro Phe Leu Val Met Ile Ile
65 70 75 80
Lys Asn Leu Lys Lys Tyr Phe Thr Phe Glu Val Gln Val Leu Asp Asp
85 90 95
Lys Asn Val Arg Arg Arg Phe Arg Ala Ser Asn Tyr Gln Ser Thr Thr
100 105 110
Arg Val Lys Pro Phe Ile Cys Thr Met Pro Met Arg Leu Asp Asp Gly
115 120 125
Trp Asn Gln Ile Gln Phe Asn Leu Leu Asp Phe Thr Arg Arg Ala Tyr
130 135 140
Gly Thr Asn Tyr Ile Glu Thr Leu Arg Val Gln Ile His Ala Asn Cys
145 150 155 160
Arg Ile Arg Arg Val Tyr Phe Ser Asp Arg Leu Tyr Ser Glu Asp Glu
165 170 175
Leu Pro Ala Glu Phe Lys Leu Tyr Leu Pro Val Gln Asn Lys Ala Lys
180 185 190
Gln

<210> 4151
<211> 1372
<212> DNA
<213> Homo sapiens

<400> 4151
ttatattttt ttttttttt ttttttttt cacggacaga cagggtcgtt tgtcacagca
60

gagaagcacc tcacggctcc tacccgcact catcgcggac agtgcctgca gcgggagcgg
120
cgcgagcacc ctccccagat gaaaacacca gcaccaggag gtgggccgta gcccaggctg
180
agggaggagg ctgggggctg gggctcaggg ccccccccgg gccacagcgc caccctgagt
240
ggccctgaaa atagtgcaca gtgctgggta ctgccccggc tggaggcacc tagttgttga
300
gcattccggc cacaggccac ccgctggccc ttccttggtg tggcacgaga ccacgggcac
360
ttgcaggagc tccctgcatg ctgttttgtg ctttggtctc agggagcacc ctcctacctc
420
ggggtcccag agtgggcagc cgggcaggtg tgaacagtgt gacaagggta ccgtggggca
480
cctggtagtg ccaacccaga ggggcagccg gtgctcctgg tggtgtggca gcaacagtta
540
caaactcacc ccaagtccaa accccagaaa tcctgtttct ctggccctcc gggtccagaa
600
tgccctgcac tgcctcctgg cctcaggggc tgctgcggtg gtgggaaggc tgcccagcag
660
tgaggaaggc gagtgcaggg gctgcggccg cggtcagaga aggagagaca ccagcagagg
720
acgcgaagct ggaccggcca ggttcagagc ccgcctcggt tgctcccaat cagaatctgc
780
tttgtgctcc acggcctcca agcactttca tgagcgttct gctcctacgt ggccaggtcc
840
taccttccct gacggctctg gccaggccag ctcggtttcc ctctaaccca tgaggcctgg
900
gggggctgtg acagaggctg gaaccgcggc cagagcccag gggcaggccc gcctggtcac
960
agcaggatga ggctggggtg gcgcagctgc cggtacacct gtagcagcct ctgggcggtg
1020
gcacaggagc tggcctcatc ctccgtgcag agccggtcgc gcagggtctg cacctcccgc
1080
agcagtgtct cgtggttggc gtggatctgg cggaggtact gcacacggag atcaggagcg
1140
ctggagccct gggcggcctg ctctgtcacc atcgtctgca tgcgcccgac aacggcatgg
1200
tgcgccctgc aaatgtcggc cagagaggag ctttccactt gaatctccac ggcctggatg
1260
gcgctgctgg gcacaggtcg gtcatggcca cctctcggac gatgaggtga acgttggcgc
1320
catcaggggc cactccctgg atggaagata gtgctcgggc cctcacgacg tc
1372

<210> 4152
<211> 97
<212> PRT
<213> Homo sapiens

<400> 4152
Met Pro Cys Thr Ala Ser Trp Pro Gln Gly Leu Leu Arg Trp Trp Glu
1 5 10 15
Gly Cys Pro Ala Val Arg Lys Ala Ser Ala Gly Ala Ala Ala Ala Val

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            20                  25                  30
Arg Glu Gly Glu Thr Pro Ala Glu Asp Ala Lys Leu Asp Arg Pro Gly
        35                  40                  45
Ser Glu Pro Ala Ser Val Ala Pro Asn Gln Asn Leu Leu Cys Ala Pro
    50                  55                  60
Arg Pro Pro Ser Thr Phe Met Ser Val Leu Leu Leu Arg Gly Gln Val
65                  70                  75                  80
Leu Pro Ser Leu Thr Ala Leu Ala Arg Pro Ala Arg Phe Pro Ser Asn
                85                  90                  95
Pro
```

<210> 4153
<211> 395
<212> DNA
<213> Homo sapiens

<400> 4153
tgatcagacc tgagtgaaca gaaggaaaga gcattttacc gatggtatca actgcttggg
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aaatcctccg attggcaaga aaggctttga tttcctcttt tatcacactg ctgtccctcc
120
tcattaattc ttccacttta tcatttacat ctaggtcctc ttctgaggct tcaaaactgt
180
atgacctctg acccatgctg tttgcatgga agcgagttgg tgacatcttt ccattggatg
240
tagataatcg ctcattattc tccctcccat tttgattggt agtgcaaggc tgtggggaag
300
tatcataact gttgctaggt gacggggaca ttcccgaatg ctgcgtctgt gtggaagctg
360
tagctgtaga ggaagatgct gggacattgt tagtn
395

<210> 4154
<211> 110
<212> PRT
<213> Homo sapiens

<400> 4154

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Met Ser Pro Ser Pro Ser Asn Ser Tyr Asp Thr Ser Pro Gln Pro Cys
 1               5                  10                  15
Thr Thr Asn Gln Asn Gly Arg Glu Asn Asn Glu Arg Leu Ser Thr Ser
            20                  25                  30
Asn Gly Lys Met Ser Pro Thr Arg Phe His Ala Asn Ser Met Gly Gln
        35                  40                  45
Arg Ser Tyr Ser Phe Glu Ala Ser Glu Glu Asp Leu Asp Val Asn Asp
    50                  55                  60
Lys Val Glu Glu Leu Met Arg Arg Asp Ser Ser Val Ile Lys Glu Glu
65                  70                  75                  80
Ile Lys Ala Phe Leu Ala Asn Arg Arg Ile Ser Gln Ala Val Asp Thr
                85                  90                  95
Ile Gly Lys Met Leu Phe Pro Ser Val His Ser Gly Leu Ile
            100                 105                 110
```

<210> 4155
<211> 1191
<212> DNA
<213> Homo sapiens

<400> 4155
aggcccgagc cgcagggaaa gcggcgcggg ccgggcgggg cgcggcgccc agagctcagg
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gggagacaaa ggggaccggt tcctctctag gcgccaagat gtggatacag gttcgcacca
120
ttgatggctc caagacgtgc accattgagg acgtgtctcg caaagccacg attgaggagc
180
tgcgcgagcg ggtgtgggcg ctgttcgacg tgcggcccga atgccagcgc ctcttctacc
240
ggggcaagca gttggaaaat ggatatacct tatttgatta tgatgttgga ctgaatgata
300
taattcagct gctagttcgc ccagaccctg atcatcttcc tggcacatct acacagattg
360
aggctaaacc ctgttctaat agtccaccta aagtaaagaa agctccgagg gtaggacctt
420
ccaatcagcc atctacatca gctcgtgccc gtcttattga tcctggcttt ggaatatata
480
agatacccag aaagcggtac tctagaaatg aatgtcaagg atcttagacc acgagctaga
540
accattttga aatggaatga actaaatgtt ggtgatgtgg taatggttaa ttataatgta
600
gaaagtcctg gacaaagagg attctggttt gatgcagaaa ttaccacatt gaagacaatc
660
tcaaggacca aaaaagaact tcgtgtgaaa attttcctgg ggggttctga aggaacatta
720
aatgactgca agataatatc tgtagatgaa atcttcaaga ttgagagacc tggagcccat
780
ccccttttcat ttgcagatgg aaagttttta aggcgaaatg accctgaatg tgacctgtgt
840
ggtggagacc cagaaaagaa atgtcattct tgctcctgtc gtgtatgtgg tgggaaacat
900
gaacccaaca tgcagcttct gtgtgatgaa tgtaatgtgg cttatcatat ttactgtctg
960
aatccacctt tggataaagt cccagaagag gaatactggt attgtccttc ttgtaaaact
1020
gattccagtg aagttgtaaa ggctggtgaa agactcaaga tgagtaaaaa gaaagcaaag
1080
atgccgtcag ctagtactga aagccgaaga gactgaggca ggggagggga ggggagggaa
1140
tgaggcagct ctaggatcta tactgtagct aataaaatgt aaaaacacct g
1191

<210> 4156
<211> 233
<212> PRT
<213> Homo sapiens

<400> 4156
Asp Leu Pro Ile Ser His Leu His Gln Leu Val Pro Val Leu Leu Ile

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 1               5                  10                  15
Leu Ala Leu Glu Tyr Ile Arg Tyr Pro Glu Ser Gly Thr Leu Glu Met
            20                  25                  30
Asn Val Lys Asp Leu Arg Pro Arg Ala Arg Thr Ile Leu Lys Trp Asn
        35                  40                  45
Glu Leu Asn Val Gly Asp Val Val Met Val Asn Tyr Asn Val Glu Ser
    50                  55                  60
Pro Gly Gln Arg Gly Phe Trp Phe Asp Ala Glu Ile Thr Thr Leu Lys
65                  70                  75                  80
Thr Ile Ser Arg Thr Lys Lys Glu Leu Arg Val Lys Ile Phe Leu Gly
                85                  90                  95
Gly Ser Glu Gly Thr Leu Asn Asp Cys Lys Ile Ile Ser Val Asp Glu
            100                 105                 110
Ile Phe Lys Ile Glu Arg Pro Gly Ala His Pro Leu Ser Phe Ala Asp
        115                 120                 125
Gly Lys Phe Leu Arg Arg Asn Asp Pro Glu Cys Asp Leu Cys Gly Gly
    130                 135                 140
Asp Pro Glu Lys Lys Cys His Ser Cys Ser Cys Arg Val Cys Gly Gly
145                 150                 155                 160
Lys His Glu Pro Asn Met Gln Leu Leu Cys Asp Glu Cys Asn Val Ala
                165                 170                 175
Tyr His Ile Tyr Cys Leu Asn Pro Pro Leu Asp Lys Val Pro Glu Glu
            180                 185                 190
Glu Tyr Trp Tyr Cys Pro Ser Cys Lys Thr Asp Ser Ser Glu Val Val
        195                 200                 205
Lys Ala Gly Glu Arg Leu Lys Met Ser Lys Lys Lys Ala Lys Met Pro
    210                 215                 220
Ser Ala Ser Thr Glu Ser Arg Arg Asp
225                 230
```

<210> 4157
<211> 3460
<212> DNA
<213> Homo sapiens

<400> 4157

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cattagtatc cgcagagatt cgaggacatg ccgttgacct tgttacagga ctggtgtcgg
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ggggaacacc tgaacacccg gaggtgcatg ctcatcctgg ggatccccga ggactgtggc
120
gaggatgagt ttgaggagac actccaggag gcttgcaggc acctgggcag atacagggtg
180
attggcagga tgtttaggag ggaggagaac gcccaggcga ttctactgga gctggcacaa
240
gatatcgact atgctttgct cccaagggaa ataccaggaa agggggggcc ctgggaagtg
300
attgtaaaac cccgtaactc agatggggaa tttctcaaca gactgaaccg cttcttagag
360
gaggagaggc ggaccgtgtc agatatgaac cgagtcctcg ggtcggacac caattgttcg
420
gctccaagag tgactatatc accagagttc tggacctggg cccagactct gggggcagca
480
gtgcagcctc tgctagaaca aatgttgtac cgagaactaa gagtgttttc tgggaacacc
540
```

atatccatcc caggtgcact ggcctttgat gcctggcttg agcacaccac tgagatgcta
600
cagatgtggc aggtgcccga gggggaaaag aggcggaggc tgatggaatg cttacggggc
660
cctgctctcc aggtggtcag tgggctccgg gccagcaatg cttccataac tgtggaggag
720
tgcctggctg ccttgcagca ggtgttcgga cctgtggaga gccataaaat tgcccaggtg
780
aagttgtgta aagcctatca ggaggcagga gagaaagtat ctagctttgt gttacgtttg
840
gaacccctgc tccaaagagc tgtagaaaac aatgtggtat cacgtagaaa cgtgaatcag
900
actcgcctga aacgagtctt aagtggggcc acccttcctg acaaactccg agataagctt
960
aagctgatga aacagcgaag gaagcctcct ggtttcctgg ccctggtgaa gctcctgcgt
1020
gaggaggagg aatgggaggc cactttaggt ccagataggg agagtctgga ggggctggaa
1080
gtagccccaa ggccacctgc caggatcact ggggttgggg cagtacctct ccctgcctct
1140
ggcaacagtt ttgatgcgag gccttcccag ggctaccggc gccggagggg cagaggccaa
1200
caccgaaggg gtggtgtggc aagggctggc tctcgaggct caagaaaacg gaaacgccac
1260
acattctgct atagctgtgg ggaagacggc cacatcaggg tacagtgcat caacccctcc
1320
aacctgctct tggtaaagca gaagaaacag gctgcagttg agtcgggaaa cgggaactgg
1380
gcttgggaca agagccatcc caagtccaag gccaagtagg ctcgggagaa cagggcaaca
1440
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1500
gacaaacagc agatgagttg agtggggcag agggacaggg cagccagacc aaggccaagc
1560
cttctcaccc ttggccagct ggaagggact ttcagcaacc aagaccacct ggcaacaggc
1620
tcagtggggg tcaggtccag gtccccgaag aggtgctgga gaggaaagca gggagccact
1680
gcatccagca catggggtgc ctgggcctca gatggggacc ccaaagaagc agaagctgaa
1740
gaaggtacgg ctgggggttc tgtcctgctc atccaaccac ccctaaatac ccaccctgtg
1800
gactttgagc tgaacatgcc cactggcccc caggccacat gggacctgga ggagcctacc
1860
tggggcctgc ccctgccagc aggtgccagg gctggtgagg aagagctggg gggcagaggt
1920
aaagccctgc aggggaggcc acagggtcca tcccgtcttc aggatcatct acactgcact
1980
aggggagccc caggaaggca gcaccctgga ggccctgtgc cagtgaggac aggagaccct
2040
aaggccccgg gagcccagtg ccagccagag gttgtgcagg caaggagacc aaagattgat
2100
gagaagaccc ccagcagggg tactgggtac ccggcaggcc agtgccctca cagttgactt
2160

ggaccagggt ggctgtgaag ggaagtcttt gttgcaaagg aggaggagga aaagggagga
2220
cttggtaggg ttttgtttct tctgcttgtt tctgtacagg gccaccagac tcctggagag
2280
atcaagcaag gagaacctgg ggctgccatg gccaaagcaa ctcaacagat gccaatgcca
2340
attccaaggc cagccacaac cctgccacct tggggaatcc agcctggagg catcccctaa
2400
gcagccagcc atggcctggg tggaggcacc tgaagacgtc tgtcccaaac tcccccagcc
2460
ctgagctggg agatgacagg gggaaagagg ccctctcaag ggtgccagat gcctgggtct
2520
cccaagaggg gtcccccaac tcaccgttcc cgggacaggc tgccccctgt tccaggaagc
2580
tcatcctcac ctgtgtaggc ccctgtagtg acccacgcgt ccagcagacg cccacccacc
2640
gctagccgtt gttcctgtgc aaagtagtgt gctatgcacc cacccaggtg gccgcctctg
2700
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2760
gtcatgagca ccacctctgc tttccctgtg tagatctagg ccagtggctg cttgtttttg
2820
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2880
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2940
tgaccgtgac tgtgggagga agaactggac ccaggacgga gtggggctgc cctgtctgag
3000
tttccccagt gaactttgtg ctttggtgtt ccacccctgt tgttactcat gactcagttt
3060
ccttgacctg gtagggtgtt ccctgctgtg ttttccagtg tcctgtgact gtcctgtgcg
3120
ggccataggg cagggccctg tcccagcaga tgggcttggg agggggctcc ctaaagccag
3180
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3240
gggagttggc agcgggggct gcagcaggag taggagcaga tgaggcgtct tgccaggaac
3300
ctcaggagga gggggcccgg gacctgtgtg ggacctgtgt cctgtggtgg ccgtttgcag
3360
tttctctctg tgttgtgatt cccttctctt caacggtttc agtacgtgtt tctcttcaat
3420
aaacttcatt cagtgttcca aaaaaaaaaa aaaaaaaaaa
3460

<210> 4158
<211> 463
<212> PRT
<213> Homo sapiens

<400> 4158
Met Pro Leu Thr Leu Leu Gln Asp Trp Cys Arg Gly Glu His Leu Asn
1 5 10 15
Thr Arg Arg Cys Met Leu Ile Leu Gly Ile Pro Glu Asp Cys Gly Glu

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            20                  25                  30
Asp Glu Phe Glu Glu Thr Leu Gln Glu Ala Cys Arg His Leu Gly Arg
        35                  40                  45
Tyr Arg Val Ile Gly Arg Met Phe Arg Arg Glu Glu Asn Ala Gln Ala
    50                  55                  60
Ile Leu Leu Glu Leu Ala Gln Asp Ile Asp Tyr Ala Leu Leu Pro Arg
65                  70                  75                  80
Glu Ile Pro Gly Lys Gly Gly Pro Trp Glu Val Ile Val Lys Pro Arg
                85                  90                  95
Asn Ser Asp Gly Glu Phe Leu Asn Arg Leu Asn Arg Phe Leu Glu Glu
            100                 105                 110
Glu Arg Arg Thr Val Ser Asp Met Asn Arg Val Leu Gly Ser Asp Thr
        115                 120                 125
Asn Cys Ser Ala Pro Arg Val Thr Ile Ser Pro Glu Phe Trp Thr Trp
    130                 135                 140
Ala Gln Thr Leu Gly Ala Ala Val Gln Pro Leu Leu Glu Gln Met Leu
145                 150                 155                 160
Tyr Arg Glu Leu Arg Val Phe Ser Gly Asn Thr Ile Ser Ile Pro Gly
                165                 170                 175
Ala Leu Ala Phe Asp Ala Trp Leu Glu His Thr Thr Glu Met Leu Gln
            180                 185                 190
Met Trp Gln Val Pro Glu Gly Glu Lys Arg Arg Arg Leu Met Glu Cys
        195                 200                 205
Leu Arg Gly Pro Ala Leu Gln Val Val Ser Gly Leu Arg Ala Ser Asn
    210                 215                 220
Ala Ser Ile Thr Val Glu Glu Cys Leu Ala Ala Leu Gln Gln Val Phe
225                 230                 235                 240
Gly Pro Val Glu Ser His Lys Ile Ala Gln Val Lys Leu Cys Lys Ala
                245                 250                 255
Tyr Gln Glu Ala Gly Glu Lys Val Ser Ser Phe Val Leu Arg Leu Glu
            260                 265                 270
Pro Leu Leu Gln Arg Ala Val Glu Asn Asn Val Val Ser Arg Arg Asn
        275                 280                 285
Val Asn Gln Thr Arg Leu Lys Arg Val Leu Ser Gly Ala Thr Leu Pro
    290                 295                 300
Asp Lys Leu Arg Asp Lys Leu Lys Leu Met Lys Gln Arg Arg Lys Pro
305                 310                 315                 320
Pro Gly Phe Leu Ala Leu Val Lys Leu Leu Arg Glu Glu Glu Glu Trp
                325                 330                 335
Glu Ala Thr Leu Gly Pro Asp Arg Glu Ser Leu Glu Gly Leu Glu Val
            340                 345                 350
Ala Pro Arg Pro Pro Ala Arg Ile Thr Gly Val Gly Ala Val Pro Leu
        355                 360                 365
Pro Ala Ser Gly Asn Ser Phe Asp Ala Arg Pro Ser Gln Gly Tyr Arg
    370                 375                 380
Arg Arg Arg Gly Arg Gly Gln His Arg Arg Gly Gly Val Ala Arg Ala
385                 390                 395                 400
Gly Ser Arg Gly Ser Arg Lys Arg Lys Arg His Thr Phe Cys Tyr Ser
                405                 410                 415
Cys Gly Glu Asp Gly His Ile Arg Val Gln Cys Ile Asn Pro Ser Asn
            420                 425                 430
Leu Leu Leu Val Lys Gln Lys Lys Gln Ala Ala Val Glu Ser Gly Asn
        435                 440                 445
Gly Asn Trp Ala Trp Asp Lys Ser His Pro Lys Ser Lys Ala Lys
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450 455 460

<210> 4159
<211> 1491
<212> DNA
<213> Homo sapiens

<400> 4159
catcctagtc gtgcttgttg tgtgtaacct ggattgtgtg ctgggcatag tagcaagcac
60
aagtacagtt ctttatgtgt actttgtaag gcagaaatat gtggccagtt ttagggtcca
120
ggagcaccgt ggagaatgga gagttttctg ttgctttcag tcgttgccct tacccatcct
180
tgcctacccc tggttattgc taaaatgggt aactgacaat aaagagatta gaagtgggtt
240
ataggaagcg aggtgggttc tagatgcaaa actaataccc tgtcccatgt gaaattgttt
300
ttgtgatttt gtggcgttgg ggatgacaga tgagacttga ggaatgcaaa tgtgctaatt
360
tcccacttga tgtattggaa agtgtggagc atgtatacat cacctggtta atttcatttg
420
gcactatttt cttccggtca gctcactgca tttgacagaa caaatactga gtctgcaaag
480
attcgagcaa tagaaaagtc tgtggtgcct tgggtcaacg accaggatgt ccctttctgt
540
ccagactgtg ggaataagtt cagcatccgg aaccgccgcc accactgccg cctctgcggg
600
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840
cagcagattg atgagaagga gcacacacct gacatcgtga agctctacga gaaattacga
900
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960
aatgctgggg agacaaccta cagtctggaa catgccagtg accttcgagt ggaagtgcag
1020
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1080
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1140
ctttttgtgc aggaaaagtt gcttggtttg atgtcactgc caaccaaaga acagtttgag
1200
gaactgaaaa agaaaaggaa ggaggaaatg gagaggaaga gggccgtgga gagacaagct
1260
gccctggagt cccagcgaag gcttgaggaa aggcagagtg gcctggcttc tcgagcggcc
1320
aacggggagg tggcatctct ccgcaggggc cctgcccccc tgaaaaaggc tgagggctgg
1380

ctcccactgt caggaggtca ggggcagagt gaggactcag acccgctcct ccagcagatc
1440
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1491

<210> 4160
<211> 360
<212> PRT
<213> Homo sapiens

<400> 4160
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1 5 10 15
Thr Asn Thr Glu Ser Ala Lys Ile Arg Ala Ile Glu Lys Ser Val Val
20 25 30
Pro Trp Val Asn Asp Gln Asp Val Pro Phe Cys Pro Asp Cys Gly Asn
35 40 45
Lys Phe Ser Ile Arg Asn Arg Arg His His Cys Arg Leu Cys Gly Ser
50 55 60
Ile Met Cys Lys Lys Cys Met Glu Leu Ile Ser Leu Pro Leu Ala Asn
65 70 75 80
Lys Leu Thr Ser Ala Ser Lys Glu Ser Leu Ser Thr His Thr Ser Pro
85 90 95
Ser Gln Ser Pro Asn Ser Val His Gly Ser Arg Arg Gly Ser Ile Ser
100 105 110
Ser Met Ser Ser Val Ser Ser Val Leu Asp Glu Lys Asp Asp Asp Arg
115 120 125
Ile Arg Cys Cys Thr His Cys Lys Asp Thr Leu Leu Lys Arg Glu Gln
130 135 140
Gln Ile Asp Glu Lys Glu His Thr Pro Asp Ile Val Lys Leu Tyr Glu
145 150 155 160
Lys Leu Arg Leu Cys Met Glu Lys Val Asp Gln Lys Ala Pro Glu Tyr
165 170 175
Ile Arg Met Ala Ala Ser Leu Asn Ala Gly Glu Thr Thr Tyr Ser Leu
180 185 190
Glu His Ala Ser Asp Leu Arg Val Glu Val Gln Lys Val Tyr Glu Leu
195 200 205
Ile Asp Ala Leu Ser Lys Lys Ile Leu Thr Leu Gly Leu Asn Gln Asp
210 215 220
Pro Pro Pro His Pro Ser Asn Leu Arg Leu Gln Arg Met Ile Arg Tyr
225 230 235 240
Ser Ala Thr Leu Phe Val Gln Glu Lys Leu Leu Gly Leu Met Ser Leu
245 250 255
Pro Thr Lys Glu Gln Phe Glu Glu Leu Lys Lys Lys Arg Lys Glu Glu
260 265 270
Met Glu Arg Lys Arg Ala Val Glu Arg Gln Ala Ala Leu Glu Ser Gln
275 280 285
Arg Arg Leu Glu Glu Arg Gln Ser Gly Leu Ala Ser Arg Ala Ala Asn
290 295 300
Gly Glu Val Ala Ser Leu Arg Arg Gly Pro Ala Pro Leu Lys Lys Ala
305 310 315 320
Glu Gly Trp Leu Pro Leu Ser Gly Gly Gln Gly Gln Ser Glu Asp Ser
325 330 335
Asp Pro Leu Leu Gln Gln Ile His Asn Ile Thr Ser Phe Ile Arg Gln

340 345 350
Ala Lys Ala Ala Gly Pro His Gly
355 360

<210> 4161
<211> 3316
<212> DNA
<213> Homo sapiens

<400> 4161
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120
ggaaatggtg ctcttgcaga acattctgaa aatgtgcata tttcaggagt gtcaactgct
180
tgtggagaga ctccagagca aatacgagca ccaagtggca taatcacaag cccaggctgg
240
ccttctgaat atcctgcaaa aatcaactgt agctggttca taagggcaaa cccaggcgaa
300
atcattacta taagttttca ggattttgat attcaaggat ccagaaggtg caatttggac
360
tggttgacaa tagaaacata caagaatatt gaaagttaca gagcttgtgg ttccacaatt
420
ccacctccgt atatctcttc acaagaccac atctggatta ggtttcattc ggatgacaac
480
atctctagaa agggtttcag actggcatat ttttcaggga aatctgagga accaaattgt
540
gcttgtgatc agtttcgttg tggtaatgga aagtgtatac cagaagcctg gaaatgtaat
600
aacatggatg aatgtggaga tagttccgat gaagagatct gtgccaaaga agcaaatcct
660
ccaactgctg ctgcttttca accctgtgct tacaaccagt tccagtgttt atcccgtttt
720
accaaagttt acacttgcct ccccgaatct ttaaaatgtg atgggaacat tgactgcctt
780
gacctaggag atgagataga ctgtgatgtg ccaacatgtg ggcaatggct aaaatatttt
840
tatggtactt ttaattctcc caattatcca gacttttatc ctcctggaag caattgcacc
900
tggttaatag acactggtga tcaccgtaaa gtcattttac gcttcactga ctttaaactt
960
gatggtactg gttatggtga ttatgtcaaa atatatgatg gattagagga gaatccacac
1020
aagcttttgc gtgtgttgac agcttttgat tctcatgcac ctcttacagt tgtttcttct
1080
tctggacaga taagggtaca tttttgtgct gataaagtga atgctgcaag gggatttaat
1140
gctacttacc aagtagatgg gttctgtttg ccatgggaaa taccctgtgg aggtaactgg
1200
gggtgttata ctgagcagca gcgttgtgat gggtattggc attgcccaaa tggaagggat
1260
gaaaccaatt gtaccatgtg ccagaaggaa gaatttccat gttcccgaaa tggtgtctgt
1320

tatcctcgtt ctgatcgctg caactaccag aatcattgcc caaatggctc agatgaaaaa
1380
aactgctttt tttgccaacc aggaaatttc cattgtaaaa acaatcgttg tgtgtttgaa
1440
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1500
gtaatcgtgc ctacaagagt catcactgct gccgtcatag ggagcctcat ctgtggcctg
1560
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1620
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1680
ccctcgtatg gacaattgat tgctcagggt ttaattccac cagttgaaga ttttcctgtt
1740
tgttcaccta atcaggcttc tgttttggaa aatctgaggc tagcggtacg atctcagctt
1800
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1860
tttaattttg caagatcacg tcattctggg tcattggctt tggtctcagc agatggagat
1920
gaggttgtcc ctagtcagag taccagtaga gaacctgaga gaaatcatac tcacagaagt
1980
ttgttttccg tggagtctga tgatacagac acagaaaatg agagaagaga tatggcagga
2040
gcatctggtg gggttgcagc tcctttgcct caaaaagtcc ctcccacaac ggcagtagaa
2100
gcgacagtag gagcatgtgc aagttcctca actcagagta cccgaggtgg tcatgcagat
2160
aatggaaggg atgtgacaag tgtggaaccc ccaagtgtga gtccagcacg tcaccagctt
2220
acaagtgcac tcagtcgtat gactcagggg ctacgctggg tacgttttac attaggacga
2280
tcaagttccc taagtcagaa ccagagtcct ttgagacaac ttgataatgg ggtaagtgga
2340
agagaagatg atgatgatgt tgaaatgcta attccaattt ctgatggatc ttcagacttt
2400
gatgtgaatg actgctccag acctcttctt gatcttgcct cagatcaagg acaagggctt
2460
agacaaccat ataatgcaac aaatcctgga gtaaggccaa gtaatcgaga tggcccctgt
2520
gagcgctgtg gtattgtcca cactgcccag ataccagaca cttgcttaga agtaacactg
2580
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2640
agattgtata caagttggag caatatccgt ttattatttt gtaactttac agttaaacta
2700
gttttagttt aaaaagaaaa aatgcagggt gatttcttat tattatatgt tagcctgcat
2760
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2820
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2880
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2940

ttatctatcc tatgttaaat ggtttgtttt tacaaaataa taccttattt taattgaaac
3000
gtttatgctt ttgccaagca catcttgtaa cttaatatag ctagatgtta aggttgttaa
3060
tgtaccaaaa aaaaaaaccc ttatactcac ctgcgttttc atttgtttga catttgtcta
3120
ttattggata tcattatcat atgaacttgt cagtgggaaa caaactgtct aaaaatttat
3180
ctcttacgtt taacatacaa tcatgtgaga tttaggcaga gttcgataaa ttactggcaa
3240
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3300
accanatggt aaaatc
3316

<210> 4162
<211> 859
<212> PRT
<213> Homo sapiens

<400> 4162
Met Ala Cys Arg Trp Ser Thr Lys Glu Ser Pro Arg Trp Arg Ser Ala
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Leu Leu Leu Leu Phe Leu Ala Gly Val Tyr Gly Asn Gly Ala Leu Ala
20 25 30
Glu His Ser Glu Asn Val His Ile Ser Gly Val Ser Thr Ala Cys Gly
35 40 45
Glu Thr Pro Glu Gln Ile Arg Ala Pro Ser Gly Ile Ile Thr Ser Pro
50 55 60
Gly Trp Pro Ser Glu Tyr Pro Ala Lys Ile Asn Cys Ser Trp Phe Ile
65 70 75 80
Arg Ala Asn Pro Gly Glu Ile Ile Thr Ile Ser Phe Gln Asp Phe Asp
85 90 95
Ile Gln Gly Ser Arg Arg Cys Asn Leu Asp Trp Leu Thr Ile Glu Thr
100 105 110
Tyr Lys Asn Ile Glu Ser Tyr Arg Ala Cys Gly Ser Thr Ile Pro Pro
115 120 125
Pro Tyr Ile Ser Ser Gln Asp His Ile Trp Ile Arg Phe His Ser Asp
130 135 140
Asp Asn Ile Ser Arg Lys Gly Phe Arg Leu Ala Tyr Phe Ser Gly Lys
145 150 155 160
Ser Glu Glu Pro Asn Cys Ala Cys Asp Gln Phe Arg Cys Gly Asn Gly
165 170 175
Lys Cys Ile Pro Glu Ala Trp Lys Cys Asn Asn Met Asp Glu Cys Gly
180 185 190
Asp Ser Ser Asp Glu Glu Ile Cys Ala Lys Glu Ala Asn Pro Pro Thr
195 200 205
Ala Ala Ala Phe Gln Pro Cys Ala Tyr Asn Gln Phe Gln Cys Leu Ser
210 215 220
Arg Phe Thr Lys Val Tyr Thr Cys Leu Pro Glu Ser Leu Lys Cys Asp
225 230 235 240
Gly Asn Ile Asp Cys Leu Asp Leu Gly Asp Glu Ile Asp Cys Asp Val
245 250 255
Pro Thr Cys Gly Gln Trp Leu Lys Tyr Phe Tyr Gly Thr Phe Asn Ser

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            260                 265                 270
Pro Asn Tyr Pro Asp Phe Tyr Pro Pro Gly Ser Asn Cys Thr Trp Leu
        275                 280                 285
Ile Asp Thr Gly Asp His Arg Lys Val Ile Leu Arg Phe Thr Asp Phe
    290                 295                 300
Lys Leu Asp Gly Thr Gly Tyr Gly Asp Tyr Val Lys Ile Tyr Asp Gly
305                 310                 315                 320
Leu Glu Glu Asn Pro His Lys Leu Leu Arg Val Leu Thr Ala Phe Asp
                325                 330                 335
Ser His Ala Pro Leu Thr Val Val Ser Ser Ser Gly Gln Ile Arg Val
            340                 345                 350
His Phe Cys Ala Asp Lys Val Asn Ala Ala Arg Gly Phe Asn Ala Thr
        355                 360                 365
Tyr Gln Val Asp Gly Phe Cys Leu Pro Trp Glu Ile Pro Cys Gly Gly
    370                 375                 380
Asn Trp Gly Cys Tyr Thr Glu Gln Gln Arg Cys Asp Gly Tyr Trp His
385                 390                 395                 400
Cys Pro Asn Gly Arg Asp Glu Thr Asn Cys Thr Met Cys Gln Lys Glu
                405                 410                 415
Glu Phe Pro Cys Ser Arg Asn Gly Val Cys Tyr Pro Arg Ser Asp Arg
            420                 425                 430
Cys Asn Tyr Gln Asn His Cys Pro Asn Gly Ser Asp Glu Lys Asn Cys
        435                 440                 445
Phe Phe Cys Gln Pro Gly Asn Phe His Cys Lys Asn Asn Arg Cys Val
    450                 455                 460
Phe Glu Ser Trp Val Cys Asp Ser Gln Asp Asp Cys Gly Asp Gly Ser
465                 470                 475                 480
Asp Glu Glu Asn Cys Pro Val Ile Val Pro Thr Arg Val Ile Thr Ala
                485                 490                 495
Ala Val Ile Gly Ser Leu Ile Cys Gly Leu Leu Leu Val Ile Ala Leu
            500                 505                 510
Gly Cys Thr Cys Lys Leu Tyr Ser Leu Arg Met Phe Glu Arg Arg Ser
        515                 520                 525
Phe Glu Thr Gln Leu Ser Arg Val Glu Ala Glu Leu Leu Arg Arg Glu
    530                 535                 540
Ala Pro Pro Ser Tyr Gly Gln Leu Ile Ala Gln Gly Leu Ile Pro Pro
545                 550                 555                 560
Val Glu Asp Phe Pro Val Cys Ser Pro Asn Gln Ala Ser Val Leu Glu
                565                 570                 575
Asn Leu Arg Leu Ala Val Arg Ser Gln Leu Gly Phe Thr Ser Val Arg
            580                 585                 590
Leu Pro Met Ala Gly Arg Ser Ser Asn Ile Trp Asn Arg Ile Phe Asn
        595                 600                 605
Phe Ala Arg Ser Arg His Ser Gly Ser Leu Ala Leu Val Ser Ala Asp
    610                 615                 620
Gly Asp Glu Val Val Pro Ser Gln Ser Thr Ser Arg Glu Pro Glu Arg
625                 630                 635                 640
Asn His Thr His Arg Ser Leu Phe Ser Val Glu Ser Asp Asp Thr Asp
                645                 650                 655
Thr Glu Asn Glu Arg Arg Asp Met Ala Gly Ala Ser Gly Gly Val Ala
            660                 665                 670
Ala Pro Leu Pro Gln Lys Val Pro Pro Thr Thr Ala Val Glu Ala Thr
        675                 680                 685
Val Gly Ala Cys Ala Ser Ser Ser Thr Gln Ser Thr Arg Gly Gly His
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    690                 695                 700
Ala Asp Asn Gly Arg Asp Val Thr Ser Val Glu Pro Pro Ser Val Ser
705                 710                 715                 720
Pro Ala Arg His Gln Leu Thr Ser Ala Leu Ser Arg Met Thr Gln Gly
                725                 730                 735
Leu Arg Trp Val Arg Phe Thr Leu Gly Arg Ser Ser Ser Leu Ser Gln
            740                 745                 750
Asn Gln Ser Pro Leu Arg Gln Leu Asp Asn Gly Val Ser Gly Arg Glu
        755                 760                 765
Asp Asp Asp Asp Val Glu Met Leu Ile Pro Ile Ser Asp Gly Ser Ser
    770                 775                 780
Asp Phe Asp Val Asn Asp Cys Ser Arg Pro Leu Leu Asp Leu Ala Ser
785                 790                 795                 800
Asp Gln Gly Gln Gly Leu Arg Gln Pro Tyr Asn Ala Thr Asn Pro Gly
                805                 810                 815
Val Arg Pro Ser Asn Arg Asp Gly Pro Cys Glu Arg Cys Gly Ile Val
            820                 825                 830
His Thr Ala Gln Ile Pro Asp Thr Cys Leu Glu Val Thr Leu Lys Asn
        835                 840                 845
Glu Thr Ser Asp Asp Glu Ala Leu Leu Leu Cys
    850                 855
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<210> 4163
<211> 568
<212> DNA
<213> Homo sapiens

<400> 4163
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actccagggc tcccaggtca gagtggccat ggtagcttac aatgcggcct gcaggaccca
120
gcaggcagcc ggcccctctc ccctcccttt tcccgcctgc gctctgaagg ctccaagtca
180
gtgttgcccc agtggctctg ggggatgaag gggatcccgg tcccatctgg acaccctcaa
240
gctgatggac gcagagctct ggtgcgggca gtgggtcacc cccaggacct gctgaccgaa
300
gcctctcccc gctgcccggc aggcccttca ccgctgagat ctaccggcag aaagcctccg
360
ggtcccccaa gaggaggtga tttagctgcc ccagttttgt ttaaggcctg ggccacctcc
420
ttggcttgcc ccaagtggca ggccttgcgc agggcgagaa tggtgcctgt tgttcagggc
480
tcgccccccgg cgtgggctgc cccagtgcct tggaacctgc tgccttgggg accctggacg
540
tgccgacata tggccattga gctccaac
568

<210> 4164
<211> 187
<212> PRT
<213> Homo sapiens

<400> 4164
Asn Leu Ser Leu Trp Pro Gly Gln Ala Gln Asp Arg Leu Pro Ser Ala
1 5 10 15
Arg Pro Thr Pro Gly Leu Pro Gly Gln Ser Gly His Gly Ser Leu Gln
20 25 30
Cys Gly Leu Gln Asp Pro Ala Gly Ser Arg Pro Leu Ser Pro Pro Phe
35 40 45
Ser Arg Leu Arg Ser Glu Gly Ser Lys Ser Val Leu Pro Gln Trp Leu
50 55 60
Trp Gly Met Lys Gly Ile Pro Val Pro Ser Gly His Pro Gln Ala Asp
65 70 75 80
Gly Arg Arg Ala Leu Val Arg Ala Val Gly His Pro Gln Asp Leu Leu
85 90 95
Thr Glu Ala Ser Pro Arg Cys Pro Ala Gly Pro Ser Pro Leu Arg Ser
100 105 110
Thr Gly Arg Lys Pro Pro Gly Pro Pro Arg Gly Gly Asp Leu Ala Ala
115 120 125
Pro Val Leu Phe Lys Ala Trp Ala Thr Ser Leu Ala Cys Pro Lys Trp
130 135 140
Gln Ala Leu Arg Arg Ala Arg Met Val Pro Val Val Gln Gly Ser Pro
145 150 155 160
Pro Ala Trp Ala Ala Pro Val Pro Trp Asn Leu Leu Pro Trp Gly Pro
165 170 175
Trp Thr Cys Arg His Met Ala Ile Glu Leu Gln
180 185

<210> 4165
<211> 717
<212> DNA
<213> Homo sapiens

<400> 4165
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taccctatgg aggtgctgaa gacgcggctg accttgcgcc ggacgggcca gtataagggg
120
ctgctggact gcgccaggcg tatcctggag agggaggggc cccgtgcctt ctaccgcggc
180
tacctcccca acgtgctggg catcatcccc tatgcgggca tcgacctggc cgtctacgag
240
actctgaaga actggtggct tcagcagtac agccacgact cggcagaccc aggcatcctc
300
gtgctcctgg cctgcggtac catatccagc acctgcggcc agatagccag ttacccgctg
360
gccctggtcc ggacccgcat gcaggcacaa ggatttcatc atgttgccca ggctcatctc
420
gaactcgtgg ggtcaaggaa ttcgccagcc ttcagcctcc caacgtgctg ggattacagg
480
aagccggtgg tcatgccatg agcagcctta tggagaggac catgtggtaa ggaactcagc
540
caatagccat gtaactgagc ttggaagagg atcttgctgt cctggccaac atctcactgc
600
aattctatca gttgaattcc ctggatagtc caagctttgt ggatccctcc accagaacaa
660

ctggatccca gtacctgaat cctgaatctt agactcttat acttcaaaca ctgatca
717

<210> 4166
<211> 166
<212> PRT
<213> Homo sapiens

<400> 4166
Xaa Val Gln Glu Arg Phe Val Ala Gly Ser Leu Ala Gly Ala Thr Ala
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Gln Thr Ile Ile Tyr Pro Met Glu Val Leu Lys Thr Arg Leu Thr Leu
20 25 30
Arg Arg Thr Gly Gln Tyr Lys Gly Leu Leu Asp Cys Ala Arg Arg Ile
35 40 45
Leu Glu Arg Glu Gly Pro Arg Ala Phe Tyr Arg Gly Tyr Leu Pro Asn
50 55 60
Val Leu Gly Ile Ile Pro Tyr Ala Gly Ile Asp Leu Ala Val Tyr Glu
65 70 75 80
Thr Leu Lys Asn Trp Trp Leu Gln Gln Tyr Ser His Asp Ser Ala Asp
85 90 95
Pro Gly Ile Leu Val Leu Leu Ala Cys Gly Thr Ile Ser Ser Thr Cys
100 105 110
Gly Gln Ile Ala Ser Tyr Pro Leu Ala Leu Val Arg Thr Arg Met Gln
115 120 125
Ala Gln Gly Phe His His Val Ala Gln Ala His Leu Glu Leu Val Gly
130 135 140
Ser Arg Asn Ser Pro Ala Phe Ser Leu Pro Thr Cys Trp Asp Tyr Arg
145 150 155 160
Lys Pro Val Val Met Pro
165

<210> 4167
<211> 897
<212> DNA
<213> Homo sapiens

<400> 4167
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cgagaacgtg cgggaagaga agatcatcga gcatttcaaa cggctggtgt gcaatggcgt
120
gatctcagcc caccgcaact tccgcctcct gggatcaagc aatcctcctg cttcagcctc
180
ctgagtagct tggactacag atatggccgc gtggaaagtg tcaaaattct tcccaagagg
240
ggatctgaag gaggagtggc tgcctttgtg gattttgtgg acatcaaaag tgcacagaaa
300
gctcacaact cggtcaacaa aatgggtgac agagacctac gcacggatta taatgaacca
360
ggcaccatcc cgagtgctgc tcggggattg gatgatacag tttccatagc atctcgtagt
420
agagaggttt ctgggttcag aggaggtggt ggagggcctg cttatggtcc cccaccgtca
480

cttcatgcac gagaaggacg ttatgagcgg agacttgatg gggcttcaga taacagggag
540
cgtgcttatg aacatagtgc ctatggacac catgaacggg ggacgggagg atttgatcgg
600
acaagacatt acgatcagga ttactataga gatcctcgag agcggacttt acaacatggg
660
ctctattacg cttctcggag tcgaagtcca aatcgctttg atgctcatga cccccgatat
720
gaacctaggg ctcgcgagca gtttacactg cccagtgtgg tacacaggga tatctacagg
780
gatgatatta cccgggaggt acgaggcaga aggccagagc ggaattacca gcacagcagg
840
agtcggtcac cacattcatc ccagtctaga aatcagtctc ctcagagact ggctagc
897

<210> 4168
<211> 299
<212> PRT
<213> Homo sapiens

<400> 4168
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Gly Gln Phe Thr Arg Glu Arg Ala Gly Arg Glu Asp His Arg Ala Phe
20 25 30
Gln Thr Ala Gly Val Gln Trp Arg Asp Leu Ser Pro Pro Gln Leu Pro
35 40 45
Pro Pro Gly Ile Lys Gln Ser Ser Cys Phe Ser Leu Leu Ser Ser Leu
50 55 60
Asp Tyr Arg Tyr Gly Arg Val Glu Ser Val Lys Ile Leu Pro Lys Arg
65 70 75 80
Gly Ser Glu Gly Gly Val Ala Ala Phe Val Asp Phe Val Asp Ile Lys
85 90 95
Ser Ala Gln Lys Ala His Asn Ser Val Asn Lys Met Gly Asp Arg Asp
100 105 110
Leu Arg Thr Asp Tyr Asn Glu Pro Gly Thr Ile Pro Ser Ala Ala Arg
115 120 125
Gly Leu Asp Asp Thr Val Ser Ile Ala Ser Arg Ser Arg Glu Val Ser
130 135 140
Gly Phe Arg Gly Gly Gly Gly Gly Pro Ala Tyr Gly Pro Pro Pro Ser
145 150 155 160
Leu His Ala Arg Glu Gly Arg Tyr Glu Arg Arg Leu Asp Gly Ala Ser
165 170 175
Asp Asn Arg Glu Arg Ala Tyr Glu His Ser Ala Tyr Gly His His Glu
180 185 190
Arg Gly Thr Gly Gly Phe Asp Arg Thr Arg His Tyr Asp Gln Asp Tyr
195 200 205
Tyr Arg Asp Pro Arg Glu Arg Thr Leu Gln His Gly Leu Tyr Tyr Ala
210 215 220
Ser Arg Ser Arg Ser Pro Asn Arg Phe Asp Ala His Asp Pro Arg Tyr
225 230 235 240
Glu Pro Arg Ala Arg Glu Gln Phe Thr Leu Pro Ser Val Val His Arg
245 250 255
Asp Ile Tyr Arg Asp Asp Ile Thr Arg Glu Val Arg Gly Arg Arg Pro

260 265 270
Glu Arg Asn Tyr Gln His Ser Arg Ser Arg Ser Pro His Ser Ser Gln
275 280 285
Ser Arg Asn Gln Ser Pro Gln Arg Leu Ala Ser
290 295

<210> 4169
<211> 4743
<212> DNA
<213> Homo sapiens

<400> 4169
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cccccgcctc caccacccat gcccctgcag ctcgaggccc acctccgcag ccatggcctg
120
gagcccgcgg cccccagccc ccgcctgcga cccgaggaga gcctggatcc gccaggcgcc
180
atgcaggaat tgctcggggc tctggagccg ctgcccccgg cgcctgggga tactggcgta
240
ggcccaccaa actcggaggg caaggatccc gcaggcgcct accgcagccc cagcccgcaa
300
ggcaccaagg cgccgcgttt cgtgccgctc acctccatct gcttccctga ctccttgctc
360
caagacgagg agcgcagctt cttccccacc atggaggaga tgttcggtgg aggggccgcg
420
gacgactacg gcaaggccgg gccacctgag gacgaggggg accccaaggc tggcgctggg
480
ccacccccgg gccccccctgc ttatgatccc tatgggccct actgtcctgg ccgggcgtcg
540
ggagccgggc ccgagacacc gggcctgggc ctggacccca acaaaccgcc tgaactgccc
600
tccacggtca acgccgagcc gctgggcctg atccagagtg gcccccacca ggcggcgcca
660
ccacccccgc ctccgccacc gccgcctccc gcgccggcct ccgaacccaa gggtggcctc
720
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780
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4743

<210> 4170
<211> 900
<212> PRT
<213> Homo sapiens

<400> 4170
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Ala His Leu Arg Ser His Gly Leu Glu Pro Ala Ala Pro Ser Pro Arg
35 40 45
Leu Arg Pro Glu Glu Ser Leu Asp Pro Pro Gly Ala Met Gln Glu Leu
50 55 60
Leu Gly Ala Leu Glu Pro Leu Pro Pro Ala Pro Gly Asp Thr Gly Val
65 70 75 80
Gly Pro Pro Asn Ser Glu Gly Lys Asp Pro Ala Gly Ala Tyr Arg Ser
85 90 95
Pro Ser Pro Gln Gly Thr Lys Ala Pro Arg Phe Val Pro Leu Thr Ser
100 105 110
Ile Cys Phe Pro Asp Ser Leu Leu Gln Asp Glu Glu Arg Ser Phe Phe
115 120 125
Pro Thr Met Glu Glu Met Phe Gly Gly Gly Ala Ala Asp Asp Tyr Gly
130 135 140
Lys Ala Gly Pro Pro Glu Asp Glu Gly Asp Pro Lys Ala Gly Ala Gly
145 150 155 160
Pro Pro Pro Gly Pro Pro Ala Tyr Asp Pro Tyr Gly Pro Tyr Cys Pro
165 170 175
Gly Arg Ala Ser Gly Ala Gly Pro Glu Thr Pro Gly Leu Gly Leu Asp
180 185 190
Pro Asn Lys Pro Pro Glu Leu Pro Ser Thr Val Asn Ala Glu Pro Leu
195 200 205
Gly Leu Ile Gln Ser Gly Pro His Gln Ala Ala Pro Pro Pro Pro Pro
210 215 220
Pro Pro Pro Pro Pro Pro Ala Pro Ala Ser Glu Pro Lys Gly Gly Leu
225 230 235 240
Thr Ser Pro Ile Phe Cys Ser Thr Lys Pro Lys Lys Leu Leu Lys Thr
245 250 255
Ser Ser Phe His Leu Leu Arg Arg Arg Asp Pro Pro Phe Gln Thr Pro
260 265 270
Lys Lys Leu Tyr Ala Gln Glu Tyr Glu Phe Glu Ala Asp Glu Asp Lys
275 280 285
Ala Asp Val Pro Ala Asp Ile Arg Leu Asn Pro Arg Arg Leu Pro Asp

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    290                 295                 300
Leu Val Ser Ser Cys Arg Ser Arg Pro Ala Leu Ser Pro Leu Gly Asp
305                 310                 315                 320
Ile Asp Phe Cys Leu Pro Asn Pro Gly Pro Asp Gly Pro Arg Arg Arg
                325                 330                 335
Gly Arg Lys Pro Thr Lys Ala Lys Arg Asp Gly Pro Pro Arg Pro Arg
            340                 345                 350
Gly Arg Pro Arg Ile Arg Pro Leu Glu Val Pro Thr Thr Ala Gly Pro
        355                 360                 365
Ala Ser Ala Ser Thr Pro Thr Asp Gly Ala Lys Lys Pro Arg Gly Arg
    370                 375                 380
Gly Arg Gly Arg Gly Arg Lys Ala Glu Glu Ala Gly Gly Thr Arg Leu
385                 390                 395                 400
Glu Pro Leu Lys Pro Leu Lys Ile Lys Leu Ser Val Pro Lys Ala Gly
                405                 410                 415
Glu Gly Leu Gly Thr Ser Ser Gly Asp Ala Ile Ser Gly Thr Asp His
            420                 425                 430
Asn Ser Leu Asp Ser Ser Leu Thr Arg Glu Lys Ile Glu Ala Lys Ile
        435                 440                 445
Lys Glu Val Glu Glu Lys Gln Pro Glu Met Lys Ser Gly Phe Met Ala
    450                 455                 460
Ser Phe Leu Asp Phe Leu Lys Ser Gly Lys Arg His Pro Pro Leu Tyr
465                 470                 475                 480
Gln Ala Gly Leu Thr Pro Pro Leu Ser Pro Pro Lys Ser Val Pro Pro
                485                 490                 495
Ser Val Pro Ala Arg Gly Leu Gln Pro Gln Pro Pro Ala Thr Pro Ala
            500                 505                 510
Val Pro His Pro Pro Pro Ser Gly Ala Phe Gly Leu Gly Gly Ala Leu
        515                 520                 525
Glu Ala Ala Glu Ser Glu Gly Leu Gly Leu Gly Cys Pro Ser Pro Cys
    530                 535                 540
Lys Arg Leu Asp Glu Glu Leu Lys Arg Asn Leu Glu Thr Leu Pro Ser
545                 550                 555                 560
Phe Ser Ser Asp Glu Glu Asp Ser Val Ala Lys Asn Arg Asp Leu Gln
                565                 570                 575
Glu Ser Ile Ser Ser Ala Ile Ser Ala Leu Asp Asp Pro Pro Leu Ala
            580                 585                 590
Gly Pro Lys Asp Thr Ser Thr Pro Asp Gly Pro Pro Leu Ala Pro Ala
        595                 600                 605
Ala Ala Val Pro Gly Pro Pro Pro Leu Pro Gly Leu Pro Ser Ala Asn
    610                 615                 620
Ser Asn Gly Thr Pro Glu Pro Pro Leu Leu Glu Glu Lys Pro Pro Pro
625                 630                 635                 640
Thr Pro Pro Pro Ala Pro Thr Pro Gln Pro Gln Pro Pro Pro Pro Pro
                645                 650                 655
Pro Pro Pro Gln Pro Ala Leu Pro Ser Pro Pro Pro Leu Val Ala Pro
            660                 665                 670
Thr Pro Ser Ser Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro
        675                 680                 685
Ala Met Pro Ser Pro Pro Pro Pro Pro Pro Pro Ala Ala Ala Pro Leu
    690                 695                 700
Ala Ala Pro Pro Glu Glu Pro Ala Ala Pro Ser Pro Glu Asp Pro Glu
705                 710                 715                 720
Leu Pro Asp Thr Arg Pro Leu His Leu Ala Lys Lys Gln Glu Thr Ala
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                725                 730                 735
Ala Val Cys Gly Glu Thr Asp Glu Glu Ala Gly Glu Ser Gly Gly Glu
            740                 745                 750
Gly Ile Phe Arg Glu Arg Asp Glu Phe Val Ile Arg Ala Glu Asp Ile
        755                 760                 765
Pro Ser Leu Lys Leu Ala Leu Gln Thr Gly Arg Glu Pro Pro Pro Ile
    770                 775                 780
Trp Arg Val Gln Lys Ala Leu Leu Gln Lys Phe Thr Pro Glu Ile Lys
785                 790                 795                 800
Asp Gly Gln Arg Gln Phe Cys Ala Thr Ser Asn Tyr Leu Gly Tyr Phe
                805                 810                 815
Gly Asp Ala Lys Asn Arg Tyr Gln Arg Leu Tyr Val Lys Phe Leu Glu
            820                 825                 830
Asn Val Asn Lys Lys Asp Tyr Val Arg Val Cys Ala Arg Lys Pro Trp
        835                 840                 845
His Arg Pro Pro Val Pro Val Arg Arg Ser Gly Gln Ala Lys Asn Pro
    850                 855                 860
Val Ser Ala Gly Gly Ser Ser Ala Pro Pro Pro Lys Ala Pro Ala Pro
865                 870                 875                 880
Pro Pro Lys Pro Glu Thr Pro Glu Lys Thr Thr Ser Glu Lys Pro Pro
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<211> 889
<212> DNA
<213> Homo sapiens

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120
gtgagcctaa ggcggaacgc gtgaggcgct tttgagtctg gggtccgggg ccgagagcag
180
gcggaaagag aggggacccg gcagaccccg agtggccgcc gctgcggggc ccaagtcctt
240
ggctgctgag tggtgacagt agcccagccc gccggccaga tatggtccag acctgtacat
300
gaataacttt ggttagtcag agtgaaatat tcaataatga gtggtgcagc tttgggactt
360
gagattgttt ttgtcttttt tctggcatta tttctgcttc atcgatatgg agactttaag
420
aaacagcata gacttgtgat tattggaaca ctgcttgctt ggtatctctg ctttcttatt
480
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660
ttctggaggg tagtgtattg gacgtcacaa tttttaacat ggattctctt acctttttatg
720

cagtcatatg caagatcagg agggttttcc atcactggaa agatcaaaac tgcactaatt
780
gagaatgcaa tctactatgg cacctatttg ctgatttttg gagcattttt aatttatgta
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889

<210> 4172
<211> 184
<212> PRT
<213> Homo sapiens

<400> 4172
Met Ser Gly Ala Ala Leu Gly Leu Glu Ile Val Phe Val Phe Phe Leu
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Ala Leu Phe Leu Leu His Arg Tyr Gly Asp Phe Lys Lys Gln His Arg
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Leu Val Ile Ile Gly Thr Leu Leu Ala Trp Tyr Leu Cys Phe Leu Ile
35 40 45
Val Phe Ile Leu Pro Leu Asp Val Ser Thr Thr Ile Tyr Asn Arg Cys
50 55 60
Lys His Ala Ala Gln Ile Gln Ala Leu Leu Arg Ile Ala Thr Leu Gln
65 70 75 80
Asp Cys Ala Thr Ala Asn Pro Val Pro Ser Gln His Pro Cys Phe Lys
85 90 95
Pro Trp Ser Tyr Ile Pro Asp Gly Ile Met Pro Ile Phe Trp Arg Val
100 105 110
Val Tyr Trp Thr Ser Gln Phe Leu Thr Trp Ile Leu Leu Pro Phe Met
115 120 125
Gln Ser Tyr Ala Arg Ser Gly Gly Phe Ser Ile Thr Gly Lys Ile Lys
130 135 140
Thr Ala Leu Ile Glu Asn Ala Ile Tyr Tyr Gly Thr Tyr Leu Leu Ile
145 150 155 160
Phe Gly Ala Phe Leu Ile Tyr Val Ala Val Asn Pro His Leu His Leu
165 170 175
Glu Trp Asn Gln Leu Gln Thr Ile
180

<210> 4173
<211> 404
<212> DNA
<213> Homo sapiens

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404

<210> 4174
<211> 91
<212> PRT
<213> Homo sapiens

<400> 4174
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Gly Thr Pro Val Ser Lys Cys Ala Arg Ala Leu Gly Ser Ala Lys Gly
35 40 45
Pro Leu Leu Cys Cys Cys Val Gln Ala Trp His Leu Gln Asp Gly Asp
50 55 60
Ser Phe Leu Thr His Asp His Tyr Tyr Met Leu Asn Asp Leu Pro Asp
65 70 75 80
Ser Ser Ser Pro Val Ala Ala Thr Phe Met Phe
85 90

<210> 4175
<211> 2778
<212> DNA
<213> Homo sapiens

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180
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420
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720

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1920
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2340

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2760
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2778

<210> 4176
<211> 586
<212> PRT
<213> Homo sapiens

<400> 4176
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Ala Gly Leu Arg Ala Ala Met Gly Pro Gly Ile Ser Arg Met Asn Asp
35 40 45
Leu Thr Ile Ile Gln Thr Thr Gln Gly Phe Cys Arg Tyr Leu Glu Lys
50 55 60
Gln Phe Ser Asp Leu Lys Gln Lys Gly Ile Val Ile Ser Phe Asp Ala
65 70 75 80
Arg Ala His Pro Ser Ser Gly Gly Ser Ser Arg Arg Phe Ala Arg Leu
85 90 95
Ala Ala Thr Thr Phe Ile Ser Gln Gly Ile Pro Val Tyr Leu Phe Ser
100 105 110
Asp Ile Thr Pro Thr Pro Phe Val Pro Phe Thr Val Ser His Leu Lys
115 120 125
Leu Cys Ala Gly Ile Met Ile Thr Ala Ser His Asn Pro Lys Gln Asp
130 135 140
Asn Gly Tyr Lys Val Tyr Trp Asp Asn Gly Ala Gln Ile Ile Ser Pro
145 150 155 160
His Asp Lys Gly Ile Ser Gln Ala Ile Glu Glu Asn Leu Glu Pro Trp
165 170 175
Pro Gln Ala Trp Asp Asp Ser Leu Ile Asp Ser Ser Pro Leu Leu His
180 185 190
Asn Pro Ser Ala Ser Ile Asn Asn Asp Tyr Phe Glu Asp Leu Lys Lys
195 200 205
Tyr Cys Phe His Arg Ser Val Asn Arg Glu Thr Lys Val Lys Phe Val
210 215 220
His Thr Ser Val His Gly Val Gly His Ser Phe Val Gln Ser Ala Phe
225 230 235 240
Lys Ala Phe Xaa Pro Cys Ser Ser Xaa Glu Ala Val Pro Glu Gln Lys

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                245                 250                 255
Asp Pro Asp Pro Glu Phe Pro Thr Val Lys Tyr Pro Asn Pro Glu Glu
            260                 265                 270
Gly Lys Gly Val Leu Thr Leu Ser Phe Ala Leu Ala Asp Lys Thr Lys
        275                 280                 285
Ala Arg Ile Val Leu Ala Asn Asp Pro Asp Ala Asp Arg Leu Ala Val
    290                 295                 300
Ala Glu Lys Gln Asp Ser Gly Glu Trp Arg Val Phe Ser Gly Asn Glu
305                 310                 315                 320
Leu Gly Ala Leu Leu Gly Trp Trp Leu Phe Thr Ser Trp Lys Glu Lys
                325                 330                 335
Asn Gln Asp Arg Ser Ala Leu Lys Asp Thr Tyr Met Leu Ser Ser Thr
            340                 345                 350
Val Ser Ser Lys Ile Leu Arg Ala Ile Ala Leu Lys Glu Gly Phe His
        355                 360                 365
Phe Glu Glu Thr Leu Thr Gly Phe Lys Trp Met Gly Asn Arg Ala Lys
    370                 375                 380
Gln Leu Ile Asp Gln Gly Lys Thr Val Leu Phe Ala Phe Glu Glu Ala
385                 390                 395                 400
Ile Gly Tyr Met Cys Cys Pro Phe Val Leu Asp Lys Asp Gly Val Ser
                405                 410                 415
Ala Ala Val Ile Ser Ala Glu Leu Ala Ser Phe Leu Ala Thr Lys Asn
            420                 425                 430
Leu Ser Leu Ser Gln Gln Leu Lys Ala Ile Tyr Val Glu Tyr Gly Tyr
        435                 440                 445
His Ile Thr Lys Ala Ser Tyr Phe Ile Cys His Asp Gln Glu Thr Ile
    450                 455                 460
Lys Lys Leu Phe Glu Asn Leu Arg Asn Tyr Asp Gly Lys Asn Asn Tyr
465                 470                 475                 480
Pro Lys Ala Cys Gly Lys Phe Glu Ile Ser Ala Ile Arg Asp Leu Thr
                485                 490                 495
Thr Gly Tyr Asp Asp Ser Gln Pro Asp Lys Lys Ala Val Leu Pro Thr
            500                 505                 510
Ser Lys Ser Ser Gln Met Ile Thr Phe Thr Phe Ala Asn Gly Gly Val
        515                 520                 525
Ala Thr Met Arg Thr Ser Gly Thr Glu Pro Lys Ile Lys Tyr Tyr Ala
    530                 535                 540
Glu Leu Cys Ala Pro Pro Gly Asn Ser Asp Pro Glu Gln Leu Lys Lys
545                 550                 555                 560
Glu Leu Asn Glu Leu Val Ser Ala Ile Glu Glu His Phe Phe Gln Pro
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<210> 4177
<211> 4763
<212> DNA
<213> Homo sapiens

<400> 4177
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120

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3360

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3720
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<211> 398
<212> PRT
<213> Homo sapiens

<400> 4178
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35 40 45
Ser Arg Thr Asn Glu Asn Asp Pro Ala Lys His Gly Asp Gln His Glu
50 55 60
Gly Gln His Tyr Asn Ile Ser Pro Gln Asp Leu Glu Thr Val Phe Pro
65 70 75 80
His Gly Leu Pro Pro Arg Phe Val Met Gln Val Lys Thr Phe Ser Glu
85 90 95
Ala Cys Leu Met Val Arg Lys Pro Ala Leu Glu Leu Leu His Tyr Leu
100 105 110
Lys Asn Thr Ser Phe Ala Tyr Pro Ala Ile Arg Tyr Leu Leu Tyr Gly
115 120 125
Glu Lys Gly Thr Gly Lys Thr Leu Ser Leu Cys His Val Phe His Phe
130 135 140
Cys Ala Lys Gln Asp Trp Leu Ile Leu His Ile Pro Asp Ala His Leu
145 150 155 160
Trp Val Lys Asn Cys Arg Asp Leu Leu Gln Ser Ser Tyr Asn Lys Gln
165 170 175
Arg Phe Asp Gln Pro Leu Glu Ala Ser Thr Trp Leu Lys Asn Phe Lys
180 185 190
Thr Thr Asn Glu Arg Phe Leu Asn Gln Ile Lys Val Gln Glu Lys Tyr
195 200 205
Val Trp Asn Lys Arg Glu Leu Thr Glu Lys Gly Ser Pro Leu Gly Glu
210 215 220
Val Val Glu Gln Gly Ile Thr Arg Val Arg Asn Ala Thr Asp Ala Val
225 230 235 240
Gly Ile Val Leu Lys Glu Leu Lys Arg Gln Ser Ser Leu Gly Met Phe
245 250 255
His Leu Leu Val Ala Val Asp Gly Ile Asn Ala Leu Trp Gly Arg Thr
260 265 270
Thr Leu Lys Arg Glu Asp Lys Ser Pro Ile Ala Pro Glu Glu Leu Ala
275 280 285
Leu Val His Asn Leu Arg Lys Met Met Lys Asn Asp Trp His Gly Gly
290 295 300
Ala Ile Val Ser Ala Leu Ser Gln Thr Gly Ser Leu Phe Lys Pro Arg
305 310 315 320
Lys Ala Tyr Leu Pro Gln Glu Leu Leu Gly Lys Glu Gly Phe Asp Ala
325 330 335
Leu Asp Pro Phe Ile Pro Ile Leu Val Ser Asn Tyr Asn Pro Lys Glu
340 345 350
Phe Glu Ser Cys Ile Gln Tyr Tyr Leu Glu Asn Asn Trp Leu Gln His
355 360 365
Glu Lys Ala Pro Thr Glu Glu Gly Lys Lys Glu Leu Leu Phe Leu Ser
370 375 380
Asn Ala Asn Pro Ser Leu Leu Glu Arg His Cys Ala Tyr Leu
385 390 395

<210> 4179
<211> 2208

<212> DNA
<213> Homo sapiens

<400> 4179
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ggcacccatt aaagactcaa cagtcaaaat gagacaaatc agtcctttag acgttcacag
180
acaattgaaa ggcactttaa aaatccactt tttaaactac cacttgagaa cacatggtag
240
cacagtctta aattcatcct agttgatcgg gaatgatgaa tgagtgttgg caccagaaaa
300
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480
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720
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2100
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<210> 4180
<211> 257
<212> PRT
<213> Homo sapiens

<400> 4180
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Thr Asp Cys Val Met Ile Ser Thr Arg Leu Val Ser Ser Val His Ala
35 40 45
Val Leu Ala Thr Gly Ser Gly Ile Val Ile Ile Arg Ser Cys Asp Asp
50 55 60
Val Ile Thr Gly Arg His Trp Leu Ala Arg Glu Tyr Val Trp Phe Leu
65 70 75 80
Ile Pro Tyr Met Ile Tyr Asp Ser Tyr Ala Met Tyr Leu Cys Glu Trp
85 90 95
Cys Arg Thr Arg Asp Gln Asn Arg Ala Pro Ser Leu Thr Leu Arg Asn
100 105 110
Phe Leu Ser Arg Asn Arg Leu Met Ile Thr His His Ala Val Ile Leu
115 120 125
Phe Val Leu Val Pro Val Ala Gln Arg Leu Arg Gly Asp Leu Gly Asp
130 135 140
Phe Phe Val Gly Cys Ile Phe Thr Ala Glu Leu Ser Thr Pro Phe Val
145 150 155 160
Ser Leu Gly Arg Val Leu Ile Gln Leu Lys Gln Gln His Thr Leu Leu
165 170 175
Tyr Lys Val Asn Gly Ile Leu Thr Leu Ala Thr Phe Leu Ser Cys Arg

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            180                 185                 190
Ile Leu Leu Phe Pro Phe Met Tyr Trp Ser Tyr Gly Arg Gln Gln Gly
        195                 200                 205
Leu Ser Leu Leu Gln Val Pro Phe Ser Ile Pro Phe Tyr Cys Asn Val
    210                 215                 220
Ala Asn Ala Phe Leu Val Ala Pro Gln Ile Tyr Trp Phe Cys Leu Leu
225                 230                 235                 240
Cys Arg Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys Asp
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Gly
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<211> 735
<212> DNA
<213> Homo sapiens

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360
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420
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540
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735

<210> 4182
<211> 192
<212> PRT
<213> Homo sapiens

<400> 4182
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Val Ser Tyr Thr Phe Leu Tyr Trp Leu Pro Leu Tyr Ile Ala Asn Val
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            20                  25                  30
Ala His Phe Ser Ala Lys Glu Ala Gly Asp Leu Ser Thr Leu Phe Asp
        35                  40                  45
Val Gly Gly Ile Ile Gly Gly Ile Val Ala Gly Leu Val Ser Asp Tyr
    50                  55                  60
Thr Asn Gly Arg Ala Thr Thr Cys Cys Val Met Leu Ile Leu Ala Ala
65                  70                  75                  80
Pro Met Met Phe Leu Tyr Asn Tyr Ile Gly Gln Asp Gly Ile Ala Ser
                85                  90                  95
Ser Ile Val Met Leu Ile Ile Cys Gly Gly Leu Val Asn Gly Pro Tyr
            100                 105                 110
Ala Xaa Ile Thr Thr Ala Val Ser Ala Asp Leu Gly Thr His Lys Ser
        115                 120                 125
Leu Lys Gly Asn Ala Lys Ala Leu Ser Thr Val Thr Ala Ile Ile Asp
    130                 135                 140
Gly Thr Gly Ser Ile Gly Ala Ala Leu Gly Pro Leu Leu Ala Gly Leu
145                 150                 155                 160
Ile Ser Pro Thr Gly Trp Asn Asn Val Phe Tyr Met Leu Ile Ser Ala
                165                 170                 175
Asp Val Leu Ala Cys Leu Leu Leu Cys Arg Leu Val Tyr Lys Glu Ile
            180                 185                 190
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<210> 4183
<211> 1129
<212> DNA
<213> Homo sapiens

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420
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480
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720
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780

gtcctcactt gaaccatgtc taggattatc agcatgatga ttagctgaat tgccagacaa
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900
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960
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1020
aaatctgttc ccagagcttg tctgtggtgg cacaaaccgg ctggaggggc tatgtgagat
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agtggtttgt tgataattgg aagatgcagg actactgtgc atggaattc
1129

<210> 4184
<211> 374
<212> PRT
<213> Homo sapiens

<400> 4184
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35 40 45
Gln Ser Pro Ala Gly Tyr Met Pro Tyr Ser His Pro Ser Ser Tyr Thr
50 55 60
Thr His Pro Gln Met Gln Gln Ala Ser Val Ser Ser Pro Ile Val Ala
65 70 75 80
Gly Gly Leu Arg Asn Ile His Asp Asn Lys Val Ser Gly Pro Leu Ser
85 90 95
Gly Asn Ser Ala Asn His His Ala Asp Asn Pro Arg His Gly Ser Ser
100 105 110
Glu Asp Tyr Leu His Met Val His Arg Leu Ser Ser Asp Asp Gly Asp
115 120 125
Ser Ser Thr Met Arg Asn Ala Ala Ser Phe Pro Leu Arg Ser Pro Gln
130 135 140
Pro Val Cys Ser Pro Ala Gly Ser Glu Gly Thr Pro Lys Gly Ser Arg
145 150 155 160
Pro Pro Leu Ile Leu Gln Ser Gln Ser Leu Pro Cys Ser Ser Pro Arg
165 170 175
Asp Val Pro Pro Asp Ile Leu Leu Asp Ser Pro Glu Arg Lys Gln Lys
180 185 190
Lys Gln Lys Lys Met Lys Leu Gly Lys Asp Glu Lys Glu Gln Ser Glu
195 200 205
Lys Ala Ala Met Tyr Asp Ile Ile Ser Ser Pro Ser Lys Asp Ser Thr
210 215 220
Lys Leu Thr Leu Arg Leu Ser Arg Val Arg Ser Ser Asp Met Asp Gln
225 230 235 240
Gln Glu Asp Met Leu Ser Gly Met Glu Asn Ser Asn Val Ser Glu Asn
245 250 255
Asp Ile Pro Phe Asn Val Gln Tyr Gln Gly Gln Thr Ser Lys Thr Pro
260 265 270
Ile Thr Pro Gln Asp Val Asn Arg Pro Leu Asn Ala Ala Gln Cys Leu

```
        275                 280                 285
Ser Gln Gln Glu Gln Thr Ala Phe Leu Pro Ala Asn Gln Val Pro Val
    290                 295                 300
Leu Gln Gln Asn Thr Ser Val Ala Thr Lys Gln Pro Gln Thr Ser Val
305                 310                 315                 320
Val Gln Asn Gln Gln Gln Ile Ser Gln Gln Gly Pro Ile Tyr Asp Glu
                325                 330                 335
Val Glu Leu Asp Ala Leu Ala Glu Ile Glu Arg Ile Glu Arg Glu Ser
            340                 345                 350
Ala Ile Glu Arg Glu Arg Phe Ser Lys Glu Val Gln Asp Lys Asp Lys
        355                 360                 365
Pro Leu Lys Lys Lys Lys
    370
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<210> 4185
<211> 1481
<212> DNA
<213> Homo sapiens

<400> 4185
ntggtgttta agagtttgga caaaaagaat gatggacgca ttgacgcgca ggagatcatg
60
cagtccctgc gggacttggg agtcaagata tctgaacagc aggcagaaaa aattctcaag
120
agcatggata aaaacggcac gatgaccatc gactggaacg agtggagaga ctaccacctc
180
ctccaccccg tggaaaacat ccccgagatc atcctctact ggaagcattc cacgatcttt
240
gatgtgggtg agaatctaac ggtcccggat gagttcacag tggaggagag gcagacgggg
300
atgtggtgga gacacctggt ggcaggaggt ggggcagggg ccgtatccag aacctgcacg
360
gccccctgg acaggctcaa ggtgctcatg caggtccatg cctcccgcag caacaacatg
420
ggcatcgttg gtggcttcac tcagatgatt cgagaaggag gggccaggtc actctggcgg
480
ggcaatggca tcaacgtcct caaaattgcc cccgaatcag ccatcaaatt catggcctat
540
gagcagatca agcgccttgt tggtagtgac caggagactc tgaggattca cgagaggctt
600
gtggcagggt ccttggcagg ggccatcgcc cagagcagca tctacccaat ggaggtcctg
660
aagacccgga tggcgctgcg gaagacaggc cagtactcag gaatgctgga ctgcgccagg
720
aggatcctgg ccagagaggg ggtggccgcc ttctacaaag gctatgtccc caacatgctg
780
ggcatcatcc cctatgccgg catcgacctt gcagtctacg agacgctcaa gaatgcctgg
840
ctgcagcact atgcagtgaa cagcgcggac cccggcgtgt ttgtgctcct ggcctgtggc
900
accatgtcca gtacctgtgg ccagctggcc agctaccccc tggccctagt caggacccgg
960
atgcaggcgc aagcctctat tgagggcgct ccggaggtga ccatgagcag cctcttcaaa
1020

catatcctgc ggaccgaggg ggccttcggg ctgtacaggg ggctggcccc caacttcatg
1080
aaggtcatcc cagctgtgag catcagctac gtggtctacg agaacctgaa gatcaccctg
1140
ggcgtgcagt cgcggtgacg gggggagggc cgcccggcag tggactcgct gatcctgggc
1200
cgcagcctgg ggtgtgcagc catctcattc tgtgaatgtg ccaacactaa gctgtctcga
1260
gccaagctgt gaaaacccta gacgcacccg cagggagggt ggggagagct ggcaggccca
1320
gggcttgtcc tgctgacccc agcagaccct cctgttggtt ccagcgaaga ccacaggcat
1380
tccttagggt ccagggtcag caggctccgg gctcacatgt gtaaggacag gacattttct
1440
gcagtgcctg ccaatagtga gcttggagcc tggaggccgg c
1481

<210> 4186
<211> 385
<212> PRT
<213> Homo sapiens

<400> 4186
Xaa Val Phe Lys Ser Leu Asp Lys Lys Asn Asp Gly Arg Ile Asp Ala
 1   5   10   15
Gln Glu Ile Met Gln Ser Leu Arg Asp Leu Gly Val Lys Ile Ser Glu
            20   25   30
Gln Gln Ala Glu Lys Ile Leu Lys Ser Met Asp Lys Asn Gly Thr Met
        35   40   45
Thr Ile Asp Trp Asn Glu Trp Arg Asp Tyr His Leu Leu His Pro Val
    50   55   60
Glu Asn Ile Pro Glu Ile Ile Leu Tyr Trp Lys His Ser Thr Ile Phe
65   70   75   80
Asp Val Gly Glu Asn Leu Thr Val Pro Asp Glu Phe Thr Val Glu Glu
                85   90   95
Arg Gln Thr Gly Met Trp Trp Arg His Leu Val Ala Gly Gly Gly Ala
            100   105   110
Gly Ala Val Ser Arg Thr Cys Thr Ala Pro Leu Asp Arg Leu Lys Val
        115   120   125
Leu Met Gln Val His Ala Ser Arg Ser Asn Asn Met Gly Ile Val Gly
    130   135   140
Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Arg Ser Leu Trp Arg
145   150   155   160
Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro Glu Ser Ala Ile Lys
                165   170   175
Phe Met Ala Tyr Glu Gln Ile Lys Arg Leu Val Gly Ser Asp Gln Glu
            180   185   190
Thr Leu Arg Ile His Glu Arg Leu Val Ala Gly Ser Leu Ala Gly Ala
        195   200   205
Ile Ala Gln Ser Ser Ile Tyr Pro Met Glu Val Leu Lys Thr Arg Met
    210   215   220
Ala Leu Arg Lys Thr Gly Gln Tyr Ser Gly Met Leu Asp Cys Ala Arg
225   230   235   240
Arg Ile Leu Ala Arg Glu Gly Val Ala Ala Phe Tyr Lys Gly Tyr Val

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                245                 250                 255
Pro Asn Met Leu Gly Ile Ile Pro Tyr Ala Gly Ile Asp Leu Ala Val
            260                 265                 270
Tyr Glu Thr Leu Lys Asn Ala Trp Leu Gln His Tyr Ala Val Asn Ser
        275                 280                 285
Ala Asp Pro Gly Val Phe Val Leu Leu Ala Cys Gly Thr Met Ser Ser
    290                 295                 300
Thr Cys Gly Gln Leu Ala Ser Tyr Pro Leu Ala Leu Val Arg Thr Arg
305                 310                 315                 320
Met Gln Ala Gln Ala Ser Ile Glu Gly Ala Pro Glu Val Thr Met Ser
                325                 330                 335
Ser Leu Phe Lys His Ile Leu Arg Thr Glu Gly Ala Phe Gly Leu Tyr
            340                 345                 350
Arg Gly Leu Ala Pro Asn Phe Met Lys Val Ile Pro Ala Val Ser Ile
        355                 360                 365
Ser Tyr Val Val Tyr Glu Asn Leu Lys Ile Thr Leu Gly Val Gln Ser
    370                 375                 380
Arg
385
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<210> 4187
<211> 1087
<212> DNA
<213> Homo sapiens

<400> 4187
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60
gctgattctt ttcctgacag ttccccttat gagggttaca actatggctc ctttgagaat
120
gtttctggat ctaccgatgg tctggttgac agcgctggca ctggggacct ctcttacggt
180
taccagggcc gctcctttga acctgtaggt actcggcccc gagtggactc catgagctct
240
gtggaggagg atgactacga cacattgacc gacatcgatt ccgacaagaa tgtcattcgc
300
accaagcaat acctctatgt ggctgacctg gcacggaagg acaagcgtgt tctgcggaaa
360
aagtaccaga tctacttctg gaacattgcc accattgctg tcttctatgc ccttcctgtg
420
gtgcagctgg tgatcaccta cccagaggnn ggnggatgta cnaggggatc nagggacatc
480
tgctcntcna acttcctctg cgcccaccca ctgggcaatc tcagcgcctt caacaacatc
540
ctcagcaacc tggggtacat cctgctgggg ctgcttttcc tgctcatcat cctgcaacgg
600
gagatcaacc acaaccgggc cctgctgcgc aatgacctct gtgccctgga atgtgggatc
660
cccaaacact ttgggctttt ctacgccatg ggcacagccc tgatgatgga ggggctgctc
720
agtgcttgct atcatgtgtg ccccaactat accaatttcc agtttggtga gtggggcgtc
780
cttcttttct ggctcaacct acagcaggga cctgcctgag tccttcacta tccccaagtc
840

acccacaggg atcgctaaga cacccctgta ggaaactcca aggctggcgt gcctgggtgt
900
gcacacatcc tagcctatgg aacatgggca cctagatgct gcttcattca tctgtcaagc
960
tattcctatg taaaggcatg tgccgcagtg aagaaaacag tataattaag aaggggtccc
1020
tggccgggtg cagtggctca cgcctgtaat cccagcactt tgggaggcag aggcgggtgg
1080
atcatga
1087

<210> 4188
<211> 272
<212> PRT
<213> Homo sapiens

<400> 4188
Xaa Ala Ile Asp Arg Ala Cys Pro Glu Ser Ala Ser Leu Leu Gly His
1 5 10 15
Pro Arg Val Leu Ala Asp Ser Phe Pro Asp Ser Ser Pro Tyr Glu Gly
20 25 30
Tyr Asn Tyr Gly Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu
35 40 45
Val Asp Ser Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg
50 55 60
Ser Phe Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser
65 70 75 80
Val Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys
85 90 95
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala Arg
100 105 110
Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn
115 120 125
Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val
130 135 140
Ile Thr Tyr Pro Glu Xaa Gly Gly Cys Thr Arg Gly Ser Arg Asp Ile
145 150 155 160
Cys Ser Ser Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala
165 170 175
Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu
180 185 190
Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu
195 200 205
Leu Arg Asn Asp Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe
210 215 220
Gly Leu Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu
225 230 235 240
Ser Ala Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Gly
245 250 255
Glu Trp Gly Val Leu Leu Phe Trp Leu Asn Leu Gln Gln Gly Pro Ala
260 265 270

<210> 4189
<211> 1570

<212> DNA
<213> Homo sapiens

<400> 4189
agatctattc gatcttttgc taatgatgat cgccatgtta tggtgaaaca ttcaacaatc
60
tatccatctc cggaggaact tgaagctgtt cagaatatgg tatctactgt tgaatgtgct
120
cttaaacatg tctcagattg gttggatgaa acaaataaag gcacaaaaac agagggtgag
180
acagaagtga agaaagatga ggccggagaa aactattcca aggatcaagg tggtcggaca
240
ttgtgtggtg taatgaggat tggcctggtt gcaaaaggct tgctgattaa agatgatatg
300
gacttggagc tggttttaat gtgcaaagac aaacccacag agaccctgtt aaatacagtc
360
aaagataatc ttcctattca gattcagaaa ctcacagaag agaaatatca agtggaacaa
420
tgtgtaaatg aggcatctat tataattcgg aatacaaaag agcccacgct aactttgaag
480
gtgatactta cctcacctct aattagggac gaattggaga agaaggatgg agaaaatgtt
540
tcgatgaaag atcctccgga cttattggac aggcagaaat gcctgaacgc cttggcgtct
600
cttcgacatg ccaaatggtt tcaggcaagg gcaaatggat taaaatcatg tgtaattgtc
660
ctccgcattc tgcgtgattt gtgcaacaga gtccccacat gggcaccatt gaaaggatgg
720
ccactagaac ttatatgtga aaagtctata ggtacttgta atagaccttt gggcgctggg
780
gaggccttga gacgagtaat ggagtgtttg gcatctggaa tactacttcc tgggggtcct
840
ggtcttcatg atccttgtga gcgagaccca acagatgctc tgagctatat gaccatccag
900
caaaaagaag atattaccca cagtgcacag catgcactca gactatcagc ctttggtcag
960
atttacaaag tgctggagat ggacccccct ccatctagta agccttttca gaagtattcc
1020
tggtcagtta ctgataaaga aggtgctggg tcttcagctc taaagaggcc atttgaagat
1080
ggattagggg atgataaaga ccccaacaag aagatgaaac gaaacttaag gaaaattctg
1140
gatagtaaag caatagacct tatgaatgca ctaatgaggc taaatcagat caggcctggg
1200
cttcagtata agctcctatc tcagtctggc tccgttcatg ccccagtctt cacaatgtct
1260
gtagatgtgg atggcacaac atatgaagcc tcaggaccat ccaagaaaac agcaaaactt
1320
cacgtagcgg tgaaggtatt gcaggcaatg ggatatccaa caggctttga tgcagatatt
1380
gaatgtatga gttccgatga aaaaagaaga ggtctcaagt atgaactcat ctcagagact
1440
ggtggaagcc atgacaagcg ctttgtaatg gaggtagaag tagatggaca gaaattcaga
1500

ggcgcaggtc caaataagaa agtggcaaag gcgagtgcag ctttactcgc tnntggagaa
1560
actgtttttct
1570

<210> 4190
<211> 523
<212> PRT
<213> Homo sapiens

<400> 4190
Arg Ser Ile Arg Ser Phe Ala Asn Asp Asp Arg His Val Met Val Lys
1 5 10 15
His Ser Thr Ile Tyr Pro Ser Pro Glu Glu Leu Glu Ala Val Gln Asn
20 25 30
Met Val Ser Thr Val Glu Cys Ala Leu Lys His Val Ser Asp Trp Leu
35 40 45
Asp Glu Thr Asn Lys Gly Thr Lys Thr Glu Gly Glu Thr Glu Val Lys
50 55 60
Lys Asp Glu Ala Gly Glu Asn Tyr Ser Lys Asp Gln Gly Gly Arg Thr
65 70 75 80
Leu Cys Gly Val Met Arg Ile Gly Leu Val Ala Lys Gly Leu Leu Ile
85 90 95
Lys Asp Asp Met Asp Leu Glu Leu Val Leu Met Cys Lys Asp Lys Pro
100 105 110
Thr Glu Thr Leu Leu Asn Thr Val Lys Asp Asn Leu Pro Ile Gln Ile
115 120 125
Gln Lys Leu Thr Glu Glu Lys Tyr Gln Val Glu Gln Cys Val Asn Glu
130 135 140
Ala Ser Ile Ile Ile Arg Asn Thr Lys Glu Pro Thr Leu Thr Leu Lys
145 150 155 160
Val Ile Leu Thr Ser Pro Leu Ile Arg Asp Glu Leu Glu Lys Lys Asp
165 170 175
Gly Glu Asn Val Ser Met Lys Asp Pro Pro Asp Leu Leu Asp Arg Gln
180 185 190
Lys Cys Leu Asn Ala Leu Ala Ser Leu Arg His Ala Lys Trp Phe Gln
195 200 205
Ala Arg Ala Asn Gly Leu Lys Ser Cys Val Ile Val Leu Arg Ile Leu
210 215 220
Arg Asp Leu Cys Asn Arg Val Pro Thr Trp Ala Pro Leu Lys Gly Trp
225 230 235 240
Pro Leu Glu Leu Ile Cys Glu Lys Ser Ile Gly Thr Cys Asn Arg Pro
245 250 255
Leu Gly Ala Gly Glu Ala Leu Arg Arg Val Met Glu Cys Leu Ala Ser
260 265 270
Gly Ile Leu Leu Pro Gly Gly Pro Gly Leu His Asp Pro Cys Glu Arg
275 280 285
Asp Pro Thr Asp Ala Leu Ser Tyr Met Thr Ile Gln Gln Lys Glu Asp
290 295 300
Ile Thr His Ser Ala Gln His Ala Leu Arg Leu Ser Ala Phe Gly Gln
305 310 315 320
Ile Tyr Lys Val Leu Glu Met Asp Pro Leu Pro Ser Ser Lys Pro Phe
325 330 335
Gln Lys Tyr Ser Trp Ser Val Thr Asp Lys Glu Gly Ala Gly Ser Ser

```
            340                 345                 350
Ala Leu Lys Arg Pro Phe Glu Asp Gly Leu Gly Asp Asp Lys Asp Pro
        355                 360                 365
Asn Lys Lys Met Lys Arg Asn Leu Arg Lys Ile Leu Asp Ser Lys Ala
    370                 375                 380
Ile Asp Leu Met Asn Ala Leu Met Arg Leu Asn Gln Ile Arg Pro Gly
385                 390                 395                 400
Leu Gln Tyr Lys Leu Leu Ser Gln Ser Gly Pro Val His Ala Pro Val
                405                 410                 415
Phe Thr Met Ser Val Asp Val Asp Gly Thr Thr Tyr Glu Ala Ser Gly
            420                 425                 430
Pro Ser Lys Lys Thr Ala Lys Leu His Val Ala Val Lys Val Leu Gln
        435                 440                 445
Ala Met Gly Tyr Pro Thr Gly Phe Asp Ala Asp Ile Glu Cys Met Ser
    450                 455                 460
Ser Asp Glu Lys Arg Arg Gly Leu Lys Tyr Glu Leu Ile Ser Glu Thr
465                 470                 475                 480
Gly Gly Ser His Asp Lys Arg Phe Val Met Glu Val Glu Val Asp Gly
                485                 490                 495
Gln Lys Phe Arg Gly Ala Gly Pro Asn Lys Lys Val Ala Lys Ala Ser
            500                 505                 510
Ala Ala Leu Leu Ala Xaa Gly Glu Thr Val Phe
        515                 520
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<210> 4191
<211> 1661
<212> DNA
<213> Homo sapiens

<400> 4191
nngccggcga cagtcggggt tgcgagcggc ccggggccgg ggcggccagg gccgctgcag
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gacgagaccc tgggtgtggc gtccgtgccc tcgcagtgga gggccgtcca gggcatccgc
120
ggggagacga aaagttgcca gacggccagc attgccactg ccagtgcatc cgcccaggcc
180
aggaatcatg tggacgccca ggtgcagacg gaggcccccg tgcctgtcag cgtgcagccc
240
ccgtcccagt acgacatacc caggctcgca gcctttcttc ggagagtgga ggccatggtc
300
atccgagagc tgaacaagaa ttggcagagc cacgcgtttg atggcttcga ggtgaactgg
360
accgagcagc agcagatggt gtcttgtctg tataccctgg gctacccgcc agcccaagcg
420
cagggtctgc atgtgaccag catctcctgg aactccactg gctctgtggt ggcctgtgcc
480
tacggccggc tggaccatgg ggactggagc acgcttaagt ccttcgtgtg tgcctggaac
540
ctggaccggc gagacctgcg tccccagcaa ccgtcggccg tggtggaggt ccccagcgct
600
gtcctgtgtc tggccttcca ccccacgcag ccctcccacg tcgcaggagg gctgtacagt
660
ggtgaggtgt tggtgtggga cctgagccgt cttgaggacc cgctgctgtg gcgcacaggc
720

ctgacggatg acacccacac agaccctgtg tcccaggtgg tgtggctgcc cgagcctggg
780
cacagccacc gcttccaggt gctgagtgtg gccactgacg ggaaggtgct actctggcag
840
ggcatcgggg taggccagct gcagctcaca gagggcttcg ccctggtcat gcagcagctg
900
ccacggagca ccaagctcaa gaagcatccc cgcggggaga ccgaggtggg cgccacggca
960
gtggccttct ccagctttga ccctaggctg ttcattctgg gcacggaagg cggcttcccg
1020
ctcaagtgtt ccctggcagc tggagaggca gccctcacgc ggatgcccag ctccgtgccc
1080
ctgcgggccc cagcacagtt taccttctcc ccccacggcg gtcccatcta ctctgtgagc
1140
tgttcccccc tccacaggaa tctcttcctg agcgctggga ctgacgggca tgtccacctg
1200
tactccatgc tgcaggcccc tcccttgact tcgctgcagc tctccctcaa gtatctgttt
1260
gctgtgcgct ggtccccagt gcggcccttg gtttttgcag ctgcctctgg gaaaggtgac
1320
gtgcagctgt ttgatctcca gaaaagctcc cagaaaccca cagttttgat caagcaaacc
1380
caggatgaaa gccctgtcta ctgtctggag ttcaacagcc agcagactca gctcttggct
1440
gcgggcgatg cccagggcac agtgaaggtg tggcagctga gcacagagtt cacggaacaa
1500
gggccccggg aagctgagga cctggactgc ctggcagcag aggtggcggc ctgaggggtc
1560
ccgggaggcg ggtgcaagcc ttcgctgtgc cgagccttgt gtttctgacg caagccaaat
1620
gaagaaaagc aaagctttaa aaaaaaaaaa aaaaaaaaaa a
1661

<210> 4192
<211> 517
<212> PRT
<213> Homo sapiens

<400> 4192
Xaa Pro Ala Thr Val Gly Val Ala Ser Gly Pro Gly Pro Gly Arg Pro
1 5 10 15
Gly Pro Leu Gln Asp Glu Thr Leu Gly Val Ala Ser Val Pro Ser Gln
20 25 30
Trp Arg Ala Val Gln Gly Ile Arg Gly Glu Thr Lys Ser Cys Gln Thr
35 40 45
Ala Ser Ile Ala Thr Ala Ser Ala Ser Ala Gln Ala Arg Asn His Val
50 55 60
Asp Ala Gln Val Gln Thr Glu Ala Pro Val Pro Val Ser Val Gln Pro
65 70 75 80
Pro Ser Gln Tyr Asp Ile Pro Arg Leu Ala Ala Phe Leu Arg Arg Val
85 90 95
Glu Ala Met Val Ile Arg Glu Leu Asn Lys Asn Trp Gln Ser His Ala
100 105 110
Phe Asp Gly Phe Glu Val Asn Trp Thr Glu Gln Gln Gln Met Val Ser

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        115                 120                 125
Cys Leu Tyr Thr Leu Gly Tyr Pro Pro Ala Gln Ala Gln Gly Leu His
    130                 135                 140
Val Thr Ser Ile Ser Trp Asn Ser Thr Gly Ser Val Val Ala Cys Ala
145                 150                 155                 160
Tyr Gly Arg Leu Asp His Gly Asp Trp Ser Thr Leu Lys Ser Phe Val
                165                 170                 175
Cys Ala Trp Asn Leu Asp Arg Arg Asp Leu Arg Pro Gln Gln Pro Ser
            180                 185                 190
Ala Val Val Glu Val Pro Ser Ala Val Leu Cys Leu Ala Phe His Pro
        195                 200                 205
Thr Gln Pro Ser His Val Ala Gly Gly Leu Tyr Ser Gly Glu Val Leu
    210                 215                 220
Val Trp Asp Leu Ser Arg Leu Glu Asp Pro Leu Leu Trp Arg Thr Gly
225                 230                 235                 240
Leu Thr Asp Asp Thr His Thr Asp Pro Val Ser Gln Val Val Trp Leu
                245                 250                 255
Pro Glu Pro Gly His Ser His Arg Phe Gln Val Leu Ser Val Ala Thr
            260                 265                 270
Asp Gly Lys Val Leu Leu Trp Gln Gly Ile Gly Val Gly Gln Leu Gln
        275                 280                 285
Leu Thr Glu Gly Phe Ala Leu Val Met Gln Gln Leu Pro Arg Ser Thr
    290                 295                 300
Lys Leu Lys Lys His Pro Arg Gly Glu Thr Glu Val Gly Ala Thr Ala
305                 310                 315                 320
Val Ala Phe Ser Ser Phe Asp Pro Arg Leu Phe Ile Leu Gly Thr Glu
                325                 330                 335
Gly Gly Phe Pro Leu Lys Cys Ser Leu Ala Ala Gly Glu Ala Ala Leu
            340                 345                 350
Thr Arg Met Pro Ser Ser Val Pro Leu Arg Ala Pro Ala Gln Phe Thr
        355                 360                 365
Phe Ser Pro His Gly Gly Pro Ile Tyr Ser Val Ser Cys Ser Pro Phe
    370                 375                 380
His Arg Asn Leu Phe Leu Ser Ala Gly Thr Asp Gly His Val His Leu
385                 390                 395                 400
Tyr Ser Met Leu Gln Ala Pro Pro Leu Thr Ser Leu Gln Leu Ser Leu
                405                 410                 415
Lys Tyr Leu Phe Ala Val Arg Trp Ser Pro Val Arg Pro Leu Val Phe
            420                 425                 430
Ala Ala Ala Ser Gly Lys Gly Asp Val Gln Leu Phe Asp Leu Gln Lys
        435                 440                 445
Ser Ser Gln Lys Pro Thr Val Leu Ile Lys Gln Thr Gln Asp Glu Ser
    450                 455                 460
Pro Val Tyr Cys Leu Glu Phe Asn Ser Gln Gln Thr Gln Leu Leu Ala
465                 470                 475                 480
Ala Gly Asp Ala Gln Gly Thr Val Lys Val Trp Gln Leu Ser Thr Glu
                485                 490                 495
Phe Thr Glu Gln Gly Pro Arg Glu Ala Glu Asp Leu Asp Cys Leu Ala
            500                 505                 510
Ala Glu Val Ala Ala
        515
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<210> 4193
<211> 6439

<212> DNA
<213> Homo sapiens

<400> 4193
gaattccggc gtcgcggacg catcccagtc tgggcgggac gctcggccgc ggcgaggcgg
60
gcaagcctgg cagggcagag ggagccccgg ctccgaggtt gctcttcgcc cccgaggatc
120
agtcttggcc ccaaagcgcg acgcacaaat ccacataacc tgaggaccat ggatgctgat
180
gagggtcaag acatgtccca agtttcaggg aaggaaagcc cccctgtaag cgatactcca
240
gatgagggcg atgagcccat gccgatcccc gaggacctct ccaccacctc gggaggacag
300
caaagctcca agagtgacag agtcgtggcc agtaatgtta aagtagagac tcagagtgat
360
gaagagaatg ggcgtgcctg tgaaatgaat ggggaagaat gtgcggagga tttacgaatg
420
cttgatgcct cgggagagaa aatgaatggc tcccacaggg accaaggcag ctcggctttg
480
tcgggagttg gaggcattcg acttcctaac ggaaaactaa agtgtgatat ctgtgggatc
540
atttgcatcg ggcccaatgt gctcatggtt cacaaaagaa gccacactgg agaacggccc
600
ttccagtgca atcagtgcgg ggcctcattc acccagaagg gcaacctgct ccggcacatc
660
aagctgcatt ccggggagaa gcccttcaaa tgccacctct gcaactacgc ctgccgccgg
720
agggacgccc tcactggcca cctgaggacg cactccgttg gtaaacctca caaatgtgga
780
tattgtggcc gaagctataa acagcgaagc tctttagagg aacataaaga gcgctgccac
840
aactacttgg aaagcatggg ccttccgggc acactgtacc cagtcattaa agaagaaact
900
aatcacagtg aaatggcaga agacctgtgc aagataggat cagagagatc tctcgtgctg
960
gacagactag caagtaacgt cgccaaacgt aagagctcta tgcctcagaa atttcttggg
1020
gacaagggcc tgtccgacac gccctacgac agcagcgcca gctacgagaa ggagaacgaa
1080
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6439

<210> 4194
<211> 519
<212> PRT
<213> Homo sapiens

<400> 4194
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Ile Pro Glu Asp Leu Ser Thr Thr Ser Gly Gly Gln Gln Ser Ser Lys
35 40 45
Ser Asp Arg Val Val Ala Ser Asn Val Lys Val Glu Thr Gln Ser Asp
50 55 60
Glu Glu Asn Gly Arg Ala Cys Glu Met Asn Gly Glu Glu Cys Ala Glu
65 70 75 80
Asp Leu Arg Met Leu Asp Ala Ser Gly Glu Lys Met Asn Gly Ser His
85 90 95
Arg Asp Gln Gly Ser Ser Ala Leu Ser Gly Val Gly Gly Ile Arg Leu
100 105 110
Pro Asn Gly Lys Leu Lys Cys Asp Ile Cys Gly Ile Ile Cys Ile Gly
115 120 125
Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro
130 135 140
Phe Gln Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu
145 150 155 160
Leu Arg His Ile Lys Leu His Ser Gly Glu Lys Pro Phe Lys Cys His
165 170 175
Leu Cys Asn Tyr Ala Cys Arg Arg Arg Asp Ala Leu Thr Gly His Leu
180 185 190
Arg Thr His Ser Val Gly Lys Pro His Lys Cys Gly Tyr Cys Gly Arg
195 200 205
Ser Tyr Lys Gln Arg Ser Ser Leu Glu Glu His Lys Glu Arg Cys His
210 215 220
Asn Tyr Leu Glu Ser Met Gly Leu Pro Gly Thr Leu Tyr Pro Val Ile
225 230 235 240
Lys Glu Glu Thr Asn His Ser Glu Met Ala Glu Asp Leu Cys Lys Ile
245 250 255
Gly Ser Glu Arg Ser Leu Val Leu Asp Arg Leu Ala Ser Asn Val Ala
260 265 270
Lys Arg Lys Ser Ser Met Pro Gln Lys Phe Leu Gly Asp Lys Gly Leu
275 280 285
Ser Asp Thr Pro Tyr Asp Ser Ser Ala Ser Tyr Glu Lys Glu Asn Glu
290 295 300
Met Met Lys Ser His Val Met Asp Gln Ala Ile Asn Asn Ala Ile Asn
305 310 315 320
Tyr Leu Gly Ala Glu Ser Leu Arg Pro Leu Val Gln Thr Pro Pro Gly
325 330 335
Gly Ser Glu Val Val Pro Val Ile Ser Pro Met Tyr Gln Leu His Lys

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            340                 345                 350
Pro Leu Ala Glu Gly Thr Pro Arg Ser Asn His Ser Ala Gln Asp Ser
        355                 360                 365
Ala Val Glu Asn Leu Leu Leu Leu Ser Lys Ala Lys Leu Val Pro Ser
    370                 375                 380
Glu Arg Glu Ala Ser Pro Ser Asn Ser Cys Gln Asp Ser Thr Asp Thr
385                 390                 395                 400
Glu Ser Asn Asn Glu Glu Gln Arg Ser Gly Leu Ile Tyr Leu Thr Asn
                405                 410                 415
His Ile Ala Pro His Ala Arg Asn Gly Leu Ser Leu Lys Glu Glu His
            420                 425                 430
Arg Ala Tyr Asp Leu Leu Arg Ala Ala Ser Glu Asn Ser Gln Asp Ala
        435                 440                 445
Leu Arg Val Val Ser Thr Ser Gly Glu Gln Met Lys Val Tyr Lys Cys
    450                 455                 460
Glu His Cys Arg Val Leu Phe Leu Asp His Val Met Tyr Thr Ile His
465                 470                 475                 480
Met Gly Cys His Gly Phe Arg Asp Pro Phe Glu Cys Asn Met Cys Gly
                485                 490                 495
Tyr His Ser Gln Asp Arg Tyr Glu Phe Ser Ser His Ile Thr Arg Gly
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Glu His Arg Phe His Met Ser
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<210> 4195
<211> 1200
<212> DNA
<213> Homo sapiens

<400> 4195
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120
ctggtgctgc tggaggctct ggcccaggcg gacacacaga agatggtgga agcccagcgt
180
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240
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360
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420
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480
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540
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720

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780
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1080
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<210> 4196
<211> 318
<212> PRT
<213> Homo sapiens

<400> 4196
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Phe Ala Thr Leu Ala Leu Ile Leu Leu Val Leu Leu Glu Ala Leu Ala
35 40 45
Gln Ala Asp Thr Gln Lys Met Val Glu Ala Gln Arg Gly Val Gly Pro
50 55 60
Arg Ala Cys Tyr Ser Ile Trp Leu Leu Leu Ala Pro Thr Pro Pro Leu
65 70 75 80
Ser His Cys Leu Gln Ser Pro Gln Lys Gln His Gln Val Cys Gly Asp
85 90 95
Arg Arg Leu Lys Ala Ser Ser Thr Asn Cys Pro Ser Glu Lys Cys Thr
100 105 110
Ala Trp Ala Arg Tyr Ser His Arg Met Asp Ser Leu Gln Lys Gln Asp
115 120 125
Leu Arg Arg Pro Lys Ile His Gly Ala Val Gln Ala Ser Pro Tyr Gln
130 135 140
Pro Pro Thr Leu Ala Ser Leu Gln Arg Leu Leu Trp Val Arg Gln Ala
145 150 155 160
Ala Thr Leu Asn His Ile Asp Glu Val Trp Pro Ser Leu Phe Leu Gly
165 170 175
Asp Ala Tyr Ala Ala Arg Asp Lys Ser Lys Leu Ile Gln Leu Gly Ile
180 185 190
Thr His Val Val Asn Ala Ala Ala Gly Lys Phe Gln Val Asp Thr Gly
195 200 205
Ala Lys Phe Tyr Arg Gly Met Ser Leu Glu Tyr Tyr Gly Ile Glu Ala
210 215 220
Asp Asp Asn Pro Phe Phe Asp Leu Ser Val Tyr Phe Leu Pro Val Ala
225 230 235 240
Arg Tyr Ile Arg Ala Ala Leu Ser Val Pro Gln Gly Arg Val Leu Val

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                245                 250                 255
His Cys Ala Met Gly Val Ser Arg Ser Ala Thr Leu Val Leu Ala Phe
            260                 265                 270
Leu Met Ile Tyr Glu Asn Met Thr Leu Val Glu Ala Ile Gln Thr Val
        275                 280                 285
Gln Ala His Arg Asn Ile Cys Pro Asn Ser Gly Phe Leu Arg Gln Leu
    290                 295                 300
Gln Val Leu Asp Asn Arg Leu Gly Arg Glu Thr Gly Arg Phe
305                 310                 315
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<210> 4197
<211> 597
<212> DNA
<213> Homo sapiens

<400> 4197
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120
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240
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300
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420
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480
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597

<210> 4198
<211> 148
<212> PRT
<213> Homo sapiens

<400> 4198
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Asn Trp Ser Ser Ala Arg Asn Ser Ala Ser Ala Ala Glu Ala Arg Ser
            20                  25                  30
Met Ala Leu Pro Thr Gln Ala Gln Val Val Ile Cys Gly Gly Gly Ile
        35                  40                  45
Thr Gly Thr Ser Val Ala His His Gln Ser Lys Met Gly Trp Lys Asp
    50                  55                  60
Ile Val Leu Leu Glu Gln Gly Arg Leu Ala Ala Gly Ser Thr Arg Phe
65                  70                  75                  80
Cys Ala Gly Ile Leu Ser Thr Ala Arg His Leu Thr Ile Glu Gln Lys
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                85                  90                  95
Met Ala Asp Tyr Ser Asn Lys Leu Tyr Tyr Gln Leu Glu Gln Glu Thr
            100                 105                 110
Gly Ile Gln Thr Gly Tyr Thr Arg Thr Gly Ser Ile Phe Leu Ala Gln
        115                 120                 125
Thr Gln Asp Arg Leu Ile Ser Leu Lys Arg Ile Asn Ala Gly Leu Lys
    130                 135                 140
Tyr Val Arg Val
145
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<210> 4199
<211> 1769
<212> DNA
<213> Homo sapiens

<400> 4199
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240
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300
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1769

<210> 4200
<211> 186
<212> PRT
<213> Homo sapiens

<400> 4200
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Lys Thr Thr Phe Val Asn Val Ile Ala Ser Gly Gln Phe Ser Glu Asp
35 40 45
Met Ile Pro Thr Val Gly Phe Asn Met Arg Lys Val Thr Lys Gly Asn
50 55 60
Val Thr Ile Lys Ile Trp Asp Ile Gly Gly Gln Pro Arg Phe Arg Ser
65 70 75 80
Met Trp Glu Arg Tyr Cys Arg Gly Val Asn Ala Ile Val Tyr Met Ile
85 90 95
Asp Ala Ala Asp Arg Glu Lys Ile Glu Ala Ser Arg Asn Glu Leu His
100 105 110
Asn Leu Leu Asp Lys Pro Gln Leu Gln Gly Ile Pro Val Leu Val Leu
115 120 125
Gly Asn Lys Arg Asp Leu Pro Gly Ala Leu Asp Glu Lys Glu Leu Ile
130 135 140
Glu Lys Met Asn Leu Ser Ala Ile Gln Asp Arg Glu Ile Cys Cys Tyr
145 150 155 160
Ser Ile Ser Cys Lys Glu Lys Asp Asn Ile Asp Ile Thr Leu Gln Trp
165 170 175
Leu Ile Gln His Ser Lys Ser Arg Arg Ser
180 185

<210> 4201
<211> 917
<212> DNA
<213> Homo sapiens

<400> 4201
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120
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180
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240
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His Ser Arg Lys Ser Thr Val Thr Asp Glu Ser Glu Met Gln Asp Met
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Met Thr Arg Gly Asn Leu Gly Leu Leu Glu Gln Ala Ile Ala Leu Lys
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Ala Glu Gln Val Arg Thr Val Cys Glu Pro Gly Cys Pro Pro Ala Glu
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Gln Ser Gln Leu Gly Leu Gly Glu Pro Gly Lys Ala Ala Lys Pro Leu
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Asp Thr Val Arg Lys Ser Tyr Tyr Ser Lys Asp Pro Ser Arg Ala Glu
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Val Thr Gly Leu Tyr Pro His His Arg Ser Leu Ser Gly Cys Pro His
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Arg Asn Thr His Arg Ser Leu Ser Gly Cys Pro Ile Ala Ala Ala Glu
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Ser Lys Val Thr Phe Asp Tyr Ala Ser Phe Asp Ala Gln Val Phe Gly
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Lys Arg Met Leu Ala Pro Lys Ile Gln Thr Ser Glu Thr Ser Pro Lys
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Ala Phe Gln Cys Phe Asp Tyr Ser Gln Asp Ala Glu Ala Ala His Met
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Glu Asn Leu Ser Thr Lys Pro Gln Asp Leu Pro Ser Lys Ser Val Asp
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Ile Glu Val Asp Glu Asn Gly Thr Leu Asp Leu Ser Met His Lys His
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Arg Lys Arg Glu Asn Ala Phe Pro Ser Ser Ser Ser Cys Ser Ser Ser
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Cys Asp Gly Ser Gly His Ile Thr Gly Asn Tyr Ala Ser His Arg Ser
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Ala His Ser Ala Asp Leu Lys Cys Pro Thr Pro Gly Cys Asp Gly Ser
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Gly His Ile Thr Gly Asn Tyr Ala Ser His Arg Ser Leu Ser Gly Cys
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Lys Glu Asp Pro Glu Leu Met Lys Cys Pro Val Pro Gly Cys Val Gly
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Leu Gly His Ile Ser Gly Lys Tyr Ala Ser His Arg Ser Ala Ser Gly
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Gln Ser Gln Ile Ser Ser Met Glu Lys Asn Leu Lys Asn Ile Glu Glu
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<212> DNA
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tgtgttcttc aatgccctct gctccttttt taacaacttc agatacataa tctgtacaac
720
cctgaccatt tgtagtattg gctataggag ccaaacattt tttctcacca tcttgaactg
780
aattattatc gtctggatga tcttgccaaa ctgaaaacac ttcagatgaa ctttcaaact
840
caaaacactg agaatcagat tcctcaaact gaaaaagagt ctctgtcttt tcttccttta
900
ctggattctt ttcctcctta ctattaactg ttgaaacgtg ctgctctgga tgttccctct
960
caaggcatat tttgtcctgt ttagtgagtt tctcaagact caggattctt tcatca
1016

<210> 4208
<211> 193
<212> PRT
<213> Homo sapiens

<400> 4208
Met Ala Glu Asp Pro Val Arg Ser Ser Ser Ser Val Arg Asn Glu Gly
 1   5   10   15
Gln Ser Asp Thr Asn Lys Arg Glu Leu Val Gly Asn Asp Phe Lys Ser
            20   25   30
Ile Asp Arg Arg Thr Ser Thr Pro Asn Ser Arg Ile Gln Arg Ala Thr
        35   40   45
Thr Val Ser Gln Lys Lys Ser Ser Lys Leu Cys Thr Cys Thr Glu Pro
    50   55   60
Ile Arg Lys Val Pro Val Ser Lys Thr Pro Lys Lys Thr His Ser Asp
65   70   75   80
Ala Lys Lys Gly Gln Asn Arg Ser Ser Asn Tyr Leu Ser Cys Arg Thr

```
                85                  90                  95
Thr Pro Ala Ile Val Pro Pro Lys Lys Phe Arg Gln Cys Pro Glu Pro
            100                 105                 110
Thr Ser Thr Ala Glu Lys Leu Gly Leu Lys Lys Gly Pro Arg Lys Ala
        115                 120                 125
Tyr Glu Leu Ser Gln Arg Ser Leu Asp Tyr Val Ala Gln Leu Arg Asp
    130                 135                 140
His Gly Lys Thr Val Gly Val Val Asp Thr Arg Lys Lys Thr Lys Leu
145                 150                 155                 160
Ile Ser Pro Gln Asn Leu Ser Val Arg Asn Asn Lys Lys Leu Leu Thr
                165                 170                 175
Ser Gln Glu Leu Gln Met Gln Arg Gln Ile Arg Pro Lys Ser Gln Lys
            180                 185                 190
Lys
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<210> 4209
<211> 2661
<212> DNA
<213> Homo sapiens

<400> 4209
ntctcctgta cctgggcatc cagaaaaatg gtggtgatgg cgcgactttc gcggcccgag
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cggccggacc ttgtcttcga ggaagaggac ctcccctatg aggaggaaat catgcggaac
120
caattctctg tcaaatgctg gcttcgctac atcgagttca aacagggcgc cccgaagccc
180
aggctcaatc agctatacga gcgggcactc aagctgctgc cctgcagcta caaactctgg
240
taccgatacc tgaaggcgcg tcgggcacag gtgaagcatc gctgtgtgac cgaccctgcc
300
tatgaagatg tcaacaactg tcatgagagg gcctttgtgt tcatgcacaa gatgcctcgt
360
ctgtggctag attactgcca gttcctcatg gaccaggggc gcgtcacaca cacccgccgc
420
accttcgacc gtgccctccg ggcactgccc atcacgcagc actctcgaat ttggcccctg
480
tatctgcgct tcctgcgctc acacccactg cctgagacag ctgtgcgagg ctatcggcgc
540
ttcctcaagc tgagtcctga gagtgcagag gagtacattg agtacctcaa gtcaagtgac
600
cggctggatg aggccgccca gcgcctggcc accgtggtga acgacgagcg tttcgtgtct
660
aaggccggca agtccaacta ccagctgtgg cacgagctgt gcgacctcat ctcccagaat
720
ccggacaagg tacagtccct caatgtggac gccatcatcc gcgggggcct cacccgcttc
780
accgaccagc tgggcaagct ctggtgttct ctcgccgact actacatccg cagcggccat
840
ttcgagaagg ctcgggacgt gtacgaggag gccatccgga cagtgatgac cgtgcgggac
900
ttcacacagg tgtttgacag ctacgcccag ttcgaggaga gcatgatcgc tgcaaagatg
960

gagaccgcct cggagctggg tcgcgaggag gaggatgatg tggacctgga gctgcgcctg
1020
gcccgcttcg agcacctcat cagccggcgg cccctgcacc tcagcagcgt cttgctgcgc
1080
caaaacccac accacgtgca cgagtggcac aagcgtgtcg ccctgcacca gggccgcccc
1140
cgggagatca tcaacaccta cacagaggct gtgcagacgg tggacccctt caaggccaca
1200
ggcaagcccc acactctgtg ggtggcgttt gccaagtttt atgaggacaa cggacagctg
1260
gacgatgccc gtgtcatcct ggagaaggcc accaaggtga acttcaagca ggtggatgac
1320
ctggcaagcg tgtggtgtca gtgcggagag ctggagctcc gacacgagaa ctacgatgag
1380
gccttgcggc tgctgcgaaa ggccacggcg ctgcctccgc cgggccgagt atttgatggt
1440
tcagagcccg tgcagaaccg cgtgtacaag tcactgaagg tctggtccat gctcgccgac
1500
ctggaggaga gcctcggcac cttccagtcc accaaggccg tgtacgaccg catcctggac
1560
ctgcgtatcg caacacccca gatcgtcatc aactatgcca tgttcctgga ggagcacaag
1620
tacttcgagg agagcttcaa ggcgtacgag cgcggcatct cgctgttcaa gtggcccaac
1680
gtgtccgaca tctggagcac ctacctgacc aaattcattg cccgctatgg gggccgcaag
1740
ctggagcggg cacgggacct gtttgaacag gctctggacg gctgcccccc aaaatatgcc
1800
aagaccttgt acctgctgta cgcacagctg gaggaggagt ggggcctggc ccggcatgcc
1860
atggccgtgt acgagcgtgc caccagggcc gtggagcccg cccagcagta tgacatgttc
1920
aacatctaca tcaagcgggc ggccgagatc tatggggtca cccacacccg cggcatctac
1980
cagaaggcca ttgaggtgct gtcggacgag cacgcgcgtg agatgtgcct gcggtttgca
2040
gacatggagt gcaagctcgg ggagatcgac cgcgcccggg ctatctacag cttctgctcc
2100
cagatctgtg atccccggac aactggggca ttctggcaaa cgtggaagga ctttgaggtc
2160
cggcatggca acgaggacac catcagggag atgctgagga tacggcggag tgtgcaggcc
2220
acgtacaaca ctcaggtcaa cttcatggcc tcgcagatgc tcaaggtgtc gggcagtgcc
2280
acgggcaccg tgtctgacct ggctcccggg cagagcggca tggatgacat gaagttgctg
2340
gaacagagag cagaacagct ggcggctgag gcggagcgtg accagccctt gcgcgcccag
2400
agcaagatcc tgttcgtgag gagtgacgcc tcccgggagg agctggcaga gctggcacag
2460
caggtcaacc ccgaggagat ccagctgggc gaggacgagg acgaggacga gatggacctg
2520
gagcccaacg aggttcggct ggagcagcag agcgtgccag ccgcagtgtt tgggagcctg
2580

aaggaagact gacccgtccc tcccccatcc cccctcccca ccccctcccc aatacagcta
2640
cgtttgtaca tcaaaaaaaa a
2661

<210> 4210
<211> 863
<212> PRT
<213> Homo sapiens

<400> 4210
Xaa Ser Cys Thr Trp Ala Ser Arg Lys Met Val Val Met Ala Arg Leu
1 5 10 15
Ser Arg Pro Glu Arg Pro Asp Leu Val Phe Glu Glu Glu Asp Leu Pro
20 25 30
Tyr Glu Glu Glu Ile Met Arg Asn Gln Phe Ser Val Lys Cys Trp Leu
35 40 45
Arg Tyr Ile Glu Phe Lys Gln Gly Ala Pro Lys Pro Arg Leu Asn Gln
50 55 60
Leu Tyr Glu Arg Ala Leu Lys Leu Leu Pro Cys Ser Tyr Lys Leu Trp
65 70 75 80
Tyr Arg Tyr Leu Lys Ala Arg Arg Ala Gln Val Lys His Arg Cys Val
85 90 95
Thr Asp Pro Ala Tyr Glu Asp Val Asn Asn Cys His Glu Arg Ala Phe
100 105 110
Val Phe Met His Lys Met Pro Arg Leu Trp Leu Asp Tyr Cys Gln Phe
115 120 125
Leu Met Asp Gln Gly Arg Val Thr His Thr Arg Arg Thr Phe Asp Arg
130 135 140
Ala Leu Arg Ala Leu Pro Ile Thr Gln His Ser Arg Ile Trp Pro Leu
145 150 155 160
Tyr Leu Arg Phe Leu Arg Ser His Pro Leu Pro Glu Thr Ala Val Arg
165 170 175
Gly Tyr Arg Arg Phe Leu Lys Leu Ser Pro Glu Ser Ala Glu Glu Tyr
180 185 190
Ile Glu Tyr Leu Lys Ser Ser Asp Arg Leu Asp Glu Ala Ala Gln Arg
195 200 205
Leu Ala Thr Val Val Asn Asp Glu Arg Phe Val Ser Lys Ala Gly Lys
210 215 220
Ser Asn Tyr Gln Leu Trp His Glu Leu Cys Asp Leu Ile Ser Gln Asn
225 230 235 240
Pro Asp Lys Val Gln Ser Leu Asn Val Asp Ala Ile Ile Arg Gly Gly
245 250 255
Leu Thr Arg Phe Thr Asp Gln Leu Gly Lys Leu Trp Cys Ser Leu Ala
260 265 270
Asp Tyr Tyr Ile Arg Ser Gly His Phe Glu Lys Ala Arg Asp Val Tyr
275 280 285
Glu Glu Ala Ile Arg Thr Val Met Thr Val Arg Asp Phe Thr Gln Val
290 295 300
Phe Asp Ser Tyr Ala Gln Phe Glu Glu Ser Met Ile Ala Ala Lys Met
305 310 315 320
Glu Thr Ala Ser Glu Leu Gly Arg Glu Glu Glu Asp Asp Val Asp Leu
325 330 335
Glu Leu Arg Leu Ala Arg Phe Glu His Leu Ile Ser Arg Arg Pro Leu

```
            340                 345                 350
His Leu Ser Ser Val Leu Leu Arg Gln Asn Pro His His Val His Glu
        355                 360                 365
Trp His Lys Arg Val Ala Leu His Gln Gly Arg Pro Arg Glu Ile Ile
    370                 375                 380
Asn Thr Tyr Thr Glu Ala Val Gln Thr Val Asp Pro Phe Lys Ala Thr
385                 390                 395                 400
Gly Lys Pro His Thr Leu Trp Val Ala Phe Ala Lys Phe Tyr Glu Asp
                405                 410                 415
Asn Gly Gln Leu Asp Asp Ala Arg Val Ile Leu Glu Lys Ala Thr Lys
            420                 425                 430
Val Asn Phe Lys Gln Val Asp Asp Leu Ala Ser Val Trp Cys Gln Cys
        435                 440                 445
Gly Glu Leu Glu Leu Arg His Glu Asn Tyr Asp Glu Ala Leu Arg Leu
    450                 455                 460
Leu Arg Lys Ala Thr Ala Leu Pro Pro Pro Gly Arg Val Phe Asp Gly
465                 470                 475                 480
Ser Glu Pro Val Gln Asn Arg Val Tyr Lys Ser Leu Lys Val Trp Ser
                485                 490                 495
Met Leu Ala Asp Leu Glu Glu Ser Leu Gly Thr Phe Gln Ser Thr Lys
            500                 505                 510
Ala Val Tyr Asp Arg Ile Leu Asp Leu Arg Ile Ala Thr Pro Gln Ile
        515                 520                 525
Val Ile Asn Tyr Ala Met Phe Leu Glu Glu His Lys Tyr Phe Glu Glu
    530                 535                 540
Ser Phe Lys Ala Tyr Glu Arg Gly Ile Ser Leu Phe Lys Trp Pro Asn
545                 550                 555                 560
Val Ser Asp Ile Trp Ser Thr Tyr Leu Thr Lys Phe Ile Ala Arg Tyr
                565                 570                 575
Gly Gly Arg Lys Leu Glu Arg Ala Arg Asp Leu Phe Glu Gln Ala Leu
            580                 585                 590
Asp Gly Cys Pro Pro Lys Tyr Ala Lys Thr Leu Tyr Leu Leu Tyr Ala
        595                 600                 605
Gln Leu Glu Glu Glu Trp Gly Leu Ala Arg His Ala Met Ala Val Tyr
    610                 615                 620
Glu Arg Ala Thr Arg Ala Val Glu Pro Ala Gln Gln Tyr Asp Met Phe
625                 630                 635                 640
Asn Ile Tyr Ile Lys Arg Ala Ala Glu Ile Tyr Gly Val Thr His Thr
                645                 650                 655
Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu Ser Asp Glu His Ala
            660                 665                 670
Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu Cys Lys Leu Gly Glu
        675                 680                 685
Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys Ser Gln Ile Cys Asp
    690                 695                 700
Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp Lys Asp Phe Glu Val
705                 710                 715                 720
Arg His Gly Asn Glu Asp Thr Ile Arg Glu Met Leu Arg Ile Arg Arg
                725                 730                 735
Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn Phe Met Ala Ser Gln
            740                 745                 750
Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr Val Ser Asp Leu Ala
        755                 760                 765
Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu Leu Glu Gln Arg Ala
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    770                 775                 780
Glu Gln Leu Ala Ala Glu Ala Glu Arg Asp Gln Pro Leu Arg Ala Gln
785                 790                 795                 800
Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser Arg Glu Glu Leu Ala
                805                 810                 815
Glu Leu Ala Gln Gln Val Asn Pro Glu Glu Ile Gln Leu Gly Glu Asp
            820                 825                 830
Glu Asp Glu Asp Glu Met Asp Leu Glu Pro Asn Glu Val Arg Leu Glu
        835                 840                 845
Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser Leu Lys Glu Asp
    850                 855                 860
```

<210> 4211
<211> 456
<212> DNA
<213> Homo sapiens

<400> 4211
ggggatcgct agcccccagc ttctcagaac taaatatgaa agctcttgct cgtctacgct
60
tagttacaac agactccctg ggcctactgt aggggtcaag agcagatttc cagactctca
120
agctggaaaa gagacgctcc acactgcgac gacaaccaac acatgggaca agctgagaaa
180
gtgcactcag gacttcgcgt gatgtcacca ccatggcaat acttagatcc tgttgcttaa
240
gcataccatg tcgctgaaag agggaaagaa aatgaaagag cgtcctttaa aaagacgtaa
300
aattacactt tcactactac tggttcctat ccttgtgcag taaagtacaa cctggccagg
360
gtttaccagc tctacctgca actgagtcag aaaggcaaag tagtcagctt tgtccatgct
420
gtacggaatt tgctccacaa acccccttgc tctaga
456

<210> 4212
<211> 81
<212> PRT
<213> Homo sapiens

<400> 4212
```
Met Leu Lys Gln Gln Asp Leu Ser Ile Ala Met Val Val Thr Ser Arg
 1               5                  10                  15
Glu Val Leu Ser Ala Leu Ser Gln Leu Val Pro Cys Val Gly Cys Arg
            20                  25                  30
Arg Ser Val Glu Arg Leu Phe Ser Ser Leu Arg Val Trp Lys Ser Ala
        35                  40                  45
Leu Asp Pro Tyr Ser Arg Pro Arg Glu Ser Val Val Thr Lys Arg Arg
    50                  55                  60
Arg Ala Arg Ala Phe Ile Phe Ser Ser Glu Lys Leu Gly Ala Ser Asp
65                  70                  75                  80
Pro
```

<210> 4213
<211> 383
<212> DNA
<213> Homo sapiens

<400> 4213
nacgcgtacc tgtgccagcg cgcgcgcttc ttcgcagaga acgagggcct agacgactac
60
atggaggcac gcgagggcat gcacctcaag aacgtggact tccgtgagtt catggtggcc
120
ttcccggacc cggcccggcc gccctggtac gcctgctcgt cggccttctg ggccgcggcg
180
ctgctcacgc tgtcgtggcc gctgcgagtg ctggccgagt accgcacggc ctacgcgcac
240
taccacgtgg agaagctgtt tggcctggag ggcccgggct cggccagcag cgcaggcggt
300
ggcctcagcc ccagcgatga gctgctgccc ccgctcaccc accgcctgcc gcgggtcaac
360
acagtagaca gcacggagct cgg
383

<210> 4214
<211> 127
<212> PRT
<213> Homo sapiens

<400> 4214
Xaa Ala Tyr Leu Cys Gln Arg Ala Arg Phe Phe Ala Glu Asn Glu Gly
 1   5   10   15
Leu Asp Asp Tyr Met Glu Ala Arg Glu Gly Met His Leu Lys Asn Val
            20   25   30
Asp Phe Arg Glu Phe Met Val Ala Phe Pro Asp Pro Ala Arg Pro Pro
        35   40   45
Trp Tyr Ala Cys Ser Ser Ala Phe Trp Ala Ala Ala Leu Leu Thr Leu
    50   55   60
Ser Trp Pro Leu Arg Val Leu Ala Glu Tyr Arg Thr Ala Tyr Ala His
65   70   75   80
Tyr His Val Glu Lys Leu Phe Gly Leu Glu Gly Pro Gly Ser Ala Ser
                85   90   95
Ser Ala Gly Gly Gly Leu Ser Pro Ser Asp Glu Leu Leu Pro Pro Leu
            100   105   110
Thr His Arg Leu Pro Arg Val Asn Thr Val Asp Ser Thr Glu Leu
        115   120   125

<210> 4215
<211> 939
<212> DNA
<213> Homo sapiens

<400> 4215
nggtacctcg gctgaataaa aattcaaaaa aacagcaatg gacaggaact tgagaagacg
60
ctggaagaaa gcaaagaaat ggatatcaaa cgtaaagaaa ataaaggcaa tgatacccct
120

ttggccctag agagtacaaa cactgaaaag gagacaagcc tggaggaaac aaaaatcggg
180
gagatcctga tccagggctt gacagaagat atggtgactg ttttaatccg ggcctgcgtg
240
agcatgctgg gagtccctgt ggacccagat actttgcatg ccacccttg tttctgtttg
300
agggtcactc ggggccccca attagccatg atgtttgcag aactgaagaa tacccgcatg
360
atcttgaatt tgacccagag ctcaggcttc aatgggttta ctcccctggt cacccttctc
420
ttaagacaca tcattgagga cccctgtacc cttcgtcata ccatggaaaa ggttgttcgc
480
tcagcagcta caagtggagc tggtagcact acctctggtg ttgtgtctgg cagcctcggc
540
tctcgggaga tcaactacat ccttcgtgtc cttgggccag ccgcatgccg caatccagac
600
atattcacag aagtggccaa ctgctgtatc cgcatcgccc ttcctgcccc tcgaggctca
660
ggaactgctt cagatgatga atttgagaat cttagaatta aaggccctaa tgctgtacag
720
ctggtgaaga ccaccccttt gaagccctca cctctgcctg tcatccctga tactatcaag
780
gaagtgatct atgatatgct gaatgctctg gctgcatacc atgctccaga ggaagcagat
840
aaatctgatc ctaaacctgg ggttatgacc caagaggttg gccagctcct gcaagacatg
900
ggtgatgatg tataccagca gtaccggtca cttacgcgt
939

<210> 4216
<211> 287
<212> PRT
<213> Homo sapiens

<400> 4216
Met Asp Ile Lys Arg Lys Glu Asn Lys Gly Asn Asp Thr Pro Leu Ala
1 5 10 15
Leu Glu Ser Thr Asn Thr Glu Lys Glu Thr Ser Leu Glu Glu Thr Lys
20 25 30
Ile Gly Glu Ile Leu Ile Gln Gly Leu Thr Glu Asp Met Val Thr Val
35 40 45
Leu Ile Arg Ala Cys Val Ser Met Leu Gly Val Pro Val Asp Pro Asp
50 55 60
Thr Leu His Ala Thr Leu Cys Phe Cys Leu Arg Val Thr Arg Gly Pro
65 70 75 80
Gln Leu Ala Met Met Phe Ala Glu Leu Lys Asn Thr Arg Met Ile Leu
85 90 95
Asn Leu Thr Gln Ser Ser Gly Phe Asn Gly Phe Thr Pro Leu Val Thr
100 105 110
Leu Leu Leu Arg His Ile Ile Glu Asp Pro Cys Thr Leu Arg His Thr
115 120 125
Met Glu Lys Val Val Arg Ser Ala Ala Thr Ser Gly Ala Gly Ser Thr
130 135 140
Thr Ser Gly Val Val Ser Gly Ser Leu Gly Ser Arg Glu Ile Asn Tyr

```
145                 150                 155                 160
Ile Leu Arg Val Leu Gly Pro Ala Ala Cys Arg Asn Pro Asp Ile Phe
                165                 170                 175
Thr Glu Val Ala Asn Cys Cys Ile Arg Ile Ala Leu Pro Ala Pro Arg
            180                 185                 190
Gly Ser Gly Thr Ala Ser Asp Asp Glu Phe Glu Asn Leu Arg Ile Lys
        195                 200                 205
Gly Pro Asn Ala Val Gln Leu Val Lys Thr Thr Pro Leu Lys Pro Ser
    210                 215                 220
Pro Leu Pro Val Ile Pro Asp Thr Ile Lys Glu Val Ile Tyr Asp Met
225                 230                 235                 240
Leu Asn Ala Leu Ala Ala Tyr His Ala Pro Glu Glu Ala Asp Lys Ser
                245                 250                 255
Asp Pro Lys Pro Gly Val Met Thr Gln Glu Val Gly Gln Leu Leu Gln
            260                 265                 270Met Gly Asp Asp
Val Tyr Gln Gln Tyr Arg Ser Leu Thr Arg
        275                 280                 285
```

<210> 4217
<211> 619
<212> DNA
<213> Homo sapiens

<400> 4217
acacacacac gcacacaaaa ctcagccaca ggctcaccag ggtctctctc aacatgcaca
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catacacaca cacacccctc agtcataggc tcacaagagt ctctcttgtc tctctctcat
120
acatacacac acacacacaa ccagccacag gcccacaaag gtgtctctct ctttgtccct
180
gtctgctctc tcgcactcac acacacacat ctcagccaca ggcccaccag agtctgtctg
240
tctctttgtc tctctcactc tctctcacac acatacacct cagccacagg cccacaaggg
300
tctctctcct tgtccctggc tcctctctct cgcacactcc cacacacaca catacagctc
360
agccacaggc ccacgagggt gtctctctct ctctctctct ctcacacaca cacacacaca
420
cacacacgcc tgtgcagctc cacaggggcc tggggcagga gacagatctg aatacacata
480
ccaccctgtg ctgtgagtgg ccactcccat ccaacaactg agactttctg ttactgggcc
540
aaggttttct gccaaactca cttcccttat aatgaatgaa ttatccctca gaaggttcca
600
cagtcctccc ctggcgcgc
619

<210> 4218
<211> 155
<212> PRT
<213> Homo sapiens

<400> 4218
Met His Thr Tyr Thr His Thr Pro Leu Ser His Arg Leu Thr Arg Val

```
 1               5                  10                  15
Ser Leu Val Ser Leu Ser Tyr Ile His Thr His Thr Gln Pro Ala Thr
            20                  25                  30
Gly Pro Gln Arg Cys Leu Ser Leu Cys Pro Cys Leu Leu Ser Arg Thr
        35                  40                  45
His Thr His Thr Ser Gln Pro Gln Ala His Gln Ser Leu Ser Val Ser
    50                  55                  60
Leu Ser Leu Ser Leu Ser Leu Thr His Ile His Leu Ser His Arg Pro
65                  70                  75                  80
Thr Arg Val Ser Leu Leu Val Pro Gly Ser Ser Leu Ser His Thr Pro
                85                  90                  95
Thr His Thr His Thr Ala Gln Pro Gln Ala His Glu Gly Val Ser Leu
            100                 105                 110
Ser Leu Ser Leu Ser His Thr His Thr His Thr His Thr Pro Val Gln
        115                 120                 125
Leu His Arg Gly Leu Gly Gln Glu Thr Asp Leu Asn Thr His Thr Thr
    130                 135                 140
Leu Cys Cys Glu Trp Pro Leu Pro Ser Asn Asn
145                 150                 155
```

<210> 4219
<211> 774
<212> DNA
<213> Homo sapiens

<400> 4219
ngcggccgcg cacctgctcc cgtcgcccta cagcaagatc acgcccccgc ggaggcccca
60
ccgctgcagc agcggccacg gcagcgacaa cagcagcgtg ctgagcgggg agctcccgcc
120
ggccatgggg aagacggccc tgttctacca cagcggcggc agcagcggct acgagagcgt
180
gatgcgggac agcgaggcca ccggcagcgc gtcctcggcg caggactcca cgagcgagaa
240
cagcagctcc gtgggcggca ggtgccggag cctcaagacc ccgaagaaac gctccaatcc
300
aggttctcag agacggaggc ttatcccagc actatccctg gacacctctt cccctgtgag
360
aaaaacccccc aacagcacag gcgtccgctg ggtggatggn ncccttgcg gagcagcccg
420
aggggccttg gggaaccttt gagattaaag tctnatgaaa tcgatgacgt ggagcgcctg
480
cagcggcgac gaggggggtgc cagcaaggag gccatgtgct tcaatgcaaa gctgaagatt
540
ctggaacacc gccagcagag gatcgccgag gtccgcgcga agtacgagtg gctgatgaag
600
gagctggagg cgaccaaaca gtatctgatg ctggatccca acaagtggct cagtgaattt
660
gacttggagc aggtttggga gctggattcc ctggagtacc tggaggcact ggagtgtgtg
720
acggagcgcc tggagagccg tgtcaacttc tgcaaggccc atctcatgat gctc
774

<210> 4220

<211> 258
<212> PRT
<213> Homo sapiens

<400> 4220
Xaa Gly Arg Ala Pro Ala Pro Val Ala Leu Gln Gln Asp His Ala Pro
1 5 10 15
Ala Glu Ala Pro Pro Leu Gln Gln Arg Pro Arg Gln Arg Gln Gln Gln
20 25 30
Arg Ala Glu Arg Gly Ala Pro Ala Gly His Gly Glu Asp Gly Pro Val
35 40 45
Leu Pro Gln Arg Arg Gln Gln Arg Leu Arg Glu Arg Asp Ala Gly Gln
50 55 60
Arg Gly His Arg Gln Arg Val Leu Gly Ala Gly Leu His Glu Arg Glu
65 70 75 80
Gln Gln Leu Arg Gly Arg Gln Val Pro Glu Pro Gln Asp Pro Glu Glu
85 90 95
Thr Leu Gln Ser Arg Phe Ser Glu Thr Glu Ala Tyr Pro Ser Thr Ile
100 105 110
Pro Gly His Leu Phe Pro Cys Glu Lys Thr Pro Gln Gln His Arg Arg
115 120 125
Pro Leu Gly Gly Trp Xaa Pro Leu Arg Ser Ser Pro Arg Gly Leu Gly
130 135 140
Glu Pro Leu Arg Leu Lys Ser Xaa Glu Ile Asp Asp Val Glu Arg Leu
145 150 155 160
Gln Arg Arg Arg Gly Gly Ala Ser Lys Glu Ala Met Cys Phe Asn Ala
165 170 175
Lys Leu Lys Ile Leu Glu His Arg Gln Gln Arg Ile Ala Glu Val Arg
180 185 190
Ala Lys Tyr Glu Trp Leu Met Lys Glu Leu Glu Ala Thr Lys Gln Tyr
195 200 205
Leu Met Leu Asp Pro Asn Lys Trp Leu Ser Glu Phe Asp Leu Glu Gln
210 215 220
Val Trp Glu Leu Asp Ser Leu Glu Tyr Leu Glu Ala Leu Glu Cys Val
225 230 235 240
Thr Glu Arg Leu Glu Ser Arg Val Asn Phe Cys Lys Ala His Leu Met
245 250 255
Met Leu

<210> 4221
<211> 789
<212> DNA
<213> Homo sapiens

<400> 4221
aatgtgaaga ggattaaaga ataaagaaaa aacaaaaaag tcttatacta aaataagaaa
60
tcagccccat cttggcacag ttctcatgca gaatattgca cccagtgtga actaacgcta
120
gaagcttcaa actgtataaa tttaaatgta tttgcatatt ataaaaataa agataaacat
180
atacatattt tacactagtt atggaacagc aatgaacgtc agtcgatccc tctttcacat
240

ttaacagaac tgaaatctga gtgctctaaa tactgccacc tgtactgtaa ctatggctta
300
tatgtgcacg gaaaacaaaa tccctgagaa gccattcgac ttttttttt tttcttttct
360
tcaagtagcg cgctccttgg aggatcacag ttctgaggtt caggttgtaa aacatttgct
420
ccatgttctc gtccatgctt ccccccacca ccccctcccc acctcttccc cagtcgtcca
480
aaaagcaccc tgcaagcacg cgttgtcact caagttcaca gaacacgctg gggtgagtgc
540
agagggtctg ccaggtgcaa aagatggtcc aggtgttcag atgctctctt ttctccatgg
600
aaattccaca gccacaaacg tcactggttt ctgtgctttt caccaacatt cttcccttaa
660
aaattggtgc tcctaaagtc acagtttggg tacagtaaaa atgatggcat aaggaaaaga
720
agcactatct tttccactta attttccaag aaagtatgaa gatacttgga acaggggctg
780
atcacagtc
789

<210> 4222
<211> 127
<212> PRT
<213> Homo sapiens

<400> 4222
Met Ala Tyr Met Cys Thr Glu Asn Lys Ile Pro Glu Lys Pro Phe Asp
1 5 10 15
Phe Phe Phe Phe Ser Phe Leu Gln Val Ala Arg Ser Leu Glu Asp His
20 25 30
Ser Ser Glu Val Gln Val Val Lys His Leu Leu His Val Leu Val His
35 40 45
Ala Ser Pro His His Pro Leu Pro Thr Ser Ser Pro Val Val Gln Lys
50 55 60
Ala Pro Cys Lys His Ala Leu Ser Leu Lys Phe Thr Glu His Ala Gly
65 70 75 80
Val Ser Ala Glu Gly Leu Pro Gly Ala Lys Asp Gly Pro Gly Val Gln
85 90 95
Met Leu Ser Phe Leu His Gly Asn Ser Thr Ala Thr Asn Val Thr Gly
100 105 110
Phe Cys Ala Phe His Gln His Ser Ser Leu Lys Asn Trp Cys Ser
115 120 125

<210> 4223
<211> 852
<212> DNA
<213> Homo sapiens

<400> 4223
atcctggacc agggctacta ctcggagcga gacacaagca acgtggtacg gcaagtcctg
60
gaggccgtgg cctatttgca ctcactcaag atcgtgcaca ggaatctcaa gctggagaac
120

ctggtttact acaaccggct gaagaactcg aagattgtca tcagtgactt ccatctggct
180
aagctagaaa atggcctcat caaggagccc tgtgggaccc ccgaagattt tgccccccaa
240
ggggaaggcc ggcagcggta tggacgccct gtggactgct gggccattgg agtcatcatg
300
tacatcctgc tttcaggcaa tccacctttc tatgaggagg tggaagaaga tgattatgag
360
aaccatgata agaatctctt ccgcaagatc ctggctggtg actatgagtt tgactctcca
420
tattgggatg atatttcgca ggcagccaaa gacctggtca caaggctgat ggaggtggag
480
caagaccagc ggatcactgc agaagaggcc atctcccatg agtggatttc tggcaatgct
540
gcttctgata agaacatcaa ggatggtgtc tgtgcccaga ttgaaaagaa ctttgccagg
600
gccaagtgga agaaggctgt ccgagtgacc accctcatga aacggctccg ggcaccagag
660
cagtccagca cggctgcagc ccagtcggcc tcagccacag acactgccac ccccggggct
720
gcagaccgta gtgccacccc agccacagat ggaagtgcca ccccagccac tgatggcagt
780
gtcaccccag ccaccgatgg aagcatcact ccagccattg atgggagtgt caccccagcc
840
actgacagga gc
852

<210> 4224
<211> 284
<212> PRT
<213> Homo sapiens

<400> 4224
Ile Leu Asp Gln Gly Tyr Tyr Ser Glu Arg Asp Thr Ser Asn Val Val
1 5 10 15
Arg Gln Val Leu Glu Ala Val Ala Tyr Leu His Ser Leu Lys Ile Val
20 25 30
His Arg Asn Leu Lys Leu Glu Asn Leu Val Tyr Tyr Asn Arg Leu Lys
35 40 45
Asn Ser Lys Ile Val Ile Ser Asp Phe His Leu Ala Lys Leu Glu Asn
50 55 60
Gly Leu Ile Lys Glu Pro Cys Gly Thr Pro Glu Asp Phe Ala Pro Gln
65 70 75 80
Gly Glu Gly Arg Gln Arg Tyr Gly Arg Pro Val Asp Cys Trp Ala Ile
85 90 95
Gly Val Ile Met Tyr Ile Leu Leu Ser Gly Asn Pro Pro Phe Tyr Glu
100 105 110
Glu Val Glu Glu Asp Asp Tyr Glu Asn His Asp Lys Asn Leu Phe Arg
115 120 125
Lys Ile Leu Ala Gly Asp Tyr Glu Phe Asp Ser Pro Tyr Trp Asp Asp
130 135 140
Ile Ser Gln Ala Ala Lys Asp Leu Val Thr Arg Leu Met Glu Val Glu
145 150 155 160
Gln Asp Gln Arg Ile Thr Ala Glu Glu Ala Ile Ser His Glu Trp Ile

```
                165                 170                 175
Ser Gly Asn Ala Ala Ser Asp Lys Asn Ile Lys Asp Gly Val Cys Ala
            180                 185                 190
Gln Ile Glu Lys Asn Phe Ala Arg Ala Lys Trp Lys Lys Ala Val Arg
        195                 200                 205
Val Thr Thr Leu Met Lys Arg Leu Arg Ala Pro Glu Gln Ser Ser Thr
    210                 215                 220
Ala Ala Ala Gln Ser Ala Ser Ala Thr Asp Thr Ala Thr Pro Gly Ala
225                 230                 235                 240
Ala Asp Arg Ser Ala Thr Pro Ala Thr Asp Gly Ser Ala Thr Pro Ala
                245                 250                 255
Thr Asp Gly Ser Val Thr Pro Ala Thr Asp Gly Ser Ile Thr Pro Ala
            260                 265                 270
Ile Asp Gly Ser Val Thr Pro Ala Thr Asp Arg Ser
        275                 280
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<210> 4225
<211> 470
<212> DNA
<213> Homo sapiens

<400> 4225
nntgtacaag aaagtgagcc agtcatcgtc aatattcaag tgatggatgc aaatgataac
60
acgccaacct tccctgaaat atcctatgat gtgtatgttt atacagacat gagacctggg
120
gacagggtcc tacagttaac tgcagtcgac gcagacgaag ggtcaaatgg ggagatcaca
180
tatgaaatcc ttgttggggc tcagggagac ttcatcatca ataaaacaac agggcttatc
240
accatcgctc caggggtgga aatgatagtc gggcggactt acgcactccc ggtccaagca
300
gcggataatg ctcctcctgc aaagcaaagg actcccatct gcactgtgta tattgaagtg
360
cttccaccaa ataatcaaag ccctcctcgc ttcccacagc tgatgtatag ccttgaaatt
420
agtgaagcca tgagggttgg tgctgtttta ttaaatctac aggcaactga
470

<210> 4226
<211> 156
<212> PRT
<213> Homo sapiens

<400> 4226
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Xaa Val Gln Glu Ser Glu Pro Val Ile Val Asn Ile Gln Val Met Asp
 1               5                  10                  15
Ala Asn Asp Asn Thr Pro Thr Phe Pro Glu Ile Ser Tyr Asp Val Tyr
            20                  25                  30
Val Tyr Thr Asp Met Arg Pro Gly Asp Arg Val Leu Gln Leu Thr Ala
        35                  40                  45
Val Asp Ala Asp Glu Gly Ser Asn Gly Glu Ile Thr Tyr Glu Ile Leu
    50                  55                  60
Val Gly Ala Gln Gly Asp Phe Ile Ile Asn Lys Thr Thr Gly Leu Ile
```

65 70 75 80
Thr Ile Ala Pro Gly Val Glu Met Ile Val Gly Arg Thr Tyr Ala Leu
85 90 95
Pro Val Gln Ala Ala Asp Asn Ala Pro Pro Ala Lys Gln Arg Thr Pro
100 105 110
Ile Cys Thr Val Tyr Ile Glu Val Leu Pro Pro Asn Asn Gln Ser Pro
115 120 125
Pro Arg Phe Pro Gln Leu Met Tyr Ser Leu Glu Ile Ser Glu Ala Met
130 135 140
Arg Val Gly Ala Val Leu Leu Asn Leu Gln Ala Thr
145 150 155

<210> 4227
<211> 1199
<212> DNA
<213> Homo sapiens

<400> 4227
nnaagcttat ggccagtgtt aatttgttat ttcttaaata actttccctt tcatttttaa
60
attataaatt taacttctaa catgttttat ggttaaaatt gtacttttt cctttagcga
120
cattcaaatg catcacaatc actttgtgaa attgttcgcc tgagcagaga ccagatgtta
180
caaattcaga acagtacaga gcccgacccc ctgcttgcca ctctagaaaa gcaagaaatt
240
atagagcagc ttctatcaaa tattttccac aaggagaaaa atgagtcagc catagtcagt
300
gcaatccaga tattgctgac tttacttgag acacgacgac caacatttga aggccatata
360
gagatctgcc caccaggcat gagccattca gcttgttcag taaacaagag tgttctagaa
420
gccatcagag gaagacttgg atcttttcat gaactcctgc tggagccacc caagaaaagt
480
gtgatgaaga ccacatgggg tgtgctggat cctcctgtgg ggaatacccg gttgaatgtc
540
attaggttga tatccagcct gcttcaaacc aataccagca gtataaatgg ggaccttatg
600
gagctgaata gcattggagt catattgaac atgttcttca agtatacatg gaataacttt
660
ttgcatacac aagtggaaat ttgtattgca ctgattcttg caagtccttt tgaaaacaca
720
gaaaatgcca caattaccga tcaagactcc actggtgata atttgttatt aaaacatctt
780
ttccaaaaat gtcaattaat agaacgaata cttgaagcct gggaaatgaa tgagaagaaa
840
caggctgagg gaggaagacg gcatggttac atgggacacc taacgaggat agctaactgt
900
atcgtgcaca gcactgacaa gggccccaac agtgcattag tgcagcagct tatcaaaggt
960
aagttatttg tgaaatttga attacatttt tgttgggttg caggaaggat ttaagggtca
1020
agtagaaatg catgtagcat ttttaatagt gatttgtggg acttctttat atttggcaaa
1080

ttatgtattt gaatgaggtt cttgagaatg tgtttgaaca gggttgtttt ttgggttgta
1140
ttttatgttc atgtagttac agaccattcc ataagcattg gcaggcttgg ctggattca
1199

<210> 4228
<211> 298
<212> PRT
<213> Homo sapiens

<400> 4228
Arg His Ser Asn Ala Ser Gln Ser Leu Cys Glu Ile Val Arg Leu Ser
1 5 10 15
Arg Asp Gln Met Leu Gln Ile Gln Asn Ser Thr Glu Pro Asp Pro Leu
20 25 30
Leu Ala Thr Leu Glu Lys Gln Glu Ile Ile Glu Gln Leu Leu Ser Asn
35 40 45
Ile Phe His Lys Glu Lys Asn Glu Ser Ala Ile Val Ser Ala Ile Gln
50 55 60
Ile Leu Leu Thr Leu Leu Glu Thr Arg Arg Pro Thr Phe Glu Gly His
65 70 75 80
Ile Glu Ile Cys Pro Pro Gly Met Ser His Ser Ala Cys Ser Val Asn
85 90 95
Lys Ser Val Leu Glu Ala Ile Arg Gly Arg Leu Gly Ser Phe His Glu
100 105 110
Leu Leu Leu Glu Pro Pro Lys Lys Ser Val Met Lys Thr Thr Trp Gly
115 120 125
Val Leu Asp Pro Pro Val Gly Asn Thr Arg Leu Asn Val Ile Arg Leu
130 135 140
Ile Ser Ser Leu Leu Gln Thr Asn Thr Ser Ser Ile Asn Gly Asp Leu
145 150 155 160
Met Glu Leu Asn Ser Ile Gly Val Ile Leu Asn Met Phe Phe Lys Tyr
165 170 175
Thr Trp Asn Asn Phe Leu His Thr Gln Val Glu Ile Cys Ile Ala Leu
180 185 190
Ile Leu Ala Ser Pro Phe Glu Asn Thr Glu Asn Ala Thr Ile Thr Asp
195 200 205
Gln Asp Ser Thr Gly Asp Asn Leu Leu Leu Lys His Leu Phe Gln Lys
210 215 220
Cys Gln Leu Ile Glu Arg Ile Leu Glu Ala Trp Glu Met Asn Glu Lys
225 230 235 240
Lys Gln Ala Glu Gly Gly Arg Arg His Gly Tyr Met Gly His Leu Thr
245 250 255
Arg Ile Ala Asn Cys Ile Val His Ser Thr Asp Lys Gly Pro Asn Ser
260 265 270
Ala Leu Val Gln Gln Leu Ile Lys Gly Lys Leu Phe Val Lys Phe Glu
275 280 285
Leu His Phe Cys Trp Val Ala Gly Arg Ile
290 295

<210> 4229
<211> 1612
<212> DNA
<213> Homo sapiens

<400> 4229
ncgggggtct ccatcctgga ccaggacctg gactacctgt ccgaaggcct cgaaggccga
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tcccaaagcc ccgtggccct gctctttgat gcccttctac gcccagacac agactttggg
120
ggaaacatga agtcggtcct cacctggaag caccggaagg agcacgccat cccccacgtg
180
gttctgggcc ggaacctccc cgggggagcc tggcactcca tcgaaggctc catggtgatc
240
ctgagccaag gccagtggat ggggctcccg gacctggagg tcaaggactg gatgcagaag
300
aagcgaagag gtcttcgcaa cagccgggcc actgccgggg acatcgccca ctactacagg
360
gactacgtgg tcaagaaggg tctggggcat aactttgtgt ccggtgctgt agtcacagcc
420
gtggagtggg ggacccccga tcccagcagc tgtggggccc aggactccag ccccctcttc
480
caggtgagcg gcttcctgac caggaaccag gcccagcagc ccttctcgct gtgggcccgc
540
aacgtggtcc tcgccacagg cacgttcgac agcccggccc ggctgggcat ccccggggag
600
gccctgccct tcatccacca tgagctgtct gccctggagg ccgccacaag ggtgggtgcg
660
gtgaccccgg cctcagaccc tgtcctcatc attggcgcgg ggctgtcagc ggccgacgcc
720
gtcctctacg cccgccacta caacatcccg gtgatccatg ccttccgccg ggccgtggac
780
gaccctggcc tggtgttcaa ccagctgccc aagatgctgt accccgagta ccacaaggtg
840
caccagatga tgcgggagca gtccatcctg tcgcccagcc cctatgaggg ttaccgcagc
900
ctccccaggc accagctgct gtgcttcaag gaagactgcc aggccgtgtt ccaggacctc
960
gagggtgtcg agaaggtgtt tggggtctcc ctggtgctgg tcctcatcgg ctcccacccc
1020
gacctctcct tcctgcctgg ggcaggggct gactttgcag tggatcctga ccagccgctg
1080
agcgccaaga ggaaccccat tgacgtggac cccttcacct accagagcac ccgccaggag
1140
ggcctgtacg ccatggggcc gctggccggg gacaacttcg tgaggtttgt gcaggggggc
1200
gccttggctg tggccagctc cctgctaagg aaggagacca ggaagccacc ctaacactcg
1260
gccagacccg ctggctccca ggccctgaga ggacagagat gaccacatcc ctgctggatg
1320
caggacccgt ccaaagatgc cccggggagg ggtgtcagcc cacgttgctg gcctttgggg
1380
tcaagaggag tagggatccc aggctgccct ggacttagac cagtgtctga ggttggactt
1440
agaccagtgt gtgaggtggt aacagcggcc gcagcagggg gttggcctag acctgggatt
1500
tgtggggaaa gctgctggtg tgaccagctg agcacccagc caggagacct gcagccctgc
1560

gccttccaga agcaggtccc aaataaagcc agtgcccacc tgaaaaaaaa aa
1612

<210> 4230
<211> 417
<212> PRT
<213> Homo sapiens

<400> 4230
Xaa Gly Val Ser Ile Leu Asp Gln Asp Leu Asp Tyr Leu Ser Glu Gly
 1   5   10   15
Leu Glu Gly Arg Ser Gln Ser Pro Val Ala Leu Leu Phe Asp Ala Leu
            20   25   30
Leu Arg Pro Asp Thr Asp Phe Gly Gly Asn Met Lys Ser Val Leu Thr
        35   40   45
Trp Lys His Arg Lys Glu His Ala Ile Pro His Val Val Leu Gly Arg
    50   55   60
Asn Leu Pro Gly Gly Ala Trp His Ser Ile Glu Gly Ser Met Val Ile
65   70   75   80
Leu Ser Gln Gly Gln Trp Met Gly Leu Pro Asp Leu Glu Val Lys Asp
                85   90   95
Trp Met Gln Lys Lys Arg Arg Gly Leu Arg Asn Ser Arg Ala Thr Ala
            100   105   110
Gly Asp Ile Ala His Tyr Tyr Arg Asp Tyr Val Val Lys Lys Gly Leu
        115   120   125
Gly His Asn Phe Val Ser Gly Ala Val Val Thr Ala Val Glu Trp Gly
    130   135   140
Thr Pro Asp Pro Ser Ser Cys Gly Ala Gln Asp Ser Ser Pro Leu Phe
145   150   155   160
Gln Val Ser Gly Phe Leu Thr Arg Asn Gln Ala Gln Gln Pro Phe Ser
                165   170   175
Leu Trp Ala Arg Asn Val Val Leu Ala Thr Gly Thr Phe Asp Ser Pro
            180   185   190
Ala Arg Leu Gly Ile Pro Gly Glu Ala Leu Pro Phe Ile His His Glu
        195   200   205
Leu Ser Ala Leu Glu Ala Ala Thr Arg Val Gly Ala Val Thr Pro Ala
    210   215   220
Ser Asp Pro Val Leu Ile Ile Gly Ala Gly Leu Ser Ala Ala Asp Ala
225   230   235   240
Val Leu Tyr Ala Arg His Tyr Asn Ile Pro Val Ile His Ala Phe Arg
                245   250   255
Arg Ala Val Asp Asp Pro Gly Leu Val Phe Asn Gln Leu Pro Lys Met
            260   265   270
Leu Tyr Pro Glu Tyr His Lys Val His Gln Met Met Arg Glu Gln Ser
        275   280   285
Ile Leu Ser Pro Ser Pro Tyr Glu Gly Tyr Arg Ser Leu Pro Arg His
    290   295   300
Gln Leu Leu Cys Phe Lys Glu Asp Cys Gln Ala Val Phe Gln Asp Leu
305   310   315   320
Glu Gly Val Glu Lys Val Phe Gly Val Ser Leu Val Leu Val Leu Ile
                325   330   335
Gly Ser His Pro Asp Leu Ser Phe Leu Pro Gly Ala Gly Ala Asp Phe
            340   345   350
Ala Val Asp Pro Asp Gln Pro Leu Ser Ala Lys Arg Asn Pro Ile Asp

```
        355                 360                 365
Val Asp Pro Phe Thr Tyr Gln Ser Thr Arg Gln Glu Gly Leu Tyr Ala
    370                 375                 380
Met Gly Pro Leu Ala Gly Asp Asn Phe Val Arg Phe Val Gln Gly Gly
385                 390                 395                 400
Ala Leu Ala Val Ala Ser Ser Leu Leu Arg Lys Glu Thr Arg Lys Pro
                405                 410                 415
Pro
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<210> 4231
<211> 1588
<212> DNA
<213> Homo sapiens

<400> 4231
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attaaagaac ttcgagatca aattgtatct gttcaggagg aaaagaagat tttagccatt
120
gagctggaaa atctcaagag caaactcgta gaagtaattg aagaagtaaa taaagttaaa
180
caagaaaaga ctgttttaaa ttcagaagtt cttgaacaga gaaaagtctt agaaaaatgc
240
aatagagtgt ccatgttagc tgtagaagag tatgaggaga tgcaagtaaa cctggagctg
300
gagaaggacc ttcgaaagaa agcagagtca tttgcccaag agatgttcct tgagccaaac
360
cagggtaaaa agacaaagcc ccccttggg cggcagagtt ccatccttga tcagcagtta
420
gctttagacg aaaatgcaaa actcacccag caacttgaag aagagagaat tcagcatcaa
480
caaaaggtca aagaattaga agagcaacta gaaaatgaaa cactccacaa agaaatacac
540
aacctcaaac agcaactgga gcttctagag gaagataaaa aggaattgga attgaaatat
600
cagaattctg aagagaaagc cagaaattta aagcactctg ttgatgaact ccagaaacga
660
gtgaaccagt ctgagaattc agtacctcca ccacctcctc ctccaccacc acttcccccct
720
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780
ggcagtggtg ctaagaaaga aaaggcaact caaccagaaa caactgaaga agtcacagat
840
ctaaagaggc aagcagttga agagatgatg gatagaatta aaaagggagt tcatcttaga
900
cccgttaatc agacagccag accgaagaca aagccagaat cttcgaaagg ctgcgaaagt
960
gcagtggatg aactaaaagg aatactgggg acacttaaca aatccactag ttcaagaagc
1020
ttaaaatccc ttgaccctga aaacagtgaa actgagttag aaaggatttt gcgtcgcaga
1080
aaggtgacag cagaagcaga tagcagtagt ccaactggga tattagccac ctcagagtcc
1140

aaatccatgc cagtgttggg ttctgtatcc agtgtaacaa aaacagcctt gaacaagaaa
1200
actctggagg cagaattcaa cagcccgtcc cccccaacac ctgagccagg tgaagggccc
1260
cgtaaattgg aaggatgcac aagttccaag gttacgtttc agtaagtaac gatgctcttt
1320
actaagtggt gtatagaaga atctgtaatg actaacttgt gtgtttcttt gatttgtttc
1380
ctttagagag attttgattg gctcgccggt aaattctctt cttcttttca tttgatgggc
1440
cagctttttc attctaggct cctagataag agatctaatt aagatccaaa gcaagtacca
1500
tgtacaaaga gaattacttc ccctaaactg gtttggtaat caggttctta tacacaaata
1560
attgatctgg atgatacaga ctctgcag
1588

<210> 4232
<211> 434
<212> PRT
<213> Homo sapiens

<400> 4232
Xaa Thr Thr Asp Thr Asp Gly Ala Ala Glu Thr Cys Val Ser Val Gln
1 5 10 15
Cys Gln Lys Gln Ile Lys Glu Leu Arg Asp Gln Ile Val Ser Val Gln
20 25 30
Glu Glu Lys Lys Ile Leu Ala Ile Glu Leu Glu Asn Leu Lys Ser Lys
35 40 45
Leu Val Glu Val Ile Glu Glu Val Asn Lys Val Lys Gln Glu Lys Thr
50 55 60
Val Leu Asn Ser Glu Val Leu Glu Gln Arg Lys Val Leu Glu Lys Cys
65 70 75 80
Asn Arg Val Ser Met Leu Ala Val Glu Glu Tyr Glu Glu Met Gln Val
85 90 95
Asn Leu Glu Leu Glu Lys Asp Leu Arg Lys Lys Ala Glu Ser Phe Ala
100 105 110
Gln Glu Met Phe Leu Glu Pro Asn Gln Gly Lys Lys Thr Lys Pro Pro
115 120 125
Phe Gly Arg Gln Ser Ser Ile Leu Asp Gln Gln Leu Ala Leu Asp Glu
130 135 140
Asn Ala Lys Leu Thr Gln Gln Leu Glu Glu Glu Arg Ile Gln His Gln
145 150 155 160
Gln Lys Val Lys Glu Leu Glu Glu Gln Leu Glu Asn Glu Thr Leu His
165 170 175
Lys Glu Ile His Asn Leu Lys Gln Gln Leu Glu Leu Leu Glu Glu Asp
180 185 190
Lys Lys Glu Leu Glu Leu Lys Tyr Gln Asn Ser Glu Glu Lys Ala Arg
195 200 205
Asn Leu Lys His Ser Val Asp Glu Leu Gln Lys Arg Val Asn Gln Ser
210 215 220
Glu Asn Ser Val Pro Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro Pro
225 230 235 240
Pro Pro Pro Asn Pro Ile Arg Ser Leu Met Ser Met Ile Arg Lys Arg

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                245                 250                 255
Ser His Pro Ser Gly Ser Gly Ala Lys Lys Glu Lys Ala Thr Gln Pro
            260                 265                 270
Glu Thr Thr Glu Glu Val Thr Asp Leu Lys Arg Gln Ala Val Glu Glu
        275                 280                 285
Met Met Asp Arg Ile Lys Lys Gly Val His Leu Arg Pro Val Asn Gln
    290                 295                 300
Thr Ala Arg Pro Lys Thr Lys Pro Glu Ser Ser Lys Gly Cys Glu Ser
305                 310                 315                 320
Ala Val Asp Glu Leu Lys Gly Ile Leu Gly Thr Leu Asn Lys Ser Thr
                325                 330                 335
Ser Ser Arg Ser Leu Lys Ser Leu Asp Pro Glu Asn Ser Glu Thr Glu
            340                 345                 350
Leu Glu Arg Ile Leu Arg Arg Arg Lys Val Thr Ala Glu Ala Asp Ser
        355                 360                 365
Ser Ser Pro Thr Gly Ile Leu Ala Thr Ser Glu Ser Lys Ser Met Pro
    370                 375                 380
Val Leu Gly Ser Val Ser Ser Val Thr Lys Thr Ala Leu Asn Lys Lys
385                 390                 395                 400
Thr Leu Glu Ala Glu Phe Asn Ser Pro Ser Pro Pro Thr Pro Glu Pro
                405                 410                 415
Gly Glu Gly Pro Arg Lys Leu Glu Gly Cys Thr Ser Ser Lys Val Thr
            420                 425                 430
Phe Gln
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<210> 4233
<211> 2827
<212> DNA
<213> Homo sapiens

<400> 4233

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ggatccctga aaggagacca tatactgtac catttgatac tcatttgggg cattatattt
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120
cctatgtact ctctggatcg aatatttgct ggatttcgaa cacgaagtca gatgctgttg
180
ggtcacatag aagaacaaga taaggtcctc cactgccaat tttctgataa cagtgatgat
240
gaagaatcag aaggccaaga gaaatctgga actagatgta gaagtcgttc atggattcag
300
aagccagact ctgtttgttc ccttgttgaa ttgagtgata ctcaggatga aacacaaaag
360
tcagatttgg agaatgaaga tttaaagatt gattgtctcc aggagagtca agaattgaat
420
ttgcaaaaat taaagaattc agaacgcata cttactgaag ccaaacaaaa aatgagagaa
480
cttacagtta acatcaagat gaaggaagat ctgattaaag aattaataaa aacaggtaac
540
gatgccaagt ctgtaagcaa gcagtatact ttgaaagtaa caaagctaga gcatgatgca
600
gaacaggcaa aagtcgaact aactgaaaca caaaagcagc tacaggagct ggaaaacaaa
660
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gatctttctg atgttgcaat gaaggtaaaa ttacagaaag agtttcgtaa aaaggtggat
720
gctgcaaagc tgagagttca ggtcttacag aagaagcaac aagatagtaa gaaactggca
780
tcactgtcaa tccaaaatga gaaacgtgct aatgaactag agcagagtgt agatcacatg
840
aaatatcaaa agatacagct acaaagaaaa ctacgagaag aaaatgaaaa aaggaagcaa
900
ctggatgcag taattaagcg ggaccagcaa aaaatcaaag taatacaatt aaaaacagga
960
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1020
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<211> 833
<212> PRT
<213> Homo sapiens

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Thr Cys Lys Val His Thr Ser Pro Pro Met Tyr Ser Leu Asp Arg Ile
35 40 45
Phe Ala Gly Phe Arg Thr Arg Ser Gln Met Leu Leu Gly His Ile Glu
50 55 60
Glu Gln Asp Lys Val Leu His Cys Gln Phe Ser Asp Asn Ser Asp Asp
65 70 75 80
Glu Glu Ser Glu Gly Gln Glu Lys Ser Gly Thr Arg Cys Arg Ser Arg
85 90 95
Ser Trp Ile Gln Lys Pro Asp Ser Val Cys Ser Leu Val Glu Leu Ser
100 105 110
Asp Thr Gln Asp Glu Thr Gln Lys Ser Asp Leu Glu Asn Glu Asp Leu
115 120 125
Lys Ile Asp Cys Leu Gln Glu Ser Gln Glu Leu Asn Leu Gln Lys Leu
130 135 140
Lys Asn Ser Glu Arg Ile Leu Thr Glu Ala Lys Gln Lys Met Arg Glu
145 150 155 160
Leu Thr Val Asn Ile Lys Met Lys Glu Asp Leu Ile Lys Glu Leu Ile
165 170 175
Lys Thr Gly Asn Asp Ala Lys Ser Val Ser Lys Gln Tyr Thr Leu Lys
180 185 190
Val Thr Lys Leu Glu His Asp Ala Glu Gln Ala Lys Val Glu Leu Thr
195 200 205
Glu Thr Gln Lys Gln Leu Gln Glu Leu Glu Asn Lys Asp Leu Ser Asp

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Val Ala Met Lys Val Lys Leu Gln Lys Glu Phe Arg Lys Lys Val Asp
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Ala Ala Lys Leu Arg Val Gln Val Leu Gln Lys Lys Gln Gln Asp Ser
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Lys Lys Leu Ala Ser Leu Ser Ile Gln Asn Glu Lys Arg Ala Asn Glu
            260                 265                 270
Leu Glu Gln Ser Val Asp His Met Lys Tyr Gln Lys Ile Gln Leu Gln
        275                 280                 285
Arg Lys Leu Arg Glu Glu Asn Glu Lys Arg Lys Gln Leu Asp Ala Val
    290                 295                 300
Ile Lys Arg Asp Gln Gln Lys Ile Lys Val Ile Gln Leu Lys Thr Gly
305                 310                 315                 320
Gln Glu Glu Gly Leu Lys Pro Lys Ala Glu Asp Leu Asp Ala Cys Asn
                325                 330                 335
Leu Lys Arg Arg Lys Gly Ser Phe Gly Ser Ile Asp His Leu Gln Lys
            340                 345                 350
Leu Asp Glu Gln Lys Lys Trp Leu Asp Glu Glu Val Glu Lys Val Leu
        355                 360                 365
Asn Gln Arg Gln Glu Leu Glu Glu Leu Glu Ala Asp Leu Lys Lys Arg
    370                 375                 380
Glu Ala Ile Val Ser Lys Lys Glu Ala Leu Leu Gln Glu Lys Ser His
385                 390                 395                 400
Leu Glu Asn Lys Lys Leu Arg Ser Ser Gln Ala Leu Asn Thr Asp Ser
                405                 410                 415
Leu Lys Ile Ser Thr Arg Leu Asn Leu Leu Glu Gln Glu Leu Ser Glu
            420                 425                 430
Lys Asn Val Gln Leu Gln Thr Ser Thr Ala Glu Glu Lys Thr Lys Ile
        435                 440                 445
Ser Glu Gln Val Glu Val Leu Gln Lys Glu Lys Asp Gln Leu Gln Lys
    450                 455                 460
Arg Arg His Asp Val Asp Glu Lys Leu Lys Asn Gly Arg Val Leu Ser
465                 470                 475                 480
Pro Glu Glu Glu His Val Leu Phe Gln Leu Glu Glu Gly Ile Glu Ala
                485                 490                 495
Leu Glu Ala Ala Ile Glu Tyr Arg Asn Glu Ser Ile Gln Asn Arg Gln
            500                 505                 510
Lys Ser Leu Arg Ala Ser Phe His Asn Leu Ser Arg Gly Glu Ala Asn
        515                 520                 525
Val Leu Glu Lys Leu Ala Cys Leu Ser Pro Val Glu Ile Arg Thr Ile
    530                 535                 540
Leu Phe Arg Tyr Phe Asn Lys Val Val Asn Leu Arg Glu Ala Glu Arg
545                 550                 555                 560
Lys Gln Gln Leu Tyr Asn Glu Glu Met Lys Met Lys Val Leu Glu Arg
                565                 570                 575
Asp Asn Met Val Arg Glu Leu Glu Ser Ala Leu Asp His Leu Lys Leu
            580                 585                 590
Gln Cys Asp Arg Arg Leu Thr Leu Gln Gln Lys Glu His Glu Gln Lys
        595                 600                 605
Met Gln Leu Leu Leu His His Phe Lys Glu Gln Asp Gly Glu Gly Ile
    610                 615                 620
Met Glu Thr Phe Lys Thr Tyr Glu Asp Lys Ile Gln Gln Leu Glu Lys
625                 630                 635                 640
Asp Leu Tyr Phe Tyr Lys Lys Thr Ser Arg Asp His Lys Lys Lys Leu
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645 650 655
Lys Glu Leu Val Gly Glu Ala Ile Arg Arg Gln Leu Ala Ser Ser Glu
660 665 670
Tyr Gln Glu Ala Gly Asp Gly Val Leu Lys Pro Glu Gly Gly Gly Met
675 680 685
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690 695 700
Ser Gly Arg Glu Arg Glu Met Asp Ser Ser Ala Ser Ser Leu Arg Thr
705 710 715 720
Gln Pro Asn Pro Gln Lys Leu Trp Glu Asp Ile Pro Glu Leu Pro Pro
725 730 735
Ile His Ser Ser Leu Ala Pro Pro Ser Gly His Met Leu Gly Asn Glu
740 745 750
Asn Lys Thr Glu Thr Asp Asp Asn Gln Phe Thr Lys Ser His Ser Arg
755 760 765
Leu Ser Ser Gln Ile Gln Val Val Gly Asn Val Gly Arg Leu His Gly
770 775 780
Val Thr Pro Val Lys Leu Cys Arg Lys Glu Leu Arg Gln Ile Ser Ala
785 790 795 800
Leu Glu Leu Ser Leu Arg Arg Ser Ser Leu Gly Val Gly Ile Gly Ser
805 810 815
Met Ala Ala Asp Ser Ile Glu Val Ser Arg Lys Pro Arg Asp Leu Lys
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Thr

<210> 4235
<211> 971
<212> DNA
<213> Homo sapiens

<400> 4235
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120
gctattgggc tctcatttac aacttcaacg actaccaccg ccactttcac caccaacact
180
actaccacaa tcaccagtgg ctttactgtg aaccaaaacc aactgttatc aagagggttt
240
gaaaaccttg taccttatac ttcaactgtt agtgtagtag caactcctgt gatgacatat
300
ggtcatctgg agggtcttat aaatgagtgg aaccttgagc tggaagatca agagaagtac
360
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420
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480
caagaattgg attttatcct gtcacagcag caggaactag aatttctgtt gacttattta
540
gaggagtcta cgcgtgacca gagtggactt cattatctgc aggatgcaga tgaggagcat
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gtggagatct ccaccagatc tgcagaattc tgaatgccca tatggactcc ctgcagtgga
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780
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<210> 4236
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<212> PRT
<213> Homo sapiens

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Ser Phe Thr Thr Ser Thr Thr Thr Thr Ala Thr Phe Thr Thr Asn Thr
35 40 45
Thr Thr Thr Ile Thr Ser Gly Phe Thr Val Asn Gln Asn Gln Leu Leu
50 55 60
Ser Arg Gly Phe Glu Asn Leu Val Pro Tyr Thr Ser Thr Val Ser Val
65 70 75 80
Val Ala Thr Pro Val Met Thr Tyr Gly His Leu Glu Gly Leu Ile Asn
85 90 95
Glu Trp Asn Leu Glu Leu Glu Asp Gln Glu Lys Tyr Phe Leu Leu Gln
100 105 110
Ala Thr Gln Val Asn Ala Trp Asp His Thr Leu Ile Glu Asn Gly Glu
115 120 125
Met Ile Arg Ile Leu His Gly Glu Val Asn Lys Val Lys Leu Asp Gln
130 135 140
Lys Arg Leu Glu Gln Glu Leu Asp Phe Ile Leu Ser Gln Gln Gln Glu
145 150 155 160
Leu Glu Phe Leu Leu Thr Tyr Leu Glu Glu Ser Thr Arg Asp Gln Ser
165 170 175
Gly Leu His Tyr Leu Gln Asp Ala Asp Glu Glu His Val Glu Ile Ser
180 185 190
Thr Arg Ser Ala Glu Phe
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<210> 4237
<211> 560
<212> DNA
<213> Homo sapiens

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240
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360
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<211> 124
<212> PRT
<213> Homo sapiens

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35 40 45
Phe Leu Asp Ser Leu Ser Cys Phe Leu Asp Ser Leu Gln Ile Ala Arg
50 55 60
Ala Met Gly Val Ala Asp Glu Ala Leu Gly Asn Val Arg Thr Val Arg
65 70 75 80
Ala Phe Ala Met Glu Gln Arg Glu Glu Glu Arg Tyr Gly Ala Glu Leu
85 90 95
Glu Ala Cys Arg Cys Arg Ala Glu Glu Leu Gly Arg Gly Ile Ala Leu
100 105 110
Phe Gln Gly Leu Ser Asn Ile Ala Phe Asn Cys Glu
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<210> 4239
<211> 3127
<212> DNA
<213> Homo sapiens

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180

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<210> 4240
<211> 860
<212> PRT
<213> Homo sapiens

<400> 4240
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Arg Arg Ser Ser Ala Ser Ile Ser Arg Gln Ser His Leu Glu Pro Asp
        35                  40                  45
Thr Phe Glu Ala Thr Gln Asp Asp Met Val Thr Val Pro Lys Ser Pro
    50                  55                  60
Pro Ala Tyr Ala Arg Ser Ser Asp Met Tyr Ser His Met Gly Thr Met
65                  70                  75                  80
Pro Arg Pro Ser Ile Lys Lys Ala Gln Asn Ser Gln Ala Ala Arg Gln
                85                  90                  95
Ala Gln Glu Ala Gly Pro Lys Pro Asn Leu Val Pro Gly Gly Val Pro
            100                 105                 110
Asp Pro Pro Gly Leu Glu Ala Ala Lys Glu Val Met Val Lys Ala Thr
        115                 120                 125
Gly Pro Leu Glu Asp Thr Pro Ala Met Glu Pro Asn Pro Ser Ala Val
    130                 135                 140
Glu Val Asp Pro Ile Arg Lys Pro Glu Val Pro Thr Gly Asp Val Glu
145                 150                 155                 160
Glu Glu Arg Pro Pro Arg Asp Val His Ser Glu Arg Ala Ala Gly Glu
                165                 170                 175
Pro Glu Ala Gly Ser Asp Tyr Val Lys Phe Ser Lys Glu Lys Tyr Ile
            180                 185                 190
Leu Asp Ser Ser Pro Glu Lys Leu His Lys Glu Leu Glu Glu Glu Leu
        195                 200                 205
Lys Leu Ser Ser Thr Asp Leu Arg Ser His Ala Trp Tyr His Gly Arg
    210                 215                 220
Ile Pro Arg Glu Val Ser Glu Thr Leu Val Gln Arg Asn Gly Asp Phe
225                 230                 235                 240
Leu Ile Arg Asp Ser Leu Thr Ser Leu Gly Asp Tyr Val Leu Thr Cys
                245                 250                 255
Arg Trp Arg Asn Gln Ala Leu His Phe Lys Ile Asn Lys Val Val Val
            260                 265                 270
Lys Ala Gly Glu Ser Tyr Thr His Ile Gln Tyr Leu Phe Glu Gln Glu
        275                 280                 285
Ser Phe Asp His Val Pro Ala Leu Val Arg Tyr His Val Gly Ser Arg
    290                 295                 300
Lys Ala Val Ser Glu Gln Ser Gly Ala Ile Ile Tyr Cys Pro Val Asn
305                 310                 315                 320
Arg Thr Phe Pro Leu Arg Tyr Leu Glu Ala Ser Tyr Gly Leu Gly Gln
                325                 330                 335
Gly Ser Ser Lys Pro Ala Ser Pro Val Ser Pro Ser Gly Pro Lys Gly
            340                 345                 350
Ser His Met Lys Arg Arg Ser Val Thr Met Thr Asp Gly Leu Thr Ala
        355                 360                 365
Asp Lys Val Thr Arg Ser Asp Gly Cys Pro Thr Ser Thr Ser Leu Pro
    370                 375                 380
Arg Pro Arg Asp Ser Ile Arg Ser Cys Ala Leu Ser Met Asp Gln Ile
385                 390                 395                 400
Pro Asp Leu His Ser Pro Met Ser Pro Ile Ser Glu Ser Pro Ser Ser
                405                 410                 415
Pro Ala Tyr Ser Thr Val Thr Arg Val His Ala Ala Pro Ala Ala Pro
            420                 425                 430
Ser Ala Thr Ala Leu Pro Ala Ser Pro Val Ala Arg Cys Ser Ser Glu
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        435                 440                 445
Pro Gln Leu Cys Pro Gly Ser Ala Pro Lys Thr His Gly Glu Ser Asp
    450                 455                 460
Lys Gly Pro His Thr Ser Pro Ser His Thr Leu Gly Lys Ala Ser Pro
465                 470                 475                 480
Ser Pro Ser Leu Ser Ser Tyr Ser Asp Pro Asp Ser Gly His Tyr Cys
                485                 490                 495
Gln Leu Gln Pro Pro Val Arg Gly Ser Arg Glu Trp Ala Ala Thr Glu
            500                 505                 510
Thr Ser Ser Gln Gln Ala Arg Ser Tyr Gly Glu Arg Leu Lys Glu Leu
        515                 520                 525
Ser Glu Asn Gly Ala Pro Glu Gly Asp Trp Gly Lys Thr Phe Thr Val
    530                 535                 540
Pro Ile Val Glu Val Thr Ser Ser Phe Asn Pro Ala Thr Phe Gln Ser
545                 550                 555                 560
Leu Leu Ile Pro Arg Asp Asn Arg Pro Leu Glu Val Gly Leu Leu Arg
                565                 570                 575
Lys Val Lys Glu Leu Leu Ala Glu Val Asp Ala Arg Thr Leu Ala Arg
            580                 585                 590
His Val Thr Lys Val Asp Cys Leu Val Ala Arg Ile Leu Gly Val Thr
        595                 600                 605
Lys Glu Met Gln Thr Leu Met Gly Val Arg Trp Gly Met Glu Leu Leu
    610                 615                 620
Thr Leu Pro His Gly Arg Gln Leu Arg Leu Asp Leu Leu Glu Arg Phe
625                 630                 635                 640
His Thr Met Ser Ile Met Leu Ala Val Asp Ile Leu Gly Cys Thr Gly
                645                 650                 655
Ser Ala Glu Glu Arg Ala Ala Leu Leu His Lys Thr Ile Gln Leu Ala
            660                 665                 670
Ala Glu Leu Arg Gly Thr Met Gly Asn Met Phe Ser Phe Ala Ala Val
        675                 680                 685
Met Gly Ala Leu Asp Met Ala Gln Ile Ser Arg Leu Glu Gln Thr Trp
    690                 695                 700
Val Thr Leu Arg Gln Arg His Thr Glu Gly Ala Ile Leu Tyr Glu Lys
705                 710                 715                 720
Lys Leu Lys Pro Phe Leu Lys Ser Leu Asn Glu Gly Lys Glu Gly Pro
                725                 730                 735
Pro Leu Ser Asn Thr Thr Phe Pro His Val Leu Pro Leu Ile Thr Leu
            740                 745                 750
Leu Glu Cys Asp Ser Ala Pro Pro Glu Gly Pro Glu Pro Trp Gly Ser
        755                 760                 765
Thr Glu His Gly Val Glu Val Val Leu Ala His Leu Glu Ala Ala Arg
    770                 775                 780
Thr Val Ala His His Gly Gly Leu Tyr His Thr Asn Ala Glu Val Lys
785                 790                 795                 800
Leu Gln Gly Phe Gln Ala Arg Pro Glu Leu Leu Glu Val Phe Ser Thr
                805                 810                 815
Glu Phe Gln Met Arg Leu Leu Trp Gly Ser Gln Gly Ala Ser Ser Ser
            820                 825                 830
Gln Ala Arg Arg Tyr Glu Lys Phe Asp Lys Val Leu Thr Ala Leu Ser
        835                 840                 845
His Lys Leu Glu Pro Ala Val Arg Ser Ser Glu Leu
    850                 855                 860
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<211> 479
<212> DNA
<213> Homo sapiens

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<210> 4242
<211> 159
<212> PRT
<213> Homo sapiens

<400> 4242
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Cys Trp Lys Val Ser Pro His Ile Lys Met Asp Leu Leu Gln Trp Ile
        35   40   45
Gln Ser Lys Thr Gln Ser Asp Gly Ser Thr Leu Gln Gln Gly Ser Leu
    50   55   60
Glu Phe Phe Ser Cys Leu Tyr Glu Ile Gln Glu Glu Glu Phe Ile Gln
65   70   75   80
Gln Ala Leu Ser His Phe Gln Val Ile Val Val Ser Asn Ile Ala Ser
                85   90   95
Lys Met Glu His Met Val Ser Ser Phe Cys Leu Lys Arg Cys Arg Ser
            100   105   110
Ala Gln Val Leu His Leu Tyr Gly Ala Thr Tyr Ser Ala Asp Gly Glu
        115   120   125
Asp Arg Ala Arg Cys Pro Gln Glu Arg Thr Arg Cys Trp Cys Ser Tyr
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Gln Arg Gly Pro Phe Cys Trp Thr Pro Thr Val Asn Ile Trp Gln
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<210> 4243
<211> 3159
<212> DNA
<213> Homo sapiens

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<211> 849
<212> PRT
<213> Homo sapiens

<400> 4244
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35 40 45
Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
50 55 60
Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu
65 70 75 80
Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro
85 90 95
Leu Ile Leu Arg Gly Met Phe Gln Arg Lys Tyr Leu Tyr Gln Lys Val
100 105 110
Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
115 120 125
Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
130 135 140
Gln Leu Arg Val Ser Arg Met Asp Asp Phe Val Leu Arg Thr Gly Glu
145 150 155 160
Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
165 170 175
Glu Phe Pro Glu Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn
180 185 190
Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
195 200 205
Val Tyr Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr
210 215 220
Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
225 230 235 240
Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
245 250 255
Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro Val Asp
260 265 270
Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
275 280 285
Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys Leu Gly Ile Phe
290 295 300
Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
305 310 315 320
Arg Gln Lys Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
325 330 335
Glu Ser Ala Ser Leu Leu Gly His Pro Arg Val Leu Ala Asp Ser Phe
340 345 350
Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn
355 360 365
Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser Ala Gly Thr Gly Asp

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Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu
            420                 425                 430
Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile
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Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr
465                 470                 475                 480
Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr
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Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn
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Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile
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Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile
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Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp
545                 550                 555                 560
Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr
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Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr
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His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met
        595                 600                 605
Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His
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Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile
625                 630                 635                 640
Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr
                645                 650                 655
Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu
            660                 665                 670
Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly
        675                 680                 685
Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln
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Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly
705                 710                 715                 720
Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro
                725                 730                 735
Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu
            740                 745                 750
Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg
        755                 760                 765
Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp
    770                 775                 780
Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys
785                 790                 795                 800
Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp
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Thr

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<211> 909
<212> DNA
<213> Homo sapiens

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<210> 4246
<211> 303
<212> PRT
<213> Homo sapiens

<400> 4246
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Gly Arg Gln Leu Gln Ala Ala Glu Glu Ala Val Glu Lys Leu Lys Ala
    50                  55                  60
Thr Gln Ala Asp Met Gly Glu Lys Leu Ser Cys Thr Ser Asn His Leu
65                  70                  75                  80
Ala Glu Cys Gln Ala Ala Met Leu Arg Lys Asp Lys Glu Gly Ala Ala
                85                  90                  95
Leu Arg Glu Asp Leu Glu Arg Thr Gln Lys Glu Leu Glu Lys Ala Thr
            100                 105                 110
Thr Lys Ile Gln Glu Tyr Tyr Asn Lys Leu Cys Gln Glu Val Thr Asn
        115                 120                 125
Arg Glu Arg Asn Asp Gln Lys Met Leu Ala Asp Leu Asp Asp Leu Asn
    130                 135                 140
Arg Thr Lys Lys Tyr Leu Glu Glu Arg Leu Ile Glu Leu Leu Arg Asp
145                 150                 155                 160
Lys Asp Ala Leu Trp Gln Lys Ser Asp Ala Leu Glu Phe Gln Gln Lys
                165                 170                 175
Leu Ser Ala Glu Glu Arg Trp Leu Gly Asp Thr Glu Ala Asn His Cys
            180                 185                 190
Leu Asp Cys Lys Arg Glu Phe Ser Trp Met Val Arg Arg His His Cys
        195                 200                 205
Arg Ile Cys Gly Arg Ile Phe Cys Tyr Tyr Cys Cys Asn Asn Tyr Val
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Leu Ser Lys His Gly Gly Lys Lys Glu Arg Cys Cys Arg Ala Cys Phe
225                 230                 235                 240
Gln Lys Leu Ser Glu Gly Pro Gly Ser Pro Asp Ser Ser Gly Ser Gly
                245                 250                 255
Thr Ser Gln Gly Glu Leu Ser Pro Ala Leu Ser Pro Ala Ser Pro Gly
            260                 265                 270
Pro Gln Ala Thr Gly Gly Gln Gly Ala Asn Thr Asp Tyr Arg Pro Pro
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<210> 4247
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<212> DNA
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<400> 4247

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5755

<210> 4248
<211> 1297
<212> PRT
<213> Homo sapiens

<400> 4248
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Gly Glu Asp Arg Arg Gly Ala Pro Ala Gly Ala Thr Ser Phe Pro Ala
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Ala Pro Ser Pro Leu Pro Leu His Thr His Ala Arg Ser Leu Ala Gly
35 40 45
Ala Arg Thr Pro Pro Ala Pro Asp Pro His Leu Gly Gly Arg His Thr
50 55 60
Leu Gly Ser Pro Ser Arg Gly Ser Arg Ser Gly Met Glu Ala Ala Arg
65 70 75 80
Thr Glu Arg Pro Ala Gly Arg Pro Gly Ala Pro Leu Val Arg Thr Gly
85 90 95
Leu Leu Leu Leu Ser Thr Trp Val Leu Ala Gly Ala Glu Ile Thr Trp
100 105 110
Asp Ala Thr Gly Gly Pro Gly Arg Pro Ala Ala Pro Ala Ser Arg Pro
115 120 125
Pro Ala Leu Ser Pro Leu Ser Pro Arg Ala Val Ala Ser Gln Trp Pro
130 135 140
Glu Glu Leu Ala Ser Ala Arg Arg Ala Ala Val Leu Gly Arg Arg Ala
145 150 155 160
Gly Pro Glu Leu Leu Pro Gln Gln Gly Gly Gly Arg Gly Gly Glu Met
165 170 175
Gln Val Glu Ala Gly Gly Thr Ser Pro Ala Gly Glu Arg Arg Gly Arg
180 185 190
Gly Ile Pro Ala Pro Ala Lys Leu Gly Gly Ala Arg Arg Ser Arg Arg
195 200 205
Ala Gln Pro Pro Ile Thr Gln Glu Arg Gly Asp Ala Trp Ala Thr Ala

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    210                 215                 220
Pro Ala Asp Gly Ser Arg Gly Ser Arg Pro Leu Ala Lys Gly Ser Arg
225                 230                 235                 240
Glu Glu Val Lys Ala Pro Arg Ala Gly Gly Ser Ala Ala Glu Asp Leu
                245                 250                 255
Arg Leu Pro Ser Thr Ser Phe Ala Leu Thr Gly Asp Ser Ala His Asn
            260                 265                 270
Gln Ala Met Val His Trp Ser Gly His Asn Ser Ser Val Ile Leu Ile
        275                 280                 285
Leu Thr Lys Leu Tyr Asp Phe Asn Leu Gly Ser Val Thr Glu Ser Ser
    290                 295                 300
Leu Trp Arg Ser Thr Asp Tyr Gly Thr Thr Tyr Glu Lys Leu Asn Asp
305                 310                 315                 320
Lys Val Gly Leu Lys Thr Val Leu Ser Tyr Leu Tyr Val Asn Pro Thr
                325                 330                 335
Asn Lys Arg Lys Ile Met Leu Leu Ser Asp Pro Glu Met Glu Ser Ser
            340                 345                 350
Ile Leu Ile Ser Ser Asp Glu Gly Ala Thr Tyr Gln Lys Tyr Arg Leu
        355                 360                 365
Thr Phe Tyr Ile Gln Ser Leu Leu Phe His Pro Lys Gln Glu Asp Trp
    370                 375                 380
Val Leu Ala Tyr Ser Leu Asp Gln Lys Leu Tyr Ser Ser Met Asp Phe
385                 390                 395                 400
Gly Arg Arg Trp Gln Leu Met His Glu Arg Ile Thr Pro Asn Arg Phe
                405                 410                 415
Tyr Trp Ser Val Ala Gly Leu Asp Lys Glu Ala Asp Leu Val His Met
            420                 425                 430
Glu Val Arg Thr Thr Asp Gly Tyr Ala His Tyr Leu Thr Cys Arg Ile
        435                 440                 445
Gln Glu Cys Ala Glu Thr Thr Arg Ser Gly Pro Phe Ala Arg Ser Ile
    450                 455                 460
Asp Ile Ser Ser Leu Val Val Gln Asp Glu Tyr Ile Phe Ile Gln Val
465                 470                 475                 480
Thr Thr Ser Gly Arg Ala Ser Tyr Tyr Val Ser Tyr Arg Arg Glu Ala
                485                 490                 495
Phe Ala Gln Ile Lys Leu Pro Lys Tyr Ser Leu Pro Lys Asp Met His
            500                 505                 510
Ile Ile Ser Thr Asp Glu Asn Gln Val Phe Ala Ala Val Gln Glu Trp
        515                 520                 525
Asn Gln Asn Asp Thr Tyr Asn Leu Tyr Ile Ser Asp Thr Arg Gly Ile
    530                 535                 540
Tyr Phe Thr Leu Ala Met Glu Asn Ile Lys Ser Ser Arg Gly Leu Met
545                 550                 555                 560
Gly Asn Ile Ile Ile Glu Leu Tyr Glu Val Ala Gly Ile Lys Gly Ile
                565                 570                 575
Phe Leu Ala Asn Lys Lys Val Asp Asp Gln Val Lys Thr Tyr Ile Thr
            580                 585                 590
Tyr Asn Lys Gly Arg Asp Trp Arg Leu Leu Gln Ala Pro Asp Val Asp
        595                 600                 605
Leu Arg Gly Ser Pro Val His Cys Leu Leu Pro Phe Cys Ser Leu His
    610                 615                 620
Leu His Leu Gln Leu Ser Glu Asn Pro Tyr Ser Ser Gly Arg Ile Ser
625                 630                 635                 640
Ser Lys Glu Thr Ala Pro Gly Leu Val Val Ala Thr Gly Asn Ile Gly
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                645                 650                 655
Pro Glu Leu Ser Tyr Thr Asp Ile Gly Val Phe Ile Ser Ser Asp Gly
            660                 665                 670
Gly Asn Thr Trp Arg Gln Ile Phe Asp Glu Glu Tyr Asn Val Trp Phe
        675                 680                 685
Leu Asp Trp Gly Gly Ala Leu Val Ala Met Lys His Thr Pro Leu Pro
    690                 695                 700
Val Arg His Leu Trp Val Ser Phe Asp Glu Gly His Ser Trp Asp Lys
705                 710                 715                 720
Tyr Gly Phe Thr Ser Val Pro Leu Phe Val Asp Gly Ala Leu Val Glu
                725                 730                 735
Ala Gly Met Glu Thr His Ile Met Thr Val Phe Gly His Phe Ser Leu
            740                 745                 750
Arg Ser Glu Trp Gln Leu Val Lys Val Asp Tyr Lys Ser Ile Phe Ser
        755                 760                 765
Arg His Cys Thr Lys Glu Asp Tyr Gln Thr Trp His Leu Leu Asn Gln
    770                 775                 780
Gly Glu Pro Cys Val Met Gly Glu Arg Lys Ile Phe Lys Lys Arg Lys
785                 790                 795                 800
Pro Gly Ala Gln Cys Ala Leu Gly Arg Asp His Ser Gly Ser Val Val
                805                 810                 815
Ser Glu Pro Cys Val Cys Ala Asn Trp Asp Phe Glu Cys Asp Tyr Gly
            820                 825                 830
Tyr Glu Arg His Gly Glu Ser Gln Cys Val Pro Ala Phe Trp Tyr Asn
        835                 840                 845
Pro Ala Ser Pro Ser Lys Asp Cys Ser Leu Gly Gln Ser Tyr Leu Asn
    850                 855                 860
Ser Thr Gly Tyr Arg Arg Ile Val Ser Asn Asn Cys Thr Asp Gly Leu
865                 870                 875                 880
Arg Glu Lys Tyr Thr Ala Lys Ala Gln Met Cys Pro Gly Lys Ala Pro
                885                 890                 895
Arg Gly Leu His Val Val Thr Thr Asp Gly Arg Leu Val Ala Glu Gln
            900                 905                 910
Gly His Asn Ala Thr Phe Ile Ile Leu Met Glu Glu Gly Asp Leu Gln
        915                 920                 925
Arg Thr Asn Ile Gln Leu Asp Phe Gly Asp Gly Ile Ala Val Ser Tyr
    930                 935                 940
Ala Asn Phe Ser Pro Ile Glu Asp Gly Ile Lys His Val Tyr Lys Ser
945                 950                 955                 960
Ala Gly Ile Phe Gln Val Thr Ala Tyr Ala Glu Asn Asn Leu Gly Ser
                965                 970                 975
Asp Thr Ala Val Leu Phe Leu His Val Val Cys Pro Val Glu His Val
            980                 985                 990
His Leu Arg Val Pro Phe Val Ala Ile Arg Asn Lys Glu Val Asn Ile
        995                 1000                1005
Ser Ala Val Val Trp Pro Ser Gln Leu Gly Thr Leu Thr Tyr Phe Trp
    1010                1015                1020
Trp Phe Gly Asn Ser Thr Lys Pro Leu Ile Thr Leu Asp Ser Ser Ile
1025                1030                1035                1040
Ser Phe Thr Phe Leu Ala Glu Gly Thr Asp Thr Ile Thr Val Gln Val
                1045                1050                1055
Ala Ala Gly Asn Ala Leu Ile Gln Asp Thr Lys Glu Ile Ala Val His
            1060                1065                1070
Glu Tyr Phe Gln Ser Gln Leu Leu Ser Phe Ser Pro Asn Leu Asp Tyr
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        1075                1080                1085
His Asn Pro Asp Ile Pro Glu Trp Arg Lys Asp Ile Gly Asn Val Ile
    1090                1095                1100
Lys Arg Ala Leu Val Lys Val Thr Ser Val Pro Glu Asp Gln Ile Leu
1105                1110                1115                1120
Ile Ala Val Phe Pro Gly Leu Pro Thr Ser Ala Glu Leu Phe Ile Leu
                1125                1130                1135
Pro Pro Lys Asn Leu Thr Glu Arg Arg Lys Gly Asn Glu Gly Asp Leu
            1140                1145                1150
Glu Gln Ile Val Glu Thr Leu Phe Asn Ala Leu Asn Gln Asn Leu Val
        1155                1160                1165
Gln Phe Glu Leu Lys Pro Gly Val Gln Val Ile Val Tyr Val Thr Gln
    1170                1175                1180
Leu Thr Leu Ala Pro Leu Val Asp Ser Ser Ala Gly His Ser Ser Ser
1185                1190                1195                1200
Ala Met Leu Met Leu Leu Ser Val Val Phe Val Gly Leu Ala Val Phe
                1205                1210                1215
Leu Ile Tyr Lys Phe Lys Arg Lys Ile Pro Trp Ile Asn Ile Tyr Ala
            1220                1225                1230
Gln Val Gln His Asp Lys Glu Gln Glu Met Ile Gly Ser Val Ser Gln
        1235                1240                1245
Ser Glu Asn Ala Pro Lys Ile Thr Leu Ser Asp Phe Thr Glu Pro Glu
    1250                1255                1260
Glu Leu Leu Asp Lys Glu Leu Asp Thr Arg Val Ile Gly Gly Ile Ala
1265                1270                1275                1280
Thr Ile Ala Asn Ser Glu Ser Thr Lys Glu Ile Pro Asn Cys Thr Ser
                1285                1290                1295
Val
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<210> 4249
<211> 553
<212> DNA
<213> Homo sapiens

<400> 4249
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ctaagaaact caactgcatc cagaacaaag attaagatga tttataaaaa tgctaaaaca
120
cccagcacgc aacatggtaa aattcgcaat gcctcaggca tcaacccgag agtaccaggc
180
ccacaggaag gcagcataat aggaccccaa acaaggagga aaagcagcct cctgaaaccg
240
accctgatat cagaaccagc agacatgggc actcagcagt tcttacaact gaatcccaat
300
ctgcaaaagt ttagtagaga catggaagac gtaaagggga ccccaagcaa gcctctagag
360
aattataaca tgttggctgg gcttggtggc tcacgcgtgt catcgcagca ctttgggagg
420
ctgaggcagg aggatcgctt gagcccagga gttcaagacc agcctggacc acatagtgag
480
acccccatct cataaaaaat aaaaaaaaat tgaattacaa cacgaggtga caaaagcact
540

ggatgagatt aac
553

<210> 4250
<211> 164
<212> PRT
<213> Homo sapiens

<400> 4250
Xaa Arg Ala Leu Pro Lys Lys Asp Gln Val Val Gln Lys Ser Glu Gln
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Leu Lys Leu Phe Leu Arg Asn Ser Thr Ala Ser Arg Thr Lys Ile Lys
 20 25 30
Met Ile Tyr Lys Asn Ala Lys Thr Pro Ser Thr Gln His Gly Lys Ile
 35 40 45
Arg Asn Ala Ser Gly Ile Asn Pro Arg Val Pro Gly Pro Gln Glu Gly
 50 55 60
Ser Ile Ile Gly Pro Gln Thr Arg Arg Lys Ser Ser Leu Leu Lys Pro
65 70 75 80
Thr Leu Ile Ser Glu Pro Ala Asp Met Gly Thr Gln Gln Phe Leu Gln
 85 90 95
Leu Asn Pro Asn Leu Gln Lys Phe Ser Arg Asp Met Glu Asp Val Lys
 100 105 110
Gly Thr Pro Ser Lys Pro Leu Glu Asn Tyr Asn Met Leu Ala Gly Leu
 115 120 125
Gly Gly Ser Arg Val Ser Ser Gln His Phe Gly Arg Leu Arg Gln Glu
 130 135 140
Asp Arg Leu Ser Pro Gly Val Gln Asp Gln Pro Gly Pro His Ser Glu
145 150 155 160
Thr Pro Ile Ser

<210> 4251
<211> 1574
<212> DNA
<213> Homo sapiens

<400> 4251
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aaaagggcgg cgcgggggg gtcccccaca caaaaaaagg gggggaaagg aattcgcccc
120
gggggggggc caggccctaa ccccatttat ttcattccac agatgagggc aaccttaaga
180
gggaaggggg agatggcagg gccagcgggc gcaggaagtg ccttcccacc cccaggacct
240
gacacatctc gtctcccctc ttttccgcac tgtgggcaca aagacacttt ttcttccgca
300
ggggcgggag cccctagttc caacactgag gacgcgtgac atggtgggca ccggaaagga
360
ggggacttct cctgcacccc aagaagtggt ggggagattg ctgcccctat agccatatct
420
cggccccttc ccactcacca cccccacccc aggtgctggg ggtcccttat ttttatgcaa
480

taactgagct tgatgggggt gggcaggggg ccagttgagc caatcaccag cctccatatc
540
acagatcctg accctgaatc tcaggagctg cagatcgggg gcacctgccc tgacatcacc
600
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660
ttgaaaaagt cgctgtgcat ggtcaagtgc cactggaaag agaagcagga ctacgcgttt
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840
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agacagcctc tggt
1574

<210> 4252
<211> 352
<212> PRT
<213> Homo sapiens

<400> 4252
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Thr Asp Pro Asp Pro Glu Ser Gln Glu Leu Gln Ile Gly Gly Thr Cys
20 25 30
Pro Asp Ile Thr Lys Arg Tyr Leu Arg Leu Thr Cys Ala Pro Asp Pro
35 40 45
Ser Thr Val Arg Pro Val Ala Val Leu Lys Lys Ser Leu Cys Met Val
50 55 60
Lys Cys His Trp Lys Glu Lys Gln Asp Tyr Ala Phe Ala Cys Glu Gln

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65                  70                  75                  80
Met Lys Ser Ile Arg Gln Asp Leu Thr Val Gln Gly Ile Arg Thr Glu
                85                  90                  95
Phe Thr Val Glu Val Tyr Glu Thr His Ala Arg Ile Ala Leu Glu Lys
            100                 105                 110
Gly Asp His Glu Glu Phe Asn Gln Cys Gln Thr Gln Leu Lys Ser Leu
        115                 120                 125
Tyr Ala Glu Asn Leu Pro Gly Asn Val Gly Glu Phe Thr Ala Tyr Arg
    130                 135                 140
Ile Leu Tyr Tyr Ile Phe Thr Lys Asn Ser Gly Asp Ile Thr Thr Glu
145                 150                 155                 160
Leu Ala Tyr Leu Thr Arg Glu Leu Lys Ala Asp Pro Cys Val Ala His
                165                 170                 175
Ala Leu Ala Leu Arg Thr Ala Trp Ala Leu Gly Asn Tyr His Arg Phe
            180                 185                 190
Phe Arg Leu Tyr Cys His Ala Pro Cys Met Ser Gly Tyr Leu Val Asp
        195                 200                 205
Lys Phe Ala Asp Arg Glu Arg Lys Val Ala Leu Lys Ala Met Ile Lys
    210                 215                 220
Thr Tyr Val Val Pro Ser Ser Leu Leu Pro Leu Leu Phe Pro Ser Phe
225                 230                 235                 240
Arg Leu Ala Pro Pro Leu Arg Pro Ala Pro Gly Arg Arg Pro Pro Pro
                245                 250                 255
Ala Pro Asn Pro Cys Pro Gly Pro Cys Phe Pro Ile Ile Phe Leu His
            260                 265                 270
Ser Ala Leu Pro Ser Pro Val Pro Leu Ala Leu Leu Val Gly His Leu
        275                 280                 285
Cys Val Pro Gly His Ser Ser Pro Ser Pro His Cys Ser Gln Leu Thr
    290                 295                 300
Ala Ser Gly Ala Ser Ser Pro Pro His Leu Cys Val Ser Ser Ser Cys
305                 310                 315                 320
Ser Leu Leu Pro Gly Pro Pro Ser Ser Leu Leu Ala Leu Gly Phe Leu
                325                 330                 335
Arg Thr Leu Arg Ser Leu Leu Ser Gln Leu Val Ala Val Leu Pro Pro
            340                 345                 350
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<210> 4253
<211> 1287
<212> DNA
<213> Homo sapiens

<400> 4253
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120
gtttccttgt gggtggaggg tactttcccg ccccctggtt tcgggcttgc ccacgtggct
180
tgctctggcc atggaatgaa gcagaaacga aagcctgcca gttctgagcc tatgccggaa
240
gacgccttgg gcggttccgc ggtccctgtg cgcttccacc ttcacccaga aggacttctc
300
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360

gcaggtctgc agggagccac agagcgcagc ggccggccca gcgttcaagc ccaagcacag
420
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480
gcggtagctc accaatccag tgcgtgcacc cgctccttta ttaggctata gagccagtgg
540
ctcccacagg gacctgatac aacagtgcgt taaataagga gcatattgag ctctcatgtc
600
gtaagccagt ggagaagtcc agggctagtg tgggggctcc ggcgggggct gtggccccca
660
tccgcatgga gcctccccat ggttcacagg tctcagtctt cggagccttc ggccctgcga
720
gcccgaacgg tccacagggc ggcgccagac cctctttcga acgccatcct ctaaagcggc
780
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900
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960
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1020
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1080
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1260
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1287

<210> 4254
<211> 114
<212> PRT
<213> Homo sapiens

<400> 4254
Met Val Ser Leu Trp Val Glu Gly Thr Phe Pro Pro Pro Gly Phe Gly
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Leu Ala His Val Ala Cys Ser Gly His Gly Met Lys Gln Lys Arg Lys
20 25 30
Pro Ala Ser Ser Glu Pro Met Pro Glu Asp Ala Leu Gly Gly Ser Ala
35 40 45
Val Pro Val Arg Phe His Leu His Pro Glu Gly Leu Leu Trp Cys Ser
50 55 60
Arg Cys Phe Phe Ser His Gly Pro Lys Gly Ser Glu Pro Pro Gly Arg
65 70 75 80
Ser Ala Gly Leu Gln Gly Ala Thr Glu Arg Ser Gly Arg Pro Ser Val
85 90 95
Gln Ala Gln Ala Gln Ala Cys Glu Asn Leu Val Pro Ala Thr Val Trp
100 105 110
Asp Gly

<210> 4255
<211> 2205
<212> DNA
<213> Homo sapiens

<400> 4255
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120
aacacccaat ggcgtcctca gaatttattc tgggtccctc atgggacaag cattggatcc
180
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240
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300
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360
cagatacttc tacaaagttc tgatggacct attacctgtc tgtaaccaag atggtggcaa
420
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480
cgaccccaaa ggacatgcac ctgtggagca gcagcacatc acccacaagg agcccctggt
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600
tgacagaacg gtccagaggt tttataaatt caacaccagc cttgcggggg atttgacgaa
660
ccttgtgcat ggcagccact gttccaaata cagattagca aggatcccag gaaccaacgc
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780
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960
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1020
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1140
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ccaagaaatg tcagtgcgta tgtccaacct ggagaatgac agagatgaaa gggacgacga
1380

cagccacgaa gacagaggca tcatcagcaa cactcggttt atagctgcgg tcatcgaacg
1440
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1500
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1560
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1920
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1980
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2040
gaacctgcaa gtgaagctga gccagaggaa tgttccaaag agccagaagc attcagctct
2100
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2205

<210> 4256
<211> 384
<212> PRT
<213> Homo sapiens

<400> 4256
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Gly Val Leu Arg Ile Tyr Ser Gly Ser Leu Met Gly Gln Ala Leu Asp
35 40 45
Pro Thr Arg Lys Gln Trp Tyr Leu His Ala Val Ala Asn Pro Gly Leu
50 55 60
Ile Ser Leu Thr Gly Pro Tyr Leu Asp Val Gly Gly Ala Gly Tyr Val
65 70 75 80
Val Thr Ile Ser His Thr Ile His Ser Ser Ser Thr Gln Leu Ser Ser
85 90 95
Gly His Thr Val Ala Val Met Gly Ile Asp Phe Thr Leu Arg Tyr Phe
100 105 110
Tyr Lys Val Leu Met Asp Leu Leu Pro Val Cys Asn Gln Asp Gly Gly
115 120 125
Asn Lys Ile Arg Cys Phe Ile Met Glu Asp Arg Gly Tyr Leu Val Ala
130 135 140
His Pro Thr Leu Ile Asp Pro Lys Gly His Ala Pro Val Glu Gln Gln

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145                 150                 155                 160
His Ile Thr His Lys Glu Pro Leu Val Ala Asn Asp Ile Leu Asn His
                165                 170                 175
Pro Asn Phe Val Lys Lys Asn Leu Cys Asn Ser Phe Ser Asp Arg Thr
            180                 185                 190
Val Gln Arg Phe Tyr Lys Phe Asn Thr Ser Leu Ala Gly Asp Leu Thr
        195                 200                 205
Asn Leu Val His Gly Ser His Cys Ser Lys Tyr Arg Leu Ala Arg Ile
    210                 215                 220
Pro Gly Thr Asn Ala Phe Val Gly Ile Val Asn Glu Thr Cys Asp Ser
225                 230                 235                 240
Leu Ala Phe Cys Ala Cys Ser Met Val Asp Arg Leu Cys Leu Asn Cys
                245                 250                 255
His Arg Met Glu Gln Asn Glu Cys Glu Cys Pro Cys Glu Cys Pro Leu
            260                 265                 270
Glu Val Asn Glu Cys Thr Gly Asn Leu Thr Asn Ala Glu Asn Arg Asn
        275                 280                 285
Pro Ser Cys Glu Val His Gln Glu Pro Val Thr Tyr Thr Ala Ile Asp
    290                 295                 300
Pro Gly Leu Gln Asp Ala Leu His Gln Cys Val Asn Ser Arg Cys Ser
305                 310                 315                 320
Gln Arg Leu Glu Ser Gly Asp Cys Phe Gly Val Leu Asp Cys Glu Trp
                325                 330                 335
Cys Met Val Asp Ser Asp Gly Lys Thr His Leu Asp Lys Pro Tyr Cys
            340                 345                 350
Ala Pro Gln Lys Glu Cys Phe Gly Gly Ile Val Gly Ala Lys Ser Pro
        355                 360                 365
Tyr Val Asp Asp Met Gly Ala Ile Gly Asp Glu Val Ile Thr Leu Lys
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<210> 4257
<211> 1541
<212> DNA
<213> Homo sapiens

<400> 4257
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120
tgagtgccct gaggagtgac acagagcctg ggatggatct ttgggagttc tgcagcgaaa
180
ctttccaaag accttaccag tatttaagac gattcaatcc aaacccagac cttaacccgg
240
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300
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360
aattatcagc tcagagattg tgaggcctct ctcttctgca atccgagttt tattggcgac
420
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480
gccacaccat cactccacac ctctgaccaa agcccgggga agcacatggt caccatggat
540

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600
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660
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1080
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1541

<210> 4258
<211> 314
<212> PRT
<213> Homo sapiens

<400> 4258
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Asp Gln Ser Pro Gly Lys His Met Val Thr Met Asp Gly Val Arg Glu
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Glu Asp Leu Ala Pro Phe Ser Leu Arg Lys Arg Trp Glu Ser Glu Pro
35 40 45
His Pro Tyr Val Phe Phe Asn Asp Asp His Thr Thr Met Thr Phe Ile
50 55 60
Gly Phe His Leu Gln Pro Asn Ile Asn Gly Ser Val Asp Ala Ile Ser
65 70 75 80
His Leu Thr Gly Lys Val Ile Lys Arg Asp Val Met Thr Arg Asp Leu
85 90 95
Tyr Gln Gly Leu Leu Leu Gln Arg Val Pro Phe Asn Val Asp Phe Asp

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            100                 105                 110
Lys Leu Pro Arg His Lys Lys Leu Glu Arg Leu Cys Leu Thr Leu Gly
        115                 120                 125
Ile Pro Gln Ala Thr Asp Pro Asp Lys Thr Tyr Glu Leu Thr Thr Asp
    130                 135                 140
Asn Met Leu Lys Ile Leu Ala Ile Glu Met Arg Phe Arg Cys Gly Ile
145                 150                 155                 160
Pro Val Ile Ile Met Gly Glu Thr Gly Cys Gly Lys Thr Arg Leu Ile
                165                 170                 175
Lys Phe Leu Ser Asp Leu Arg Arg Gly Gly Thr Asn Ala Asp Thr Ile
            180                 185                 190
Lys Leu Val Lys Val His Gly Gly Thr Thr Ala Asp Met Ile Tyr Ser
        195                 200                 205
Arg Val Arg Glu Ala Glu Asn Val Ala Phe Ala Asn Lys Asp Gln His
    210                 215                 220
Gln Leu Asp Thr Ile Leu Phe Phe Asp Glu Ala Asn Thr Thr Glu Ala
225                 230                 235                 240
Ile Ser Cys Ile Lys Glu Val Leu Cys Asp His Met Val Asp Gly Gln
                245                 250                 255
Pro Leu Ala Glu Asp Ser Gly Leu His Ile Ile Ala Ala Cys Asn Pro
            260                 265                 270
Tyr Pro Glu Asn Ser Glu Glu Met Ile Cys Arg Leu Glu Ser Ala Gly
        275                 280                 285
Leu Gly Tyr Arg Val Ser Met Glu Glu Thr Ala Asp Arg Leu Gly Ser
    290                 295                 300
Ile Pro Leu Gly Tyr Thr Cys Thr Gln Arg
305                 310
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<210> 4259
<211> 377
<212> DNA
<213> Homo sapiens

<400> 4259
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120
gaagcgcagc ccgttgtggt gatacgagcc ggagatgcct tctgcaggga ctgtttcaag
180
gccttctacg tccacaagtt cagagccatg ctgggcaaga accggctcat ctttccaggc
240
gagaaggtgc tcttggcgtg gtctgggggg ccttcgtcca gctccatggt ctggcaggtt
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360
gttgacgagg gagcagc
377

<210> 4260
<211> 125
<212> PRT
<213> Homo sapiens

<400> 4260
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Gly Glu Pro Ala Pro Glu Glu Pro Pro Pro Ala Pro Arg Pro Ser Arg
20 25 30
Glu Gln Lys Cys Val Lys Cys Lys Glu Ala Gln Pro Val Val Val Ile
35 40 45
Arg Ala Gly Asp Ala Phe Cys Arg Asp Cys Phe Lys Ala Phe Tyr Val
50 55 60
His Lys Phe Arg Ala Met Leu Gly Lys Asn Arg Leu Ile Phe Pro Gly
65 70 75 80
Glu Lys Val Leu Leu Ala Trp Ser Gly Gly Pro Ser Ser Ser Ser Met
85 90 95
Val Trp Gln Val Leu Glu Gly Leu Ser Gln Asp Ser Ala Lys Arg Leu
100 105 110
Arg Phe Val Ala Gly Val Ile Phe Val Asp Glu Gly Ala
115 120 125

<210> 4261
<211> 592
<212> DNA
<213> Homo sapiens

<400> 4261
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180
aaggacaaag gtgtctgggg aaataagcaa gatcatagag gagctttctt aattgaccga
240
agtcctgagt acttcgaacc cattttgaac tacttgcgtc atggacagct cattgtaaat
300
gatggcatta atttattggg tgtgttagaa gaagcaagat tttttggtat tgactcattg
360
attgaacacc tagaagtggc aataaagaat tctcaaccac cggaggatca ttcaccaata
420
tcccgaaagg aatttgtccg atttttgcta gcaactccaa ccaagtcaga actgcgatgc
480
cagggtttga acttcagtgg tgctgatctt tctcgtttgg accttcgata cattaacttc
540
aaaatggcca atttaagccg ctgtaatctt gcacatgcaa atctttgctg tg
592

<210> 4262
<211> 156
<212> PRT
<213> Homo sapiens

<400> 4262
Ile Leu Arg Ser Thr Leu Val Asn Lys Glu Pro Asp Ser Met Leu Ala
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His Met Phe Lys Asp Lys Gly Val Trp Gly Asn Lys Gln Asp His Arg

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Gly Ala Phe Leu Ile Asp Arg Ser Pro Glu Tyr Phe Glu Pro Ile Leu
        35                  40                  45
Asn Tyr Leu Arg His Gly Gln Leu Ile Val Asn Asp Gly Ile Asn Leu
    50                  55                  60
Leu Gly Val Leu Glu Glu Ala Arg Phe Phe Gly Ile Asp Ser Leu Ile
65                  70                  75                  80
Glu His Leu Glu Val Ala Ile Lys Asn Ser Gln Pro Pro Glu Asp His
                85                  90                  95
Ser Pro Ile Ser Arg Lys Glu Phe Val Arg Phe Leu Leu Ala Thr Pro
            100                 105                 110
Thr Lys Ser Glu Leu Arg Cys Gln Gly Leu Asn Phe Ser Gly Ala Asp
        115                 120                 125
Leu Ser Arg Leu Asp Leu Arg Tyr Ile Asn Phe Lys Met Ala Asn Leu
    130                 135                 140
Ser Arg Cys Asn Leu Ala His Ala Asn Leu Cys Cys
145                 150                 155
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<210> 4263
<211> 7710
<212> DNA
<213> Homo sapiens

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240
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360
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420
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480
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720
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780
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840
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900

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<210> 4264
<211> 797
<212> PRT
<213> Homo sapiens

<400> 4264
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Met Gln Lys Phe Leu Gly Ser Tyr Phe Ile Thr Trp Asp Glu Asp Met
35 40 45
Phe Asp Glu Glu Thr Gly Glu Gly Pro Leu Val Asn Thr Ser Asp Leu
50 55 60
Asn Glu Glu Leu Gly Gln Val Glu Tyr Ile Phe Thr Asp Lys Thr Gly
65 70 75 80
Thr Leu Thr Glu Asn Asn Met Glu Phe Lys Glu Cys Cys Ile Glu Gly
85 90 95
His Val Tyr Val Pro His Val Ile Cys Asn Gly Gln Val Leu Pro Glu
100 105 110
Ser Ser Gly Ile Asp Met Ile Asp Ser Ser Pro Ser Val Asn Gly Arg
115 120 125
Glu Arg Glu Glu Leu Phe Phe Arg Ala Leu Cys Leu Cys His Thr Val
130 135 140
Gln Val Lys Asp Asp Asp Ser Val Asp Gly Pro Arg Lys Ser Pro Asp
145 150 155 160
Gly Gly Lys Ser Cys Val Tyr Ile Ser Ser Ser Pro Asp Glu Val Ala
165 170 175
Leu Val Glu Gly Val Gln Arg Leu Gly Phe Thr Tyr Leu Arg Leu Lys
180 185 190
Asp Asn Tyr Met Glu Ile Leu Asn Arg Glu Asn His Ile Glu Arg Phe
195 200 205
Glu Leu Leu Glu Ile Leu Ser Phe Asp Ser Val Arg Arg Arg Met Ser
210 215 220
Val Ile Val Lys Ser Ala Thr Gly Glu Ile Tyr Leu Phe Cys Lys Gly
225 230 235 240
Ala Asp Ser Ser Ile Phe Pro Arg Val Ile Glu Gly Lys Val Asp Gln
245 250 255
Ile Arg Ala Arg Val Glu Arg Asn Ala Val Glu Gly Leu Arg Thr Leu
260 265 270
Cys Val Ala Tyr Lys Arg Leu Ile Gln Glu Glu Tyr Glu Gly Ile Cys

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Ala Thr Ala Val Glu Asp Arg Leu Gln Glu Lys Ala Ala Asp Thr Ile
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Glu Ala Leu Gln Lys Ala Gly Ile Lys Val Trp Val Leu Thr Gly Asp
            340                 345                 350
Lys Met Glu Thr Ala Ala Ala Thr Cys Tyr Ala Cys Lys Leu Phe Arg
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Arg Asn Thr Gln Leu Leu Glu Leu Thr Thr Lys Arg Ile Glu Glu Gln
    370                 375                 380
Ser Leu His Asp Val Leu Phe Glu Leu Ser Lys Thr Val Leu Arg His
385                 390                 395                 400
Ser Gly Ser Leu Thr Arg Asp Asn Leu Ser Gly Leu Ser Ala Asp Met
                405                 410                 415
Gln Asp Tyr Gly Leu Ile Ile Asp Gly Ala Ala Leu Ser Leu Ile Met
            420                 425                 430
Lys Pro Arg Glu Asp Gly Ser Ser Gly Asn Tyr Arg Glu Leu Phe Leu
        435                 440                 445
Glu Ile Cys Arg Ser Cys Ser Ala Val Leu Cys Cys Arg Met Ala Pro
    450                 455                 460
Leu Gln Lys Ala Gln Ile Val Lys Leu Ile Lys Phe Ser Lys Glu His
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Pro Ile Thr Leu Ala Ile Gly Asp Gly Ala Asn Asp Val Ser Met Ile
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Leu Glu Ala His Val Gly Ile Gly Val Ile Gly Lys Glu Gly Arg Gln
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Ala Ala Arg Asn Ser Asp Tyr Ala Ile Pro Lys Phe Lys His Leu Lys
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Lys Met Leu Leu Val His Gly His Phe Tyr Tyr Ile Arg Ile Ser Glu
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Leu Val Gln Tyr Phe Phe Tyr Lys Asn Val Cys Phe Ile Phe Pro Gln
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Phe Leu Tyr Gln Phe Phe Cys Gly Phe Ser Gln Gln Thr Val His Asp
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Thr Ala Tyr Leu Thr Leu Tyr Asn Ile Ser Phe Thr Ser Leu Pro Ile
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Leu Leu Tyr Ser Leu Met Glu Gln His Val Gly Ile Asp Val Leu Lys
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Arg Asp Pro Thr Leu Tyr Arg Asp Val Ala Lys Asn Ala Leu Leu Arg
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Trp Arg Val Phe Ile Tyr Trp Thr Leu Leu Gly Leu Phe Asp Ala Leu
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Val Phe Phe Phe Gly Ala Tyr Phe Val Phe Glu Asn Thr Thr Val Thr
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Ser Asn Gly Gln Ile Phe Gly Asn Trp Thr Phe Gly Thr Leu Val Phe
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Thr Val Met Val Phe Thr Val Thr Leu Lys Leu Ala Leu Asp Thr His
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Tyr Trp Thr Trp Ile Asn His Phe Val Ile Trp Gly Ser Leu Leu Phe
    690                 695                 700
Tyr Val Val Phe Ser Leu Leu Trp Gly Gly Val Ile Trp Pro Phe Leu
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Asn Tyr Gln Arg Met Tyr Tyr Val Phe Ile Gln Met Leu Ser Ser Gly
725 730 735
Pro Ala Trp Leu Ala Ile Val Leu Leu Val Thr Ile Ser Leu Leu Pro
740 745 750
Asp Val Leu Lys Lys Val Leu Cys Arg Gln Leu Trp Pro Thr Ala Thr
755 760 765
Glu Arg Val Gln Thr Lys Ser Gln Cys Leu Ser Val Glu Gln Ser Thr
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Ile Phe Met Leu Ser Gln Thr Ser Ser Ser Leu Ser Phe
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<210> 4265
<211> 2422
<212> DNA
<213> Homo sapiens

<400> 4265
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<210> 4266
<211> 613
<212> PRT
<213> Homo sapiens

<400> 4266
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Ile Leu Val Ser Ile Ala Gly Lys Asn Val Met Leu Asp Cys Gly Met
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His Met Gly Phe Asn Asp Asp Arg Arg Phe Pro Asp Phe Ser Tyr Ile
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Thr Gln Asn Gly Arg Leu Thr Asp Phe Leu Asp Cys Val Ile Ile Ser
65                  70                  75                  80
His Phe His Leu Asp His Cys Gly Ala Leu Pro Tyr Phe Ser Glu Met
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Val Gly Tyr Asp Gly Pro Ile Tyr Met Thr His Pro Thr Gln Ala Ile
            100                 105                 110
Cys Pro Ile Leu Leu Glu Asp Tyr Arg Lys Ile Ala Val Asp Lys Lys
        115                 120                 125
Gly Glu Ala Asn Phe Phe Thr Ser Gln Met Ile Lys Asp Cys Met Lys
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Lys Val Val Ala Val His Leu His Gln Thr Val Gln Val Asp Asp Glu
145                 150                 155                 160
Leu Glu Ile Lys Ala Tyr Tyr Ala Gly His Val Leu Gly Ala Ala Met
                165                 170                 175
Phe Gln Ile Lys Val Gly Ser Glu Ser Val Val Tyr Thr Gly Asp Tyr
            180                 185                 190
Asn Met Thr Pro Asp Arg His Leu Gly Ala Ala Trp Ile Asp Lys Cys
        195                 200                 205
Arg Pro Asn Leu Leu Ile Thr Glu Ser Thr Tyr Ala Thr Thr Ile Arg
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Asp Ser Lys Arg Cys Arg Glu Arg Asp Phe Leu Lys Lys Val His Glu
225                 230                 235                 240
Thr Val Glu Arg Gly Gly Lys Val Leu Ile Pro Val Phe Ala Leu Gly
                245                 250                 255
Arg Ala Gln Glu Leu Cys Ile Leu Leu Glu Thr Phe Trp Glu Arg Met
            260                 265                 270
Asn Leu Lys Val Pro Ile Tyr Phe Ser Thr Gly Leu Thr Glu Lys Ala
        275                 280                 285
Asn His Tyr Tyr Lys Leu Phe Ile Pro Trp Thr Asn Gln Lys Ile Arg
    290                 295                 300
Lys Thr Phe Val Gln Arg Asn Met Phe Glu Phe Lys His Ile Lys Ala
305                 310                 315                 320
Phe Asp Arg Ala Phe Ala Asp Asn Pro Gly Pro Met Val Val Phe Ala
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Thr Pro Gly Met Leu His Ala Gly Gln Ser Leu Gln Ile Phe Arg Lys
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Trp Ala Gly Asn Glu Lys Asn Met Val Ile Met Pro Gly Tyr Cys Val
        355                 360                 365
Gln Gly Thr Val Gly His Lys Ile Leu Ser Gly Gln Arg Lys Leu Glu
    370                 375                 380
Met Glu Gly Arg Gln Val Leu Glu Val Lys Met Gln Val Glu Tyr Met
385                 390                 395                 400
Ser Phe Ser Ala His Ala Asp Ala Lys Gly Ile Met Gln Leu Val Gly
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Gln Ala Glu Pro Glu Ser Val Leu Leu Val His Gly Glu Ala Lys Lys
            420                 425                 430
Met Glu Phe Leu Lys Gln Lys Ile Glu Gln Glu Leu Arg Val Asn Cys
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465                 470                 475                 480
Gly Leu Leu Pro Glu Ala Lys Lys Pro Arg Leu Leu His Gly Thr Leu
                485                 490                 495
Ile Met Lys Asp Ser Asn Phe Arg Leu Val Ser Ser Glu Gln Ala Leu
            500                 505                 510
Lys Glu Leu Gly Leu Ala Glu His Gln Leu Arg Phe Thr Cys Arg Val
        515                 520                 525
His Leu His Asp Thr Arg Lys Glu Gln Glu Thr Ala Leu Arg Val Tyr
    530                 535                 540
Ser His Leu Lys Ser Val Leu Lys Asp His Cys Val Gln His Leu Pro
545                 550                 555                 560
Asp Gly Ser Val Thr Val Glu Ser Val Leu Leu Gln Ala Ala Ala Pro
                565                 570                 575
Ser Glu Asp Pro Gly Thr Lys Val Leu Leu Val Ser Trp Thr Tyr Gln
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<210> 4267
<211> 2230
<212> DNA
<213> Homo sapiens

<400> 4267

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720
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<210> 4268

<211> 210
<212> PRT
<213> Homo sapiens

<400> 4268
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35 40 45
Lys Arg Cys Glu Ser Cys Ser Gln Lys Leu Glu Arg Glu Asn Asn His
50 55 60
Cys Asn Ile Ser His Ser Ile Ile Leu Asn Ser Glu Asp Gly Glu Ile
65 70 75 80
Leu Asn Asn Glu Glu His Glu Tyr Ala Ser Lys Lys Arg Lys Lys Asp
85 90 95
His Phe Arg Asn Asp Thr Asn Thr Gln Ser Phe Tyr His Glu Lys Trp
100 105 110
Ile Tyr Val His Lys Glu Ser Thr Lys Glu Arg His Gly Tyr Cys Thr
115 120 125
Leu Gly Glu Thr Phe Asn Arg Leu Asp Phe Ser Ser Ala Ile Gln Asp
130 135 140
Ile Arg Arg Phe Asn Tyr Val Val Lys Leu Leu Gln Leu Ile Ala Lys
145 150 155 160
Ser Gln Leu Thr Ser Leu Ser Gly Val Ala Gln Lys Asn Tyr Phe Asn
165 170 175
Ile Leu Asp Lys Ile Val Gln Lys Val Leu Asp Asp His His Asn Pro
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<210> 4269
<211> 5748
<212> DNA
<213> Homo sapiens

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<211> 1084
<212> PRT
<213> Homo sapiens

<400> 4270
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Gln Arg Gly Arg Val Leu Pro Pro Pro Ala Pro Leu Asp Thr Thr Asn
35 40 45
Leu Ala Gly Arg Arg Thr Leu Gln Gly Arg Ala Lys Met Ala Ser Val
50 55 60
Pro Val Tyr Cys Leu Cys Arg Leu Pro Tyr Asp Val Thr Arg Phe Met
65 70 75 80
Ile Glu Cys Asp Met Cys Gln Asp Trp Phe His Gly Ser Cys Val Gly
85 90 95
Val Glu Glu Glu Lys Ala Ala Asp Ile Asp Leu Tyr His Cys Pro Asn
100 105 110
Cys Glu Val Leu His Gly Pro Ser Ile Met Lys Lys Arg Arg Gly Ser
115 120 125
Ser Lys Gly His Asp Thr His Lys Gly Lys Pro Val Lys Thr Gly Ser
130 135 140
Pro Thr Phe Val Arg Glu Leu Arg Ser Arg Thr Phe Asp Ser Ser Asp
145 150 155 160
Glu Val Ile Leu Lys Pro Thr Gly Asn Gln Leu Thr Val Glu Phe Leu
165 170 175
Glu Glu Asn Ser Phe Ser Val Pro Ile Leu Val Leu Lys Lys Asp Gly
180 185 190
Leu Gly Met Thr Leu Pro Ser Pro Ser Phe Thr Val Arg Asp Val Glu
195 200 205
His Tyr Val Gly Ser Asp Lys Glu Ile Asp Val Ile Asp Val Thr Arg
210 215 220
Gln Ala Asp Cys Lys Met Lys Leu Gly Asp Phe Val Lys Tyr Tyr Tyr
225 230 235 240
Ser Gly Lys Arg Glu Lys Val Leu Asn Val Ile Ser Leu Glu Phe Ser

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Asp Thr Arg Leu Ser Asn Leu Val Glu Thr Pro Lys Ile Val Arg Lys
            260                 265                 270
Leu Ser Trp Val Glu Asn Leu Trp Pro Glu Glu Cys Val Phe Glu Arg
        275                 280                 285
Pro Asn Val Gln Lys Tyr Cys Leu Met Ser Val Arg Asp Ser Tyr Thr
    290                 295                 300
Asp Phe His Ile Asp Phe Gly Gly Thr Ser Val Trp Tyr His Val Leu
305                 310                 315                 320
Lys Gly Glu Lys Ile Phe Tyr Leu Ile Arg Pro Thr Asn Ala Asn Leu
                325                 330                 335
Thr Leu Phe Glu Cys Trp Ser Ser Ser Ser Asn Gln Asn Glu Met Phe
            340                 345                 350
Phe Gly Asp Gln Val Asp Lys Cys Tyr Lys Cys Ser Val Lys Gln Gly
        355                 360                 365
Gln Thr Leu Phe Ile Pro Thr Gly Trp Ile His Ala Val Leu Thr Pro
    370                 375                 380
Val Asp Cys Leu Ala Phe Gly Gly Asn Phe Leu His Ser Leu Asn Ile
385                 390                 395                 400
Glu Met Gln Leu Lys Ala Tyr Glu Ile Glu Lys Arg Leu Ser Thr Ala
                405                 410                 415
Asp Leu Phe Arg Phe Pro Asn Phe Glu Thr Ile Cys Trp Tyr Val Gly
            420                 425                 430
Lys His Ile Leu Asp Ile Phe Arg Gly Leu Arg Glu Asn Arg Arg His
        435                 440                 445
Pro Ala Ser Tyr Leu Val His Gly Gly Lys Ala Leu Asn Leu Ala Phe
    450                 455                 460
Arg Ala Trp Thr Arg Lys Glu Ala Leu Pro Asp His Glu Asp Glu Ile
465                 470                 475                 480
Pro Glu Thr Val Arg Thr Val Gln Leu Ile Lys Asp Leu Ala Arg Glu
                485                 490                 495
Ile Arg Leu Val Glu Asp Ile Phe Gln Gln Asn Val Gly Lys Thr Ser
            500                 505                 510
Asn Ile Phe Gly Leu Gln Arg Ile Phe Pro Ala Gly Ser Ile Pro Leu
        515                 520                 525
Thr Arg Pro Ala His Ser Thr Ser Val Ser Met Ser Arg Leu Ser Leu
    530                 535                 540
Pro Ser Lys Asn Gly Ser Lys Lys Lys Gly Leu Lys Pro Lys Glu Leu
545                 550                 555                 560
Phe Lys Lys Ala Glu Arg Lys Gly Lys Glu Ser Ser Ala Leu Gly Pro
                565                 570                 575
Ala Gly Gln Leu Ser Tyr Asn Leu Met Asp Thr Tyr Ser His Gln Ala
            580                 585                 590
Leu Lys Thr Gly Ser Phe Gln Lys Ala Lys Phe Asn Ile Thr Gly Ala
        595                 600                 605
Cys Leu Asn Asp Ser Asp Asp Asp Ser Pro Asp Leu Asp Leu Asp Gly
    610                 615                 620
Asn Glu Ser Pro Leu Ala Leu Leu Met Ser Asn Gly Ser Thr Lys Arg
625                 630                 635                 640
Val Lys Ser Leu Ser Lys Ser Arg Arg Thr Lys Ile Ala Lys Lys Val
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Asp Lys Ala Arg Leu Met Ala Glu Gln Val Met Glu Asp Glu Phe Asp
            660                 665                 670
Leu Asp Ser Asp Asp Glu Leu Gln Ile Asp Glu Arg Leu Gly Lys Glu
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Lys Ala Thr Leu Ile Ile Arg Pro Lys Phe Pro Arg Lys Leu Pro Arg
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Ala Lys Pro Cys Ser Asp Pro Asn Arg Val Arg Glu Pro Gly Glu Val
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Glu Phe Asp Ile Glu Glu Asp Tyr Thr Thr Asp Glu Asp Met Val Glu
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Gly Val Glu Gly Lys Leu Gly Asn Gly Ser Gly Ala Gly Gly Ile Leu
            740                 745                 750
Asp Leu Leu Lys Ala Ser Arg Gln Val Gly Gly Pro Asp Tyr Ala Ala
        755                 760                 765
Leu Thr Glu Ala Pro Ala Ser Pro Ser Thr Gln Glu Ala Ile Gln Gly
    770                 775                 780
Met Leu Cys Met Ala Asn Leu Gln Ser Ser Ser Ser Ser Pro Ala Thr
785                 790                 795                 800
Ser Ser Leu Gln Ala Trp Trp Thr Gly Gly Gln Asp Arg Ser Ser Gly
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Ser Ser Ser Ser Gly Leu Gly Thr Val Ser Asn Ser Pro Ala Ser Gln
            820                 825                 830
Arg Thr Pro Gly Lys Arg Pro Ile Lys Arg Pro Ala Tyr Trp Arg Thr
        835                 840                 845
Glu Ser Glu Glu Glu Glu Glu Asn Ala Ser Leu Asp Glu Gln Asp Ser
    850                 855                 860
Leu Gly Ala Cys Phe Lys Asp Ala Glu Tyr Ile Tyr Pro Ser Leu Glu
865                 870                 875                 880
Ser Asp Asp Asp Asp Pro Ala Leu Lys Ser Arg Pro Lys Lys Lys Lys
                885                 890                 895
Asn Ser Asp Asp Ala Pro Trp Ser Pro Lys Ala Arg Val Thr Pro Thr
            900                 905                 910
Leu Pro Lys Gln Asp Arg Pro Val Arg Glu Gly Thr Arg Val Ala Ser
        915                 920                 925
Ile Glu Thr Gly Leu Ala Ala Ala Ala Ala Lys Leu Ala Gln Gln Glu
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Leu Gln Lys Ala Gln Lys Lys Lys Tyr Ile Lys Lys Lys Pro Leu Leu
945                 950                 955                 960
Lys Glu Val Glu Gln Pro Arg Pro Gln Asp Ser Asn Leu Ser Leu Thr
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Val Pro Ala Pro Thr Val Ala Ala Thr Pro Gln Leu Val Thr Ser Ser
            980                 985                 990
Ser Pro Leu Pro Pro Pro Glu Pro Lys Gln Glu Ala Leu Ser Gly Ser
        995                 1000                1005
Leu Ala Asp His Glu Tyr Thr Ala Arg Pro Asn Ala Phe Gly Met Ala
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Gln Ala Asn Arg Ser Thr Thr Pro Met Ala Pro Gly Val Phe Leu Thr
1025                1030                1035                1040
Gln Arg Arg Pro Ser Val Gly Ser Gln Ser Asn Gln Ala Gly Gln Gly
                1045                1050                1055
Lys Arg Pro Lys Lys Gly Leu Ala Thr Ala Lys Gln Arg Leu Gly Arg
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<210> 4271
<211> 588
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<212> DNA
<213> Homo sapiens

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<210> 4272
<211> 134
<212> PRT
<213> Homo sapiens

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Ile Leu Arg Gln Leu Thr Thr Asp Phe Val His His Tyr Ile Val Ala
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Asn Asn Phe Ser Glu Leu Phe His Leu Leu Ser Ser Arg Asn Cys Lys
        35   40   45
Thr Arg Asn Leu Val Met Lys Leu Leu Leu Asn Met Ser Glu Asn Pro
    50   55   60
Thr Ala Ala Arg Asp Met Ile Asn Met Lys Ala Leu Ala Ala Leu Lys
65   70   75   80
Leu Ile Phe Asn His Lys Glu Ala Lys Ala Asn Leu Val Ser Gly Val
                85   90   95
Ala Ile Phe Ile Asn Ile Lys Glu His Ile Arg Lys Gly Ser Ile Val
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Val Asn Lys Tyr Gly His Thr Thr Asn Lys Ile Gly Phe Cys Leu Phe
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Leu Val Lys Asp Glu Phe
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<210> 4273
<211> 2081
<212> DNA
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2081

<210> 4274
<211> 235
<212> PRT
<213> Homo sapiens

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35 40 45
Arg Gly Arg Ala Ser Ser Glu Ser Gln Gly Leu Gly Ala Gly Val Arg
50 55 60
Thr Glu Xaa Asp Val Glu Glu Glu Ala Leu Arg Arg Lys Leu Glu Glu
65 70 75 80
Leu Thr Ser Asn Val Ser Asp Gln Glu Thr Phe Val Arg Gly Gly Gly
85 90 95
Ser Gln Gly Arg Lys Cys Arg Ala Gln Gln Gly Gln Ile Ser Trp Ala
100 105 110
Ser Pro Pro Gly Gly Pro Gly Arg Trp His Gly Cys Pro Ser Asn Gln
115 120 125
Gln Thr Gly Lys Lys Pro Gln Asp Pro Gly Asp Pro Val Gln Tyr Asn
130 135 140
Arg Thr Thr Asp Glu Glu Leu Ser Glu Leu Glu Asp Arg Val Ala Val
145 150 155 160
Thr Ala Ser Glu Val Gln Gln Ala Glu Ser Glu Val Ser Asp Ile Glu
165 170 175
Ser Arg Ile Ala Ala Leu Arg Ala Ala Gly Leu Thr Val Lys Pro Ser
180 185 190
Gly Lys Pro Arg Arg Lys Ser Asn Leu Pro Ile Phe Leu Pro Arg Val
195 200 205
Ala Gly Lys Leu Gly Lys Arg Pro Glu Asp Pro Asn Ala Asp Pro Ser
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Ser Glu Ala Lys Ala Met Ala Val Pro Ile Phe

225 230 235

<210> 4275
<211> 874
<212> DNA
<213> Homo sapiens

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840
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<210> 4276
<211> 264
<212> PRT
<213> Homo sapiens

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Gly Lys Ser Ser Leu Val Asn Leu Leu Ser Arg Lys Pro Val Ser Ile
35 40 45
Val Ser Pro Glu Pro Gly Thr Thr Arg Asp Val Leu Glu Thr Pro Val
50 55 60
Asp Leu Ala Gly Phe Pro Val Leu Leu Ser Asp Thr Ala Gly Leu Arg

65 70 75 80
Glu Gly Val Gly Pro Val Glu Gln Glu Gly Val Arg Arg Ala Arg Glu
85 90 95
Arg Leu Glu Gln Ala Asp Leu Ile Leu Ala Met Leu Asp Ala Ser Asp
100 105 110
Leu Ala Ser Pro Ser Ser Cys Asn Phe Leu Ala Thr Val Val Ala Ser
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Val Gly Ala Gln Ser Pro Ser Asp Ser Ser Gln Arg Leu Leu Leu Val
130 135 140
Leu Asn Lys Ser Asp Leu Leu Ser Pro Glu Gly Pro Gly Pro Gly Pro
145 150 155 160
Asp Leu Pro Pro His Leu Leu Leu Ser Cys Leu Thr Gly Glu Gly Leu
165 170 175
Asp Gly Leu Leu Glu Ala Leu Arg Lys Glu Leu Ala Ala Val Cys Gly
180 185 190
Asp Pro Ser Thr Asp Pro Pro Leu Leu Thr Arg Ala Arg His Gln His
195 200 205
His Leu Gln Gly Cys Leu Asp Ala Leu Gly His Tyr Lys Gln Ser Lys
210 215 220
Asp Leu Ala Leu Ala Ala Glu Ala Leu Arg Val Ala Arg Gly His Leu
225 230 235 240
Thr Arg Leu Thr Gly Gly Gly Gly Thr Glu Glu Ile Leu Asp Ile Ile
245 250 255
Phe Gln Asp Phe Cys Val Gly Lys
260

<210> 4277
<211> 1070
<212> DNA
<213> Homo sapiens

<400> 4277
cggccggtcg ggcctccttt tgttttagga agggcacttc actccccggg cccccacctg
60
cccgcctgcg ccgccccttt ccgcgggtcc ggagttggcg gggccctgcg ccggaggagg
120
aggaccaggc ccgcgggctc agctctcgcc gccagcgggc cgcagcattt ttgaaacgtt
180
ggggttgttg gagtggttgg attttccctg gaattgagtg agaaattcag aagactgaag
240
cccaggctta ctgtctacct ttcacggagg cctagccgtg agaggacaga agaaggcacg
300
tggcgaatca tgacagcgga caaagacaaa gacaaagaca aagagaagga ccgggaccga
360
gaccgggacc gagagagaga gaaaagagac aaagcaagag agagtgagaa ttcaaggcca
420
cgccggagct gtaccttgga aggaggagcc aaaaattatg ctgagagtga tcacagtgaa
480
gacgaggaca atgacaacaa tagtgccacc gcagaggagt ccacgaagaa gaataagaag
540
aaaccaccga aaaaaaagtc tcgttatgaa aggacagata ccggtgagat aacatcctac
600
atcactgaag atgatgtggt ctacagacca ggagactgtg tgtatatcga gagtcggagg
660

ccaaacacac cgtatttcat ctgtagcatt caagacttca aactggtcca caactcccag
720
gcctgttgca gatctccaac tcctgctttg tgtgaccccc cagcatgctc tctgccggtg
780
gcatcacagc caccacagca tctttctgaa gccgggagag ggcctgtagg gagtaagagg
840
gaccatctcc tcatgaacgt caaatggtac taccgtcaat ctgaggttcc agattctgtg
900
tatcagcatt tggttcagga tcgacataat gaaaatgact ctggaagaga acttgtcatt
960
acagacccag ttatcaagaa ccgagagctc ttcatttctg attacgttga cacttaccat
1020
gctgctgccc ttagagggaa gtgtaacatt ctccattttt ctgacatatt
1070

<210> 4278
<211> 253
<212> PRT
<213> Homo sapiens

<400> 4278
Met Thr Ala Asp Lys Asp Lys Asp Lys Asp Lys Glu Lys Asp Arg Asp
1 5 10 15
Arg Asp Arg Asp Arg Glu Arg Glu Lys Arg Asp Lys Ala Arg Glu Ser
20 25 30
Glu Asn Ser Arg Pro Arg Arg Ser Cys Thr Leu Glu Gly Gly Ala Lys
35 40 45
Asn Tyr Ala Glu Ser Asp His Ser Glu Asp Glu Asp Asn Asp Asn Asn
50 55 60
Ser Ala Thr Ala Glu Glu Ser Thr Lys Lys Asn Lys Lys Lys Pro Pro
65 70 75 80
Lys Lys Lys Ser Arg Tyr Glu Arg Thr Asp Thr Gly Glu Ile Thr Ser
85 90 95
Tyr Ile Thr Glu Asp Asp Val Val Tyr Arg Pro Gly Asp Cys Val Tyr
100 105 110
Ile Glu Ser Arg Arg Pro Asn Thr Pro Tyr Phe Ile Cys Ser Ile Gln
115 120 125
Asp Phe Lys Leu Val His Asn Ser Gln Ala Cys Cys Arg Ser Pro Thr
130 135 140
Pro Ala Leu Cys Asp Pro Pro Ala Cys Ser Leu Pro Val Ala Ser Gln
145 150 155 160
Pro Pro Gln His Leu Ser Glu Ala Gly Arg Gly Pro Val Gly Ser Lys
165 170 175
Arg Asp His Leu Leu Met Asn Val Lys Trp Tyr Tyr Arg Gln Ser Glu
180 185 190
Val Pro Asp Ser Val Tyr Gln His Leu Val Gln Asp Arg His Asn Glu
195 200 205
Asn Asp Ser Gly Arg Glu Leu Val Ile Thr Asp Pro Val Ile Lys Asn
210 215 220
Arg Glu Leu Phe Ile Ser Asp Tyr Val Asp Thr Tyr His Ala Ala Ala
225 230 235 240
Leu Arg Gly Lys Cys Asn Ile Leu His Phe Ser Asp Ile
245 250

<210> 4279
<211> 1963
<212> DNA
<213> Homo sapiens

<400> 4279
cggccgctta cggaaaactc gctgttggaa gttctggatg gcacagtcat gatgtacagt
60
ctgagcgtac accagcagct gggcaagatg gtgggtgtgt ctgatgatgt caacgagtat
120
gcaatggccc tgagagacac cgaggacaag ctacgtcggt gccccaagag gaggaaggac
180
atccttgcag agttgaccaa gagccagaag gttttctcag aaaagctgga ccacctgagc
240
cgccgtcttg cctgggtcca tgccactgtc tactcccagg agaagatgct ggacatctac
300
tggctgctgc gcgtctgcct gcggaccatt gagcacggtg atcgcacagg gtctctcttt
360
gccttcatgc ccgagttcta cctgagcgtg gccatcaaca gctacagtgc tctcaagaat
420
tactttggtc ccgtgcacag catggaggag ctcccaggct atgaagagac cctgacccgc
480
ctggctgcca ttctcgccaa acactttgcc gacgcacgca ttgtgggcac tgacatccga
540
gactcactga tgcaggccct ggccagctac gtgtgctacc cacactccct gcgggctgtg
600ccgaggagca gcgtatcgcc atggtgagga acctcctggc gccctatgag 660
cagcggccct gggcccagac caactggatc ctggtgcggc tctggagggg ctgtggcttc
720
gggtaccgct atacacggct gccacatctg ctgaaaacca aacttgagga cgccaatttg
780
cccagcctcc agaagccctg cccttccacc ctgctgcagc agcacatggc ggacctccta
840
cagcagggtc ctgatgtggc acccagcttc ctcaacagcg tcctcaatca gctcaactgg
900
gccttctctg aattcattgg catgatccaa gagatccagc aggctgctga gcgcctggag
960
cggaactttg tggacagccg gcagctcaag gtatgtgcca cctgctttga cctctcggtc
1020
agcctgctgc gtgtcttgga gatgactatc acactggtgc ctgagatatt ccttgactgg
1080
acccggccta cctctgagat gctgctgcgg cgtcttgcac agctgctaaa ccaggtgctg
1140
aaccgggtga cagctgagag gaacctgttt gatcgtgtgg tcaccctacg gctgcctggc
1200
ctagagagcg tggaccacta tcccattctg gtggcagtga cgggcatcct ggtgcagctc
1260
ctggtgcgtg gcccagcctc agagagagag caagccacat cagtgctcct ggcagatccc
1320
tgcttccagc tacgctcaat atgctatctc ctgggacagc cagagccccc agcacctggc
1380
actgctctgc cagcccctga ccggaagcgc ttctccctgc agagctatgc ggattatatc
1440
agtgccgatg agctggccca agtggaacag atgctggcgc acctgacctc tgcatctgcc
1500

caggcagcag ctgcctccct gcccaccagt gaggaggacc tctgccccat ctgctatgcc
1560
caccccatct ctgctgtgtt ccagccctgt ggccacaagt cctgcaaagc ctgtatcaac
1620
cagcacctga tgaacaacaa ggactgcttc ttctgcaaaa ccaccatcgt gtctgtagag
1680
gactgggaga agggagccaa tacgagtact acctcctcag ctgcctagcc ctcacagcct
1740
gtgccatcct ggaacctcca cctttgaacc cagagccagg ctgggcccta tttatgagct
1800
ccctttgccc ttctcctgta tcccacacca ccacatccaa cctccttgcc tgcctgtatc
1860
ctcattggtg ggagcccagc catggcccta attgtgcctg agcttgactt tcagtcaggg
1920
ccacagtgag cattaaatta ttattccata caaaaaaaaa aaa
1963

<210> 4280
<211> 575
<212> PRT
<213> Homo sapiens

<400> 4280
Arg Pro Leu Thr Glu Asn Ser Leu Leu Glu Val Leu Asp Gly Thr Val
1 5 10 15
Met Met Tyr Ser Leu Ser Val His Gln Gln Leu Gly Lys Met Val Gly
20 25 30
Val Ser Asp Asp Val Asn Glu Tyr Ala Met Ala Leu Arg Asp Thr Glu
35 40 45
Asp Lys Leu Arg Arg Cys Pro Lys Arg Arg Lys Asp Ile Leu Ala Glu
50 55 60
Leu Thr Lys Ser Gln Lys Val Phe Ser Glu Lys Leu Asp His Leu Ser
65 70 75 80
Arg Arg Leu Ala Trp Val His Ala Thr Val Tyr Ser Gln Glu Lys Met
85 90 95
Leu Asp Ile Tyr Trp Leu Leu Arg Val Cys Leu Arg Thr Ile Glu His
100 105 110
Gly Asp Arg Thr Gly Ser Leu Phe Ala Phe Met Pro Glu Phe Tyr Leu
115 120 125
Ser Val Ala Ile Asn Ser Tyr Ser Ala Leu Lys Asn Tyr Phe Gly Pro
130 135 140
Val His Ser Met Glu Glu Leu Pro Gly Tyr Glu Glu Thr Leu Thr Arg
145 150 155 160
Leu Ala Ala Ile Leu Ala Lys His Phe Ala Asp Ala Arg Ile Val Gly
165 170 175
Thr Asp Ile Arg Asp Ser Leu Met Gln Ala Leu Ala Ser Tyr Val Cys
180 185 190
Tyr Pro His Ser Leu Arg Ala Val Glu Arg Ile Pro Glu Glu Gln Arg
195 200 205
Ile Ala Met Val Arg Asn Leu Leu Ala Pro Tyr Glu Gln Arg Pro Trp
210 215 220
Ala Gln Thr Asn Trp Ile Leu Val Arg Leu Trp Arg Gly Cys Gly Phe
225 230 235 240
Gly Tyr Arg Tyr Thr Arg Leu Pro His Leu Leu Lys Thr Lys Leu Glu

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                245                 250                 255
Asp Ala Asn Leu Pro Ser Leu Gln Lys Pro Cys Pro Ser Thr Leu Leu
            260                 265                 270
Gln Gln His Met Ala Asp Leu Leu Gln Gln Gly Pro Asp Val Ala Pro
        275                 280                 285
Ser Phe Leu Asn Ser Val Leu Asn Gln Leu Asn Trp Ala Phe Ser Glu
    290                 295                 300
Phe Ile Gly Met Ile Gln Glu Ile Gln Gln Ala Ala Glu Arg Leu Glu
305                 310                 315                 320
Arg Asn Phe Val Asp Ser Arg Gln Leu Lys Val Cys Ala Thr Cys Phe
                325                 330                 335
Asp Leu Ser Val Ser Leu Leu Arg Val Leu Glu Met Thr Ile Thr Leu
            340                 345                 350
Val Pro Glu Ile Phe Leu Asp Trp Thr Arg Pro Thr Ser Glu Met Leu
        355                 360                 365
Leu Arg Arg Leu Ala Gln Leu Leu Asn Gln Val Leu Asn Arg Val Thr
    370                 375                 380
Ala Glu Arg Asn Leu Phe Asp Arg Val Val Thr Leu Arg Leu Pro Gly
385                 390                 395                 400
Leu Glu Ser Val Asp His Tyr Pro Ile Leu Val Ala Val Thr Gly Ile
                405                 410                 415
Leu Val Gln Leu Leu Val Arg Gly Pro Ala Ser Glu Arg Glu Gln Ala
            420                 425                 430
Thr Ser Val Leu Leu Ala Asp Pro Cys Phe Gln Leu Arg Ser Ile Cys
        435                 440                 445
Tyr Leu Leu Gly Gln Pro Glu Pro Pro Ala Pro Gly Thr Ala Leu Pro
    450                 455                 460
Ala Pro Asp Arg Lys Arg Phe Ser Leu Gln Ser Tyr Ala Asp Tyr Ile
465                 470                 475                 480
Ser Ala Asp Glu Leu Ala Gln Val Glu Gln Met Leu Ala His Leu Thr
                485                 490                 495
Ser Ala Ser Ala Gln Ala Ala Ala Ala Ser Leu Pro Thr Ser Glu Glu
            500                 505                 510
Asp Leu Cys Pro Ile Cys Tyr Ala His Pro Ile Ser Ala Val Phe Gln
        515                 520                 525
Pro Cys Gly His Lys Ser Cys Lys Ala Cys Ile Asn Gln His Leu Met
    530                 535                 540
Asn Asn Lys Asp Cys Phe Phe Cys Lys Thr Thr Ile Val Ser Val Glu
545                 550                 555                 560
Asp Trp Glu Lys Gly Ala Asn Thr Ser Thr Thr Ser Ser Ala Ala
                565                 570                 575
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<210> 4281
<211> 507
<212> DNA
<213> Homo sapiens

<400> 4281
acgcgtgaag ggacagagct ggggccttgt caggagcccc acagttggcc aatgggccag
60
atgccccata gtctcagccc acctctcttc tgccatgagt cccctgattc tgtcctttga
120
gctgactctg agaggcagtg ggcttcccgc cagcacctcc ccctatcaca tttgtagggc
180

tggtttatga ggccggaagt aagcaagcac cccctcatat caacctggca cttcacaccc
240
cccatggtta tcagtggggg tgctggctgg ctggcaggca gccagagaca tttcagcagg
300
tcaggcatgg atgcaggtgg aaatgagaga ggatcagtga gcgcattcat gtcttttgag
360
tggtctacag atgagtggtc tccagtctca aatgaggaga acaaataggg aagtaggagc
420
tcagggttct tgtgtgtctc ataggcagct gcctatccct gggtgataca gctccctggc
480
acacccattc ccaagggcac aggatcc
507

<210> 4282
<211> 106
<212> PRT
<213> Homo sapiens

<400> 4282
Met Asn Ala Leu Thr Asp Pro Leu Ser Phe Pro Pro Ala Ser Met Pro
 1   5   10   15
Asp Leu Leu Lys Cys Leu Trp Leu Pro Ala Ser Gln Pro Ala Pro Pro
            20   25   30
Leu Ile Thr Met Gly Gly Val Lys Cys Gln Val Asp Met Arg Gly Cys
        35   40   45
Leu Leu Thr Ser Gly Leu Ile Asn Gln Pro Tyr Lys Cys Asp Arg Gly
    50   55   60
Arg Cys Trp Arg Glu Ala His Cys Leu Ser Glu Ser Ala Gln Arg Thr
65   70   75   80
Glu Ser Gly Asp Ser Trp Gln Lys Arg Gly Gly Leu Arg Leu Trp Gly
                85   90   95
Ile Trp Pro Ile Gly Gln Leu Trp Gly Ser
            100   105

<210> 4283
<211> 315
<212> DNA
<213> Homo sapiens

<400> 4283
gaattctcaa ccagaacagc ccagcaggaa aggagccggc atggggtgcc cctctgcagc
60
cgaccgtttt cctagaaggc ctaaccgctc aaacgggcag gggaggggggg cgggcggccc
120
gggagaaacc gagtccccgc cgggtcccca ccgtgtggcg ccgaccgaaa taactccagt
180
ccagctgcaa aaaccctccc gaaaacccaa gcttgtccgg cacaacttcg gtctctccag
240
cctcattcct gcccgcactc cgccaaactg ctcgccctgc ccagcgcagc ggatgcagcg
300
ctcccggccc nacgg
315

<210> 4284

<211> 91
<212> PRT
<213> Homo sapiens

<400> 4284
Met Gly Cys Pro Ser Ala Ala Asp Arg Phe Pro Arg Arg Pro Asn Arg
1 5 10 15
Ser Asn Gly Gln Gly Arg Gly Ala Gly Gly Pro Gly Glu Thr Glu Ser
20 25 30
Pro Pro Gly Pro His Arg Val Ala Pro Thr Glu Ile Thr Pro Val Gln
35 40 45
Leu Gln Lys Pro Ser Arg Lys Pro Lys Leu Val Arg His Asn Phe Gly
50 55 60
Leu Ser Ser Leu Ile Pro Ala Arg Thr Pro Pro Asn Cys Ser Pro Cys
65 70 75 80
Pro Ala Gln Arg Met Gln Arg Ser Arg Pro Xaa
85 90

<210> 4285
<211> 591
<212> DNA
<213> Homo sapiens

<400> 4285
nagatctcag agaacttggt gaacattcag aaaatgcaga aaacgcaggt gaaatgccgc
60
aaaatcctga ccaagatgaa gcagcagggt catgagacag ccgcctgtcc ggagactgaa
120
gagataccgc agggagccag tggctgctgg aaggatgacc tccagaagga actgagtgat
180
atatggtgat gcccagcctg cagtctgacc cctgaccctc ctctgaaccc gttcccccaa
240
cgggatctgg cagtgaccac cagaacctgg agcccacctg agtccagact tccctcaccc
300
cctaggactc accccaccac ggcccccaac cttagctgta ctgctgtcta caccctgagc
360
agtgtggagt ctcccagcgc ccccagctcc ttgtcttctt gcaggtctgc tgtgcacgtg
420
ctgcaggact ccatagacag cctcactttg tgctcggggg cctgtcccaa ggcctcgagc
480
ctaagaggcc acaagggcac cagtgcctga gccctccact ccccctcctgg gactctgact
540
ccgactgtga ccaggacctc tcccagccac ctttcagcaa gagcggccgc a
591

<210> 4286
<211> 106
<212> PRT
<213> Homo sapiens

<400> 4286
Cys Pro Ala Cys Ser Leu Thr Pro Asp Pro Pro Leu Asn Pro Phe Pro
1 5 10 15
Gln Arg Asp Leu Ala Val Thr Thr Arg Thr Trp Ser Pro Pro Glu Ser

```
            20                  25                  30
Arg Leu Pro Ser Pro Pro Arg Thr His Pro Thr Thr Ala Pro Asn Leu
        35                  40                  45
Ser Cys Thr Ala Val Tyr Thr Leu Ser Ser Val Glu Ser Pro Ser Ala
    50                  55                  60
Pro Ser Ser Leu Ser Ser Cys Arg Ser Ala Val His Val Leu Gln Asp
65                  70                  75                  80
Ser Ile Asp Ser Leu Thr Leu Cys Ser Gly Ala Cys Pro Lys Ala Ser
                85                  90                  95
Ser Leu Arg Gly His Lys Gly Thr Ser Ala
            100                 105
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<210> 4287
<211> 868
<212> DNA
<213> Homo sapiens

<400> 4287
cgagggcgcg actgcggggt tcctggtgct gaggacggac gccattggag ttcccgagaa
60
ggctgagctc tcatctccct gggacccgca gcatggctga gggaagcttc agcgtgcaat
120
cggaaagcta cagtgttgaa gacatggatg agggtagcga cgaagtcggg gaggaagaga
180
tggttgaagg caacgactat gaagaattcg gtgcgtttgg tggctatggc accctcacca
240
gctttgacat ccatatcctc agagccttcg gaagcttggg tccaggcctt cgcatcttat
300
cgaatgagcc ctgggaactg gaaaaccnct gtgctggccc agaccctggt ggaggcattg
360
cagctggatc cggaaacact tgccaatgag acggccgccc gtgctgccaa cgtagcccgc
420
gccgccgcct ccaaccgtgc ggctcgggcc gctgccgccg ctgcccgtac cgccttcagt
480
caggtggtcg ctagccaccg ggtggccacg ccgcaggtct caggagagga tacccagccc
540
acgacctacg ccgccgaggc tcaggggccc acccctgagc cacccccttgc ttctccgcag
600
acctcccaga tgttagtcac cagtaagatg gctgcccccg aggctccggc aacctccgca
660
cagtcccaga caggctcccc ggcccaggag gctgctactg agggccctag tagcgcctgt
720
gcattctctc aggctccgtg tgccagggag gtggacgcca accggcccag cacagccttc
780
ctgggccaga atgatgtctt cgatttcact cagccggcag tgtcagtggc atggcttccc
840
gcgcccaaga gacctgccca gccaagag
868

<210> 4288
<211> 240
<212> PRT
<213> Homo sapiens

<400> 4288
Met Arg Val Ala Thr Lys Ser Gly Arg Lys Arg Trp Leu Lys Ala Thr
1 5 10 15
Thr Met Lys Asn Ser Val Arg Leu Val Ala Met Ala Pro Ser Pro Ala
20 25 30
Leu Thr Ser Ile Ser Ser Glu Pro Ser Glu Ala Trp Val Gln Ala Phe
35 40 45
Ala Ser Tyr Arg Met Ser Pro Gly Asn Trp Lys Thr Xaa Val Leu Ala
50 55 60
Gln Thr Leu Val Glu Ala Leu Gln Leu Asp Pro Glu Thr Leu Ala Asn
65 70 75 80
Glu Thr Ala Ala Arg Ala Ala Asn Val Ala Arg Ala Ala Ala Ser Asn
85 90 95
Arg Ala Ala Arg Ala Ala Ala Ala Ala Ala Arg Thr Ala Phe Ser Gln
100 105 110
Val Val Ala Ser His Arg Val Ala Thr Pro Gln Val Ser Gly Glu Asp
115 120 125
Thr Gln Pro Thr Thr Tyr Ala Ala Glu Ala Gln Gly Pro Thr Pro Glu
130 135 140
Pro Pro Leu Ala Ser Pro Gln Thr Ser Gln Met Leu Val Thr Ser Lys
145 150 155 160
Met Ala Ala Pro Glu Ala Pro Ala Thr Ser Ala Gln Ser Gln Thr Gly
165 170 175
Ser Pro Ala Gln Glu Ala Ala Thr Glu Gly Pro Ser Ser Ala Cys Ala
180 185 190
Phe Ser Gln Ala Pro Cys Ala Arg Glu Val Asp Ala Asn Arg Pro Ser
195 200 205
Thr Ala Phe Leu Gly Gln Asn Asp Val Phe Asp Phe Thr Gln Pro Ala
210 215 220
Val Ser Val Ala Trp Leu Pro Ala Pro Lys Arg Pro Ala Gln Pro Arg
225 230 235 240

<210> 4289
<211> 353
<212> DNA
<213> Homo sapiens

<400> 4289
ggatccctgg gaagatgact accctgcctg tgcgggatat gagggagaaa tatgggagcc
60
tcctcacttc aggtgtcact gctcagcata tatccaggct ttgttttcat attggtcttg
120
caaagagcct tttgggaaca gttttcttat tgaaacatac tcagtgttta aacctgcagg
180
tgtgggttgg tggcagtcca catggcatcc tttgctctgt ccctgttctc ctgtctctgg
240
ctattcaggt tcccgtgagg atactgtcac ccttgaataa tggagcttgc ggaagaccaa
300
gcccctgttt ttggagtcct tgtgctgagg ccgctgtaac ttgcggagag ttg
353

<210> 4290
<211> 113
<212> PRT

<213> Homo sapiens

<400> 4290
Met Thr Thr Leu Pro Val Arg Asp Met Arg Glu Lys Tyr Gly Ser Leu
1 5 10 15
Leu Thr Ser Gly Val Thr Ala Gln His Ile Ser Arg Leu Cys Phe His
20 25 30
Ile Gly Leu Ala Lys Ser Leu Leu Gly Thr Val Phe Leu Leu Lys His
35 40 45
Thr Gln Cys Leu Asn Leu Gln Val Trp Val Gly Gly Ser Pro His Gly
50 55 60
Ile Leu Cys Ser Val Pro Val Leu Leu Ser Leu Ala Ile Gln Val Pro
65 70 75 80
Val Arg Ile Leu Ser Pro Leu Asn Asn Gly Ala Cys Gly Arg Pro Ser
85 90 95
Pro Cys Phe Trp Ser Pro Cys Ala Glu Ala Ala Val Thr Cys Gly Glu
100 105 110
Leu

<210> 4291
<211> 517
<212> DNA
<213> Homo sapiens

<400> 4291
nnaaatttgc caagccaaga gttaccccag gaagattctc tcttacatgg ccaattttca
60
caagcagtca ctcccctagc ccatcatcac acagattatt caaagcccac cgatatctca
120
tggagagaca cactttctca gaagtttgga tcctcagatc acttggagaa actatttaag
180
atggatgaag caagtgccca gctccttgct tataaggaaa aaggccattc tcagagttca
240
caatttttcct ctgatcaaga aatagctcat ctgctgcctg aaaatgtgag tgcgctccca
300
gctacggtgg cagttgcttc tccacatacc acctcggcta ctccaaagcc cgccacccctt
360
ctacccacca atgcttcagt gacaccttct gggacttccc agccacagct ggccaccaca
420
gctccacctg taaccactgt cacttctcag cctcccacga ccctcatttc tacagttttt
480
acacgggctg tggctacact ccaagcaatg gctacaa
517

<210> 4292
<211> 172
<212> PRT
<213> Homo sapiens

<400> 4292
Xaa Asn Leu Pro Ser Gln Glu Leu Pro Gln Glu Asp Ser Leu Leu His
1 5 10 15
Gly Gln Phe Ser Gln Ala Val Thr Pro Leu Ala His His His Thr Asp

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            20                  25                  30
Tyr Ser Lys Pro Thr Asp Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys
        35                  40                  45
Phe Gly Ser Ser Asp His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala
    50                  55                  60
Ser Ala Gln Leu Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser
65                  70                  75                  80
Gln Phe Ser Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val
                85                  90                  95
Ser Ala Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser
            100                 105                 110
Ala Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr
        115                 120                 125
Pro Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro Val
    130                 135                 140
Thr Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr Val Phe
145                 150                 155                 160
Thr Arg Ala Val Ala Thr Leu Gln Ala Met Ala Thr
                165                 170
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<210> 4293
<211> 547
<212> DNA
<213> Homo sapiens

<400> 4293
gccggcgccc ccggcgcgga tgcctgctct gtgcctgtat ctgagatcat cgccgttgag
60
gaaacagacg ttcacgggaa acatcaaggc agtggaaaat ggcagaaaat ggaaaagcct
120
tacgctttta cagttcactg tgtaaagaga gcacgacggc accgctggaa gtgggcgcag
180
gtgactttct ggtgtccaga ggagcagctg tgtcacttgt ggctgcagac cctgcgggag
240
atgctggaga agctgacgtc cagaccaaag catttactgg tatttatcaa cccgtttgga
300
ggaaaaggac aaggcaagcg gatatatgaa agaaaagtgg caccactgtt caccttagcc
360
tccatcacca ctgacatcat cgttactgaa catgctaatc aggccaagga gactctgtat
420
gagattaaca tagacaaata cgacggcatc gtctgtgtcg gcggagatgg tatgttcagc
480
gaggtgctgc acggtctgat tgggaggacg cagaggagcg ccggggtcga ccagaaccac
540
ccccggg
547

<210> 4294
<211> 182
<212> PRT
<213> Homo sapiens

<400> 4294
Ala Gly Ala Pro Gly Ala Asp Ala Cys Ser Val Pro Val Ser Glu Ile

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 1               5                  10                  15
Ile Ala Val Glu Glu Thr Asp Val His Gly Lys His Gln Gly Ser Gly
            20                  25                  30
Lys Trp Gln Lys Met Glu Lys Pro Tyr Ala Phe Thr Val His Cys Val
        35                  40                  45
Lys Arg Ala Arg Arg His Arg Trp Lys Trp Ala Gln Val Thr Phe Trp
    50                  55                  60
Cys Pro Glu Glu Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg Glu
65                  70                  75                  80
Met Leu Glu Lys Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe Ile
                85                  90                  95
Asn Pro Phe Gly Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg Lys
            100                 105                 110
Val Ala Pro Leu Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile Ile Val
        115                 120                 125
Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu Ile Asn Ile
    130                 135                 140
Asp Lys Tyr Asp Gly Ile Val Cys Val Gly Gly Asp Gly Met Phe Ser
145                 150                 155                 160
Glu Val Leu His Gly Leu Ile Gly Arg Thr Gln Arg Ser Ala Gly Val
                165                 170                 175
Asp Gln Asn His Pro Arg
            180
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<210> 4295
<211> 431
<212> DNA
<213> Homo sapiens

<400> 4295
nntctagaaa atcactgtct ccttctaccc tgccatctct acaccagggt tacaaacaag
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agcccactgc tggctccttg ttttgtaaat aagatttgtt ggactacagc tatgcccgta
120
catgtacatt ttgtgtatgg ctgcttttgt gccacaacag cagggttgag tattgcgaca
180
gagaccccca ttgcccacaa gcctaaaaca tttgccatcg agccctttaa gaaagagttt
240
gctggccgtg cgcggtggcc gtggctcccg cctgtaatcc cagcactttg gaaggctgag
300
gcaggcggtg aggtctggag ttcgaaacca gcctggccag cgtggcgaaa ccctgtctcc
360
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420
cgtgccaacc a
431

<210> 4296
<211> 138
<212> PRT
<213> Homo sapiens

<400> 4296
Xaa Leu Glu Asn His Cys Leu Leu Leu Pro Cys His Leu Tyr Thr Arg

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 1               5                  10                  15
Val Thr Asn Lys Ser Pro Leu Leu Ala Pro Cys Phe Val Asn Lys Ile
            20                  25                  30
Cys Trp Thr Thr Ala Met Pro Val His Val His Phe Val Tyr Gly Cys
        35                  40                  45
Phe Cys Ala Thr Thr Ala Gly Leu Ser Ile Ala Thr Glu Thr Pro Ile
    50                  55                  60
Ala His Lys Pro Lys Thr Phe Ala Ile Glu Pro Phe Lys Lys Glu Phe
65                  70                  75                  80
Ala Gly Arg Ala Arg Trp Pro Trp Leu Pro Pro Val Ile Pro Ala Leu
                85                  90                  95
Trp Lys Ala Glu Ala Gly Gly Glu Val Trp Ser Ser Lys Pro Ala Trp
            100                 105                 110
Pro Ala Trp Arg Asn Pro Val Ser Pro Ser Gln Ile His Val Ile Ile
        115                 120                 125
Pro Pro Gln Pro Pro Glu Tyr Leu Gly Leu
    130                 135
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<210> 4297
<211> 1668
<212> DNA
<213> Homo sapiens

<400> 4297
nccatggact cggcctttgt gggtataaag gtcaaccaag tgtcagctgc agttggaaaa
60
gatttcaccg tgattccatc taaactgatt cagtttgacc caggaatgtc aactaagatg
120
tggaatatag caattaccta tgacggatta gaggaagatg atgaggtctt tgaagtaatt
180
ctgaactccc ctgtgaatgc agttcttggc acaaagacaa aagctgcagt gaaaattttg
240
gactcaaaag gaggacaatg ccatccttca tattcctcca accaaagcaa gcacagcaca
300
tgggagaagg gcatttggca tctgctgccc ccagggtctt cctcatccac cacttctggt
360
tcctttcatc tggaaagaag acctcttcca tcttccatgc agctagcagt catcagggga
420
gacaccctgc ggggctttga ttctacagat ctttctcaaa ggaagcttag gacccgtggg
480
aatggcaaaa cagttcgtcc atcctctgtt tatagaaatg gaacagacat catctataat
540
tatcatggga tagtttcctt gaaactggag gatgacagtt tcccaactca caaaaggaag
600
gccaaagtat ccatcattag tcagccacaa aagacaatca aagtggcaga actgcctcaa
660
gcagataagg tggaatccac aactgactca cacttcccca gacaggacca gttgccctca
720
tttccaaaga actgcactct ggaattaaag ggactcttcc attttgaaga aggcatccag
780
aagctgtatc agtgcaatgg gatcgcctgg aaagcctgga gtccccaaac caaggatgtg
840
gaagacaaat cctgtccagc cgggtggcac cagcactcag gctactgtca catcttgatc
900

acagagcaga aaggcacctg gaatgcggct gcccaagctt gcagggaaca atacctgggc
960
aaccttgtaa ctgtattctc caggcagcac atgcggtggc tctgggacat tggtgggaga
1020
aagtcctttt ggataggttt gaacgaccaa gtgcatgctg gccactggga gtggatcggt
1080
ggtgaacctg ttgccttcac caatgggaga agagggccct ctccacgctc caagcttgga
1140
aagagctgtg ttttggttca aagacaaggg aaatggcaaa caaaagactg taggagagcc
1200
aaacctcata attatgtgtg ttccagaaaa ctctaaatat aacagaccct acaggggcc
1260
acctggagtt tgtcacctat ttattcacag gatctgtgaa tattgctcca tagaaaacaa
1320
attgttatga ttgagtgggt ataccttttgt gattctgtct agtgaaaatg ggacattttt
1380
aatagtgcca gaaagattga taaataaata ttttttacaa gataagatac aatttttgta
1440
tctcaatacc ttttaaaata aatgccagca gtattaaaaa gtgtaaggtt tgtttattcc
1500
agaagaccct cacccttacc ccattccaaa tctcagggag caccagtctc atagtccttg
1560
gatttttttt aaaaaaaatt tttggtcccg ttacctctaa tgaatttatt ctgaaatatg
1620
tatcgtaggt gctcctacca ctttagtctg agtggaaagc caaaaaac
1668

<210> 4298
<211> 411
<212> PRT
<213> Homo sapiens

<400> 4298
Xaa Met Asp Ser Ala Phe Val Gly Ile Lys Val Asn Gln Val Ser Ala
 1   5   10   15
Ala Val Gly Lys Asp Phe Thr Val Ile Pro Ser Lys Leu Ile Gln Phe
            20   25   30
Asp Pro Gly Met Ser Thr Lys Met Trp Asn Ile Ala Ile Thr Tyr Asp
        35   40   45
Gly Leu Glu Glu Asp Asp Glu Val Phe Glu Val Ile Leu Asn Ser Pro
    50   55   60
Val Asn Ala Val Leu Gly Thr Lys Thr Lys Ala Ala Val Lys Ile Leu
65   70   75   80
Asp Ser Lys Gly Gly Gln Cys His Pro Ser Tyr Ser Ser Asn Gln Ser
                85   90   95
Lys His Ser Thr Trp Glu Lys Gly Ile Trp His Leu Leu Pro Pro Gly
            100   105   110
Ser Ser Ser Ser Thr Thr Ser Gly Ser Phe His Leu Glu Arg Arg Pro
        115   120   125
Leu Pro Ser Ser Met Gln Leu Ala Val Ile Arg Gly Asp Thr Leu Arg
    130   135   140
Gly Phe Asp Ser Thr Asp Leu Ser Gln Arg Lys Leu Arg Thr Arg Gly
145   150   155   160
Asn Gly Lys Thr Val Arg Pro Ser Ser Val Tyr Arg Asn Gly Thr Asp

```
                165                 170                 175
Ile Ile Tyr Asn Tyr His Gly Ile Val Ser Leu Lys Leu Glu Asp Asp
            180                 185                 190
Ser Phe Pro Thr His Lys Arg Lys Ala Lys Val Ser Ile Ile Ser Gln
        195                 200                 205
Pro Gln Lys Thr Ile Lys Val Ala Glu Leu Pro Gln Ala Asp Lys Val
    210                 215                 220
Glu Ser Thr Thr Asp Ser His Phe Pro Arg Gln Asp Gln Leu Pro Ser
225                 230                 235                 240
Phe Pro Lys Asn Cys Thr Leu Glu Leu Lys Gly Leu Phe His Phe Glu
                245                 250                 255
Glu Gly Ile Gln Lys Leu Tyr Gln Cys Asn Gly Ile Ala Trp Lys Ala
            260                 265                 270
Trp Ser Pro Gln Thr Lys Asp Val Glu Asp Lys Ser Cys Pro Ala Gly
        275                 280                 285
Trp His Gln His Ser Gly Tyr Cys His Ile Leu Ile Thr Glu Gln Lys
    290                 295                 300
Gly Thr Trp Asn Ala Ala Ala Gln Ala Cys Arg Glu Gln Tyr Leu Gly
305                 310                 315                 320
Asn Leu Val Thr Val Phe Ser Arg Gln His Met Arg Trp Leu Trp Asp
                325                 330                 335
Ile Gly Gly Arg Lys Ser Phe Trp Ile Gly Leu Asn Asp Gln Val His
            340                 345                 350
Ala Gly His Trp Glu Trp Ile Gly Gly Glu Pro Val Ala Phe Thr Asn
        355                 360                 365
Gly Arg Arg Gly Pro Ser Pro Arg Ser Lys Leu Gly Lys Ser Cys Val
    370                 375                 380
Leu Val Gln Arg Gln Gly Lys Trp Gln Thr Lys Asp Cys Arg Arg Ala
385                 390                 395                 400
Lys Pro His Asn Tyr Val Cys Ser Arg Lys Leu
                405                 410
```

<210> 4299
<211> 988
<212> DNA
<213> Homo sapiens

<400> 4299
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tcccaggagg ggagtggagg gctcaggcac tggtgccctt gtggcctctt aggctcgagg
120
ccttgggaca ggcccccgag cacaaagtga ggctgtctat ggagttctgc agcacgtgca
180
cagcagacca tatatcactc agttccttct ggaggtcatc cttccagcag ccactggctc
240
cctgcggtat ctcttcagtc tccggacagg cggctgtctc atgaccctgc tgcttcatct
300
tggtcaggat tttgcggcat ttcacctgcg ttttctgcat tttctgaatg ttcaccaagt
360
tctctgagat ctcatcctcc tgcgcttgga gcttctgata gatgaaggtc acctcctccc
420
gcaccagttc cagctcctcc cacaggaact tcttgctgtc ccggatctcc tgggccagca
480

gctgcaggca gcgagtggtg cgggcccgct gcatctcctc actgtcacgc agggtcttct
540
ccagcccctg aaggccttgg gtcagggccc catacagctc ctgccggccc tgctccatgc
600
cccacttgtg ctcctccttc tctccatggc ggcctgtggg gctcagcacc tcttcaagct
660
gctgaatctt gatttgctgc aagcagctct ccttctccaa catggtcact gagtggttca
720
ggaactcgaa agccttggtc tgggcctgta actggctctt gagtgactca agttcacatc
780
gcaggagctt ctgggagtcg ggaatcatca caatggtctt ggctttgact ttggaagagc
840
tggtctccaa gggcttcaca taccacctgt tcatgctctn cccatcaggg accacgaagc
900
cagtcctcag ctgtgacgct gaagtttgat cccgcgggga caccatcgta ttaaaacgct
960
cagagactga gtcacagaga ggggtgtc
988

<210> 4300
<211> 84
<212> PRT
<213> Homo sapiens

<400> 4300
Gly Cys Leu Trp Ser Ser Ala Ala Arg Ala Gln Gln Thr Ile Tyr His
1 5 10 15
Ser Val Pro Ser Gly Gly His Pro Ser Ser Ser His Trp Leu Pro Ala
20 25 30
Val Ser Leu Gln Ser Pro Asp Arg Arg Leu Ser His Asp Pro Ala Ala
35 40 45
Ser Ser Trp Ser Gly Phe Cys Gly Ile Ser Pro Ala Phe Ser Ala Phe
50 55 60
Ser Glu Cys Ser Pro Ser Ser Leu Arg Ser His Pro Pro Ala Leu Gly
65 70 75 80
Ala Ser Asp Arg

<210> 4301
<211> 2429
<212> DNA
<213> Homo sapiens

<400> 4301
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cccaaggtgc ggcctcgcta gcgggagagg gagcgggatc accggcccgg agagagctct
120
cagggccaga gcggggcagg aggatgcttt cccagcccca ccatggagct gcgctgtggg
180
ggattgctgt tcagttctcg ctttgattca gggaatctag cccacgtgga gaaggtggaa
240
tctttgtcca gtgatgggga aggggtagga ggtggggcgt cagccctgac cagtggcatt
300

gcctcttccc ctgactatga attcaacgtg tggacccgac cagactgtgc tgaaacggaa
360
tttgagaatg ggaacaggtc atggttctac ttcagcgtcc ggggaggaat gccaggaaaa
420
ctcatcaaga tcaacattat gaacatgaac aagcagagca agctgtattc ccagggcatg
480
gccccctttg tgcgcacact gcccacccgg ccacgctggg aacgcattcg agaccggccc
540
acctttgaga tgacagagac gcagtttgtg ttatcctttg ttcatcgttt cgtggagggc
600
cgtggggcca ccaccttctt cgccttctgc taccccttct cctacagtga ctgccaggaa
660
ctgctaaacc agctagacca gcgctttccg gagaaccacc ctacccatag cagccccctg
720
gataccatct attaccatcg ggagctcctt tgctattctc tggatggact tcgtgtagat
780
ctgctgacga tcacttcctg ccatgggctt cgagaagatc gagagccccg tctagagcag
840
ctatttcctg ataccagcac ccctcgacca ttccgtttcg caggcaagag gatattcttc
900
ttaagcagta gagtacaccc aggggagact ccatctagct ttgtcttcaa tggctttctg
960
gacttcatcc tccgacctga tgatccccgg gcccaaaccc tccgtcgcct cttcgtcttt
1020
aagctgattc ccatgttgaa ccccgatggt gtggtccggg gacactaccg cacagactca
1080
cgtggagtga atctgaaccg tcagtacctg aagcctgatg ccgtcctgca cccggccatc
1140
tatggggcca aagctgtgct tctctaccac catgtgcact ctcgtctgaa ctcccagagt
1200
tcctctgagc accagcccag ttcctgtctc cctcctgatg ctcctgtttc tgacctggag
1260
aaagccaaca atctccaaaa tgaagctcag tgtgggcact cagctgacag gcataacgct
1320
gaagcctgga aacaaacaga gccagcagaa cagaagctca acagtgtgtg gattatgcca
1380
caacagtctg cggggcttga agagtcagcc cctgatacca tccccccaa agagagtggc
1440
gttgcttact atgtggacct gcatggacat gcttccaaaa ggggctgctt catgtacgga
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1560
ttgaattcag cccacttcga cttccagggc tgcaatttct cagagaagaa tatgtatgcc
1620
cgagaccgta gagatggcca gtctaaagag ggaagcggcc gtgttgcaat ctacaaagcc
1680
tcagggataa tccacagcta cacacttgaa tgcaactaca acactggacg ctcagtaaac
1740
agcatccctg ctgcctgcca tgacaatggg cgtgccagcc cccctccccc gccggctttc
1800
ccctccagat acactgtgga actatttgag caggtgggac gagctatggc cattgcagcc
1860
ctggacatgg cggaatgtaa tccgtggccc cgaattgtac tgtcagagca cagcagcctt
1920

actaatctac gggcctggat gctgaaacat gtacgcaaca gccgaggcct aagcagcact
1980
ctgaatgtgg gtgtcaacaa gaagaggggc cttcgaactc cacccaaaag tcacaatggg
2040
ttgcctgtct cctgctccga aaacaccttg agtcgggcac gaagttttag caccggcaca
2100
agtgccggtg gtagcagcag cagccaacaa aattctccac agatgaagaa ttcccccagc
2160
tttccttttc atggcagtcg gcctgcaggg ctgccaggcc tgggctctag tacccaaaag
2220
gtcacccacc gggtgctggg ccccgtcaga ggtaagccag tctgggagcc cctgcaacat
2280
gtgttcggtt gtctggggca ttgctggggg aagtaagagc ttgaagatat actgttggcc
2340
caggaccaag gggtgaatca ataaaattag tttgtagcag aaaaaaaaaa aaaaaaaaaa
2400
aaaaaaaaaa aaaaaaaaaa aaaaaaaaa
2429

<210> 4302
<211> 717
<212> PRT
<213> Homo sapiens

<400> 4302
Met Glu Leu Arg Cys Gly Gly Leu Leu Phe Ser Ser Arg Phe Asp Ser
1 5 10 15
Gly Asn Leu Ala His Val Glu Lys Val Glu Ser Leu Ser Ser Asp Gly
20 25 30
Glu Gly Val Gly Gly Gly Ala Ser Ala Leu Thr Ser Gly Ile Ala Ser
35 40 45
Ser Pro Asp Tyr Glu Phe Asn Val Trp Thr Arg Pro Asp Cys Ala Glu
50 55 60
Thr Glu Phe Glu Asn Gly Asn Arg Ser Trp Phe Tyr Phe Ser Val Arg
65 70 75 80
Gly Gly Met Pro Gly Lys Leu Ile Lys Ile Asn Ile Met Asn Met Asn
85 90 95
Lys Gln Ser Lys Leu Tyr Ser Gln Gly Met Ala Pro Phe Val Arg Thr
100 105 110
Leu Pro Thr Arg Pro Arg Trp Glu Arg Ile Arg Asp Arg Pro Thr Phe
115 120 125
Glu Met Thr Glu Thr Gln Phe Val Leu Ser Phe Val His Arg Phe Val
130 135 140
Glu Gly Arg Gly Ala Thr Thr Phe Phe Ala Phe Cys Tyr Pro Phe Ser
145 150 155 160
Tyr Ser Asp Cys Gln Glu Leu Leu Asn Gln Leu Asp Gln Arg Phe Pro
165 170 175
Glu Asn His Pro Thr His Ser Ser Pro Leu Asp Thr Ile Tyr Tyr His
180 185 190
Arg Glu Leu Leu Cys Tyr Ser Leu Asp Gly Leu Arg Val Asp Leu Leu
195 200 205
Thr Ile Thr Ser Cys His Gly Leu Arg Glu Asp Arg Glu Pro Arg Leu
210 215 220
Glu Gln Leu Phe Pro Asp Thr Ser Thr Pro Arg Pro Phe Arg Phe Ala

```
225                 230                 235                 240
Gly Lys Arg Ile Phe Phe Leu Ser Ser Arg Val His Pro Gly Glu Thr
                245                 250                 255
Pro Ser Ser Phe Val Phe Asn Gly Phe Leu Asp Phe Ile Leu Arg Pro
            260                 265                 270
Asp Asp Pro Arg Ala Gln Thr Leu Arg Arg Leu Phe Val Phe Lys Leu
        275                 280                 285
Ile Pro Met Leu Asn Pro Asp Gly Val Val Arg Gly His Tyr Arg Thr
    290                 295                 300
Asp Ser Arg Gly Val Asn Leu Asn Arg Gln Tyr Leu Lys Pro Asp Ala
305                 310                 315                 320
Val Leu His Pro Ala Ile Tyr Gly Ala Lys Ala Val Leu Leu Tyr His
                325                 330                 335
His Val His Ser Arg Leu Asn Ser Gln Ser Ser Ser Glu His Gln Pro
            340                 345                 350
Ser Ser Cys Leu Pro Pro Asp Ala Pro Val Ser Asp Leu Glu Lys Ala
        355                 360                 365
Asn Asn Leu Gln Asn Glu Ala Gln Cys Gly His Ser Ala Asp Arg His
    370                 375                 380
Asn Ala Glu Ala Trp Lys Gln Thr Glu Pro Ala Glu Gln Lys Leu Asn
385                 390                 395                 400
Ser Val Trp Ile Met Pro Gln Gln Ser Ala Gly Leu Glu Glu Ser Ala
                405                 410                 415
Pro Asp Thr Ile Pro Pro Lys Glu Ser Gly Val Ala Tyr Tyr Val Asp
            420                 425                 430
Leu His Gly His Ala Ser Lys Arg Gly Cys Phe Met Tyr Gly Asn Ser
        435                 440                 445
Phe Ser Asp Glu Ser Thr Gln Val Glu Asn Met Leu Tyr Pro Lys Leu
    450                 455                 460
Ile Ser Leu Asn Ser Ala His Phe Asp Phe Gln Gly Cys Asn Phe Ser
465                 470                 475                 480
Glu Lys Asn Met Tyr Ala Arg Asp Arg Arg Asp Gly Gln Ser Lys Glu
                485                 490                 495
Gly Ser Gly Arg Val Ala Ile Tyr Lys Ala Ser Gly Ile Ile His Ser
            500                 505                 510
Tyr Thr Leu Glu Cys Asn Tyr Asn Thr Gly Arg Ser Val Asn Ser Ile
        515                 520                 525
Pro Ala Ala Cys His Asp Asn Gly Arg Ala Ser Pro Pro Pro Pro Pro
    530                 535                 540
Ala Phe Pro Ser Arg Tyr Thr Val Glu Leu Phe Glu Gln Val Gly Arg
545                 550                 555                 560
Ala Met Ala Ile Ala Ala Leu Asp Met Ala Glu Cys Asn Pro Trp Pro
                565                 570                 575
Arg Ile Val Leu Ser Glu His Ser Ser Leu Thr Asn Leu Arg Ala Trp
            580                 585                 590
Met Leu Lys His Val Arg Asn Ser Arg Gly Leu Ser Ser Thr Leu Asn
        595                 600                 605
Val Gly Val Asn Lys Lys Arg Gly Leu Arg Thr Pro Pro Lys Ser His
    610                 615                 620
Asn Gly Leu Pro Val Ser Cys Ser Glu Asn Thr Leu Ser Arg Ala Arg
625                 630                 635                 640
Ser Phe Ser Thr Gly Thr Ser Ala Gly Gly Ser Ser Ser Ser Gln Gln
                645                 650                 655
Asn Ser Pro Gln Met Lys Asn Ser Pro Ser Phe Pro Phe His Gly Ser
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660 665 670
Arg Pro Ala Gly Leu Pro Gly Leu Gly Ser Ser Thr Gln Lys Val Thr
675 680 685
His Arg Val Leu Gly Pro Val Arg Gly Lys Pro Val Trp Glu Pro Leu
690 695 700
Gln His Val Phe Gly Cys Leu Gly His Cys Trp Gly Lys
705 710 715

<210> 4303
<211> 768
<212> DNA
<213> Homo sapiens

<400> 4303
acgcgtgcag caagagagct ggacaatctg cagtatcgaa agatgaagaa actccttttc
60
caggaggcac ataatggacc agcagtagaa gcacaggaag aagaagagga acaagatcat
120
ggtgttggcc ggacaggaac agttaatagt gttggaagta atcaatccat tcccagcatg
180
tccatcagtg ccagcagcca aagcagtagt gttaacagtc ttccagatgt ctcagatgac
240
aagagtgagc tagacatgat ggagggagac cacacagtga tgtctaacag ttctgttatc
300
catttaaaac cagaggaaga aaattacaga gaagagggag atcctagaac aagagcatca
360
gatccacaat ctccacccca agtatctcgt cacaaatcac actatcgtaa tcgagaacac
420
tttgctacta tacggacagc atcactggtt acgaggcaaa tgcaagaaca tgagcaggac
480
tctgagctta gagaacaaat gtctggctat aagcgaatga ggcgacaaca tcaaaagcaa
540
ctgatgactc tggaaaacaa gctaaaggct gagatggatg aacatcgcct cagattagac
600
aaagatcttg aaactcagcg taacaatttt gctgcagaaa tggagaaact tatcaagaaa
660
caccaggctg ctatggagaa agaggctaaa gtgatgtcca atgaagagaa aaaatttcag
720
caacatattc aggcccaaca gaagaaagaa ctgaatagtt ttctcgag
768

<210> 4304
<211> 256
<212> PRT
<213> Homo sapiens

<400> 4304
Thr Arg Ala Ala Arg Glu Leu Asp Asn Leu Gln Tyr Arg Lys Met Lys
1 5 10 15
Lys Leu Leu Phe Gln Glu Ala His Asn Gly Pro Ala Val Glu Ala Gln
20 25 30
Glu Glu Glu Glu Glu Gln Asp His Gly Val Gly Arg Thr Gly Thr Val
35 40 45
Asn Ser Val Gly Ser Asn Gln Ser Ile Pro Ser Met Ser Ile Ser Ala

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    50                  55                  60
Ser Ser Gln Ser Ser Ser Val Asn Ser Leu Pro Asp Val Ser Asp Asp
65                  70                  75                  80
Lys Ser Glu Leu Asp Met Met Glu Gly Asp His Thr Val Met Ser Asn
                85                  90                  95
Ser Ser Val Ile His Leu Lys Pro Glu Glu Glu Asn Tyr Arg Glu Glu
            100                 105                 110
Gly Asp Pro Arg Thr Arg Ala Ser Asp Pro Gln Ser Pro Pro Gln Val
        115                 120                 125
Ser Arg His Lys Ser His Tyr Arg Asn Arg Glu His Phe Ala Thr Ile
    130                 135                 140
Arg Thr Ala Ser Leu Val Thr Arg Gln Met Gln Glu His Glu Gln Asp
145                 150                 155                 160
Ser Glu Leu Arg Glu Gln Met Ser Gly Tyr Lys Arg Met Arg Arg Gln
                165                 170                 175
His Gln Lys Gln Leu Met Thr Leu Glu Asn Lys Leu Lys Ala Glu Met
            180                 185                 190
Asp Glu His Arg Leu Arg Leu Asp Lys Asp Leu Glu Thr Gln Arg Asn
        195                 200                 205
Asn Phe Ala Ala Glu Met Glu Lys Leu Ile Lys Lys His Gln Ala Ala
    210                 215                 220
Met Glu Lys Glu Ala Lys Val Met Ser Asn Glu Glu Lys Lys Phe Gln
225                 230                 235                 240
Gln His Ile Gln Ala Gln Gln Lys Lys Glu Leu Asn Ser Phe Leu Glu
                245                 250                 255
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<210> 4305
<211> 3400
<212> DNA
<213> Homo sapiens

<400> 4305
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cgtgccagga agctgcggag caacctgcgc cagctcacgc tcaccgccgc cggggcctgc
120
cccggggccg gggccgacgc gctcgagtcc cccgcctccc cccagctcgt gctgccggcc
180
aacctcgggg acattgaggc actgaacctg gggaacaacg gcctggagga ggtacccgag
240
gggctggggt cggcgctggg cagcctgcgc gtcctggtcc tgcgcaggaa ccgcttcgcc
300
cggctgcccc cggcggtggc cgagctcggc caccacctca ccgagctgga cgtgagccac
360
aaccggctga ccgccctggg cgcggaggtg gtgagtgctc tgagggagct gcggaagctc
420
aacctcagcc acaaccagct gcccgccctg cccgcccagc tgggcgctct cgctcacctg
480
gaggagctgg atgtcagctt taaccggctg gcgcacctgc ctgactccct ctcctgcctc
540
tcccgcctgc gcaccctgga cgtggatcac aaccagctca ctgccttccc ccggcagctg
600
ctgcagctgg tggccctgga ggagctggac gtgtccagca accggctgcg gggcctgcct
660

gaggatatca gtgccctgcg tgccctcaag atcctctggc tgagtggggc cgagcttggc
720
acgctgcccg ccggcttctg cgagctggcc agtttggaga gcctcatgct agacaacaac
780
gggctgcagg ctctgcccgc ccagttcagc tgcctgcagc ggctcaaaat gctcaacctg
840
tcctccaacc tcttcgagga gttccctgcc gcgctgctgc ccctggctgg tctggaggag
900
ctctacctta gtcgcaacca gctcacctcg gtgccatccc ttatctcggg cctgggccgg
960
cttctcacct tgtggctgga taataaccgc atccgctacc tgccggactc catcgtggag
1020
ctgaccggcc tggaggagct cgtgctgcag gggaaccaga tcgcggtgct gcccgaccac
1080
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1140
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2280

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<210> 4306
<211> 1052
<212> PRT
<213> Homo sapiens

<400> 4306
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Thr Leu Thr Ala Ala Gly Ala Cys Pro Gly Ala Gly Ala Asp Ala Leu
35 40 45
Glu Ser Pro Ala Ser Pro Gln Leu Val Leu Pro Ala Asn Leu Gly Asp
50 55 60
Ile Glu Ala Leu Asn Leu Gly Asn Asn Gly Leu Glu Glu Val Pro Glu

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65                  70                  75                  80
Gly Leu Gly Ser Ala Leu Gly Ser Leu Arg Val Leu Val Leu Arg Arg
                85                  90                  95
Asn Arg Phe Ala Arg Leu Pro Pro Ala Val Ala Glu Leu Gly His His
            100                 105                 110
Leu Thr Glu Leu Asp Val Ser His Asn Arg Leu Thr Ala Leu Gly Ala
        115                 120                 125
Glu Val Val Ser Ala Leu Arg Glu Leu Arg Lys Leu Asn Leu Ser His
    130                 135                 140
Asn Gln Leu Pro Ala Leu Pro Ala Gln Leu Gly Ala Leu Ala His Leu
145                 150                 155                 160
Glu Glu Leu Asp Val Ser Phe Asn Arg Leu Ala His Leu Pro Asp Ser
                165                 170                 175
Leu Ser Cys Leu Ser Arg Leu Arg Thr Leu Asp Val Asp His Asn Gln
            180                 185                 190
Leu Thr Ala Phe Pro Arg Gln Leu Leu Gln Leu Val Ala Leu Glu Glu
        195                 200                 205
Leu Asp Val Ser Ser Asn Arg Leu Arg Gly Leu Pro Glu Asp Ile Ser
    210                 215                 220
Ala Leu Arg Ala Leu Lys Ile Leu Trp Leu Ser Gly Ala Glu Leu Gly
225                 230                 235                 240
Thr Leu Pro Ala Gly Phe Cys Glu Leu Ala Ser Leu Glu Ser Leu Met
                245                 250                 255
Leu Asp Asn Asn Gly Leu Gln Ala Leu Pro Ala Gln Phe Ser Cys Leu
            260                 265                 270
Gln Arg Leu Lys Met Leu Asn Leu Ser Ser Asn Leu Phe Glu Glu Phe
        275                 280                 285
Pro Ala Ala Leu Leu Pro Leu Ala Gly Leu Glu Glu Leu Tyr Leu Ser
    290                 295                 300
Arg Asn Gln Leu Thr Ser Val Pro Ser Leu Ile Ser Gly Leu Gly Arg
305                 310                 315                 320
Leu Leu Thr Leu Trp Leu Asp Asn Asn Arg Ile Arg Tyr Leu Pro Asp
                325                 330                 335
Ser Ile Val Glu Leu Thr Gly Leu Glu Glu Leu Val Leu Gln Gly Asn
            340                 345                 350
Gln Ile Ala Val Leu Pro Asp His Phe Gly Gln Leu Ser Arg Val Gly
        355                 360                 365
Leu Trp Lys Ile Lys Asp Asn Pro Leu Ile Gln Pro Pro Tyr Glu Val
    370                 375                 380
Cys Met Lys Gly Ile Pro Tyr Ile Ala Ala Tyr Gln Lys Glu Leu Ala
385                 390                 395                 400
His Ser Gln Pro Ala Val Gln Pro Arg Leu Lys Leu Leu Leu Met Gly
                405                 410                 415
His Lys Ala Ala Gly Lys Thr Leu Leu Arg His Cys Leu Thr Glu Glu
            420                 425                 430
Arg Val Glu Gly Cys Pro Gly Gly Gly Asp Lys Glu Lys Cys Tyr Pro
        435                 440                 445
Pro Ser Pro Pro Pro Val Ser Lys Gly Ile Glu Val Thr Ser Trp Thr
    450                 455                 460
Ala Asp Ala Ser Arg Gly Leu Arg Phe Ile Val Tyr Asp Leu Ala Gly
465                 470                 475                 480
Asp Glu Ser Tyr Glu Val Ile Gln Pro Phe Phe Leu Ser Pro Gly Ala
                485                 490                 495
Leu Tyr Val Leu Val Val Asn Leu Ala Thr Tyr Glu Pro Arg His Phe
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                500                 505                 510
Pro Thr Thr Val Gly Ser Phe Leu His Arg Val Gly Ala Arg Val Pro
        515                 520                 525
Asn Ala Val Val Cys Ile Val Gly Thr His Ala Asp Leu Cys Gly Glu
    530                 535                 540
Arg Glu Leu Glu Glu Lys Cys Leu Asp Ile His Arg Gln Ile Ala Leu
545                 550                 555                 560
Gln Glu Lys His Asp Ala Glu Gly Leu Ser Arg Leu Ala Lys Val Val
                565                 570                 575
Asp Glu Ala Leu Ala Arg Asp Phe Glu Leu Arg Ser Ala Ser Pro His
            580                 585                 590
Ala Ala Tyr Tyr Gly Val Ser Asp Lys Asn Leu Arg Arg Arg Lys Ala
        595                 600                 605
His Phe Gln Tyr Leu Leu Asn His Arg Leu Gln Ile Leu Ser Pro Val
    610                 615                 620
Leu Pro Val Ser Cys Arg Asp Pro Arg His Leu Arg Arg Leu Arg Asp
625                 630                 635                 640
Lys Leu Leu Ser Val Ala Glu His Arg Glu Ile Phe Pro Asn Leu His
                645                 650                 655
Arg Val Leu Pro Arg Ser Trp Gln Val Leu Glu Glu Leu His Phe Gln
            660                 665                 670
Pro Pro Gln Ala Gln Arg Leu Trp Leu Ser Trp Trp Asp Ser Ala Arg
        675                 680                 685
Leu Gly Leu Gln Ala Gly Leu Thr Glu Asp Arg Leu Gln Ser Ala Leu
    690                 695                 700
Ser Tyr Leu His Glu Ser Gly Lys Leu Leu Tyr Phe Glu Asp Ser Pro
705                 710                 715                 720
Ala Leu Lys Glu His Val Phe His Asn Leu Thr Arg Leu Ile Asp Ile
                725                 730                 735
Leu Asn Val Phe Phe Gln Arg Asp Pro Ser Leu Leu Leu His Lys Leu
            740                 745                 750
Leu Leu Gly Thr Ser Gly Glu Gly Lys Ala Glu Gly Glu Ser Ser Pro
        755                 760                 765
Pro Met Ala Arg Ser Thr Pro Ser Gln Glu Leu Leu Arg Ala Thr Gln
    770                 775                 780
Leu His Gln Tyr Val Glu Gly Phe Leu Leu His Gly Leu Leu Pro Ala
785                 790                 795                 800
His Val Ile Arg Leu Leu Leu Lys Pro His Val Gln Ala Gln Gln Asp
                805                 810                 815
Leu Gln Leu Leu Leu Glu Leu Leu Glu Lys Met Gly Leu Cys Tyr Cys
            820                 825                 830
Leu Asn Lys Pro Lys Gly Lys Pro Leu Asn Gly Ser Thr Ala Trp Tyr
        835                 840                 845
Lys Phe Pro Cys Tyr Val Gln Asn Glu Val Pro His Ala Glu Ala Trp
    850                 855                 860
Ile Asn Gly Thr Asn Leu Ala Gly Gln Ser Phe Val Ala Glu Gln Leu
865                 870                 875                 880
Gln Ile Glu Tyr Ser Phe Pro Phe Thr Phe Pro Pro Gly Leu Phe Ala
                885                 890                 895
Arg Tyr Ser Val Gln Ile Asn Ser His Val Val His Arg Ser Asp Gly
            900                 905                 910
Lys Phe Gln Ile Phe Ala Tyr Arg Gly Lys Val Pro Val Val Val Ser
        915                 920                 925
Tyr Arg Pro Ala Arg Gly Val Leu Gln Pro Asp Thr Leu Ser Ile Ala
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    930                 935                 940
Ser His Ala Ser Leu Pro Asn Ile Trp Thr Ala Trp Gln Ala Ile Thr
945                 950                 955                 960
Pro Leu Val Glu Glu Leu Asn Val Leu Leu Gln Glu Trp Pro Gly Leu
                965                 970                 975
His Tyr Thr Val His Ile Leu Cys Ser Lys Cys Leu Lys Arg Gly Ser
            980                 985                 990
Pro Asn Pro His Ala Phe Pro Gly Glu Leu Leu Ser Gln Pro Arg Pro
        995                 1000                1005
Glu Gly Val Ala Glu Ile Ile Cys Pro Lys Asn Gly Ser Glu Arg Val
    1010                1015                1020
Asn Val Ala Leu Val Tyr Pro Pro Thr Pro Thr Val Ile Ser Pro Cys
1025                1030                1035                1040
Ser Lys Lys Asn Val Gly Glu Lys His Arg Asn Gln
                1045                1050
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<210> 4307
<211> 947
<212> DNA
<213> Homo sapiens

<400> 4307
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120
aggacagaac tgatcgatac gtccaggctc tgaggaccgt ctctctcctc ctgggcgagc
180
cgttcttcac taccagcctg ctgccgtggc acaacctcta cttctggtac gtgcggacgc
240
tgtggaccag cacctggggc caggtgccat ggtgatgccc caggcagcct cgctgcacgc
300
tgtggttgtg gagttcaggg tgtgcaggga acagcaagat gtgcctcttg ttcttgctgc
360
cacgcttccc tgtgtcctgc gggcgggtgt ggatggggct gctccttcct cacaggancc
420
tgtggcggat ccggagccnc ctgtggtgac tgcgaaggct tcgacgtgca catcatggat
480
gacatgatta aggtaggcag ggccacactc tgcatagtcc ccccgacctg ctcctgtatc
540
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660
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720
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780
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840
tgaggagatt cccacaggtt atttacatgg taggggttag caactgggcc tacgttctcc
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947

<210> 4308
<211> 200
<212> PRT
<213> Homo sapiens

<400> 4308
Gly Pro Ser Leu Ser Ser Trp Ala Ser Arg Ser Ser Leu Pro Ala Cys
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Cys Arg Gly Thr Thr Ser Thr Ser Gly Thr Cys Gly Arg Cys Gly Pro
20 25 30
Ala Pro Gly Ala Arg Cys His Gly Asp Ala Pro Gly Ser Leu Ala Ala
35 40 45
Arg Cys Gly Cys Gly Val Gln Gly Val Gln Gly Thr Ala Arg Cys Ala
50 55 60
Ser Cys Ser Cys Cys His Ala Ser Leu Cys Pro Ala Gly Gly Cys Gly
65 70 75 80
Trp Gly Cys Ser Phe Leu Thr Gly Xaa Cys Gly Gly Ser Gly Ala Xaa
85 90 95
Cys Gly Asp Cys Glu Gly Phe Asp Val His Ile Met Asp Asp Met Ile
100 105 110
Lys Val Gly Arg Ala Thr Leu Cys Ile Val Pro Pro Thr Cys Ser Cys
115 120 125
Ile Ala Gly Leu Ser Gln Gly Pro Ser Leu Gly Ser Thr Gly Ser Ser
130 135 140
Val Gly Gly Ser Glu Val Arg Cys Cys His Phe Val Trp Phe Asn Met
145 150 155 160
Ser Ile Ala Trp Tyr Gln Pro Cys Ser Trp Leu Arg Ala Val Thr Leu
165 170 175
Cys Gln Asn Leu His Trp Ala Cys Thr Ser Cys His Cys Asn Cys Pro
180 185 190
Cys Gln Cys Pro Gln Leu Leu Phe
195 200

<210> 4309
<211> 1928
<212> DNA
<213> Homo sapiens

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180
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240
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300
aagatttgtt tcatcattca cctgttgaat tataacccct tctgaatgct ttgatttata
360
aataggcatg aaaaattcag ttggtgaagg gaatatctcg ttctcatcct ttggtgccga
420

caataacata tccaaagcct tttggtattg ttgacgttcc tgctgaattg ttacttcact
480
ttcatttttt aattcatttg gttctgaatt cccagccttt tcaaaatcaa atacattcaa
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catatcaaca tcattttgct ttaccgagtt ttcctccgat gtgcagccta agtctacttt
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720
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780
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1928

<210> 4310

<211> 599
<212> PRT
<213> Homo sapiens

<400> 4310
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Phe Cys Thr Asp Ser Ser Ser Leu Arg Leu Ser Thr Leu Gln Leu Val
35 40 45
Lys Asn His Met Ala Val His Tyr Asn Lys Ile Leu Ser Ala Lys Ala
50 55 60
Ala Val Asp Cys Ser Val Pro Val Ser Val Ser Thr Ser Ile Lys Tyr
65 70 75 80
Ala Asp Gln Gln Arg Arg Glu Lys Leu Lys Lys Glu Leu Ala Gln Cys
85 90 95
Glu Lys Glu Phe Lys Leu Thr Lys Thr Ala Met Arg Ala Asn Tyr Lys
100 105 110
Asn Asn Ser Lys Ser Leu Phe Asn Thr Leu Gln Lys Pro Ser Gly Glu
115 120 125
Pro Gln Ile Glu Asp Asp Met Leu Lys Glu Glu Met Asn Gly Phe Ser
130 135 140
Ser Phe Ala Arg Ser Leu Val Pro Ser Ser Glu Arg Leu His Leu Ser
145 150 155 160
Leu His Lys Ser Ser Lys Val Ile Thr Asn Gly Pro Glu Lys Asn Ser
165 170 175
Ser Ser Ser Pro Ser Ser Val Asp Tyr Ala Ala Ser Gly Pro Arg Lys
180 185 190
Leu Ser Ser Gly Ala Leu Tyr Gly Arg Arg Pro Arg Ser Thr Phe Pro
195 200 205
Asn Ser His Arg Phe Gln Leu Val Ile Ser Lys Ala Pro Ser Gly Asp
210 215 220
Leu Leu Asp Lys His Ser Glu Leu Phe Ser Asn Lys Gln Leu Pro Phe
225 230 235 240
Thr Pro Arg Thr Leu Lys Thr Glu Ala Lys Ser Phe Leu Ser Gln Tyr
245 250 255
Arg Tyr Tyr Thr Pro Ala Lys Arg Lys Lys Asp Phe Thr Asp Gln Arg
260 265 270
Ile Glu Ala Glu Thr Gln Thr Glu Leu Ser Phe Lys Ser Glu Leu Gly
275 280 285
Thr Ala Glu Thr Lys Asn Met Thr Asp Ser Glu Met Asn Ile Lys Gln
290 295 300
Ala Ser Asn Cys Val Thr Tyr Asp Ala Lys Glu Lys Ile Ala Pro Leu
305 310 315 320
Pro Leu Glu Gly His Asp Ser Thr Trp Asp Glu Ile Lys Asp Asp Ala
325 330 335
Leu Gln His Ser Ser Pro Arg Ala Met Cys Gln Tyr Ser Leu Lys Pro
340 345 350
Pro Ser Thr Arg Lys Ile Tyr Ser Asp Glu Glu Glu Leu Leu Tyr Leu
355 360 365
Ser Phe Ile Glu Asp Val Thr Asp Glu Ile Leu Lys Leu Gly Leu Phe
370 375 380
Ser Asn Arg Phe Leu Glu Arg Leu Phe Glu Arg His Ile Lys Gln Asn

385 390 395 400
Lys His Leu Glu Glu Glu Lys Met Arg His Leu Leu His Val Leu Lys
405 410 415
Val Asp Leu Gly Cys Thr Ser Glu Glu Asn Ser Val Lys Gln Asn Asp
420 425 430
Val Asp Met Leu Asn Val Phe Asp Phe Glu Lys Ala Gly Asn Ser Glu
435 440 445
Pro Asn Glu Leu Lys Asn Glu Ser Glu Val Thr Ile Gln Gln Glu Arg
450 455 460
Gln Gln Tyr Gln Lys Ala Leu Asp Met Leu Leu Ser Ala Pro Lys Asp
465 470 475 480
Glu Asn Glu Ile Phe Pro Ser Pro Thr Glu Phe Phe Met Pro Ile Tyr
485 490 495
Lys Ser Lys His Ser Glu Gly Val Ile Ile Gln Gln Val Asn Asp Glu
500 505 510
Thr Asn Leu Glu Thr Ser Thr Leu Asp Glu Asn His Pro Ser Ile Ser
515 520 525
Asp Ser Leu Thr Asp Arg Glu Thr Ser Val Asn Val Ile Glu Gly Asp
530 535 540
Ser Asp Pro Glu Lys Val Glu Ile Ser Asn Gly Leu Cys Gly Leu Asn
545 550 555 560
Thr Ser Pro Ser Gln Ser Val Gln Phe Ser Ser Val Lys Gly Asp Asn
565 570 575
Asn His Asp Met Glu Leu Ser Thr Leu Lys Ile Met Glu Met Ser Ile
580 585 590
Glu Asp Cys Pro Leu Asp Val
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<210> 4311
<211> 432
<212> DNA
<213> Homo sapiens

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120
aaaaacataa ccactggggc atctgcagca tcccagactc agatgcctac gggccagaca
180
ggcaactgtg agtccccttt agggagcaag gaggacctca actccaaaga gaacctggat
240
gccgatgagg gagatgggaa aagtaacgac ctcgtcctta gttgtcctta ctttagaaat
300
gagactggag gggaaggcga caggcggatt gcgctctctc gagccaactc atcctctttc
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432

<210> 4312
<211> 144
<212> PRT

<213> Homo sapiens

<400> 4312
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His Tyr Asp Val Gln Ser Ile Leu Phe Asn Ile Asn Glu Ala Met Ala
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Thr Arg Ala Asn Val Gly Lys Arg Lys Asn Ile Thr Thr Gly Ala Ser
35 40 45
Ala Ala Ser Gln Thr Gln Met Pro Thr Gly Gln Thr Gly Asn Cys Glu
50 55 60
Ser Pro Leu Gly Ser Lys Glu Asp Leu Asn Ser Lys Glu Asn Leu Asp
65 70 75 80
Ala Asp Glu Gly Asp Gly Lys Ser Asn Asp Leu Val Leu Ser Cys Pro
85 90 95
Tyr Phe Arg Asn Glu Thr Gly Gly Glu Gly Asp Arg Arg Ile Ala Leu
100 105 110
Ser Arg Ala Asn Ser Ser Ser Phe Ser Ser Gly Glu Ser Cys Ser Phe
115 120 125
Glu Ser Ser Leu Ser Ser His Cys Thr Asn Ala Gly Val Ser Val Leu
130 135 140

<210> 4313
<211> 936
<212> DNA
<213> Homo sapiens

<400> 4313
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120
attcagtatc caaccatcct ctccattctc ctctggacct caccactctc agagctgctt
180
gtcctggcag aatctacagt tcaccccaac tctatgcctt acccctccca acccaacagc
240
atttgcagtt tgcaaaatat acagacccaa gtcctgaggg gactgaggac atgatgctgg
300
gcccaagtct cctgctcagg gcttctctcc aatgccagcc ctgccactcc ttcctcaccc
360
tccttggagc ctcctctgct gcttgtctat cccaacggcc ctgctccccc cccttcctgc
420
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780

gtttacttct ctgcacgggg gactcacccc aagaccattt ccagcagctt cccaggtgat
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936

<210> 4314
<211> 110
<212> PRT
<213> Homo sapiens

<400> 4314
Met Ser Ser Leu Leu Leu Pro Ser Gln Ser Cys Asp Pro Val Met Ser
1 5 10 15
Thr Arg Met Ala Leu Trp Ser Leu Glu His Pro Ser Cys Cys Arg Val
20 25 30
Leu Gln Pro His Pro Phe Ser Thr Gly Pro Trp Tyr Pro Gly Ser Ser
35 40 45
Leu Ser Ser Ala Thr Asp Leu Cys Ala Leu Val Tyr Phe Ser Ala Arg
50 55 60
Gly Thr His Pro Lys Thr Ile Ser Ser Ser Phe Pro Gly Asp Val Val
65 70 75 80
Pro Gln Gly Trp Ala Leu Gln Leu Trp Pro Ser Ser Leu Val Leu Pro
85 90 95
Arg Arg His Gln Ala Ala Gln Asn Glu Val Thr Ala Gly Asn
100 105 110

<210> 4315
<211> 573
<212> DNA
<213> Homo sapiens

<400> 4315
nncctaatcc aatatgactg gtgtccttat aagaagagga aattaggaca cagacaggca
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cagagcgatg accatgtgaa gacacaggga agagatggcc acctaccacc acgccatggt
120
cacctaccat ccaagccatg gtcaccttca ccaagccaca gtcatctacc atccaagcca
180
ccgtcaccta ccatccaagc catggccacc tacctgccaa gccatggcca cctacccgcc
240
aagccatggt cacctaccca ccaagtcatg gtcgcctacc atccaaggag caggcctgga
300
acagatcctt ccccagagcc ctcagtagga gccaaccctg ctgacacctt gatctcagac
360
ttcaagcctc cagaactgtg ggacaatcct tcactgtcat ttaatccacc cagcatgtgg
420
tctcttgtca cagttgcatt agccagtgaa cctacccggg cccttctgca gtcgcctggc
480
tcaggagtgg ttctggtcag gaagttctga ggccaggcag gatcgggaca ctccctggaa
540
agacccgagg gagatatttg ggaaacaaga tgg
573

<210> 4316
<211> 169
<212> PRT
<213> Homo sapiens

<400> 4316
Xaa Leu Ile Gln Tyr Asp Trp Cys Pro Tyr Lys Lys Arg Lys Leu Gly
1 5 10 15
His Arg Gln Ala Gln Ser Asp Asp His Val Lys Thr Gln Gly Arg Asp
20 25 30
Gly His Leu Pro Pro Arg His Gly His Leu Pro Ser Lys Pro Trp Ser
35 40 45
Pro Ser Pro Ser His Ser His Leu Pro Ser Lys Pro Pro Ser Pro Thr
50 55 60
Ile Gln Ala Met Ala Thr Tyr Leu Pro Ser His Gly His Leu Pro Ala
65 70 75 80
Lys Pro Trp Ser Pro Thr His Gln Val Met Val Ala Tyr His Pro Arg
85 90 95
Ser Arg Pro Gly Thr Asp Pro Ser Pro Glu Pro Ser Val Gly Ala Asn
100 105 110
Pro Ala Asp Thr Leu Ile Ser Asp Phe Lys Pro Pro Glu Leu Trp Asp
115 120 125
Asn Pro Ser Leu Ser Phe Asn Pro Pro Ser Met Trp Ser Leu Val Thr
130 135 140
Val Ala Leu Ala Ser Glu Pro Thr Arg Ala Leu Leu Gln Ser Pro Gly
145 150 155 160
Ser Gly Val Val Leu Val Arg Lys Phe
165

<210> 4317
<211> 744
<212> DNA
<213> Homo sapiens

<400> 4317
nntgaagaga agtcaaaaaa ctcatgacct gtcagagatt tggggtccat ttcaggatca
60
tcccatgccg aaaacatact ccagatattt aatgaatttc gtgatagccg cttattcaca
120
gatgttatca tttgggtgga aggaaaagaa tttccttgcc atagagctgt gctctcagcc
180
tgtagcagct acttcagagc tatgttttgt aatgaccaca gggaaagccg agaaatgttg
240
gttgagatca atggtatttt agctgaagct atggaatgtt ttttgcagta tgtttatact
300
ggaaaggtga agatcactac agagaatgta cagtatctct ttgagacatc aagcctcttt
360
cagattagtg ttctccgtga tgcatgtgcc aagttcttgg aggagcaact tgatccttgt
420
aattgcttag gaatccagcg ctttgctgat acccattcac tcaaaacact cttcacaaaa
480
tgcaaaaatt ttgcgttaca gacttttgag gatgtatccc agcacgaaga atttcttgag
540

cttgacaaag atgaacttat tgattatatt tgtagtgatg aacttgttat tggtaaagag
600
gagatggttt ttgaagccgt catgcgttgg gtctatcgtg ccgttgatct gagaagacca
660
ctgttacacg agctcctgac acatgtgaga ctcccctctgt tgcatcccaa ctactttgtt
720
caaacagttg aagtggacca attg
744

<210> 4318
<211> 239
<212> PRT
<213> Homo sapiens

<400> 4318
Pro Val Arg Asp Leu Gly Ser Ile Ser Gly Ser Ser His Ala Glu Asn
1 5 10 15
Ile Leu Gln Ile Phe Asn Glu Phe Arg Asp Ser Arg Leu Phe Thr Asp
20 25 30
Val Ile Ile Trp Val Glu Gly Lys Glu Phe Pro Cys His Arg Ala Val
35 40 45
Leu Ser Ala Cys Ser Ser Tyr Phe Arg Ala Met Phe Cys Asn Asp His
50 55 60
Arg Glu Ser Arg Glu Met Leu Val Glu Ile Asn Gly Ile Leu Ala Glu
65 70 75 80
Ala Met Glu Cys Phe Leu Gln Tyr Val Tyr Thr Gly Lys Val Lys Ile
85 90 95
Thr Thr Glu Asn Val Gln Tyr Leu Phe Glu Thr Ser Ser Leu Phe Gln
100 105 110
Ile Ser Val Leu Arg Asp Ala Cys Ala Lys Phe Leu Glu Glu Gln Leu
115 120 125
Asp Pro Cys Asn Cys Leu Gly Ile Gln Arg Phe Ala Asp Thr His Ser
130 135 140
Leu Lys Thr Leu Phe Thr Lys Cys Lys Asn Phe Ala Leu Gln Thr Phe
145 150 155 160
Glu Asp Val Ser Gln His Glu Glu Phe Leu Glu Leu Asp Lys Asp Glu
165 170 175
Leu Ile Asp Tyr Ile Cys Ser Asp Glu Leu Val Ile Gly Lys Glu Glu
180 185 190
Met Val Phe Glu Ala Val Met Arg Trp Val Tyr Arg Ala Val Asp Leu
195 200 205
Arg Arg Pro Leu Leu His Glu Leu Leu Thr His Val Arg Leu Pro Leu
210 215 220
Leu His Pro Asn Tyr Phe Val Gln Thr Val Glu Val Asp Gln Leu
225 230 235

<210> 4319
<211> 388
<212> DNA
<213> Homo sapiens

<400> 4319
nccatggaga aaagtattga tgctgtgatt gcaactgcct ctgcaccacc ttcttccagt
60

ccaggccgta gccacagcaa ggaccgaacc ctgggaaaac cagacagcct tttagtgcct
120
gcagtcgcaa gtgactcttg caataatagc atctcactcc tatctgaaaa gttgacaagc
180
agctgttccc cccatcatat caagagaagt gtagtggaag ctatgcaacg ccaagctcgg
240
aaaatgtgca attacgacaa aatcttggcc acaaagaaaa acctagacca tgtcaataaa
300
atcttaaaag ccaaaaaact tcaaaggcag gccaggacag ggaataactt tgtgaaacgt
360
aggccaggtc gaccgcggtc ggagagag
388

<210> 4320
<211> 129
<212> PRT
<213> Homo sapiens

<400> 4320
Xaa Met Glu Lys Ser Ile Asp Ala Val Ile Ala Thr Ala Ser Ala Pro
1 5 10 15
Pro Ser Ser Ser Pro Gly Arg Ser His Ser Lys Asp Arg Thr Leu Gly
20 25 30
Lys Pro Asp Ser Leu Leu Val Pro Ala Val Ala Ser Asp Ser Cys Asn
35 40 45
Asn Ser Ile Ser Leu Leu Ser Glu Lys Leu Thr Ser Ser Cys Ser Pro
50 55 60
His His Ile Lys Arg Ser Val Val Glu Ala Met Gln Arg Gln Ala Arg
65 70 75 80
Lys Met Cys Asn Tyr Asp Lys Ile Leu Ala Thr Lys Lys Asn Leu Asp
85 90 95
His Val Asn Lys Ile Leu Lys Ala Lys Lys Leu Gln Arg Gln Ala Arg
100 105 110
Thr Gly Asn Asn Phe Val Lys Arg Arg Pro Gly Arg Pro Arg Ser Glu
115 120 125
Arg

<210> 4321
<211> 278
<212> DNA
<213> Homo sapiens

<400> 4321
ngcccagaac ctgccacagt cccctgagaa caccgacctg caggttattc caggcagcca
60
gaccaggctc cttggtgaga agaccaccac agcggcaggg tccagccaca gcaggcccgg
120
cgtcccggtg gaaggcagcc ctgggcggaa cccaggcgtt taacggctca ctaggcagcc
180
ccagatctgg ggaacagatg agcacgtggg gagctggagt gagctgagca gaagttttgt
240
gcccgcctgc ccccatcccc tccaggccac gttttaga
278

<210> 4322
<211> 85
<212> PRT
<213> Homo sapiens

<400> 4322
Met Gly Ala Gly Gly His Lys Thr Ser Ala Gln Leu Thr Pro Ala Pro
1 5 10 15
His Val Leu Ile Cys Ser Pro Asp Leu Gly Leu Pro Ser Glu Pro Leu
20 25 30
Asn Ala Trp Val Pro Pro Arg Ala Ala Phe His Arg Asp Ala Gly Pro
35 40 45
Ala Val Ala Gly Pro Cys Arg Cys Gly Gly Leu Leu Thr Lys Glu Pro
50 55 60
Gly Leu Ala Ala Trp Asn Asn Leu Gln Val Gly Val Leu Arg Gly Leu
65 70 75 80
Trp Gln Val Leu Gly
85

<210> 4323
<211> 1542
<212> DNA
<213> Homo sapiens

<400> 4323
ngttacagta aagatggagc aaagtccttg aaaggagatg tgcctgcctc tgaggtgaca
60
ctgaaagact cgacattcag ccagtttagc ccgatctcca gtgctgaaga gtttgatgac
120
gacgagaaga ttgaggtgga tgacccccct gacaaggagg acatgcgatc aagcttcagg
180
tcgaatgtgt tgacggggtc ggctccccag caggactacg ataagctgaa ggcactcgga
240
ggggaaaact ccagcaaaac tggactctct acgtcaggca atgtggagaa aaacaaagct
300
gttaagagag aaacagaagc cagttctata aacctgagtg tttatgaacc ttttaaagtc
360
agaaaagcag aggataaatt gaaggaaagc tctgacaagg tgctggaaaa cagagtccta
420
gatgggaagc tgagctccga gaagaatgac accagcctcc ccagcgttgc gccatcaaag
480
acaaagtcgt cctccaagct ctcgtcctgc atcgctgcca tcgcggctct cagcgctaaa
540
aaggcggctt cagactcctg caaagaacca gtggccaatt cgagggaatc ctccccgtta
600
ccaaaagaag taaatgacag tccgagagcc gctgacaagt ctcctgaatc ccagaatctc
660
atcgacggga ccaaaaaacc atccctgaag caaccggata gtcccagaag catctcaagt
720
gagaacagca gcaaaggatc cccgtcctct cccgcggggt ccacaccagc aatccccaaa
780
gtccgcataa aaaccattaa gacatcttct ggggaaatca agagaacagt gaccagggta
840

ttgccagaag tggatcttga ctctggaaag aaaccttccg agcagacagc gtccgtcatg
900
gcctctgtga catcccttct gtcgtctcca gcatcagccg ccgtcctttc ctctcccccc
960
agggcgcctc tccagtctgc ggtcgtgacc aatgcagttt cccctgcaga gctcaccccc
1020
aaacaggtca caatcaagcc tgtggctact gctttcctcc cagtgtctgc tgtgaagacg
1080
gcaggatccc aagtcattaa tttgaagctc gctaacaaca ccacggtgaa agccacggtc
1140
atatctgctg cctctgtcca gagtgccagc agcgccatca ttaaagctgc caacgccatc
1200
cagcagcaaa ctgtcgtggt gccggcatcc agcctggcca atgccaaact cgtgccaaag
1260
actgtgcacc ttgccaacct taacctttg cctcagggtg cccaggccac ctctgaactc
1320
cgccaagtgc taaccaaacc tcagcaacaa ataaagcagg caataatcaa tgcagcagcc
1380
tcgcaacccc ccaaaaaggt gtctcgagtc caggtggtgt cgtccttgca gagttctgtg
1440
gtggaagctt tcaacaaggt gctgagcagt gtcaatccag tccctgttta catcccaaac
1500
ctcagtcctc ccgccaatgc agggatcacg ttaccgacgc gt
1542

<210> 4324
<211> 514
<212> PRT
<213> Homo sapiens

<400> 4324
Xaa Tyr Ser Lys Asp Gly Ala Lys Ser Leu Lys Gly Asp Val Pro Ala
 1   5   10   15
Ser Glu Val Thr Leu Lys Asp Ser Thr Phe Ser Gln Phe Ser Pro Ile
            20   25   30
Ser Ser Ala Glu Glu Phe Asp Asp Asp Glu Lys Ile Glu Val Asp Asp
        35   40   45
Pro Pro Asp Lys Glu Asp Met Arg Ser Ser Phe Arg Ser Asn Val Leu
    50   55   60
Thr Gly Ser Ala Pro Gln Gln Asp Tyr Asp Lys Leu Lys Ala Leu Gly
65   70   75   80
Gly Glu Asn Ser Ser Lys Thr Gly Leu Ser Thr Ser Gly Asn Val Glu
                85   90   95
Lys Asn Lys Ala Val Lys Arg Glu Thr Glu Ala Ser Ser Ile Asn Leu
            100   105   110
Ser Val Tyr Glu Pro Phe Lys Val Arg Lys Ala Glu Asp Lys Leu Lys
        115   120   125
Glu Ser Ser Asp Lys Val Leu Glu Asn Arg Val Leu Asp Gly Lys Leu
    130   135   140
Ser Ser Glu Lys Asn Asp Thr Ser Leu Pro Ser Val Ala Pro Ser Lys
145   150   155   160
Thr Lys Ser Ser Ser Lys Leu Ser Ser Cys Ile Ala Ala Ile Ala Ala
                165   170   175
Leu Ser Ala Lys Lys Ala Ala Ser Asp Ser Cys Lys Glu Pro Val Ala

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            180                 185                 190
Asn Ser Arg Glu Ser Ser Pro Leu Pro Lys Glu Val Asn Asp Ser Pro
        195                 200                 205
Arg Ala Ala Asp Lys Ser Pro Glu Ser Gln Asn Leu Ile Asp Gly Thr
    210                 215                 220
Lys Lys Pro Ser Leu Lys Gln Pro Asp Ser Pro Arg Ser Ile Ser Ser
225                 230                 235                 240
Glu Asn Ser Ser Lys Gly Ser Pro Ser Ser Pro Ala Gly Ser Thr Pro
                245                 250                 255
Ala Ile Pro Lys Val Arg Ile Lys Thr Ile Lys Thr Ser Ser Gly Glu
            260                 265                 270
Ile Lys Arg Thr Val Thr Arg Val Leu Pro Glu Val Asp Leu Asp Ser
        275                 280                 285
Gly Lys Lys Pro Ser Glu Gln Thr Ala Ser Val Met Ala Ser Val Thr
    290                 295                 300
Ser Leu Leu Ser Ser Pro Ala Ser Ala Ala Val Leu Ser Ser Pro Pro
305                 310                 315                 320
Arg Ala Pro Leu Gln Ser Ala Val Val Thr Asn Ala Val Ser Pro Ala
                325                 330                 335
Glu Leu Thr Pro Lys Gln Val Thr Ile Lys Pro Val Ala Thr Ala Phe
            340                 345                 350
Leu Pro Val Ser Ala Val Lys Thr Ala Gly Ser Gln Val Ile Asn Leu
        355                 360                 365
Lys Leu Ala Asn Asn Thr Thr Val Lys Ala Thr Val Ile Ser Ala Ala
    370                 375                 380
Ser Val Gln Ser Ala Ser Ser Ala Ile Ile Lys Ala Ala Asn Ala Ile
385                 390                 395                 400
Gln Gln Gln Thr Val Val Val Pro Ala Ser Ser Leu Ala Asn Ala Lys
                405                 410                 415
Leu Val Pro Lys Thr Val His Leu Ala Asn Leu Asn Leu Leu Pro Gln
            420                 425                 430
Gly Ala Gln Ala Thr Ser Glu Leu Arg Gln Val Leu Thr Lys Pro Gln
        435                 440                 445
Gln Gln Ile Lys Gln Ala Ile Ile Asn Ala Ala Ala Ser Gln Pro Pro
    450                 455                 460
Lys Lys Val Ser Arg Val Gln Val Val Ser Ser Leu Gln Ser Ser Val
465                 470                 475                 480
Val Glu Ala Phe Asn Lys Val Leu Ser Ser Val Asn Pro Val Pro Val
                485                 490                 495
Tyr Ile Pro Asn Leu Ser Pro Pro Ala Asn Ala Gly Ile Thr Leu Pro
            500                 505                 510
Thr Arg
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<210> 4325
<211> 1405
<212> DNA
<213> Homo sapiens

<400> 4325
acgcgtgccc ggggtctgct gtgcagcgca gcccgttgtg gtgatacgag ccggagatgc
60
cttctgcagg gactgtttca aggccttcta cgtccacaag ttcatagcca tgctgggcaa
120

gaaccggctc atctttccag gcgagaaggt agcgtctggg tcctgggggt ctgactgagc
180
agcctggccc ctcgaggtcc ctgcttgtcc ctcccacagg cagcctggcc tgctgcagcc
240
cgccagctcc tccttggcct ttgaggacag actcgatgtc ctagatgtcc acgaggtggg
300
gtgtctgcct gtgttggagg tgcggtgccc tgagtgatgt tttttctccc ccaggtgctc
360
ttggcgtggt ctgggggggcc ttcgtccagc tccatggtct ggcaggttct tgagggcctg
420
agccaagatt ctgccaaaag actgcgcttt gtggcaggag tcatctttgt tgacgaggga
480
gcagcctgtg gccagagcct agaggagaga tcaaagaccc tggccgaagt gaagcccatt
540
ctgcaagcaa ctgggttccc atggcatgtg gtggccttag aggaggtgtt cagcctgcca
600
ccgtcggtgc tttggtgctc tgcccaggag ctggtgggat ccgaggggggc ctacaaggcg
660
gccgtggaca gcttcctcca gcagcagtat gtgctggggg ccgggggtgg tcctggcccg
720
actcaagggg aggaacagcc accccagccc ccgctggacc cccagaacct ggcaagaccg
780
cctgcccctg cccagactga ggctctttcc caactgttct gctcagtgag gacactgact
840
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900
cacggctact ccaaggtcat gactggggac agctgcacac gcttggctat caagctcatg
960
accaacctgg cgctgggtcg aggggccttc ctggcctggg atacgggctt ctcggatgag
1020
cggcacgggg acgtggtggt ggtgcggccc atgcgggacc acaccctgaa ggaggtcgct
1080
ttctacaacc gcctgttctc cgttccttct gtcttcacac cagccgtcga caccaaggcc
1140
cctgaaaagg ccagcatcca ccggctgatg gaggccttca tcctcaggct gcagacccag
1200
ttcccctcca ctgtcagcac tgtgtacagg tgtgtgtggg tgtgtgcggg gggtgcgcgg
1260
gtgtgtgctg tgtgcgggtg tgtgcgggtg gtgagctcac cactcgtgct caggccaggg
1320
cttagggtgg agccccagcc cgtgtgattc acctgctcct cccacaatcc ggccacagga
1380
caagtgagaa gcttgtgaag ggccc
1405

<210> 4326
<211> 336
<212> PRT
<213> Homo sapiens

<400> 4326
Met Phe Phe Leu Pro Gln Val Leu Leu Ala Trp Ser Gly Gly Pro Ser
1 5 10 15
Ser Ser Ser Met Val Trp Gln Val Leu Glu Gly Leu Ser Gln Asp Ser

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            20                  25                  30
Ala Lys Arg Leu Arg Phe Val Ala Gly Val Ile Phe Val Asp Glu Gly
        35                  40                  45
Ala Ala Cys Gly Gln Ser Leu Glu Glu Arg Ser Lys Thr Leu Ala Glu
    50                  55                  60
Val Lys Pro Ile Leu Gln Ala Thr Gly Phe Pro Trp His Val Val Ala
65                  70                  75                  80
Leu Glu Glu Val Phe Ser Leu Pro Pro Ser Val Leu Trp Cys Ser Ala
                85                  90                  95
Gln Glu Leu Val Gly Ser Glu Gly Ala Tyr Lys Ala Ala Val Asp Ser
            100                 105                 110
Phe Leu Gln Gln Gln Tyr Val Leu Gly Ala Gly Gly Gly Pro Gly Pro
        115                 120                 125
Thr Gln Gly Glu Glu Gln Pro Pro Gln Pro Pro Leu Asp Pro Gln Asn
    130                 135                 140
Leu Ala Arg Pro Pro Ala Pro Ala Gln Thr Glu Ala Leu Ser Gln Leu
145                 150                 155                 160
Phe Cys Ser Val Arg Thr Leu Thr Ala Lys Glu Glu Leu Leu Gln Thr
                165                 170                 175
Leu Arg Thr His Leu Ile Leu His Met Ala Arg Ala His Gly Tyr Ser
            180                 185                 190
Lys Val Met Thr Gly Asp Ser Cys Thr Arg Leu Ala Ile Lys Leu Met
        195                 200                 205
Thr Asn Leu Ala Leu Gly Arg Gly Ala Phe Leu Ala Trp Asp Thr Gly
    210                 215                 220
Phe Ser Asp Glu Arg His Gly Asp Val Val Val Val Arg Pro Met Arg
225                 230                 235                 240
Asp His Thr Leu Lys Glu Val Ala Phe Tyr Asn Arg Leu Phe Ser Val
                245                 250                 255
Pro Ser Val Phe Thr Pro Ala Val Asp Thr Lys Ala Pro Glu Lys Ala
            260                 265                 270
Ser Ile His Arg Leu Met Glu Ala Phe Ile Leu Arg Leu Gln Thr Gln
        275                 280                 285
Phe Pro Ser Thr Val Ser Thr Val Tyr Arg Cys Val Trp Val Cys Ala
    290                 295                 300
Gly Gly Ala Arg Val Cys Ala Val Cys Gly Cys Val Arg Val Val Ser
305                 310                 315                 320
Ser Pro Leu Val Leu Arg Pro Gly Leu Arg Val Glu Pro Gln Pro Val
                325                 330                 335
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<210> 4327
<211> 551
<212> DNA
<213> Homo sapiens

<400> 4327
tggccacagg cagagccgcc tctgcaggtg acacccaccc caggccgtgc accccacctc
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caccctcgca ggccacccag acggcagctt ggggaaacct gggaggtccc gtaccctcac
120
tgtgcaggtg gggaaattta gaccctgaaa aagggatgcc ctgagatcac catgagattg
180
aggggcaagc agggctcacc ctgactggct cacttcccag gcacccccat gagcccaggc
240

accgcctgcc accctcactc tccaggaaga gccaccgcgt ggtggccggg atcgtgtggt
300
ggccagggcg tctgaccttg gctctcaccc ggaggccatc caggtgctga ggatggctaa
360
cgctaaggcc acacagccag ggagaggagg tggctcgtga caccacgatg ggacacaccc
420
acctctggga gaggagggtg actccgacag cccttgcctg ccaggatgga gcctggactc
480
tggagggcat cgtgtcctgg agcagcacca gcacctcctg ttgtcaccag gcgtggatgc
540
ccgcatcatg a
551

<210> 4328
<211> 107
<212> PRT
<213> Homo sapiens

<400> 4328
Met Pro Ser Arg Val Gln Ala Pro Ser Trp Gln Ala Arg Ala Val Gly
1 5 10 15
Val Thr Leu Leu Ser Gln Arg Trp Val Cys Pro Ile Val Val Ser Arg
20 25 30
Ala Thr Ser Ser Pro Trp Leu Cys Gly Leu Ser Val Ser His Pro Gln
35 40 45
His Leu Asp Gly Leu Arg Val Arg Ala Lys Val Arg Arg Pro Gly His
50 55 60
His Thr Ile Pro Ala Thr Thr Arg Trp Leu Phe Leu Glu Ser Glu Gly
65 70 75 80
Gly Arg Arg Cys Leu Gly Ser Trp Gly Cys Leu Gly Ser Glu Pro Val
85 90 95
Arg Val Ser Pro Ala Cys Pro Ser Ile Ser Trp
100 105

<210> 4329
<211> 3192
<212> DNA
<213> Homo sapiens

<400> 4329
cttaagactt tcaaagccca ataaaaatat atccaggagg gccagctaca atgagcccaa
60
gccagaggtc acctacatca gccagaaaat ctatgacctc tcagacagca agatttatct
120
tgtacctaaa actttggctc gaaagcgaat ctggaataaa aagtacccca tttgtatcga
180
gcttggtcag caagatgact ttatgtctaa agctcagact gataaggaga cttcagaaga
240
gaagccgcca gctggaggaa gggaggaccc ttagaagcca ccccgccctc aggaggaaca
300
agatctagcc agcgagatca gatactctat ctctttggga gaactggccg agaaaaagag
360
gaatggttta ggagatttat tctggcatct aagctaaagt cggaaatcaa gaagtcatcg
420

ggtgtctctg gaggtaaacc agggcttttg cctgcacaca gcagacacaa cagtccgtcc
480
gggcacctga cccacagccg cagcagcagc aaaggcagtg tggaggagat catgtcacag
540
ccaaagcaga aggagctggc aggcagcgtg cggcagaaga tgcttctcga ctacagcgtg
600
tacatgggca ggtgtgtccc ccaggaaagc cgaagccccc agaggagccc cctgcagagt
660
gcggagagca gccccacagc tgggaagaag ttgccagagg ttccaccctc tgaggaggaa
720
gaacaggaag cctgggtgaa tgccttgctt ggaagaatat tttgggactt cttaggagag
780
aaatactggt ctgatctggt gtctaagaag atccaaatga aactcagcaa aataaagctc
840
ccctacttta tgaatgagct cactctgacg gaacttgaca tgggcgtggc tgtgccaaaa
900
atcctccagg ccttcaagcc ttacgttgat caccaaggac tctggattga tttggaaatg
960
tcctacaatg ggtcctttct gatgactctc gagaccaaaa tgaatttgcc taaactaggt
1020
aaagagcctc ttgttgaagc cctgaaggtt ggagaaattg gcaaagaagg ttgcaggccc
1080
cgggcattct gtctggcgga cagcgatgag gaatcctcca gcgctggctc ctccgaggaa
1140
gacgatgccc cagagcccgc gggggagaca aacagctcct cccaggggga agggtacgtt
1200
ggaggtcatc gaacaagtaa gattatgagg tttgttgata aaattaccaa gtcaaaatat
1260
ttccaaaaag caacagagac agagtttata aaaaganaga tcgaagaagt ctccaacaca
1320
cccctgctgc tcactgttga agtacaagaa tgtagaggaa ccttggcggt caacattcca
1380
ccacccccga ctgaccgagt atggtatggt ttccgaaagc caccacatgt ggagctgaaa
1440
gctcggccaa aacttggaga gagagaagtg actttagttc atgtgacaga ctggatagag
1500
aagaaactgg agcaagagtt tcagaaagtt tttgtcatgc caaacatgga tgatgtttat
1560
atcactataa tgcactcagc catggaccct cgctctactt cctgcctcct gaaagaccca
1620
cctgtggagg ctgctgatcg gccatgatgg gtgatgtcag atgttcccca tattgtgaca
1680
tcgagctgga tgtgtggggt tcttggccgc catctgtact gtagcactgg cctctgtgcc
1740
acagctactg tttcttaaag gactgcttct gccctctgcc tgccagtgcc cattccactg
1800
tgaggtgtca ttccctgcat ctagtgacaa ctgtctggat tgcctgctgc aaagctttga
1860
tttggcaaag gagaccatgg aagaatcatg gtggatccag aagttatacg tgacccacac
1920
catggctttt aaaagtctac ccatgtttgt ggcagcaaat gagcacagta agagcaaagc
1980
tgaacaactt gcctcctcta ctcctccaaa gcttttcttc aggcagccgg tgcacagtgg
2040

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acttttttcac ttctatactt tgtatgcggc cttccacact tccagagaat gtcagtgtgc
2100
aatgtgtctg gagggtgggg agaggaattc tgtgagcctt ttcatttcgg tgacagaaga
2160
gatgggcaga gcaacttatt ttccacatta aattgtgcat ttgggaagca agtagccata
2220
gtacacacac aacacgctat cagcttgggt aaggacagtg ggatttatgt gaacatcagg
2280
caaagccatg agatcaaacc atcccaagcc tttcaccaat gaggtacaac cacctggggg
2340
ctagctaatc ttgaatgttt tcctgagaca ggagcgtatg tgaaaacatc aaacactgca
2400
catgacagga tgggtcctct catacagatg ggatggggtt agaaagccag agccagtttt
2460
tccatctggc gtttcctgtg tcctccaggt ttatatggga atcgaaacag tttgttaatc
2520
tgattgggag agttccatgg gcagatttcc cttcctgaag gccaaaacgg agaactgctc
2580
tctttaatta tttcaagagt caagaccaaa agtttgctca gcatcacact acatctcaaa
2640
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2700
gggctctctt tgcttcgaga agtaaaccta ataccatttt tttattgttt aaagctgcat
2760
tcaacgtcaa aattaccttg ggtaactttt gataacttac atgtgtggac aaagctaata
2820
gtggtttttt aaacagcacc ttgcctgaac atgactttaa agaaattaat atattgaaaa
2880
catgtttgaa cccttatttt aattgcacca ttaaaacatt tgacttaaat tgtttgacca
2940
ttccagttgg tgtactgttc tgatttttcg ttgtgtaggc cgatctgcct gtcagagtcc
3000
acgtgtcctg gtcactggtc tttataattg ttgtgcaata actaaaggct aaggactaga
3060
tgcactatcg tgtaaagaga ttacacatga ctgtaccatg ttgcacttaa tcaaatagta
3120
tgtggggatt taaaatcgct tgcattgttt cacaaaataa atatctcaat gtcaaatact
3180
aaaaaaaaaa aa
3192

<210> 4330
<211> 371
<212> PRT
<213> Homo sapiens

<400> 4330
Met Ser Gln Pro Lys Gln Lys Glu Leu Ala Gly Ser Val Arg Gln Lys
 1               5                  10                  15
Met Leu Leu Asp Tyr Ser Val Tyr Met Gly Arg Cys Val Pro Gln Glu
            20                  25                  30
Ser Arg Ser Pro Gln Arg Ser Pro Leu Gln Ser Ala Glu Ser Ser Pro
        35                  40                  45
Thr Ala Gly Lys Lys Leu Pro Glu Val Pro Pro Ser Glu Glu Glu Glu
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    50                  55                  60
Gln Glu Ala Trp Val Asn Ala Leu Leu Gly Arg Ile Phe Trp Asp Phe
65                  70                  75                  80
Leu Gly Glu Lys Tyr Trp Ser Asp Leu Val Ser Lys Lys Ile Gln Met
                85                  90                  95
Lys Leu Ser Lys Ile Lys Leu Pro Tyr Phe Met Asn Glu Leu Thr Leu
            100                 105                 110
Thr Glu Leu Asp Met Gly Val Ala Val Pro Lys Ile Leu Gln Ala Phe
        115                 120                 125
Lys Pro Tyr Val Asp His Gln Gly Leu Trp Ile Asp Leu Glu Met Ser
    130                 135                 140
Tyr Asn Gly Ser Phe Leu Met Thr Leu Glu Thr Lys Met Asn Leu Pro
145                 150                 155                 160
Lys Leu Gly Lys Glu Pro Leu Val Glu Ala Leu Lys Val Gly Glu Ile
                165                 170                 175
Gly Lys Glu Gly Cys Arg Pro Arg Ala Phe Cys Leu Ala Asp Ser Asp
            180                 185                 190
Glu Glu Ser Ser Ser Ala Gly Ser Ser Glu Glu Asp Asp Ala Pro Glu
        195                 200                 205
Pro Ala Gly Glu Thr Asn Ser Ser Ser Gln Gly Glu Gly Tyr Val Gly
    210                 215                 220
Gly His Arg Thr Ser Lys Ile Met Arg Phe Val Asp Lys Ile Thr Lys
225                 230                 235                 240
Ser Lys Tyr Phe Gln Lys Ala Thr Glu Thr Glu Phe Ile Lys Arg Xaa
                245                 250                 255
Ile Glu Glu Val Ser Asn Thr Pro Leu Leu Leu Thr Val Glu Val Gln
            260                 265                 270
Glu Cys Arg Gly Thr Leu Ala Val Asn Ile Pro Pro Pro Pro Thr Asp
        275                 280                 285
Arg Val Trp Tyr Gly Phe Arg Lys Pro Pro His Val Glu Leu Lys Ala
    290                 295                 300
Arg Pro Lys Leu Gly Glu Arg Glu Val Thr Leu Val His Val Thr Asp
305                 310                 315                 320
Trp Ile Glu Lys Lys Leu Glu Gln Glu Phe Gln Lys Val Phe Val Met
                325                 330                 335
Pro Asn Met Asp Asp Val Tyr Ile Thr Ile Met His Ser Ala Met Asp
            340                 345                 350
Pro Arg Ser Thr Ser Cys Leu Leu Lys Asp Pro Pro Val Glu Ala Ala
        355                 360                 365
Asp Arg Pro
    370
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<210> 4331
<211> 1355
<212> DNA
<213> Homo sapiens

<400> 4331
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60
ttaaaagatg gcagtttatt ttggcagtca ccaaagaggc caccctctcc aataaaattt
120
gatttaaatg agcctttgca cctcagtttc cttcagaatg ctgcaaaact atatgctaca
180

gtatattgta ttccatttgc agaagaggac ttatcagcag atgccctctt gaatattctt
240
tcagaagtaa agattcagga attcaagcct tccaataagg ttgttcaaac agatgaaact
300
gcaaggaaac cagaccatgt tcctattagc agtgaagatg agaggaatgc aattttccaa
360
ctagaaaagg ctattttatc taatgaagcc accaaaagtg accttcagat ggcagtgctt
420
tcatttgaaa aagatgatga tcataatgga cacatagatt tcatcacagc tgcatcaaat
480
cttcgtgcca aaatgtacag cattgaacca gctgaccgtt tcaaaacaaa gcgcatagct
540
ggtaaaatta tacctgctat agcaacaacc actgctacag tttctggctt ggttgccttg
600
gagatgatca aagtaactgg tggctatcca tttgaagctt acaaaaattg ttttcttaac
660
ttagccattc caattgtagt atttacagag acaactgaag taaggaaaac taaaatcaga
720
aatggaatat catttacaat ttgggatcga tggaccgtac atggaaaaga agatttcacc
780
ctcttggatt tcataaatgc agtcaaagag aagtatggaa ttgagccaac aatggtggta
840
cagggagtca aaatgcttta tgttcctgta atgcctggtc atgcaaaaag attgaagtta
900
acaatgcata aacttgtaaa acctactact gaaaagaaat atgtggatct tactgtgtca
960
tttgctccag acattgatgg agatgaagat ttgccgggac ctccagtaag atactacttc
1020
agtcatgaca ctgattaata caagttgtct taacgttact ccaggaccac ttgattttgg
1080
aaagagtgca cttaattcag aagctaaaga aaatcagttc ataatactat ggatttctct
1140
ttcattaagc cttaatttta agggaaacat cagtaagaaa ctgcactgaa gaattataaa
1200
acattttggg gcatagcata cacttgtcta acggttcaca cgtggctatg atcacaagca
1260
actttgaact ggaatgctat ttataaaagt tttgtgtatt aatctgtgta ttaatctctc
1320
tggataaaaa gaaggaaaaa atatgtatga ccggt
1355

<210> 4332
<211> 345
<212> PRT
<213> Homo sapiens

<400> 4332
Glu Lys Tyr Phe Asn His Lys Ala Leu Gln Leu Leu His Cys Phe Pro
1 5 10 15
Leu Asp Ile Arg Leu Lys Asp Gly Ser Leu Phe Trp Gln Ser Pro Lys
20 25 30
Arg Pro Pro Ser Pro Ile Lys Phe Asp Leu Asn Glu Pro Leu His Leu
35 40 45
Ser Phe Leu Gln Asn Ala Ala Lys Leu Tyr Ala Thr Val Tyr Cys Ile

```
    50                  55                  60
Pro Phe Ala Glu Glu Asp Leu Ser Ala Asp Ala Leu Leu Asn Ile Leu
65                  70                  75                  80
Ser Glu Val Lys Ile Gln Glu Phe Lys Pro Ser Asn Lys Val Val Gln
                85                  90                  95
Thr Asp Glu Thr Ala Arg Lys Pro Asp His Val Pro Ile Ser Ser Glu
            100                 105                 110
Asp Glu Arg Asn Ala Ile Phe Gln Leu Glu Lys Ala Ile Leu Ser Asn
        115                 120                 125
Glu Ala Thr Lys Ser Asp Leu Gln Met Ala Val Leu Ser Phe Glu Lys
    130                 135                 140
Asp Asp Asp His Asn Gly His Ile Asp Phe Ile Thr Ala Ala Ser Asn
145                 150                 155                 160
Leu Arg Ala Lys Met Tyr Ser Ile Glu Pro Ala Asp Arg Phe Lys Thr
                165                 170                 175
Lys Arg Ile Ala Gly Lys Ile Ile Pro Ala Ile Ala Thr Thr Thr Ala
            180                 185                 190
Thr Val Ser Gly Leu Val Ala Leu Glu Met Ile Lys Val Thr Gly Gly
        195                 200                 205
Tyr Pro Phe Glu Ala Tyr Lys Asn Cys Phe Leu Asn Leu Ala Ile Pro
    210                 215                 220
Ile Val Val Phe Thr Glu Thr Thr Glu Val Arg Lys Thr Lys Ile Arg
225                 230                 235                 240
Asn Gly Ile Ser Phe Thr Ile Trp Asp Arg Trp Thr Val His Gly Lys
                245                 250                 255
Glu Asp Phe Thr Leu Leu Asp Phe Ile Asn Ala Val Lys Glu Lys Tyr
            260                 265                 270
Gly Ile Glu Pro Thr Met Val Val Gln Gly Val Lys Met Leu Tyr Val
        275                 280                 285
Pro Val Met Pro Gly His Ala Lys Arg Leu Lys Leu Thr Met His Lys
    290                 295                 300
Leu Val Lys Pro Thr Thr Glu Lys Lys Tyr Val Asp Leu Thr Val Ser
305                 310                 315                 320
Phe Ala Pro Asp Ile Asp Gly Asp Glu Asp Leu Pro Gly Pro Pro Val
                325                 330                 335
Arg Tyr Tyr Phe Ser His Asp Thr Asp
            340                 345
```

<210> 4333
<211> 1278
<212> DNA
<213> Homo sapiens

<400> 4333
cggccgcagc gccgtctgct cagcgcccgg gtcaatagga gccagtcctt cgcaggcgtc
60
ctcggcagcc acgagcgggg gcccaggagt ttcccggtct tcagcccgcc ggggccccca
120
cggaagcccc ccgcgctctc ccgagtgtcc aggatgtttt ccgtggctca cccagccgcc
180
aaggtgccgc agcccgagcg gctggacctg gtgtacacgg cgctgaagcg gggcctgacg
240
gcctacttgg aagtgcacca gcaggagcaa gagaaactcc aggggcagat aagggagtcc
300

aagaggaatt cccgcttggg cttcctgtat gatctggaca agcaagtcaa gtccattgaa
360
cgcttcctgc gacgactgga gttccatgcc agcaagatcg atgagctgta tgaggcatac
420
tgtgtccagc ggcgtctccg ggatggtgcc tacaacatgg tccgtgccta caccactggg
480
tccccgggaa gccgagaggc ccgggacagc ctggcagagg ccactcgggg gcatcgcgag
540
tacacggagg taggggatgg gggcccatga agcagaggca cagggtgtgg cagggctagt
600
ggctggccct tgacccccctc ctgtccctgc ccctccctcc caagcatgtg tctgctggag
660
agcgagctgg aggcacagct gggcgagttt catctccgaa tgaaagggct ggctggcttc
720
gccaggctgt gtgtaggcga tcagtatgag atctgcatga aatatgggcg tcagcgctgg
780
aaactacggg gccgaattga gggtagtgga aagcaggtgt gggacagtga agaaaccatc
840
tttctccctc tactcacgga atttctgtct attaaggtga cagaactgaa gggcctggcc
900
aaccatgtgg ttgtgggcag tgtctcctgt gagaccaagg acctgtttgc cgccctgccc
960
caggttgtgg ctgtggatat caatgacctt ggtaccatca agctcagcct ggaagtcaca
1020
tggagcccct tcgacaagga tgaccagccc tcagctgctt cttctgtcaa caaggcctcc
1080
acagtcacca agcgcttctc cacctatagc cagagcccac cggacacacc ctcacttcgg
1140
gaacaggctt tctataacat gctgcgacgg caggaggagc tggagaatgg gacagcatgg
1200
tccctgtcat ctgaatcttc agacgactca tccagcccac agctctcagg cactgcccgc
1260
cactcaccag cccctagg
1278

<210> 4334
<211> 189
<212> PRT
<213> Homo sapiens

<400> 4334
Arg Pro Gln Arg Arg Leu Leu Ser Ala Arg Val Asn Arg Ser Gln Ser
1 5 10 15
Phe Ala Gly Val Leu Gly Ser His Glu Arg Gly Pro Arg Ser Phe Pro
20 25 30
Val Phe Ser Pro Pro Gly Pro Pro Arg Lys Pro Pro Ala Leu Ser Arg
35 40 45
Val Ser Arg Met Phe Ser Val Ala His Pro Ala Ala Lys Val Pro Gln
50 55 60
Pro Glu Arg Leu Asp Leu Val Tyr Thr Ala Leu Lys Arg Gly Leu Thr
65 70 75 80
Ala Tyr Leu Glu Val His Gln Gln Glu Gln Glu Lys Leu Gln Gly Gln
85 90 95
Ile Arg Glu Ser Lys Arg Asn Ser Arg Leu Gly Phe Leu Tyr Asp Leu

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            100                 105                 110
Asp Lys Gln Val Lys Ser Ile Glu Arg Phe Leu Arg Arg Leu Glu Phe
        115                 120                 125
His Ala Ser Lys Ile Asp Glu Leu Tyr Glu Ala Tyr Cys Val Gln Arg
    130                 135                 140
Arg Leu Arg Asp Gly Ala Tyr Asn Met Val Arg Ala Tyr Thr Thr Gly
145                 150                 155                 160
Ser Pro Gly Ser Arg Glu Ala Arg Asp Ser Leu Ala Glu Ala Thr Arg
                165                 170                 175
Gly His Arg Glu Tyr Thr Glu Val Gly Asp Gly Gly Pro
            180                 185
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<210> 4335
<211> 1211
<212> DNA
<213> Homo sapiens

<400> 4335
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60
gatggggagg agtggctccc cccacttaaa acatttgtgc cctctgtatc cccattccag
120
ctggccttgg gtgcggcact cgtgaatgta cagatccccc tgctcctggg ccagctggta
180
gaggtcgtgg ccaagtacac aagggaccac gtagggagtt tcatgactga gtctcagaat
240
ctcagcaccc acctgcttat cctctatggt gtccagggac tgctgacctt cgggtacctg
300
gtgctgctgt cccacgttgg cgagcgcatg gctgtggaca tgcggagggc cctcttcagc
360
tccctgctcc gacaagacat caccttcttt gacgccaata agacagggca gctggtgagc
420
cgcttgacaa ctgacgtgca ggagtttaag tcatccttca agcttgtcat ctcccagggg
480
ctgcgaagct gcacccaggt ggcaggctgc ctggtgtccc tgtccatgct gtcgacacgc
540
ctcacgctgc tgctgatggt ggccacacca gccctgatgg gagtgggcac cctgatgggc
600
tcaggcctcc gaaaattgtc tcgccagtgt caggagcaga tcgccagggc aatgggcgta
660
gcagacgagg ccctgggcaa tgtgcggact gtgcgtgcct tcgccatgga gcaacgggaa
720
gaggagcgct atggggcaga gctggaagcc tgccgctgcc gggcagagga gctgggccgc
780
ggcatcgcct tgttccaagg gctttccaac atcgccttca actgcatggt cttgggtacc
840
ctatttattg ggggctccct tgtggccgga cagcagctga caggggggaga cctcatgtcc
900
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960
cttccgctgc aggctgtgac actccatgca tggaaggacc atccttgaca ggctgtgtga
1020
gctgcccttc cccatgcctg ccacttccag ggatgacaag ctgacccctg tccccacaca
1080

ccccaccctt atagcttatt gctttgcgtt ggtccaaaac cacccgctca gctgagcctc
1140
tgggatgacc agagctgatc accagacagc tcaaggcggg cctcccccca gaggctggag
1200
tgtgctcgcg a
1211

<210> 4336
<211> 325
<212> PRT
<213> Homo sapiens

<400> 4336
Trp Glu Arg Lys Gly Gln Asp Leu Ala Gly Asp Gly Glu Glu Trp Leu
1 5 10 15
Pro Pro Leu Lys Thr Phe Val Pro Ser Val Ser Pro Phe Gln Leu Ala
20 25 30
Leu Gly Ala Ala Leu Val Asn Val Gln Ile Pro Leu Leu Leu Gly Gln
35 40 45
Leu Val Glu Val Val Ala Lys Tyr Thr Arg Asp His Val Gly Ser Phe
50 55 60
Met Thr Glu Ser Gln Asn Leu Ser Thr His Leu Leu Ile Leu Tyr Gly
65 70 75 80
Val Gln Gly Leu Leu Thr Phe Gly Tyr Leu Val Leu Leu Ser His Val
85 90 95
Gly Glu Arg Met Ala Val Asp Met Arg Arg Ala Leu Phe Ser Ser Leu
100 105 110
Leu Arg Gln Asp Ile Thr Phe Phe Asp Ala Asn Lys Thr Gly Gln Leu
115 120 125
Val Ser Arg Leu Thr Thr Asp Val Gln Glu Phe Lys Ser Ser Phe Lys
130 135 140
Leu Val Ile Ser Gln Gly Leu Arg Ser Cys Thr Gln Val Ala Gly Cys
145 150 155 160
Leu Val Ser Leu Ser Met Leu Ser Thr Arg Leu Thr Leu Leu Leu Met
165 170 175
Val Ala Thr Pro Ala Leu Met Gly Val Gly Thr Leu Met Gly Ser Gly
180 185 190
Leu Arg Lys Leu Ser Arg Gln Cys Gln Glu Gln Ile Ala Arg Ala Met
195 200 205
Gly Val Ala Asp Glu Ala Leu Gly Asn Val Arg Thr Val Arg Ala Phe
210 215 220
Ala Met Glu Gln Arg Glu Glu Glu Arg Tyr Gly Ala Glu Leu Glu Ala
225 230 235 240
Cys Arg Cys Arg Ala Glu Glu Leu Gly Arg Gly Ile Ala Leu Phe Gln
245 250 255
Gly Leu Ser Asn Ile Ala Phe Asn Cys Met Val Leu Gly Thr Leu Phe
260 265 270
Ile Gly Gly Ser Leu Val Ala Gly Gln Gln Leu Thr Gly Gly Asp Leu
275 280 285
Met Ser Phe Leu Val Ala Ser Gln Thr Val Gln Ser Phe Leu Arg Val
290 295 300
Ala Pro Cys Pro Asn Ser Leu Pro Leu Gln Ala Val Thr Leu His Ala
305 310 315 320
Trp Lys Asp His Pro

325

<210> 4337
<211> 461
<212> DNA
<213> Homo sapiens

<400> 4337
tctattatgt tgtcctgatt acatatcagc aaaatgtttt tctggggcat tgtgcataaa
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acaaaggaga aaacaacatc tctagccggc cagcgtgcct gtccctccct cccgcagagg
120
cctgggaggc tgagggtgag gaaggccagc tgtgctggct gcagagggct ttgctgtttc
180
tccacagagc agcaggtcgc cccttccctt ctccctccct ccacctcacc tccatgggct
240
ccactggatg ggaaccatgt gcttgttctc cccaccccta gactgggatc tcctggggca
300
gaagaggctt cccaagtggc acagacagag ccaggctgac tgaatgtgag attcatgaat
360
gaacagtgat accaggcata gccctgccct ttagcatcct gagggccacg tggagttttc
420
tgcaacactg cccgccgtgt tccagcatct gccttccact t
461

<210> 4338
<211> 118
<212> PRT
<213> Homo sapiens

<400> 4338
Met Asn Leu Thr Phe Ser Gln Pro Gly Ser Val Cys Ala Thr Trp Glu
 1   5   10   15
Ala Ser Ser Ala Pro Gly Asp Pro Ser Leu Gly Val Gly Arg Thr Ser
            20   25   30
Thr Trp Phe Pro Ser Ser Gly Ala His Gly Gly Glu Val Glu Gly Gly
        35   40   45
Arg Arg Glu Gly Ala Thr Cys Cys Ser Val Glu Lys Gln Gln Ser Pro
    50   55   60
Leu Gln Pro Ala Gln Leu Ala Phe Leu Thr Leu Ser Leu Pro Gly Leu
65   70   75   80
Cys Gly Arg Glu Gly Gln Ala Arg Trp Pro Ala Arg Asp Val Val Phe
                85   90   95
Ser Phe Val Leu Cys Thr Met Pro Gln Lys Asn Ile Leu Leu Ile Cys
            100   105   110
Asn Gln Asp Asn Ile Ile
        115

<210> 4339
<211> 5269
<212> DNA
<213> Homo sapiens

<400> 4339

nnagccatgc ccacgaactt tacggtggtg cccgtggagg ctcacgccga cggcggcggg
60
gacgagactg ccgagcggac ggaggctccg ggcacccccg agggccccga gcccgagcgc
120
cccagcccgg gagatggaaa tccaagagaa aacagcccat tcctcaacaa tgtcgaggtg
180
gaacaagaga gcttctttga agggaagaac atggcacttt tcgaggagga gatggacagt
240
aaccccatgg tgtcctcgct gctcaacaag ctggccaact acaccaacct gagccagggc
300
gtggtggagc acgaggagga cgaggagagc cggcggcggg aggccaaggc tccgcgcatg
360
ggcaccttca tcggcgtcta cctgccgtgc ctgcagaaca tcctgggcgt catcctcttc
420
ctgcgcctga cgtggatcgt gggggtggct ggtgtcctgg agtccttcct catcgtggcc
480
atgtgctgca catgtacaat gctgaccgcc atttccatga gtgcgatcgc taccaacggt
540
gtggtcccag ctggcgggtc ctactacatg atatcgcgct cgctgggacc cgagtttgga
600
ggcgctgtcg gcctctgctt ctacctgggc acgacgtttg caggggccat gtatattttg
660
gggaccatcg agatttttct gacgtacatc tccccgggtg cggccatctt ccaggcggag
720
gctgcaggtg gcgaggcggc cgccatgctg cacaacatgc gtgtgtacgg cacgtgcacg
780
ctcgtgctca tggccctggt ggtcttcgtg ggcgtcaagt atgtcaacaa gctggcgctg
840
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900
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960
agcttcgatg cctgcgtcaa ggcctacggc atccacaaca actcagccac ctccgcgctc
1020
tggggcctct tctgcaacgg ctcccagccc agcgccgcct gtgacgagta cttcatccag
1080
aacaacgtca ccgaaatcca gggcatcccg ggcgcggcca gtggtgtctt cctggagaac
1140
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1200
cccgtggcag aggagagccg tgccagcgca ctgccctacg tgctcaccga catcgcggcc
1260
tccttcaccc tgctggttgg catctacttc ccttccgtga ccggtatcat ggcgggttca
1320
aaccggtccg gggacctcaa ggatgcacag aagtccatcc ccacggggac catcctggcc
1380
atagtgacga cgtctttcat ctatctctcc tgcattgtgc tgtttggggc ctgcattgaa
1440
ggcgtggtct tacgagataa gttcggggag gccctgcagg ggaacctggt catcggcatg
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1560
ggcctgcaga ccctcacggg ggcaccgcgc ctactgcagg ccattgcccg tgacggcatc
1620

gtccccttcc tgcaggtgtt tggccacggg aaggccaacg gggagcccac gtgggcgctg
1680
ctgctgacag tcctcatctg cgagactggc atcctcatcg cctctctgga cagcgtggcc
1740
ccgatcctct ccatgttctt cctcatgtgc tacctgttcg tgaacctggc ctgcgccgtg
1800
cagaccctgc tacgtacccc caactggcgt ccacgcttca agttctacca ctggaccctg
1860
tcctttctgg gtatgagcct gtgcctggcg ctgatgttca tctgctcctg gtactacgcg
1920
ctgtccgcca tgctcatcgc tggctgcatc tacaagtaca tcgagtaccg cggggccgag
1980
aaggagtggg gcgatggcat ccgtggccta tccctgaacg ccgcccgcta cgccctgctg
2040
cgcgtggagc acggtccccc ccacaccaag aactggaggc cccaggtgct ggtgatgctg
2100
aacctggacg cggagcaggc cgtgaagcac ccccgcctgc tgtccttcac gtcgcagctg
2160
aaggccggca agggcctgac catcgtgggc tcggtgctgg aggggacgta cctggacaag
2220
cacatggagg ctcagcgggc cgaggagaac atacggtccc taatgagcac agagaagacc
2280
aagggcttct gccagctggt ggtctcgtcc agcctgcggg atggcatgtc ccacctgatc
2340
cagtcggccg gcctgggcgg cctgaagcac aacacggtgc tcatggcctg gcccgcatcc
2400
tggaagcagg aggacaaccc cttctcctgg aagaactttg tagacaccgt ccgcgacacc
2460
accgccgcgc accaggctct gctggtggcc aagaacgtcg actcgtttcc gcaaaaccag
2520
gagcgcttcg gcgggggcca catcgacgtg tggtggatcg tgcacgacgg cggcatgctc
2580
atgctgctgc ccttcctgct gcgccagcac aaggtgtgga ggaagtgccg gatgcgtatc
2640
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<211> 1088
<212> PRT
<213> Homo sapiens

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Gly Pro Glu Pro Glu Arg Pro Ser Pro Gly Asp Gly Asn Pro Arg Glu
35 40 45
Asn Ser Pro Phe Leu Asn Asn Val Glu Val Glu Gln Glu Ser Phe Phe
50 55 60
Glu Gly Lys Asn Met Ala Leu Phe Glu Glu Glu Met Asp Ser Asn Pro
65 70 75 80
Met Val Ser Ser Leu Leu Asn Lys Leu Ala Asn Tyr Thr Asn Leu Ser
85 90 95
Gln Gly Val Val Glu His Glu Glu Asp Glu Glu Ser Arg Arg Arg Glu
100 105 110
Ala Lys Ala Pro Arg Met Gly Thr Phe Ile Gly Val Tyr Leu Pro Cys
115 120 125
Leu Gln Asn Ile Leu Gly Val Ile Leu Phe Leu Arg Leu Thr Trp Ile
130 135 140
Val Gly Val Ala Gly Val Leu Glu Ser Phe Leu Ile Val Ala Met Cys
145 150 155 160
Cys Thr Cys Thr Met Leu Thr Ala Ile Ser Met Ser Ala Ile Ala Thr
165 170 175
Asn Gly Val Val Pro Ala Gly Gly Ser Tyr Tyr Met Ile Ser Arg Ser
180 185 190
Leu Gly Pro Glu Phe Gly Gly Ala Val Gly Leu Cys Phe Tyr Leu Gly
195 200 205
Thr Thr Phe Ala Gly Ala Met Tyr Ile Leu Gly Thr Ile Glu Ile Phe
210 215 220
Leu Thr Tyr Ile Ser Pro Gly Ala Ala Ile Phe Gln Ala Glu Ala Ala
225 230 235 240
Gly Gly Glu Ala Ala Ala Met Leu His Asn Met Arg Val Tyr Gly Thr
245 250 255
Cys Thr Leu Val Leu Met Ala Leu Val Val Phe Val Gly Val Lys Tyr

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            260                 265                 270
Val Asn Lys Leu Ala Leu Val Phe Leu Ala Cys Val Val Leu Ser Ile
        275                 280                 285
Leu Ala Ile Tyr Ala Gly Val Ile Lys Ser Ala Phe Asp Pro Pro Asp
    290                 295                 300
Ile Pro Val Cys Leu Leu Gly Asn Arg Thr Leu Ser Arg Arg Ser Phe
305                 310                 315                 320
Asp Ala Cys Val Lys Ala Tyr Gly Ile His Asn Asn Ser Ala Thr Ser
                325                 330                 335
Ala Leu Trp Gly Leu Phe Cys Asn Gly Ser Gln Pro Ser Ala Ala Cys
            340                 345                 350
Asp Glu Tyr Phe Ile Gln Asn Asn Val Thr Glu Ile Gln Gly Ile Pro
        355                 360                 365
Gly Ala Ala Ser Gly Val Phe Leu Glu Asn Leu Trp Ser Thr Tyr Ala
    370                 375                 380
His Ala Gly Ala Phe Val Glu Lys Lys Gly Val Pro Ser Val Pro Val
385                 390                 395                 400
Ala Glu Glu Ser Arg Ala Ser Ala Leu Pro Tyr Val Leu Thr Asp Ile
                405                 410                 415
Ala Ala Ser Phe Thr Leu Leu Val Gly Ile Tyr Phe Pro Ser Val Thr
            420                 425                 430
Gly Ile Met Ala Gly Ser Asn Arg Ser Gly Asp Leu Lys Asp Ala Gln
        435                 440                 445
Lys Ser Ile Pro Thr Gly Thr Ile Leu Ala Ile Val Thr Thr Ser Phe
    450                 455                 460
Ile Tyr Leu Ser Cys Ile Val Leu Phe Gly Ala Cys Ile Glu Gly Val
465                 470                 475                 480
Val Leu Arg Asp Lys Phe Gly Glu Ala Leu Gln Gly Asn Leu Val Ile
                485                 490                 495
Gly Met Leu Ala Trp Pro Ser Pro Trp Val Ile Val Ile Gly Ser Phe
            500                 505                 510
Phe Ser Thr Cys Gly Ala Gly Leu Gln Thr Leu Thr Gly Ala Pro Arg
        515                 520                 525
Leu Leu Gln Ala Ile Ala Arg Asp Gly Ile Val Pro Phe Leu Gln Val
    530                 535                 540
Phe Gly His Gly Lys Ala Asn Gly Glu Pro Thr Trp Ala Leu Leu Leu
545                 550                 555                 560
Thr Val Leu Ile Cys Glu Thr Gly Ile Leu Ile Ala Ser Leu Asp Ser
                565                 570                 575
Val Ala Pro Ile Leu Ser Met Phe Phe Leu Met Cys Tyr Leu Phe Val
            580                 585                 590
Asn Leu Ala Cys Ala Val Gln Thr Leu Leu Arg Thr Pro Asn Trp Arg
        595                 600                 605
Pro Arg Phe Lys Phe Tyr His Trp Thr Leu Ser Phe Leu Gly Met Ser
    610                 615                 620
Leu Cys Leu Ala Leu Met Phe Ile Cys Ser Trp Tyr Tyr Ala Leu Ser
625                 630                 635                 640
Ala Met Leu Ile Ala Gly Cys Ile Tyr Lys Tyr Ile Glu Tyr Arg Gly
                645                 650                 655
Ala Glu Lys Glu Trp Gly Asp Gly Ile Arg Gly Leu Ser Leu Asn Ala
            660                 665                 670
Ala Arg Tyr Ala Leu Leu Arg Val Glu His Gly Pro Pro His Thr Lys
        675                 680                 685
Asn Trp Arg Pro Gln Val Leu Val Met Leu Asn Leu Asp Ala Glu Gln
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    690                 695                 700
Ala Val Lys His Pro Arg Leu Leu Ser Phe Thr Ser Gln Leu Lys Ala
705                 710                 715                 720
Gly Lys Gly Leu Thr Ile Val Gly Ser Val Leu Glu Gly Thr Tyr Leu
                725                 730                 735
Asp Lys His Met Glu Ala Gln Arg Ala Glu Glu Asn Ile Arg Ser Leu
            740                 745                 750
Met Ser Thr Glu Lys Thr Lys Gly Phe Cys Gln Leu Val Val Ser Ser
        755                 760                 765
Ser Leu Arg Asp Gly Met Ser His Leu Ile Gln Ser Ala Gly Leu Gly
    770                 775                 780
Gly Leu Lys His Asn Thr Val Leu Met Ala Trp Pro Ala Ser Trp Lys
785                 790                 795                 800
Gln Glu Asp Asn Pro Phe Ser Trp Lys Asn Phe Val Asp Thr Val Arg
                805                 810                 815
Asp Thr Thr Ala Ala His Gln Ala Leu Leu Val Ala Lys Asn Val Asp
            820                 825                 830
Ser Phe Pro Gln Asn Gln Glu Arg Phe Gly Gly Gly His Ile Asp Val
        835                 840                 845
Trp Trp Ile Val His Asp Gly Gly Met Leu Met Leu Leu Pro Phe Leu
    850                 855                 860
Leu Arg Gln His Lys Val Trp Arg Lys Cys Arg Met Arg Ile Phe Thr
865                 870                 875                 880
Val Ala Gln Val Asp Asp Asn Ser Ile Gln Met Lys Lys Asp Leu Gln
                885                 890                 895
Met Phe Leu Tyr His Leu Arg Ile Ser Ala Glu Val Glu Val Val Glu
            900                 905                 910
Met Val Glu Asn Asp Ile Ser Ala Phe Thr Tyr Glu Arg Thr Leu Met
        915                 920                 925
Met Glu Gln Arg Ser Gln Met Leu Lys Gln Met Gln Leu Ser Lys Asn
    930                 935                 940
Glu Gln Glu Arg Glu Ala Gln Leu Ile His Asp Arg Asn Thr Ala Ser
945                 950                 955                 960
His Thr Ala Ala Ala Ala Arg Thr Gln Ala Pro Pro Thr Pro Asp Lys
                965                 970                 975
Val Gln Met Thr Trp Thr Arg Glu Lys Leu Ile Ala Glu Lys Tyr Arg
            980                 985                 990
Ser Arg Asp Thr Ser Leu Ser Gly Phe Lys Asp Leu Phe Ser Met Lys
        995                 1000                1005
Pro Glu Trp Gly Asn Leu Asp Gln Ser Asn Val Arg Arg Met His Thr
    1010                1015                1020
Ala Val Lys Leu Asn Gly Val Val Leu Asn Lys Ser Gln Asp Ala Gln
1025                1030                1035                1040
Leu Val Leu Leu Asn Met Pro Gly Pro Pro Lys Asn Arg Gln Gly Asp
                1045                1050                1055
Glu Asn Tyr Met Glu Phe Leu Glu Val Leu Thr Glu Gly Leu Asn Arg
            1060                1065                1070
Val Leu Leu Val Arg Gly Gly Gly Arg Glu Val Ile Thr Ile Tyr Ser
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<211> 693
<212> DNA
<213> Homo sapiens

<400> 4341
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120
gacctgaggg agccatatgc atcaagtgag tgtttctcca taacagaata tttataagag
180
aacatgtata gtgccctctt ttgagtgatg ccgacagaca ccaagccctc cttttcacca
240
agtcccaggc ttgcattcca gcctcttgag ctctgccctc tctcaggtgg atctttgtgt
300
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360
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420
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<210> 4342
<211> 103
<212> PRT
<213> Homo sapiens

<400> 4342
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Arg Gly Gln Ser Ser Arg Gly Trp Asn Ala Ser Leu Gly Leu Gly Glu
20 25 30
Lys Glu Gly Leu Val Ser Val Gly Ile Thr Gln Lys Arg Ala Leu Tyr
35 40 45
Met Phe Ser Tyr Lys Tyr Ser Val Met Glu Lys His Ser Leu Asp Ala
50 55 60
Tyr Gly Ser Leu Arg Ser Phe Phe Phe His Pro Leu Phe Leu Glu Lys
65 70 75 80
Lys Phe Phe Lys Ala Tyr Asn Leu Lys Ser Thr Ser Thr Tyr Ser Arg
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Asn Ile Val Ala Phe Ser Ile
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<210> 4343
<211> 499
<212> DNA
<213> Homo sapiens

<400> 4343

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120
ttcagaacag ggcgcccgac gttgggcgcg tggacagagt cctccggcgg ccgcgccgct
180
gggccaggcg gagagaggcg gacggacttc aggggaggcc cgggccacgc cgcggaaact
240
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300
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360
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499

<210> 4344
<211> 118
<212> PRT
<213> Homo sapiens

<400> 4344
Met Ala Pro Ser Arg Pro Arg Leu Pro Pro Ser Pro Pro Gln Arg Leu
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20 25 30
Thr Leu Gly Ala Trp Thr Glu Ser Ser Gly Gly Arg Ala Ala Gly Pro
35 40 45
Gly Gly Glu Arg Arg Thr Asp Phe Arg Gly Gly Pro Gly His Ala Ala
50 55 60
Glu Thr Thr Arg Leu Pro Gly Gly Gly Gln Asp Arg Pro Cys Pro Asp
65 70 75 80
Lys Met Glu Phe Pro Val Trp Leu Gln Leu Ala Ala Arg Ser Gln Ser
85 90 95
Ser Ser Val Ile Arg Leu Ser Asp Cys Ser Pro Phe Ile Ser Phe Ala
100 105 110
Val Val Gln Ile Leu Ile
115

<210> 4345
<211> 349
<212> DNA
<213> Homo sapiens

<400> 4345
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120
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180

ctgaggagtg ggctgncgcg cacggccatc tccgagctcc acgggaacat gtacattgaa
240
ggagtacgtg cgggtgttcg atgtgacgga gcgcactgcc ctccacagac accagacagg
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349

<210> 4346
<211> 116
<212> PRT
<213> Homo sapiens

<400> 4346
Ala Ser Ile Pro Asp Tyr Arg Gly Pro Asn Gly Val Trp Thr Leu Leu
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Gln Lys Gly Arg Ser Val Ser Ala Ala Asp Xaa Glu Arg Ala Glu Pro
20 25 30
Thr Leu Thr His Met Ser Ile Thr Arg Leu His Glu Gln Lys Leu Val
35 40 45
Gln His Val Val Ser Gln Asn Cys Asp Gly Leu His Leu Arg Ser Gly
50 55 60
Leu Xaa Arg Thr Ala Ile Ser Glu Leu His Gly Asn Met Tyr Ile Glu
65 70 75 80
Gly Val Arg Ala Gly Val Arg Cys Asp Gly Ala His Cys Pro Pro Gln
85 90 95
Thr Pro Asp Arg Pro Asp Leu Pro Gln Val Trp Asp Pro Ala Ala Gly
100 105 110
His His Cys Ala
115

<210> 4347
<211> 353
<212> DNA
<213> Homo sapiens

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240
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353

<210> 4348
<211> 72
<212> PRT
<213> Homo sapiens

<400> 4348
Asp Ser Ser Gly Ile Ser Thr Pro Arg Pro Pro Pro Arg Gly Ser Arg
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20 25 30
Arg Gln Cys Arg Gly Arg Ser Arg Arg Arg Val Ala Arg Ser Ser Leu
35 40 45
Pro Ser Pro Ser Ala Arg Pro Gly Arg Gly Gly Arg Pro Gly Pro Gly
50 55 60
Gly Ser Ala Gly Cys Pro Gly Leu
65 70

<210> 4349
<211> 2040
<212> DNA
<213> Homo sapiens

<400> 4349
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120
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180
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1080

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1560
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1680
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1860
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1920
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2040

<210> 4350
<211> 113
<212> PRT
<213> Homo sapiens

<400> 4350
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Phe Pro Pro Leu Ala His Ala Pro Leu Thr Gly Thr Arg Pro Ser Cys
35 40 45
Gly Pro Arg Leu Trp His Gly Thr Cys Pro Ser Ala Gln His Gly Pro
50 55 60
Gly Ala Thr Leu Leu Ala Glu Gly Gln Gly Pro Leu Cys Arg Gln Trp
65 70 75 80
Gly Gly Gly Pro Arg Phe Pro Asp Arg Gly Arg Gln Gly Thr Gly Glu
85 90 95
Pro Ala Ser Pro Ser Gly Gln His Gly Pro Gly Gln Thr Glu Gln Gly
100 105 110
Pro

<210> 4351
<211> 4703
<212> DNA
<213> Homo sapiens

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120
ctggttgtca acacatattg aagaaatgta agcaaaatac agaaagtgat gattttcaaa
180
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240
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300
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360
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420
aaatagatta tctctcaata caatacttct ctgtcttggt aaaaataata aagcaaagaa
480
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720
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780
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840
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960
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<212> PRT
<213> Homo sapiens

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Leu Gln Pro Pro Pro Pro Gly Phe Glu Leu Phe Ser Cys Leu Ser Phe
35 40 45
Gln Ser Ser Trp Gly Tyr Arg His Ser Pro Pro Arg Leu Ala Asn Phe
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Gln Thr Pro Asn Leu Lys
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35 40 45
Pro Ala Glu Val Asp Glu Glu Gly Lys Asp Ile Asn Pro His Ile Pro
50 55 60
Gln Tyr Ile Ser Ser Val Pro Trp Tyr Ile Asp Pro Ser Lys Arg Pro
65 70 75 80
Thr Leu Lys His Gln Arg Pro Gln Pro Glu Lys Gln Lys Gln Phe Ser
85 90 95
Ser Ser Gly Glu Trp Tyr Lys Arg Gly Val Lys Glu Asn Ser Ile Ile
100 105 110
Thr Lys Tyr Arg Lys Gly Ala Cys Glu Asn Cys Gly Ala Met Thr His
115 120 125
Lys Lys Lys Asp Cys Phe Glu Arg Pro Arg Arg Val Gly Ala Lys Phe
130 135 140
Thr Gly Thr Asn Ile Ala Pro Asp Glu His Val Gln Pro Gln Leu Met
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Phe Asp Tyr Asp Gly Lys Arg Asp Arg Trp Asn Gly Tyr Asn Pro Glu
165 170 175
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Arg Thr Leu Lys Ala Gln Lys Leu Gln Glu Glu Leu Ala Ser Gly Lys
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Pro Asn Ser Gln Thr Glu Lys Asp His Asn Ser Glu Asp Glu Asp Glu
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260 265 270
Lys Tyr Leu Arg Asn Leu Asp Pro Asn Ser Ala Tyr Tyr Asp Pro Lys
275 280 285
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Leu Tyr Lys Ser Phe Lys Val Lys Lys Glu Asp Phe Lys Glu Gln Gln
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Lys Glu Ser Ile Leu Glu Lys Tyr Gly Gly Gln Glu His Leu Asp Ala
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Pro Pro Ala Glu Leu Leu Leu Ala Gln Thr Glu Asp Tyr Val Glu Tyr
385                 390                 395                 400
Ser Arg His Gly Thr Val Ile Lys Gly Gln Glu Arg Ala Val Ala Cys
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Ser Lys Tyr Glu Glu Asp Val Lys Ile His Asn His Thr His Ile Trp
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Gly Ser Tyr Trp Lys Glu Gly Arg Trp Gly Tyr Lys Cys Cys His Ser
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Phe Phe Lys Tyr Ser Tyr Cys Thr Gly Glu Ala Gly Lys Glu Ile Val
    450                 455                 460
Asn Ser Glu Glu Cys Ile Ile Asn Glu Ile Thr Gly Glu Glu Ser Val
465                 470                 475                 480
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Glu Lys Lys Lys Lys Lys Lys Lys Lys Lys His Arg Lys Ser Ser
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Ser Asp Ser Asp Asp Glu Glu Lys Lys His Glu Lys Leu Lys Lys Ala
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Leu Asn Ala Glu Glu Ala Arg Leu Leu His Val Lys Glu Thr Met Gln
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Ile Asp Glu Arg Lys Arg Pro Tyr Asn Ser Met Tyr Glu Thr Arg Glu
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<213> Homo sapiens

<400> 4355

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<212> PRT
<213> Homo sapiens

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Gly Leu Ala Ala Lys Gln Ser Arg Ile Arg Asn Ile Ser Asn Thr Val
    50                  55                  60
Met Lys Val Lys Gln Ile Leu Gly Arg Ser Ser Ser Asp Pro Gln Ala
65                  70                  75                  80
Gln Lys Tyr Ile Ala Glu Ser Lys Cys Leu Val Ile Glu Lys Asn Gly
                85                  90                  95
Lys Leu Arg Tyr Glu Ile Asp Thr Gly Glu Glu Thr Lys Phe Val Asn
            100                 105                 110
Pro Glu Asp Val Ala Arg Leu Ile Phe Ser Lys Met Lys Glu Thr Ala
        115                 120                 125
His Ser Val Leu Gly Ser Asp Ala Asn Asp Val Val Ile Thr Val Pro
    130                 135                 140
Phe Asp Phe Gly Glu Lys Gln Lys Asn Ala Leu Gly Glu Ala Ala Arg
145                 150                 155                 160
Ala Ala Gly Phe Asn Val Leu Arg Leu Ile His Glu Pro Ser Ala Ala
                165                 170                 175
Leu Leu Ala Tyr Gly Ile Gly Gln Asp Ser Pro Thr Gly Lys Ser Asn
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Ile Leu Val Phe Lys Leu Gly Gly Thr Ser Leu Ser Leu Ser Val Met
        195                 200                 205
Glu Val Asn Ser Gly Ile Tyr Arg Val Leu Ser Thr Asn Thr Asp Asp
    210                 215                 220
Asn Ile Gly Gly Ala His Phe Thr Glu Thr Leu Ala Gln Tyr Leu Ala
225                 230                 235                 240
Ser Glu Phe Gln Arg Ser Phe Lys His Asp Val Arg Gly Asn Ala Arg
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Ala Met Met Lys Leu Thr Asn Ser Ala Glu Val Ala Lys His Ser Leu
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Ser Thr Leu Gly Ser Ala Asn Cys Phe Leu Asp Ser Leu Tyr Glu Gly
        275                 280                 285
Gln Asp Phe Asp Cys Asn Val Ser Arg Ala Arg Phe Glu Leu Leu Cys
    290                 295                 300
Ser Pro Leu Phe Asn Lys Cys Ile Glu Ala Ile Arg Gly Leu Leu Asp
305                 310                 315                 320
Gln Asn Gly Phe Thr Ala Asp Asp Ile Asn Lys Val Val Leu Cys Gly
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Gly Ser Ser Arg Ile Pro Lys Leu Gln Gln Leu Ile Lys Asp Leu Phe
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Pro Ala Val Glu Leu Leu Asn Ser Ile Pro Pro Asp Glu Val Ile Pro
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Ile Gly Ala Ala Ile Glu Ala Gly Ile Leu Ile Gly Lys Glu Asn Leu
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Leu Val Glu Asp Ser Leu Met Ile Glu Cys Ser Ala Arg Asp Ile Leu
385                 390                 395                 400
Val Lys Gly Val Asp Glu Ser Gly Ala Ser Arg Phe Thr Val Leu Phe
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Pro Gly Ser Ile Ser Ser Val Cys Leu Glu Leu Tyr Glu Ser Asp Gly
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    450                 455                 460
Asp Leu Asp Lys Lys Glu Asn Gly Leu Arg Asp Ile Leu Ala Val Leu
465                 470                 475                 480
Thr Met Lys Arg Asp Gly Ser Leu His Val Thr Cys Thr Asp Gln Glu
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<211> 421
<212> DNA
<213> Homo sapiens

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<210> 4358
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<212> PRT
<213> Homo sapiens

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            20                  25                  30
Gln Lys Pro Trp Pro Ser Pro Ala Val Phe Phe Arg Arg Asn Val Arg
        35                  40                  45
Gly Leu Pro Pro Arg Phe Ser Ser Pro Thr Pro Leu Trp Arg Lys Val
    50                  55                  60
Leu Ser Thr Ala Val Val Gly Ala Pro Leu Leu Leu Gly Ala Arg Tyr
65                  70                  75                  80
Val Met Ala Glu Ala Arg Glu Lys Arg Arg Met Arg Leu Val Val Asp
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115

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3661

<210> 4360
<211> 670
<212> PRT
<213> Homo sapiens

<400> 4360
Met Ser Ser Gly Lys Ser Ala Arg Tyr Asn Arg Phe Ser Gly Gly Pro
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Ser Asn Leu Pro Thr Pro Asp Val Thr Thr Gly Thr Arg Met Glu Thr
            20   25   30
Thr Phe Gly Pro Ala Phe Ser Ala Val Thr Thr Ile Thr Lys Ala Asp
        35   40   45
Gly Thr Ser Thr Tyr Lys Gln His Cys Arg Thr Pro Ser Ser Ser Ser
    50   55   60
Thr Leu Ala Tyr Ser Pro Arg Asp Glu Glu Asp Ser Met Pro Pro Ile
65   70   75   80
Ser Thr Pro Arg Arg Ser Asp Ser Ala Ile Ser Val Arg Ser Leu His
                85   90   95
Ser Glu Ser Ser Met Ser Leu Arg Ser Thr Phe Ser Leu Pro Glu Glu
            100   105   110
Glu Glu Glu Pro Glu Pro Leu Val Phe Ala Glu Gln Pro Ser Val Lys
        115   120   125
Leu Cys Cys Gln Leu Cys Cys Ser Val Phe Lys Asp Pro Val Ile Thr
    130   135   140
Thr Cys Gly His Thr Phe Cys Arg Arg Cys Ala Leu Lys Ser Glu Lys
145   150   155   160
Cys Pro Val Asp Asn Val Lys Leu Thr Val Val Val Asn Asn Ile Ala
                165   170   175
Val Ala Glu Gln Ile Gly Glu Leu Phe Ile His Cys Arg His Gly Cys

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            180                 185                 190
Arg Val Ala Gly Ser Gly Lys Pro Pro Ile Phe Glu Val Asp Pro Arg
        195                 200                 205
Gly Cys Pro Phe Thr Ile Lys Leu Ser Ala Arg Lys Asp His Glu Gly
    210                 215                 220
Ser Cys Asp Tyr Arg Pro Val Arg Cys Pro Asn Asn Pro Ser Cys Pro
225                 230                 235                 240
Pro Leu Leu Arg Met Asn Leu Glu Ala His Leu Lys Glu Cys Glu His
                245                 250                 255
Ile Lys Cys Pro His Ser Lys Tyr Gly Cys Thr Phe Ile Gly Asn Gln
            260                 265                 270
Asp Thr Tyr Glu Thr His Leu Glu Thr Cys Arg Phe Glu Gly Leu Lys
        275                 280                 285
Glu Phe Leu Gln Gln Thr Asp Asp Arg Phe His Glu Met His Val Ala
    290                 295                 300
Leu Ala Gln Lys Asp Gln Glu Ile Ala Phe Leu Arg Ser Met Leu Gly
305                 310                 315                 320
Lys Leu Ser Glu Lys Ile Asp Gln Leu Glu Lys Ser Leu Glu Leu Lys
                325                 330                 335
Phe Asp Val Leu Asp Glu Asn Gln Ser Lys Leu Ser Glu Asp Leu Met
            340                 345                 350
Glu Phe Arg Arg Asp Ala Ser Met Leu Asn Asp Glu Leu Ser His Ile
        355                 360                 365
Asn Ala Arg Leu Asn Met Gly Ile Leu Gly Ser Tyr Asp Pro Gln Gln
    370                 375                 380
Ile Phe Lys Cys Lys Gly Thr Phe Val Gly His Gln Gly Pro Val Trp
385                 390                 395                 400
Cys Leu Cys Val Tyr Ser Met Gly Asp Leu Leu Phe Ser Gly Ser Ser
                405                 410                 415
Asp Lys Thr Ile Lys Val Trp Asp Thr Cys Thr Thr Tyr Lys Cys Gln
            420                 425                 430
Lys Thr Leu Glu Gly His Asp Gly Ile Val Leu Ala Leu Cys Ile Gln
        435                 440                 445
Gly Cys Lys Leu Tyr Ser Gly Ser Ala Asp Cys Thr Ile Ile Val Trp
    450                 455                 460
Asp Ile Gln Asn Leu Gln Lys Val Asn Thr Ile Arg Ala His Asp Asn
465                 470                 475                 480
Pro Val Cys Thr Leu Val Ser Ser His Asn Val Leu Phe Ser Gly Ser
                485                 490                 495
Leu Lys Ala Ile Lys Val Trp Asp Ile Val Gly Thr Glu Leu Lys Leu
            500                 505                 510
Lys Lys Glu Leu Thr Gly Leu Asn His Trp Val Arg Ala Leu Val Ala
        515                 520                 525
Ala Gln Ser Tyr Leu Tyr Ser Gly Ser Tyr Gln Thr Ile Lys Ile Trp
    530                 535                 540
Asp Ile Arg Thr Leu Asp Cys Ile His Val Leu Gln Thr Ser Gly Gly
545                 550                 555                 560
Ser Val Tyr Ser Ile Ala Val Thr Asn His His Ile Val Cys Gly Thr
                565                 570                 575
Tyr Glu Asn Leu Ile His Val Trp Asp Ile Glu Ser Lys Glu Gln Val
            580                 585                 590
Arg Thr Leu Thr Gly His Val Gly Thr Val Tyr Ala Leu Ala Val Ile
        595                 600                 605
Ser Thr Pro Asp Gln Thr Lys Val Phe Ser Ala Ser Tyr Asp Arg Ser
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    610                 615                 620
Leu Arg Val Trp Ser Met Asp Asn Met Ile Cys Thr Gln Thr Leu Leu
625                 630                 635                 640
Arg His Gln Gly Ser Val Thr Ala Leu Ala Val Ser Arg Gly Arg Leu
                645                 650                 655
Phe Ser Gly Ala Val Asp Ser Thr Val Lys Val Trp Thr Cys
            660                 665                 670
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<210> 4361
<211> 574
<212> DNA
<213> Homo sapiens

<400> 4361
nggatccaga acccattgct atcaggctgt acagccttca atcacaacgg gaacctgctg
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gtcacagggg cagctgatgg cgtcatccgg ctgtttgaca tgcagcagca tgagtgcgcg
120
atgagctgga gggcccacta cggggaggtc tactctgtgg agttcagcta tgatgagaac
180
accgtgtaca gcatcggcga ggacgggaag gtaggcggct ccaggattca gataagagag
240
caccgggatg acatgtgggc cggctgcagg ttgtggccat acctgttact agctctgcaa
300
cctggggcct ctttttgcag ctttgttatc tgtagaatag ggataaacta gtaattcgtc
360
ttacaatcct tgcgaggttt tagtgaattc agtgggagtt ggctatcctt atgaaaggaa
420
gtaccaaaaa ttactcatct taccatagat gtatctgtgg ggtctggatt tagggctgag
480
tttgctttgc tgggcttggt agtgagtggt cccaggacca ctcatggatg tgtagtttgc
540
tgagtggctg gggacagctt cttacatgtg taca
574

<210> 4362
<211> 116
<212> PRT
<213> Homo sapiens

<400> 4362
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Xaa Ile Gln Asn Pro Leu Leu Ser Gly Cys Thr Ala Phe Asn His Asn
 1               5                  10                  15
Gly Asn Leu Leu Val Thr Gly Ala Ala Asp Gly Val Ile Arg Leu Phe
            20                  25                  30
Asp Met Gln Gln His Glu Cys Ala Met Ser Trp Arg Ala His Tyr Gly
        35                  40                  45
Glu Val Tyr Ser Val Glu Phe Ser Tyr Asp Glu Asn Thr Val Tyr Ser
    50                  55                  60
Ile Gly Glu Asp Gly Lys Val Gly Gly Ser Arg Ile Gln Ile Arg Glu
65                  70                  75                  80
His Arg Asp Asp Met Trp Ala Gly Cys Arg Leu Trp Pro Tyr Leu Leu
                85                  90                  95
Leu Ala Leu Gln Pro Gly Ala Ser Phe Cys Ser Phe Val Ile Cys Arg
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100 105 110
Ile Gly Ile Asn
115

<210> 4363
<211> 1222
<212> DNA
<213> Homo sapiens

<400> 4363
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tggctttaat ttgaaaaatc tgattggggt ctcttcccgt atcagagaag gaacagccca
120
agctatgacc ccagggccag ggaattcagt ccccaccaga ccctgtcatt ccatcactag
180
ggggtaattc caggctcccc ctgccagccc tgagacagga ggacggatgt gaagttgccc
240
aggactagat tctgtctctc caaagtggcc caagccctgt tctctgtact agggaagcca
300
gctgtgtctt ttcgaggaca gttggtccag ccagcaggct cagttcagat accagacaac
360
cattccagca cgagggctca gcgccctggc cccggcggtc gctccagtgc ctgtgtgccc
420
accagcacat ccatgaggta gtccaattcg gcctcgtcca gctccggagc ttcctccttg
480
cccggcccat cctcagggcc tggtttgagg ccctcagagg ctggtgccca aagttcattg
540
tcatacatag aggtgtcaat atcctcaaac aggccctcga gcccatcgtc cagtagacag
600
ccagtggctg ggcccagcag gtccaaggca cccaggctgg gcgctgctcc cccgatgcta
660
cggcctggtg gcccctcgtc tgccaagggt tggggagcct gactcaggcc ctcaatgtgg
720
ctgaggtcct ccaggaggct ggccatggag gctgaaaggg cagcgtccga gcttgccagt
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960
gagctagagg ccacggccgg gggtgcctgt gccaccgctg cgtggccagg atctagccac
1020
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1080
ttgctcagca tcttgctcac tagcggccaa tcagaacgaa gaggtagcca cccacaacca
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1200
tcgcgagacg cagttctagc ga
1222

<210> 4364

<211> 75
<212> PRT
<213> Homo sapiens

<400> 4364
Asp Arg Arg Thr Asp Val Lys Leu Pro Arg Thr Arg Phe Cys Leu Ser
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Lys Val Ala Gln Ala Leu Phe Ser Val Leu Gly Lys Pro Ala Val Ser
20 25 30
Phe Arg Gly Gln Leu Val Gln Pro Ala Gly Ser Val Gln Ile Pro Asp
35 40 45
Asn His Ser Ser Thr Arg Ala Gln Arg Pro Gly Pro Gly Gly Arg Ser
50 55 60
Ser Ala Cys Val Pro Thr Ser Thr Ser Met Arg
65 70 75

<210> 4365
<211> 469
<212> DNA
<213> Homo sapiens

<400> 4365
gacgtgctcg atggcaaggt cgcaccgggc aagaacgtgc cggtctacga caccatctgc
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gagttcaccg gcatgtcggt cgccgacttc ctcgctgaca agggcagcca ggttgagatc
120
gtcaccgacg acatcaagcc gggtgtggcg attggcggta cgtcgttccc gacctactac
180
cgcagcatgt acccgaaaga agtgatcatg accggcgaca tgatgctgga aaaggtctat
240
cgcgagggcg acaagctggt ggcggtgctg gagaacgaat acaccggcgc caaggaagag
300
cgggtggtcg accaggtggt ggtggagaac ggtgtgcgtc cggatgagga aatctactac
360
gggctcaagg aaggttcgcg caacaagggc agatcgatg tcgaagccct gttcgcgatc
420
aagccgcagc cttcgctgaa tactcttaat gaagaggcag cgggtgacg
469

<210> 4366
<211> 156
<212> PRT
<213> Homo sapiens

<400> 4366
Asp Val Leu Asp Gly Lys Val Ala Pro Gly Lys Asn Val Pro Val Tyr
1 5 10 15
Asp Thr Ile Cys Glu Phe Thr Gly Met Ser Val Ala Asp Phe Leu Ala
20 25 30
Asp Lys Gly Ser Gln Val Glu Ile Val Thr Asp Asp Ile Lys Pro Gly
35 40 45
Val Ala Ile Gly Gly Thr Ser Phe Pro Thr Tyr Tyr Arg Ser Met Tyr
50 55 60
Pro Lys Glu Val Ile Met Thr Gly Asp Met Met Leu Glu Lys Val Tyr

65 70 75 80
Arg Glu Gly Asp Lys Leu Val Ala Val Leu Glu Asn Glu Tyr Thr Gly
85 90 95
Ala Lys Glu Glu Arg Val Val Asp Gln Val Val Val Glu Asn Gly Val
100 105 110
Arg Pro Asp Glu Glu Ile Tyr Tyr Gly Leu Lys Glu Gly Ser Arg Asn
115 120 125
Lys Gly Gln Ile Asp Val Glu Ala Leu Phe Ala Ile Lys Pro Gln Pro
130 135 140
Ser Leu Asn Thr Leu Asn Glu Glu Ala Ala Gly Asp
145 150 155

<210> 4367
<211> 852
<212> DNA
<213> Homo sapiens

<400> 4367
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120
atctacgaga ctccccgggg cccagaccca gccctcctgg aggccacagg gggagcagct
180
ggagctggtg gggctggccg cggggaggat gaagagaacc gagagcaccg tgtccgcagg
240
atccatgtcc ggcgccatat cacccacgac gagcgtcctc atggccaaca aattgtcttc
300
aaggactgac ctctgaccct ccccctgcct tcctcttgcc ttgggaccca gtccctctct
360
ctttccctcc ccttcccaga cttttgcccc ggctctgctg gccaagtcgt gggtcctcct
420
ctgtcccttc attgcatggc acagctcact ttggcccttc tccacccgtc ccaaccccat
480
tgctaacaac atggtacatt ccggccccac cactcagagc cttccgaagc caacacttgt
540
ccccaccctg gccctgcgtc cttccctctc cagctggtta agagggattt agaattccct
600
ttctcttttt ttagtgcatc gtccatgcca aagtgtgcgg cccttcctga catcaccaca
660
gtctgagcag cctcccgcgt cctgcagggt agtccgcccc ctcctcccca ccatcctccc
720
tacctcctta actttgtact agactggcct gggcctgccc agctcagcgt tatcagtctg
780
tttcatatta tttattattt taatttttcta ttaaattatt gaaataaagt taagttgaga
840
aactaaaaaa aa
852

<210> 4368
<211> 102
<212> PRT
<213> Homo sapiens

<400> 4368
Xaa Leu Gly Arg Gly Met Ala Leu Arg Asp Cys Thr Arg Arg Lys Glu
1 5 10 15
Leu Gly Pro Ala Gly Leu Leu Gln Val Glu Phe Pro Glu Ala Arg Ile
20 25 30
Phe Glu Glu Thr Leu Asn Ile Leu Ile Tyr Glu Thr Pro Arg Gly Pro
35 40 45
Asp Pro Ala Leu Leu Glu Ala Thr Gly Gly Ala Ala Gly Ala Gly Gly
50 55 60
Ala Gly Arg Gly Glu Asp Glu Glu Asn Arg Glu His Arg Val Arg Arg
65 70 75 80
Ile His Val Arg Arg His Ile Thr His Asp Glu Arg Pro His Gly Gln
85 90 95
Gln Ile Val Phe Lys Asp
100

<210> 4369
<211> 1264
<212> DNA
<213> Homo sapiens

<400> 4369
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60
tcctccatca gcgagctctc tgcacgactt cacctctggg cattcaaaat ggattatgaa
120
actacagaaa aggaagtagc agaaccactc ctggacctga aggaaggaat agaccagttg
180
gagaacaata aaaccttggg ctttatcctg tctactctct tagccattgg gaactttcta
240
aatggaacta atgccaaagc gtttgagtta agctacctcg agaaggttcc agaagtcaaa
300
gacacagtgc acaagcagtc gcttctccac catgtgtgca ccatggtggt agaaaacttc
360
ccagacagct ccgatctgta ctcggagatc ggggccatca ccaggtcagc caaggttgac
420
tttgatcaac ttcaggataa tttatgtcag atggagagaa gatgcaaagc ttcatgggat
480
cacctcaagg caattgcaaa acatgaaatg aaaccagttt taaaacaacg gatgtcagag
540
ttcctgaaag actgtgcaga gcgaattata attttaaaga ttgtccatag aaggataatc
600
aacagattcc actccttttt actctttatg ggccatccac cttatgcaat tcgggaagtg
660
aacataaaca aattctgcag gattattagt gaatttgcac tagagtatcg cacaaccagg
720
gaaagggttt tgcagcagaa acagaaacgg gccaaccaca gagagagaaa taagaccaga
780
gggaagatga tcaccgattc tggcaagttc tccggcagtt ctccggcgcc cccaagccag
840
ccgcagggtc tgagctatgc ggaggacgcg gctgagcacg agaacatgaa ggctgtgctg
900
aaaacctcgt ccccctccag gagtcccctg cacatacctt ctccatcgtg tcagctgtgt
960

ttctcttgat tccgtgacac ccggtttatt agttcaaaag tgtgacacct tttctgggca
1020
aggaacagcc cctttaagga gcaaatcact tctgtcacag ttattatggt aatatgaggc
1080
aatctgatta gcttcacaga ctgagtctcc acaacaccaa aatatccaga tgtaaacccc
1140
aaacttgtac acaaaagaaa gcacagattg tttacctgtt gtggatttta gatgtaacaa
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atgtttatac aaatacatac atgtacacca tgtttcaaat actaaataaa tagagtttaa
1260
tgcc
1264

<210> 4370
<211> 322
<212> PRT
<213> Homo sapiens

<400> 4370
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Leu Leu Thr Leu Ser Ser Ile Ser Glu Leu Ser Ala Arg Leu His Leu
20 25 30
Trp Ala Phe Lys Met Asp Tyr Glu Thr Thr Glu Lys Glu Val Ala Glu
35 40 45
Pro Leu Leu Asp Leu Lys Glu Gly Ile Asp Gln Leu Glu Asn Asn Lys
50 55 60
Thr Leu Gly Phe Ile Leu Ser Thr Leu Leu Ala Ile Gly Asn Phe Leu
65 70 75 80
Asn Gly Thr Asn Ala Lys Ala Phe Glu Leu Ser Tyr Leu Glu Lys Val
85 90 95
Pro Glu Val Lys Asp Thr Val His Lys Gln Ser Leu Leu His His Val
100 105 110
Cys Thr Met Val Val Glu Asn Phe Pro Asp Ser Ser Asp Leu Tyr Ser
115 120 125
Glu Ile Gly Ala Ile Thr Arg Ser Ala Lys Val Asp Phe Asp Gln Leu
130 135 140
Gln Asp Asn Leu Cys Gln Met Glu Arg Arg Cys Lys Ala Ser Trp Asp
145 150 155 160
His Leu Lys Ala Ile Ala Lys His Glu Met Lys Pro Val Leu Lys Gln
165 170 175
Arg Met Ser Glu Phe Leu Lys Asp Cys Ala Glu Arg Ile Ile Ile Leu
180 185 190
Lys Ile Val His Arg Arg Ile Ile Asn Arg Phe His Ser Phe Leu Leu
195 200 205
Phe Met Gly His Pro Pro Tyr Ala Ile Arg Glu Val Asn Ile Asn Lys
210 215 220
Phe Cys Arg Ile Ile Ser Glu Phe Ala Leu Glu Tyr Arg Thr Thr Arg
225 230 235 240
Glu Arg Val Leu Gln Gln Lys Gln Lys Arg Ala Asn His Arg Glu Arg
245 250 255
Asn Lys Thr Arg Gly Lys Met Ile Thr Asp Ser Gly Lys Phe Ser Gly
260 265 270
Ser Ser Pro Ala Pro Pro Ser Gln Pro Gln Gly Leu Ser Tyr Ala Glu

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        275                 280                 285
Asp Ala Ala Glu His Glu Asn Met Lys Ala Val Leu Lys Thr Ser Ser
    290                 295                 300
Pro Ser Arg Ser Pro Leu His Ile Pro Ser Pro Ser Cys Gln Leu Cys
305                 310                 315                 320
Phe Ser
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<210> 4371
<211> 907
<212> DNA
<213> Homo sapiens

<400> 4371
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aagagcatca cgctgccccc cgacgagatc ttccgcaacc tggagaacgc caagcgcttc
120
gccatcgaca taggcgggtc gttaaccaag ctggcctact attcaacggt acagcacaaa
180
gtcgccaagg tgcggtcttt cgaccactcc ggaaaggaca cagaacgtga acatgagccg
240
ccctatgaga tttcagttca agaagagatc actgctcgac tgcacttcat taagtttgag
300
aatacctaca tcgaagcctg cctggacttc atcaaagacc atctcgtcaa cacagagacc
360
aaggtcatcc aggcgaccgg gggcggggcc tacaagttca aggacctcat cgaagagaag
420
ctgcggctga aagtcgacaa ggaggacgtg atgacgtgcc tgattaaggg gtgcaacttc
480
gtgctcaaga acatccccca tgaggccttc gtgtaccaga aggattccga ccctgagttc
540
cggttccaga ccaaccaccc ccacattttc ccctatcttc ttgtcaatat cggctctgga
600
gtctccatcg tgaaggtgga gacggaggac aggttcgagt gggtcggcgg cagctccatt
660
ggaggcggca ccttctgggg gcttggcgct ctgctcacca aaacgaagaa gtttgacgag
720
ctcctgcacc tggcctcgag gggccagcac agcaatgtgg acatgctggt gcgggacgtc
780
tacggcggcg cccaccagac tctcgggctg agcgggaacc tcatcgccag cagcttcggg
840
aagtcggcca ccgccgacca agagttctcc aaagaagaca tggcgaagag cctgctgcac
900
atgatca
907

<210> 4372
<211> 302
<212> PRT
<213> Homo sapiens

<400> 4372
Thr Phe Lys Met Ala Glu Cys Gly Ala Ser Gly Ser Gly Ser Ser Gly

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 1               5                  10                  15
Asp Ser Leu Asp Lys Ser Ile Thr Leu Pro Pro Asp Glu Ile Phe Arg
            20                  25                  30
Asn Leu Glu Asn Ala Lys Arg Phe Ala Ile Asp Ile Gly Gly Ser Leu
        35                  40                  45
Thr Lys Leu Ala Tyr Tyr Ser Thr Val Gln His Lys Val Ala Lys Val
    50                  55                  60
Arg Ser Phe Asp His Ser Gly Lys Asp Thr Glu Arg Glu His Glu Pro
65                  70                  75                  80
Pro Tyr Glu Ile Ser Val Gln Glu Glu Ile Thr Ala Arg Leu His Phe
                85                  90                  95
Ile Lys Phe Glu Asn Thr Tyr Ile Glu Ala Cys Leu Asp Phe Ile Lys
            100                 105                 110
Asp His Leu Val Asn Thr Glu Thr Lys Val Ile Gln Ala Thr Gly Gly
        115                 120                 125
Gly Ala Tyr Lys Phe Lys Asp Leu Ile Glu Glu Lys Leu Arg Leu Lys
    130                 135                 140
Val Asp Lys Glu Asp Val Met Thr Cys Leu Ile Lys Gly Cys Asn Phe
145                 150                 155                 160
Val Leu Lys Asn Ile Pro His Glu Ala Phe Val Tyr Gln Lys Asp Ser
                165                 170                 175
Asp Pro Glu Phe Arg Phe Gln Thr Asn His Pro His Ile Phe Pro Tyr
            180                 185                 190
Leu Leu Val Asn Ile Gly Ser Gly Val Ser Ile Val Lys Val Glu Thr
        195                 200                 205
Glu Asp Arg Phe Glu Trp Val Gly Gly Ser Ser Ile Gly Gly Gly Thr
    210                 215                 220
Phe Trp Gly Leu Gly Ala Leu Leu Thr Lys Thr Lys Lys Phe Asp Glu
225                 230                 235                 240
Leu Leu His Leu Ala Ser Arg Gly Gln His Ser Asn Val Asp Met Leu
                245                 250                 255
Val Arg Asp Val Tyr Gly Gly Ala His Gln Thr Leu Gly Leu Ser Gly
            260                 265                 270
Asn Leu Ile Ala Ser Ser Phe Gly Lys Ser Ala Thr Ala Asp Gln Glu
        275                 280                 285
Phe Ser Lys Glu Asp Met Ala Lys Ser Leu Leu His Met Ile
    290                 295                 300
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<210> 4373
<211> 1017
<212> DNA
<213> Homo sapiens

<400> 4373
acgcgtcatc acggctgcgc cgggggaatc cgtgcgggcg ccttccgtcc cggtcccatc
60
ctcgccgcgc tccagcacct ctgaagtttt gcagcgccca gaaaggaggc gaggaaggag
120
ggagtgtgtg agaggaggga gcaaaaagct caccctaaaa catttatttc aaggagaaaa
180
gaaaaagggg gggcgcaaaa atggctgggg caattataga aaacatgagc accaagaagc
240
tgtgcattgt tggtgggatt ctgctcgtgt tccaaatcat cgcctttctg gtgggaggct
300

tgattgctcc agggcccaca acggcagtgt cctacatgtc ggtgaaatgt gtggatgccc
360
gtaagaacca tcacaagaca aaatggttcg tgccttgggg acccaatcat tgtgacaaga
420
tccgagacat tgaagaggca attccaaggg aaattgaagc caatgacatc gtgttttctg
480
ttcacattcc cctcccccac atggagatga gtccttggtt ccaattcatg ctgtttatcc
540
tgcagctgga cattgccttc aagctaaaca accaaatcag agaaaatgca gaagtctcca
600
tggacgtttc cctggcttac cgtgatgacg cgtttgctga gtggactgaa atggcccatg
660
aaagagtacc acggaaactc aaatgcacct tcacatctcc caagactcca gagcatgagg
720
gccgttacta tgaatgtgat gtccttcctt tcatggaaat tgggtctgtg gcccataagt
780
tttacctttt aaacatccgg ctgcctgtga atgagaagaa gaaaatcaat gtgggaattg
840
gggagataaa ggatatccgg ttggtgggga tccaccaaaa tggaggcttc accaaggtgt
900
ggtttgccat gaagaccttc cttacgccca gcatcttcat cattatggtg tggtattgga
960
ggaggatcac catgatgtcc cgacccccag tgcttctgga aaaagtcatc tttgccc
1017

<210> 4374
<211> 272
<212> PRT
<213> Homo sapiens

<400> 4374
Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile
1 5 10 15
Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
20 25 30
Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
35 40 45
Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
50 55 60
Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65 70 75 80
Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
85 90 95
Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
100 105 110
Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu
115 120 125
Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala
130 135 140
Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu
145 150 155 160
Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr
165 170 175
Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His

```
            180                 185                 190
Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys
        195                 200                 205
Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile
    210                 215                 220
His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe
225                 230                 235                 240
Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile
                245                 250                 255
Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala
            260                 265                 270
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<210> 4375
<211> 1966
<212> DNA
<213> Homo sapiens

<400> 4375
aaggtgcctg cattgtatac caccacgtcg ggcaggtgct cctggaggga tttcttgatg
60
ttcctctcca ccttatccag gtactcatca tcctctgtgc cccactccag ctccaccttc
120
cgcctgacgg ccagctttgg gagggccggc cccgggatgc tacacacaac ccagctgtac
180
cagcatgtgc cagagacacg ctggccaatc gtgtactcgc cgcgctacaa catcaccttc
240
atgggcctgg agaagctgca tccctttgat gccggaaaat ggggcaaagt gatcaatttc
300
ctaaaagaag agaagcttct gtctgacagc atgctggtgg aggcgcggga ggcctcggag
360
gaggacctgc tggtggtgca cacgaggcgc tatcttaatg agctcaagtg gtcctttgct
420
gttgctacca tcacagaaat ccccccccgtt atcttcctcc ccaacttcct tgtgcagagg
480
aaggtgctga ggccccttcg gacccagaca ggaggaacca taatggcggg gaagctggct
540
gtggagcgag gctgggccat caacgtgggg ggtggcttcc accactgctc cagcgaccgt
600
ggcgggggct tctgtgccta tgcggacatc acgctcgcca tcaagtttct gtttgagcgt
660
gtggagggca tctccagggc taccatcatt gatcttgatg cccatcaggg caatgggcat
720
gagcgagact tcatggacga caagtgtgtg acatgcatgg atgtctacaa ccgccacatc
780
tacccagggg accgctttgc caagcaggcc atcaggcgga aggtggagct ggagtggggc
840
acagaggatg atgagtacct ggataaggtg gagaggaaca tcaagaaatc cctccaggag
900
cacctgcccg acgtggtggt atacaatgca ggcaccgaca tcctcgaggg ggaccgcctt
960
gggggctgt ccatcagccc agcgggcatc gtgaagcggg atgagctggt gttccggatg
1020
gtccgtggcc gccgggtgcc catccttatg gtgacctcag gcgggtacca gaagcgcaca
1080

gcccgcatca ttgctgactc catacttaat ctgtttggcc tggggctcat tgggcctgag
1140
tcacccagcg tctccgcaca gaactcagac acaccgctgc ttccccctgc agtgccctga
1200
cccttgctgc cctgcctgtc acgtggccct gcctatccgc cccttagtgc tttttgtttt
1260
ctaacctcat ggggtggtgg aggcagcctt cagtgagcat ggaggggcag ggccatccct
1320
ggctggggcc tggagctggc ccttcctcta cttttccctg ctggaagcca gaagggcttg
1380
aggcctctat gggtgggggc agaaagcaga gcctgtgtcc caggggaccc acacgaagtc
1440
accagcccat aggtccaggg aggcaggcag ttaactgaga attggagagg acaggctagg
1500
tcccaggcac agcgagggcc ctgggcttgg ggtgttctgg ttttgagaac ggcagaccca
1560
ggtcggagtg aggaagcttc cacctccatc ctgactaggc ctgcatccta actgggcctc
1620
cctccctccc cttggtcatg ggatttgctg ccctctttgc cccagagctg aagagctata
1680
ggcactggtg tggatggccc aggaggtgct ggagctaggt ctccaggtgg gcctggttcc
1740
caggcagcag gtgggaaccc tgggcctgga tgtgaggggc ggtcaggaag gggtacaggt
1800
gggttccctc atctggagtt ccccctcaat aaagcaaggt ctggacctgc cttcccaggc
1860
ccttctgtgg gggtgaaggt ggggaaggcc tgcggcgccc agatcactgc cttagcagta
1920
gtcttgcctg ttcagtgcaa ggggcaggtt ttgggggggag gaattc
1966

<210> 4376
<211> 399
<212> PRT
<213> Homo sapiens

<400> 4376
Lys Val Pro Ala Leu Tyr Thr Thr Thr Ser Gly Arg Cys Ser Trp Arg
 1   5   10   15
Asp Phe Leu Met Phe Leu Ser Thr Leu Ser Arg Tyr Ser Ser Ser Ser
            20   25   30
Val Pro His Ser Ser Ser Thr Phe Arg Leu Thr Ala Ser Phe Gly Arg
        35   40   45
Ala Gly Pro Gly Met Leu His Thr Thr Gln Leu Tyr Gln His Val Pro
    50   55   60
Glu Thr Arg Trp Pro Ile Val Tyr Ser Pro Arg Tyr Asn Ile Thr Phe
65   70   75   80
Met Gly Leu Glu Lys Leu His Pro Phe Asp Ala Gly Lys Trp Gly Lys
                85   90   95
Val Ile Asn Phe Leu Lys Glu Glu Lys Leu Leu Ser Asp Ser Met Leu
            100   105   110
Val Glu Ala Arg Glu Ala Ser Glu Glu Asp Leu Leu Val Val His Thr
        115   120   125
Arg Arg Tyr Leu Asn Glu Leu Lys Trp Ser Phe Ala Val Ala Thr Ile

```
    130                 135                 140
Thr Glu Ile Pro Pro Val Ile Phe Leu Pro Asn Phe Leu Val Gln Arg
145                 150                 155                 160
Lys Val Leu Arg Pro Leu Arg Thr Gln Thr Gly Gly Thr Ile Met Ala
                165                 170                 175
Gly Lys Leu Ala Val Glu Arg Gly Trp Ala Ile Asn Val Gly Gly Gly
            180                 185                 190
Phe His His Cys Ser Ser Asp Arg Gly Gly Gly Phe Cys Ala Tyr Ala
        195                 200                 205
Asp Ile Thr Leu Ala Ile Lys Phe Leu Phe Glu Arg Val Glu Gly Ile
    210                 215                 220
Ser Arg Ala Thr Ile Ile Asp Leu Asp Ala His Gln Gly Asn Gly His
225                 230                 235                 240
Glu Arg Asp Phe Met Asp Asp Lys Cys Val Thr Cys Met Asp Val Tyr
                245                 250                 255
Asn Arg His Ile Tyr Pro Gly Asp Arg Phe Ala Lys Gln Ala Ile Arg
            260                 265                 270
Arg Lys Val Glu Leu Glu Trp Gly Thr Glu Asp Asp Glu Tyr Leu Asp
        275                 280                 285
Lys Val Glu Arg Asn Ile Lys Lys Ser Leu Gln Glu His Leu Pro Asp
    290                 295                 300
Val Val Val Tyr Asn Ala Gly Thr Asp Ile Leu Glu Gly Asp Arg Leu
305                 310                 315                 320
Gly Gly Leu Ser Ile Ser Pro Ala Gly Ile Val Lys Arg Asp Glu Leu
                325                 330                 335
Val Phe Arg Met Val Arg Gly Arg Arg Val Pro Ile Leu Met Val Thr
            340                 345                 350
Ser Gly Gly Tyr Gln Lys Arg Thr Ala Arg Ile Ile Ala Asp Ser Ile
        355                 360                 365
Leu Asn Leu Phe Gly Leu Gly Leu Ile Gly Pro Glu Ser Pro Ser Val
    370                 375                 380
Ser Ala Gln Asn Ser Asp Thr Pro Leu Leu Pro Pro Ala Val Pro
385                 390                 395
```

<210> 4377
<211> 812
<212> DNA
<213> Homo sapiens

<400> 4377
ntcctgggga ggcggtgccc cccatggcga ggccggcgag agcagggcct gcttcccccc
60
gaggacagcc gcctgtggca gtatcttctg agccgctcca tgcgggagca cccggcgctg
120
cgaagcctga ggctgctgac cctggagcag ccgcaggggg attctatgat gacctgcgag
180
caggcccagc tcttggccaa cctggcgcgg ctcatccagg ccaagaaggc gctggacctg
240
ggcaccttca cgggctactc cgccctggcc ctggccctgg cgctgcccgc ggacgggcgc
300
gtggtgacct gcgaggtgga cgcgcagccc ccggagctgg gacggcccct gtggaggcag
360
gccgaggcgg agcacaagat tcgactccgg ctgaagcccg ccttggagac cctggacgag
420

ctgctggcgg cgggcgaggc cggcaccttc gacgtggccg tggtggatgc ggacaaggag
480
aactgctccg cctactacga gcgctgcctg cagctgctgc gacccggagg catcctcgcc
540
gtcctcagag tcctgtggcg cgggaaggtg ctgcaacctc cgaaagggga cgtggcggcc
600
gagtgtgtgc gaaacctaaa cgaacgcatc cggcgggacg tcagggtcta catcagcctc
660
ctgcccctgg gcgatggact caccttggcc ttcaagatct agggctggcc cctagtgagt
720
gggctcgagg gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa
780
ataaagtggg gctgggacac acgaaaaaaa aa
812

<210> 4378
<211> 233
<212> PRT
<213> Homo sapiens

<400> 4378
Xaa Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Gly
1 5 10 15
Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser Arg
20 25 30
Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu Thr Leu
35 40 45
Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln Ala Gln Leu
50 55 60
Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys Ala Leu Asp Leu
65 70 75 80
Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu Ala Leu Ala Leu Pro
85 90 95
Ala Asp Gly Arg Val Val Thr Cys Glu Val Asp Ala Gln Pro Pro Glu
100 105 110
Leu Gly Arg Pro Leu Trp Arg Gln Ala Glu Ala Glu His Lys Ile Arg
115 120 125
Leu Arg Leu Lys Pro Ala Leu Glu Thr Leu Asp Glu Leu Leu Ala Ala
130 135 140
Gly Glu Ala Gly Thr Phe Asp Val Ala Val Val Asp Ala Asp Lys Glu
145 150 155 160
Asn Cys Ser Ala Tyr Tyr Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly
165 170 175
Gly Ile Leu Ala Val Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln
180 185 190
Pro Pro Lys Gly Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu
195 200 205
Arg Ile Arg Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly
210 215 220
Asp Gly Leu Thr Leu Ala Phe Lys Ile
225 230

<210> 4379
<211> 2347

<212> DNA
<213> Homo sapiens

<400> 4379
ngaggaccaa gccatgcgtg cctttgagct aatgaggagc aacgcggccc tgttccagct
60
gggctcggcc ccgcggtgtg ctggattgtg tgcacgactc tgaagctgca gatggagaag
120
ggggaggacc cggtccccac ctgcctcacc cgcacggggc tgttcctgcg tttcctctgc
180
agccggttcc cgcggggcgc acagctgcgg ggcgcgctgc ggacgctgag cctcctggcc
240
gcgcagggcc tgtgggcgca gacgtccgtg cttcaccgag aggatctgga aaggctcggg
300
gtgcaggagt ccgacctccg tctgttcctg gacggagaca tcctccgcca ggacagagtc
360
tccaaaggct gctactcctt catccacctc agcttccagc agtttctcac tgccctgttc
420
tacaccctgg agaaggagga ggaagaggat agggacggcc acacctggga cattggggac
480
gtacagaagc tgctttccgg agtagaaaga ctcaggaacc ccgacctgat ccaagcaggc
540
tactactcct ttggcctcgc taacgagaag agagccaagg agttggaggc cacttttggc
600
tgccggatgt caccggacat caaacaggaa ttgctgcgat gcgacataag ttgtaagggt
660
ggacattcaa cggtgacaga cctgcaggag ctgctcggct gtctgtacga gtctcaggag
720
gaggagctgg tgaaggaggt gatggctcag ttcaaagaaa tatccctgca cttaaatgca
780
gtagacgttg tgccatcttc attctgcgtc aagcactgtc gaaacctgca gaaaatgtca
840
ctgcaggtaa taaaggagaa tctcccggag aatgtcactg cgtctgaatc agacgccgag
900
gttgagagat cccaggatga tcagcacatg cttcctttct ggacggacct ttgttccata
960
tttggatcaa ataaggatct gatgggtcta gcaatcaatg atagctttct cagtgcctcc
1020
ctagtaagga tcctgtgtga acaaatagcc tctgacacct gtcatctcca gagagtggtg
1080
ttcaaaaaca tttccccagc tgatgctcat cggaacctcn tgcctnnagc tcttcgaggt
1140
cacaagactg taacgtatct gacccttcaa ggcaatgacc aggatgatat gtttcccgca
1200
ttgtgtgagg tcttgagaca tccagaatgt aacctgcgat atctcgggtt ggtgtcttgt
1260
tccgctacca ctcagcagtg ggctgatctc tccttggccc ttgaagtcaa ccagtccctg
1320
acgtgcgtaa acctctccga caatgagctt ctggatgagg gtgctaagtt gctgtacaca
1380
actttgagac accccaagtg ctttctgcag aggttgtcgt tggaaaactg tcaccttaca
1440
gaagccaatt gcaaggacct tgctgctgtg ttggttgtca gccgggagct gacacacctg
1500

tgcttggcca agaaccccat tgggaataca ggggtgaagt ttctgtgtga gggcttgagg
1560
taccccgagt gtaaactgca gaccttggtg ctttggaact gcgacataac tagcgatggc
1620
tgctgcgatc tcacaaagct tctccaagaa aaatcaagcc tgttgtgttt ggatctgggg
1680
ctgaatcaca taggagttaa gggaatgaag ttcctgtgtg aggctttgag gaaaccactg
1740
tgcaacttga gatgtctgtg gttgtgggga tgttccatcc ctccgttcag ttgtgaagac
1800
gtctgctctg ccctcagctg caaccagagc ctcgtcactc tggacctggg tcagaatccc
1860
ttggggtcta gtggagtgaa gatgctgttt gaaaccttga catgttccag tggcaccctc
1920
cggacactca ggttgaaaat agatgacttt aatgatgaac tcaataagct gctggaagaa
1980
atagaagaaa aaaacccaca actgattatt gatactgaga aacatcatcc ctgggaagaa
2040
aggccttctt ctcatgactt catgatctga atccccccga gtcattcatt ctccatgaag
2100
tcatcgattt tccaggtgtg ggtgaactgc ctgtgactcc tctcctcccc cgcccctacc
2160
cctcagggat aatgagttca ttgctgggct agatgtttta gccatgattc tgcctctgtt
2220
ttatacctgc acacatcctt atctttgtta catatgaaat atctgtatca cgggtatatt
2280
gagagaaata aaggtgagag cattcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
2340
aaaaaaa
2347

<210> 4380
<211> 652
<212> PRT
<213> Homo sapiens

<400> 4380
Met Glu Lys Gly Glu Asp Pro Val Pro Thr Cys Leu Thr Arg Thr Gly
1 5 10 15
Leu Phe Leu Arg Phe Leu Cys Ser Arg Phe Pro Arg Gly Ala Gln Leu
20 25 30
Arg Gly Ala Leu Arg Thr Leu Ser Leu Leu Ala Ala Gln Gly Leu Trp
35 40 45
Ala Gln Thr Ser Val Leu His Arg Glu Asp Leu Glu Arg Leu Gly Val
50 55 60
Gln Glu Ser Asp Leu Arg Leu Phe Leu Asp Gly Asp Ile Leu Arg Gln
65 70 75 80
Asp Arg Val Ser Lys Gly Cys Tyr Ser Phe Ile His Leu Ser Phe Gln
85 90 95
Gln Phe Leu Thr Ala Leu Phe Tyr Thr Leu Glu Lys Glu Glu Glu Glu
100 105 110
Asp Arg Asp Gly His Thr Trp Asp Ile Gly Asp Val Gln Lys Leu Leu
115 120 125
Ser Gly Val Glu Arg Leu Arg Asn Pro Asp Leu Ile Gln Ala Gly Tyr

```
    130                 135                 140
Tyr Ser Phe Gly Leu Ala Asn Glu Lys Arg Ala Lys Glu Leu Glu Ala
145                 150                 155                 160
Thr Phe Gly Cys Arg Met Ser Pro Asp Ile Lys Gln Glu Leu Leu Arg
                165                 170                 175
Cys Asp Ile Ser Cys Lys Gly Gly His Ser Thr Val Thr Asp Leu Gln
            180                 185                 190
Glu Leu Leu Gly Cys Leu Tyr Glu Ser Gln Glu Glu Glu Leu Val Lys
        195                 200                 205
Glu Val Met Ala Gln Phe Lys Glu Ile Ser Leu His Leu Asn Ala Val
    210                 215                 220
Asp Val Val Pro Ser Ser Phe Cys Val Lys His Cys Arg Asn Leu Gln
225                 230                 235                 240
Lys Met Ser Leu Gln Val Ile Lys Glu Asn Leu Pro Glu Asn Val Thr
                245                 250                 255
Ala Ser Glu Ser Asp Ala Glu Val Glu Arg Ser Gln Asp Asp Gln His
            260                 265                 270
Met Leu Pro Phe Trp Thr Asp Leu Cys Ser Ile Phe Gly Ser Asn Lys
        275                 280                 285
Asp Leu Met Gly Leu Ala Ile Asn Asp Ser Phe Leu Ser Ala Ser Leu
    290                 295                 300
Val Arg Ile Leu Cys Glu Gln Ile Ala Ser Asp Thr Cys His Leu Gln
305                 310                 315                 320
Arg Val Val Phe Lys Asn Ile Ser Pro Ala Asp Ala His Arg Asn Leu
                325                 330                 335
Xaa Pro Xaa Ala Leu Arg Gly His Lys Thr Val Thr Tyr Leu Thr Leu
            340                 345                 350
Gln Gly Asn Asp Gln Asp Asp Met Phe Pro Ala Leu Cys Glu Val Leu
        355                 360                 365
Arg His Pro Glu Cys Asn Leu Arg Tyr Leu Gly Leu Val Ser Cys Ser
    370                 375                 380
Ala Thr Thr Gln Gln Trp Ala Asp Leu Ser Leu Ala Leu Glu Val Asn
385                 390                 395                 400
Gln Ser Leu Thr Cys Val Asn Leu Ser Asp Asn Glu Leu Leu Asp Glu
                405                 410                 415
Gly Ala Lys Leu Leu Tyr Thr Thr Leu Arg His Pro Lys Cys Phe Leu
            420                 425                 430
Gln Arg Leu Ser Leu Glu Asn Cys His Leu Thr Glu Ala Asn Cys Lys
        435                 440                 445
Asp Leu Ala Ala Val Leu Val Val Ser Arg Glu Leu Thr His Leu Cys
    450                 455                 460
Leu Ala Lys Asn Pro Ile Gly Asn Thr Gly Val Lys Phe Leu Cys Glu
465                 470                 475                 480
Gly Leu Arg Tyr Pro Glu Cys Lys Leu Gln Thr Leu Val Leu Trp Asn
                485                 490                 495
Cys Asp Ile Thr Ser Asp Gly Cys Cys Asp Leu Thr Lys Leu Leu Gln
            500                 505                 510
Glu Lys Ser Ser Leu Leu Cys Leu Asp Leu Gly Leu Asn His Ile Gly
        515                 520                 525
Val Lys Gly Met Lys Phe Leu Cys Glu Ala Leu Arg Lys Pro Leu Cys
    530                 535                 540
Asn Leu Arg Cys Leu Trp Leu Trp Gly Cys Ser Ile Pro Pro Phe Ser
545                 550                 555                 560
Cys Glu Asp Val Cys Ser Ala Leu Ser Cys Asn Gln Ser Leu Val Thr
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                565                 570                 575
Leu Asp Leu Gly Gln Asn Pro Leu Gly Ser Ser Gly Val Lys Met Leu
            580                 585                 590
Phe Glu Thr Leu Thr Cys Ser Ser Gly Thr Leu Arg Thr Leu Arg Leu
        595                 600                 605
Lys Ile Asp Asp Phe Asn Asp Glu Leu Asn Lys Leu Leu Glu Glu Ile
    610                 615                 620
Glu Glu Lys Asn Pro Gln Leu Ile Ile Asp Thr Glu Lys His His Pro
625                 630                 635                 640
Trp Glu Glu Arg Pro Ser Ser His Asp Phe Met Ile
                645                 650
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<210> 4381
<211> 1638
<212> DNA
<213> Homo sapiens

<400> 4381
nnagagcccg gggcgagtgg gcctctgctc gtgggtggtt ctcgtggagg tcagctcccg
60
cgtgtctccg ctcgacaggg tgcttgggca gagcccatcg ggtaggcgcg ggccatggcg
120
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180
aggcagcggg agcagatgga ggtgctgaag cagcgcatcg ccgaggagac catcctcaag
240
tcgcaggtgg acaagaggtt ctcggcgcat tacgacgccg tggaggccga gctgaagtcc
300
agcgcggtgg gcctggtgac cctgaacgac atgaaggccc ggcaggaggc cctggtcagg
360
gagcgcgagc ggcagctggc caagcgccag cacctggagg agcagcggct gcagcaggag
420
cggcagcggg agcaggagca gcggcgcgag cgcaagcgta agatctcctg cctgtccttt
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540
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600
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720
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780
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960
gagaaggacg agtcgcacgc gggcaaggtg gtgctgcgca gctggtacga gaagaacaag
1020
cacatcttcc ccgccagccg ctgggaggcc tatgaccccg agaagaagtg ggacaagtac
1080

accatccgct aacacccgcc tgccagagcg gaaaccgggg gtggggggag acactcattt
1140
ctaggcccca tcaccagtca cttgatttcg tgaccttgat ttcttccccc aaatttaata
1200
aagacagagg gttctcatga ttcacattgg ttgtgctatt gctgatgtta tgctttggtt
1260
gcttggttgg tcttttctga gtattttagt gttgccacct ggatttgctg cattgctctg
1320
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1380
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1440
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1620
aaaaaaaaaa aaaaaaaa
1638

<210> 4382
<211> 325
<212> PRT
<213> Homo sapiens

<400> 4382
Met Ala Gln Tyr Lys Gly Thr Met Arg Glu Ala Gly Arg Ala Met His
1 5 10 15
Leu Leu Lys Lys Arg Glu Arg Gln Arg Glu Gln Met Glu Val Leu Lys
20 25 30
Gln Arg Ile Ala Glu Glu Thr Ile Leu Lys Ser Gln Val Asp Lys Arg
35 40 45
Phe Ser Ala His Tyr Asp Ala Val Glu Ala Glu Leu Lys Ser Ser Ala
50 55 60
Val Gly Leu Val Thr Leu Asn Asp Met Lys Ala Arg Gln Glu Ala Leu
65 70 75 80
Val Arg Glu Arg Glu Arg Gln Leu Ala Lys Arg Gln His Leu Glu Glu
85 90 95
Gln Arg Leu Gln Gln Glu Arg Gln Arg Glu Gln Glu Gln Arg Arg Glu
100 105 110
Arg Lys Arg Lys Ile Ser Cys Leu Ser Phe Ala Leu Asp Asp Leu Asp
115 120 125
Asp Gln Ala Asp Ala Ala Glu Ala Arg Arg Ala Gly Asn Leu Gly Lys
130 135 140
Asn Pro Asp Val Asp Thr Ser Phe Leu Pro Asp Arg Asp Arg Glu Glu
145 150 155 160
Glu Glu Asn Arg Leu Arg Glu Glu Leu Arg Gln Glu Trp Glu Ala Gln
165 170 175
Arg Glu Lys Val Lys Asp Glu Glu Met Glu Val Thr Phe Ser Tyr Trp
180 185 190
Asp Gly Ser Gly His Arg Arg Thr Val Arg Val Arg Lys Gly Asn Thr
195 200 205
Val Gln Gln Phe Leu Lys Lys Ala Leu Gln Gly Leu Arg Lys Asp Phe

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    210                 215                 220
Leu Glu Leu Arg Ser Ala Gly Val Glu Gln Leu Met Phe Ile Lys Glu
225                 230                 235                 240
Asp Leu Ile Leu Pro His Tyr His Thr Phe Tyr Asp Phe Ile Ile Ala
                245                 250                 255
Arg Ala Arg Gly Lys Ser Gly Pro Leu Phe Ser Phe Asp Val His Asp
            260                 265                 270
Asp Val Arg Leu Leu Ser Asp Ala Thr Met Glu Lys Asp Glu Ser His
        275                 280                 285
Ala Gly Lys Val Val Leu Arg Ser Trp Tyr Glu Lys Asn Lys His Ile
    290                 295                 300
Phe Pro Ala Ser Arg Trp Glu Ala Tyr Asp Pro Glu Lys Lys Trp Asp
305                 310                 315                 320
Lys Tyr Thr Ile Arg
                325
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<210> 4383
<211> 419
<212> DNA
<213> Homo sapiens

<400> 4383
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aaaatgaaat ataaagcgcc cactgactat tgctttgttt taaagcaccc ccaaattcag
120
aaggagtccc agtatatcaa gtatctctgc tgtgatgaca caagaaccct taaccagtgg
180
gtcatgggaa tacggatagc caagtatggg aagactctct atgataacta ccagcgggct
240
gtggcaaagg ctggacttgc ctctcggtgg acaaacttgg ggacagtcaa tgcagctgca
300
ccagctcagc catttacagg acctaaaaca ggcaccaccc agcccaatgg acagattccc
360
caggctacac atttcttcag tgctgttctc caagaagccc agagacatgc tgaaaactn
419

<210> 4384
<211> 139
<212> PRT
<213> Homo sapiens

<400> 4384
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Arg Asp Leu Ala Cys Phe Ile Gln Phe Glu Asn Val Asn Ile Tyr Tyr
 1               5                  10                  15
Gly Thr Gln His Lys Met Lys Tyr Lys Ala Pro Thr Asp Tyr Cys Phe
            20                  25                  30
Val Leu Lys His Pro Gln Ile Gln Lys Glu Ser Gln Tyr Ile Lys Tyr
        35                  40                  45
Leu Cys Cys Asp Asp Thr Arg Thr Leu Asn Gln Trp Val Met Gly Ile
    50                  55                  60
Arg Ile Ala Lys Tyr Gly Lys Thr Leu Tyr Asp Asn Tyr Gln Arg Ala
65                  70                  75                  80
Val Ala Lys Ala Gly Leu Ala Ser Arg Trp Thr Asn Leu Gly Thr Val
```

```
                85                  90                  95
Asn Ala Ala Ala Pro Ala Gln Pro Phe Thr Gly Pro Lys Thr Gly Thr
            100                 105                 110
Thr Gln Pro Asn Gly Gln Ile Pro Gln Ala Thr His Phe Phe Ser Ala
        115                 120                 125
Val Leu Gln Glu Ala Gln Arg His Ala Glu Asn
    130                 135
```

<210> 4385
<211> 754
<212> DNA
<213> Homo sapiens

<400> 4385
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60
tcccggctgc tcaagcgggt gggaaggagc ggccactctt gctgaaaggt ggctgggaga
120
ggtcctggtc agagtcggag tcagagtccc aggaggggag tggagggctc aggcactggt
180
gccccttgtg gcctcttagg ctcgaggcct tgggacaggc ccccgagcac aaagtgaggc
240
tgtctatgga gttctgcagc acgtgcacag cagaccatat atcactcagt tccttctgga
300
ggtcatcctt ccagcagcca ctggctccct gcggtatctc ttcagtctcc ggacaggcgg
360
ctgtctcatg accctgctgc ttcatcttgg tcaggatttt gcggcatttc acctgcgttt
420
tctgcatttt ctgaatgttc accaagttct ctgagatctc atcctcctgc gcttcttcaa
480
gctgctgaat cttgatttgc tgcaagcagc tctccttctc caacatggtc actgagtggt
540
tcaggaactc gaaagccttg gtctgggcct gtaactggct cttgagtgac ccaagttcac
600
atcgcaggag cttctgggag tcgggaatca tcacaatggt cttggctttg actttggaag
660
agctggtctc caagggcttc acataccacc tgttcatgct ctcccatcag ggaccacgaa
720
gaaagtcctc agctgtgacg ctgaagtttg atca
754

<210> 4386
<211> 85
<212> PRT
<213> Homo sapiens

<400> 4386
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Gly Cys Leu Trp Ser Ser Ala Ala Arg Ala Gln Gln Thr Ile Tyr His
 1               5                  10                  15
Ser Val Pro Ser Gly Gly His Pro Ser Ser Ser His Trp Leu Pro Ala
            20                  25                  30
Val Ser Leu Gln Ser Pro Asp Arg Arg Leu Ser His Asp Pro Ala Ala
        35                  40                  45
Ser Ser Trp Ser Gly Phe Cys Gly Ile Ser Pro Ala Phe Ser Ala Phe
```

```
    50                  55                  60
Ser Glu Cys Ser Pro Ser Ser Leu Arg Ser His Pro Pro Ala Leu Leu
65                  70                  75                  80
Gln Ala Ala Glu Ser
                85
```

<210> 4387
<211> 341
<212> DNA
<213> Homo sapiens

<400> 4387
ggggggggcc ttcccatctt tttccctttt atgggggggg ggtttttaa aaaaaaaggg
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gggccccccc aaaaggggggg gggggaagg gggttttccc accccaaaaa acccccccc
120
ccccccgggn gggggggaag gggggggggg ttttcccccc ctccccccc ccctaaaaaa
180
aaaacccgga aaatttttt tccccccccc ccaaaaaaaa aaaaaaaacc gggggcccc
240
cctttttttg gggggggggg ttttttttt ttttttttt ttttttttt ttttttttac
300
aaaacagaga atgtttattg tgccagaggg tggagtgtgc n
341

<210> 4388
<211> 113
<212> PRT
<213> Homo sapiens

<400> 4388
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Gly Gly Gly Leu Pro Ile Phe Phe Pro Phe Met Gly Gly Gly Phe Phe
 1               5                  10                  15
Lys Lys Lys Gly Gly Pro Pro Gln Lys Gly Gly Gly Gly Arg Gly Phe
            20                  25                  30
Ser His Pro Lys Lys Pro Pro Pro Pro Pro Gly Xaa Gly Gly Arg Gly
        35                  40                  45
Gly Gly Phe Phe Pro Pro Pro Pro Pro Pro Lys Lys Lys Thr Arg Lys
    50                  55                  60
Ile Phe Phe Pro Pro Pro Pro Lys Lys Lys Lys Lys Pro Gly Gly Pro
65                  70                  75                  80
Pro Phe Phe Gly Gly Gly Gly Phe Phe Phe Phe Phe Phe Phe Phe Phe
                85                  90                  95
Phe Phe Phe Tyr Lys Thr Glu Asn Val Tyr Cys Ala Arg Gly Trp Ser
            100                 105                 110
Val
```

<210> 4389
<211> 1895
<212> DNA
<213> Homo sapiens

<400> 4389

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gctgccgagg gccgcgcggt gtacgtggtg gacgacgcag ctgtcctggg cgcagaggac
120
ccagcggtgt acggcgattc tgcccgtgag aaggcattgc gtggagctct gcgagcctcc
180
gtggaacgac gcctgagtcg ccacgacgtc gtcatcctgg actcgcttaa ctacatcaaa
240
ggtttccgtt acgagctcta ctgcctggca cgggcggcgc gcaccccgct ctgcctggtc
300
tactgcgtac ggcccggcgg cccgatcgcg ggacctcagg tggcgggcgc gaacgagaac
360
cctggccgga acgtcagtgt gagttggcgg ccacgcgctg aggaggacgg gagagcccag
420
gcggcgggca gcagcgtcct cagggaactg catactgcgg actctgtagt aaatggaagt
480
gcccaggccg acgtacccaa ggaactggag cgagaagaat ccggggctgc ggagtctcca
540
gctcttgtga ctccggattc agagaaatct gcaaagcatg ggtccggtgc cttttactct
600
cccgaactcc tggaggccct aacgctgcgc tttgaggctc ccgattctcg gaatcgctgg
660
gaccggcctt tattcacttt ggtgggcata gaggagccgt tgcccccggc ggggatccgc
720
tctgccctgt ttgagaaccg ggccccacca ccccatcagt ctacgcagtc ccagcccctc
780
gcctccggca gctttctgca ccagttggac caggtcacga gtcaagtact ggccggattg
840
atggaagcgc agaagagcgc tgtccccggg gacttgctca cgcttcctgg taccacagag
900
cacttgcggt ttacccggcc cttgaccatg gcagaactga gtcgccttcg tcgccagttt
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1020
cttcagtatt tgagccagag cctgcactaa ccagaggagg taggggggaa gccatggctt
1080
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1140
cgatgcagta ctgtactaga gctgttgtga ctgattcact caaactttcc tgcatacccc
1200
tgtgccaggc cttgggttta cagcataagt tcagactaaa gagaatggag aactattgtg
1260
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1320
gatcctactt gggctatcac agagcattga ccattggctt ccctcatctg aggcgtggga
1380
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1440
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1560
atccttgaga aactttgttt ttgtggaagt aagaaagtta tctactagat tatttcctct
1620

aataaaatct tttaaaatag tctactggaa tctctttcac ttaatgttcc ctgtgtaact
1680
tcatgtaaca ttttaggtat acttgtcatt gttctgcctt taagtgaagt agtattttga
1740
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1800
gtaactgttt tgcttcattc tgcatttcaa ggcaaatatc attgtaagct tgtctttcat
1860
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1895

<210> 4390
<211> 335
<212> PRT
<213> Homo sapiens

<400> 4390
Arg Val Ala Arg Gly Val Ala Ala Glu Gly Arg Ala Val Tyr Val Val
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Asp Asp Ala Ala Val Leu Gly Ala Glu Asp Pro Ala Val Tyr Gly Asp
20 25 30
Ser Ala Arg Glu Lys Ala Leu Arg Gly Ala Leu Arg Ala Ser Val Glu
35 40 45
Arg Arg Leu Ser Arg His Asp Val Val Ile Leu Asp Ser Leu Asn Tyr
50 55 60
Ile Lys Gly Phe Arg Tyr Glu Leu Tyr Cys Leu Ala Arg Ala Ala Arg
65 70 75 80
Thr Pro Leu Cys Leu Val Tyr Cys Val Arg Pro Gly Gly Pro Ile Ala
85 90 95
Gly Pro Gln Val Ala Gly Ala Asn Glu Asn Pro Gly Arg Asn Val Ser
100 105 110
Val Ser Trp Arg Pro Arg Ala Glu Glu Asp Gly Arg Ala Gln Ala Ala
115 120 125
Gly Ser Ser Val Leu Arg Glu Leu His Thr Ala Asp Ser Val Val Asn
130 135 140
Gly Ser Ala Gln Ala Asp Val Pro Lys Glu Leu Glu Arg Glu Glu Ser
145 150 155 160
Gly Ala Ala Glu Ser Pro Ala Leu Val Thr Pro Asp Ser Glu Lys Ser
165 170 175
Ala Lys His Gly Ser Gly Ala Phe Tyr Ser Pro Glu Leu Leu Glu Ala
180 185 190
Leu Thr Leu Arg Phe Glu Ala Pro Asp Ser Arg Asn Arg Trp Asp Arg
195 200 205
Pro Leu Phe Thr Leu Val Gly Ile Glu Glu Pro Leu Pro Pro Ala Gly
210 215 220
Ile Arg Ser Ala Leu Phe Glu Asn Arg Ala Pro Pro Pro His Gln Ser
225 230 235 240
Thr Gln Ser Gln Pro Leu Ala Ser Gly Ser Phe Leu His Gln Leu Asp
245 250 255
Gln Val Thr Ser Gln Val Leu Ala Gly Leu Met Glu Ala Gln Lys Ser
260 265 270
Ala Val Pro Gly Asp Leu Leu Thr Leu Pro Gly Thr Thr Glu His Leu
275 280 285
Arg Phe Thr Arg Pro Leu Thr Met Ala Glu Leu Ser Arg Leu Arg Arg

290 295 300
Gln Phe Ile Ser Tyr Thr Lys Met His Pro Asn Asn Glu Asn Leu Pro
305 310 315 320
Gln Leu Ala Asn Met Phe Leu Gln Tyr Leu Ser Gln Ser Leu His
325 330 335

<210> 4391
<211> 988
<212> DNA
<213> Homo sapiens

<400> 4391
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120
ggaggtggca tgcgaccccc acccaactcc ctcgccggcc caggcctgcc tgccatgaac
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atgggcccag gagttcgtgg cccgtgggcc agccccagtg gaaactcgat cccctactcc
240
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300
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360
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420
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660
tgcgggccta ggcttctgcc cagcgccccc gctcagggcg aggggctgag gtcacacctc
720
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780
tcttaccatt ttattaaaaa cgcaaggacc tcagagacgt tcttttctgt atggaccctt
840
cctgccattt gtattttgtc ccagagagaa aggctctttg gggggccccc ctccccagga
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960
aaaaaaaaaa aaaaaaaaaa aaaaaaaa
988

<210> 4392
<211> 211
<212> PRT
<213> Homo sapiens

<400> 4392
Xaa Pro Phe Ser Trp Pro His Gly Ala Ser Pro Arg Ala Gln Gly His

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 1               5                  10                  15
Pro Ser Met Gly Gly Pro Met Gln Arg Val Thr Pro Pro Arg Gly Met
            20                  25                  30
Ala Ser Val Gly Pro Gln Ser Tyr Gly Gly Gly Met Arg Pro Pro Pro
        35                  40                  45
Asn Ser Leu Ala Gly Pro Gly Leu Pro Ala Met Asn Met Gly Pro Gly
    50                  55                  60
Val Arg Gly Pro Trp Ala Ser Pro Ser Gly Asn Ser Ile Pro Tyr Ser
65                  70                  75                  80
Ser Ser Ser Pro Gly Ser Tyr Thr Gly Pro Pro Gly Gly Gly Gly Pro
                85                  90                  95
Pro Gly Thr Pro Ile Met Pro Ser Pro Gly Asp Ser Thr Asn Ser Ser
            100                 105                 110
Glu Asn Met Tyr Thr Ile Met Asn Pro Ile Gly Gln Gly Ala Gly Arg
        115                 120                 125
Ala Asn Phe Pro Leu Gly Pro Gly Pro Glu Gly Pro Met Ala Ala Met
    130                 135                 140
Ser Ala Met Glu Pro His His Val Asn Gly Ser Leu Gly Ser Gly Asp
145                 150                 155                 160
Met Asp Gly Leu Pro Lys Ser Ser Pro Gly Ala Val Ala Gly Leu Ser
                165                 170                 175
Asn Ala Pro Gly Thr Pro Arg Asp Asp Gly Glu Met Ala Ala Ala Gly
            180                 185                 190
Thr Phe Leu His Pro Phe Pro Ser Glu Ser Tyr Ser Pro Gly Met Thr
        195                 200                 205
Met Ser Val
    210
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<210> 4393
<211> 2171
<212> DNA
<213> Homo sapiens

<400> 4393

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gaggccaccc gccccggggc ctgggctcgc tgtggactcg tcatggcgac cgagcagagg
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cctttccacc tggtggtgtt cggcgcgtct ggcttcaccg gccagttcgt gaccgaggag
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gtggcccggg agcaggtgga cccggagcgg agctcccctg ccctgggcgt ggcgggccgc
180
tcccgggaga agctgcagcg ggtgctggag aaggcggccc tgaagctggg aagaccaaca
240
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300
atggctaaac aggcaacagt tgtcctcaat tgcgtaggac catatcggtt ttatggagaa
360
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420
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480
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540
aataaaatga atggtacttt gactgctgtg gaaagtttcc tgactataca ttcaggacct
600
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gaggggttga gcattcatga tggtacctgg aagtcagcaa tttatggttt tggagatcag
660
agtaatttga gaaaactaag aaatgtatca aatctgaaac ctgtcccgct cattggtcca
720
aaattgaaga gaaggtggcc aatttcttat tgtcgggaac tcaaaggtta ttccattcct
780
tttatgggat ctgatgtgtc tgttgtaagg aggactcaac gttacttgta tgaaaattta
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960
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1020
caaaaacaga ttgatgctgc ctcattcacg ctgacattct ttggtcaagg atacagccaa
1080
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1260
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1380
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1500
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1560
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1680
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1860
aatggtggtt taatgtttgg acctgccgat gtatttgtat agtggtagaa acatgctgct
1920
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1980
ctatatctgt gactaggttt ttaaggatac agcttataag ttgctatcaa ttttcactac
2040
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2160
tagcaaattg a
2171

<210> 4394
<211> 428
<212> PRT
<213> Homo sapiens

<400> 4394
Met Ala Thr Glu Gln Arg Pro Phe His Leu Val Val Phe Gly Ala Ser
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Gly Phe Thr Gly Gln Phe Val Thr Glu Glu Val Ala Arg Glu Gln Val
20 25 30
Asp Pro Glu Arg Ser Ser Pro Ala Leu Gly Val Ala Gly Arg Ser Arg
35 40 45
Glu Lys Leu Gln Arg Val Leu Glu Lys Ala Ala Leu Lys Leu Gly Arg
50 55 60
Pro Thr Leu Ser Ser Glu Val Gly Ile Ile Ile Cys Asp Ile Ala Asn
65 70 75 80
Pro Ala Ser Leu Asp Glu Met Ala Lys Gln Ala Thr Val Val Leu Asn
85 90 95
Cys Val Gly Pro Tyr Arg Phe Tyr Gly Glu Pro Val Ile Lys Ala Cys
100 105 110
Ile Glu Asn Gly Ala Ser Cys Ile Asp Ile Ser Gly Glu Pro Gln Phe
115 120 125
Leu Glu Leu Met Gln Leu Lys Tyr His Glu Lys Ala Ala Asp Lys Gly
130 135 140
Val Tyr Ile Ile Gly Ser Ser Gly Phe Asp Ser Ile Pro Ala Asp Leu
145 150 155 160
Gly Val Ile Tyr Thr Arg Asn Lys Met Asn Gly Thr Leu Thr Ala Val
165 170 175
Glu Ser Phe Leu Thr Ile His Ser Gly Pro Glu Gly Leu Ser Ile His
180 185 190
Asp Gly Thr Trp Lys Ser Ala Ile Tyr Gly Phe Gly Asp Gln Ser Asn
195 200 205
Leu Arg Lys Leu Arg Asn Val Ser Asn Leu Lys Pro Val Pro Leu Ile
210 215 220
Gly Pro Lys Leu Lys Arg Arg Trp Pro Ile Ser Tyr Cys Arg Glu Leu
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Lys Gly Tyr Ser Ile Pro Phe Met Gly Ser Asp Val Ser Val Val Arg
245 250 255
Arg Thr Gln Arg Tyr Leu Tyr Glu Asn Leu Glu Glu Ser Pro Val Gln
260 265 270
Tyr Ala Ala Tyr Val Thr Val Gly Gly Ile Thr Ser Val Ile Lys Leu
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Met Phe Ala Gly Leu Phe Phe Leu Phe Phe Val Arg Phe Gly Ile Gly
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Arg Gln Leu Leu Ile Lys Phe Pro Trp Phe Phe Ser Phe Gly Tyr Phe
305 310 315 320
Ser Lys Gln Gly Pro Thr Gln Lys Gln Ile Asp Ala Ala Ser Phe Thr
325 330 335
Leu Thr Phe Phe Gly Gln Gly Tyr Ser Gln Gly Thr Gly Thr Asp Lys
340 345 350
Asn Lys Pro Asn Ile Lys Ile Cys Thr Gln Val Lys Gly Pro Glu Ala
355 360 365
Gly Tyr Val Ala Thr Pro Ile Ala Met Val Gln Ala Ala Met Thr Leu

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Leu Ser Asp Ala Ser His Leu Pro Lys Ala Gly Gly Val Phe Thr Pro
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Gly Ala Ala Phe Ser Lys Thr Lys Leu Ile Asp Arg Leu Asn Lys His
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Gly Ile Glu Phe Ser Val Ile Ser Ser Ser Glu Val
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<211> 1893
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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35 40 45
Ser Thr Glu Ser Ile Arg Leu Glu Val Gly Val Thr Gly Glu Ser Gly
50 55 60
Ala Gly Lys Ser Ser Leu Ile Asn Ala Leu Arg Gly Leu Glu Ala Glu
65 70 75 80
Asp Pro Gly Ala Ala Leu Thr Gly Val Met Glu Thr Thr Met Gln Pro
85 90 95
Ser Pro Tyr Pro His Pro Gln Phe Pro Asp Val Thr Leu Trp Asp Leu
100 105 110
Pro Gly Ala Gly Ser Pro Gly Cys Pro Ala Asp Lys Tyr Leu Lys Gln
115 120 125
Val Asp Phe Ser Arg Tyr Asp Phe Phe Leu Leu Val Ser Pro Arg Arg
130 135 140
Cys Gly Ala Val Glu Thr Arg Leu Ala Ala Glu Ile Leu Cys Gln Gly
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Lys Lys Phe Tyr Phe Val Arg Thr Lys Val Asp Glu Asp Leu Ala Ala
165 170 175
Thr Arg Thr Gln Arg Pro Ser Gly Phe Arg Glu Ala Ala Val Leu Gln

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            180                 185                 190
Glu Ile Arg Asp His Cys Ala Glu Arg Leu Arg Glu Ala Gly Val Ala
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Asp Pro Arg Ile Phe Leu Val Ser Asn Leu Ser Pro Ala Arg Tyr Asp
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Phe Pro Thr Leu Val Ser Thr Trp Glu His Asp Leu Pro Ser His Arg
225                 230                 235                 240
Arg His Ala Gly Leu Leu Ser Leu Pro Asp Ile Ser Leu Glu Ala Leu
                245                 250                 255
Gln Lys Lys Lys Ala Met Leu Gln Glu Gln Val Leu Lys Thr Ala Leu
            260                 265                 270
Val Leu Gly Val Ile Gln Ala Leu Pro Val Pro Gly Leu Ala Ala Ala
        275                 280                 285
Tyr Asp Asp Ala Leu Leu Ile His Ser Leu Arg Gly Tyr His Arg Ser
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Phe Gly Leu Asp Asp Asp Ser Leu Ala Lys Leu Ala Glu Gln Val Gly
305                 310                 315                 320
Lys Gln Ala Gly Asp Leu Arg Ser Val Ile Arg Ser Pro Leu Ala Asn
                325                 330                 335
Glu Val Ser Pro Glu Thr Val Leu Arg Leu Tyr Ser Gln Ser Ser Asp
            340                 345                 350
Gly Ala Met Arg Val Ala Arg Ala Phe Glu Arg Gly Ile Pro Val Phe
        355                 360                 365
Gly Thr Leu Val Ala Gly Gly Ile Ser Phe Gly Ala Val Tyr Thr Met
    370                 375                 380
Leu Gln Gly Cys Leu Asn Glu Met Ala Glu Asp Ala Gln Arg Val Arg
385                 390                 395                 400
Ile Lys Ala Leu Glu Asp Asp Glu Pro Gln Pro Glu Val Ser Leu Glu
                405                 410                 415
Val Ala Ser Asp Asn Gly Val Glu Lys Gly Gly Ser Gly Glu Gly Gly
            420                 425                 430
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<211> 2543
<212> DNA
<213> Homo sapiens

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5945

<210> 3170
<211> 412
<212> PRT
<213> Homo sapiens

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20 25 30
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35 40 45
Pro Glu Gln Gln Met Ile Ala Asp Ile His Cys Met Ile Ala Ala Gly
50 55 60
Gln Asp Leu Asp Trp Ile Asp Ala Gln Gly Ala Thr Leu Leu His Ile
65 70 75 80
Ala Gly Ala Asn Gly Tyr Leu Arg Ala Ala Glu Leu Leu Leu Asp His
85 90 95
Gly Val Arg Val Asp Val Lys Asp Trp Asp Gly Trp Glu Pro Leu His
100 105 110
Ala Ala Ala Phe Trp Gly Gln Met Gln Met Ala Glu Leu Leu Val Ser
115 120 125
His Gly Ala Ser Leu Ser Ala Arg Thr Ser Met Asp Glu Met Pro Ile
130 135 140
Asp Leu Cys Glu Glu Glu Glu Phe Lys Val Leu Leu Leu Glu Leu Lys
145 150 155 160
His Lys His Asp Val Ile Met Lys Ser Gln Leu Arg His Lys Ser Ser
165 170 175
Leu Ser Arg Arg Thr Ser Ser Ala Gly Ser Arg Gly Lys Val Val Arg
180 185 190
Arg Ala Ser Leu Ser Asp Arg Thr Asn Leu Tyr Arg Lys Glu Tyr Glu
195 200 205
Gly Glu Ala Ile Leu Trp Gln Arg Ser Ala Ala Glu Asp Gln Arg Thr
210 215 220
Ser Thr Tyr Asn Gly Asp Ile Arg Glu Thr Arg Thr Asp Gln Glu Asn
225 230 235 240
Lys Asp Pro Asn Pro Arg Leu Glu Lys Pro Val Leu Leu Ser Glu Phe
245 250 255
Pro Thr Lys Ile Pro Arg Gly Glu Leu Asp Met Pro Val Glu Asn Gly
260 265 270
Leu Arg Ala Pro Val Ser Ala Tyr Gln Tyr Ala Leu Ala Asn Gly Asp

275 280 285
Val Trp Lys Val His Glu Val Pro Asp Tyr Ser Met Ala Tyr Gly Asn
290 295 300
Pro Gly Val Ala Asp Ala Thr Pro Pro Trp Ser Ser Tyr Lys Glu Gln
305 310 315 320
Ser Pro Gln Thr Leu Leu Glu Leu Lys Arg Gln Arg Ala Ala Ala Lys
325 330 335
Leu Leu Ser His Pro Phe Leu Ser Thr His Leu Gly Ser Ser Met Ala
340 345 350
Arg Thr Gly Glu Ser Ser Ser Glu Gly Lys Ala Xaa Leu Ile Gly Gly
355 360 365
Arg Thr Ser Pro Tyr Ser Ser Asn Gly Thr Ser Val Tyr Tyr Thr Val
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Thr Ser Gly Asp Pro Pro Leu Leu Lys Phe Lys Ala Pro Ile Glu Glu
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Met Glu Glu Lys Val His Gly Cys Cys Arg Ile Ser
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<212> DNA
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<211> 228
<212> PRT

<213> Homo sapiens

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35 40 45
Ser Leu Ala Met Asp Val Ser Ser Val His His Asn Ser Thr Leu Leu
50 55 60
Arg Tyr Ser Val Ser Leu Leu Gly Tyr Gly Phe Tyr Gly Asp Ile Ile
65 70 75 80
Lys Asp Ser Glu Lys Lys Arg Trp Leu Gly Leu Ala Arg Tyr Asp Phe
85 90 95
Ser Gly Leu Lys Thr Phe Leu Ser His His Cys Tyr Glu Gly Thr Val
100 105 110
Ser Phe Leu Pro Ala Gln His Thr Val Gly Ser Pro Arg Asp Arg Lys
115 120 125
Pro Cys Arg Ala Gly Cys Phe Val Cys Arg Gln Ser Lys Gln Gln Leu
130 135 140
Glu Glu Glu Gln Lys Lys Ala Leu Tyr Gly Leu Glu Ala Ala Glu Asp
145 150 155 160
Val Glu Glu Trp Gln Val Val Cys Gly Lys Phe Leu Ala Ile Asn Ala
165 170 175
Thr Asn Met Ser Cys Ala Cys Arg Arg Ser Pro Arg Gly Leu Ser Pro
180 185 190
Ala Ala His Leu Gly Asp Gly Ser Ser Asp Leu Ile Leu Ile Arg Lys
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Cys Ser Arg Phe Asn Phe Leu Arg Phe Leu Ile Trp His Glu Val Cys
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Lys Lys Pro Leu
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<211> 573
<212> DNA
<213> Homo sapiens

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<210> 3174
<211> 152
<212> PRT
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Gln Thr Phe Pro Leu Gln Leu Glu Asn Gly Gln Thr Val Glu Arg Thr
35 40 45
Val Ala Gln Tyr Phe Arg Glu Lys Tyr Thr Leu Gln Leu Lys Tyr Pro
50 55 60
His Leu Pro Cys Leu Gln Val Gly Gln Glu Gln Lys His Thr Tyr Leu
65 70 75 80
Pro Leu Glu Val Cys Asn Ile Val Ala Gly Gln Arg Cys Ile Lys Lys
85 90 95
Leu Thr Asp Asn Gln Thr Ser Thr Met Ile Lys Ala Thr Ala Arg Ser
100 105 110
Ala Pro Asp Arg Gln Glu Glu Ile Ser Arg Leu Val Arg Ser Ala Asn
115 120 125
Tyr Glu Thr Asp Pro Phe Val Gln Glu Phe Gln Phe Lys Val Arg Asp
130 135 140
Glu Met Ala His Val Thr Gly Arg
145 150

<210> 3175
<211> 948
<212> DNA
<213> Homo sapiens

<400> 3175
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120
tgggctccgg aatcgcccgc agccggtact gcgggaccca ctgcggatat ggctgtcttg
180
gctggatccc tgttgggccc cacgagtagg tcggcagcgt tgctgggtgg caggtggctc
240
cagccccggg cctggctggg gttcccagac gcctggggcc tccccacccc gcagcaggcc
300
cggggcaagg ctcgcgggaa tgagtatcag ccgagcaaca tcaaacgcaa gaacaagcac
360
ggctgggtcc ggcgcctgag cacgccggcc ggcgtgcagg tcatccttcg ccgaatgctc
420

aagggccgca agtcgctgag ccattgagga tcgcgacgca gtcggcggga ccctcatgga
480
agcatcgccc tcgcctcgga ccttgcctgg cgctattttt gcagggagct ggggagcagg
540
aacgcctcgg acctgagtgc tctccatatt gtggggttga agtctggatg ggagcttgcc
600
aagtcccttt ttaggctttt taattaggaa gcatttcgaa cctgcgcaac agaccaaaga
660
acagtacaaa gaacatccgt gtacccagta ccctgactac cgactaccta caacccgtcc
720
ctgccccatc ctgagttctt ttgaagctga tctcaggcat cggattattt cttctgtaaa
780
tatttcagaa tgtatctctc caagatgaga gctcattaaa agataattac aaagcttatc
840
acatccaaaa gaattatcaa taattttgaa atattattaa acgtgtaata aatgttcaaa
900
gttccacttg caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa
948

<210> 3176
<211> 92
<212> PRT
<213> Homo sapiens

<400> 3176
Met Ala Val Leu Ala Gly Ser Leu Leu Gly Pro Thr Ser Arg Ser Ala
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Ala Leu Leu Gly Gly Arg Trp Leu Gln Pro Arg Ala Trp Leu Gly Phe
            20   25   30
Pro Asp Ala Trp Gly Leu Pro Thr Pro Gln Gln Ala Arg Gly Lys Ala
        35   40   45
Arg Gly Asn Glu Tyr Gln Pro Ser Asn Ile Lys Arg Lys Asn Lys His
    50   55   60
Gly Trp Val Arg Arg Leu Ser Thr Pro Ala Gly Val Gln Val Ile Leu
65   70   75   80
Arg Arg Met Leu Lys Gly Arg Lys Ser Leu Ser His
                85   90

<210> 3177
<211> 1857
<212> DNA
<213> Homo sapiens

<400> 3177
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tccccgtctt ttgtaccaac aggggagaag ccatgtgagc aagtccagtt ccagcccaac
120
acagtgaaca ctttggcctg cccgctcctc tccaacctgg cgacccgact ctggctacgc
180
aacggggccc ccgtcaatgc ctcggcctcc tgccacgtgc tacccactgg ggacctgctg
240
ctggtgggca cccaacagct gggggagttc cagtgctggt cactagagga gggcttccag
300

cagctggtag ccagctactg cccagaggtg gtggaggacg gggtggcaga ccaaacagat
360
gagggtggca gtgtacccgt cattatcagc acatcgcgtg tgagtgcacc agctggtggc
420
aaggccagct ggggtgcaga caggtcctac tggaaggagt tcctggtgat gtgcacgctc
480
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540
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cgagggtacc agtccctgtc agacagcccc ccgggggccc gagtcttcac tgagtcagag
720
aagaggccac tcagcatcca agacagcttc gtggaggtat ccccagtgtg cccccggccc
780
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900
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1020
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tgtaaactga gccctttgtt tagaaaacaa ttccaaatgt gaaactagaa tgagagggaa
1140
gagatagcat ggcatgcagc acacacggct gctccagttc atggcctccc aggggtgctg
1200
gggatgcatc caaagtggtt gtctgagaca gagttggaaa ccctcaccaa ctggcctctt
1260
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1320
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1380
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1500
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1620
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1680
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1740
cccagcacag gggccctgaa tttatgtggt ttttatacat tttttaataa gatgcacttt
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1857

<210> 3178

<211> 273
<212> PRT
<213> Homo sapiens

<400> 3178
Xaa Ile Gln Asp Ile Glu Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala
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Ser Ser Val Val Ser Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys
20 25 30
Glu Gln Val Gln Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro
35 40 45
Leu Leu Ser Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro
50 55 60
Val Asn Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu
65 70 75 80
Leu Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu
85 90 95
Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val Glu
100 105 110
Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro Val Ile
115 120 125
Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly Lys Ala Ser Trp
130 135 140
Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val Met Cys Thr Leu
145 150 155 160
Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe Leu Leu Tyr Arg His
165 170 175
Arg Asn Ser Met Lys Val Phe Leu Lys Gln Gly Glu Cys Ala Ser Val
180 185 190
His Pro Lys Thr Cys Pro Val Val Leu Pro Pro Glu Thr Arg Pro Leu
195 200 205
Asn Gly Leu Gly Pro Pro Ser Thr Pro Leu Asp His Arg Gly Tyr Gln
210 215 220
Ser Leu Ser Asp Ser Pro Pro Gly Ala Arg Val Phe Thr Glu Ser Glu
225 230 235 240
Lys Arg Pro Leu Ser Ile Gln Asp Ser Phe Val Glu Val Ser Pro Val
245 250 255
Cys Pro Arg Pro Arg Val Arg Leu Gly Ser Glu Ile Arg Asp Ser Val
260 265 270
Val

<210> 3179
<211> 3447
<212> DNA
<213> Homo sapiens

<400> 3179
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tgtttaatga atgcataaaa aggcagaaaa atatataaag ccaaaagctc ataataaaat
120
taaatcatga tacaaccacc acaggcaatt accatcaaat acattcccat gatttacaaa
180

tgtatcgctt atacagagga agttgcaaaa tcactgccag tacagacaca tccagtctaa
240
ttaactatcg tctattcata caacagcaac aactgcagct cctgagacca cagaaggaca
300
cagtgagcag ctggtgactg agccagggta gcctccgatc aataactgat cagagtaatg
360
agacttcgag aggaatgcct ataagaaatc tcaaaaggta tttgtttggg tgcagaaaca
420
aatgcaccct ccacatttgg attttctcta gaagaatctg tggccaaatc tcttatccaa
480
tggaggtact gagtggctgg atcagttacc atgcaagctc acgatgaatg agattgaatt
540
tggttctgtg tgcacactgg gctctgggga gggaggacac ccctgtgtgt tgctgctgcc
600
ttccgtgctg tctactgtat ccttcatgtg tctccaaatg gtacacgccc catgggatta
660
cagaacacag ctacagaatt aggatctcat ggtaacaatg aggaattagg ttactgtaga
720
actaaaatat gtttaatgaa attaaaatgc aatggaaaaa aaatcaggca acagaacatt
780
ctgatgaatt tacaggactg attatatccc acggcactga atgacaaaca gttcttctcc
840
atacagtcgc aattagaggc atagaagtca tactgaatgc tgaatagaag aacactgaga
900
agagcaggtt ataaatgaag gttttcacat aaaacagaaa aatagacaaa atcatcggta
960
agaagctagc tttcgaaaac ctccctaaaa gtacacggca cggagaagtg gggtactggg
1020
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1080
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1140
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1260
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1320
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1620
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1680
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1740
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1800

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1860
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1920
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1980
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2100
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2160
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2280
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2340
ttaccataaa ggaagaaaaa catctatgtg tgtcaatatt gttttgagat aaagtcacaa
2400
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2460
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2520
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2580
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2640
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2700
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2760
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2820
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3000
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3180
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3240
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3300
tctgaatggc actcagggac cagcgctttg atgaaccagc agccacaggt tctccactga
3360
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3420

gttatacttt ttttttccact tttgctt
3447

<210> 3180
<211> 127
<212> PRT
<213> Homo sapiens

<400> 3180
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1 5 10 15
Thr Gln Thr Asp Gly Arg Asp Val Asn Ser Cys Leu Lys Leu Arg Cys
20 25 30
Ala Phe Thr Pro Thr Gly Lys Val Lys Leu Thr Phe Val Phe Leu Phe
35 40 45
Asn Asn Phe Met Ile Asn Lys Glu Leu Gln Leu Glu Thr Lys Ala Asn
50 55 60
Ser Arg Asn Ser Leu Thr Pro Ser Cys Pro Met Val Phe Met Ile Ala
65 70 75 80
Cys Tyr Gln Asn Glu Ala Leu Cys Ser Thr Leu Tyr Ser Lys Ala Phe
85 90 95
Tyr Ala Pro Thr Arg Pro Ser Gly Ile Pro Glu Ser Ala Leu His Thr
100 105 110
Gly Arg Lys Thr Ala Ser Ser Tyr Arg Leu Cys Glu Asn Thr Gln
115 120 125

<210> 3181
<211> 287
<212> DNA
<213> Homo sapiens

<400> 3181
natggcttcc tccccggcgg tggacgtgtc ctgcaggcgg cggggagaac ggcggcagct
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ggacgcgcgc cgcaacaagt gccgcattcg cctgggcggg cacatgaagc agggggggcct
120
cctcaaggac ggctgggctt ctccctgcac tcgcagctcg ccaagttcct gttggaccgg
180
tacacttctt caggctgtgt cctctgtgca ggtcctgagc ttttgcctcc aaaaggtctg
240
cagtatctgg tgctcttgtc tcatgcccca caccggagat gcaccct
287

<210> 3182
<211> 95
<212> PRT
<213> Homo sapiens

<400> 3182
Met Ala Ser Ser Pro Ala Val Asp Val Ser Cys Arg Arg Arg Gly Glu
1 5 10 15
Arg Arg Gln Leu Asp Ala Arg Arg Asn Lys Cys Arg Ile Arg Leu Gly
20 25 30
Gly His Met Lys Gln Gly Gly Leu Leu Lys Asp Gly Trp Ala Ser Pro

35 40 45
Cys Thr Arg Ser Ser Pro Ser Ser Cys Trp Thr Gly Thr Leu Leu Gln
50 55 60
Ala Val Ser Ser Val Gln Val Leu Ser Phe Cys Leu Gln Lys Val Cys
65 70 75 80
Ser Ile Trp Cys Ser Cys Leu Met Pro His Thr Gly Asp Ala Pro
85 90 95

<210> 3183
<211> 1457
<212> DNA
<213> Homo sapiens

<400> 3183
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acacatatcc cacgtaatgc agggtactcc tttgtccaga cccagctcct ggttcccaaa
120
aaagttctcc ctgagagctg caggctgtcc tggaatctcc tcggggatga ggcagctgcc
180
gagctggccc aggtgctgcc gcagatgggc cggctgaaga gagtggacct ggagaagaat
240
cagatcacag ctttgggggc ctggctcctg gctgaaggac tggcccaggg gtctagcatc
300
caagtcatcc gcctctggaa taaccccatt ccctgcgaca tggcccagca cctgaagagc
360
caggagccca ggctggactt tgccttcttt gacaaccagc cccaggcccc ttggggtact
420
tgatggcccc ctcaagacct ttggaatcca gccaagtgat gcacccaaat gatccacctt
480
tcgcccactg ggataaatga ctcaggaaag aagagcctcg gcagggcgct ctgcactcca
540
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600
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660
ggacatgcga cacacaatga gggtgtcatg acaatgcatg acacgtacgg ttatatgtgg
720
cagtgtgacc ccttgacatg tggcgttaca tgaaagtcag tgtggcacgt gttctgtggc
780
atgggtgctg gcatcccaag tggcaggata catgattgtt ggtctatata tgacacatga
840
caaatgtcca tgtcacagga ctcatggctg gccagatgac ctcaggctgg cccaagatct
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960
caggaaaagt cttccgcccg agctgggagg ggagagtgtc catgcactga ccagtccagg
1020
ggctcaaggg ccagggctct ggaacaagcc agggactcag ccattaagtc ccctcctgcc
1080
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tccaaggaca ggtggaggta gggccagcct ggcgggagtg gagaagccca gtctgtccta
1200

tgtaagggac aaagccaggt ctaatggtac tgggtagggg gcactgccaa gacaataagc
1260
taggctactg ggtccagcta ctactttggt gggattcagg tgagtctcca tgcacttcac
1320
atgttaccca gtgttcttgt tacttccaag gagaaccaag aatggctctg tcacactcga
1380
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1440
aaaaaaaaaa aaaaaaa
1457

<210> 3184
<211> 140
<212> PRT
<213> Homo sapiens

<400> 3184
Xaa Tyr Val Ser Cys Ile Val Met Thr Pro Ser Leu Cys Val Ala Cys
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Pro Gln Leu Ile Thr His Ile Pro Arg Asn Ala Gly Tyr Ser Phe Val
            20   25   30
Gln Thr Gln Leu Leu Val Pro Lys Lys Val Leu Pro Glu Ser Cys Arg
        35   40   45
Leu Ser Trp Asn Leu Leu Gly Asp Glu Ala Ala Ala Glu Leu Ala Gln
    50   55   60
Val Leu Pro Gln Met Gly Arg Leu Lys Arg Val Asp Leu Glu Lys Asn
65   70   75   80
Gln Ile Thr Ala Leu Gly Ala Trp Leu Leu Ala Glu Gly Leu Ala Gln
                85   90   95
Gly Ser Ser Ile Gln Val Ile Arg Leu Trp Asn Asn Pro Ile Pro Cys
            100   105   110
Asp Met Ala Gln His Leu Lys Ser Gln Glu Pro Arg Leu Asp Phe Ala
        115   120   125
Phe Phe Asp Asn Gln Pro Gln Ala Pro Trp Gly Thr
    130   135   140

<210> 3185
<211> 1433
<212> DNA
<213> Homo sapiens

<400> 3185
gccgcgtcga ctttttttttt ttttttttct aattgcatca ctttatttca ccgacctcca
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120
cctggtaacc tgaggaggtg tagagcaccc agaaggaagg gtaaaagcag ggggcaaagc
180
ggtggccctc cctttctggg ggtcacttct gggctggggc cagctgaaac ctgtgtccaa
240
gtagctttca gggctggcca caccctaagc cttgcaaaag ggcctcctgc aagggctggc
300
ccatggggtc cccaccttcc cagccagtga ggttagcatg gttaggagtc cacatgtgtg
360

caagtgcttg tgtggaggct catgtatgca tgtgtgtata tgcaaagctg cacatgacaa
420
tgtgcatgcc agtccagagt tagatgtacc tatgcagttg ccctcaagcg aagggtcata
480
tttggaaaca aggatggctc taaacatgta agcgtgcatg tgggcatgta tgtatctggg
540
gcctaaggag gtggggaagt gggtgttggg gtaagggctg gccttcaggg catttgcaga
600
aggaggagtg ggtgggaggg aaaggctggg cagagcaggg gaaggagtga aagccaggca
660
ggaaagtgga agaacaggag aagctcatgt aatggattac cctccacagg attatgttcc
720
ttgattcctg agagtttttt ctcttgattt tacccccctca gtctatcact gcaagagaaa
780
gaggtagaaa agacaaacag accacaaaag acaagaaccc agacatatag acagacgcac
840
ctgttgcatg tgcatgagcc agagcctggg agagaagaga gagcgtgcaa gagagagctc
900
agagcaggca ggcagcccac cccctgcagc agtgctgggc ttcactggag cccctgcagg
960
aagtccagca gccctgtatg ccactcctct ggtttgtcca ggtaacaggg gtgccccgcc
1020
cccttcatga tcagcacccg gtggttgggc agctgcttca ggtgctcaaa gctggtctga
1080
cccatggggt cctggtctcc atatacaatc agagctggag tctgagagga aggatagggg
1140
ggtggggcag agtcaacagg acctgccata gcatccccag ccctccccac ttcagtctct
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1320
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1380
ccccagatga ggaaagccca ggatgcaccc ttccttgctc ctggcagggc acc
1433

<210> 3186
<211> 112
<212> PRT
<213> Homo sapiens

<400> 3186
Met Pro Leu Leu Trp Phe Val Gln Val Thr Gly Val Pro Arg Pro Leu
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His Asp Gln His Pro Val Val Gly Gln Leu Leu Gln Val Leu Lys Ala
            20   25   30
Gly Leu Thr His Gly Val Leu Val Ser Ile Tyr Asn Gln Ser Trp Ser
        35   40   45
Leu Arg Gly Arg Ile Gly Gly Trp Gly Arg Val Asn Arg Thr Cys His
    50   55   60
Ser Ile Pro Ser Pro Pro His Phe Ser Leu Phe Leu Gly Pro Pro His
65   70   75   80
Met Arg Glu Arg Asp Lys Leu Ala Gln Trp Val Gly Ala Gln Ile Gly

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                85                  90                  95
Val Cys Pro Arg Thr Gln Phe Ser Thr Gly Leu Gly Thr Val Val Cys
            100                 105                 110
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<210> 3187
<211> 860
<212> DNA
<213> Homo sapiens

<400> 3187
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tatctaccag gagacggagt ttcgctatgt ttcccagact ggttttgaac tcctggccta
120
aagtggtcct cccgcctcgg cctcctgagt agctgggatt acagatatgt tcctaaaaca
180
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240
caccatgcag aggtcgtgaa gaaggtgaat gagatgatcg tcacggggca gtatggcagg
300
ctctttgccg tggtgcactt tgccagccgc cagtggaagg tgacctctga agacctgatc
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420
ctggttgggg cagacaactt cacgctgctt ggcaagccac tcctcgggta atggctgtga
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agtgctgggc tttgtctggg gctccagggc tggacatgca gacagtggtc acagtgcaat
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taggccagaa aggatcttgt tcgagtagaa gccacagtca ttgaaaagac agaatcatgg
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ccaagaatca ttatgagatt caggaaaagg aaaaacttca agaagaaaag aagtaagtta
660
gagaaagtac cgctgggccc tgttgcacgg tgctggttgc ccaggcgcat gcggacggag
720
ggtgtggggc acgtgggtct cgggacagga agcccaggca ggtctcaacc tggctgccac
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840
ctcctccacg ctccacgcgt
860

<210> 3188
<211> 120
<212> PRT
<213> Homo sapiens

<400> 3188

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Thr Pro Gly Leu Lys Trp Ser Ser Arg Leu Gly Leu Leu Ser Ser Trp
 1               5                  10                  15
Asp Tyr Arg Tyr Val Pro Lys Thr Ser Leu Ser Ser Pro Pro Trp Pro
            20                  25                  30
Glu Val Val Leu Pro Asp Pro Val Glu Glu Thr Arg His His Ala Glu
        35                  40                  45
Val Val Lys Lys Val Asn Glu Met Ile Val Thr Gly Gln Tyr Gly Arg
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    50                  55                  60
Leu Phe Ala Val Val His Phe Ala Ser Arg Gln Trp Lys Val Thr Ser
65                  70                  75                  80
Glu Asp Leu Ile Leu Ile Gly Asn Glu Leu Asp Leu Ala Cys Gly Glu
                85                  90                  95
Arg Ile Arg Leu Glu Lys Val Leu Leu Val Gly Ala Asp Asn Phe Thr
            100                 105                 110
Leu Leu Gly Lys Pro Leu Leu Gly
        115                 120
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<210> 3189
<211> 440
<212> DNA
<213> Homo sapiens

<400> 3189
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agcctgggga agcaagtccc tgttttcagt accacctgca tcccccaggg cagcatcctt
120
gactcccctt ctgggccagt gctgccctgc tttctctgtc tctttcaggg tgtgctgtcc
180
gacctcacca aagtgacccg gatgcatgga atcgaccctg tggtgctggt cctgatggtg
240
ggcatggtga tgttcaccct ggggttcgcc ggctgcgtgg gggctctgcg ggagaatatc
300
tgcttgctca actttgtgag tggccacaga gacaagagtg ggatatgatg caatggggta
360
caggctctgc tgggcaggat tatatgttac ctggtcagag caggtggcag ctcttaggag
420
cctcccctat ggcccctgcc
440

<210> 3190
<211> 111
<212> PRT
<213> Homo sapiens

<400> 3190
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Gly His Gly Trp Gly Arg Thr Leu Ala Trp Leu Ser Thr Arg Gly Leu
 1               5                  10                  15
Ser Leu Gly Lys Gln Val Pro Val Phe Ser Thr Thr Cys Ile Pro Gln
            20                  25                  30
Gly Ser Ile Leu Asp Ser Pro Ser Gly Pro Val Leu Pro Cys Phe Leu
        35                  40                  45
Cys Leu Phe Gln Gly Val Leu Ser Asp Leu Thr Lys Val Thr Arg Met
    50                  55                  60
His Gly Ile Asp Pro Val Val Leu Val Leu Met Val Gly Met Val Met
65                  70                  75                  80
Phe Thr Leu Gly Phe Ala Gly Cys Val Gly Ala Leu Arg Glu Asn Ile
                85                  90                  95
Cys Leu Leu Asn Phe Val Ser Gly His Arg Asp Lys Ser Gly Ile
            100                 105                 110
```

<210> 3191
<211> 266
<212> DNA
<213> Homo sapiens

<400> 3191
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acctttttgcg gcagtcgcta aattgccacg ggtcgtcttt gctctctcta cttcggagcg
120
aacagcagga caatccacac ttccgtagcc tcctggggtc ggccgccgag ccagcccggg
180
gcccgccgcc ccagcacccg ttgcagggca gaaaagagaa gagagttgac aacatcgaga
240
tacagaaatt catctcccaa aaagcg
266

<210> 3192
<211> 84
<212> PRT
<213> Homo sapiens

<400> 3192
Met Asn Phe Cys Ile Ser Met Leu Ser Thr Leu Phe Ser Phe Leu Pro
1 5 10 15
Cys Asn Gly Cys Trp Gly Gly Gly Pro Arg Ala Gly Ser Ala Ala Asp
20 25 30
Pro Arg Arg Leu Arg Lys Cys Gly Leu Ser Cys Cys Ser Leu Arg Ser
35 40 45
Arg Glu Ser Lys Asp Asp Pro Trp Gln Phe Ser Asp Cys Arg Lys Arg
50 55 60
Ser Arg Ser Met Ala Gln Val Ala Asp Thr Glu Gln Gly Thr Ile Ser
65 70 75 80
Pro Ser Ala Ser

<210> 3193
<211> 567
<212> DNA
<213> Homo sapiens

<400> 3193
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120
tggagtgagt tgttttgccc ctctgagcct cagtttctcc atctgtgaaa tggggacaac
180
agcagttcct tccaggaggg taaaaggagg agaaaaagaa tgcagatcca gccctcggca
240
gagtcagcgg ttcatgcttt gcatgcaaag tgcccagccc ctggctcaaa gtctgtgttc
300
atccagacct gggttaacta ctgtcttcct tatgttgttc ctgtggggac gcctggggct
360

gctggcctcg tgattcctct ctttccctgc aggccacggt tcacctactt ccccttctcc
420
ctgggccacc gctcctgcat cgggcagcag tttgctcaga tggaggtgaa ggtggtcatg
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540
gagcaggcca cactcaagcc actggac
567

<210> 3194
<211> 116
<212> PRT
<213> Homo sapiens

<400> 3194
Met Gln Ile Gln Pro Ser Ala Glu Ser Ala Val His Ala Leu His Ala
 1   5   10   15
Lys Cys Pro Ala Pro Gly Ser Lys Ser Val Phe Ile Gln Thr Trp Val
            20   25   30
Asn Tyr Cys Leu Pro Tyr Val Val Pro Val Gly Thr Pro Gly Ala Ala
        35   40   45
Gly Leu Val Ile Pro Leu Phe Pro Cys Arg Pro Arg Phe Thr Tyr Phe
    50   55   60
Pro Phe Ser Leu Gly His Arg Ser Cys Ile Gly Gln Gln Phe Ala Gln
65   70   75   80
Met Glu Val Lys Val Val Met Ala Lys Leu Leu Gln Arg Leu Glu Phe
                85   90   95
Arg Leu Val Pro Gly Gln Arg Phe Gly Leu Gln Glu Gln Ala Thr Leu
            100   105   110
Lys Pro Leu Asp
        115

<210> 3195
<211> 987
<212> DNA
<213> Homo sapiens

<400> 3195
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120
agccccagac acctacctcc ttggctggat cagccaaagg tgggcaagac ggttcacagc
180
gttcaagcat ccactttgaa acggaagagg ctaaccgttc ctttctctcg gggatcaaga
240
ccattttgaa gaagagcccg gagcccaagg aggatcccgc tcacctgtct gactcgtcct
300
catcctccgg ctccatcgtg tccttcaaaa gtgctgacag catcaaaagt cgaccaggaa
360
tcccacgact tgcgggtgac ggtggcgagc gaacgtcccc cgagcggaga gagccaggga
420
cggggaggaa agacgacgat gttgcgagca taatgaagaa atacctccag aagtaggaac
480

cagttcagcc tccttgaagc tgcccttgaa gacttcccga ctctacaata acttggagac
540
agagagactg gccaggcctc cccggtggcc agagccagcc agcatggcca ccctcaagag
600
gcgagatgag cccacagagg catatcctgc ggggatgctg ggctcccagt gtggttggcc
660
tgaacaaaat aaagtgttga ctcctgggca tctgtgcctt ctctatggcc ttgctacctg
720
ggattccaga gagttgatgg ggtgcagata ggggtaggac tgttagaata gaaccaaccc
780
aaactgtgtg tagtttgggg tgtatacttc tatttctctt cctacatgtc tacatgccat
840
gaccttcctc ctcctcttca cttggccagt ttcagctcac ttcctccagg aagtctttcc
900
tgatatatca aactgaaaca aatgctcctc ctccatgctc ccttaatccc catgcttgtc
960
gattatattc ctttgccaat tcatttc
987

<210> 3196
<211> 153
<212> PRT
<213> Homo sapiens

<400> 3196
Met Glu Glu Pro Leu Gly Ser Asp Pro Phe Ser Trp Lys Leu Pro Ser
 1   5   10   15
Leu Asp Tyr Glu Arg Lys Thr Lys Val Asp Phe Asp Asp Phe Leu Pro
            20   25   30
Ala Ile Arg Lys Pro Gln Thr Pro Thr Ser Leu Ala Gly Ser Ala Lys
        35   40   45
Gly Gly Gln Asp Gly Ser Gln Arg Ser Ser Ile His Phe Glu Thr Glu
    50   55   60
Glu Ala Asn Arg Ser Phe Leu Ser Gly Ile Lys Thr Ile Leu Lys Lys
65   70   75   80
Ser Pro Glu Pro Lys Glu Asp Pro Ala His Leu Ser Asp Ser Ser Ser
                85   90   95
Ser Ser Gly Ser Ile Val Ser Phe Lys Ser Ala Asp Ser Ile Lys Ser
            100   105   110
Arg Pro Gly Ile Pro Arg Leu Ala Gly Asp Gly Gly Glu Arg Thr Ser
        115   120   125
Pro Glu Arg Arg Glu Pro Gly Thr Gly Arg Lys Asp Asp Asp Val Ala
    130   135   140
Ser Ile Met Lys Lys Tyr Leu Gln Lys
145   150

<210> 3197
<211> 5575
<212> DNA
<213> Homo sapiens

<400> 3197
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ctggctgaca cagcaagact atgtttaaaa aaaaagagag agaaaaaaaa acaagaagga
120
agagcaatgg cgacactgga tcgcaaagtg cccagtccgg aggcgtttct gggcaaaccc
180
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240
gctggaaaag agggtggaaa aagcagggag gttatgaggc ttaataaaga agatatgcac
300
ttatttggcc attacccagc acatgacgac ttctatctcg tagtgtgcag tgcctgtaac
360
caggtcgtca agccacaggt tttccagtcg cactgcgaga gaagacacgg ttcaatgtgt
420
agaccttctc cctctccagt gtctccagcc tccaatccca ggacatcact agtacaggtg
480
aaaacaaaag cctgtctcag cggccatcac tctgccagca gcacctcaaa gccattcaaa
540
acgcccaaag acaatctact tacctccagc agcaaacagc acacagtctt tcctgcgaaa
600
ggatcaaggg ataaaccatg tgttccagtt cctgtagtca gtttagagaa aattcctaac
660
ctagtgaagg cagatggtgc caatgtcaaa atgaactcca caaccactac tgcagtttct
720
gcctcccccа cctcgtcctc tgccgtctcc acccctcctt taattaagcc tgtcctgatg
780
tccaagtcag tgccaccttc accagagaag atcttaaatg gcaaaggaat tctgccaacc
840
accatagaca agaaacacca aaatggcacc aaaaacagca acaagcctta caggagactt
900
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960
ccttgcacaa gatccctcac ctgcaagaca cattcgctaa gccatcggag ggcagtccca
1020
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1080
gaagttaaag ataaagagca tctcctgact tccacgaggg aaatacttcc aagccaatcc
1140
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1320
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1380
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1440
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1560
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gttccagcat ccgttttgca gcctttcagc aaccccagtg ctgtgtatct tccttcagct
1680

cccatcagct cgagactcac ctcttcttac ataatgacat cagccatgct ctcagacgca
1740
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4920

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5575

<210> 3198
<211> 833
<212> PRT
<213> Homo sapiens

<400> 3198
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Lys Pro Trp Ser Ser Trp Ile Asp Ala Ala Lys Leu His Cys Ser Asp
20 25 30
Asn Val Asp Leu Glu Glu Ala Gly Lys Glu Gly Gly Lys Ser Arg Glu
35 40 45
Val Met Arg Leu Asn Lys Glu Asp Met His Leu Phe Gly His Tyr Pro
50 55 60
Ala His Asp Asp Phe Tyr Leu Val Val Cys Ser Ala Cys Asn Gln Val
65 70 75 80
Val Lys Pro Gln Val Phe Gln Ser His Cys Glu Arg Arg His Gly Ser
85 90 95
Met Cys Arg Pro Ser Pro Ser Pro Val Ser Pro Ala Ser Asn Pro Arg
100 105 110
Thr Ser Leu Val Gln Val Lys Thr Lys Ala Cys Leu Ser Gly His His
115 120 125
Ser Ala Ser Ser Thr Ser Lys Pro Phe Lys Thr Pro Lys Asp Asn Leu
130 135 140
Leu Thr Ser Ser Ser Lys Gln His Thr Val Phe Pro Ala Lys Gly Ser
145 150 155 160
Arg Asp Lys Pro Cys Val Pro Val Pro Val Val Ser Leu Glu Lys Ile
165 170 175
Pro Asn Leu Val Lys Ala Asp Gly Ala Asn Val Lys Met Asn Ser Thr
180 185 190
Thr Thr Thr Ala Val Ser Ala Ser Pro Thr Ser Ser Ser Ala Val Ser

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        195                 200                 205
Thr Pro Pro Leu Ile Lys Pro Val Leu Met Ser Lys Ser Val Pro Pro
    210                 215                 220
Ser Pro Glu Lys Ile Leu Asn Gly Lys Gly Ile Leu Pro Thr Thr Ile
225                 230                 235                 240
Asp Lys Lys His Gln Asn Gly Thr Lys Asn Ser Asn Lys Pro Tyr Arg
                245                 250                 255
Arg Leu Ser Glu Arg Glu Phe Asp Pro Asn Lys His Cys Gly Val Leu
            260                 265                 270
Asp Pro Glu Thr Lys Lys Pro Cys Thr Arg Ser Leu Thr Cys Lys Thr
        275                 280                 285
His Ser Leu Ser His Arg Arg Ala Val Pro Gly Arg Lys Lys Gln Phe
    290                 295                 300
Asp Leu Leu Leu Ala Glu His Lys Ala Lys Ser Arg Glu Lys Glu Val
305                 310                 315                 320
Lys Asp Lys Glu His Leu Leu Thr Ser Thr Arg Glu Ile Leu Pro Ser
                325                 330                 335
Gln Ser Gly Pro Ala Gln Asp Ser Leu Leu Gly Ser Ser Gly Ser Ser
            340                 345                 350
Gly Pro Glu Pro Lys Val Ala Ser Pro Ala Lys Ser Arg Pro Pro Asn
        355                 360                 365
Ser Val Leu Pro Arg Pro Ser Ser Ala Asn Ser Ile Ser Ser Ser Thr
    370                 375                 380
Ser Ser Asn His Ser Gly His Thr Pro Glu Pro Pro Leu Pro Pro Val
385                 390                 395                 400
Gly Gly Asp Leu Ala Ser Arg Leu Ser Ser Asp Glu Gly Glu Met Asp
                405                 410                 415
Gly Ala Asp Glu Ser Glu Lys Leu Asp Cys Gln Phe Ser Thr His His
            420                 425                 430
Pro Arg Pro Leu Ala Phe Cys Ser Phe Gly Ser Arg Leu Met Gly Arg
        435                 440                 445
Gly Tyr Tyr Val Phe Asp Arg Arg Trp Asp Arg Phe Arg Phe Ala Leu
    450                 455                 460
Asn Ser Met Val Glu Lys His Leu Asn Ser Gln Met Trp Lys Lys Ile
465                 470                 475                 480
Pro Pro Ala Ala Asp Ser Pro Met Pro Ser Pro Ala Ala His Ile Thr
                485                 490                 495
Thr Pro Val Pro Ala Ser Val Leu Gln Pro Phe Ser Asn Pro Ser Ala
            500                 505                 510
Val Tyr Leu Pro Ser Ala Pro Ile Ser Ser Arg Leu Thr Ser Ser Tyr
        515                 520                 525
Ile Met Thr Ser Ala Met Leu Ser Asp Ala Ala Phe Val Thr Ser Pro
    530                 535                 540
Asp Pro Ser Ala Leu Met Ser His Thr Thr Ala Phe Pro His Val Ala
545                 550                 555                 560
Ala Thr Leu Ser Ile Met Asp Ser Thr Phe Lys Ala Pro Ser Ala Val
                565                 570                 575
Ser Pro Ile Pro Ala Val Ile Pro Ser Pro Ser His Lys Pro Ser Lys
            580                 585                 590
Thr Lys Thr Ser Lys Ser Ser Lys Val Lys Asp Leu Ser Thr Arg Ser
        595                 600                 605
Asp Glu Ser Pro Ser Asn Lys Lys Arg Lys Pro Gln Ser Ser Thr Ser
    610                 615                 620
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Leu Gln Thr Ser Leu Ser Ser
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625 630 635 640
Pro Leu Ser Gly Pro His Lys Lys Asn Cys Val Leu Asn Ala Ser Ser
645 650 655
Ala Leu Asn Ser Tyr Gln Ala Ala Pro Pro Tyr Asn Ser Leu Ser Val
660 665 670
His Asn Ser Asn Asn Gly Val Ser Pro Leu Ser Ala Lys Leu Glu Pro
675 680 685
Ser Gly Arg Thr Ser Leu Pro Gly Gly Pro Ala Asp Ile Val Arg Gln
690 695 700
Val Gly Ala Val Gly Gly Ser Ser Asp Ser Cys Pro Leu Ser Val Pro
705 710 715 720
Ser Leu Ala Leu His Ala Gly Asp Leu Ser Leu Ala Ser His Asn Ala
725 730 735
Val Ser Ser Leu Pro Leu Ser Phe Asp Lys Ser Glu Gly Lys Lys Arg
740 745 750
Lys Asn Ser Ser Ser Ser Ser Lys Ala Cys Lys Ile Thr Lys Met Pro
755 760 765
Gly Met Asn Ser Val His Lys Lys Asn Pro Pro Ser Leu Leu Ala Pro
770 775 780
Val Pro Asp Pro Val Asn Ser Thr Ser Ser Arg Gln Val Gly Lys Asn
785 790 795 800
Ser Ser Leu Ala Leu Ser Gln Ser Ser Pro Ser Ser Ile Ser Ser Pro
805 810 815
Gly His Ser Arg Gln Asn Thr Asn Arg Thr Gly Arg Ile Arg Thr Leu
820 825 830
Pro

<210> 3199
<211> 777
<212> DNA
<213> Homo sapiens

<400> 3199
acgcgtgagg tccggccact gcgcagtcag acacgccggc tgctgcagtg gggcaggcag
60
ctccaggtgc tggtgagggc cccagctctc tgcgaggctg tggctggacc aggcatacag
120
caagcagctc ccacagctgg cactggggaa cgtggtgaca cccagaagct tggagatgcc
180
aggaaccgca aggccccaaa gagagtgtca cagccctggc ttagggagct cctaggtctg
240
ggctgcccga agagcaaggg ctcttccttc cttctttctt ttctccttct tgctacctgc
300
aacatggcga gcaaggggca tgtctcagcc ctgtttgtga tacagctctt ttagccctgc
360
catccagtgg gtcctgagtt cttgtccggc aaccaggaag aatgaggtac ccagacaagt
420
gtagagtgac caagacaaag aggagcttta ctgagtgaca atagctcaga ggaggccctg
480
gagagggcag ttcctcacta cagctggtca tccgacgtct gctcagctct ggctgagcct
540
ggggcttctg tcagcctcag agaggggaa gttcatgctg actggtccat gggcggccat
600

gggcaggccc agaaaaggca acacaagttc gcactccagt ccacggcact gacagcctgg
660
cccccagcct tcagggcctc cctggcctga aggtgggcct caccagggac tcacccccctt
720
ctgcccagaa acctgtctgc ctcctgctgc cattcatggc gcccaggcta taggtat
777

<210> 3200
<211> 92
<212> PRT
<213> Homo sapiens

<400> 3200
Met Leu Gln Val Ala Arg Arg Arg Lys Glu Arg Arg Lys Glu Glu Pro
1 5 10 15
Leu Leu Phe Gly Gln Pro Arg Pro Arg Ser Ser Leu Ser Gln Gly Cys
20 25 30
Asp Thr Leu Phe Gly Ala Leu Arg Phe Leu Ala Ser Pro Ser Phe Trp
35 40 45
Val Ser Pro Arg Ser Pro Val Pro Ala Val Gly Ala Ala Cys Cys Met
50 55 60
Pro Gly Pro Ala Thr Ala Ser Gln Arg Ala Gly Ala Leu Thr Ser Thr
65 70 75 80
Trp Ser Cys Leu Pro His Cys Ser Ser Arg Arg Val
85 90

<210> 3201
<211> 390
<212> DNA
<213> Homo sapiens

<400> 3201
acacgcgcag tgcgtctcct actgaacccg agcccctgct atgggtacgc ggaagcagct
60
cccgtcgcgc ctgccccagg ctggacggaa gggccacgct gcagccgggg tgagcacagc
120
gaagccgaca gcctttggga ccgaggtcag cagctgcacc ggcgcaagaa ttccaaacac
180
agctgtggct gaagggcctg ggggtgtgca ggtcccaaac cccagtgagc ctgatcccga
240
catgggtcct gtctcctggg ggccaccttt gtgtcccgtg gtggctgacc ctgagaggga
300
gggctgtggg gatgctcaca tgacactggg gtcccagcga cagcccctcc tcacgctgcg
360
tgtccctggg gcctctcagg agggacgcgt
390

<210> 3202
<211> 116
<212> PRT
<213> Homo sapiens

<400> 3202
Met Gly Thr Arg Lys Gln Leu Pro Ser Arg Leu Pro Gln Ala Gly Arg

```
 1               5                  10                  15
Lys Gly His Ala Ala Ala Gly Val Ser Thr Ala Lys Pro Thr Ala Phe
            20                  25                  30
Gly Thr Glu Val Ser Ser Cys Thr Gly Ala Arg Ile Pro Asn Thr Ala
        35                  40                  45
Val Ala Glu Gly Pro Gly Gly Val Gln Val Pro Asn Pro Ser Glu Pro
    50                  55                  60
Asp Pro Asp Met Gly Pro Val Ser Trp Gly Pro Pro Leu Cys Pro Val
65                  70                  75                  80
Val Ala Asp Pro Glu Arg Glu Gly Cys Gly Asp Ala His Met Thr Leu
                85                  90                  95
Gly Ser Gln Arg Gln Pro Leu Leu Thr Leu Arg Val Pro Gly Ala Ser
            100                 105                 110
Gln Glu Gly Arg
        115
```

<210> 3203
<211> 1906
<212> DNA
<213> Homo sapiens

<400> 3203
ngaattcggc acgagctcgt gccgaatcgg cacgagcgcg ggcccaggag cggcaggact
60
cgggccggag cgtggccgga cccccacccg ccgaggggcc cagggaggac gcggcagagt
120
cacggtggca gcattgagag ttggacaccc gggtccttga agtgatctct aggccccagc
180
cccaaatccg ccaccattcc gtgctgcggg gacaccatgg ctccagaaga ggacgctgga
240
ggggaggcct taggggggcag tttctgggag gctggcaact acaggcgcac ggtacagcgg
300
gtggaggacg ggcaccggct gtgcggggac ctggtcagct gcttccagga gcgcgcccgc
360
atcgagaagg cttatgccca gcagttggct gactgggccc gaaagtggag ggggaccgtg
420
gagaagggcc cccagtatgg cacactggag aaggcctggc atgccttttt cacggcggct
480
gagcggctga gcgcgctgca cctggaggtg cgggagaagc tgcaagggca ggacagtgag
540
cgggtgcgcg cctggcagcg gggggctttc caccggcctg tgctgggcgg cttccgcgag
600
agccgggcgg ccgaggacgg cttccgcaag gcccagaagc cctggctgaa gaggctgaag
660
gaggttgagg cttccaagaa aagctaccac gcagcccgga aggatgagaa gaccgcccag
720
acgagggaga gccacgcaaa ggcagacagc gccgtctccc aggagcagct gcgcaaactg
780
caggaacggg tggaacgctg tgccaaggag gccgagaaga caaaagctca gtatgagcag
840
acgctggcag agctgcatcg ctacactcca cgctacatgg aggacatgga acaggccttt
900
gagacctgcc aggccgccga gcgccagcgg cttcttttct tcaaggatat gctgctcacc
960

ttacaccagc acctggacct ttccagcagt gagaagttcc atgaactcca ccgtgacttg
1020
caccagggca ttgaggcagc cagtgacgaa gaggatctgc gctggtggcg cagcacccac
1080
gggccaggca tggccatgaa ctggccacag ttcgaggagt ggtccttgga cacacagagg
1140
acaatcagcc ggaaagagaa gggtggccgg agccctgatg aggttaccct gaccagcatt
1200
gtgcctacaa gagatggcac cgcaccccca ccccagtccc cggggtcccc aggcacgggg
1260
caggatgagg agtggtcaga tgaagagagt ccccggaagg ctgccaccgg ggttcgggtg
1320
agggcactct atgactacgc tggccaggaa gctgatgagc tgagcttccg agcaggggag
1380
gagctgctga agatgagtga ggaggacgag cagggctggt gccaaggcca gttgcagagt
1440
ggccgcattg gcctgtaccc tgccaactac gtggagtgtg tgggcgcctg agtgtcctga
1500
cagcccttct gcaacgttta cccaccctgg ttcagagccc agcttctcct ggagagccgg
1560
accctcaggg ccctgaaccg tcgctctctg gctgctcctc tgtcccttga gggaggaagt
1620
cctgggaccc agggagggga ggggcctttg tctagggaag ggactggtag ggaagggacg
1680
agtctaggct gagggcaaga tgggaggtca gaggtgacag aagcgttcag gggtgcctgg
1740
gcctccccag gagctgtgga ctcagttcct gacctctgct ttggggttcc tggggtgggc
1800
ttggggtgag tgtagttctg gcctagcagc accctcttgt ggcttgttct agcgtgtatt
1860
aaaacttgac acacacccac acacaaaaac aaaaacacca aaaaaa
1906

<210> 3204
<211> 424
<212> PRT
<213> Homo sapiens

<400> 3204
Met Ala Pro Glu Glu Asp Ala Gly Gly Glu Ala Leu Gly Gly Ser Phe
1 5 10 15
Trp Glu Ala Gly Asn Tyr Arg Arg Thr Val Gln Arg Val Glu Asp Gly
20 25 30
His Arg Leu Cys Gly Asp Leu Val Ser Cys Phe Gln Glu Arg Ala Arg
35 40 45
Ile Glu Lys Ala Tyr Ala Gln Gln Leu Ala Asp Trp Ala Arg Lys Trp
50 55 60
Arg Gly Thr Val Glu Lys Gly Pro Gln Tyr Gly Thr Leu Glu Lys Ala
65 70 75 80
Trp His Ala Phe Phe Thr Ala Ala Glu Arg Leu Ser Ala Leu His Leu
85 90 95
Glu Val Arg Glu Lys Leu Gln Gly Gln Asp Ser Glu Arg Val Arg Ala
100 105 110
Trp Gln Arg Gly Ala Phe His Arg Pro Val Leu Gly Gly Phe Arg Glu

```
        115                 120                 125
Ser Arg Ala Ala Glu Asp Gly Phe Arg Lys Ala Gln Lys Pro Trp Leu
    130                 135                 140
Lys Arg Leu Lys Glu Val Glu Ala Ser Lys Lys Ser Tyr His Ala Ala
145                 150                 155                 160
Arg Lys Asp Glu Lys Thr Ala Gln Thr Arg Glu Ser His Ala Lys Ala
                165                 170                 175
Asp Ser Ala Val Ser Gln Glu Gln Leu Arg Lys Leu Gln Glu Arg Val
            180                 185                 190
Glu Arg Cys Ala Lys Glu Ala Glu Lys Thr Lys Ala Gln Tyr Glu Gln
        195                 200                 205
Thr Leu Ala Glu Leu His Arg Tyr Thr Pro Arg Tyr Met Glu Asp Met
    210                 215                 220
Glu Gln Ala Phe Glu Thr Cys Gln Ala Ala Glu Arg Gln Arg Leu Leu
225                 230                 235                 240
Phe Phe Lys Asp Met Leu Leu Thr Leu His Gln His Leu Asp Leu Ser
                245                 250                 255
Ser Ser Glu Lys Phe His Glu Leu His Arg Asp Leu His Gln Gly Ile
            260                 265                 270
Glu Ala Ala Ser Asp Glu Glu Asp Leu Arg Trp Trp Arg Ser Thr His
        275                 280                 285
Gly Pro Gly Met Ala Met Asn Trp Pro Gln Phe Glu Glu Trp Ser Leu
    290                 295                 300
Asp Thr Gln Arg Thr Ile Ser Arg Lys Glu Lys Gly Gly Arg Ser Pro
305                 310                 315                 320
Asp Glu Val Thr Leu Thr Ser Ile Val Pro Thr Arg Asp Gly Thr Ala
                325                 330                 335
Pro Pro Pro Gln Ser Pro Gly Ser Pro Gly Thr Gly Gln Asp Glu Glu
            340                 345                 350
Trp Ser Asp Glu Glu Ser Pro Arg Lys Ala Ala Thr Gly Val Arg Val
        355                 360                 365
Arg Ala Leu Tyr Asp Tyr Ala Gly Gln Glu Ala Asp Glu Leu Ser Phe
    370                 375                 380
Arg Ala Gly Glu Glu Leu Leu Lys Met Ser Glu Glu Asp Glu Gln Gly
385                 390                 395                 400
Trp Cys Gln Gly Gln Leu Gln Ser Gly Arg Ile Gly Leu Tyr Pro Ala
                405                 410                 415
Asn Tyr Val Glu Cys Val Gly Ala
            420
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<210> 3205
<211> 1482
<212> DNA
<213> Homo sapiens

<400> 3205
nnggagatgg agggaacctc cccgagcagc ccaccaccca gtggggtgcg gtccccccg
60
ggtctggcca agacacccct atctgctctg ggcctgaaac ctcacaaccc agcggacatc
120
ctgttgcacc ccacaggaga gccccggagc tatgtggagt ctgtggcacg gacagcggtg
180
gctggacccc gagctcagga ctctgagccc aagagcttta gtgctccagc cacccaggcc
240

tatggccatg agataccccct gaggaacggg accctgggtg gctcctttgt ctcccccagc
300
cccctctcca ccagcagccc catcctcagt gctgacagca cttcagtggg gagtttcccg
360
tcgggagaga gcagtgacca gggtccccgg acgcccaccc agcctctgtt ggagtctggc
420
ttccgctcag gcagcctggg acagcccagc ccgtctgccc agagaaacta ccagagctct
480
tctcctctcc cgactgtggg cagtagctac agcagccccg actactcact tcagcatttc
540
agctcctctc cggaaagcca ggctcgagct cagttcagtg tggctggcgt ccacacggtg
600
cctgggagcc ctcaggcgcg tcacagaaca gtgggcacca acactccccc tagtcctggc
660
ttcggctggc gggccatcaa tcccagcatg gctgccccca gcagtcccag tttgagccat
720
caccagatga tgggtccacc aggcactggc ttccatggta gcactgtctc cagcccccag
780
agcagtgcag cgaccacccc ggggagcccc agcctgtgtc ggcacccagc aggggtctac
840
caggtttctg gcctccacaa caaagtggcc accaccccgg ggagtcccag cctgggccgg
900
caccctgggg ctcaccaagg caacctggcc tccggtcttc atagcaatgc aatagccagc
960
cctggaagcc ccagcctggg ccgtcacctc ggagggtctg gatctgtggt tcccggcagc
1020
ccctgcttgg accggcatgt ggcctatggc ggctattcta ccccggagga tcggagaccc
1080
acactgtccc ggcagagcag tgcctctggc taccaggctc cttccacgcc ctccttccct
1140
gtctcccctg cctactaccc tggcctgagc agccctgcca cctccccgtc accagactcc
1200
gcagccttcc ggcaagggag cccaacacca gccttgccag agaagcgaag gatgtcagtg
1260
ggagaccggg caggcagcct ccccaactat gccaccatca atgggaaggt gtcttcgcct
1320
gtcgccagcg gcatgtccag tcccagtggg ggcagcaccg tctccttctc ccacactctg
1380
cccgacttct ccaagtactc catgccagac aacagcccgg agacgcgggc taaagtgaag
1440
tttgtccagg acacttctaa gtattggtac aagcctaaga tc
1482

<210> 3206
<211> 494
<212> PRT
<213> Homo sapiens

<400> 3206
Xaa Glu Met Glu Gly Thr Ser Pro Ser Ser Pro Pro Pro Ser Gly Val
 1   5   10   15
Arg Ser Pro Pro Gly Leu Ala Lys Thr Pro Leu Ser Ala Leu Gly Leu
            20   25   30
Lys Pro His Asn Pro Ala Asp Ile Leu Leu His Pro Thr Gly Glu Pro

```
        35                  40                  45
Arg Ser Tyr Val Glu Ser Val Ala Arg Thr Ala Val Ala Gly Pro Arg
    50                  55                  60
Ala Gln Asp Ser Glu Pro Lys Ser Phe Ser Ala Pro Ala Thr Gln Ala
65                  70                  75                  80
Tyr Gly His Glu Ile Pro Leu Arg Asn Gly Thr Leu Gly Gly Ser Phe
                85                  90                  95
Val Ser Pro Ser Pro Leu Ser Thr Ser Ser Pro Ile Leu Ser Ala Asp
            100                 105                 110
Ser Thr Ser Val Gly Ser Phe Pro Ser Gly Glu Ser Ser Asp Gln Gly
        115                 120                 125
Pro Arg Thr Pro Thr Gln Pro Leu Leu Glu Ser Gly Phe Arg Ser Gly
    130                 135                 140
Ser Leu Gly Gln Pro Ser Pro Ser Ala Gln Arg Asn Tyr Gln Ser Ser
145                 150                 155                 160
Ser Pro Leu Pro Thr Val Gly Ser Ser Tyr Ser Ser Pro Asp Tyr Ser
                165                 170                 175
Leu Gln His Phe Ser Ser Ser Pro Glu Ser Gln Ala Arg Ala Gln Phe
            180                 185                 190
Ser Val Ala Gly Val His Thr Val Pro Gly Ser Pro Gln Ala Arg His
        195                 200                 205
Arg Thr Val Gly Thr Asn Thr Pro Pro Ser Pro Gly Phe Gly Trp Arg
    210                 215                 220
Ala Ile Asn Pro Ser Met Ala Ala Pro Ser Ser Pro Ser Leu Ser His
225                 230                 235                 240
His Gln Met Met Gly Pro Pro Gly Thr Gly Phe His Gly Ser Thr Val
                245                 250                 255
Ser Ser Pro Gln Ser Ser Ala Ala Thr Thr Pro Gly Ser Pro Ser Leu
            260                 265                 270
Cys Arg His Pro Ala Gly Val Tyr Gln Val Ser Gly Leu His Asn Lys
        275                 280                 285
Val Ala Thr Thr Pro Gly Ser Pro Ser Leu Gly Arg His Pro Gly Ala
    290                 295                 300
His Gln Gly Asn Leu Ala Ser Gly Leu His Ser Asn Ala Ile Ala Ser
305                 310                 315                 320
Pro Gly Ser Pro Ser Leu Gly Arg His Leu Gly Gly Ser Gly Ser Val
                325                 330                 335
Val Pro Gly Ser Pro Cys Leu Asp Arg His Val Ala Tyr Gly Gly Tyr
            340                 345                 350
Ser Thr Pro Glu Asp Arg Arg Pro Thr Leu Ser Arg Gln Ser Ser Ala
        355                 360                 365
Ser Gly Tyr Gln Ala Pro Ser Thr Pro Ser Phe Pro Val Ser Pro Ala
    370                 375                 380
Tyr Tyr Pro Gly Leu Ser Ser Pro Ala Thr Ser Pro Ser Pro Asp Ser
385                 390                 395                 400
Ala Ala Phe Arg Gln Gly Ser Pro Thr Pro Ala Leu Pro Glu Lys Arg
                405                 410                 415
Arg Met Ser Val Gly Asp Arg Ala Gly Ser Leu Pro Asn Tyr Ala Thr
            420                 425                 430
Ile Asn Gly Lys Val Ser Ser Pro Val Ala Ser Gly Met Ser Ser Pro
        435                 440                 445
Ser Gly Gly Ser Thr Val Ser Phe Ser His Thr Leu Pro Asp Phe Ser
    450                 455                 460
Lys Tyr Ser Met Pro Asp Asn Ser Pro Glu Thr Arg Ala Lys Val Lys
```

```
465                 470                 475                 480
Phe Val Gln Asp Thr Ser Lys Tyr Trp Tyr Lys Pro Lys Ile
                485                 490

<210> 3207
<211> 495
<212> DNA
<213> Homo sapiens

<400> 3207
ngcgggacgc gcagcgctat ggcagagggc agcggggaag tggtcgcagt gtctgcgacc
60
ggggctgcca acggcctcaa caatggggca ggcgggacct cggcgacgac ctgcaacccg
120
ctgtcgcgca agctgcataa gatcctggag acgcggctgg acaacgacaa ggagatgtta
180
gaagctctca aggcactttc aacctttttt gttgaaaata gtctgcggac tcgaagaaat
240
ttacgtggag atattgaacg taaaagttta gccatcaatg aagaatttgt aagcattttc
300
aaggaagtga aggaggaact tgaaagcata agcgaagatg ttcaagcaat gagcaactgt
360
tgtcaagata tgacaagtcg cctacaggca gcaaaggaac agactcaaga tttaatagta
420
aataccacta agcttcaatc tgaaagccaa aaattagaga taagagctca agttgcagat
480
gccttcttat ccaag
495

<210> 3208
<211> 107
<212> PRT
<213> Homo sapiens

<400> 3208
Met Leu Glu Ala Leu Lys Ala Leu Ser Thr Phe Phe Val Glu Asn Ser
 1               5                  10                  15
Leu Arg Thr Arg Arg Asn Leu Arg Gly Asp Ile Glu Arg Lys Ser Leu
            20                  25                  30
Ala Ile Asn Glu Glu Phe Val Ser Ile Phe Lys Glu Val Lys Glu Glu
        35                  40                  45
Leu Glu Ser Ile Ser Glu Asp Val Gln Ala Met Ser Asn Cys Cys Gln
    50                  55                  60
Asp Met Thr Ser Arg Leu Gln Ala Ala Lys Glu Gln Thr Gln Asp Leu
65                  70                  75                  80
Ile Val Asn Thr Thr Lys Leu Gln Ser Glu Ser Gln Lys Leu Glu Ile
                85                  90                  95
Arg Ala Gln Val Ala Asp Ala Phe Leu Ser Lys
            100                 105

<210> 3209
<211> 346
<212> DNA
<213> Homo sapiens
```

<400> 3209
tgttcctcta ggtggggcag gtaggggtc cagcttcctg cttgctggtg gttcaggtca
60
tgcgtccagc cttgtccctt ctgacctggg ccctacccac ggggaaatgt tcccatagca
120
gaagaatcag ccccacagtg caggggtgtg ttagtgggga acgggctctg ggctcctgtg
180
ggaaccaggg acccccctatc ttggtaccgg tcattggatg tatccccagc tcatgcctgt
240
gtctgtcttg gcccgtgtgg tcaccctgtg ttcatctctc tcccagccat ggcctctcaa
300
actggggttt tcgtctccct atgaggggt cctggtatgt acgcgt
346

<210> 3210
<211> 95
<212> PRT
<213> Homo sapiens

<400> 3210
Met Arg Pro Ala Leu Ser Leu Leu Thr Trp Ala Leu Pro Thr Gly Lys
1 5 10 15
Cys Ser His Ser Arg Arg Ile Ser Pro Thr Val Gln Gly Cys Val Ser
20 25 30
Gly Glu Arg Ala Leu Gly Ser Cys Gly Asn Gln Gly Pro Pro Ile Leu
35 40 45
Val Pro Val Ile Gly Cys Ile Pro Ser Ser Cys Leu Cys Leu Ser Trp
50 55 60
Pro Val Trp Ser Pro Cys Val His Leu Ser Pro Ser His Gly Leu Ser
65 70 75 80
Asn Trp Gly Phe Arg Leu Pro Met Arg Gly Ser Trp Tyr Val Arg
85 90 95

<210> 3211
<211> 1728
<212> DNA
<213> Homo sapiens

<400> 3211
tccggaaata taaagttgag ctaccagttt tcagaaatcc atgaagactc taccgtctgc
60
tggacaaaag attccaagtc gatagcccag gccaagaaaa gcgcagggga caactccagt
120
gtttccttgg ccatcgtgca agccagtccg aaggaccagg gactctatta ctgctgcatc
180
aagaacagct acggaaaagt gactgctgaa tttaacctca cagctgaagt tctcaaacag
240
ctgtcaagtc acacagaata ctaaaggatg tgaagagatt gaattcagcc aactcatctt
300
caaagaagac ttcctccatg acagctactt tgggggccgc ctgcgtggtc agatcgccac
360
ggaggagctg cactttggag aaggggttca ccgcaaagcc ttccgcagca cagtgatgca
420

cggcctcatg cctgtcttca aacctggcca tgcctgtgtg cttaaggtgc acaatgccat
480
tgcctatggg accagaaata atgatgagct catccaaagg aactacaaac tcgctgccca
540
ggaatgctat gttcaaaata ctgccaggta ttatgccaag atctacgctg ctgaagcaca
600
gcctctggaa ggctttggag aagtacctga gatcattcct atttttctta tccatcggcc
660
tgagaacaat atcccgtatg ctacagtgga ggaggagctg attggagaat ttgtgaagta
720
ttccatcagg gatgggaaag aaataaactt cttgagaaga gaatcagaag ctggtcagaa
780
atgttgcacc ttccagcact gggtgtacca gaaaacaagt ggctgcctcc tggtgacgga
840
catgcaaggt gtaggaatga agctaactga cgttggcata gcaacgctgg ctaaagggta
900
caagggattt aaaggcaact gttccatgac cttcattgat cagtttaaag cactacacca
960
gtgtaacaag tattgcaaaa tgctgggact gaaatccctt caaaacaaca accagaaaca
1020
gaagcagccg agcattggga aaagcaaagt tcaaacaaac tctatgacag taaagaaggc
1080
agggcctgag accccaggcg aaaagaaaac ctaacgtccc cgggtaacct aatggccact
1140
ggctagcagc acacaatctc gccagggaaa atctgaggcc acacaggaga gaatatacag
1200
cctgcagaga gtgcgtggca atccttactc ccagccgact gtgcgccaag atgcttctaa
1260
acccatcacc tgctgtcttc actcaaatga tttcagaaca ggatttgcga ccaggtttat
1320
ggggagattg aatcaacgat tggtctcaaa gacagtccat tctttatata catgtttagc
1380
atttttacca acctcacatc atgtgtatat ttgtgtattt gcacatggtt gtgctgtcga
1440
ggacctggtg ctgagaagag tctgttcaca gccaaaattc ttcccactgt cattcctaac
1500
ctgggatttc tagacacatc ctgctgtgat gtaaacagaa atcacgaatt cgctcactgg
1560
atcaagttgt tccactggtg tctaatacgc tattgttgcc ggaggtgggt tctgtgacgt
1620
gaagccattt cccatcattc aacagccagt tacaattttc tgtttaatta aattcatatt
1680
taaacaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa
1728

<210> 3212
<211> 87
<212> PRT
<213> Homo sapiens

<400> 3212
Ser Gly Asn Ile Lys Leu Ser Tyr Gln Phe Ser Glu Ile His Glu Asp
 1   5   10   15
Ser Thr Val Cys Trp Thr Lys Asp Ser Lys Ser Ile Ala Gln Ala Lys

```
            20                  25                  30
Lys Ser Ala Gly Asp Asn Ser Ser Val Ser Leu Ala Ile Val Gln Ala
        35                  40                  45
Ser Pro Lys Asp Gln Gly Leu Tyr Tyr Cys Cys Ile Lys Asn Ser Tyr
    50                  55                  60
Gly Lys Val Thr Ala Glu Phe Asn Leu Thr Ala Glu Val Leu Lys Gln
65                  70                  75                  80
Leu Ser Ser His Thr Glu Tyr
                85
```

<210> 3213
<211> 348
<212> DNA
<213> Homo sapiens

<400> 3213
acgcgtgaag gggaagcggc ggggtagtaa cagattatgg gcaacagtcc ttttaattaa
60
tctaccgtca tcatggctaa tgaggactgt cccaaggctg ctgatagtcc tttttcatca
120
gataaacatg cccaactcat cttggcccaa atcaataaga tgagaaatgg acagcatttc
180
tgtgatgtgc agctgcaagt tggacaggaa agttttaaag ctcatcggct ggttttggct
240
gccagcagtc cttactttgc agctttgttc actggaggaa tgaaagagtc ctcaaaagat
300
gttgtaccga ttctaggaat tgaagcagga atctttcaga tacttcta
348

<210> 3214
<211> 92
<212> PRT
<213> Homo sapiens

<400> 3214
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Met Ala Asn Glu Asp Cys Pro Lys Ala Ala Asp Ser Pro Phe Ser Ser
 1               5                  10                  15
Asp Lys His Ala Gln Leu Ile Leu Ala Gln Ile Asn Lys Met Arg Asn
            20                  25                  30
Gly Gln His Phe Cys Asp Val Gln Leu Gln Val Gly Gln Glu Ser Phe
        35                  40                  45
Lys Ala His Arg Leu Val Leu Ala Ala Ser Ser Pro Tyr Phe Ala Ala
    50                  55                  60
Leu Phe Thr Gly Gly Met Lys Glu Ser Ser Lys Asp Val Val Pro Ile
65                  70                  75                  80
Leu Gly Ile Glu Ala Gly Ile Phe Gln Ile Leu Leu
                85                  90
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<210> 3215
<211> 597
<212> DNA
<213> Homo sapiens

<400> 3215

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120
accttcaagt tcgacttgga cggggacgca cccgatgaaa ttgccacgta tatggtggag
180
catgacttta tcctgcaggc cgagcgggaa acgttcatcg agcagatgaa ggatgtcatg
240
gacaaggcag aggacatgct cagcgaggac acagacgccg accgtggctc cgacccaggg
300
accagcccgc cacacctcag cacctgcggc ctgggcaccg gggaggagag ccgacaatcc
360
caagccaacg cccccgtgta tcagcagaac gtcctgcaca ccgggaagag gtggttcatc
420
atctgtccgg tgcctgagcc ccccgccccc gagggccctt gaatcttcgc ccccacttcc
480
tctaagctcc ctgccgccag aagccagcca agattcagcg ccctataaag accagctgtc
540
ctcgaaggaa caacccagct ttctagccag tcagcagctc ctgggccagg cgggccc
597

<210> 3216
<211> 153
<212> PRT
<213> Homo sapiens

<400> 3216
Thr Arg Ala Arg Ser Arg Gln Glu Arg Ala Ser Arg Pro Arg Leu Thr
 1   5   10   15
Ile Leu Asn Val Cys Asn Thr Gly Asp Lys Met Val Glu Cys Gln Leu
            20   25   30
Glu Thr His Asn His Lys Met Val Thr Phe Lys Phe Asp Leu Asp Gly
        35   40   45
Asp Ala Pro Asp Glu Ile Ala Thr Tyr Met Val Glu His Asp Phe Ile
    50   55   60
Leu Gln Ala Glu Arg Glu Thr Phe Ile Glu Gln Met Lys Asp Val Met
65   70   75   80
Asp Lys Ala Glu Asp Met Leu Ser Glu Asp Thr Asp Ala Asp Arg Gly
                85   90   95
Ser Asp Pro Gly Thr Ser Pro Pro His Leu Ser Thr Cys Gly Leu Gly
            100   105   110
Thr Gly Glu Glu Ser Arg Gln Ser Gln Ala Asn Ala Pro Val Tyr Gln
        115   120   125
Gln Asn Val Leu His Thr Gly Lys Arg Trp Phe Ile Ile Cys Pro Val
    130   135   140
Pro Glu Pro Pro Ala Pro Glu Gly Pro
145   150

<210> 3217
<211> 2570
<212> DNA
<213> Homo sapiens

<400> 3217

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gactttgtaa agctgcggga aatgctcatt tgtacaaata tggaggacct gcgagagcag
120
acccatacca ggcactatga gctttacagg cgctgcaaac tggaggaaat gggctttaca
180
gatgtgggcc cagaaaacaa gccagtcagt gttcaagaga cctatgaagc caaaagacat
240
gagttccatg gtgaacgtca gaggaaggaa gaagaaatga aacagatgtt tgtgcagcga
300
gtaaaggaga aagaagccat attgaaagaa gctgagagag agctacaggc caaatttgag
360
caccttaaga gacttcacca agaagagaga atgaagcttg aagaacaaag aagacttttg
420
gaagaagaaa taattgcttt ctctaaaaag aaagctacct ccgagatatt tcacagccag
480
tccttttctgg caacaggcag caacctgagt aaggacaagg accataagaa ctccaatttt
540
ttgtaaaaca gaagttccag agcacagaag gtcatcatca caagcaaact ttattaaaaa
600
aaaactagaa gtgtgctttg attttgctgt tatttgtttt atcacttcta tatttggtga
660
acagccacag ttactgatat ttatggaaaa gtactttcaa gtacaaggtc aatacataag
720
ccagagtgaa tgatactaca agttgagcat ctctaattca aaaatctgaa atccagaagc
780
ttcaaaatct gaatcttttt gagcactgac ttgaccccac aagtggaaaa ttccccaccc
840
gacacctttg ctttctgatg gttcagttta aacagatttt gtttcttgca caaaatttct
900
gtataaatta ctttcaggct atatgtataa ggtggatgtg aaacatgaat tatgtaatta
960
gagtcgggtc ccgttgtgta tatgcagata ttccaaacct gaaatccaaa acacttctgg
1020
tccctagcat tttggataag ggatactcag cttgtaccta tatattcata tatattcact
1080
gttgttagaa atgtttaagt tgctgttctg tgatgaatct aaatcttttc tcttgctacc
1140
aagctattgt cactgcagtg cattatacca aagagcgaag tcagtgccac tgaaaataca
1200
gaacccatta atatcgtggc tatctgatta catttatatt ccaagatgaa cctttttttа
1260
tatatgctaa aaattttggg gaatatgttt tgggatgtat tatggagcta aaactctaac
1320
ctcttaatag ttttatagaa cttaaaaatt ttttatacaa ttacccaatt ggtgatatga
1380
tcttaagctt ttgtgtcaga ttatttaata tgatgacttc atgctttatt atgccttatt
1440
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1500
ataagctatt ttttcctaag gataaagtac ctttgagcat gagtgtatca cagctttcat
1560
taggaaaact tttcattaca tacttgttta aactctgtct tccagggtaa aaataataag
1620

gttgaatcat tttattaaaa atacttttta agaaaataac tatgaacatc tgaatattaa
1680
agatataaaa atgcacataa ttcatatttc aggtggtatt tgcattcagt gccttactgg
1740
tattctcaga acattttaat gatttctaac atttcttaac agtcatagat atatacattt
1800
tcatttttg tacttgaata ttctaaataa aactgacatt tactcttgac aaataaaaca
1860
tatatttact aaaaaaaaaa aaaaaaaacc tcgtgccgaa ttcggagagt ctaggaatac
1920
tgttaaagga aaaaaaagag gggggaagat caggtcatac tatctactct cctcatctct
1980
aacagctcag gatctcttag cattttaatt agatgtaatt gtttgtcttt aactgtcaaa
2040
aagtttggtt ctgtgtctgt gttttaataa gacgagagga cgagcgattg aggtgtatgg
2100
agagaaaaca gacctaatgc tccttgttcc tagagtagag tggagggagg gtggcctaag
2160
agttgagctc tcggaactgc atgctgctgg acagtatcac tgtctttcct agatggcagt
2220
cactgaattc catttttca aggtaatttc ttgtgcctct aatagcccaa gaatgggagg
2280
ttgatcagat ctgacatgat tccttcctgt tctgaactgt ggggtgtgca catctctgct
2340
tgagtcaggt ttgagtagag gcttagagac agttgggtga gaacaaccaa aatcttatca
2400
tggtctcagt cataatcatt agggggaact ctagccaaat ggtttaactt ctgcctgtgg
2460
aactggggat tgggtgggca ggaaaaggtg atatccattc tttctgataa ctagatggtg
2520
ctgagaagct tttgaataaa aactttgcta aatgaaaaaa aaaaaaaaaa
2570

<210> 3218
<211> 181
<212> PRT
<213> Homo sapiens

<400> 3218
Gly Val Lys Ala Arg Gln Tyr Pro Trp Gly Val Val Gln Val Glu Asn
1 5 10 15
Glu Asn His Cys Asp Phe Val Lys Leu Arg Glu Met Leu Ile Cys Thr
20 25 30
Asn Met Glu Asp Leu Arg Glu Gln Thr His Thr Arg His Tyr Glu Leu
35 40 45
Tyr Arg Arg Cys Lys Leu Glu Glu Met Gly Phe Thr Asp Val Gly Pro
50 55 60
Glu Asn Lys Pro Val Ser Val Gln Glu Thr Tyr Glu Ala Lys Arg His
65 70 75 80
Glu Phe His Gly Glu Arg Gln Arg Lys Glu Glu Glu Met Lys Gln Met
85 90 95
Phe Val Gln Arg Val Lys Glu Lys Glu Ala Ile Leu Lys Glu Ala Glu
100 105 110
Arg Glu Leu Gln Ala Lys Phe Glu His Leu Lys Arg Leu His Gln Glu

```
        115                 120                 125
Glu Arg Met Lys Leu Glu Glu Gln Arg Arg Leu Leu Glu Glu Glu Ile
    130                 135                 140
Ile Ala Phe Ser Lys Lys Lys Ala Thr Ser Glu Ile Phe His Ser Gln
145                 150                 155                 160
Ser Phe Leu Ala Thr Gly Ser Asn Leu Ser Lys Asp Lys Asp His Lys
                165                 170                 175
Asn Ser Asn Phe Leu
            180
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<210> 3219
<211> 1241
<212> DNA
<213> Homo sapiens

<400> 3219
gcgcgccatg taccacaccc agcacctcag gtcccgccca gcaggggget cggctgtgcc
60
tcctctggac gccacgttgt cccagcccag gttcatgtca atggtgggng cgttacatct
120
gagcgggaga cagacatcct ggacgatgaa ttgccaaacc aggatggtca cagtgcgggc
180
agcatgggca cactctcttc tctggacggg gtcaccaaca tcagtgaggg gggctaccca
240
gaggccctgt ccccactgac caacggtctg gacaagtcct accccatgga gcctatggtc
300
aatggaggag gctaccccta cgagtctgcc agccgggcgg ggcctgccca tgctggccac
360
acggcccccа tgcggccctc ctactctgca caggagggtt tagctggcta ccagagggag
420
gggccccacc cagcctggcc acagccagtg accacctccc actatgccca tgaccccagc
480
ggtatgttcc gctctcaatc cttttcggaa gctgaacccc agctgccccc agctccggtc
540
cgaggggaa gcagccggga ggctgtgcaa aggggactga attcgtggca gcagcagcag
600
cagcagcagc agcagcctcg cccacctcca cgccagcagg aaagagccca cttggagagt
660
cttgtagcca gcaggcccag ccctcagcca ttggcagaga cccccatccc cagtctccct
720
gagttcccgc gagcagcctc ccagcaggag attgaacagt ccatcgaaac actcaatatg
780
ctgatgctgg acctggagcc agcctccgct gctgccccac tacacaagtc ccagagtgtc
840
cccggggcct ggccaggggc ttctccactc tcctcccagc ccctctctgg atcctcccgt
900
cagtcccatc cactgaccca gtccagatct ggctatatcc ccagtgggca ttcgttggga
960
acccctgagc cagccccacg ggcctctctg gagtctgtcc ctcctggcag gtcttactca
1020
ccttatgact atcagccatg tttggctggg cctaaccagg atttccattc aaagagccca
1080
gcctcttcct ccttgcctgc cttccttccg accacccaca gccctccagg gcctcagcaa
1140

ccccagcct ctctccctgg cctcactgct cagcctctgc tctcaccaaa ggaagcgact
1200
tcagaccct cccggactcc agaggaggag ccattgaatt c
1241

<210> 3220
<211> 413
<212> PRT
<213> Homo sapiens

<400> 3220
Ala Arg His Val Pro His Pro Ala Pro Gln Val Pro Pro Ser Arg Gly
1 5 10 15
Leu Gly Cys Ala Ser Ser Gly Arg His Val Val Pro Ala Gln Val His
20 25 30
Val Asn Gly Gly Xaa Val Thr Ser Glu Arg Glu Thr Asp Ile Leu Asp
35 40 45
Asp Glu Leu Pro Asn Gln Asp Gly His Ser Ala Gly Ser Met Gly Thr
50 55 60
Leu Ser Ser Leu Asp Gly Val Thr Asn Ile Ser Glu Gly Gly Tyr Pro
65 70 75 80
Glu Ala Leu Ser Pro Leu Thr Asn Gly Leu Asp Lys Ser Tyr Pro Met
85 90 95
Glu Pro Met Val Asn Gly Gly Gly Tyr Pro Tyr Glu Ser Ala Ser Arg
100 105 110
Ala Gly Pro Ala His Ala Gly His Thr Ala Pro Met Arg Pro Ser Tyr
115 120 125
Ser Ala Gln Glu Gly Leu Ala Gly Tyr Gln Arg Glu Gly Pro His Pro
130 135 140
Ala Trp Pro Gln Pro Val Thr Thr Ser His Tyr Ala His Asp Pro Ser
145 150 155 160
Gly Met Phe Arg Ser Gln Ser Phe Ser Glu Ala Glu Pro Gln Leu Pro
165 170 175
Pro Ala Pro Val Arg Gly Gly Ser Ser Arg Glu Ala Val Gln Arg Gly
180 185 190
Leu Asn Ser Trp Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Arg Pro
195 200 205
Pro Pro Arg Gln Gln Glu Arg Ala His Leu Glu Ser Leu Val Ala Ser
210 215 220
Arg Pro Ser Pro Gln Pro Leu Ala Glu Thr Pro Ile Pro Ser Leu Pro
225 230 235 240
Glu Phe Pro Arg Ala Ala Ser Gln Gln Glu Ile Glu Gln Ser Ile Glu
245 250 255
Thr Leu Asn Met Leu Met Leu Asp Leu Glu Pro Ala Ser Ala Ala Ala
260 265 270
Pro Leu His Lys Ser Gln Ser Val Pro Gly Ala Trp Pro Gly Ala Ser
275 280 285
Pro Leu Ser Ser Gln Pro Leu Ser Gly Ser Ser Arg Gln Ser His Pro
290 295 300
Leu Thr Gln Ser Arg Ser Gly Tyr Ile Pro Ser Gly His Ser Leu Gly
305 310 315 320
Thr Pro Glu Pro Ala Pro Arg Ala Ser Leu Glu Ser Val Pro Pro Gly
325 330 335
Arg Ser Tyr Ser Pro Tyr Asp Tyr Gln Pro Cys Leu Ala Gly Pro Asn

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            340                 345                 350
Gln Asp Phe His Ser Lys Ser Pro Ala Ser Ser Ser Leu Pro Ala Phe
        355                 360                 365
Leu Pro Thr Thr His Ser Pro Pro Gly Pro Gln Gln Pro Pro Ala Ser
    370                 375                 380
Leu Pro Gly Leu Thr Ala Gln Pro Leu Leu Ser Pro Lys Glu Ala Thr
385                 390                 395                 400
Ser Asp Pro Ser Arg Thr Pro Glu Glu Glu Pro Leu Asn
                405                 410
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<210> 3221
<211> 1585
<212> DNA
<213> Homo sapiens

<400> 3221
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ccccaacgct cctgcaccgc gcggagatgg cacatccagg ccaccggtgg ggtcgagccc
120
gcaggctgga aggagatgcg atgccacctg cgcgccaacg gctacctgtg caagtaccag
180
tttgaggtct tgtgtcctgc gccgcgcccc ggggccgcct ctaacttgag ctatcgcgcg
240
cccttccagc tgcacagcgc cgctctggac ttcagtccac ctgggaccga ggtgagtgcg
300
ctctgccggg gacagctccc gatctcagtt acttgcatcg cggacgaaat cggcgctcgc
360
tgggacaaac tctcgggcga tgtgttgtgt ccctgccccg ggaggtacct ccgtgctggc
420
aaatgcgcag agctccctaa ctgcctagac gacttgggag gctttgcctg cgaatgtgct
480
acgggcttcg agctggggaa ggacggccgc tcttgtgtga ccagtgggga aggacagccg
540
acccttgggg ggaccggggt gcccaccagg cgcccgccgg ccactgcaac cagccccgtg
600
ccgcagagaa catggccaat cagggtcgac gagaagctgg gagagacacc acttgtccct
660
gaacaagaca attcagtaac atctattcct gagattcctc gatggggatc acagagcacg
720
atgtctaccc ttcaaatgtc ccttcaagcc gagtcaaagg ccactatcac cccatcaggg
780
agcgtgattt ccaagtttaa ttctacgact tcctctgcca ctcctcaggc tttcgactcc
840
tcctctgccg tggtcttcat atttgtgagc acagcagtag tagtgttggt gatcttgacc
900
atgacagtac ttgggcttgt caagctctgc tttcacgaaa gcccctcttc ccagccaagg
960
aaggagtcta tgggcccgcc gggctgtgat gagtgatcct gagcccgctg ctttgggctc
1020
cagtttgcac attgcacaaa caatggggtg aaagtcgggg actgtgatct gcgggacaga
1080
gcagagggtg ccttgctgcg gagtccccgt ctttgggctc tagtgatgca tagggaaaca
1140

ggggacatgg gcactcctgt gaacagtttt tcacttttga tgaaacgggg aaccaagagg
1200
aacttacttg tgtaactgac aatttctgca gaaatccccc ttcctctaaa ttcccttttac
1260
tccactgagg agctaaatca gaactgcaca ctccttccct gatgatagag gaagtggaag
1320
tgcctttagg atggtgatac tgggggaccg ggtagtgctg gggagagata ttttcttatg
1380
tttattcgga gaatttggag aagtgattga acttttcaag acattggaaa caaatagaac
1440
acaatataat ttacattaaa aaataatttc taccaaaatg gaaaggaaat gttctatgtt
1500
gttcaggcta ggagtatatt ggttcgaaat cccagggaaa aaaaataaaa ataaaaaatt
1560
aaaggattgt tgataaaaaa aaaaa
1585

<210> 3222
<211> 331
<212> PRT
<213> Homo sapiens

<400> 3222
Leu Leu Ala Val Leu Arg Pro Arg Arg Ser Arg Lys Arg His Val Gln
1 5 10 15
Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Trp His Ile
20 25 30
Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met Arg Cys
35 40 45
His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu Val Leu
50 55 60
Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr Arg Ala
65 70 75 80
Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro Gly Thr
85 90 95
Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val Thr Cys
100 105 110
Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly Asp Val
115 120 125
Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys Ala Glu
130 135 140
Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu Cys Ala
145 150 155 160
Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr Ser Gly
165 170 175
Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg Arg Pro
180 185 190
Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro Ile Arg
195 200 205
Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln Asp Asn
210 215 220
Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln Ser Thr
225 230 235 240
Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala Thr Ile

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                245                 250                 255
Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr Ser Ser
            260                 265                 270
Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe Ile Phe
        275                 280                 285
Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr Val Leu
    290                 295                 300
Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln Pro Arg
305                 310                 315                 320
Lys Glu Ser Met Gly Pro Pro Gly Cys Asp Glu
                325                 330
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<210> 3223
<211> 985
<212> DNA
<213> Homo sapiens

<400> 3223
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agcctgattt ttggggcact gaccatcatg accggcgtca ttggggtcat cttgggggca
120
gaagcttcga ggaggtacaa gaaagtcatt ccaggagctg agcccctcat ctgcgcctcc
180
agcctgcttg ccacagcccc ctgcctctac ctggctctcg tcctggcccc gaccaccctg
240
ctggcctcct atgtgttcct gggccttggg gagctgcttc tgtcctgcaa ctgggcagtg
300
gttgccgaca tcctgctgtc tgtggtggtg cccagatgcc gggggacggc agaggcactt
360
cagatcacgg tgggccacat cctgggagac gctggcagcc cctatctcac aggacttatc
420
tctagtgtcc tgcggccagg cgccctgact cctctgcagc gcttccgcag cctgcagcag
480
agcttcctgt gctgcgcctt tgtcatcgcc ctgggggggcg gctgcttcct gctgactgcg
540
ctgtacctgg agagagacga gacccgggcc tggcagcctg tcacagggac cccagacagc
600
aatgatgtgg acagcaacga cctggagaga caaggcctac tttcgggcgc tggcgcctct
660
acagaggagc cctgaggtcc ctgcctacac tcgtcctgcc tgcaagcctc ccgttggtcc
720
ccacagcagc agtgcctcgg ttcctctttg gctgtcctcg gggactccgg ctgaggcaca
780
tctgccactt ttgaattccc ggctggagag ctggcaggac cctgtggctg ggctgggaat
840
ggagctgtca gcactctgcg tgggaggcct gggcctgtgc ctgcatcccg ctcaaggctg
900
ccccagcctg gggtccccag cctggctgct gctgggccct gaataaagag aggccagtac
960
aaagcccatg gattttgggc ctgta
985

<210> 3224

<211> 224
<212> PRT
<213> Homo sapiens

<400> 3224
Xaa Arg Val Val His Gly Leu Gln Pro Pro Cys Phe Gln Glu Pro Cys
1 5 10 15
Ser Asn Pro Asp Ser Leu Ile Phe Gly Ala Leu Thr Ile Met Thr Gly
20 25 30
Val Ile Gly Val Ile Leu Gly Ala Glu Ala Ser Arg Arg Tyr Lys Lys
35 40 45
Val Ile Pro Gly Ala Glu Pro Leu Ile Cys Ala Ser Ser Leu Leu Ala
50 55 60
Thr Ala Pro Cys Leu Tyr Leu Ala Leu Val Leu Ala Pro Thr Thr Leu
65 70 75 80
Leu Ala Ser Tyr Val Phe Leu Gly Leu Gly Glu Leu Leu Leu Ser Cys
85 90 95
Asn Trp Ala Val Val Ala Asp Ile Leu Leu Ser Val Val Val Pro Arg
100 105 110
Cys Arg Gly Thr Ala Glu Ala Leu Gln Ile Thr Val Gly His Ile Leu
115 120 125
Gly Asp Ala Gly Ser Pro Tyr Leu Thr Gly Leu Ile Ser Ser Val Leu
130 135 140
Arg Pro Gly Ala Leu Thr Pro Leu Gln Arg Phe Arg Ser Leu Gln Gln
145 150 155 160
Ser Phe Leu Cys Cys Ala Phe Val Ile Ala Leu Gly Gly Gly Cys Phe
165 170 175
Leu Leu Thr Ala Leu Tyr Leu Glu Arg Asp Glu Thr Arg Ala Trp Gln
180 185 190
Pro Val Thr Gly Thr Pro Asp Ser Asn Asp Val Asp Ser Asn Asp Leu
195 200 205
Glu Arg Gln Gly Leu Leu Ser Gly Ala Gly Ala Ser Thr Glu Glu Pro
210 215 220

<210> 3225
<211> 506
<212> DNA
<213> Homo sapiens

<400> 3225
cgcctgcccc agtccatctg tgacaggcgg gcgtgagtgt agaggaatag ctaggctgta
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gcagtcgaaa ttctttctga accccatata ggatgaaggt tatatttcca aaattaaaac
120
agaggaacat tttaaatggc ctacgtccat gcaccttctt tattcaagaa gctaccaaga
180
attctgcctg tttcccagtc cctaaaatgc ctgtgccatg tgccctgggt gaagaactag
240
tcccatgcca caggggtaca ggccccgctg tagtttggcc agcccaaccg cagcaagggg
300
aagtggaacc acagcctcaa cccacacaga ggatggaacc accttctgca gctaaaaata
360
accacaccgc ctttgaggtg agccacccaa gatgcaggtg gggctgtatg aaactccacg
420

aacatgggat gagtttcatt ttcagggttc cgaggggcca tgagtggtac caagatccct
480
ggaggtgccc ttggtttccc atgtag
506

<210> 3226
<211> 137
<212> PRT
<213> Homo sapiens

<400> 3226
Met Lys Val Ile Phe Pro Lys Leu Lys Gln Arg Asn Ile Leu Asn Gly
1 5 10 15
Leu Arg Pro Cys Thr Phe Phe Ile Gln Glu Ala Thr Lys Asn Ser Ala
20 25 30
Cys Phe Pro Val Pro Lys Met Pro Val Pro Cys Ala Leu Gly Glu Glu
35 40 45
Leu Val Pro Cys His Arg Gly Thr Gly Pro Ala Val Val Trp Pro Ala
50 55 60
Gln Pro Gln Gln Gly Glu Val Glu Pro Gln Pro Gln Pro Thr Gln Arg
65 70 75 80
Met Glu Pro Pro Ser Ala Ala Lys Asn Asn His Thr Ala Phe Glu Val
85 90 95
Ser His Pro Arg Cys Arg Trp Gly Cys Met Lys Leu His Glu His Gly
100 105 110
Met Ser Phe Ile Phe Arg Val Pro Arg Gly His Glu Trp Tyr Gln Asp
115 120 125
Pro Trp Arg Cys Pro Trp Phe Pro Met
130 135

<210> 3227
<211> 1623
<212> DNA
<213> Homo sapiens

<400> 3227
nngtgtaggg gtagattttc gctgcagtgt tccccgagcc tgttagacgc agcggccggg
60
agactgagag aggaaaggat agaggaagtg ctgccctagg ctgcatgagt cgaagcaagc
120
gtgtttcctt cccgccaggc aagtgccctt agaaaccggg ccccgccccc ttcctggcct
180
gcattcccat cccctctccc ggggcggagg tgaggacctc cttggttcct ttggttctgt
240
cagtgagccc cttccttggc catgaagctc gtgaggaaga acatcgagaa ggacaatgcg
300
ggccaggtga ccctggtccc cgaggagcct gaggacatgt ggcacactta caacctcgtg
360
caggtgggcg acagcctgcg cgcctccacc atccgcaagg tacagacaga gtcctccacg
420
ggcagcgtgg gcagcaaccg ggtccgcact accctcactc tctgcgtgga ggccatcgac
480
ttcgactctc aagcctgcca gctgcgggtt aaggggacca acatccaaga gaatgagtat
540

gtcaagatgg gggcttacca caccatcgag ctggagccca accgccagtt caccctggcc
600
aagaagcagt gggatagtgt ggtactggag cgcatcgagc aggcctgtga cccagcctgg
660
agcgctgatg tggcggctgt ggtcatgcag gaaggcctcg cccatatctg cttagtcact
720
cccagcatga ccctcactcg ggccaaggtg gaggtgaaca tccctaggaa aaggaaaggc
780
aattgctctc agcatgaccg ggccttggag cggttctatg aacaggtggt ccaggctatc
840
cagcgccaca tacactttga tgttgtaaag tgcatcctgg tggccagccc aggatttgtg
900
agggagcagt tctgcgacta catgtttcaa caagcagtga agaccgacaa caaactgctc
960
ctggaaaacc ggtccaaatt tcttcaggta catgcctcct ccggacacaa gtactccctg
1020
aaagaggccc tttgtgaccc tactgtggct agccgccttt cagacactaa agctgctggg
1080
gaagtcaaag ccttggatga cttctataaa atgttacagc atgaaccgga tcgagctttc
1140
tatggactca agcaggtgga gaaggccaat gaagccatgg caattgacac attgctcatc
1200
agcgatgagc tcttcaggca tcaggatgta gccacacgga gccggtatgt gaggctggtg
1260
gacagtgtga aagagaatgc aggcaccgtt aggatattct ctagtcttca cgtttctggg
1320
gaacagctca gccagttgac tggggtagct gccattctcc gcttccctgt tcccgaactt
1380
tctgaccaag agggtgattc cagttctgaa gaggattaat gattgaaact taaaattgag
1440
acaatcttgt gtttcctaaa ctgttacagt acatttctca gcatccttgt gacagaaagc
1500
tgcaagaatg gcacttttg attcatacag ggatttctta tgtctttggc tacactagat
1560
attttgtgat tggcaagaca tgtatttaaa caataaacta aaaggaaata aaaaaaaaaa
1620
aaa
1623

<210> 3228
<211> 385
<212> PRT
<213> Homo sapiens

<400> 3228
Met Lys Leu Val Arg Lys Asn Ile Glu Lys Asp Asn Ala Gly Gln Val
 1   5   10   15
Thr Leu Val Pro Glu Glu Pro Glu Asp Met Trp His Thr Tyr Asn Leu
            20   25   30
Val Gln Val Gly Asp Ser Leu Arg Ala Ser Thr Ile Arg Lys Val Gln
        35   40   45
Thr Glu Ser Ser Thr Gly Ser Val Gly Ser Asn Arg Val Arg Thr Thr
    50   55   60
Leu Thr Leu Cys Val Glu Ala Ile Asp Phe Asp Ser Gln Ala Cys Gln

65 70 75 80
Leu Arg Val Lys Gly Thr Asn Ile Gln Glu Asn Glu Tyr Val Lys Met
85 90 95
Gly Ala Tyr His Thr Ile Glu Leu Glu Pro Asn Arg Gln Phe Thr Leu
100 105 110
Ala Lys Lys Gln Trp Asp Ser Val Val Leu Glu Arg Ile Glu Gln Ala
115 120 125
Cys Asp Pro Ala Trp Ser Ala Asp Val Ala Ala Val Val Met Gln Glu
130 135 140
Gly Leu Ala His Ile Cys Leu Val Thr Pro Ser Met Thr Leu Thr Arg
145 150 155 160
Ala Lys Val Glu Val Asn Ile Pro Arg Lys Arg Lys Gly Asn Cys Ser
165 170 175
Gln His Asp Arg Ala Leu Glu Arg Phe Tyr Glu Gln Val Val Gln Ala
180 185 190
Ile Gln Arg His Ile His Phe Asp Val Val Lys Cys Ile Leu Val Ala
195 200 205
Ser Pro Gly Phe Val Arg Glu Gln Phe Cys Asp Tyr Met Phe Gln Gln
210 215 220
Ala Val Lys Thr Asp Asn Lys Leu Leu Leu Glu Asn Arg Ser Lys Phe
225 230 235 240
Leu Gln Val His Ala Ser Ser Gly His Lys Tyr Ser Leu Lys Glu Ala
245 250 255
Leu Cys Asp Pro Thr Val Ala Ser Arg Leu Ser Asp Thr Lys Ala Ala
260 265 270
Gly Glu Val Lys Ala Leu Asp Asp Phe Tyr Lys Met Leu Gln His Glu
275 280 285
Pro Asp Arg Ala Phe Tyr Gly Leu Lys Gln Val Glu Lys Ala Asn Glu
290 295 300
Ala Met Ala Ile Asp Thr Leu Leu Ile Ser Asp Glu Leu Phe Arg His
305 310 315 320
Gln Asp Val Ala Thr Arg Ser Arg Tyr Val Arg Leu Val Asp Ser Val
325 330 335
Lys Glu Asn Ala Gly Thr Val Arg Ile Phe Ser Ser Leu His Val Ser
340 345 350
Gly Glu Gln Leu Ser Gln Leu Thr Gly Val Ala Ala Ile Leu Arg Phe
355 360 365
Pro Val Pro Glu Leu Ser Asp Gln Glu Gly Asp Ser Ser Ser Glu Glu
370 375 380
Asp
385

<210> 3229
<211> 1008
<212> DNA
<213> Homo sapiens

<400> 3229
nngcgcgcct cgcgctccag ggagccccgc cctcccgcgg cacctccgca gcaaccgccg
60
cctgcactgg gcgcgcgaga gctgctaggg cggtttctct gcctcgggcc tgttgggcag
120
ggccggctaa ggtgcgcgtg ctcgctggtt ctaacccttc tgttgggcgt ttctgctgag
180

aggcgggagg cgctgagagt ctgtgcggag gtccgtggac agactgcttt gctcgttgtt
240
gctcttcgga ggcggcgatc cccgaaggcg agctgaaata cggctgcagg ctacaatttg
300
cagccgacca ttatggaaga cggcaagcgg gagaggtggc ccaccctcat ggagcgcttg
360
tgctcggatg gcttcgcatt tccccaatac cccattaaac cgtatcatct gaagaggatc
420
cacagagctg tcttacgtgg taatctggag gaactgaagt accttctgct cacgtattat
480
gacatcaata agagagacag gaaggaaagg accgccctac atttggcctg tgccactggc
540
caaccggaaa tggtacatct cctggtgtcc agaagatgtg agcttaacct ctgcgaccgt
600
gaagacagga cacctctgat caaggctgta caactgaggc aggaggcttg tgcaactctt
660
ctgctgcaaa atggcgccga tccaaatatt acggatgtct ttggaaggac tgctctgcac
720
tacgctgtgt ataatgaaga tacatccatg atagaaaaac ttctttcaca tggtacaaat
780
attgaagaat gcagcaagaa tgaatatcag ccactgttac ttgctgtgag tcgaagaaaa
840
gtgaaaatgg tggaattttt attaaagaaa aaagcaaatg taaatgccat tgattatctt
900
ggcagatcag ccctcatact tgctgttact cttggagaaa aagatatagt cattcttctt
960
ctgcagcaca atattgatgt gttttctcga gatgtgtatg gaaagctt
1008

<210> 3230
<211> 232
<212> PRT
<213> Homo sapiens

<400> 3230
Met Glu Asp Gly Lys Arg Glu Arg Trp Pro Thr Leu Met Glu Arg Leu
 1   5   10   15
Cys Ser Asp Gly Phe Ala Phe Pro Gln Tyr Pro Ile Lys Pro Tyr His
            20   25   30
Leu Lys Arg Ile His Arg Ala Val Leu Arg Gly Asn Leu Glu Glu Leu
        35   40   45
Lys Tyr Leu Leu Leu Thr Tyr Tyr Asp Ile Asn Lys Arg Asp Arg Lys
    50   55   60
Glu Arg Thr Ala Leu His Leu Ala Cys Ala Thr Gly Gln Pro Glu Met
65   70   75   80
Val His Leu Leu Val Ser Arg Arg Cys Glu Leu Asn Leu Cys Asp Arg
                85   90   95
Glu Asp Arg Thr Pro Leu Ile Lys Ala Val Gln Leu Arg Gln Glu Ala
            100   105   110
Cys Ala Thr Leu Leu Leu Gln Asn Gly Ala Asp Pro Asn Ile Thr Asp
        115   120   125
Val Phe Gly Arg Thr Ala Leu His Tyr Ala Val Tyr Asn Glu Asp Thr
    130   135   140
Ser Met Ile Glu Lys Leu Leu Ser His Gly Thr Asn Ile Glu Glu Cys

```
145                 150                 155                 160
Ser Lys Asn Glu Tyr Gln Pro Leu Leu Leu Ala Val Ser Arg Arg Lys
                165                 170                 175
Val Lys Met Val Glu Phe Leu Leu Lys Lys Lys Ala Asn Val Asn Ala
            180                 185                 190
Ile Asp Tyr Leu Gly Arg Ser Ala Leu Ile Leu Ala Val Thr Leu Gly
        195                 200                 205
Glu Lys Asp Ile Val Ile Leu Leu Leu Gln His Asn Ile Asp Val Phe
    210                 215                 220
Ser Arg Asp Val Tyr Gly Lys Leu
225                 230
```

<210> 3231
<211> 1367
<212> DNA
<213> Homo sapiens

<400> 3231
nnacgcgtga aggggaagtt tcgcctcaga aggctgcctc gctggtccga attcggtggc
60
gccacgtccg cccgtctccg ccttctgcat cgcggcttcg gcggcttcca cctagacacc
120
taacagtcgc ggagccggcc gcgtcgtgag ggggtcggca cggggagtcg ggcggtcttg
180
tgcatcttgg ctacctgtgg gtcgaagatg tcggacatcg gagactggtt caggagcatc
240
ccggcgatca cgcgctattg gttcgccgcc accgtcgccg tgcccttggt cggcaaactc
300
ggcctcatca gcccggccta cctcttcctc tggcccgaag ccttccttta tcgctttcag
360
atttggaggc caatcactgc caccttttat ttccctgtgg gtccaggaac tggatttctt
420
tatttggtca atttatattt cttatatcag tattctacgc gacttgaaac aggagctttt
480
gatgggaggc cagcagacta tttattcatg ctcctcttta actggatttg catcgtgatt
540
actggcttag caatggatat gcagttgctg atgattcctc tgatcatgtc agtactttat
600
gtctgggccc agctgaacag agacatgatt gtatcatttt ggtttggaac acgatttaag
660
gcctgctatt taccctgggt tatccttgga ttcaactata tcatcggagg ctcggtaatc
720
aatgagctta ttggaaatct ggttggacat ctttatttttt tcctaatgtt cagataccca
780
atggacttgg gaggaagaaa ttttctatcc acacctcagt ttttgtaccg ctggctgccc
840
agtaggagag gaggagtatc aggatttggt gtgccccctg ctagcatgag gcgagctgct
900
gatcagaatg gcggaggcgg gagacacaac tggggccagg gctttcgact tggagaccag
960
tgaaggggcg gcctcgggca gccgctcctc tcaagccaca tttcctccca gtgctgggtg
1020
cacttaacaa ctgcgttctg gctaacactg ttggacctga cccacactga atgtagtctt
1080

tcagtacgag acaaagtttc ttaaatcccg aagaaaaata taagtgttcc acaagtttca
1140
cgattctcat tcaagtcctt actgctgtga agaacaaata ccaactgtgc aaattgcaaa
1200
actgactaca ttttttggtg ttttttttt tccccttcc gttctgaata atgggtttta
1260
gcgggtccta gtctgctggc attgagctgg ggctgggtca ccaaaccctt cccaaaagga
1320
cccttatctc tttcttgcac acatgcctct ctccccccctt cacgcgt
1367

<210> 3232
<211> 251
<212> PRT
<213> Homo sapiens

<400> 3232
Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala Ile Thr Arg
1 5 10 15
Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly Lys Leu Gly
20 25 30
Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala Phe Leu Tyr
35 40 45
Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr Phe Pro Val
50 55 60
Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr Phe Leu Tyr
65 70 75 80
Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly Arg Pro Ala
85 90 95
Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile Val Ile Thr
100 105 110
Gly Leu Ala Met Asp Met Gln Leu Leu Met Ile Pro Leu Ile Met Ser
115 120 125
Val Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile Val Ser Phe
130 135 140
Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp Val Ile Leu
145 150 155 160
Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu Leu Ile Gly
165 170 175
Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg Tyr Pro Met
180 185 190
Asp Leu Gly Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe Leu Tyr Arg
195 200 205
Trp Leu Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly Val Pro Pro
210 215 220
Ala Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly Gly Arg His
225 230 235 240
Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln
245 250

<210> 3233
<211> 975
<212> DNA
<213> Homo sapiens

<400> 3233
nacgcgtacg tggtggagct ctgcgtgttt actatttttg gaaatgaaga aaatggaaag
60
accgttgttt accttgtggc tttccatctg ttctttgtta tgtttgtatg gtcctattgg
120
atgacaattt tcacatctcc cgcttccccc tccaaagagt tctacttgtc caattctgaa
180
aaggaacgtt atgaaaaaga attcagccaa gaaagacaac aagaaatttt gagaagagca
240
gcaagagctt tacctatcta taccacatca gcttcaaaaa ctatcagata ttgtgaaaaa
300
tgtcagctga ttaaacctga tcgggcgcat cactgctcag cctgtgactc atgtattctt
360
aagatggatc atccctgtcc ttgggtgaat aactgtgtgg gattttctaa ttacaaattc
420
ttcctgctgt ttttattgta ttccctatta tattgccttt tcgtggccgc acagttttag
480
agtacttaaa aaattttgga cgaaagaacc gaccaaaacc cgggccaaaa ttccacgtac
540
ttttttcttt tctttgtgtc tgcaatgttc ttcatcagcg tcctctcact tttcagctac
600
cactgctggc tttaaacagc attgtccaca gctccgtctg cagggtcagg gcatggcctc
660
tctccgtgtt cctgtgaaga gccttcattg gaatcatccc gggacataca gcttgaatgt
720
gctgtctggc tagcccctcc acaagtcggt cactctgcac aaggaatccg agagctcatc
780
aaggatcagc acggtctggg gcccaggtgg ggtggaacac gcacggtcca caagcaattc
840
tgtctttctc aaggcttttt cttgtgcagt atgaaatcct tcatatttca tatgaagtat
900
gtgccttctg gggcactgag ctcaggaact ccaaaaagac cccttcgggc cggatcccgg
960
cttcaaggct gcccc
975

<210> 3234
<211> 159
<212> PRT
<213> Homo sapiens

<400> 3234
Xaa Ala Tyr Val Val Glu Leu Cys Val Phe Thr Ile Phe Gly Asn Glu
1 5 10 15
Glu Asn Gly Lys Thr Val Val Tyr Leu Val Ala Phe His Leu Phe Phe
20 25 30
Val Met Phe Val Trp Ser Tyr Trp Met Thr Ile Phe Thr Ser Pro Ala
35 40 45
Ser Pro Ser Lys Glu Phe Tyr Leu Ser Asn Ser Glu Lys Glu Arg Tyr
50 55 60
Glu Lys Glu Phe Ser Gln Glu Arg Gln Gln Glu Ile Leu Arg Arg Ala
65 70 75 80
Ala Arg Ala Leu Pro Ile Tyr Thr Thr Ser Ala Ser Lys Thr Ile Arg

```
                85                  90                  95
Tyr Cys Glu Lys Cys Gln Leu Ile Lys Pro Asp Arg Ala His His Cys
            100                 105                 110
Ser Ala Cys Asp Ser Cys Ile Leu Lys Met Asp His Pro Cys Pro Trp
        115                 120                 125
Val Asn Asn Cys Val Gly Phe Ser Asn Tyr Lys Phe Phe Leu Leu Phe
    130                 135                 140
Leu Leu Tyr Ser Leu Leu Tyr Cys Leu Phe Val Ala Ala Gln Phe
145                 150                 155
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<210> 3235
<211> 551
<212> DNA
<213> Homo sapiens

<400> 3235
ntggaaactg agcttcaaac atataagcat tctcgtcagg ggctagatga aatgtacaat
60
gaagccagaa ggcagcttcg agatgaatct cagttacgac aggatgtaga gaatgagcta
120
gcagtacaag ttagtatgaa gcatgagatt gaacttgcca tgaagttgct ggagaaagat
180
atccatgaga aacaagatac tctgataggc cttcgacaac aactagagga agttaaagca
240
attaacatag agatgtatca aaagttgcag ggttctgaag atggcttgaa agaaaaaaat
300
gaaataattg cccgactaga agaaaaaacc aataaaatta ctgcagccat gaggcagctg
360
gaacaaagat tgcagcaagc agagaaggcg caaatggaag ctgaagatga ggatgagaaa
420
tatctacaag aatgtctcag taaatctgat agtctgcaga aacaaatctc ccaaaaggag
480
aaacagctgg tgcaactgga aactgacttg aagattgaga aggaatggag gcagactttg
540
caggaagatc t
551

<210> 3236
<211> 183
<212> PRT
<213> Homo sapiens

<400> 3236
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Xaa Glu Thr Glu Leu Gln Thr Tyr Lys His Ser Arg Gln Gly Leu Asp
 1               5                  10                  15
Glu Met Tyr Asn Glu Ala Arg Arg Gln Leu Arg Asp Glu Ser Gln Leu
            20                  25                  30
Arg Gln Asp Val Glu Asn Glu Leu Ala Val Gln Val Ser Met Lys His
        35                  40                  45
Glu Ile Glu Leu Ala Met Lys Leu Leu Glu Lys Asp Ile His Glu Lys
    50                  55                  60
Gln Asp Thr Leu Ile Gly Leu Arg Gln Gln Leu Glu Glu Val Lys Ala
65                  70                  75                  80
Ile Asn Ile Glu Met Tyr Gln Lys Leu Gln Gly Ser Glu Asp Gly Leu
```

85 90 95
Lys Glu Lys Asn Glu Ile Ile Ala Arg Leu Glu Glu Lys Thr Asn Lys
100 105 110
Ile Thr Ala Ala Met Arg Gln Leu Glu Gln Arg Leu Gln Gln Ala Glu
115 120 125
Lys Ala Gln Met Glu Ala Glu Asp Glu Asp Glu Lys Tyr Leu Gln Glu
130 135 140
Cys Leu Ser Lys Ser Asp Ser Leu Gln Lys Gln Ile Ser Gln Lys Glu
145 150 155 160
Lys Gln Leu Val Gln Leu Glu Thr Asp Leu Lys Ile Glu Lys Glu Trp
165 170 175
Arg Gln Thr Leu Gln Glu Asp
180

<210> 3237
<211> 1323
<212> DNA
<213> Homo sapiens

<400> 3237
nctctgggct gcgacctacc tcgcagaggg gtttgcacta aggcgctggg cgccgggctc
60
cgggcgctgt ggaccatggc tccgcccgcg gcgcctggcc gggaccgtgt gggccgtgag
120
gatgaggacc gttgggaagt acgggggggac cgcaaggccc ggaagcccct ggtggagaag
180
aagcgacgcg cgcggatcaa cgagagtctt caggagttgc ggctgctgct ggcgggcgcc
240
gaggtgcagg ccaagctgga gaacgccgaa gtgctggagc tgacggtgcg gcgggtccag
300
ggtgtgctgc ggggccgggc gcgcgagcgc gagcagctgc aggcggaagc gagcgagcgc
360
ttcgctgccg gctacatcca gtgcatgcac gaggtgcaca cgttcgtgtc cacgtgccag
420
gccatcgacg ctaccgtcgc tgccgagctc ctgaaccatc tgctcgagtc catgccgctg
480
cgtgagggca gcagcttcca ggatctgctg ggggacgccc tggcggggcc acctagagcc
540
cctggacgga gtggctggcc tgcgggggggc gctccgggat ccccaatacc cagccccccg
600
ggtcctgggg acgacctgtg ctccgacctg gaggaggccc ctgaggctga actgagtcag
660
gctcctgctg aggggcccga cttggtgccc gcagccctgg gcagcctgac cacagcccaa
720
attgcccgga gtgtctggag gccttggtga ccaatgccag ccagagtcct gcgggggtgg
780
gcccggccct ccctggatct cctccctcct cccaggggtt cagatgtggt ggggtagggc
840
cctggaagtc tcccaggtct tccctccctc ctctgatgga tggcttgcag ggcagcccct
900
ggtaaccagc ccagtcaggc cccagccccg tttcttaaga aacttttagg gaccctgcag
960
ctctggagtg ggtggaggga gggagctacg ggcaggagga agaattttgt agagctgcca
1020

gcgctctccc aggttcaccc acccaggctt caccagccct gtgcgggctc tgggggcaga
1080
ggtggcagaa atggtgctgg gcactagtgt tccaggcagc cctgggctaa acaaaagctt
1140
gaacttgcca cttcagcggg gagatgagag gcaggtgcac tcagctgcac tgcccagagc
1200
tgtgatgctc tgtacatctt gtttgtagca cacttgagtt tgtgtattcc attgacatca
1260
aatgtgacaa ttttactaaa taaagaattt tggagttagt tacccttgaa aaaaaagtcg
1320
acg
1323

<210> 3238
<211> 249
<212> PRT
<213> Homo sapiens

<400> 3238
Xaa Leu Gly Cys Asp Leu Pro Arg Arg Gly Val Cys Thr Lys Ala Leu
 1   5   10   15
Gly Ala Gly Leu Arg Ala Leu Trp Thr Met Ala Pro Pro Ala Ala Pro
            20   25   30
Gly Arg Asp Arg Val Gly Arg Glu Asp Glu Asp Arg Trp Glu Val Arg
        35   40   45
Gly Asp Arg Lys Ala Arg Lys Pro Leu Val Glu Lys Lys Arg Arg Ala
    50   55   60
Arg Ile Asn Glu Ser Leu Gln Glu Leu Arg Leu Leu Leu Ala Gly Ala
65   70   75   80
Glu Val Gln Ala Lys Leu Glu Asn Ala Glu Val Leu Glu Leu Thr Val
                85   90   95
Arg Arg Val Gln Gly Val Leu Arg Gly Arg Ala Arg Glu Arg Glu Gln
            100   105   110
Leu Gln Ala Glu Ala Ser Glu Arg Phe Ala Ala Gly Tyr Ile Gln Cys
        115   120   125
Met His Glu Val His Thr Phe Val Ser Thr Cys Gln Ala Ile Asp Ala
    130   135   140
Thr Val Ala Ala Glu Leu Leu Asn His Leu Leu Glu Ser Met Pro Leu
145   150   155   160
Arg Glu Gly Ser Ser Phe Gln Asp Leu Leu Gly Asp Ala Leu Ala Gly
                165   170   175
Pro Pro Arg Ala Pro Gly Arg Ser Gly Trp Pro Ala Gly Gly Ala Pro
            180   185   190
Gly Ser Pro Ile Pro Ser Pro Pro Gly Pro Gly Asp Asp Leu Cys Ser
        195   200   205
Asp Leu Glu Glu Ala Pro Glu Ala Glu Leu Ser Gln Ala Pro Ala Glu
    210   215   220
Gly Pro Asp Leu Val Pro Ala Ala Leu Gly Ser Leu Thr Thr Ala Gln
225   230   235   240
Ile Ala Arg Ser Val Trp Arg Pro Trp
                245

<210> 3239
<211> 432

<212> DNA
<213> Homo sapiens

<400> 3239
aaaaccaaag attctcctgg agttttctct aaactgggtg ttctcctgag gagagtgaca
60
agaaacttgg tgagaaataa gctggcagtg attacgcgtc tccttcagaa tctgatcatg
120
ggtttgttcc tccttttctt cgttctgcgg gtccgaagca atgtgctaaa gggtgctatc
180
caggaccgcg taggtctcct ttaccagttt gtgggcgcca ccccgtacac aggcatgctg
240
aacgctgtga atctgtttcc cgtgctgcga gctgtcagcg accaggagag tcaggacggc
300
ctctaccaga agtggcagat gatgctggcc tatgcactgc acgtcctccc cttcagcgtt
360
gttgccacca tgattttcag cagtgtgtgc tactggacgc tgggcttaca tcctgaggtt
420
gcccgattgg gt
432

<210> 3240
<211> 144
<212> PRT
<213> Homo sapiens

<400> 3240
Lys Thr Lys Asp Ser Pro Gly Val Phe Ser Lys Leu Gly Val Leu Leu
 1   5   10   15
Arg Arg Val Thr Arg Asn Leu Val Arg Asn Lys Leu Ala Val Ile Thr
            20   25   30
Arg Leu Leu Gln Asn Leu Ile Met Gly Leu Phe Leu Leu Phe Phe Val
        35   40   45
Leu Arg Val Arg Ser Asn Val Leu Lys Gly Ala Ile Gln Asp Arg Val
    50   55   60
Gly Leu Leu Tyr Gln Phe Val Gly Ala Thr Pro Tyr Thr Gly Met Leu
65   70   75   80
Asn Ala Val Asn Leu Phe Pro Val Leu Arg Ala Val Ser Asp Gln Glu
                85   90   95
Ser Gln Asp Gly Leu Tyr Gln Lys Trp Gln Met Met Leu Ala Tyr Ala
            100   105   110
Leu His Val Leu Pro Phe Ser Val Val Ala Thr Met Ile Phe Ser Ser
        115   120   125
Val Cys Tyr Trp Thr Leu Gly Leu His Pro Glu Val Ala Arg Leu Gly
    130   135   140

<210> 3241
<211> 492
<212> DNA
<213> Homo sapiens

<400> 3241
gtggaatttt tttagacaaa gtctcaaaaa acaaacaaac aaacaaaagg taagataaat
60

acgaaataca aaataagagg caggaagagc ccaaagcatc agaaatgtgc cagttataat
120
gggccaaaat cccctcttgt gtctccagaa gtatttgaaa aatacgttag gatctgcctc
180
acagacatgc tcccaggaca ctcgacagca aggaggtacg gcgggcccag ccagccaagg
240
cagaggagga catcactgcc acagcagggg gcctgactgg cagcaaaagg gacgactccg
300
gcgaaaagtc agcaggaaac aggacagggg ctggaccaat ggcctccctc agccccacac
360
cccacccagg caggagcggt gcctggcccg gggcaggcgg gtgggagagc tcactgagtg
420
ggcagcaggg catggcccct gatgctgcag gtacccaggc tgcagctgca gaaacctcag
480
tgggaaccca gg
492

<210> 3242
<211> 107
<212> PRT
<213> Homo sapiens

<400> 3242
Met Gly Gln Asn Pro Leu Leu Cys Leu Gln Lys Tyr Leu Lys Asn Thr
1 5 10 15
Leu Gly Ser Ala Ser Gln Thr Cys Ser Gln Asp Thr Arg Gln Gln Gly
20 25 30
Gly Thr Ala Gly Pro Ala Ser Gln Gly Arg Gly Gly His His Cys His
35 40 45
Ser Arg Gly Pro Asp Trp Gln Gln Lys Gly Arg Leu Arg Arg Lys Val
50 55 60
Ser Arg Lys Gln Asp Arg Gly Trp Thr Asn Gly Leu Pro Gln Pro His
65 70 75 80
Thr Pro Pro Arg Gln Glu Arg Cys Leu Ala Arg Gly Arg Arg Val Gly
85 90 95
Glu Leu Thr Glu Trp Ala Ala Gly His Gly Pro
100 105

<210> 3243
<211> 944
<212> DNA
<213> Homo sapiens

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240
tacggtttcg atggacgagg actcaaggca gaaaatggac aatttgagga atttggccag
300

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480
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gtgattctga tggtgggact acccggatct ggaaagaccc agtgggcact gaaatatgca
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720
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840
attcttgatc agtgtaatgt gtacaattct ggccaacggc ggaagctatt gctgttcaag
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944

<210> 3244
<211> 314
<212> PRT
<213> Homo sapiens

<400> 3244
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Gly Val Thr Lys Gly Lys Val Cys Phe Glu Ala Lys Val Thr Gln Asn
        35                  40                  45
Leu Pro Met Lys Glu Gly Cys Thr Glu Val Ser Leu Leu Arg Val Gly
    50                  55                  60
Trp Ser Val Asp Phe Ser Arg Pro Gln Leu Gly Glu Asp Glu Phe Ser
65                  70                  75                  80
Tyr Gly Phe Asp Gly Arg Gly Leu Lys Ala Glu Asn Gly Gln Phe Glu
                85                  90                  95
Glu Phe Gly Gln Thr Phe Gly Glu Asn Asp Val Ile Gly Cys Phe Ala
            100                 105                 110
Asn Phe Glu Thr Glu Glu Val Glu Leu Ser Phe Ser Lys Asn Gly Glu
        115                 120                 125
Asp Leu Gly Val Ala Phe Trp Ile Ser Lys Asp Ser Leu Ala Asp Arg
    130                 135                 140
Ala Leu Leu Pro His Val Leu Cys Lys Asn Cys Val Val Glu Leu Asn
145                 150                 155                 160
Phe Gly Gln Lys Glu Glu Pro Phe Phe Pro Pro Pro Glu Glu Phe Val
                165                 170                 175
Phe Ile His Ala Val Pro Val Glu Glu Arg Val Arg Thr Ala Val Pro
            180                 185                 190
Pro Lys Thr Ile Glu Glu Cys Glu Val Ile Leu Met Val Gly Leu Pro
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        195                 200                 205
Gly Ser Gly Lys Thr Gln Trp Ala Leu Lys Tyr Ala Lys Glu Asn Pro
    210                 215                 220
Glu Lys Arg Tyr Asn Val Leu Gly Ala Glu Thr Val Leu Asn Gln Met
225                 230                 235                 240
Arg Met Lys Gly Leu Glu Glu Pro Glu Met Asp Pro Lys Ser Arg Asp
                245                 250                 255
Leu Leu Val Gln Gln Ala Ser Gln Cys Leu Ser Lys Leu Val Gln Ile
            260                 265                 270
Ala Ser Arg Thr Lys Arg Asn Phe Ile Leu Asp Gln Cys Asn Val Tyr
        275                 280                 285
Asn Ser Gly Gln Arg Arg Lys Leu Leu Leu Phe Lys Thr Phe Ser Arg
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Lys Val Val Val Val Val Pro Asn Glu Glu
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<210> 3245
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<212> DNA
<213> Homo sapiens

<400> 3245

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240
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360
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480
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840
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960
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980

<210> 3246
<211> 219
<212> PRT
<213> Homo sapiens

<400> 3246
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Asp Leu Phe Arg Gly Cys Thr Ala Leu Glu Leu Gly Ala Gly Thr Gly
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Leu Ala Ser Ile Ile Ala Ala Thr Met Ala Arg Thr Val Tyr Cys Thr
35 40 45
Asp Val Gly Ala Asp Leu Leu Ser Met Cys Gln Arg Asn Ile Ala Leu
50 55 60
Asn Ser His Leu Ala Ala Thr Gly Gly Gly Ile Val Arg Val Lys Glu
65 70 75 80
Leu Asp Trp Leu Lys Asp Asp Leu Cys Thr Asp Pro Lys Val Pro Phe
85 90 95
Ser Trp Ser Gln Glu Glu Ile Ser Asp Leu Tyr Asp His Thr Thr Ile
100 105 110
Leu Phe Ala Ala Glu Val Phe Tyr Asp Asp Asp Leu Thr Asp Ala Val
115 120 125
Phe Lys Thr Leu Ser Arg Leu Ala His Arg Leu Lys Asn Ala Cys Thr
130 135 140
Ala Ile Leu Ser Val Glu Lys Arg Leu Asn Phe Thr Leu Arg His Leu
145 150 155 160
Asp Val Thr Cys Glu Ala Tyr Asp His Phe Arg Ser Cys Leu His Ala
165 170 175
Leu Glu Gln Leu Thr Asp Gly Lys Leu Arg Phe Val Val Glu Pro Val
180 185 190
Glu Ala Ser Phe Pro Gln Leu Leu Val Tyr Glu Arg Leu Gln Gln Leu
195 200 205
Glu Leu Trp Lys Ile Ile Ala Glu Pro Val Thr
210 215

<210> 3247
<211> 977
<212> DNA
<213> Homo sapiens

<400> 3247
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180
ccgggtgggc ccagccccgg gagccgggtg cttaccatcc tggagcagat ccccggcatg
240
gtggtggtgg ctgacaagac ctcggagctc taccagaaga cctactgggc cagctacaac
300

ataccgtcct tcgagactgt gttcaatgcc agtgggctgc aggccctagt ggcccagtat
360
ggggactggt tttcttatga cgggagcccc cgggcccaga tcttccggcg gaaccagtca
420
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480
cctctgtcac tgtgcaaagc ctgcaacccc cagcccaatg gggagaatgc tatctccgcc
540
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720
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977

<210> 3248
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<212> PRT
<213> Homo sapiens

<400> 3248
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35 40 45
Trp Met Ile Val Asp Tyr Lys Ala Phe Ile Pro Gly Gly Pro Ser Pro
50 55 60
Gly Ser Arg Val Leu Thr Ile Leu Glu Gln Ile Pro Gly Met Val Val
65 70 75 80
Val Ala Asp Lys Thr Ser Glu Leu Tyr Gln Lys Thr Tyr Trp Ala Ser
85 90 95
Tyr Asn Ile Pro Ser Phe Glu Thr Val Phe Asn Ala Ser Gly Leu Gln
100 105 110
Ala Leu Val Ala Gln Tyr Gly Asp Trp Phe Ser Tyr Asp Gly Ser Pro
115 120 125
Arg Ala Gln Ile Phe Arg Arg Asn Gln Ser Leu Val Gln Asp Met Asp
130 135 140
Ser Met Val Arg Leu Met Arg Tyr Asn Asp Phe Leu His Asp Pro Leu
145 150 155 160
Ser Leu Cys Lys Ala Cys Asn Pro Gln Pro Asn Gly Glu Asn Ala Ile
165 170 175
Ser Ala Arg Ser Asp Leu Asn Pro Ala Asn Gly Ser Tyr Pro Phe Gln

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            180                 185                 190
Ala Leu Arg Gln Arg Ser His Gly Gly Ile Asp Val Lys Val Thr Ser
        195                 200                 205
Met Ser Leu Ala Arg Ile Leu Ser Leu Leu Ala Ala Ser Gly Pro Thr
    210                 215                 220
Trp Asp Gln Val Pro Pro Phe Gln Trp Ser Thr Ser Pro Phe Ser Gly
225                 230                 235                 240
Leu Leu His Met Gly Gln Pro Asp Leu Trp Lys Phe Ala Pro Val Lys
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Val Ser Trp Asp
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<210> 3249
<211> 4487
<212> DNA
<213> Homo sapiens

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1080

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4320

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4487

<210> 3250
<211> 849
<212> PRT
<213> Homo sapiens

<400> 3250
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Trp Val Pro Thr Asp Cys Phe Ser Leu Ser Leu Ser Pro Pro His Ser
35 40 45
Arg Cys Ser Gly Ala Arg Cys His Arg Pro Leu Ser Arg Gln Leu Cys
50 55 60
Ala Ser Gln Arg Ser Met Trp Thr Leu Glu Asp Ser Ser Gly Thr Val
65 70 75 80
Leu His Arg Leu Ile Gln Glu Gln Leu Arg Tyr Gly Asn Leu Thr Glu
85 90 95
Thr Arg Thr Leu Leu Ala Ile Gln Gln Gln Ala Leu Arg Gly Gly Ala
100 105 110
Gly Thr Gly Gly Thr Gly Ser Pro Gln Ala Ser Leu Glu Ile Leu Ala
115 120 125
Pro Glu Asp Ser Gln Val Leu Gln Gln Ala Thr Arg Gln Glu Pro Gln
130 135 140
Gly Gln Glu His Gln Gly Gly Glu Asn His Leu Ala Glu Asn Thr Leu
145 150 155 160
Tyr Arg Leu Cys Pro Gln Pro Ser Lys Gly Glu Glu Leu Pro Thr Tyr
165 170 175
Glu Glu Ala Lys Ala His Ser Gln Tyr Tyr Ala Ala Gln Gln Ala Gly
180 185 190
Thr Arg Pro His Ala Gly Asp Arg Asp Pro Arg Gly Ala Pro Gly Gly
195 200 205
Ser Arg Arg Gln Asp Glu Ala Leu Arg Glu Leu Arg His Gly His Val
210 215 220
Arg Ser Leu Ser Glu Arg Leu Leu Gln Leu Ser Leu Glu Arg Asn Gly
225 230 235 240
Ala Arg Ala Pro Ser His Met Ser Ser Ser His Ser Phe Pro Gln Leu
245 250 255
Ala Arg Asn Gln Gln Gly Pro Pro Leu Arg Gly Pro Pro Ala Glu Gly
260 265 270
Pro Glu Ser Arg Gly Pro Pro Pro Gln Tyr Pro His Val Val Leu Ala
275 280 285
His Glu Thr Thr Thr Ala Val Thr Asp Pro Arg Tyr Arg Ala Arg Gly
290 295 300
Ser Pro His Phe Gln His Ala Glu Val Arg Ile Leu Gln Ala Gln Val
305 310 315 320
Pro Pro Val Phe Leu Gln Gln Gln Gln Gln Tyr Gln Tyr Leu Gln Gln

325 330 335
Ser Gln Glu His Pro Pro Pro Pro His Pro Ala Ala Leu Gly His Gly
340 345 350
Pro Leu Ser Ser Leu Ser Pro Pro Ala Val Glu Gly Pro Val Ser Ala
355 360 365
Gln Ala Ser Ser Ala Thr Ser Gly Ser Ala His Leu Ala Gln Met Glu
370 375 380
Ala Val Leu Arg Glu Asn Ala Arg Leu Gln Arg Asp Asn Glu Arg Leu
385 390 395 400
Gln Arg Glu Leu Glu Ser Ser Ala Glu Lys Ala Gly Arg Ile Glu Lys
405 410 415
Leu Glu Ser Glu Ile Gln Arg Leu Ser Glu Ala His Glu Ser Leu Thr
420 425 430
Arg Ala Ser Ser Lys Arg Glu Ala Leu Glu Lys Thr Met Arg Asn Lys
435 440 445
Met Asp Ser Glu Met Arg Arg Leu Gln Asp Phe Asn Arg Asp Leu Arg
450 455 460
Glu Arg Leu Glu Ser Ala Asn Arg Arg Leu Ala Ser Lys Thr Gln Glu
465 470 475 480
Ala Gln Ala Gly Ser Gln Asp Met Val Ala Lys Leu Leu Ala Gln Ser
485 490 495
Tyr Glu Gln Gln Gln Glu Gln Glu Lys Leu Glu Arg Glu Met Ala Leu
500 505 510
Leu Arg Gly Ala Ile Glu Asp Gln Arg Arg Arg Ala Glu Leu Leu Glu
515 520 525
Gln Ala Leu Gly Asn Ala Gln Gly Arg Ala Ala Arg Ala Glu Glu Glu
530 535 540
Leu Arg Lys Lys Gln Ala Tyr Val Glu Lys Val Glu Arg Leu Gln Gln
545 550 555 560
Ala Leu Gly Gln Leu Gln Ala Ala Cys Glu Lys Arg Glu Gln Leu Glu
565 570 575
Leu Arg Leu Arg Thr Arg Leu Glu Gln Glu Leu Lys Ala Leu Arg Ala
580 585 590
Gln Gln Arg Gln Ala Gly Ala Pro Gly Gly Ser Ser Gly Ser Gly Gly
595 600 605
Ser Pro Glu Leu Ser Ala Leu Arg Leu Ser Glu Gln Leu Arg Glu Lys
610 615 620
Glu Glu Gln Ile Leu Ala Leu Glu Ala Asp Met Thr Lys Trp Glu Gln
625 630 635 640
Lys Tyr Leu Glu Glu Arg Ala Met Arg Gln Phe Ala Met Asp Ala Ala
645 650 655
Ala Thr Ala Ala Ala Gln Arg Asp Thr Thr Leu Ile Arg His Ser Pro
660 665 670
Gln Pro Ser Pro Ser Ser Ser Phe Asn Glu Gly Leu Leu Thr Gly Gly
675 680 685
His Arg His Gln Glu Met Glu Ser Arg Leu Lys Val Leu His Ala Gln
690 695 700
Ile Leu Glu Lys Asp Ala Val Ile Lys Val Leu Gln Gln Arg Ser Arg
705 710 715 720
Arg Asp Pro Gly Lys Ala Ile Gln Gly Ser Leu Arg Pro Ala Lys Ser
725 730 735
Val Pro Ser Val Phe Ala Ala Ala Ala Ala Gly Thr Gln Gly Trp Gln
740 745 750
Gly Leu Ser Ser Ser Glu Arg Gln Thr Ala Asp Ala Pro Ala Arg Leu

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        755                 760                 765
Thr Thr Ala Asp Arg Ala Pro Thr Glu Glu Pro Val Val Thr Ala Pro
    770                 775                 780
Pro Ala Ala His Ala Lys His Gly Ser Arg Asp Gly Ser Thr Gln Thr
785                 790                 795                 800
Asp Gly Pro Pro Asp Ser Thr Ser Thr Cys Leu Pro Pro Glu Pro Asp
                805                 810                 815
Ser Leu Leu Gly Cys Ser Ser Ser Gln Arg Ala Ala Ser Leu Asp Ser
            820                 825                 830
Val Ala Thr Ser Arg Val Gln Asp Leu Ser Asp Met Val Glu Ile Leu
        835                 840                 845
Ile
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<210> 3251
<211> 2595
<212> DNA
<213> Homo sapiens

<400> 3251
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120
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420
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480
gagggagtgc gtgggggcca ccctccagcc atccagagcc tcatcaacct gctggcagac
540
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600
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660
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720
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960
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1020

ttcccaaggg ctttttggcc agccttccag tcgcctggca cctgctagca acatgactag
1080
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1140
ggataccctg atccagagtg gccctgctct ctcccacctg gttagccaga ccacagcaca
1200
gatggggcag ccacaggccc ccatgggatc ttaccagagg cattactgaa gctaaatctt
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1320
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1380
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1440
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1680
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1740
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1800
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1920
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1980
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tctgagactc tggccgtgaa cacccgtttc ttcagtgatt tgttttgggc ttttggctca
2100
aaaccccagg ctcttgtttt tgtctagact cttattctgt ttcctgagca gcaggaggta
2160
gggaccactt tgatgtcaga cttctggtag ctggacatgt tctcgagatg ggtggctgtt
2220
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2280
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2400
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2460
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2520
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2580
aaaaaaaaaa aaaaa
2595

<210> 3252
<211> 254
<212> PRT
<213> Homo sapiens

<400> 3252
Cys Arg Lys Ala Val Asp Cys Ser Val Ile Val Val Asn Lys Gln Thr
1 5 10 15
Lys Asp Tyr Ala Glu Ser Val Gly Arg Lys Val Arg Asp Leu Gly Met
20 25 30
Val Val Asp Leu Ile Phe Leu Asn Thr Glu Val Ser Leu Ser Gln Ala
35 40 45
Leu Glu Asp Val Ser Arg Gly Gly Ser Pro Phe Ala Ile Val Ile Thr
50 55 60
Gln Gln His Gln Ile His Arg Ser Cys Thr Val Asn Ile Met Phe Gly
65 70 75 80
Thr Pro Gln Glu His Arg Asn Met Pro Gln Ala Asp Ala Met Val Leu
85 90 95
Val Ala Arg Asn Tyr Glu Arg Tyr Lys Asn Glu Cys Arg Glu Lys Glu
100 105 110
Arg Glu Glu Ile Ala Arg Gln Ala Ala Lys Met Ala Asp Glu Ala Ile
115 120 125
Leu Gln Glu Arg Glu Arg Gly Gly Pro Glu Glu Gly Val Arg Gly Gly
130 135 140
His Pro Pro Ala Ile Gln Ser Leu Ile Asn Leu Leu Ala Asp Asn Arg
145 150 155 160
Tyr Leu Thr Ala Glu Glu Thr Asp Lys Ile Ile Asn Tyr Leu Arg Glu
165 170 175
Arg Lys Glu Arg Leu Met Arg Ser Ser Thr Asp Ser Leu Pro Gly Glu
180 185 190
Leu Arg Gly Arg Pro Arg Pro Asp Phe Pro Pro Thr Thr Arg Gly Asp
195 200 205
Leu Gly Cys Leu Ala Glu Asp Thr Ala Lys Leu Pro Thr Ala Pro Glu
210 215 220
Arg Pro Ser Ala Pro Leu Cys Tyr Thr His Ser Ile Cys Thr Pro His
225 230 235 240
Leu Pro Ala Arg Ala Ser Gly Gln Asn Pro Gln Pro Leu Gln
245 250

<210> 3253
<211> 686
<212> DNA
<213> Homo sapiens

<400> 3253
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cataggattt ccacatgccc ttggaagagc ctttggaagg tattttcatc cttcctactg
120
gtaaaatggc atcaagggtc cccaccggtt caagatgggg accttgacta tatggcaatg
180
aagacaggga caccctggca gtagcaggta gcctttggcc atctctgcag caggctggtg
240

tttgggatcc acgaggcacg gaaagtcagc actctggagg acctggttgg ggtcaccctg
300
ggccaggtgc agatcgtggg aagctggata tgtgaaatgg caggtgctgg tgaacttgcg
360
ctcgtcctcc ctcgtggcct catgttcctg tgatgggaag aagccgggga gtcccaggtc
420
tttggcagtc atgtggggtc ttttgaaagc agggtaccca tctgttagct tggggttggg
480
gttagggatg ggcctgtaaa actctttgtc ccggagttga gcatcgagct ttgcctgctc
540
ttgcggcgtg accctggagt atttgtgctt cctgtagggc tgatagtcga ccatgtggga
600
gctttggtat atgtctaaat ccacagggtc ctgtcccggg tatttcacac ctgccatggc
660
aaacgacaga cagcttctct cctagg
686

<210> 3254
<211> 180
<212> PRT
<213> Homo sapiens

<400> 3254
Met Ala Gly Val Lys Tyr Pro Gly Gln Asp Pro Val Asp Leu Asp Ile
1 5 10 15
Tyr Gln Ser Ser His Met Val Asp Tyr Gln Pro Tyr Arg Lys His Lys
20 25 30
Tyr Ser Arg Val Thr Pro Gln Glu Gln Ala Lys Leu Asp Ala Gln Leu
35 40 45
Arg Asp Lys Glu Phe Tyr Arg Pro Ile Pro Asn Pro Asn Pro Lys Leu
50 55 60
Thr Asp Gly Tyr Pro Ala Phe Lys Arg Pro His Met Thr Ala Lys Asp
65 70 75 80
Leu Gly Leu Pro Gly Phe Phe Pro Ser Gln Glu His Glu Ala Thr Arg
85 90 95
Glu Asp Glu Arg Lys Phe Thr Ser Thr Cys His Phe Thr Tyr Pro Ala
100 105 110
Ser His Asp Leu His Leu Ala Gln Gly Asp Pro Asn Gln Val Leu Gln
115 120 125
Ser Ala Asp Phe Pro Cys Leu Val Asp Pro Lys His Gln Pro Ala Ala
130 135 140
Glu Met Ala Lys Gly Tyr Leu Leu Leu Pro Gly Cys Pro Cys Leu His
145 150 155 160
Cys His Ile Val Lys Val Pro Ile Leu Asn Arg Trp Gly Pro Leu Met
165 170 175
Pro Phe Tyr Gln
180

<210> 3255
<211> 724
<212> DNA
<213> Homo sapiens

<400> 3255

nntgtacatg cgtgtgcgtc tgtgattgtg tgggtgtgtg atagtgtagg ggagccagga
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gcgagaggag aggacggcga tcgtagggga cacctgagag tcagaggccc gaggggggctg
120
ggactcatgt cgaggtcggg gaaggatgta aaacccggac ggacatcact gtaggccgca
180
cctgctgaga ggccagagct gcctccttga gagtgaagtt gtttacagac aagagaagag
240
atcttggcgg acacatcaca gctagccgcg aatcccgaag ggtcagcaga gcctagaaag
300
gaatatgagg ggggtcggaa tgaggcaggc gaaaggcacg gacgtgggag ggcacggcta
360
cccaacgggg acacctacga agggagctac gaattcggta aaagacatgg ccaggggatc
420
tacaaattta aaaatggtgc tcgatatatc ggagaatatg ttagaaataa aaagcacggt
480
caaggcactt ttatatatcc agatggatcc agatatgaag gagagtgggc aaatgacctg
540
cggcacggcc atggcgtata ctactacatc aataatgaca cctacactgg agagtggttt
600
gctcatcaaa ggcatgggca aggcacctat ttatacgcag agacgggcag taagtatgtt
660
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720
tacc
724

<210> 3256
<211> 169
<212> PRT
<213> Homo sapiens

<400> 3256
Ser Cys Leu Gln Thr Arg Glu Glu Ile Leu Ala Asp Thr Ser Gln Leu
1 5 10 15
Ala Ala Asn Pro Glu Gly Ser Ala Glu Pro Arg Lys Glu Tyr Glu Gly
20 25 30
Gly Arg Asn Glu Ala Gly Glu Arg His Gly Arg Gly Arg Ala Arg Leu
35 40 45
Pro Asn Gly Asp Thr Tyr Glu Gly Ser Tyr Glu Phe Gly Lys Arg His
50 55 60
Gly Gln Gly Ile Tyr Lys Phe Lys Asn Gly Ala Arg Tyr Ile Gly Glu
65 70 75 80
Tyr Val Arg Asn Lys Lys His Gly Gln Gly Thr Phe Ile Tyr Pro Asp
85 90 95
Gly Ser Arg Tyr Glu Gly Glu Trp Ala Asn Asp Leu Arg His Gly His
100 105 110
Gly Val Tyr Tyr Tyr Ile Asn Asn Asp Thr Tyr Thr Gly Glu Trp Phe
115 120 125
Ala His Gln Arg His Gly Gln Gly Thr Tyr Leu Tyr Ala Glu Thr Gly
130 135 140
Ser Lys Tyr Val Gly Thr Trp Val Asn Gly Gln Gln Glu Gly Thr Ala
145 150 155 160
Glu Leu Ile His Leu Asn His Arg Tyr

165

<210> 3257
<211> 368
<212> DNA
<213> Homo sapiens

<400> 3257
nncccggggt acatagactc ccccacctac agccggcagg gcatgtcccc caccttctcc
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cgctcacctc accactacta ccgctctggt gatttgtcta cagcaaccaa gagcgaaaca
120
agtgaagaca tcagccagac ctccaagtac agtcccatct actcgccaga cccctactat
180
gcttcggagt ctgagtactg gacctaccat gggtccccca aagtgccccg agccagaagg
240
ttctcgtctg gaggagagga ggatgatttt gaccgcagca tgcacaagct ccaaagtgga
300
attggccggc tgattctgaa ggaagaaatg aaggcccggt cgagctccta tgcagatccc
360
tggcgcgc
368

<210> 3258
<211> 122
<212> PRT
<213> Homo sapiens

<400> 3258
Xaa Pro Gly Tyr Ile Asp Ser Pro Thr Tyr Ser Arg Gln Gly Met Ser
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Pro Thr Phe Ser Arg Ser Pro His His Tyr Tyr Arg Ser Gly Asp Leu
            20   25   30
Ser Thr Ala Thr Lys Ser Glu Thr Ser Glu Asp Ile Ser Gln Thr Ser
        35   40   45
Lys Tyr Ser Pro Ile Tyr Ser Pro Asp Pro Tyr Tyr Ala Ser Glu Ser
    50   55   60
Glu Tyr Trp Thr Tyr His Gly Ser Pro Lys Val Pro Arg Ala Arg Arg
65   70   75   80
Phe Ser Ser Gly Gly Glu Glu Asp Asp Phe Asp Arg Ser Met His Lys
                85   90   95
Leu Gln Ser Gly Ile Gly Arg Leu Ile Leu Lys Glu Glu Met Lys Ala
            100   105   110
Arg Ser Ser Ser Tyr Ala Asp Pro Trp Arg
        115   120

<210> 3259
<211> 747
<212> DNA
<213> Homo sapiens

<400> 3259
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60

gtgctcagcc ttcgtacagc tctgggccgg cctgcagccc atcttgtgtg gcaacaaccg
120
caccattgaa cccggagcgc tgcggcgggg caacatgagc tccctgggct ttacgagcaa
180
ggagcagcgg aacctgggcc ttctcgtgca cctcatgacc agcaacccca aaatcctgta
240
cgcgcctgcg ggctctgagg tcgaccgcgt catcctcaag gccaacgaga cttttgcttt
300
tgtgggcaac gtgactcact atgcccaggt ctggctcaac atctcggcgg agatccgcag
360
cttcctggag cagggcaggc tgcagcaaca cctgcgctgg ctgcagcagt atgtagcaga
420
gctgcggctg caccccgagg cactgaacct gtcactggat gagctgccgc cggccctgag
480
acaggacaac ttctcgctgc ccagtggcat ggccctcctg cagcagctgg ataccattga
540
caacgcggcc tgcggctgga tccagttcat gtccaaggtg agcgtggaca tcttcaaggg
600
cttccccgac gaggagagca ttgtcaacta caccctcaac caggcctacc aggacaacgt
660
cactgttttt gccagtgtga tcttccagac ccggaaggac ggctcgtccc gcctcacgtg
720
cactacaaga tccgccagaa ctccagc
747

<210> 3260
<211> 197
<212> PRT
<213> Homo sapiens

<400> 3260
Met Ser Ser Leu Gly Phe Thr Ser Lys Glu Gln Arg Asn Leu Gly Leu
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Leu Val His Leu Met Thr Ser Asn Pro Lys Ile Leu Tyr Ala Pro Ala
            20   25   30
Gly Ser Glu Val Asp Arg Val Ile Leu Lys Ala Asn Glu Thr Phe Ala
        35   40   45
Phe Val Gly Asn Val Thr His Tyr Ala Gln Val Trp Leu Asn Ile Ser
    50   55   60
Ala Glu Ile Arg Ser Phe Leu Glu Gln Gly Arg Leu Gln Gln His Leu
65   70   75   80
Arg Trp Leu Gln Gln Tyr Val Ala Glu Leu Arg Leu His Pro Glu Ala
                85   90   95
Leu Asn Leu Ser Leu Asp Glu Leu Pro Pro Ala Leu Arg Gln Asp Asn
            100   105   110
Phe Ser Leu Pro Ser Gly Met Ala Leu Leu Gln Gln Leu Asp Thr Ile
        115   120   125
Asp Asn Ala Ala Cys Gly Trp Ile Gln Phe Met Ser Lys Val Ser Val
    130   135   140
Asp Ile Phe Lys Gly Phe Pro Asp Glu Glu Ser Ile Val Asn Tyr Thr
145   150   155   160
Leu Asn Gln Ala Tyr Gln Asp Asn Val Thr Val Phe Ala Ser Val Ile
                165   170   175
Phe Gln Thr Arg Lys Asp Gly Ser Ser Arg Leu Thr Cys Thr Thr Arg

180 185 190
Ser Ala Arg Thr Pro
195

<210> 3261
<211> 1323
<212> DNA
<213> Homo sapiens

<400> 3261
nnacgcgtac agccaccttc cttaccgccg gccctgccgg gagcctgctt cttatcattt
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gcacctcatt gctttcctca cctgccatct cacacgtggc tgccctgtgt tgcccctgtg
120
tgctgtgcca attgtgtttt tttgctctgt gtacattttg gttttatttg gggttgctgt
180
tgatgatttc ctttgttccg gtgttctgtc tcccctcgct ggctgtgtgg gggctgcctg
240
gcccgctgct tgccgcctcc atagatcccc gttgcgcagc catctgtcat ggacgacatt
300
gaggtgtggc tcaggaccga cctgaagggt gatgatctgg aggagggtgt cacaagtgaa
360
gagtttgata aattccttga agaaagagcc aaagctgctg aaatggttcc cgacctcccc
420
tcgcccccca tggaggctcc tgccccagcc tcaaaccctt ctggccggaa gaagccagag
480
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600
cacggcctgc acacctgtgt ttccatggaa atgccaccgt gtctgctccc aggcctccca
660
ctagtcagga ccagcttcag ccacttcttt tctctgagtg gtgggacaac tgcagccaga
720
gactctctcc cctcccacca tgggcccctc tgcccatgtt tcctcccagg aagagcgggc
780
agagtggccc agccccaggc agtgcttcct gagcagacca cccggactgt ctttcctcca
840
cccgcccatg gagaaagagc acgcccggcc ccgccctgtg ctcacctctg cctggctcag
900
tgaccttctc aggcattctg ccctcctggg cccctctctc cctgaagggg ctttgtggca
960
tctctggaag agcagggtgt gctgcactca tgggcctggt ctcactcctt ggacttgtca
1020
ccttgtgaca tttggcttac cagcatttga gaaggctctg ctgggtctcc atggtggggg
1080
tctctcacct tcttgaccct ctctccatca ttcagctgcc agcccaggct tcacacccaa
1140
gctggctcag cagccgagcc tggcaccgag ggtccctgca ggctccctgg gcagggagag
1200
ggccaaggac aattgggagg gcagcaggca gcccgcagat ggtggccatg tggcacgctg
1260
ctgagacgac actaccaata aaccaaactg ccacgcacaa aaaaaaaaaa aaaaaaaaaa
1320

aaa
1323

<210> 3262
<211> 81
<212> PRT
<213> Homo sapiens

<400> 3262
Ile Pro Val Ala Gln Pro Ser Val Met Asp Asp Ile Glu Val Trp Leu
1 5 10 15
Arg Thr Asp Leu Lys Gly Asp Asp Leu Glu Glu Gly Val Thr Ser Glu
20 25 30
Glu Phe Asp Lys Phe Leu Glu Glu Arg Ala Lys Ala Ala Glu Met Val
35 40 45
Pro Asp Leu Pro Ser Pro Pro Met Glu Ala Pro Ala Pro Ala Ser Asn
50 55 60
Pro Ser Gly Arg Lys Lys Pro Glu Arg Ser Glu Asp Ala Leu Phe Ala
65 70 75 80
Leu

<210> 3263
<211> 1128
<212> DNA
<213> Homo sapiens

<400> 3263
agccgctacc gccgcagcag cggggacgag ctcagggagg acgatgagcc cgtcaagaag
60
cggggacgca agggccgggg ccggggtccc ccgtcctcct ctgactccga gcccgaggcc
120
gagctggaga gagaggccaa gaaatcagcg aagaagccgc agtcctcaag cacagagccc
180
gccaggaaac ctggccagaa ggagaagaga gtgcggcccg aggagaagca acaagccaag
240
cccgtgaagg tggagcggac ccggaagcgg tccgagggct tctcgatgga caggaaggta
300
gagaagaaga aagagccctc cgtggaggag aagctgcaga agctgcacag tgagatcaag
360
tttgccctaa aggtcgacag cccggacgtg aaggggtgcc tgaatgccct agaggagctg
420
ggaaccctgc aggtgacctc tcagatcctc cagaagaaca cagacgtggt ggccaccttg
480
aagaagattc gccgttacaa agcgaacaag gacgtaatgg agaaggcagc agaagtctat
540
acccggctca agtcgcgggt cctcggccca aagatcgagg cggtgcagaa agtgaacaag
600
gctgggatgg agaaggagaa ggccgaggag aagctggccg gggaggagct ggccggggag
660
gaggcccccc aggagaaggc ggaggacaag cccagcaccg atctctcagc cccagtgaat
720
ggcgaggcca catcacagaa gggggagagc gcagaggaca aggagcacga ggagggtcgg
780

gactcggagg aggggccaag gtgtggctcc tctgaagacc tgcacgacag cgtacgggag
840
ggtcccgacc tggacaggcc tgggagcgac cggcaggagc gcgagagggc acgggggggac
900
tcggaggccc tggacgagga gagctgagcc gcgggcagcc aggcccagcc cccgcccgag
960
ctcaggctgc ccctctcctt ccccggctcg caggagagca gagcagagaa ctgtggggaa
1020
cgctgtgctg tttgtatttg ttcccttggg ttttttttttc ctgcctaatt tctgtgattt
1080
ccaaccaaca tgaaatgact ataaatggtt tttttaatga aaaaaaaa
1128

<210> 3264
<211> 308
<212> PRT
<213> Homo sapiens

<400> 3264
Ser Arg Tyr Arg Arg Ser Ser Gly Asp Glu Leu Arg Glu Asp Asp Glu
1 5 10 15
Pro Val Lys Lys Arg Gly Arg Lys Gly Arg Gly Arg Gly Pro Pro Ser
20 25 30
Ser Ser Asp Ser Glu Pro Glu Ala Glu Leu Glu Arg Glu Ala Lys Lys
35 40 45
Ser Ala Lys Lys Pro Gln Ser Ser Ser Thr Glu Pro Ala Arg Lys Pro
50 55 60
Gly Gln Lys Glu Lys Arg Val Arg Pro Glu Glu Lys Gln Gln Ala Lys
65 70 75 80
Pro Val Lys Val Glu Arg Thr Arg Lys Arg Ser Glu Gly Phe Ser Met
85 90 95
Asp Arg Lys Val Glu Lys Lys Lys Glu Pro Ser Val Glu Glu Lys Leu
100 105 110
Gln Lys Leu His Ser Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro
115 120 125
Asp Val Lys Gly Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln
130 135 140
Val Thr Ser Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu
145 150 155 160
Lys Lys Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala
165 170 175
Ala Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
180 185 190
Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys Ala
195 200 205
Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala Pro Gln
210 215 220
Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala Pro Val Asn
225 230 235 240
Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu Asp Lys Glu His
245 250 255
Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg Cys Gly Ser Ser Glu
260 265 270
Asp Leu His Asp Ser Val Arg Glu Gly Pro Asp Leu Asp Arg Pro Gly

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        275                 280                 285
Ser Asp Arg Gln Glu Arg Glu Arg Ala Arg Gly Asp Ser Glu Ala Leu
    290                 295                 300
Asp Glu Glu Ser
305
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<210> 3265
<211> 524
<212> DNA
<213> Homo sapiens

<400> 3265
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60
ctttttcgtg gttttcaaaa tgtttccatt gagggcgtat tacttttata atcaacaaaa
120
gagaaagtat aacttcattt tagaaattct cacctaaggc atttgaaaaa taatccaaaa
180
ggtacattat tgttgatttt tcttcctttct agaaaggatc ttgttcgagt agaagccaca
240
gtcattgaaa agacagaatc atggccaaga atcattatga gattcaggaa aaggaaaaac
300
ttcaagaaga aaagaagtaa gttagagaaa gtaccgctgg gccctgttgc acggtgctgg
360
ttgcccaggc gcatgcggac ggagggtgtg gggcacgtgg gtctcgggac aggaagccca
420
ggcaggtctc aacctggctg ccactgccca cttgccaccc tcatcctaga gggagcaccc
480
agagggtcca gcctcgctcc ccttctcctc cacgctccac gcgt
524

<210> 3266
<211> 82
<212> PRT
<213> Homo sapiens

<400> 3266
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Met Arg Phe Arg Lys Arg Lys Asn Phe Lys Lys Lys Arg Ser Lys Leu
 1               5                  10                  15
Glu Lys Val Pro Leu Gly Pro Val Ala Arg Cys Trp Leu Pro Arg Arg
            20                  25                  30
Met Arg Thr Glu Gly Val Gly His Val Gly Leu Gly Thr Gly Ser Pro
        35                  40                  45
Gly Arg Ser Gln Pro Gly Cys His Cys Pro Leu Ala Thr Leu Ile Leu
    50                  55                  60
Glu Gly Ala Pro Arg Gly Ser Ser Leu Ala Pro Leu Leu Leu His Ala
65                  70                  75                  80
Pro Arg
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<210> 3267
<211> 393
<212> DNA
<213> Homo sapiens

<400> 3267
gtcgaatatg catgcagagt acagggttta gaacatgaca tggaagagat caatgctcga
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tggaatacat tgaataaaaa ggtcgcacaa agaattgcac agctacagga agctttgttg
120
cattgtggga agtttcaaga tgccttggag ccattgctca gctggttggc agataccgag
180
gagctcatag ccaatcagaa acctccatct gctgagtata aagtggtgaa agcacagatc
240
caagaacaga agttgctcca gcggctccta gatgatcgaa aggccacagt agacatgctt
300
caagcagaag gaggcagaat agcccagtca gcagagctgg ctgatagaga gaaaatcact
360
ggacagctgg agagtcttga aagtagatgg act
393

<210> 3268
<211> 131
<212> PRT
<213> Homo sapiens

<400> 3268
Val Glu Tyr Ala Cys Arg Val Gln Gly Leu Glu His Asp Met Glu Glu
 1   5   10   15
Ile Asn Ala Arg Trp Asn Thr Leu Asn Lys Lys Val Ala Gln Arg Ile
            20   25   30
Ala Gln Leu Gln Glu Ala Leu Leu His Cys Gly Lys Phe Gln Asp Ala
        35   40   45
Leu Glu Pro Leu Leu Ser Trp Leu Ala Asp Thr Glu Glu Leu Ile Ala
    50   55   60
Asn Gln Lys Pro Pro Ser Ala Glu Tyr Lys Val Val Lys Ala Gln Ile
65   70   75   80
Gln Glu Gln Lys Leu Leu Gln Arg Leu Leu Asp Asp Arg Lys Ala Thr
                85   90   95
Val Asp Met Leu Gln Ala Glu Gly Gly Arg Ile Ala Gln Ser Ala Glu
            100   105   110
Leu Ala Asp Arg Glu Lys Ile Thr Gly Gln Leu Glu Ser Leu Glu Ser
        115   120   125
Arg Trp Thr
    130

<210> 3269
<211> 1423
<212> DNA
<213> Homo sapiens

<400> 3269
ctgtatcaaa aataatagta acttttgaa tatacacaat ttatctagaa tctattttcc
60
tttgaagctg taactttatg agcgattatt tactaccttt gagaaatgtg ttttagtata
120
aaatatagga tgtggaagcg aaaaaatatc tgggtagcaa gtgaggtgta ctcaaaaata
180

agcaaaagtc acgtgggtct gattttatac cctcgctgga aagcttgttc tcagacacac
240
tgttactgca agtgtgtgtg agggggaaac tctcacacac tttgcagttg aggacagggc
300
tagactttga ggtggaccct ggctcccagg gctgtgtact cccagcccgt gtttctcttt
360
tgctcagact gaacaagtgg aacgaaatta cattaaagaa aagaaggcag cagtgaaaga
420
atttgaagac aagaaggttg agctgaaaga gaacctgatt gctgagctag aagaaaagaa
480
gaaaatgatt gaaaacgaaa tgctgacaat ggaactgaat ggagattcta tggaggtgaa
540
acctatcatg accagaaagt tgcggaggcg accaaatgat cccgtcccca tcccagacaa
600
gaggaggaaa cctgctccag cccagctaaa ctatttgtta acagatgaac agatcatgga
660
ggatctgaga acattaaata agcttaagtc acccaagaga ccagcatctc catcctctcc
720
tgagcacttg cctgcaacac ccgcggaatc tccagcacag agatttgagg cgcggataga
780
agatggcaaa ctgtattatg acaaaagatg gtaccacaag agccaggcca tctatctgga
840
gtcaaaggac aaccagaaac tgagctgcgt gatcagttct gtaggagcca atgagatctg
900
ggtgaggaag acaagtgaca gcaccaagat gaggatctac ctgggtcagc ttcagcgcgg
960
gctcttcgtg atccgccggc gctcagctgc ttgactttct acagtgctct tctcttgacc
1020
ctttttctgg agtgggtttt atttttgttt tgtttcgttt tctccttaat agaaaaatgt
1080
taacttactg ggaatagcta ctcagccttg gaaatggaga gcactgcagt gaattcttta
1140
gggcactttt gtggccggat gcttccaact ttgtcagtct tttctgcctc aacttcttcc
1200
agacatcagt caccatgaga ctgttttact ttcaggcgta ttgggggttt tgatttactt
1260
tccttttatt tctttatttt ttgcttatac ttgtttttga aaacctcctc tgagtttgaa
1320
gggacagcta tttttattga ttatctttaa gtctctctac catggagaag agcaggaagg
1380
gatacactct ccagtgcatt ttcatgtttt gaatcggatt agt
1423

<210> 3270
<211> 169
<212> PRT
<213> Homo sapiens

<400> 3270
Met Ile Glu Asn Glu Met Leu Thr Met Glu Leu Asn Gly Asp Ser Met
 1   5   10   15
Glu Val Lys Pro Ile Met Thr Arg Lys Leu Arg Arg Arg Pro Asn Asp
            20   25   30
Pro Val Pro Ile Pro Asp Lys Arg Arg Lys Pro Ala Pro Ala Gln Leu

```
        35                  40                  45
Asn Tyr Leu Leu Thr Asp Glu Gln Ile Met Glu Asp Leu Arg Thr Leu
    50                  55                  60
Asn Lys Leu Lys Ser Pro Lys Arg Pro Ala Ser Pro Ser Ser Pro Glu
65                  70                  75                  80
His Leu Pro Ala Thr Pro Ala Glu Ser Pro Ala Gln Arg Phe Glu Ala
                85                  90                  95
Arg Ile Glu Asp Gly Lys Leu Tyr Tyr Asp Lys Arg Trp Tyr His Lys
            100                 105                 110
Ser Gln Ala Ile Tyr Leu Glu Ser Lys Asp Asn Gln Lys Leu Ser Cys
        115                 120                 125
Val Ile Ser Ser Val Gly Ala Asn Glu Ile Trp Val Arg Lys Thr Ser
    130                 135                 140
Asp Ser Thr Lys Met Arg Ile Tyr Leu Gly Gln Leu Gln Arg Gly Leu
145                 150                 155                 160
Phe Val Ile Arg Arg Arg Ser Ala Ala
                165
```

<210> 3271
<211> 464
<212> DNA
<213> Homo sapiens

<400> 3271
tcatgagcag ggcccaattc tggcttctct gtggtcgcca tccatgtgct gggcgtcact
60
gaaggcactg gggatacagc cgagcacaag atggacagag atccctggcc cctcggagca
120
ggcagtctgt ggctctggcc cctccagttc cttgtcacca ggagataggc aatgcagctg
180
atgagaaggg ccccggcagc aagagatcca atgatggtgg ccgccaggat cccagcgttg
240
gtgggcaggt gtgtactggg cagctcctta ttcttttcag ctacctggac ctcagtcttg
300
gccttcatag tccattcaga gttgatggta atggctactt ggtaggtgcc actgtctgta
360
ggctgggcgc ggcgcagcag catggaacca ttggggaagc ccacgatgtc tcgctgtccc
420
atggcactgc catccctctg aggccgttgt atccccaggg atgt
464

<210> 3272
<211> 140
<212> PRT
<213> Homo sapiens

<400> 3272

```
Met Gly Gln Arg Asp Ile Val Gly Phe Pro Asn Gly Ser Met Leu Leu
 1               5                  10                  15
Arg Arg Ala Gln Pro Thr Asp Ser Gly Thr Tyr Gln Val Ala Ile Thr
            20                  25                  30
Ile Asn Ser Glu Trp Thr Met Lys Ala Lys Thr Glu Val Gln Val Ala
        35                  40                  45
Glu Lys Asn Lys Glu Leu Pro Ser Thr His Leu Pro Thr Asn Ala Gly
```

```
    50                  55                  60
Ile Leu Ala Ala Thr Ile Ile Gly Ser Leu Ala Ala Gly Ala Leu Leu
65                  70                  75                  80
Ile Ser Cys Ile Ala Tyr Leu Leu Val Thr Arg Asn Trp Arg Gly Gln
                85                  90                  95
Ser His Arg Leu Pro Ala Pro Arg Gly Gln Gly Ser Leu Ser Ile Leu
            100                 105                 110
Cys Ser Ala Val Ser Pro Val Pro Ser Val Thr Pro Ser Thr Trp Met
        115                 120                 125
Ala Thr Thr Glu Lys Pro Glu Leu Gly Pro Ala His
    130                 135                 140
```

<210> 3273
<211> 387
<212> DNA
<213> Homo sapiens

<400> 3273
ngcgcgccag ggatggaaaa ctttattctg tatgaggaga tcggaagagg aagcaagact
60
gttgtctata aagggcgacg gaagggaaca atcaattttg tagccattct ttgtactgat
120
aagtgcagaa ggcctgaaat aaccaactgg gtccgtctca cccgtgaaat aaaacacaag
180
aatattgtaa cttttcatga atggtatgaa acaagcaacc acctctggct agtggtggaa
240
ctccgcacag gtggttcctt aaaaacagtt attgctcaag atgaaaacct cccagaagat
300
gttgtgagag aatttggaat tgacctgatt agtggattac atcatcttca taaacttggc
360
attctctttg tgacatttct cctagga
387

<210> 3274
<211> 129
<212> PRT
<213> Homo sapiens

<400> 3274

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Xaa Ala Pro Gly Met Glu Asn Phe Ile Leu Tyr Glu Glu Ile Gly Arg
 1               5                  10                  15
Gly Ser Lys Thr Val Val Tyr Lys Gly Arg Arg Lys Gly Thr Ile Asn
            20                  25                  30
Phe Val Ala Ile Leu Cys Thr Asp Lys Cys Arg Arg Pro Glu Ile Thr
        35                  40                  45
Asn Trp Val Arg Leu Thr Arg Glu Ile Lys His Lys Asn Ile Val Thr
    50                  55                  60
Phe His Glu Trp Tyr Glu Thr Ser Asn His Leu Trp Leu Val Val Glu
65                  70                  75                  80
Leu Arg Thr Gly Gly Ser Leu Lys Thr Val Ile Ala Gln Asp Glu Asn
                85                  90                  95
Leu Pro Glu Asp Val Val Arg Glu Phe Gly Ile Asp Leu Ile Ser Gly
            100                 105                 110
Leu His His Leu His Lys Leu Gly Ile Leu Phe Val Thr Phe Leu Leu
```

115 120 125
Gly

<210> 3275
<211> 1266
<212> DNA
<213> Homo sapiens

<400> 3275
tttttttaa tcagttaaga ttcttgttga cacaaattgt tttacatcaa ctgttgttat
60
agaacacatg aaaggaatac atggggaaga aataaagtag aacccaagag ttcttttaag
120
ttttctttta tagagacatg aataacagat acactgaagt ataaacaaaa attggcctga
180
agcgtccggt ggccggctta gttaggagct atggctaaac atcatcctga tttgatcttt
240
tgccgcaagc aggctggtgt tgccatcgga agactgtgtg aaaaatgtga tggcaagtgt
300
gtgatttgtg actcctatgt gcgtccctgc actctggtgc gcatatgtga tgagtgtaac
360
tatggatctt accaggggcg ctgtgtgatc tgtggaggac ctggggtctc tgatgcctat
420
tattgtaagg agtgcaccat ccaggagaag gacagagatg gctgcccaaa gattgtcaat
480
ctggggagct ctaagacaga cctcttctat gaacgcaaaa aatacggctt caagaagagg
540
tgattggtgg gtggcccctt cctcccccca acatcagtct gctgcagctg ccagaaaaca
600
tgcctactac taccagcaga aagggagcag agcccagagc atcaccagga gtgcctgcta
660
gtgtactggc agcttgccac ccctcctct cccttcaccc agacacgtgg tagggatgga
720
aaaggattct tcacagagca ctctggcaca ccatatcgga gaaaaattga tagattagtt
780
aatggttttt cttgaattcg agaagcatag atctgttctc catattggta tgttctccct
840
caaccaagat cttctaaaaa gaaataatat tttagtcttc tgcttgagga actgactgtg
900
aagcgacgcc cagtgaaaaa catgatcttg cagcagctct ggtggcagct gtccttgagg
960
aacctttggt gtgtggtggg aagctatcag aacaagaaat gtaggcattt cccgtttttt
1020
ttgggggggg ggtgggggggg cagggctctg ccctcttgaa aggcatttac ttgtttaaca
1080
cttgtccagc tacagtgggg tacagtagct ggctatttcac aggcatcatc atagcccact
1140
agtctcatat tattttcctt ttgagaaatt ggaaactctt tctgttgcta ttatattaat
1200
aaagttggtg tttatttttct ggtaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
1260
aaaaaa
1266

<210> 3276
<211> 110
<212> PRT
<213> Homo sapiens

<400> 3276
Met Ala Lys His His Pro Asp Leu Ile Phe Cys Arg Lys Gln Ala Gly
1 5 10 15
Val Ala Ile Gly Arg Leu Cys Glu Lys Cys Asp Gly Lys Cys Val Ile
20 25 30
Cys Asp Ser Tyr Val Arg Pro Cys Thr Leu Val Arg Ile Cys Asp Glu
35 40 45
Cys Asn Tyr Gly Ser Tyr Gln Gly Arg Cys Val Ile Cys Gly Gly Pro
50 55 60
Gly Val Ser Asp Ala Tyr Tyr Cys Lys Glu Cys Thr Ile Gln Glu Lys
65 70 75 80
Asp Arg Asp Gly Cys Pro Lys Ile Val Asn Leu Gly Ser Ser Lys Thr
85 90 95
Asp Leu Phe Tyr Glu Arg Lys Lys Tyr Gly Phe Lys Lys Arg
100 105 110

<210> 3277
<211> 1435
<212> DNA
<213> Homo sapiens

<400> 3277
ncctccgtct ccgagaacaa caacaacagc aacaagaaaa caacaataaa aaaaataagg
60
ctgcgtggga ggcagaaaga gctaatgcgg ccacgcttgt ccctcggcca ccgtcccacc
120
cagacttccg tctccttaaa atgttcatgc gtaagtgcgt ggcagaagcg gctcaagcgc
180
actcgtgcgt cattgctgtc agggccgagg gagcggtgca aggccgccgc gtgacgtcag
240
gacgccgcgg tcaggacgtc gaagccaaag aagaccagag ccagccgggt ggcacagcgg
300
tgtcgtggcc gtgttgctga tcgcctgggt ggttgttggc gtgtccctgc agcgaaggat
360
cctggttggc agtgaaaaag cagtctggct cccgaggtcc acccccttata ccccaaggtc
420
cagatggcgg ccaacgtggg tgatcaacgt agcacagatt ggtcttctca gtacagcatg
480
gtggctgggg caggccgaga gaatggcatg gagacgccga tgcacgagaa cccggagtgg
540
gagaaggccc gtcaggccct ggccagcatc agcaagtcag gagctgccgg cggctctgcc
600
aagtccagca gcaatgggcc tgtggccagt gcaagtacgt gtcccaggca gaagcctcag
660
ctttgcagca gcagcagtac taccagtggt accagcagta caactatgcc taccctaca
720
gctactacta tcccatgagc atgtaccaga gctatggctc cccttcccag tatgggatgg
780

ccggctccta tggctagcca caccccagca gccatccgca ccccaacacc aagggactct
840
gaaccagccc ccagtccccg gcatggatga gagcatgtcc taccaggctc cccctcagca
900
gctgccgtcg gctcagcccc ctcagccctc aaatccccca catggggctc acacgctgaa
960
cagtggccct cagcctggga cagctccagc cacacagcan ncagccaggc ggggcccgcc
1020
acgggccagg cctatgggcc acacacctac accgaacctg ccaagcccaa gaagggccaa
1080
cagctgtgga accgcatgaa acccgccccc gggactggag gttcaagttc aacatccaga
1140
agcgaccctt tgctgttacc acccagagct ttggctccaa cgcagagggc cagcacagtg
1200
gttttggccc ccagcccaac cctgagaaag ttcagaacca cagcgggtcc tctgcccggg
1260
ggaacctgtc tgggaagccc gatgactggc cccaggacat gaaagagtat gtggagcgct
1320
gcttcaccgc ctgtgagtcg gaggaggaca aggaccgcac ggaaaagctg ctcaaggagg
1380
tgctgcaggc gcggctgcag gacggctcgg cctataccat tgactggagc cggga
1435

<210> 3278
<211> 104
<212> PRT
<213> Homo sapiens

<400> 3278
Met Ala Ala Asn Val Gly Asp Gln Arg Ser Thr Asp Trp Ser Ser Gln
 1   5   10   15
Tyr Ser Met Val Ala Gly Ala Gly Arg Glu Asn Gly Met Glu Thr Pro
            20   25   30
Met His Glu Asn Pro Glu Trp Glu Lys Ala Arg Gln Ala Leu Ala Ser
        35   40   45
Ile Ser Lys Ser Gly Ala Ala Gly Gly Ser Ala Lys Ser Ser Ser Asn
    50   55   60
Gly Pro Val Ala Ser Ala Ser Thr Cys Pro Arg Gln Lys Pro Gln Leu
65   70   75   80
Cys Ser Ser Ser Ser Thr Thr Ser Gly Thr Ser Ser Thr Thr Met Pro
                85   90   95
Thr Pro Thr Ala Thr Thr Ile Pro
            100

<210> 3279
<211> 1130
<212> DNA
<213> Homo sapiens

<400> 3279
nngcgcgccc accgcgccgc atccatgttc gacaccacac cccactctgg ccggagcacg
60
ccaagcagct ccccatcgct ccggaaacgg ctgcagctcc tgcccccaag ccggccccca
120

cctgagccag aaccaggcac catggtggag aagggatcag atagctcctc agagaagggt
180
ggggtgcctg ggacccccag cacccagagc ctaggcagcc ggaacttcat ccgcaacagc
240
aagaagatgc agagctggta cagtatgctg agccccactt ataagcagcg taatgaggac
300
ttccggaaac tgttcagcaa actccccgaa gcagaacgcc tcattgtgga ttactcctgc
360
gccctgcagc gtgagatcct gctccagggc cgcctctacc tctctgagaa ctggatctgc
420
ttctacagca acatcttccg ctgggagacc acgatctcca tccagctgaa ggaagtgaca
480
tgtctgaaga aggaaaagac ggccaagctg atccccaacg ccatccagat ctgcacggag
540
agcgagaagc atttcttcac ttcctttggg gcccgtgacc gctgcttcct cctcatcttc
600
cgcctctggc agaatgcact gcttgaaaag acgctgagtc cccgcgagct ctggcacctg
660
gtgcatcagt gctacggctc agagctgggc ctcaccagtg aggatgagga ctatgtctcc
720
cccttgcagc tgaacggtct ggggaccccc aaggaagtgg gagatgtgat cgccctgagc
780
gacatcacct cctcgggggc agctgaccgc agccaggagc caagcccagt gggttcgcgc
840
cgtggccatg tcacgcccaa cctttcccga gccagcagcg acgcagacca tggggcagag
900
gaggacaagg aggagcaggt agacagccag ccagacgcct cctccagcca gacagtgacc
960
ccggtggctg aacccccgag cacagagccc acccagcctg acgggcccac caccctgggc
1020
cccttggatc tgctgcccag tgaggagcta ttgacagaca caagtaactc ctcttcatcc
1080
actggggagg aagcggactt ggctgccctg cttcccgacc tctccggccg
1130

<210> 3280
<211> 376
<212> PRT
<213> Homo sapiens

<400> 3280
Xaa Arg Ala His Arg Ala Ala Ser Met Phe Asp Thr Thr Pro His Ser
1 5 10 15
Gly Arg Ser Thr Pro Ser Ser Ser Pro Ser Leu Arg Lys Arg Leu Gln
20 25 30
Leu Leu Pro Pro Ser Arg Pro Pro Pro Glu Pro Glu Pro Gly Thr Met
35 40 45
Val Glu Lys Gly Ser Asp Ser Ser Ser Glu Lys Gly Gly Val Pro Gly
50 55 60
Thr Pro Ser Thr Gln Ser Leu Gly Ser Arg Asn Phe Ile Arg Asn Ser
65 70 75 80
Lys Lys Met Gln Ser Trp Tyr Ser Met Leu Ser Pro Thr Tyr Lys Gln
85 90 95
Arg Asn Glu Asp Phe Arg Lys Leu Phe Ser Lys Leu Pro Glu Ala Glu

```
            100                 105                 110
Arg Leu Ile Val Asp Tyr Ser Cys Ala Leu Gln Arg Glu Ile Leu Leu
        115                 120                 125
Gln Gly Arg Leu Tyr Leu Ser Glu Asn Trp Ile Cys Phe Tyr Ser Asn
    130                 135                 140
Ile Phe Arg Trp Glu Thr Thr Ile Ser Ile Gln Leu Lys Glu Val Thr
145                 150                 155                 160
Cys Leu Lys Lys Glu Lys Thr Ala Lys Leu Ile Pro Asn Ala Ile Gln
                165                 170                 175
Ile Cys Thr Glu Ser Glu Lys His Phe Phe Thr Ser Phe Gly Ala Arg
            180                 185                 190
Asp Arg Cys Phe Leu Leu Ile Phe Arg Leu Trp Gln Asn Ala Leu Leu
        195                 200                 205
Glu Lys Thr Leu Ser Pro Arg Glu Leu Trp His Leu Val His Gln Cys
    210                 215                 220
Tyr Gly Ser Glu Leu Gly Leu Thr Ser Glu Asp Glu Asp Tyr Val Ser
225                 230                 235                 240
Pro Leu Gln Leu Asn Gly Leu Gly Thr Pro Lys Glu Val Gly Asp Val
                245                 250                 255
Ile Ala Leu Ser Asp Ile Thr Ser Ser Gly Ala Ala Asp Arg Ser Gln
            260                 265                 270
Glu Pro Ser Pro Val Gly Ser Arg Arg Gly His Val Thr Pro Asn Leu
        275                 280                 285
Ser Arg Ala Ser Ser Asp Ala Asp His Gly Ala Glu Glu Asp Lys Glu
    290                 295                 300
Glu Gln Val Asp Ser Gln Pro Asp Ala Ser Ser Ser Gln Thr Val Thr
305                 310                 315                 320
Pro Val Ala Glu Pro Pro Ser Thr Glu Pro Thr Gln Pro Asp Gly Pro
                325                 330                 335
Thr Thr Leu Gly Pro Leu Asp Leu Leu Pro Ser Glu Glu Leu Leu Thr
            340                 345                 350
Asp Thr Ser Asn Ser Ser Ser Ser Thr Gly Glu Glu Ala Asp Leu Ala
        355                 360                 365
Ala Leu Leu Pro Asp Leu Ser Gly
    370                 375
```

<210> 3281
<211> 842
<212> DNA
<213> Homo sapiens

<400> 3281
gaattctgcc ttgccgtgtg cctcattggc caaaggaaag caacagagtc tgcagccagg
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gcaggacccg caggaggggc ctggacccgg ggggctcctg gcagcgctgt gcctttctga
120
ggcaaggagg tagagccagc ggctgaggac ctgtcagggc cagtcccagc tctgcagctt
180
gctgtgtgac ctggcacaca tcctctccct gcctccctca gtctcttccc ctgcaagacg
240
gggtcctgac acggatctca tgggattgct ctgaggccca ggcagtccca ggctcaacca
300
ctggttcaca aagtgtgttg tttccaggaa gaacagatgg gggcgcctga gggcaaaggg
360

cctgagtgtg ggtcgaggat atgccggctg ctcgctcagg ggctgggttt tcatcttgtg
420
tgtcttgaca gggtgtgaca cttggcacca cactgttccc tgtcccttca tggatgtggc
480
ccacatgatg ttcctttcct cttgcaaaag aagttgctgg aaggcccact gtccagcagc
540
ccccaggttg cctgggccac ggtgcctttg tgggcccagc tacaaggagg acttgcaggc
600
tcgtgtctgg gacagatact ggcgccaggg ccaagtgaag cccgggattg gtgggcatct
660
ctagctggtc cctgagagag ggtggagggt gctgacaggc cttggcgctt tcatctgtca
720
actccagagg cccttgtgct tgcagcaggg aggtcaaggc cagggcgtct gaccccggcc
780
gctcctccac actgagcctc ctgcacgtgc tcacaggtag agaagcggcg ggtcaatctg
840
tc
842

<210> 3282
<211> 146
<212> PRT
<213> Homo sapiens

<400> 3282
Met Pro Thr Asn Pro Gly Leu His Leu Ala Leu Ala Pro Val Ser Val
 1   5   10   15
Pro Asp Thr Ser Leu Gln Val Leu Leu Val Ala Gly Pro Thr Lys Ala
            20   25   30
Pro Trp Pro Arg Gln Pro Gly Gly Cys Trp Thr Val Gly Leu Pro Ala
        35   40   45
Thr Ser Phe Ala Arg Gly Lys Glu His His Val Gly His Ile His Glu
    50   55   60
Gly Thr Gly Asn Ser Val Val Pro Ser Val Thr Pro Cys Gln Asp Thr
65   70   75   80
Gln Asp Glu Asn Pro Ala Pro Glu Arg Ala Ala Gly Ile Ser Ser Thr
                85   90   95
His Thr Gln Ala Leu Cys Pro Gln Ala Pro Pro Ser Val Leu Pro Gly
            100   105   110
Asn Asn Thr Leu Cys Glu Pro Val Val Glu Pro Gly Thr Ala Trp Ala
        115   120   125
Ser Glu Gln Ser His Glu Ile Arg Val Arg Thr Pro Ser Cys Arg Gly
    130   135   140
Arg Asp
145

<210> 3283
<211> 3268
<212> DNA
<213> Homo sapiens

<400> 3283
nggatcagag cggctgtggt gctccagaaa cattaccgca tgcagagggc ccgccaggcc
60

taccagaggg tccgcagagc tgccgttgtt atccaggcct tcacccggng ccatgtttgt
120
gcggagaacc taccgccagt cctcatggag cacaaggcca ccaccatcca gaagcacgtg
180
cggggctgga tggcacgcag gcacttccag cggctgcggg atgcagccat tgtcatccag
240
tgtgccttcc ggatgctcaa ggccaggcgg gagctgaagg ccctcaggat tgaggcccgc
300
tcagcagagc atctgaaacg tctcaacgtg ggcatggaga acaaggtggt ccagctgcag
360
cggaagatcg atgagcagaa caaagagttc aagacacttt cagagcagtt gtccgtgacc
420
acctcaacat acaccatgga ggtagagcgg ctgaagaagg agctggtgca ctaccagcag
480
agcccaggtg aggacaccag cctcaggctg caggaggagg tggagagcct gcgcacagag
540
ctgcagaggg cccactcgga gcgcaagatc ttggaggacg cccacagcag ggagaaagat
600
gagctgagga agcgagttgc agacctggag caagaaaatg ctctcttgaa agatgagaaa
660
gaacagctca acaaccaaat cctgtgccag tctaaagatg aatttgccca gaactctgtg
720
aaggaaaatc tcctcatgaa gaaagaactg gaggaggagc gatcccggta ccagaacctt
780
gtgaaggaat attcacagtt ggagcagaga tacgacaacc ttcgggatga aatgaccatc
840
ataaagcaaa ctccaggtca taggcggaac ccatcaaacc aaagtagctt agaatctgac
900
tccaattacc cctccatctc cacatctgag atcggagaca ctgaggatgc cctccagcag
960
gtggaggaaa ttggcctgga gaaggcagcc atggacatga cggtcttcct gaagctgcag
1020
aagagagtac gggagctgga gcaggagagg aaaaagctgc aagtgcagct ggagaagaga
1080
gaacagcagg acagcaagaa agtccaggcg gaaccaccac agactgacat agatttggac
1140
ccgaatgcag atctggccta caatagtctg aagaggcaag agctggagtc agagaacaaa
1200
aagctgaaga atgacctgaa tgagctgagg aaagccgtgg ccgaccaagc cacgcagaat
1260
aactccagcc acggctcccc agatagctac agcctcctgc tgaaccagct caagctggcc
1320
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1680

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1800
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1920
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2940
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3060
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3120
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3268

<210> 3284
<211> 1012
<212> PRT
<213> Homo sapiens

<400> 3284
Xaa Ile Arg Ala Ala Val Val Leu Gln Lys His Tyr Arg Met Gln Arg
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Ala Arg Gln Ala Tyr Gln Arg Val Arg Arg Ala Ala Val Val Ile Gln
20 25 30
Ala Phe Thr Arg Xaa His Val Cys Ala Glu Asn Leu Pro Pro Val Leu
35 40 45
Met Glu His Lys Ala Thr Thr Ile Gln Lys His Val Arg Gly Trp Met
50 55 60
Ala Arg Arg His Phe Gln Arg Leu Arg Asp Ala Ala Ile Val Ile Gln
65 70 75 80
Cys Ala Phe Arg Met Leu Lys Ala Arg Arg Glu Leu Lys Ala Leu Arg
85 90 95
Ile Glu Ala Arg Ser Ala Glu His Leu Lys Arg Leu Asn Val Gly Met
100 105 110
Glu Asn Lys Val Val Gln Leu Gln Arg Lys Ile Asp Glu Gln Asn Lys
115 120 125
Glu Phe Lys Thr Leu Ser Glu Gln Leu Ser Val Thr Thr Ser Thr Tyr
130 135 140
Thr Met Glu Val Glu Arg Leu Lys Lys Glu Leu Val His Tyr Gln Gln
145 150 155 160
Ser Pro Gly Glu Asp Thr Ser Leu Arg Leu Gln Glu Glu Val Glu Ser
165 170 175
Leu Arg Thr Glu Leu Gln Arg Ala His Ser Glu Arg Lys Ile Leu Glu
180 185 190
Asp Ala His Ser Arg Glu Lys Asp Glu Leu Arg Lys Arg Val Ala Asp
195 200 205
Leu Glu Gln Glu Asn Ala Leu Leu Lys Asp Glu Lys Glu Gln Leu Asn
210 215 220
Asn Gln Ile Leu Cys Gln Ser Lys Asp Glu Phe Ala Gln Asn Ser Val
225 230 235 240
Lys Glu Asn Leu Leu Met Lys Lys Glu Leu Glu Glu Glu Arg Ser Arg
245 250 255
Tyr Gln Asn Leu Val Lys Glu Tyr Ser Gln Leu Glu Gln Arg Tyr Asp
260 265 270
Asn Leu Arg Asp Glu Met Thr Ile Ile Lys Gln Thr Pro Gly His Arg
275 280 285
Arg Asn Pro Ser Asn Gln Ser Ser Leu Glu Ser Asp Ser Asn Tyr Pro
290 295 300
Ser Ile Ser Thr Ser Glu Ile Gly Asp Thr Glu Asp Ala Leu Gln Gln
305 310 315 320
Val Glu Glu Ile Gly Leu Glu Lys Ala Ala Met Asp Met Thr Val Phe
325 330 335
Leu Lys Leu Gln Lys Arg Val Arg Glu Leu Glu Gln Glu Arg Lys Lys
340 345 350
Leu Gln Val Gln Leu Glu Lys Arg Glu Gln Gln Asp Ser Lys Lys Val
355 360 365
Gln Ala Glu Pro Pro Gln Thr Asp Ile Asp Leu Asp Pro Asn Ala Asp

```
    370                 375                 380
Leu Ala Tyr Asn Ser Leu Lys Arg Gln Glu Leu Glu Ser Glu Asn Lys
385                 390                 395                 400
Lys Leu Lys Asn Asp Leu Asn Glu Leu Arg Lys Ala Val Ala Asp Gln
                405                 410                 415
Ala Thr Gln Asn Asn Ser Ser His Gly Ser Pro Asp Ser Tyr Ser Leu
            420                 425                 430
Leu Leu Asn Gln Leu Lys Leu Ala His Glu Glu Leu Glu Val Arg Lys
        435                 440                 445
Glu Glu Val Leu Ile Leu Arg Thr Gln Ile Val Ser Ala Asp Gln Arg
    450                 455                 460
Arg Leu Ala Gly Arg Asn Ala Glu Pro Asn Ile Asn Ala Arg Ser Ser
465                 470                 475                 480
Trp Pro Asn Ser Glu Arg His Val Asp Gln Glu Asp Ala Ile Glu Ala
                485                 490                 495
Tyr His Gly Val Cys Gln Thr Asn Arg Leu Leu Glu Ala Gln Leu Gln
            500                 505                 510
Ala Gln Ser Leu Glu His Glu Glu Glu Val Glu His Leu Lys Ala Gln
        515                 520                 525
Leu Glu Ala Leu Lys Glu Glu Met Asp Lys Gln Gln Gln Thr Phe Cys
    530                 535                 540
Gln Thr Leu Leu Leu Ser Pro Glu Ala Gln Val Glu Phe Gly Val Gln
545                 550                 555                 560
Gln Glu Ile Ser Arg Leu Thr Asn Glu Asn Leu Asp Leu Lys Glu Leu
                565                 570                 575
Val Glu Lys Leu Glu Lys Asn Glu Arg Lys Leu Lys Lys Gln Leu Lys
            580                 585                 590
Ile Tyr Met Lys Lys Ala Gln Asp Leu Glu Ala Ala Gln Ala Leu Ala
        595                 600                 605
Gln Ser Glu Arg Lys Arg His Glu Leu Asn Arg Gln Val Thr Val Gln
    610                 615                 620
Arg Lys Glu Lys Asp Phe Gln Gly Met Leu Glu Tyr His Lys Glu Asp
625                 630                 635                 640
Glu Ala Leu Leu Ile Arg Asn Leu Val Thr Asp Leu Lys Pro Gln Met
                645                 650                 655
Leu Ser Gly Thr Val Pro Cys Leu Pro Ala Tyr Ile Leu Tyr Met Cys
            660                 665                 670
Ile Arg His Ala Asp Tyr Thr Asn Asp Asp Leu Lys Val His Ser Leu
        675                 680                 685
Leu Thr Ser Thr Ile Asn Gly Ile Lys Lys Val Leu Lys Lys His Asn
    690                 695                 700
Asp Asp Phe Glu Met Thr Ser Phe Trp Leu Ser Asn Thr Cys Arg Leu
705                 710                 715                 720
Leu His Cys Leu Lys Gln Tyr Ser Gly Asp Glu Gly Phe Met Thr Gln
                725                 730                 735
Asn Thr Ala Lys Gln Asn Glu His Cys Leu Lys Asn Phe Asp Leu Thr
            740                 745                 750
Glu Tyr Arg Gln Val Leu Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln
        755                 760                 765
Leu Ile Lys Ile Ala Glu Gly Val Leu Gln Pro Met Ile Val Ser Ala
    770                 775                 780
Met Leu Glu Asn Glu Ser Ile Gln Gly Leu Ser Gly Val Lys Pro Thr
785                 790                 795                 800
Gly Tyr Arg Lys Arg Ser Ser Ser Met Ala Asp Gly Asp Asn Ser Tyr
```

```
                805                 810                 815
Cys Leu Glu Ala Ile Ile Arg Gln Met Asn Ala Phe His Thr Val Met
            820                 825                 830
Cys Asp Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys Gln
        835                 840                 845
Leu Phe Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu Leu Arg
    850                 855                 860
Lys Asp Val Cys Ser Trp Ser Thr Gly Met Gln Leu Arg Tyr Asn Ile
865                 870                 875                 880
Ser Gln Leu Glu Glu Trp Leu Arg Gly Arg Asn Leu His Gln Ser Gly
                885                 890                 895
Ala Val Gln Thr Met Glu Pro Leu Ile Gln Ala Ala Gln Leu Leu Gln
            900                 905                 910
Leu Lys Lys Lys Thr Gln Glu Asp Ala Glu Ala Ile Cys Ser Leu Cys
        915                 920                 925
Thr Ser Leu Ser Thr Gln Gln Ile Val Lys Ile Leu Asn Leu Tyr Thr
    930                 935                 940
Pro Leu Asn Glu Phe Glu Glu Arg Val Thr Val Ala Phe Ile Arg Thr
945                 950                 955                 960
Ile Gln Ala Gln Leu Gln Glu Arg Asn Asp Pro Gln Gln Leu Leu Leu
                965                 970                 975
Asp Ala Lys His Met Phe Pro Val Leu Phe Pro Phe Asn Pro Ser Ser
            980                 985                 990
Leu Thr Met Asp Ser Ile His Ile Pro Ala Cys Leu Asn Leu Glu Phe
        995                 1000                1005
Leu Asn Glu Val
    1010
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<210> 3285
<211> 1518
<212> DNA
<213> Homo sapiens

<400> 3285
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aacctgatga caccaccact ttattttgag ctaaatcctc atttaagtga gaacaggaca
120
ggtttcacca ctgcctcctt tggcaacttg agtggtggtg ttcccaccga gtttatggct
180
gcaaagatag gtcttttctc gtatttatgt ataaacaggt accagttttg attttattta
240
atcatttcat acattaacat acatgacaca tcaaaatgag aaatgcacag tttaaccgtt
300
caacagctgg ccttacttca aaagaacact atattcatat taaacattta cagtctttcc
360
atctaacttt acacatgtcc taaatcattt tccagcactt ctcacataga agtctagttt
420
tgctctttaa aatcaccatc tgtatcaccc ctagtagacg cgagggtttc cccaattaca
480
tgctgaagag agccagccac caccccacct aaagacatcc aagcagctcc agagcctgcc
540
tccgaggcca ccccttcgcc acggcagtct cgattccaag aactgattat ctgacactag
600

tgaaccagca ctaaaggctg taggatgtga ctacatcaca gttccagaag gaaggggacc
660
atggccaaga gaagccctaa atgacagaag ctcattaaaa ccaagtcccc caaacctcct
720
gaaacatcgt tagcaaggag ctactgcttt cctttcttaa acatgttttg ggcatgacca
780
cactctggaa gtggtgaact gttacacatt tggtgtgtgt gtacataaca tcaaaaacta
840
ctgtgtgaaa cttgagaatg tctgattaaa gatttcaatg tatatctaaa aactaactca
900
aatcgttgac cagcactttc ccagtatcat aacaatgcgg ctgacctct tctgccttca
960
ctttacaccc catcatagca cattatttgt gcacaactag tgaggtctgt gcggctcatc
1020
atccccataa ccaagtcggt ctgtgttgag tcatatcatt ctgtgctggt tttagaagtc
1080
accataggaa acatgaagtc acatcctggt caaaaaactg tccatttctc aaaaacagag
1140
aaaaacctga gatacgaggc agcaactagc gacacttaca ggaagggaaa gaacaatgac
1200
aacacccgcc cagccccacc cccaaaaagc tgctgttgtg aattaaggct tcaaaagagg
1260
acccacactg tagctgataa aactcaagcc aggaggatgt ttgaaagcca atctgcacta
1320
tcacttgttc cagtgacctc ctatgttcag ctgccaggac cgattccata cagtgattgt
1380
aggttgagga ctgaggacgc ccctttgctc tcgctccatt ttgatttgct ttttccactg
1440
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1500
actgatcaaa actcaatt
1518

<210> 3286
<211> 142
<212> PRT
<213> Homo sapiens

<400> 3286
Met Lys Ser His Pro Gly Gln Lys Thr Val His Phe Ser Lys Thr Glu
 1   5   10   15
Lys Asn Leu Arg Tyr Glu Ala Ala Thr Ser Asp Thr Tyr Arg Lys Gly
            20   25   30
Lys Asn Asn Asp Asn Thr Arg Pro Ala Pro Pro Pro Lys Ser Cys Cys
        35   40   45
Cys Glu Leu Arg Leu Gln Lys Arg Thr His Thr Val Ala Asp Lys Thr
    50   55   60
Gln Ala Arg Arg Met Phe Glu Ser Gln Ser Ala Leu Ser Leu Val Pro
65   70   75   80
Val Thr Ser Tyr Val Gln Leu Pro Gly Pro Ile Pro Tyr Ser Asp Cys
                85   90   95
Arg Leu Arg Thr Glu Asp Ala Pro Leu Leu Ser Leu His Phe Asp Leu
            100   105   110
Leu Phe Pro Leu Lys Thr Arg Arg Pro Ala Phe Pro Lys Thr Ala Trp

```
        115                 120                 125
Pro Trp Leu Cys Thr Leu Phe Thr Thr Asp Gln Asn Ser Ile
    130                 135                 140
```

<210> 3287
<211> 921
<212> DNA
<213> Homo sapiens

<400> 3287
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gagcgcgcgg cttggcggag taggggggcac ggccagcgca gtcagagctg gcgccctcct
120
gcgtaagccc aatccgggaa actcgttgcc cctctcctgg gaaaggaacg tccctcccca
180
gggttgcgag tgactcgggc accatcaccc tgtgctgtaa agacctgcga gtgctgcagc
240
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300
ggagctcccg agcccttaa gctctccctg tctcgcgtag aggggaataa aaaggtgctt
360
ctgttcaaag aggctccgca gccgcagcta aatggcaggg ggatgcaggg tggtccgggg
420
tacttggaga ggccgaagct gaagctacag gactgagggg ctggaaaggg cgcgggcgag
480
acaattccga ccctccccag agcccctgac ttccttctcc ggacgctgtc ctccctggaa
540
tcagtcatca cctccttccc tttattctac cgtcccaagg gcctgagatt gggcgactcc
600
tggcacttcc tcccgcccga actctactgc aagagagtag ctcgcgaagt gggcgcggtc
660
gtaggggccc gggaaggtgg aagcgccggg cctggaagag gcgcggggac agggcactcc
720
ctgggtgccc tagacctggc ctctctcctc cctgcgctgc agaccaacgc ggccggaaaa
780
aggctggagg gggcttggca gccaagctaa ttcgggcgaa tttctatgat tatgattttt
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921

<210> 3288
<211> 148
<212> PRT
<213> Homo sapiens

<400> 3288
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Met Thr Asp Ser Arg Glu Asp Ser Val Arg Arg Arg Lys Ser Gly Ala
 1               5                  10                  15
Leu Gly Arg Val Gly Ile Val Ser Pro Ala Pro Phe Pro Ala Pro Gln
            20                  25                  30
Ser Cys Ser Phe Ser Phe Gly Leu Ser Lys Tyr Pro Gly Pro Pro Cys
```

```
        35                  40                  45
Ile Pro Leu Pro Phe Ser Cys Gly Cys Gly Ala Ser Leu Asn Arg Ser
    50                  55                  60
Thr Phe Leu Phe Pro Ser Thr Arg Asp Arg Glu Ser Leu Lys Gly Ser
65                  70                  75                  80
Gly Ala Pro Ser Ala His Leu Asp Gly Ala Gly Asp Ala Gln Arg Arg
                85                  90                  95
Phe Arg Ala Leu Tyr Phe Gln Leu Gln His Ser Gln Val Phe Thr Ala
            100                 105                 110
Gln Gly Asp Gly Ala Arg Val Thr Arg Asn Pro Gly Glu Gly Arg Ser
        115                 120                 125
Phe Pro Arg Arg Gly Ala Thr Ser Phe Pro Asp Trp Ala Tyr Ala Gly
    130                 135                 140
Gly Arg Gln Leu
145
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<210> 3289
<211> 554
<212> DNA
<213> Homo sapiens

<400> 3289
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cacagcatgg actcttccct gtgtcccgtt cctgccttcg cctcctccca gctcttctct
120
cccagcctcc tagcccaata tcagggccgg aggcactgga gaacttccgg ctaaggcagg
180
cctcccctcc cattcacaga gccctgccag ggtggctggc aatggtgaag tccagggcag
240
agatggggac agaggggacg ccttggattc gactctgtgg tgggtggacc acctccctga
300
gaccaggcat ccacgtcggg cagcacatgc tacccagtcc acagaagagg aaacagaggc
360
tccgagagga agggactgtg tccagggcgg gacccaggcc cttctgcact gggtcaatga
420
gccaagcaca tcaccccagc ccttggggag caggagccgg gccttgcagg gtgaggagct
480
gggaaaagca aagctccatg gaaggcaacc gggaatcatc acaaatagga cataactagt
540
ataagctgca attg
554

<210> 3290
<211> 129
<212> PRT
<213> Homo sapiens

<400> 3290
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Met Ile Pro Gly Cys Leu Pro Trp Ser Phe Ala Phe Pro Ser Ser Ser
 1               5                  10                  15
Pro Cys Lys Ala Arg Leu Leu Leu Pro Lys Gly Trp Gly Asp Val Leu
            20                  25                  30
Gly Ser Leu Thr Gln Cys Arg Arg Ala Trp Val Pro Pro Trp Thr Gln
```

```
        35                  40                  45
Ser Leu Pro Leu Gly Ala Ser Val Ser Ser Ser Val Asp Trp Val Ala
    50                  55                  60
Cys Ala Ala Arg Arg Gly Cys Leu Val Ser Gly Arg Trp Ser Thr His
65                  70                  75                  80
His Arg Val Glu Ser Lys Ala Ser Pro Leu Ser Pro Ser Leu Pro Trp
                85                  90                  95
Thr Ser Pro Leu Pro Ala Thr Leu Ala Gly Leu Cys Glu Trp Glu Gly
            100                 105                 110
Arg Pro Ala Leu Ala Gly Ser Ser Pro Val Pro Pro Ala Leu Ile Leu
        115                 120                 125
Gly
```

<210> 3291
<211> 1075
<212> DNA
<213> Homo sapiens

<400> 3291
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ggctggaggc ccccgcgcgt gccttcgcct gcgccgtgga gcgcgacgcc cgggccgccg
120
tgggcccctt ctcccgccac gcctgcggtg aggctccccg ccccgtctcc taccatagct
180
gcctctgtcc ctccgcactg gctgttcacc tggctagctg tgtccgtttc tcaacccgga
240
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300
cttccctagc ctacatagcc cttggccatg gcccggcctg gtcccacctc tgatgtcccg
360
ccccccacag gtggacagac gccttcgnnt gggcctgagc acttgcggcc ggcacatgtc
420
cgctcaccgc gtgtccgggg ccctggcgcg ggtcctggaa gtaccctagc gggccacacc
480
ctgacagccg agctgatggc gcaccccggc taccccagtg tgcctccacc ggcggctgcg
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600
ccgcgcccac gctgcgggcc cagcttgccc aggatggcgt gcagctttgc gccctcgacg
660
acctggactc caagaggcca ggggaggagg tcccctgtga gcccactctg gaacccttcc
720
tggaaccctc ccnntactct gacccccctac agacaaccaa gcactaatcc ccttagtacc
780
aagaaagggg agccaggatt tagtcctggc ccagcccaga gctgggacct ggagcacgat
840
ctgttgactt ccctgggtag gacactgcca cctctgggct caggtcctca tgcctccaaa
900
tggcatctag agtttgagca gccttcttgg ctgcaggcag gcctagcctg tggcagcggg
960
ctagggcccg cagagcattt ggtgcccctc catgttgcaa tgcaaacacc ttcaccactg
1020

gggcagtggg gagagatggc tatattaata aaataacgtg tgtctttcaa aaaaa
1075

<210> 3292
<211> 102
<212> PRT
<213> Homo sapiens

<400> 3292
Xaa Xaa Met Gly Cys Ala Leu Arg Asp Cys Arg Trp Ser Ala Val Trp
 1   5   10   15
Val Ala Ala Leu Gly Trp Arg Pro Pro Arg Val Pro Ser Pro Ala Pro
            20   25   30
Trp Ser Ala Thr Pro Gly Pro Pro Trp Ala Pro Ser Pro Ala Thr Pro
        35   40   45
Ala Val Arg Leu Pro Ala Pro Ser Pro Thr Ile Ala Ala Ser Val Pro
    50   55   60
Pro His Trp Leu Phe Thr Trp Leu Ala Val Ser Val Ser Gln Pro Gly
65   70   75   80
Ser Glu Ser Xaa Arg Arg Pro Leu Pro Pro Pro Gln Leu Pro Pro Pro
                85   90   95
Thr Pro Pro Ser Leu Pro
            100

<210> 3293
<211> 2362
<212> DNA
<213> Homo sapiens

<400> 3293
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atggcttgct cgaggccccc cagccagtgt gaacccacat ccctgccccc agggccacct
120
gcaggacgcc gacacctacc cctcagcaga cgccggagag aaatgagtag caacaaagag
180
cagcggtcag cagtgttcgt gatcctcttt gccctcatca ccatcctcat cctctacagc
240
tccaacagtg ccaatgaggt cttccattac ggctccctgc ggggccgtag ccgccgacct
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actggctact cagctgatgt gggcaacaag accacctacc gcgtcgtggc ccattccagt
540
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660
cagcgagcgg gcctggtgtt ccccaacatg gaagcatatg ccgtctctcc cggccgcatg
720

cggcaatttg acgacctctt ccggggtgag acgggcaagg acagggagaa gtctcattcg
780
tggttgagca caggctggtt taccatggtg atcgcggtgg agttgtgtga ccacgtgcat
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900
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960
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1020
cagctgtatg gcatcacctt ctcccacccc tcctggacct aggccaccca gcctgtggga
1080
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1140
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1320
ggggtatttc tgagtcaatc tgaggctaag gacatgtcct ttcccatgag gccttggttc
1380
agagccccag gaatggaccc cccaatcact ccccactctg ctgggataat ggggtcctgt
1440
cccaaggagc tgggaacttg gtgttgcccc ctcaatttcc agcaccagaa agagagattg
1500
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1620
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<210> 3294
<211> 353
<212> PRT
<213> Homo sapiens

<400> 3294
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Ser Arg Arg Arg Arg Glu Met Ser Ser Asn Lys Glu Gln Arg Ser Ala
50 55 60
Val Phe Val Ile Leu Phe Ala Leu Ile Thr Ile Leu Ile Leu Tyr Ser
65 70 75 80
Ser Asn Ser Ala Asn Glu Val Phe His Tyr Gly Ser Leu Arg Gly Arg
85 90 95
Ser Arg Arg Pro Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr
100 105 110
Val Pro Ile Leu Gly Asn Lys Thr Leu Pro Ser Arg Cys His Gln Cys
115 120 125
Val Ile Val Ser Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro
130 135 140
Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro Thr
145 150 155 160
Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg Val Val
165 170 175
Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln Glu Phe Val
180 185 190
Asn Arg Thr Pro Glu Thr Val Phe Ile Phe Trp Gly Pro Pro Ser Lys
195 200 205
Met Gln Lys Pro Gln Gly Ser Leu Val Arg Val Ile Gln Arg Ala Gly
210 215 220
Leu Val Phe Pro Asn Met Glu Ala Tyr Ala Val Ser Pro Gly Arg Met
225 230 235 240
Arg Gln Phe Asp Asp Leu Phe Arg Gly Glu Thr Gly Lys Asp Arg Glu
245 250 255
Lys Ser His Ser Trp Leu Ser Thr Gly Trp Phe Thr Met Val Ile Ala
260 265 270
Val Glu Leu Cys Asp His Val His Val Tyr Gly Met Val Pro Pro Asn
275 280 285
Tyr Cys Ser Gln Arg Pro Arg Leu Gln Arg Met Pro Tyr His Tyr Tyr
290 295 300
Glu Pro Lys Gly Pro Asp Glu Cys Val Thr Tyr Ile Gln Asn Glu His
305 310 315 320
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340 345 350
Thr

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<211> 690
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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Pro Arg His Met Gly Pro Ala Leu Arg Ser Leu Gln Val Lys Lys Gly
        35   40   45
Thr Glu His Ala Asp Pro Leu Pro Phe Pro Ser Val Ser Leu Ser Gly
    50   55   60
Phe Thr Val Gly Thr Leu Ser Glu Thr Ser Thr Gly Gly Pro Ala Thr
65   70   75   80
Pro Thr Trp Lys Glu Cys Pro Ile Cys Lys Glu Arg Phe Pro Ala Glu
                85   90   95
Ser Asp Lys Asp Ala Leu Glu Asp His Met Asp Gly His Phe Phe Phe
            100   105   110
Ser Thr Gln Gly Pro Leu His Leu

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<210> 3297
<211> 3176
<212> DNA
<213> Homo sapiens

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<210> 3298
<211> 251
<212> PRT
<213> Homo sapiens

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35 40 45
Xaa Leu Cys Ala Cys Met Cys Leu Asp Val Cys Phe Cys Met Cys Leu
50 55 60
Cys Val Cys Leu Tyr Val Cys Ile Cys Val Tyr Val Cys Val Cys His
65 70 75 80
Phe Val Cys Phe Trp Val Cys Leu Ser Ala Cys Leu Cys Ile Pro Val
85 90 95
Ser Pro Cys Val Cys Leu Cys Val Cys Ile Cys Xaa Cys Leu Cys Met
100 105 110
Cys Val Arg Gly Cys Val Ser Val Cys Val Cys Val Cys Ile Glu Arg
115 120 125
Glu Gly Glu Arg Lys Gly Ala Thr Asp Gly Ser Ala Trp Lys Val Tyr
130 135 140
Pro His Ser Gln Pro Trp Glu Glu Ser Val Asn Pro Pro Thr Gly Gln
145 150 155 160
Asp Gln Leu Trp Trp Cys Leu Ala Asp Ser Gly Asn Val Thr Phe His
165 170 175
Leu Arg Met Gly Leu His Phe Leu Gly Lys Glu Cys Arg Ser Trp Ser
180 185 190
Leu Lys Glu Cys Phe Phe Phe Pro Phe Val Ile Glu Arg Ala Gln Pro
195 200 205
Cys Val His Trp Leu Thr Val Thr Asn Leu Arg Val Gly Asp Ser His
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Thr Ser Leu Pro Leu Gly Pro Asn Pro Gln Leu
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<210> 3299
<211> 1387
<212> DNA
<213> Homo sapiens

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<210> 3300
<211> 219
<212> PRT
<213> Homo sapiens

<400> 3300
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Ser Ile Gln Gln Phe Thr Glu Met Asn Leu Leu Ser Asp Tyr Arg Phe
    50                  55                  60
Leu Glu Asp Val Ala Arg Thr Ala Asp His Ile Ser Arg Asp Ala Phe
65                  70                  75                  80
Leu Lys Arg Pro Ile Ser Asn Lys Tyr Met Tyr Phe Met Lys Asn Arg
                85                  90                  95
Ala Arg Ser Lys Gly Ile Asn Leu Lys Leu Leu Pro Asn Gly Phe Thr
            100                 105                 110
Lys Arg Lys Glu Asn Ser Thr Phe Phe Asp Lys Lys Lys Gln Gln Phe
        115                 120                 125
Cys Trp His Val Lys Leu Gln Phe Pro Gln Ser Gln Ala Glu Tyr Ile
    130                 135                 140
Glu Lys Arg Val Pro Asp Asp Lys Thr Ile Asn Glu Ile Leu Lys Pro
145                 150                 155                 160
Tyr Ile Asp Pro Glu Lys Ser Asp Pro Val Ile Arg Gln Arg Leu Lys
                165                 170                 175
Ala Tyr Ile Arg Ser Gln Thr Gly Val Gln Ile Leu Met Lys Ile Glu
            180                 185                 190
Tyr Met Gln Gln Asn Leu Val Arg Tyr Tyr Glu Leu Asp Pro Tyr Lys
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Ser Leu Leu Asp Asn Leu Arg Asn Lys Val Ile
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<210> 3301
<211> 2109
<212> DNA
<213> Homo sapiens

<400> 3301

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<210> 3302

<211> 323
<212> PRT
<213> Homo sapiens

<400> 3302
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Gln Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser
35 40 45
Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala
50 55 60
Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg
65 70 75 80
Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val
85 90 95
Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro
100 105 110
Met Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala
115 120 125
Pro Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met
130 135 140
Ala Ser Met Glu Ser Pro Xaa Val Asn Ala Phe Pro Ala Gln Asn Asn
145 150 155 160
Tyr Gly Leu Tyr Asp Leu Leu Gly Asn Val Trp Glu Trp Thr Ala Ser
165 170 175
Pro Tyr Gln Ala Ala Glu Gln Asp Met Arg Val Leu Arg Gly His Pro
180 185 190
Gly Ser Thr Gln Leu Met Ala Leu Pro Ile Thr Gly Pro Gly Ser Pro
195 200 205
Pro Gly Trp Ala Thr Leu Gln Ile Gln Pro Gln Thr Thr Ser Val Ser
210 215 220
Ala Val Leu Gln Thr Gln Ala Gly Arg Gln Gly Ser Cys Lys Gln Pro
225 230 235 240
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245 250 255
His Val Ala Asn Ser Ala Ile Pro Ser Ser Arg Ala Ser Ala Ser Gly
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Lys Asn Phe Pro Phe Pro Val Ser His Pro Ser Val Ala Gly Ala Ser
275 280 285
His Gln Gly Arg Arg Gly Leu Ser Leu Leu Cys Phe Gly Glu Gly Ala
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<210> 3303
<211> 699
<212> DNA
<213> Homo sapiens

<400> 3303

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<210> 3304
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<213> Homo sapiens

<400> 3304
Pro Arg Lys Arg Asp Phe Thr Asn Glu Ala Pro Pro Ala Pro Leu Pro
1 5 10 15
Asp Ala Ser Ala Ser Pro Leu Ser Pro His Arg Arg Ala Lys Ser Leu
20 25 30
Asp Arg Arg Ser Thr Glu Pro Ser Val Thr Pro Asp Leu Leu Asn Phe
35 40 45
Lys Lys Gly Trp Leu Thr Lys Gln Tyr Glu Asp Gly Gln Trp Lys Lys
50 55 60
His Trp Phe Val Leu Ala Asp Gln Ser Leu Arg Tyr Tyr Arg Asp Ser
65 70 75 80
Val Ala Glu Glu Ala Ala Asp Leu Asp Gly Glu Ile Asp Leu Ser Ala
85 90 95
Cys Tyr Asp Val Thr Glu Tyr Pro Val Gln Arg Asn Tyr Gly Phe Gln
100 105 110
Ile His Thr Lys Glu Gly Glu Phe Thr Leu Ser Ala Met Thr Ser Gly
115 120 125
Ile Arg Arg Asn Trp Ile Gln Thr Ile Met Lys His Val His Pro Thr
130 135 140
Thr Ala Pro Asp Val Thr Ser Ser Leu Pro Glu Glu Lys Asn Lys Ser
145 150 155 160
Ser Cys Ser Phe Glu Thr Cys Pro Arg Ser Thr Glu Lys Gln Glu Ala
165 170 175
Glu Leu Gly Glu Pro Asp Pro Glu Gln Lys Arg Ser Arg Ala Arg Glu

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            180                 185                 190
Arg Arg Arg Glu Gly Arg Ser Lys Thr Phe Asp Trp Ala Glu Phe Arg
        195                 200                 205
Pro Ile Gln Gln Ala Leu Ala Gln Glu Arg Val Gly Gly Val Gly Pro
    210                 215                 220
Ala Asp Thr His Glu Pro Leu Arg Pro
225                 230
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<210> 3305
<211> 2717
<212> DNA
<213> Homo sapiens

<400> 3305
nnggatcccc gctactttct ccagatgaca gagaccactg ttaagacagc agcttggttc
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atggccaacg tgcaggtctc tggaggggga cctagcatct ccttggtgat gaagactccc
120
agggtcgcca agaatgaggc gctctggcac ccgacgctga acttgccact gagcccccag
180
gggactgtgc gaactgcagt ggagttccag gtgatgacac agacccaatc cctgagcttc
240
ctgctggggt cctcagcctc cttggactgt ggcttctcca tggcaccggg cttggacctc
300
atcagtgtgg agtggcgact gcagcacaag ggcaggggtc agttggtgta cagctggacc
360
gcagggcagg ggcaggctgt gcggaagggc gctaccctgn gagcctgcac aactgggcat
420
ggcnncaggg atgcctccct caccctgccc ggcctcacta tacaggacga ggggacctac
480
atttgccaga tcaccacctc tctgtaccga gctcagcaga tcatccagct caacatccaa
540
gcttccccta aagtacgact gagcttggca aacgaagctc tgctgcccac cctcatctgc
600
gacattgctg gctattaccc tctggatgtg gtggtgacgt ggacccgaga ggagctgggt
660
ggatccccag cccaagtctc tggtgcctcc ttctccagcc tcaggcaaag cgtggcaggc
720
acctacagca tctcctcctc tctcaccgca gaacctgggc tctgcaggtg ccacttacac
780
ctgccaggtc acacacatct ctctggagga gccccttggg gccagcaccc aggttgtccc
840
accagagcgg agaacagcct tgggagtcat ctttgccagc agtctcttcc ttcttgcact
900
gatgttcctg gggcttcaga gacggcaagc acctacagga cttgggctgc ttcaggctga
960
acgctgggag accacttcct gtgctgacac acagagctcc catctccatg aagaccgcac
1020
agcgcgtgta agccagccca gctgacctaa agcgacatga gactactaga aagaaacgac
1080
acccttcccc aagcccccac agctactcca acccaaacaa caaccaagcc agtttaatgg
1140
taggaatttg tatttttgc ctttgttcag aatacatgac attggtaaat atgccacatg
1200

cctttggtgg aagtacaact gttgttatta ctctatacaa gtatgagatc agggttagga
1260
aaaaaagaca aagaggtgat gacagacaca cagtggaaac cccacatcgt ctcatggcaa
1320
accgaagaac gggatgtggg aagctcagct tcatttgact gcaaagtccc agggttttgt
1380
tgcacatttg ctcatgcaca tgggtggtgg gaggaaaggg ggatagcaaa gacacacaga
1440
agagggtaca gggtgggtga gaaagaaagt agaagggcta ataccccaa agaacaaggc
1500
caactacacc tggtgagcct cagagggaca gaaacccagg aatgattcct gtgatagggc
1560
tgggagagcc aagaggacgg attcgctcca ggcttgggac acatcgagga cagtggtggt
1620
tcttctccag cggtgacccc ctgcattagg caaggaggag cccagaggag agtggagacc
1680
ttcgaggggg gccgttggga gggtactgac tgctttcttc cagctcttca gtcccgccct
1740
tgggcaggac gaagggaatg tgggaaacaa gggcgaaagg aaaggaagga tggttttgag
1800
caatgaaatg ctgctgcatg gaaagtgggc atccagaccc tgcccagcat ggcctcagcc
1860
tcttcctgtt cgtggaccga gggaagaagg aataaagggc catgggcatt ctccgctctg
1920
ttcccagcct gccctcctcc ccttgcacct gggcttatcc cacattaata gcccatcctg
1980
aagctcagca attgccccga agataggctg agcagatccc atcctcaggt tccactgtct
2040
atacacacaa accatgcaaa gaggaggaag agaaaggagg caaagtagaa ttcagacagg
2100
aaagggtggt tcaaagggga atatactaca ggaagaacag agaggcggct ctcaaggaga
2160
gggccccatg acagcacagc aatacacaag cacacctgac acaggctggc acgcctcccc
2220
ccaaggtggg gctggtgggt ctacatgact tctctgcatc ctgaggatcg gccgggcccc
2280
aggaagaacc acttgcctca tccctgtctt tggcaagtgc acgggtggtg tggaggaaag
2340
gattccatgg gtgtccaaag atctcacact gctaacaccc tcacgctcct tcatcaacag
2400
gaagagagga acaggaccct ctttaacgag ggcaaggagt ggcttcctct gagcttgtta
2460
ctttcaaatt aagcacttga ctcactgttt ctctataact aacaggcaat ctctctcttt
2520
atgccaacaa ttaactggga gctaggttaa attatttggc tagataaaac taccagctag
2580
atggatttat ttggtgccct catacagaat gctgtagaaa atgtaaagaa gagaaagctc
2640
cttccagcta gaagcacatg ggactgcttc taggatggaa acaagtcctg ctattttcac
2700
aatccctaag tgttctc
2717

<210> 3306

<211> 319
<212> PRT
<213> Homo sapiens

<400> 3306
Xaa Asp Pro Arg Tyr Phe Leu Gln Met Thr Glu Thr Thr Val Lys Thr
1 5 10 15
Ala Ala Trp Phe Met Ala Asn Val Gln Val Ser Gly Gly Gly Pro Ser
20 25 30
Ile Ser Leu Val Met Lys Thr Pro Arg Val Ala Lys Asn Glu Ala Leu
35 40 45
Trp His Pro Thr Leu Asn Leu Pro Leu Ser Pro Gln Gly Thr Val Arg
50 55 60
Thr Ala Val Glu Phe Gln Val Met Thr Gln Thr Gln Ser Leu Ser Phe
65 70 75 80
Leu Leu Gly Ser Ser Ala Ser Leu Asp Cys Gly Phe Ser Met Ala Pro
85 90 95
Gly Leu Asp Leu Ile Ser Val Glu Trp Arg Leu Gln His Lys Gly Arg
100 105 110
Gly Gln Leu Val Tyr Ser Trp Thr Ala Gly Gln Gly Gln Ala Val Arg
115 120 125
Lys Gly Ala Thr Leu Xaa Ala Cys Thr Thr Gly His Gly Xaa Arg Asp
130 135 140
Ala Ser Leu Thr Leu Pro Gly Leu Thr Ile Gln Asp Glu Gly Thr Tyr
145 150 155 160
Ile Cys Gln Ile Thr Thr Ser Leu Tyr Arg Ala Gln Gln Ile Ile Gln
165 170 175
Leu Asn Ile Gln Ala Ser Pro Lys Val Arg Leu Ser Leu Ala Asn Glu
180 185 190
Ala Leu Leu Pro Thr Leu Ile Cys Asp Ile Ala Gly Tyr Tyr Pro Leu
195 200 205
Asp Val Val Val Thr Trp Thr Arg Glu Glu Leu Gly Gly Ser Pro Ala
210 215 220
Gln Val Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser Val Ala Gly
225 230 235 240
Thr Tyr Ser Ile Ser Ser Ser Leu Thr Ala Glu Pro Gly Leu Cys Arg
245 250 255
Cys His Leu His Leu Pro Gly His Thr His Leu Ser Gly Gly Ala Pro
260 265 270
Trp Gly Gln His Pro Gly Cys Pro Thr Arg Ala Glu Asn Ser Leu Gly
275 280 285
Ser His Leu Cys Gln Gln Ser Leu Pro Ser Cys Thr Asp Val Pro Gly
290 295 300
Ala Ser Glu Thr Ala Ser Thr Tyr Arg Thr Trp Ala Ala Ser Gly
305 310 315

<210> 3307
<211> 352
<212> DNA
<213> Homo sapiens

<400> 3307
ggatcctggg ctggtgtcca ggatggggct cccgcgtgct cttgcgctgc cctctggtgg
60

ccgctctggg tccttgcacc ccgacccagg ggccagcctg ccctgtcctg tcctgatacc
120
gaggtgggag ccctgccttg gccagggtgg ccgtgttgac ggttcttggg actgtgacat
180
tggaaggcga ggcaggtcac cagcactgtc ctctgcagga tgggctggga ttcatttggc
240
agcttctcag ggcctgtgtc cggctggttg gtccctgtgc tgcccaaacc aggtgtccac
300
atttccggct cctatgcgca gagaaggggg caggtggtgg cttgggtgga ga
352

<210> 3308
<211> 110
<212> PRT
<213> Homo sapiens

<400> 3308
Met Gly Leu Pro Arg Ala Leu Ala Leu Pro Ser Gly Gly Arg Ser Gly
1 5 10 15
Ser Leu His Pro Asp Pro Gly Ala Ser Leu Pro Cys Pro Val Leu Ile
20 25 30
Pro Arg Trp Glu Pro Cys Leu Gly Gln Gly Gly Arg Val Asp Gly Ser
35 40 45
Trp Asp Cys Asp Ile Gly Arg Arg Gly Arg Ser Pro Ala Leu Ser Ser
50 55 60
Ala Gly Trp Ala Gly Ile His Leu Ala Ala Ser Gln Gly Leu Cys Pro
65 70 75 80
Ala Gly Trp Ser Leu Cys Cys Pro Asn Gln Val Ser Thr Phe Pro Ala
85 90 95
Pro Met Arg Arg Glu Gly Gly Arg Trp Trp Leu Gly Trp Arg
100 105 110

<210> 3309
<211> 737
<212> DNA
<213> Homo sapiens

<400> 3309
ggatcctggg cctggagaag aggcatgaat gtccaccaca ggggctctgc cggtcaggat
60
caaggtcaca ctggatgagg gagtcctgac cctctcccgg gctgagccca cctgtgctgc
120
ccccaggacc ccaagtacca gggtctgcgg gcacgtggcc gggagatccg gaaggagctt
180
gttcacctgt accccaggga ggcccagctt gaggagcagt tctacctgca ggcgctgaag
240
ctgcccaacc agacccaccc agacgtgccc gtcggggatg agagccaggc tcgagtgctc
300
cacatggtcg gagacaagcc agttttctcc ttccaacctc ggggccacct ggaaattggc
360
gagaaactcg acatcatccg tcagaagcgc ctgtcccacg tgtctggcca ccggtcctat
420
tacctgcgcg gggctggagc cctcctgcag cacggcctgg tcaacttcac attcaacaag
480

cttctccgcc ggggcttcac ccccatgacg gtgccagacc ttctccgcgg agcagtgttt
540
gaaggctgtg ggatgacacc aaatgccaac ccatcccaaa tttacaacat cgaccctgcc
600
cgcttcaaag atctcaacct tgctggaaca gcggaggtgg ggcttgcagg ctacttcatg
660
gaccacaccg tggccttcag ggacctgcca gtcaggatgg tttgctccag cacctgctac
720
cgggcagaga caaacac
737

<210> 3310
<211> 210
<212> PRT
<213> Homo sapiens

<400> 3310
Ala His Leu Cys Cys Pro Gln Asp Pro Lys Tyr Gln Gly Leu Arg Ala
1 5 10 15
Arg Gly Arg Glu Ile Arg Lys Glu Leu Val His Leu Tyr Pro Arg Glu
20 25 30
Ala Gln Leu Glu Glu Gln Phe Tyr Leu Gln Ala Leu Lys Leu Pro Asn
35 40 45
Gln Thr His Pro Asp Val Pro Val Gly Asp Glu Ser Gln Ala Arg Val
50 55 60
Leu His Met Val Gly Asp Lys Pro Val Phe Ser Phe Gln Pro Arg Gly
65 70 75 80
His Leu Glu Ile Gly Glu Lys Leu Asp Ile Ile Arg Gln Lys Arg Leu
85 90 95
Ser His Val Ser Gly His Arg Ser Tyr Tyr Leu Arg Gly Ala Gly Ala
100 105 110
Leu Leu Gln His Gly Leu Val Asn Phe Thr Phe Asn Lys Leu Leu Arg
115 120 125
Arg Gly Phe Thr Pro Met Thr Val Pro Asp Leu Leu Arg Gly Ala Val
130 135 140
Phe Glu Gly Cys Gly Met Thr Pro Asn Ala Asn Pro Ser Gln Ile Tyr
145 150 155 160
Asn Ile Asp Pro Ala Arg Phe Lys Asp Leu Asn Leu Ala Gly Thr Ala
165 170 175
Glu Val Gly Leu Ala Gly Tyr Phe Met Asp His Thr Val Ala Phe Arg
180 185 190
Asp Leu Pro Val Arg Met Val Cys Ser Ser Thr Cys Tyr Arg Ala Glu
195 200 205
Thr Asn
210

<210> 3311
<211> 486
<212> DNA
<213> Homo sapiens

<400> 3311
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tggctgcact tgctccacgg gtcaggggat cggaggggga ttgaagaatg cgccattaaa
120
aggaaagatc aaggagtaaa ccagaagaag aagaaaaaga ggacttcaaa gctgggaagg
180
atgagttctt gcagcaacgt ctgtgggtcc aggcaggcac aggctgcagc tgagggtggt
240
taccagcgct atggagtccg gtcctacctg caccagtttt atgaggactg tacagcctca
300
atttgggagt atgaggatga tttccagatc caaagatcac ctaacaggtg gagctcagta
360
ttctggaagg ttggactcat ctcaggtaca gtttttgtga tcctcggatt gactgttctg
420
gcagtgggct ttcttgtgcc ccccaaaatc gaagcatttg gcgaagccga ttttgtggtg
480
gtcgac
486

<210> 3312
<211> 102
<212> PRT
<213> Homo sapiens

<400> 3312
Met Ser Ser Cys Ser Asn Val Cys Gly Ser Arg Gln Ala Gln Ala Ala
1 5 10 15
Ala Glu Gly Gly Tyr Gln Arg Tyr Gly Val Arg Ser Tyr Leu His Gln
20 25 30
Phe Tyr Glu Asp Cys Thr Ala Ser Ile Trp Glu Tyr Glu Asp Asp Phe
35 40 45
Gln Ile Gln Arg Ser Pro Asn Arg Trp Ser Ser Val Phe Trp Lys Val
50 55 60
Gly Leu Ile Ser Gly Thr Val Phe Val Ile Leu Gly Leu Thr Val Leu
65 70 75 80
Ala Val Gly Phe Leu Val Pro Pro Lys Ile Glu Ala Phe Gly Glu Ala
85 90 95
Asp Phe Val Val Val Asp
100

<210> 3313
<211> 1791
<212> DNA
<213> Homo sapiens

<400> 3313
nggctcggga gacgtacgag gaggaccggg agtacgagag ccaggccaag cgtctcaaga
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ccgaggaggg ggagatcgac tactcggccg aggaaggcca gaaccgcggt gaagcgacgc
120
cccggggcgg gtcgagttgg cggcggcggc ggccgantgc gttctcgtca gccggaaggg
180
ctgcgaagtc atcataaagt ttctgtttca cccgtcgtcc atgttcgagg actctgtgaa
240
tctgtggtgg aagcagacct cgtggaagcg ctggaaaaat ttgggacaat atgctatgtg
300

atgatgatgc catttaaacg acaggctcta gtggaatttg aaaacataga tagtgccaaa
360
gaatgtgtga catttgctgc agatgaaccc gtgtacattg ctggtcaaca ggctttttc
420
aactattcta caagcaaaag gatcactcgg ccaggaaata ctgatgatcc atcaggaggc
480
aacaaagttc ttctgctctc aattcagaat ccgctttatc caattacagt ggatgtttta
540
tatactgtat gcaaccctgt tggcaaagtg caacgtattg ttatattcaa gagaaatggg
600
atacaagcaa tggttgagtt tgaatcagtc ctttgtgccc agaaagctaa agcagcactc
660
aatggagctg atatatatgc tggatgttgc acactaaaaa ttgaatatgc acggccaact
720
cgtctaaatg ttattaggaa tgacaatgac agttgggact acactaaacc atatttggga
780
agacgagata gaggaaaggg tcgccagaga caagccattt tgggagaaca cccttcttcg
840
tttagacatg atggctatgg atcccatggt ccattattgc ctttaccaag tcgttacaga
900
atgggctctc gagatacacc tgaacttgtt gcttatccat taccacaggc ttcttcctct
960
tacatgcatg gaggaaatcc ctctggttca gttgtaatgg ttagtggatt acatcaacta
1020
aaaatgaatt gttcaagagt cttcaacctg ttctgcttat atggaaatat tgagaaggta
1080
aaatttatga agaccattcc tggtacagca ctggtagaaa tgggtgatga gtatgctgta
1140
gaaagagctg tcacacacct taataatgtc aaattatttg ggaaaagact taatgtttgc
1200
gtgtctaaac aacattcagt tgttccaagt caaatatttg agctggagga tggtaccagc
1260
agctacaaag attttgcaat gagcaaaaat aatcgcttta caagtgctgg ccaagcatct
1320
aagaatataa tccagccacc ctcctgtgtt ttgcattatt ataatgttcc attgtgtgtc
1380
acagaagaga ccttcacaaa gttgtgtaat gaccatgaag ttcttacatt catcaaatat
1440
aaagtgtttg atgcaaaacc ttcagccaaa acactttctg ggctattaga atgggagtgc
1500
aaaactgatg cagtagaagc ccttacggca ctgaatcact atcagataag agtgccgaat
1560
ggttccaatc cctatacatt gaagctttgc ttttctacat catcccattt ataagaagag
1620
aagagcatgt tagaatttat gttcaccttt attacaattt caaagctaca cttcattaaa
1680
aaaaaatcta aaatggttga tctcatgttg ccttgcttac tttaagatcc tgttctgtaa
1740
taaacatatt ttgccttgag taaatttgtt gtaagcttaa aaaaaaaaaa a
1791

<210> 3314
<211> 537
<212> PRT

<213> Homo sapiens

<400> 3314

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Xaa Leu Gly Arg Arg Thr Arg Arg Thr Gly Ser Thr Arg Ala Arg Pro
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Ser Val Ser Arg Pro Arg Arg Gly Arg Ser Thr Thr Arg Pro Arg Lys
            20                  25                  30
Ala Arg Thr Ala Val Lys Arg Arg Pro Gly Ala Gly Arg Val Gly Gly
        35                  40                  45
Gly Gly Gly Arg Xaa Arg Ser Arg Gln Pro Glu Gly Leu Arg Ser His
    50                  55                  60
His Lys Val Ser Val Ser Pro Val Val His Val Arg Gly Leu Cys Glu
65                  70                  75                  80
Ser Val Val Glu Ala Asp Leu Val Glu Ala Leu Glu Lys Phe Gly Thr
                85                  90                  95
Ile Cys Tyr Val Met Met Met Pro Phe Lys Arg Gln Ala Leu Val Glu
            100                 105                 110
Phe Glu Asn Ile Asp Ser Ala Lys Glu Cys Val Thr Phe Ala Ala Asp
115                 120                 125
Glu Pro Val Tyr Ile Ala Gly Gln Gln Ala Phe Phe Asn Tyr Ser Thr
    130                 135                 140
Ser Lys Arg Ile Thr Arg Pro Gly Asn Thr Asp Asp Pro Ser Gly Gly
145                 150                 155                 160
Asn Lys Val Leu Leu Leu Ser Ile Gln Asn Pro Leu Tyr Pro Ile Thr
                165                 170                 175
Val Asp Val Leu Tyr Thr Val Cys Asn Pro Val Gly Lys Val Gln Arg
            180                 185                 190
Ile Val Ile Phe Lys Arg Asn Gly Ile Gln Ala Met Val Glu Phe Glu
        195                 200                 205
Ser Val Leu Cys Ala Gln Lys Ala Lys Ala Ala Leu Asn Gly Ala Asp
    210                 215                 220
Ile Tyr Ala Gly Cys Cys Thr Leu Lys Ile Glu Tyr Ala Arg Pro Thr
225                 230                 235                 240
Arg Leu Asn Val Ile Arg Asn Asp Asn Asp Ser Trp Asp Tyr Thr Lys
                245                 250                 255
Pro Tyr Leu Gly Arg Arg Asp Arg Gly Lys Gly Arg Gln Arg Gln Ala
            260                 265                 270
Ile Leu Gly Glu His Pro Ser Ser Phe Arg His Asp Gly Tyr Gly Ser
        275                 280                 285
His Gly Pro Leu Leu Pro Leu Pro Ser Arg Tyr Arg Met Gly Ser Arg
    290                 295                 300
Asp Thr Pro Glu Leu Val Ala Tyr Pro Leu Pro Gln Ala Ser Ser Ser
305                 310                 315                 320
Tyr Met His Gly Gly Asn Pro Ser Gly Ser Val Val Met Val Ser Gly
                325                 330                 335
Leu His Gln Leu Lys Met Asn Cys Ser Arg Val Phe Asn Leu Phe Cys
            340                 345                 350
Leu Tyr Gly Asn Ile Glu Lys Val Lys Phe Met Lys Thr Ile Pro Gly
        355                 360                 365
Thr Ala Leu Val Glu Met Gly Asp Glu Tyr Ala Val Glu Arg Ala Val
    370                 375                 380
Thr His Leu Asn Asn Val Lys Leu Phe Gly Lys Arg Leu Asn Val Cys
385                 390                 395                 400
Val Ser Lys Gln His Ser Val Val Pro Ser Gln Ile Phe Glu Leu Glu
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                405                 410                 415
Asp Gly Thr Ser Ser Tyr Lys Asp Phe Ala Met Ser Lys Asn Asn Arg
            420                 425                 430
Phe Thr Ser Ala Gly Gln Ala Ser Lys Asn Ile Ile Gln Pro Pro Ser
        435                 440                 445
Cys Val Leu His Tyr Tyr Asn Val Pro Leu Cys Val Thr Glu Glu Thr
    450                 455                 460
Phe Thr Lys Leu Cys Asn Asp His Glu Val Leu Thr Phe Ile Lys Tyr
465                 470                 475                 480
Lys Val Phe Asp Ala Lys Pro Ser Ala Lys Thr Leu Ser Gly Leu Leu
                485                 490                 495
Glu Trp Glu Cys Lys Thr Asp Ala Val Glu Ala Leu Thr Ala Leu Asn
            500                 505                 510
His Tyr Gln Ile Arg Val Pro Asn Gly Ser Asn Pro Tyr Thr Leu Lys
        515                 520                 525
Leu Cys Phe Ser Thr Ser Ser His Leu
    530                 535
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<210> 3315
<211> 934
<212> DNA
<213> Homo sapiens

<400> 3315
ngggcggcgg catggcagca tcttccctga cggtcacctt agggcggctg gcgtccgcgt
60
gcagccacag catcctgaga ccttcggggc ccggagcagc ctccctttgg tctgcttctc
120
gaaggttcaa ttcacagagc acttcatatc taccagggta atatcaaaat atatgttcct
180
aaaacatccc tgagttcacc accttggcca gaagttgttc tgccagaccc agttgaggag
240
accagacacc atgcagaggt cgtgaagaag gtgaatgaga tgatcgtcac ggggcagtat
300
ggcaggctct ttgccgtggt gcactttgcc agccgccagt ggaaggtgac ctctgaagac
360
ctgatcttaa ttggaaatga actagacctt gcgtgtggag agagaattcg actggagaag
420
gtcctgctgg ttggggcaga caacttcacg ctgcttggca agccactcct cggaaaggat
480
cttgttcgag tagaagccac agtcattgaa aagacagaat catggccaag aatcattatg
540
agattcagga aaaggaaaaa cttcaagaag aaaagaatcg tcacgacccc gcagactgtc
600
ctccggataa acagcattga gattgctccg tgtttgttgt gattaccgag ttaatactta
660
caaaaggata aaaataaact cctgcttccc aaggagacca ggtttctgtg ttctggttta
720
aagccgtgca tgcctgttgt agatagttta actggagcag catgtctgta agcaccaggc
780
ccccgagcca gagaaaacag gaactggggg agaatgacaa gcatggccct cccagggctg
840
gataaatagt attcttggca gccctccacc ccatgtggcg gcggcagggc ccaggggagt
900

ggggcgggga tgcagattga tcttggagct gcag
934

<210> 3316
<211> 187
<212> PRT
<213> Homo sapiens

<400> 3316
Asp Leu Arg Gly Pro Glu Gln Pro Pro Phe Gly Leu Leu Leu Glu Gly
1 5 10 15
Ser Ile His Arg Ala Leu His Ile Tyr Gln Gly Asn Ile Lys Ile Tyr
20 25 30
Val Pro Lys Thr Ser Leu Ser Ser Pro Pro Trp Pro Glu Val Val Leu
35 40 45
Pro Asp Pro Val Glu Glu Thr Arg His His Ala Glu Val Val Lys Lys
50 55 60
Val Asn Glu Met Ile Val Thr Gly Gln Tyr Gly Arg Leu Phe Ala Val
65 70 75 80
Val His Phe Ala Ser Arg Gln Trp Lys Val Thr Ser Glu Asp Leu Ile
85 90 95
Leu Ile Gly Asn Glu Leu Asp Leu Ala Cys Gly Glu Arg Ile Arg Leu
100 105 110
Glu Lys Val Leu Leu Val Gly Ala Asp Asn Phe Thr Leu Leu Gly Lys
115 120 125
Pro Leu Leu Gly Lys Asp Leu Val Arg Val Glu Ala Thr Val Ile Glu
130 135 140
Lys Thr Glu Ser Trp Pro Arg Ile Ile Met Arg Phe Arg Lys Arg Lys
145 150 155 160
Asn Phe Lys Lys Lys Arg Ile Val Thr Thr Pro Gln Thr Val Leu Arg
165 170 175
Ile Asn Ser Ile Glu Ile Ala Pro Cys Leu Leu
180 185

<210> 3317
<211> 1665
<212> DNA
<213> Homo sapiens

<400> 3317
ntcattattt tccgaaatga atgtagtaga atttcagaat ggcttctgga acatgtttcc
60
tgttaaaagg cctagaatat cctgcagtgg tagagtttgc tccattccag aagatagcca
120
aaaagaagct gagaaaaaaa gatgccaaga ctggaagcat cgaagatggt gagccctttc
180
caagtgctac gttatgaagc tgccaaatta agaacactga gcaaatgtaa ttctcccgta
240
gttgggaaag attatattta ttttcttcct acttttaat gtctagatcc agaatataag
300
aagtttttag aaacctactg tgtggaggaa gagaagacca gtgccaaccc tgagactctg
360
ctgggggaga tggaggcgaa gacaagagag ctcattgcta gaagaaccac acctcttttg
420

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1380
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1440
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ccagcgcagc actacagatg gcatcacctt tctgacagca ccaggcccca ccctggcctc
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<210> 3318
<211> 253
<212> PRT
<213> Homo sapiens

<400> 3318
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Leu Glu Tyr Ile Lys Asn Arg Lys Leu Glu Lys Gln Arg Ile Arg Glu
20 25 30
Glu Lys Arg Glu Glu Arg Arg Arg Arg Glu Leu Glu Lys Lys Arg Leu

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        35                  40                  45
Arg Glu Glu Glu Lys Arg Arg Arg Arg Glu Glu Glu Arg Cys Lys Lys
    50                  55                  60
Lys Glu Thr Asp Lys Gln Lys Lys Ile Ala Glu Lys Glu Val Arg Ile
65                  70                  75                  80
Lys Leu Leu Lys Lys Pro Glu Lys Gly Glu Glu Pro Thr Thr Glu Lys
                85                  90                  95
Pro Lys Glu Arg Gly Glu Glu Ile Asp Thr Gly Gly Gly Lys Gln Glu
            100                 105                 110
Ser Cys Ala Pro Gly Ala Val Val Lys Ala Arg Pro Met Glu Gly Ser
        115                 120                 125
Leu Glu Glu Pro Gln Glu Thr Ser His Ser Gly Ser Asp Lys Glu His
    130                 135                 140
Arg Asp Val Glu Arg Ser Gln Glu Gln Glu Ser Glu Ala Gln Arg Tyr
145                 150                 155                 160
His Val Asp Asp Gly Arg Arg His Arg Ala His His Glu Pro Glu Arg
                165                 170                 175
Leu Ser Arg Arg Ser Glu Asp Glu Gln Arg Trp Gly Lys Gly Pro Gly
            180                 185                 190
Gln Asp Arg Gly Lys Lys Gly Ser Gln Asp Ser Gly Ala Pro Gly Glu
        195                 200                 205
Ala Met Glu Arg Leu Gly Arg Ala Gln Arg Cys Asp Asp Ser Pro Ala
    210                 215                 220
Pro Arg Lys Glu Arg Leu Ala Asn Lys Val Phe Ile Lys Pro Lys Lys
225                 230                 235                 240
Lys Asn Val Ser Gly Cys Leu Lys Val Gln Ala Ala Cys
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<210> 3319
<211> 1541
<212> DNA
<213> Homo sapiens

<400> 3319

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ctctgcctcc gccgagggac agccggatcg cccctctgct tcccgcaact gccctgatca
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420
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600
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720
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1380
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1541

<210> 3320
<211> 256
<212> PRT
<213> Homo sapiens

<400> 3320
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Cys Pro Ala Tyr Ala Ser Tyr Lys Ala Val Lys Thr Lys Asn Ile Arg
            20   25   30
Glu Tyr Val Arg Trp Met Met Tyr Trp Ile Val Phe Ala Leu Phe Met
        35   40   45
Ala Ala Glu Ile Val Thr Asp Ile Phe Ile Ser Trp Phe Pro Phe Tyr
    50   55   60
Tyr Glu Ile Lys Met Ala Phe Val Leu Trp Leu Leu Ser Pro Tyr Thr
65   70   75   80
Lys Gly Ala Ser Leu Leu Tyr Arg Lys Phe Val His Pro Ser Leu Ser
                85   90   95
Arg His Glu Lys Glu Ile Asp Ala Tyr Ile Val Gln Ala Lys Glu Arg
            100   105   110
Ser Tyr Glu Thr Val Leu Ser Phe Gly Lys Arg Gly Leu Asn Ile Ala

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        115                 120                 125
Ala Ser Ala Ala Val Gln Ala Ala Thr Lys Ser Gln Gly Ala Leu Ala
    130                 135                 140
Gly Arg Leu Arg Ser Phe Ser Met Gln Asp Leu Arg Ser Ile Ser Asp
145                 150                 155                 160
Ala Pro Ala Pro Ala Tyr His Asp Pro Leu Tyr Leu Glu Asp Gln Val
                165                 170                 175
Ser His Arg Arg Pro Pro Ile Gly Tyr Arg Ala Gly Gly Leu Gln Asp
            180                 185                 190
Ser Asp Thr Glu Asp Glu Cys Trp Ser Asp Thr Glu Ala Val Pro Arg
        195                 200                 205
Ala Pro Ala Arg Pro Arg Glu Lys Pro Leu Ile Arg Ser Gln Ser Leu
    210                 215                 220
Arg Val Val Lys Arg Lys Pro Pro Val Arg Glu Gly Thr Ser Arg Ser
225                 230                 235                 240
Leu Lys Val Arg Thr Arg Lys Lys Thr Val Pro Ser Asp Val Asp Ser
                245                 250                 255
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<210> 3321
<211> 1536
<212> DNA
<213> Homo sapiens

<400> 3321
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120
acgaatctgt cgtcggcggt gaccagcgag cagatgcgga cgctttttc cttcctagga
180
gaaatcgagg agctgcggct ctacccccg gacaacgcac ctcttgcttt ttcctccaaa
240
gtatgttatg ttaagtttcg tgatccatca agtgttggcg tggcccagca tctaactaac
300
acggttttta ttgacagagc tctgatagtt gttccttgtg cagaaggtaa aatcccagag
360
gaatccaaag ccctctcttt attggctcct gctccaacca tgacaagtct gatgcctggt
420
gcaggattgc ttccaatacc gaccccaaat cctttgacta ctcttggtgt ttcacttagc
480
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540
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gtttatgttg gaaatctgaa ttcccagaca acgacagctg atcaactact tgaatttttt
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720
gtaaaacccc ctgagatgac acctcaggct gcagctaagg agttagaaga agtaatgaag
780
cgagtacgag aagctcagtc atttatctca gcagctattg aaccagagtc tggaaagagc
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aatgaaagaa aaggcggtcg atctcgttcc catactcgct caaaatccag gtctagctca
900

aaatcccatt ctagaaggaa aagatcacaa tcaaaacaca ggagtagatc ccataataga
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1260
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1320
aaagacagat ccaaagagat agatgaaaaa aagaaagaag gataaaaaat ccagaacacc
1380
acccaggagt tacaatgcat cgcgaagatc tcgtagttcc agcagggaaa ggcgtaggag
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1536

<210> 3322
<211> 454
<212> PRT
<213> Homo sapiens

<400> 3322
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Gly Met Asn Ser Gly Gly Gly Phe Gly Leu Gly Leu Gly Phe Gly Leu
            20   25   30
Thr Pro Thr Ser Val Ile Gln Val Thr Asn Leu Ser Ser Ala Val Thr
        35   40   45
Ser Glu Gln Met Arg Thr Leu Phe Ser Phe Leu Gly Glu Ile Glu Glu
    50   55   60
Leu Arg Leu Tyr Pro Pro Asp Asn Ala Pro Leu Ala Phe Ser Ser Lys
65   70   75   80
Val Cys Tyr Val Lys Phe Arg Asp Pro Ser Ser Val Gly Val Ala Gln
                85   90   95
His Leu Thr Asn Thr Val Phe Ile Asp Arg Ala Leu Ile Val Val Pro
            100   105   110
Cys Ala Glu Gly Lys Ile Pro Glu Glu Ser Lys Ala Leu Ser Leu Leu
        115   120   125
Ala Pro Ala Pro Thr Met Thr Ser Leu Met Pro Gly Ala Gly Leu Leu
    130   135   140
Pro Ile Pro Thr Pro Asn Pro Leu Thr Thr Leu Gly Val Ser Leu Ser
145   150   155   160
Ser Leu Gly Ala Ile Pro Ala Ala Ala Leu Asp Pro Asn Ile Ala Thr
                165   170   175
Leu Gly Glu Ile Pro Gln Pro Pro Leu Met Gly Asn Val Asp Pro Ser
            180   185   190
Lys Ile Asp Glu Ile Arg Arg Thr Val Tyr Val Gly Asn Leu Asn Ser

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        195                 200                 205
Gln Thr Thr Thr Ala Asp Gln Leu Leu Glu Phe Phe Lys Gln Val Gly
    210                 215                 220
Glu Val Lys Phe Ala Asp Gly Arg Ile Asn His Ser Asn Asn Ala Ile
225                 230                 235                 240
Val Lys Pro Pro Glu Met Thr Pro Gln Ala Ala Ala Lys Glu Leu Glu
                245                 250                 255
Glu Val Met Lys Arg Val Arg Glu Ala Gln Ser Phe Ile Ser Ala Ala
            260                 265                 270
Ile Glu Pro Glu Ser Gly Lys Ser Asn Glu Arg Lys Gly Gly Arg Ser
        275                 280                 285
Arg Ser His Thr Arg Ser Lys Ser Arg Ser Ser Ser Lys Ser His Ser
    290                 295                 300
Arg Arg Lys Arg Ser Gln Ser Lys His Arg Ser Arg Ser His Asn Arg
305                 310                 315                 320
Ser Arg Ser Arg Gln Lys Asp Arg Arg Arg Ser Lys Ser Pro His Lys
                325                 330                 335
Lys Arg Ser Lys Ser Arg Glu Arg Arg Lys Ser Arg Ser Arg Ser His
            340                 345                 350
Ser Arg Asp Lys Arg Lys Asp Thr Arg Glu Lys Ile Lys Glu Lys Glu
        355                 360                 365
Arg Val Lys Glu Lys Asp Arg Glu Lys Glu Arg Glu Arg Glu Lys Glu
    370                 375                 380
Arg Glu Lys Glu Lys Glu Arg Gly Lys Asn Lys Asp Arg Asp Lys Glu
385                 390                 395                 400
Arg Glu Lys Asp Arg Glu Lys Asp Lys Glu Lys Asp Arg Glu Arg Glu
                405                 410                 415
Arg Glu Lys Glu His Glu Lys Asp Arg Asp Lys Glu Lys Glu Lys Glu
            420                 425                 430
Gln Asp Lys Glu Lys Glu Arg Glu Lys Asp Arg Ser Lys Glu Ile Asp
        435                 440                 445
Glu Lys Lys Lys Glu Gly
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<210> 3323
<211> 949
<212> DNA
<213> Homo sapiens

<400> 3323
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120
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180
cctggaaagg agttcaatat cttacttaac atctctcagg aagatgtgcc atcttcaact
240
ggaccattgg cttctgagta agctgtgtta ggcctgggct agacctaatg gtttattatt
300
ggtggagaga aagatctgga aatacttgag gttattacat actagattag cttctaatgt
360
gaaccatttt tcttttaaca gtgataaatt attatttccg aagttaactg ttcccttggt
420

cgtgatacac actcgattaa caaacatact gttgtatttt ttccagtttt gtttggctat
480
gccaccacag tcatccccag ggtctataca tactatgttt caactgtatt atttgccatt
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600
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720
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949

<210> 3324
<211> 122
<212> PRT
<213> Homo sapiens

<400> 3324
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Ile Asn Lys His Thr Val Val Phe Phe Pro Val Leu Phe Gly Tyr Ala
20 25 30
Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val Ser Thr Val Leu
35 40 45
Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly Leu Lys Met Ser
50 55 60
Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln Ala Glu Leu Lys
65 70 75 80
Lys Lys Asp Glu Glu Val Ser His Gly Thr Val Asp Leu Asp Gln Lys
85 90 95
Gly Thr Gln Leu Gly Ile Asn Thr Leu Gln Arg Phe Leu Ser Gly Pro
100 105 110
Ile Cys Val Ile Cys Gly Ala Thr Gln Lys
115 120

<210> 3325
<211> 5055
<212> DNA
<213> Homo sapiens

<400> 3325
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120
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180

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720
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3420

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<210> 3326
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<212> PRT
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35 40 45
His Gln Gln Gln Met Ala Pro Ser Thr Leu Ser Gln Gln Asn Arg Pro
50 55 60
Thr Gln Asn Pro Pro Ala Gly Leu Met Ser Met Pro Asn Ala Leu Thr
65 70 75 80
Thr Gln Gln Gln Gln Gln Gln Lys Leu Arg Leu Gln Arg Ile Gln Met
85 90 95
Glu Arg Glu Arg Ile Arg Met Arg Gln Glu Glu Leu Met Arg Gln Glu
100 105 110
Ala Ala Leu Cys Arg Gln Leu Pro Met Glu Ala Glu Thr Leu Ala Pro
115 120 125
Val Gln Ala Ala Val Asn Pro Pro Thr Met Thr Pro Asp Met Arg Ser
130 135 140
Ile Thr Asn Asn Ser Ser Asp Pro Phe Leu Asn Gly Gly Pro Tyr His
145 150 155 160
Ser Arg Glu Gln Ser Thr Asp Ser Gly Leu Gly Leu Gly Cys Tyr Ser
165 170 175
Val Pro Thr Thr Pro Glu Asp Phe Leu Ser Asn Val Asp Glu Met Asp
180 185 190
Thr Gly Glu Asn Ala Gly Gln Thr Pro Met Asn Ile Asn Pro Gln Gln
195 200 205
Thr Arg Phe Pro Asp Phe Leu Asp Cys Leu Pro Gly Thr Asn Val Asp
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Leu Gly Thr Leu Glu Ser Glu Asp Leu Ile Pro Leu Phe Asn Asp Val
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<210> 3327
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<212> DNA
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<212> PRT
<213> Homo sapiens

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35 40 45
Ala Leu Lys Ser Ala Arg Asp Met Trp Ala Asp Tyr Ile Leu Phe Val
50 55 60
Asp Ala Asp Asn Leu Ile Leu Asn Pro Asp Thr Leu Ser Leu Leu Ile
65 70 75 80
Ala Glu Asn Lys Thr Val Val Ala Pro Met Leu Asp Ser Arg Ala Ala
85 90 95
Tyr Ser Asn Phe Trp Cys Gly Met Thr Ser Gln Gly Tyr Tyr Lys Arg
100 105 110
Thr Pro Ala Tyr Ile Pro Ile Arg Lys Arg Asp Arg Arg Gly Cys Phe
115 120 125
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130 135 140
Ala Ser Arg Asn Leu Ala Phe Tyr Pro Pro His Pro Asp Tyr Thr Trp
145 150 155 160
Ser Phe Asp Asp Ile Ile Val Phe Ala Phe Ser Cys Lys Gln Ala Glu
165 170 175
Val Gln Met Tyr Val Cys Asn Lys Glu Glu Tyr Gly Phe Leu Pro Val
180 185 190
Pro Leu Arg Ala His Ser Thr Leu Gln Asp Glu Ala Glu Ser Phe Met
195 200 205
His Val Gln Leu Glu Val Met Val Lys His Pro Pro Ala Glu Pro Ser
210 215 220
Arg Phe Ile Ser Ala Pro Thr Lys Thr Pro Asp Lys Met Gly Phe Asp
225 230 235 240
Glu Val Phe Met Ile Asn Leu Arg Arg Arg Gln Asp Arg Arg Glu Arg
245 250 255
Met Leu Arg Ala Leu Gln Ala Gln Glu Ile Glu Cys Arg Leu Val Glu

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Thr Lys Gly Glu Leu Gly Cys Phe Leu Ser His Tyr Asn Ile Trp Lys
305                 310                 315                 320
Glu Val Val Asp Arg Gly Leu Gln Lys Ser Leu Val Phe Glu Asp Asp
                325                 330                 335
Leu Arg Phe Glu Ile Phe Phe Lys Arg Arg Leu Met Asn Leu Met Arg
            340                 345                 350
Asp Val Glu Arg Glu Gly Leu Asp Trp Asp Leu Ile Tyr Val Gly Arg
        355                 360                 365
Lys Arg Met Gln Val Glu His Pro Glu Lys Ala Val Pro Arg Val Arg
    370                 375                 380
Asn Leu Val Glu Ala Asp Tyr Ser Tyr Trp Thr Leu Ala Tyr Val Ile
385                 390                 395                 400
Ser Leu Gln Gly Ala Arg Lys Leu Leu Ala Ala Glu Pro Leu Ser Lys
                405                 410                 415
Met Leu Pro Val Asp Glu Phe Leu Pro Val Met Phe Asp Lys His Pro
            420                 425                 430
Val Ser Glu Tyr Lys Ala His Phe Ser Leu Arg Asn Leu His Ala Phe
        435                 440                 445
Ser Val Glu Pro Leu Leu Ile Tyr Pro Thr His Tyr Thr Gly Asp Asp
    450                 455                 460
Gly Tyr Val Ser Asp Thr Glu Thr Ser Val Val Trp Asn Asn Glu His
465                 470                 475                 480
Val Lys Thr Asp Trp Asp Arg Ala Lys Ser Gln Lys Met Arg Glu Gln
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Gln Ala Leu Ser Arg Glu Ala Lys Asn Ser Asp Val Leu Gln Ser Pro
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<212> DNA
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420

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<212> PRT
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35 40 45
Pro Val Pro Thr Leu Ala Phe Thr His Val Ala Arg Ala Gln Ala Gly
50 55 60
Met Tyr His Cys Leu Ala Glu Leu Pro Thr Gly Ala Ala Ala Ser Ala
65 70 75 80
Pro Val Met Leu Arg Val Leu Tyr Pro Pro Lys Thr Pro Thr Met Met
85 90 95
Val Phe Val Glu Pro Glu Gly Gly Leu Arg Gly Ile Leu Asp Cys Arg
100 105 110
Val Asp Ser Glu Pro Leu Ala Ser Leu Thr Leu His Leu Gly Ser Arg
115 120 125
Leu Val Ala Ser Ser Gln Pro Gln Gly Ala Pro Ala Glu Pro His Ile
130 135 140
His Val Leu Ala Ser Pro Asn Ala Leu Arg Val Asp Ile Glu Ala Leu
145 150 155 160
Arg Pro Ser Asp Gln Gly Glu Tyr Ile Cys Ser Ala Ser Asn Val Leu
165 170 175
Gly Ser Ala Ser Thr Ser Thr Tyr Phe Gly Val Arg Ala Leu His Arg
180 185 190
Leu His Gln Phe Gln Gln Leu Leu Trp Val Leu Gly Leu Leu Val Gly
195 200 205
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Arg Arg Val Cys Lys Gln Ser Met Gly Glu Asn
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<212> DNA
<213> Homo sapiens

<400> 3331

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<212> PRT
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35 40 45
Met Ser Ser Cys Arg Val Asp Lys Pro Ser Glu Ile Val Asp Val Gly
50 55 60
Asp Lys Val Trp Val Lys Leu Ile Gly Arg Glu Met Lys Asn Asp Arg
65 70 75 80
Ile Lys Val Ser Leu Ser Met Lys Val Val Asn Gln Gly Thr Gly Lys
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<211> 2422
<212> DNA
<213> Homo sapiens

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<211> 672
<212> PRT
<213> Homo sapiens

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35 40 45
His Met His His Val Arg Asp Arg Glu Met Pro Glu Ala Leu Glu Phe
50 55 60
Asn Leu Ser Ala Asn Pro Glu Ser Ser Thr Ile Phe Gln Arg Asn Ser
65 70 75 80
Gln Thr Glu Ala Leu Glu Phe Asn Pro Ser Ala Asn Pro Glu Ala Ser
85 90 95
Thr Ile Phe Gln Arg Asn Ser Gln Thr Asp Val Val Glu Ile Arg Arg
100 105 110
Ser Asn Cys Thr Asn His Val Ser Ala Val Arg Phe Ser Gln Gln Tyr
115 120 125
Ser Leu Cys Ser Thr Ile Phe Leu Asp Asp Ser Thr Ala Ile Gln His
130 135 140
Tyr Leu Thr Met Thr Ile Ile Ser Val Thr Leu Glu Ile Pro His His
145 150 155 160
Ile Thr Gln Arg Asp Ala Asp Arg Thr Leu Ser Ile Pro Asp Glu Gln
165 170 175
Leu His Ser Phe Ala Val Ser Thr Val His Ile Met Lys Lys Arg Asn
180 185 190
Gly Gly Gly Ser Leu Asn Asn Tyr Ser Ser Ser Ile Pro Ser Thr Pro
195 200 205
Ser Thr Ser Gln Glu Asp Pro Gln Phe Ser Val Pro Pro Thr Ala Asn
210 215 220
Thr Pro Thr Pro Val Cys Lys Arg Ser Met Arg Trp Ser Asn Leu Phe
225 230 235 240
Thr Ser Glu Lys Gly Ser His Pro Asp Lys Glu Arg Lys Ala Pro Glu
245 250 255
Asn His Ala Asp Thr Ile Gly Ser Gly Arg Ala Ile Pro Ile Lys Gln
260 265 270
Gly Met Leu Leu Lys Arg Ser Gly Lys Trp Leu Lys Thr Trp Lys Lys
275 280 285
Lys Tyr Val Thr Leu Cys Ser Asn Gly Met Leu Thr Tyr Tyr Ser Ser
290 295 300
Leu Gly Asp Tyr Met Lys Asn Ile His Lys Lys Glu Ile Asp Leu Gln
305 310 315 320
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325 330 335
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340 345 350
Met Asp Thr Gly Leu Gly Asp Ser Ile Cys Phe Ser Pro Ser Ile Ser
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385 390 395 400
Ser Ala Thr Gly Gln Thr Trp His Phe Glu Ala Thr Thr Tyr Glu Glu
405 410 415
Arg Asp Ala Trp Val Gln Ala Ile Gln Ser Gln Ile Leu Ala Ser Leu
420 425 430
Gln Ser Cys Glu Ser Ser Lys Ser Lys Ser Gln Leu Thr Ser Gln Ser
435 440 445
Glu Ala Met Ala Leu Gln Ser Ile Gln Asn Met Arg Gly Asn Ala His
450 455 460
Cys Val Asp Cys Glu Thr Gln Asn Pro Lys Trp Ala Ser Leu Asn Leu
465 470 475 480
Gly Val Leu Met Cys Ile Glu Cys Ser Gly Ile His Arg Ser Leu Gly
485 490 495
Thr Arg Leu Ser Arg Val Arg Ser Leu Glu Leu Asp Asp Trp Pro Val
500 505 510
Glu Leu Arg Lys Val Met Ser Ser Ile Gly Asn Glu Leu Ala Asn Ser
515 520 525
Ile Trp Glu Glu Ser Ser Gln Gly Arg Thr Lys Pro Ser Val Asp Ser
530 535 540
Thr Arg Glu Glu Lys Glu Arg Trp Ile Arg Ser Lys Tyr Glu Glu Lys
545 550 555 560
Leu Phe Leu Ala Pro Leu Pro Cys Thr Glu Leu Ser Leu Gly Gln Gln
565 570 575
Leu Leu Arg Ala Thr Ala Asp Glu Asp Leu Gln Thr Ala Ile Leu Leu
580 585 590
Leu Ala His Gly Ser Arg Glu Glu Val Asn Glu Thr Cys Gly Glu Gly
595 600 605
Asp Gly Cys Thr Ala Leu His Leu Ala Cys Arg Lys Gly Asn Val Val
610 615 620
Leu Ala Gln Leu Leu Ile Trp Tyr Gly Val Asp Val Met Ala Arg Asp
625 630 635 640
Ala His Gly Asn Thr Ala Leu Thr Tyr Ala Arg Gln Ala Ser Ser Gln
645 650 655
Glu Cys Ile Asn Val Leu Leu Gln Tyr Gly Cys Pro Asp Lys Cys Val
660 665 670

<210> 3335
<211> 477
<212> DNA
<213> Homo sapiens

<400> 3335
nggatccatc acgcgttcag ggcagcggaa ttccggctcc ccaggggca gctcaggcag
60
ggcctcttca ggagtgacgt ccgggacctc ctccccaggg ccctgctcat gctgtctcgg
120

cccagactgc ttgttgaagg ggttgaggtg ggcctgccgg aaacgggcca gcttctcatc
180
atattccata gcatcccacc tgcatcgcct gccagggccc aggggctcgc agggacagga
240
tggccattcc tctagggctg ctggccacgg aagcctggcc gtgggttcgg cacctgctga
300
ccgccgcctc gcatttgccc tgagacaggg ctggacagcc aggattaccg ctgtgccgag
360
tgccgggcgc ccatctctct gcggggtgtg cccagtgagg ccaggcagtg cgactacacc
420
ggccagtact actgcagccc ctgccactgg aacgccctgg ctgtgatccc tgcacgc
477

<210> 3336
<211> 59
<212> PRT
<213> Homo sapiens

<400> 3336
Pro Pro Pro Arg Ile Cys Pro Glu Thr Gly Leu Asp Ser Gln Asp Tyr
 1   5   10   15
Arg Cys Ala Glu Cys Arg Ala Pro Ile Ser Leu Arg Gly Val Pro Ser
            20   25   30
Glu Ala Arg Gln Cys Asp Tyr Thr Gly Gln Tyr Tyr Cys Ser Pro Cys
        35   40   45
His Trp Asn Ala Leu Ala Val Ile Pro Ala Arg
    50   55

<210> 3337
<211> 679
<212> DNA
<213> Homo sapiens

<400> 3337
nagatcttcc tcttgaatga tttgggcagc gagctctgta tgaagaagaa aaaggggaaa
60
aaaaagagaa agagagacac cccacagaga ggggggaagg aggttagatg gggcagtctt
120
agcttagcct ccaaagacac agatagagtg agagagagag acagagagag acacagagac
180
agacagagac caaaacagaa gcggcaaacg gcaaaaacga agcagaatca atgcaagtta
240
gagaaaaaaa taaaactaaa catcagagca gggaaaagtc atctactccg tatcacacct
300
gtgtattagc ttaaccagaa ataagctgga agaggagttc agtagcctct cagcccccta
360
aagatgttgg tcataccccc tctttcaccg tctgagtcga gaggacacca agccaaacaa
420
actgtgcccc aaactgggtc atctagtcct cccaggtcct tccttgctaa ctcgaggaaa
480
caaggaaaac caactttgga tggcaacttc aacaaggtaa ccctcctttc ttcaatggcc
540
agactgatgc ccactgacaa tggctttgag atgcttggac agcagactgt catgtcaaga
600

ctgcccagac ccccaccaca ctgtggaaaa gggcagcacc agacccactg gagatgaggc
660
tcttgagcca agtgctagc
679

<210> 3338
<211> 102
<212> PRT
<213> Homo sapiens

<400> 3338
Xaa Ile Phe Leu Leu Asn Asp Leu Gly Ser Glu Leu Cys Met Lys Lys
 1   5   10   15
Lys Lys Gly Lys Lys Lys Arg Lys Arg Asp Thr Pro Gln Arg Gly Gly
            20   25   30
Lys Glu Val Arg Trp Gly Ser Leu Ser Leu Ala Ser Lys Asp Thr Asp
        35   40   45
Arg Val Arg Glu Arg Asp Arg Glu Arg His Arg Asp Arg Gln Arg Pro
    50   55   60
Lys Gln Lys Arg Gln Thr Ala Lys Thr Lys Gln Asn Gln Cys Lys Leu
65   70   75   80
Glu Lys Lys Ile Lys Leu Asn Ile Arg Ala Gly Lys Ser His Leu Leu
                85   90   95
Arg Ile Thr Pro Val Tyr
            100

<210> 3339
<211> 1341
<212> DNA
<213> Homo sapiens

<400> 3339
ttttttttt ttttcacca aaacaatttt tatttccagt gtttaattgg gtatgcacac
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aggcatgaca caggtttgga ttcattaagt cctcatgcag aattatattc ttctcgataa
120
agaagccagt tccatccagg atccactatc tacacaccta tgttacaaca ttatatcaaa
180
tctggtatct gaagaaaaga tacacattta atatgttcat ttaagttacg tattttgcag
240
aaagattaaa aattcattca cacaaaactc aaaaactgta ttaaaagttt gaatataaaa
300
ctcagatcca cctggaatga ctaaagaatg gaagttctgt atccacctgt gttaaaactg
360
gtaaatgtaa tgatatctgt taccaataaa acgcattcgt ttattcaatg taagtaagtt
420
atctaatttt aacaatatgg caccctaaaa accaactgta tttttatgat gaggcacttt
480
tgttagtgat gaaaccaaaa gaacaaattt gctgcacact gatgccagcg attttcttca
540
gtgattttgg gtatatgcta tgtagtaagt tgcaacaaat accttgctca tttgtataca
600
actatccgat atatttttaa tatatatata tatatatgtt cttctggctg tagtaatgca
660

ctgtaaagct atttcacagt gcaaaatgat gaaaccagcc caaatgaagg ctgcataata
720
acaattctga tacaagaaaa tattgacaga gttactggaa cgtgtaacag tagttttttt
780
acttgctaga gtggacatac ccccagttta aagacaggga tgaaactctg ctttagtgcc
840
tggggtttca gacagtttat gaggttgggc attcgctgca gaactagcat ttttgctcac
900
gttctggaag ctttctccgt ttatttggtc aggtgactgt ggtggtatgg aaagaagggg
960
cctgtttgtt gaagccaagg tgctggaaga actgcctgtg ttgcaatgaa gagacaaagg
1020
tgtgtcggtc gtggctattt ctcgtgtgct tgggttctct gtctggggat ctccgatttc
1080
tcctctgcta aggtcagagg tactggtgcg taggcgttcc ctggccagcc agtctgagat
1140
ggaaaggtcc tgggctgagc attttggttt taaccggttt acagctgaaa gttcagattc
1200
tctctccccg ctctgctcat gcactttcca aaaattcaaa acgctgattt cagtagcatc
1260
tctgtgccct cctagtgtat gtctgcgccg gatgcttttc cttttagcag tctcggcatt
1320
cactttgtga ttccctactc c
1341

<210> 3340
<211> 86
<212> PRT
<213> Homo sapiens

<400> 3340
Met Ser Thr Leu Ala Ser Lys Lys Thr Thr Val Thr Arg Ser Ser Asn
1 5 10 15
Ser Val Asn Ile Phe Leu Tyr Gln Asn Cys Tyr Tyr Ala Ala Phe Ile
20 25 30
Trp Ala Gly Phe Ile Ile Leu His Cys Glu Ile Ala Leu Gln Cys Ile
35 40 45
Thr Thr Ala Arg Arg Thr Tyr Ile Tyr Ile Tyr Ile Lys Asn Ile Ser
50 55 60
Asp Ser Cys Ile Gln Met Ser Lys Val Phe Val Ala Thr Tyr Tyr Ile
65 70 75 80
Ala Tyr Thr Gln Asn His
85

<210> 3341
<211> 1132
<212> DNA
<213> Homo sapiens

<400> 3341
ttttacagca caatatatgt gctctgctct cctcccgcaa tcctgctcca agagatctta
60
agctggaggc accaggtctg aattccagac tcctccccac cacccacact tcacctccaa
120

ctggagcatg accacagacc cattcaggga ggctggcgga ctcttcatcc tggacagtcc
180
cttactgtat gtcaagtaaa gctgagaatg aagcggagag catcagacag aggagctggg
240
gaaacgtcgg ccagggccaa ggctctagga agtgggattt ctggaaataa tgcaaagaga
300
gctggaccat tcatccttgg tccccgtctg ggcaactcac cggtgccaag catagtgcag
360
tgtttggcga ggaaagatgg cacggatgac ttctatcagc tgaagatcct gaccctggag
420
gagaggggg accaaggcat agagagccag gaagagcggc agggcaagat gctgctgcac
480
accgagtact cactgctgtc tctcctgcac acgcaggatg gcgtggtgca ccaccacggc
540
ctcttccagg accgcacctg tgaaatcgtt gaggacacag aatccagccg gatggttaag
600
aagatgaaga agcgcatctg cctcgtcctg gactgcctct gtgctcatga cttcagcgat
660
aagaccgctg acctcatcaa cctgcagcac tacgtcatca aggagaagag gctcagcgag
720
agggagactg tggtaatctt ctacgacgtg gtccgcgtgg tggaggccct gcaccagaaa
780
aatatcgtgc acagagacct gaagctgggg aacatggtgc tcaacaagag gacacatcgg
840
ataaccatca ccaacttctg cctcgggaag catctggtga gcgaggggga cctgctgaag
900
gaccagagag ggagccctgc ctacatcagt cccgacgtgc tcagcggccg gccgtaccgt
960
ggcaagccca gtgacatgtg ggccctgggc gtggtgctct tcaccatgct gtatggccag
1020
ttccccttct acgacagcat cccgcaggag ctcttccgca agatcaaggc tgccgagtat
1080
accattcctg aggatggacg ggtttctgag aacaccgtgt gtctcatccg ga
1132

<210> 3342
<211> 308
<212> PRT
<213> Homo sapiens

<400> 3342
Met Lys Arg Arg Ala Ser Asp Arg Gly Ala Gly Glu Thr Ser Ala Arg
1 5 10 15
Ala Lys Ala Leu Gly Ser Gly Ile Ser Gly Asn Asn Ala Lys Arg Ala
20 25 30
Gly Pro Phe Ile Leu Gly Pro Arg Leu Gly Asn Ser Pro Val Pro Ser
35 40 45
Ile Val Gln Cys Leu Ala Arg Lys Asp Gly Thr Asp Asp Phe Tyr Gln
50 55 60
Leu Lys Ile Leu Thr Leu Glu Glu Arg Gly Asp Gln Gly Ile Glu Ser
65 70 75 80
Gln Glu Glu Arg Gln Gly Lys Met Leu Leu His Thr Glu Tyr Ser Leu
85 90 95
Leu Ser Leu Leu His Thr Gln Asp Gly Val Val His His His Gly Leu

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            100                 105                 110
Phe Gln Asp Arg Thr Cys Glu Ile Val Glu Asp Thr Glu Ser Ser Arg
        115                 120                 125
Met Val Lys Lys Met Lys Lys Arg Ile Cys Leu Val Leu Asp Cys Leu
    130                 135                 140
Cys Ala His Asp Phe Ser Asp Lys Thr Ala Asp Leu Ile Asn Leu Gln
145                 150                 155                 160
His Tyr Val Ile Lys Glu Lys Arg Leu Ser Glu Arg Glu Thr Val Val
                165                 170                 175
Ile Phe Tyr Asp Val Val Arg Val Val Glu Ala Leu His Gln Lys Asn
            180                 185                 190
Ile Val His Arg Asp Leu Lys Leu Gly Asn Met Val Leu Asn Lys Arg
        195                 200                 205
Thr His Arg Ile Thr Ile Thr Asn Phe Cys Leu Gly Lys His Leu Val
    210                 215                 220
Ser Glu Gly Asp Leu Leu Lys Asp Gln Arg Gly Ser Pro Ala Tyr Ile
225                 230                 235                 240
Ser Pro Asp Val Leu Ser Gly Arg Pro Tyr Arg Gly Lys Pro Ser Asp
                245                 250                 255
Met Trp Ala Leu Gly Val Val Leu Phe Thr Met Leu Tyr Gly Gln Phe
            260                 265                 270
Pro Phe Tyr Asp Ser Ile Pro Gln Glu Leu Phe Arg Lys Ile Lys Ala
        275                 280                 285
Ala Glu Tyr Thr Ile Pro Glu Asp Gly Arg Val Ser Glu Asn Thr Val
    290                 295                 300
Cys Leu Ile Arg
305
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<210> 3343
<211> 594
<212> DNA
<213> Homo sapiens

<400> 3343
cgcgtcatga gccaccgcat ggagggtgtc ggccagctgc ccgcctccta ccggcacaac
60
cggcctctcc tcagcggcgt gagtgacacc gaggcgcgcc agccggggaa gtcgcccccc
120
ttcagcatga actgggtcgt gggcagcgcg gacctggaga ttatcaacgc caccactggg
180
cggaggagct gtgggggccc atcccggctc tgcaagcacg tgctgtctgc acggtgggcg
240
cggctgtatg gcaggctgag cacacggaca cccagccctg gagacacgcc ctccatgtac
300
tgtgaggcca agctgggggc gcacacctac cagtctgtga aacagcagct gttcaaggcc
360
tttcagaagg ctggcctggg cacctgggtg aggaaaccac cggagcagca gcagtttcta
420
ctgactctct aggctgcggg ctcctggctg ctggagctga gcgggacgct ggagggatgg
480
gaccgtgtct ggggggcgac gtggcgggtc ggccggttcc ctgcattcgt tttactttgg
540
tgtcccagaa acacgcgagt gtgcaatgtt tggacgagca acaaaaaaaa aaaa
594

<210> 3344
<211> 143
<212> PRT
<213> Homo sapiens

<400> 3344
Arg Val Met Ser His Arg Met Glu Gly Val Gly Gln Leu Pro Ala Ser
1 5 10 15
Tyr Arg His Asn Arg Pro Leu Leu Ser Gly Val Ser Asp Thr Glu Ala
20 25 30
Arg Gln Pro Gly Lys Ser Pro Pro Phe Ser Met Asn Trp Val Val Gly
35 40 45
Ser Ala Asp Leu Glu Ile Ile Asn Ala Thr Thr Gly Arg Arg Ser Cys
50 55 60
Gly Gly Pro Ser Arg Leu Cys Lys His Val Leu Ser Ala Arg Trp Ala
65 70 75 80
Arg Leu Tyr Gly Arg Leu Ser Thr Arg Thr Pro Ser Pro Gly Asp Thr
85 90 95
Pro Ser Met Tyr Cys Glu Ala Lys Leu Gly Ala His Thr Tyr Gln Ser
100 105 110
Val Lys Gln Gln Leu Phe Lys Ala Phe Gln Lys Ala Gly Leu Gly Thr
115 120 125
Trp Val Arg Lys Pro Pro Glu Gln Gln Gln Phe Leu Leu Thr Leu
130 135 140

<210> 3345
<211> 1149
<212> DNA
<213> Homo sapiens

<400> 3345
ggatcccata ggtagctcta gggctggagc tctgcaacat tgggcaagag gaccctgtgc
60
tgggaggcag ggagcttggg cccctcagat gggccacgtg ccctcgtggg accctcattg
120
tcaccgtgag ctctttccaa ggggacgcca ccagtggggg cctgggcagg aggcagctga
180
ggtgtttcag gaaaaggctg aagatcaagg ctgtggtgtg aggactaccc actttaggga
240
agtgaaagag gccagcctca ccccagacac cccagtgtgg ttggggaaag ggggtggtcc
300
gtggtgagcc tggtacctgg ggactcatcc tggccctgcc tggccctcag gtgggatgct
360
atggaatatg atgagaagct ggcccgtttc cggcaggccc acctcaaccc cttcaacaag
420
cagtctgggc cgagacagca tgagcagggc cctggggagg aggtcccgga cgtcactcct
480
gaagaggccc tgcctgagct gccccctggg gagccggaat tccgctgccc tgaacgcgtg
540
atggatctcg gcctgtctga ggaccacttc tcccgccctg tgggtctgtt cctggcctct
600
gacgtccagc agctgcggca ggcgatcgag gagtgcaagc aggtgattct ggagctgccc
660

gagcagtcgg agaagcagaa ggatgccgtg gtgcgactca tccacctccg gctgaagctc
720
caggagctga aggaccccaa tgaggatgag ccaaacatcc gagtgctcct tgagcaccgc
780
ttttacaagg agaagagcaa gagcgtcaag cagacctgtg acaagtgtaa caccatcatc
840
tgggggctca ttcagacctg gtacacctgc acagggtgtt attaccgctg tcacagtaag
900
tgcttgaacc tcatctccaa gccctgtgtg agctccaaag tcagccacca agctgaatac
960
gaactgaaca tctgccctga gacagggctg gacagccagg attaccgctg tgccgagtgc
1020
cgggcgccca tctctctgcg gggtgtgccc agtgaggcca ggcagtgcga ctataccggc
1080
cagtactact gcagccactg ccactggaac gacctggctg tgatcccaga ggctggagtg
1140
tgctcgcga
1149

<210> 3346
<211> 263
<212> PRT
<213> Homo sapiens

<400> 3346
Met Glu Tyr Asp Glu Lys Leu Ala Arg Phe Arg Gln Ala His Leu Asn
1 5 10 15
Pro Phe Asn Lys Gln Ser Gly Pro Arg Gln His Glu Gln Gly Pro Gly
20 25 30
Glu Glu Val Pro Asp Val Thr Pro Glu Glu Ala Leu Pro Glu Leu Pro
35 40 45
Pro Gly Glu Pro Glu Phe Arg Cys Pro Glu Arg Val Met Asp Leu Gly
50 55 60
Leu Ser Glu Asp His Phe Ser Arg Pro Val Gly Leu Phe Leu Ala Ser
65 70 75 80
Asp Val Gln Gln Leu Arg Gln Ala Ile Glu Glu Cys Lys Gln Val Ile
85 90 95
Leu Glu Leu Pro Glu Gln Ser Glu Lys Gln Lys Asp Ala Val Val Arg
100 105 110
Leu Ile His Leu Arg Leu Lys Leu Gln Glu Leu Lys Asp Pro Asn Glu
115 120 125
Asp Glu Pro Asn Ile Arg Val Leu Leu Glu His Arg Phe Tyr Lys Glu
130 135 140
Lys Ser Lys Ser Val Lys Gln Thr Cys Asp Lys Cys Asn Thr Ile Ile
145 150 155 160
Trp Gly Leu Ile Gln Thr Trp Tyr Thr Cys Thr Gly Cys Tyr Tyr Arg
165 170 175
Cys His Ser Lys Cys Leu Asn Leu Ile Ser Lys Pro Cys Val Ser Ser
180 185 190
Lys Val Ser His Gln Ala Glu Tyr Glu Leu Asn Ile Cys Pro Glu Thr
195 200 205
Gly Leu Asp Ser Gln Asp Tyr Arg Cys Ala Glu Cys Arg Ala Pro Ile
210 215 220
Ser Leu Arg Gly Val Pro Ser Glu Ala Arg Gln Cys Asp Tyr Thr Gly

225 230 235 240
Gln Tyr Tyr Cys Ser His Cys His Trp Asn Asp Leu Ala Val Ile Pro
245 250 255
Glu Ala Gly Val Cys Ser Arg
260

<210> 3347
<211> 2267
<212> DNA
<213> Homo sapiens

<400> 3347
aggtgtgtaa cgtgcgctat ggagccgaaa gtcgcagagc tgaagcagaa gatcgaggac
60
acgctatgtc cttttggctt cgaggtttac cccttccagg tggcatggta caatgaactc
120
ttgcctccag ccttccacct accgctgcca ggacctaccc tggccttcct ggtactcagc
180
acgcctgcca tgtttgaccg ggccctcaag cccttcttgc agagctgcca cctccgaatg
240
ctgactgacc cagtggacca gtgtgtggcc taccatctgg gccgtgttgg agagagcctc
300
ccagagctgc agatagaaat cattgctgac tacgaggtac accccaaccg acgccccaag
360
atcctggccc agacagcagc ccatgtagct ggggctgctt actactacca acgacaagat
420
gtggaggctg acccatgggg gaaccagcgc atatcaggtg tgtgcataca cccccgattt
480
gggggctggt ttgccatccg aggggtagtg ctgctgccag ggatagaggt gccagatctg
540
ccacccagaa aacctcatga ctgtgtacct acaagagctg accgtatcgc cctactcgaa
600
ggcttcaatt tccactggcg tgattggact taccgggatg ctgtgacacc ccaggagcgc
660
tactcagaag agcagaaggc ctacttctcc actccacctg cccaacgatt ggccctattg
720
ggcttggctc agccctcaga gaagcctagt tctccctccc cggaccttcc ctttaccaca
780
cccgccccca agaagcctgg gaatcccagc agagcccgga gctggctcag ccccagggtc
840
tcaccacctg catcccctgg cccttgattt tctcccatgt ggaccctgat ttatggtggt
900
acttgctagg acttaattgg ctttggcaaa gcaaaaggtt ttgagtacaa gattactatt
960
tttgataata tagtagagat cttccatgaa gataacaagg ctcaaggaag ttaggtttgg
1020
ccaagataaa ggccagggaa ccagaattcc catctgcctt caaatgagtt ttttttttt
1080
ttttttttta gacagagtct tactctgtca cctaggctgg agtgcagtgg cacagtctct
1140
actcactgca acctctgcct cctgggctga ggcagtagaa tcatttgaac cagggaggca
1200
gagattgcag tgagccgaga ttgcatggct gcactctagc ctgggtgaca gtgtgagact
1260

ctgtctcaaa agaaaaaaaa gtacctgcct caggtaggga ctgaataaac acgtgtaagg
1320
cactttggaa aaatacctgg catatatagt aagcagtatg ttggccatta cgaaaggccc
1380
tgggaattct gtactgctgc tcatgggtgt agtcggttct agaggggtgg gcaggtggga
1440
gtagctgagg aagacaagtg gctggaatgg tatcacatga tacacagaag tatcctcagt
1500
tctgaatcta ccttggcctc aagggcccag gagaataact tttcccagct gacagcctct
1560
ctgaggacaa tgacatatga atgaggatca aaacgagctt tggccaggca ctgtggcgct
1620
cacctgtaat cccaccattt tgggaggctg aggcggagga ccacctgagg caaggaattc
1680
agaaccactc tgggcaacat aatgacacta aaaaagacta tctctaatca aggctagaac
1740
caagggaagg ctaagaattg cccagtactg tgcaactact gaaagcccta cccaaggcca
1800
ccagccttgt cttcctcttt cctctgtcag ttcaaaaaga acagaaacct ccagctcttt
1860
tacatagcag gtaccaggca tttatcagaa gaggccaagc ttctggttcc catgcagccc
1920
tttgaatagt gtgtctaaac aaaaataggt gtccaagtag tcacactgag actttaactg
1980
gtaacccacc ctgtggcgtc agtcgcagtg ctctggccaa cactatagca gggcttattc
2040
ttctccctca tgtgtagtga aacaaaatgt aacaccttgg gttcattcag ttccattccc
2100
tatgtctacc tgtgtcaata taattccctg atttggaggc agctctcctc attttcccca
2160
aaacagggaa agcaaggagt aaattcctct taaaatcaaa agctaataat atgcttccta
2220
aaataaagac tcatcaaggt ctcaaaaaaa aaaaaaaaaa aaaaatt
2267
<210> 3348
<211> 288
<212> PRT
<213> Homo sapiens

<400> 3348
Arg Cys Val Thr Cys Ala Met Glu Pro Lys Val Ala Glu Leu Lys Gln
1 5 10 15
Lys Ile Glu Asp Thr Leu Cys Pro Phe Gly Phe Glu Val Tyr Pro Phe
20 25 30
Gln Val Ala Trp Tyr Asn Glu Leu Leu Pro Pro Ala Phe His Leu Pro
35 40 45
Leu Pro Gly Pro Thr Leu Ala Phe Leu Val Leu Ser Thr Pro Ala Met
50 55 60
Phe Asp Arg Ala Leu Lys Pro Phe Leu Gln Ser Cys His Leu Arg Met
65 70 75 80
Leu Thr Asp Pro Val Asp Gln Cys Val Ala Tyr His Leu Gly Arg Val
85 90 95
Gly Glu Ser Leu Pro Glu Leu Gln Ile Glu Ile Ile Ala Asp Tyr Glu
100 105 110

```
Val His Pro Asn Arg Arg Pro Lys Ile Leu Ala Gln Thr Ala Ala His
        115                 120                 125
Val Ala Gly Ala Ala Tyr Tyr Tyr Gln Arg Gln Asp Val Glu Ala Asp
    130                 135                 140
Pro Trp Gly Asn Gln Arg Ile Ser Gly Val Cys Ile His Pro Arg Phe
145                 150                 155                 160
Gly Gly Trp Phe Ala Ile Arg Gly Val Val Leu Leu Pro Gly Ile Glu
                165                 170                 175
Val Pro Asp Leu Pro Pro Arg Lys Pro His Asp Cys Val Pro Thr Arg
            180                 185                 190
Ala Asp Arg Ile Ala Leu Leu Glu Gly Phe Asn Phe His Trp Arg Asp
        195                 200                 205
Trp Thr Tyr Arg Asp Ala Val Thr Pro Gln Glu Arg Tyr Ser Glu Glu
    210                 215                 220
Gln Lys Ala Tyr Phe Ser Thr Pro Pro Ala Gln Arg Leu Ala Leu Leu
225                 230                 235                 240
Gly Leu Ala Gln Pro Ser Glu Lys Pro Ser Ser Pro Ser Pro Asp Leu
                245                 250                 255
Pro Phe Thr Thr Pro Ala Pro Lys Lys Pro Gly Asn Pro Ser Arg Ala
            260                 265                 270
Arg Ser Trp Leu Ser Pro Arg Val Ser Pro Pro Ala Ser Pro Gly Pro
        275                 280                 285
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<210> 3349
<211> 1132
<212> DNA
<213> Homo sapiens

<400> 3349
nnaaaatcgg ggcacggtca tcgtggagcg ctggtggaag gtaccgctgg ccggggaggg
60
ccggaagccg cgcctgcacc ggcgacatcg cgtctataag ctggtggagg acacgaagca
120
tcggcccaaa gaaaacctgg agctcatcct gacgcagtcg gtggagagta aggcccgggc
180
cgaggcgctt cctctcaggc tgatgttgga gtccggggtg acctggtctc agtgaagaaa
240
tctttaggcc ggaatcgact ccttcctcag ggactggctg tatatgcatc ccctgaaaac
300
aagaagctgt ttgaagagga gaaattgctg agacaagaag gaaaattaga gaagatccag
360
accaaggcag gtgaggcgac agtgaaattt ctaaaaagct gtcgcctgga ggtagggatg
420
aagaacaatg tcaaatggga gctgaaccct gaaatagttg cccgccactt ctttaagaat
480
cttggtgttg tggttgcccc acatacatta aagttaccag cagagcctat cacacggtgg
540
ggcgagtatt ggtgtgaggt gacggtaaat gggcttgata ctgtgagagt gcctatgtct
600
gtcgtgaact ttgagaagcc caagaccaaa agatataagt actggttagc ccagcaagct
660
gccaaggcta tggcccccac cagcccccag atctaaatct actctccctc caaggcagca
720

aagcagaatc gggagcagtg gagcagaaat gtgcaagcac cctgatctca ctcccagctc
780
tgaccaaata cagaatttta gagaacatct gaagacatca gactgcactg cgtatacatg
840
ttgaattctt cattttgcc atctttaact gtcatcactg gggcagggaa gtcctgttcc
900
agaagtacca ggctgtagat ttgataagct agatgcagta gaccgaaacc atccaaaacc
960
tgtttagctt cttcctccat tggagtttat tgggacaaac aggagagcca gccattgtct
1020
ccagtacttg cctcattctc atcatccaaa ctgaacattt gtatcccaag cagaaataaa
1080
gagaatatgt tctttttaaa aaaaaaaaaa aaaaaaaaaa aaaaaaattg gc
1132

<210> 3350
<211> 174
<212> PRT
<213> Homo sapiens

<400> 3350
Gly Pro Gly Arg Gly Ala Ser Ser Gln Ala Asp Val Gly Val Arg Gly
 1   5   10   15
Asp Leu Val Ser Val Lys Lys Ser Leu Gly Arg Asn Arg Leu Leu Pro
            20   25   30
Gln Gly Leu Ala Val Tyr Ala Ser Pro Glu Asn Lys Lys Leu Phe Glu
        35   40   45
Glu Glu Lys Leu Leu Arg Gln Glu Gly Lys Leu Glu Lys Ile Gln Thr
    50   55   60
Lys Ala Gly Glu Ala Thr Val Lys Phe Leu Lys Ser Cys Arg Leu Glu
65   70   75   80
Val Gly Met Lys Asn Asn Val Lys Trp Glu Leu Asn Pro Glu Ile Val
                85   90   95
Ala Arg His Phe Phe Lys Asn Leu Gly Val Val Val Ala Pro His Thr
            100   105   110
Leu Lys Leu Pro Ala Glu Pro Ile Thr Arg Trp Gly Glu Tyr Trp Cys
        115   120   125
Glu Val Thr Val Asn Gly Leu Asp Thr Val Arg Val Pro Met Ser Val
    130   135   140
Val Asn Phe Glu Lys Pro Lys Thr Lys Arg Tyr Lys Tyr Trp Leu Ala
145   150   155   160
Gln Gln Ala Ala Lys Ala Met Ala Pro Thr Ser Pro Gln Ile
                165   170

<210> 3351
<211> 1422
<212> DNA
<213> Homo sapiens

<400> 3351
nnggaataca gaagagaaac tagaaatata cgtattttgt ttcacatttg aacagtcatt
60
cttgaggaat actccatacc tgagtagaca gccatgtggc catcgcagct actaattttc
120

atgatgctct tagctccaat aattcatggt ggcaagcaca gtgaacgaca tcctgccctc
180
gctgctgcgc cgcgatgcgc tgagcgccgc caaggaggtg ttgtaccacc tggacatcta
240
cttcagcagc cagctgcaga gcgcgccgct gcccatcgtg gacaagggcc ccgtggagct
300
gctggaggag ttcgtgttcc aggtgcccaa ggagcgcagc gcgcagccca agagactgaa
360
ttcccttcag gagcttcaac ttcttgaaat catgtgcaat tatttccagg agcaaaccaa
420
ggactctgtt cggcagatta ttttttcatc ccttttcagc cctcaaggga acaaagccga
480
tgacagccgg atgagcttgt tgggaaaact ggtctccatg gcggtggctg tgtgtcgaat
540
cccggtgttg gagtgtgctg cctcctggct tcagcggacg cccgtggttt actgtgtgag
600
gttagccaag gcccttgtag atgactactg ctgtttggtg ccgggatcca ttcagacgct
660
gaagcagata ttcagtgcca gcccgagatt ctgctgccag ttcatcacct ccgttaccgc
720
gctctatgac ctgtcatcag atgacctcat tccacctatg gacttgcttg aaatgattgt
780
cacctggatt tttgaggacc caaggttgat tctcatcact tttttaaata ctccgattgc
840
ggccaatctg ccaataggat tcttagagct caccccgctc gttggattga tccgctggtg
900
cgtgaaggca cccctggctt ataaaaggaa aaagaagccc cccttatcca atggccatgt
960
cagcaacaag gtcacaaagg acccgggcgt ggggatggac agagactccc acctcttgta
1020
ctcaaaactc cacctcagcg tcctgcaagt gctcatgacg ctgcagctgc acctgaccga
1080
gaagaatctg tatgggcgcc tggggctgat cctcttcgac cacatggtcc cgctggtaga
1140
ggagatcaac aggttggcgg atgaactgaa ccccctcaac gcctcccagg agattgagct
1200
ctcgctggac cggctggcgc aggctctgca ggtggccatg gcctcaggag ctctgctgtg
1260
cacgagagat gaccttagaa ccttgttctc caggctcccc cgtaataacc tcctccagct
1320
ggtgatctcg ggtcccgtgc agcagtcgcc tcacgccgcg ctcccccccgg ggttctaccc
1380
ccacatccac acgcccccgc tgggctacgg ggctgtcccc cc
1422

<210> 3352
<211> 97
<212> PRT
<213> Homo sapiens

<400> 3352
Met Trp Pro Ser Gln Leu Leu Ile Phe Met Met Leu Leu Ala Pro Ile
1 5 10 15
Ile His Gly Gly Lys His Ser Glu Arg His Pro Ala Leu Ala Ala Ala

```
            20                  25                  30
Pro Arg Cys Ala Glu Arg Arg Gln Gly Gly Val Val Pro Pro Gly His
        35                  40                  45
Leu Leu Gln Gln Pro Ala Ala Glu Arg Ala Ala Ala His Arg Gly Gln
    50                  55                  60
Gly Pro Arg Gly Ala Ala Gly Gly Val Arg Val Pro Gly Ala Gln Gly
65                  70                  75                  80
Ala Gln Arg Ala Ala Gln Glu Thr Glu Phe Pro Ser Gly Ala Ser Thr
                85                  90                  95
Ser
```

<210> 3353
<211> 420
<212> DNA
<213> Homo sapiens

<400> 3353
nngaagctat cctcatcctc ttcccgacct cggtcctgtg aagtccctgg aattaacatc
60
tttccatctc ctgaccagcc tgccaatgtg cctgtcctcc cacctgccat gaacacgggg
120
ggctccctac ctgacctcac caacctgcac tttcccccac cactgcccac ccccctggac
180
cctgaagaga cagcctaccc tagcctgagt gggggcaaca gtacctccaa tttgacccac
240
accatgactc acctgggcat cagcaggggc atgggcctgg gcccaggcta tgatgcacca
300
gggcgtcccc ctggatacca gtaaactgtc cactgaccag cggttacccc catacccata
360
cagttcccca agtttggtnt ctgcttaccc agccccacac cccaaagttt taacagcagc
420

<210> 3354
<211> 107
<212> PRT
<213> Homo sapiens

<400> 3354

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Xaa Lys Leu Ser Ser Ser Ser Ser Arg Pro Arg Ser Cys Glu Val Pro
 1               5                  10                  15
Gly Ile Asn Ile Phe Pro Ser Pro Asp Gln Pro Ala Asn Val Pro Val
            20                  25                  30
Leu Pro Pro Ala Met Asn Thr Gly Gly Ser Leu Pro Asp Leu Thr Asn
        35                  40                  45
Leu His Phe Pro Pro Pro Leu Pro Thr Pro Leu Asp Pro Glu Glu Thr
    50                  55                  60
Ala Tyr Pro Ser Leu Ser Gly Gly Asn Ser Thr Ser Asn Leu Thr His
65                  70                  75                  80
Thr Met Thr His Leu Gly Ile Ser Arg Gly Met Gly Leu Gly Pro Gly
                85                  90                  95
Tyr Asp Ala Pro Gly Arg Pro Pro Gly Tyr Gln
            100                 105
```

<210> 3355
<211> 474
<212> DNA
<213> Homo sapiens

<400> 3355
gaacagccag ttgaacctga tggccccctt cctggctcag acaataacca agaaaagaaa
60
gtaagattat ctccagccaa aatgtcaacc aagaattcta cagatctagt tgaatatgtt
120
gacaagagtc atgctttttct ccccatcatt ccaaacaccc agagaggtca gctagaagac
180
agactgaaca accaggcgcg taccatagct ttccttcttg aacaagcctt ccgcatcaag
240
gaggacatct ctgcttgcct gcaggggacc catggctttc gaaaagagga atcgctcgcc
300
aggaagttac tggaaagcca catccagacc atcaccagca tcgtcaaaaa actcagccaa
360
aatattgaga ttttagaaga ccaaataaga gctcgagatc aggcggccac aggaactaac
420
tttgcagtac acgagataaa catcaaacac ctacaaggag ttgggagatc tttc
474

<210> 3356
<211> 131
<212> PRT
<213> Homo sapiens

<400> 3356
Met Ser Thr Lys Asn Ser Thr Asp Leu Val Glu Tyr Val Asp Lys Ser
1 5 10 15
His Ala Phe Leu Pro Ile Ile Pro Asn Thr Gln Arg Gly Gln Leu Glu
20 25 30
Asp Arg Leu Asn Asn Gln Ala Arg Thr Ile Ala Phe Leu Leu Glu Gln
35 40 45
Ala Phe Arg Ile Lys Glu Asp Ile Ser Ala Cys Leu Gln Gly Thr His
50 55 60
Gly Phe Arg Lys Glu Glu Ser Leu Ala Arg Lys Leu Leu Glu Ser His
65 70 75 80
Ile Gln Thr Ile Thr Ser Ile Val Lys Lys Leu Ser Gln Asn Ile Glu
85 90 95
Ile Leu Glu Asp Gln Ile Arg Ala Arg Asp Gln Ala Ala Thr Gly Thr
100 105 110
Asn Phe Ala Val His Glu Ile Asn Ile Lys His Leu Gln Gly Val Gly
115 120 125
Arg Ser Phe
130

<210> 3357
<211> 2268
<212> DNA
<213> Homo sapiens

<400> 3357

nnggagcccc tggtctgatt ggtcctcacc atgataaccc tccacaacag gtactccagc
60
agcagccatt atggatttgg atgtgctctt tatacccatg tctctaattg cagatggagg
120
agggcctata aaaataattc cttcttgctt acaaagttca gcaaattcca tgttttctga
180
aagaaaaccg catcctggat ggatagcctg tgcagcagag gtcttggcca cttgaatgat
240
tttctccata gataggtagc tctgctggga ggaacgggtt tggcgtgtgg gacgcagctg
300
cctctgtact ggggagtcac ggagtggccg ggctccaggg acatggcggc ggcctctgcg
360
gtgtcggtgc tgctggtggc ggcggagagg aaccggtggc atcgtctccc gagcctgctc
420
ctgccgccga ggacatgggt gtggaggcaa agaaccatga agtacacaac agccacagga
480
agaaacatta ccaaggtcct cattgcaaac agaggagaaa ttgcctgcag ggtgatgcgc
540
acagccaaaa aactgggtgt acagactgtg gcggtttata gtgaggctga cagaaattcc
600
atgcatgtag atatggcaga tgaagcatat tccatcggcc ccgctccctc ccagcagagc
660
tacctatcta tggagaaaat cattcaagtg gccaagacct ctgctgcaca ggctatccat
720
ccaggatgcg gttttctttc agaaaacatg gaatttgctg aactttgtaa gcaagaagga
780
attatttta taggccctcc tccatctgca attagagaca tgggtataaa gagcacatcc
840
aaatccataa tggctgctgc tggagtacct gttgtggagg gttatcatgg tgaggaccaa
900
tcagaccagt gcctgaagga acacgccagg agaattggct atcctgtcat gattaaagcc
960
gtccggggtg gaggaggaaa aggaatgagg attgttagat cagaacaaga atttcaagaa
1020
cagttagagt cagcacggag agaagctaag aagtctttca atgatgatgc tatgctgatc
1080
gagaagtttg tagacacacc gaggcatgta gaagtccagg tgtttggtga tcaccatggc
1140
aatgctgtgt acttgtttga aagagactgt agtgtgcaga ggcgacatca gaagatcatt
1200
gaggaggccc cagcgcctgg tattaaatct gaagtaagaa aaaagctggg agaagctgca
1260
gtcagagctg ctaaagctgt aaattatgtt ggagcaggga ctgtggagtt tattatggac
1320
tcaaaacata atttctgttt catggagatg aatacaaggc tgcaagtgga acatcctgtt
1380
actgagatga tcacaggaac tgacttggtg gagtggcagc ttagaattgc agcaggagag
1440
aagattcctt tgagccagga agaaataact ctgcagggcc atgccttcga agctagaata
1500
tatgcagaag atcctagcaa taacttcatg cctgtggcag gcccattagt gcacctctct
1560
actcctcgag cagacccttc caccaggatt gaaactggag tacggcaagg agacgaagtt
1620

tccgtgcatt atgaccccat gattgcgaag ctggtcgtgt gggcagcaga tcgccaggcg
1680
gcattgacaa aactgaggta cagccttcgt cagtacaata ttgttggact gcacaccaac
1740
attgacttct tactcaacct gtctggccac ccagagtttg aagctgggaa cgtgcacact
1800
gatttcatcc ctcaacacca caaacagttg ttgctcagtc ggaaggctgc agccaaagag
1860
tctttatgcc aggcagccct gggtctcatc ctcaaggaga aagccatgac cgacactttc
1920
actcttcagg cacatgatca attctctcca ttttcgtcta gcagtggaag aagactgaat
1980
atctcgtata ccagaaacat gactcttaaa gatggtaaaa acagttttcg tctcctcgga
2040
taatcaacca tttccatact catgtaatct aggcatactc tggagttatt acaggtttgg
2100
ttccagacca ctacaataaa atgtagccat agctgtaacg tataaccatg atgggtctta
2160
tagcatgcag attgaagata aaactttcca agtccttggt aatctttaca gcgagggaga
2220
ctgcacttac ctgaaatgtt ctgttaatgg agttgctagt aaagcgaa
2268

<210> 3358
<211> 493
<212> PRT
<213> Homo sapiens

<400> 3358
Gln Thr Val Ala Val Tyr Ser Glu Ala Asp Arg Asn Ser Met His Val
1 5 10 15
Asp Met Ala Asp Glu Ala Tyr Ser Ile Gly Pro Ala Pro Ser Gln Gln
20 25 30
Ser Tyr Leu Ser Met Glu Lys Ile Ile Gln Val Ala Lys Thr Ser Ala
35 40 45
Ala Gln Ala Ile His Pro Gly Cys Gly Phe Leu Ser Glu Asn Met Glu
50 55 60
Phe Ala Glu Leu Cys Lys Gln Glu Gly Ile Ile Phe Ile Gly Pro Pro
65 70 75 80
Pro Ser Ala Ile Arg Asp Met Gly Ile Lys Ser Thr Ser Lys Ser Ile
85 90 95
Met Ala Ala Ala Gly Val Pro Val Val Glu Gly Tyr His Gly Glu Asp
100 105 110
Gln Ser Asp Gln Cys Leu Lys Glu His Ala Arg Arg Ile Gly Tyr Pro
115 120 125
Val Met Ile Lys Ala Val Arg Gly Gly Gly Gly Lys Gly Met Arg Ile
130 135 140
Val Arg Ser Glu Gln Glu Phe Gln Glu Gln Leu Glu Ser Ala Arg Arg
145 150 155 160
Glu Ala Lys Lys Ser Phe Asn Asp Asp Ala Met Leu Ile Glu Lys Phe
165 170 175
Val Asp Thr Pro Arg His Val Glu Val Gln Val Phe Gly Asp His His
180 185 190
Gly Asn Ala Val Tyr Leu Phe Glu Arg Asp Cys Ser Val Gln Arg Arg

```
        195                 200                 205
His Gln Lys Ile Ile Glu Glu Ala Pro Ala Pro Gly Ile Lys Ser Glu
    210                 215                 220
Val Arg Lys Lys Leu Gly Glu Ala Ala Val Arg Ala Ala Lys Ala Val
225                 230                 235                 240
Asn Tyr Val Gly Ala Gly Thr Val Glu Phe Ile Met Asp Ser Lys His
                245                 250                 255
Asn Phe Cys Phe Met Glu Met Asn Thr Arg Leu Gln Val Glu His Pro
            260                 265                 270
Val Thr Glu Met Ile Thr Gly Thr Asp Leu Val Glu Trp Gln Leu Arg
        275                 280                 285
Ile Ala Ala Gly Glu Lys Ile Pro Leu Ser Gln Glu Glu Ile Thr Leu
    290                 295                 300
Gln Gly His Ala Phe Glu Ala Arg Ile Tyr Ala Glu Asp Pro Ser Asn
305                 310                 315                 320
Asn Phe Met Pro Val Ala Gly Pro Leu Val His Leu Ser Thr Pro Arg
                325                 330                 335
Ala Asp Pro Ser Thr Arg Ile Glu Thr Gly Val Arg Gln Gly Asp Glu
            340                 345                 350
Val Ser Val His Tyr Asp Pro Met Ile Ala Lys Leu Val Val Trp Ala
        355                 360                 365
Ala Asp Arg Gln Ala Ala Leu Thr Lys Leu Arg Tyr Ser Leu Arg Gln
    370                 375                 380
Tyr Asn Ile Val Gly Leu His Thr Asn Ile Asp Phe Leu Leu Asn Leu
385                 390                 395                 400
Ser Gly His Pro Glu Phe Glu Ala Gly Asn Val His Thr Asp Phe Ile
                405                 410                 415
Pro Gln His His Lys Gln Leu Leu Leu Ser Arg Lys Ala Ala Ala Lys
            420                 425                 430
Glu Ser Leu Cys Gln Ala Ala Leu Gly Leu Ile Leu Lys Glu Lys Ala
        435                 440                 445
Met Thr Asp Thr Phe Thr Leu Gln Ala His Asp Gln Phe Ser Pro Phe
    450                 455                 460
Ser Ser Ser Ser Gly Arg Arg Leu Asn Ile Ser Tyr Thr Arg Asn Met
465                 470                 475                 480
Thr Leu Lys Asp Gly Lys Asn Ser Phe Arg Leu Leu Gly
                485                 490
```

<210> 3359
<211> 652
<212> DNA
<213> Homo sapiens

<400> 3359
ntccggacgt aatcgtggtt tttgttctgc aataggcggc ttagagggag gggctttttc
60
gcctatacct actgtagctt ctccacgtat ggaccctaaa ggctactgct gctactacgg
120
ggctagacag ttactgtctc agctctagga tgtgcgttct tccactagaa gctcttctga
180
gggaggtaat taaaaaacag tggaatggaa aaacagtgct gtagtcatcc tgtaatatgc
240
tccttgtcaa caatgtatac attcctgcta ggtgccatat tcattgcttt aagctcaagt
300

cgcatcttac tagtgaagta ttctgccaat gaagaaaaca agtatgatta tcttccaact
360
actgtgaatg tgtgctcaga actggtgaag ctagttttct gtgtgcttgt gtcattctgt
420
gttataaaga aagatcatca aagtagaaat ttgaaatatg cttcctggaa ggaattctct
480
gatttcatga agtggtccat tcctgccttt ctttatttcc tggataactt gattgtcttc
540
tatgtcctgt cctatcttca accagccatg gctgttatct tctcaaattt tagcattata
600
acaacagctc ttctattcag gatagtgctg aagaggcgtc taaactggat cc
652

<210> 3360
<211> 149
<212> PRT
<213> Homo sapiens

<400> 3360
Met Glu Lys Gln Cys Cys Ser His Pro Val Ile Cys Ser Leu Ser Thr
1 5 10 15
Met Tyr Thr Phe Leu Leu Gly Ala Ile Phe Ile Ala Leu Ser Ser Ser
20 25 30
Arg Ile Leu Leu Val Lys Tyr Ser Ala Asn Glu Glu Asn Lys Tyr Asp
35 40 45
Tyr Leu Pro Thr Thr Val Asn Val Cys Ser Glu Leu Val Lys Leu Val
50 55 60
Phe Cys Val Leu Val Ser Phe Cys Val Ile Lys Lys Asp His Gln Ser
65 70 75 80
Arg Asn Leu Lys Tyr Ala Ser Trp Lys Glu Phe Ser Asp Phe Met Lys
85 90 95
Trp Ser Ile Pro Ala Phe Leu Tyr Phe Leu Asp Asn Leu Ile Val Phe
100 105 110
Tyr Val Leu Ser Tyr Leu Gln Pro Ala Met Ala Val Ile Phe Ser Asn
115 120 125
Phe Ser Ile Ile Thr Thr Ala Leu Leu Phe Arg Ile Val Leu Lys Arg
130 135 140
Arg Leu Asn Trp Ile
145

<210> 3361
<211> 1040
<212> DNA
<213> Homo sapiens

<400> 3361
nntccggatg gtctggcgcg ctgggctcgc taggtttgtg ctggcgaggg gacggggtgg
60
gacgggcgac ccggacccaa gaagtgggag gaccgcgcgt gtcgcggcct agcggcgagg
120
ggagtcgcct gcgcgcgcag cggaggccag tgcgccggcg catagcgagc ccgggtctgt
180
gatcgccgag gcgggagtga agatagtcca agtcctaaga gacagcgcct ctctcattca
240

gtctttgatt atacatcagc atcaccagct ccctcaccac caatgcgacc atgggagatg
300
acatcaaata ggcagccccc ttcagttcga ccaagccaac atcacttctc aggggaacga
360
tgcaacacac ctgcacgcaa cagaagaagt cctcctgtca ggcgccagag aggaagaagg
420
gatcgtctgt ctcgacataa ttccattagt caagatgaaa actatcacca tctcccttac
480
gcacagcagc aagcaataga ggagcctcga gccttccacc ctccgaatgt atctccccgt
540
ctgctacatc ctgctgctca tccaccccag cagaatgcag tcatggttga catacatgat
600
cagctccatc aaggaacagt ccctgtttct tacacagtaa caacagtggc accacatggg
660
attccactct gcacaggcca gcacatccct gcttgtagta cacagcaggt cccaggatgc
720
tctgtggttt tcagtggaca gcacctccct gtctgtagtg tgcctcctcc aatgcttcag
780
gcatgttcag ttcagcactt accagtacca tatgctgcat tcccacccct tatttctagt
840
gatccatttc ttatacatcc tcctcacctt tctccccatc atcctcctca tttgccacca
900
ccaggccagt ttgtcccttt ccaaacacag caatcacgat cgcctctgca aaggatagaa
960
aatgaagtgg aactcttagg agaacatctt ccaggagccc acccccagca cccccatctg
1020
ttaataaata tctcaactcc
1040

<210> 3362
<211> 252
<212> PRT
<213> Homo sapiens

<400> 3362
Met Arg Pro Trp Glu Met Thr Ser Asn Arg Gln Pro Pro Ser Val Arg
1 5 10 15
Pro Ser Gln His His Phe Ser Gly Glu Arg Cys Asn Thr Pro Ala Arg
20 25 30
Asn Arg Arg Ser Pro Pro Val Arg Arg Gln Arg Gly Arg Arg Asp Arg
35 40 45
Leu Ser Arg His Asn Ser Ile Ser Gln Asp Glu Asn Tyr His His Leu
50 55 60
Pro Tyr Ala Gln Gln Gln Ala Ile Glu Glu Pro Arg Ala Phe His Pro
65 70 75 80
Pro Asn Val Ser Pro Arg Leu Leu His Pro Ala Ala His Pro Pro Gln
85 90 95
Gln Asn Ala Val Met Val Asp Ile His Asp Gln Leu His Gln Gly Thr
100 105 110
Val Pro Val Ser Tyr Thr Val Thr Thr Val Ala Pro His Gly Ile Pro
115 120 125
Leu Cys Thr Gly Gln His Ile Pro Ala Cys Ser Thr Gln Gln Val Pro
130 135 140
Gly Cys Ser Val Val Phe Ser Gly Gln His Leu Pro Val Cys Ser Val

```
145                 150                 155                 160
Pro Pro Pro Met Leu Gln Ala Cys Ser Val Gln His Leu Pro Val Pro
                165                 170                 175
Tyr Ala Ala Phe Pro Pro Leu Ile Ser Ser Asp Pro Phe Leu Ile His
            180                 185                 190
Pro Pro His Leu Ser Pro His His Pro Pro His Leu Pro Pro Pro Gly
        195                 200                 205
Gln Phe Val Pro Phe Gln Thr Gln Gln Ser Arg Ser Pro Leu Gln Arg
    210                 215                 220
Ile Glu Asn Glu Val Glu Leu Leu Gly Glu His Leu Pro Gly Ala His
225                 230                 235                 240
Pro Gln His Pro His Leu Leu Ile Asn Ile Ser Thr
                245                 250
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<210> 3363
<211> 718
<212> DNA
<213> Homo sapiens

<400> 3363
cagaaggacc ccaggatggc ggtcatcatg cccaggaacg ttggtgatgg ggaatgggtt
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ggccagcatg atcagggacc ccgtcatgcc catgattttt tgggtggcat tggcgaccga
120
gtagctcagg agtgtctccg gagcccactg gagaagcccc ccaacggcct cctcttcccc
180
cagcacgggg actatcagta cggccgcaac aacatctaaa cagaccactt ccaatacagc
240
cggcagagct acccaaactc gtacagtttg aaccgctatg atgtgtagag tccaaaggac
300
aggaccagac tgttggtgac tccttccccg gcccccacag cagtatcaga aacttctgac
360
aatcagtgaa tgtacaaccc agccgagggg acggtgcata actctccatc agaagccctg
420
gggttcctgg ccccccgtga gccgcaggag gatgcgttgc ctgcagtgca gacggccgtg
480
agctctgggc aaacctaaac agagaccagt gtcccatgct ctttcttcct ggagcctgtc
540
atctgagggc cgtgtccctg cggagatctt ggccacgttg tacctttcca tgtggaatta
600
ttccccaagc agtgtagctc agagcacttg tgtctgcatt ccagataaca ttcaggacct
660
gtgtgaaaag ctggggtcac tgtggctgta gaccatgaac tggcagtggg ggtgtcca
718

<210> 3364
<211> 163
<212> PRT
<213> Homo sapiens

<400> 3364
Met Gly His Trp Ser Leu Phe Arg Phe Ala Gln Ser Ser Arg Pro Ser
 1   5   10   15
Ala Leu Gln Ala Thr His Pro Pro Ala Ala His Gly Gly Pro Gly Thr

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            20                  25                  30
Pro Gly Leu Leu Met Glu Ser Tyr Ala Pro Ser Pro Arg Leu Gly Cys
        35                  40                  45
Thr Phe Thr Asp Cys Gln Lys Phe Leu Ile Leu Leu Trp Gly Pro Gly
    50                  55                  60
Lys Glu Ser Pro Thr Val Trp Ser Cys Pro Leu Asp Ser Thr His His
65                  70                  75                  80
Ser Gly Ser Asn Cys Thr Ser Leu Gly Ser Ser Ala Gly Cys Ile Gly
                85                  90                  95
Ser Gly Leu Phe Arg Cys Cys Cys Gly Arg Thr Asp Ser Pro Arg Ala
            100                 105                 110
Gly Gly Arg Gly Gly Arg Trp Gly Ala Ser Pro Val Gly Ser Gly Asp
        115                 120                 125
Thr Pro Glu Leu Leu Gly Arg Gln Cys His Pro Lys Asn His Gly His
    130                 135                 140
Asp Gly Val Pro Asp His Ala Gly Gln Pro Ile Pro His His Gln Arg
145                 150                 155                 160
Ser Trp Ala
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<210> 3365
<211> 2389
<212> DNA
<213> Homo sapiens

<400> 3365
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tcgggtggca gcgccgggcg caacgcaggg gtcacggcga cggcggcggc ggctgacggc
180
tggaagggta ggcttccttc accgctcgtc ctccttcctc gctccgctcg gtgtcaggcg
240
cggcggcggc gcggcgggcg gacttcgtcc ctcctcctgc tccccccccac accggagcgg
300
gcactcttcg cttcgccatc ccccgaccct tcaccccgag gactgggcgc ctcctccggc
360
gcagctgagg gagcgggggc cggtctcctg ctcggttgtc gagcctccat gtcggataat
420
cagaactgga actcgtcggg ctcggaggag gatccagaga cggagtctgg gccgcctgtg
480
gagcgctgcg gggtcctcag taagtggaca aactacattc atgggtggca ggatcgttgg
540
gtagttttga aaaataatgc tctgagttac tacaaatctg aagatgaaac agagtatggc
600
tgcagaggat ccatctgtct tagcaaggct gtcatcacac ctcacgattt tgatgaatgt
660
cgatttgata ttagtgtaaa tgatagtgtt tggtatcttc gtgctcagga tccagatcat
720
agacagcaat ggatagatgc cattgaacag cacaagactg aatctggata tggatctgaa
780
tccagcttgc gtcgacatgg ctcaatggtg tccctggtgt ctggagcaag tggctactct
840

gcaacatcca cctcttcatt caagaaaggc cacagtttac gtgagaagtt ggctgaaatg
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960
tgtgctgatg ctgtctctaa ggatgaactt caaagggata aagtggtaga agatgatgaa
1020
gatgactttc ctacaacgcg ttctgatggt gacttcttgc atagtaccaa cggcaataaa
1080
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1140
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1200
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agaagaacag aggaagcata taaaaatgca atgacagaac ttaagaaaaa atcccacttt
1320
ggaggaccag attatgaaga aggccctaac agtctgatta atgaagaaga gttctttgat
1380
gctgttgaag ctgctcttga cagacaagat aaaatagaag aacagtcaca gagtgaaaag
1440
gtgagattac attggcctac atccttgccc tctggagatg ccttttcttc tgtggggaca
1500
catagatttg tccaaaagcc ctatagtcgc tcttcctcca tgtcttccat tgatctagtc
1560
agtgcctctg atgatgttca cagattcagc tcccaggttg aagagatggt gcagaaccac
1620
atgacttact cattacagga tgtaggcgga gatgccaatt ggcagttggt tgtagaagaa
1680
ggagaaatga aggtatacag aagagaagta gaagaaaatg ggattgttct ggatccttta
1740
aaagctaccc atgcagttaa aggcgtcaca ggacatgaag tctgcaatta tttctggaat
1800
gttgacgttc gcaatgactg ggaaacaact atagaaaact ttcatgtggt ggaaacatta
1860
gctgataatg caatcatcat ttatcaaaca cacaagaggg tgtggcctgc ttctcagcga
1920
gacgtattat atctttctgt cattcgaaag ataccagcct tgactgaaaa tgaccctgaa
1980
acttggatag tttgtaattt ttctgtggat catgacagtg ctcctctaaa caaccgatgt
2040
gtccgtgcca aaataaatgt tgctatgatt tgtcaaacct tggtaagccc accagaggga
2100
aaccaggaaa ttagcaggga caacattcta tgcaagatta catatgtagc taatgtgaac
2160
cctggaggat gggcaccagc ctcagtgtta agggcagtgg caaagcgaga gtatcctaaa
2220
tttctaaaac gttttacttc ttacgtccaa gaaaaaactg caggaaagcc tattttgttc
2280
tagtattaac aggtactaga agatatgttt tatctttttt taactttatt tgactaatat
2340
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2389

<210> 3366

<211> 624
<212> PRT
<213> Homo sapiens

<400> 3366

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            20                  25                  30
Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
        35                  40                  45
Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
    50                  55                  60
Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
65                  70                  75                  80
Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
                85                  90                  95
Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
            100                 105                 110
Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
        115                 120                 125
Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
    130                 135                 140
Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
145                 150                 155                 160
Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
                165                 170                 175
Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp
            180                 185                 190
Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
        195                 200                 205
Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys
    210                 215                 220
Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
225                 230                 235                 240
Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
                245                 250                 255
Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser
            260                 265                 270
Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu
        275                 280                 285
Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe
    290                 295                 300
Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
305                 310                 315                 320
Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
                325                 330                 335
Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser
            340                 345                 350
Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
        355                 360                 365
Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val
    370                 375                 380
Ser Ala Ser Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met
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385 390 395 400
Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala
405 410 415
Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg
420 425 430
Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His
435 440 445
Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn
450 455 460
Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val
465 470 475 480
Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys
485 490 495
Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile
500 505 510
Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val
515 520 525
Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys
530 535 540
Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser
545 550 555 560
Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys
565 570 575
Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser
580 585 590
Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg
595 600 605
Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe
610 615 620

<210> 3367
<211> 366
<212> DNA
<213> Homo sapiens

<400> 3367
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gagaattacg ccacagaggt gttggaggct ggcatcgtgg catctcagga gcacggaggg
120
tgccttcccc acttcaggcc tcttagtgtc aaggatgtga gaggcaaggg ctgctgggag
180
agtattttac ggactgaagg aggcgtgccg cctgccctgc cctcctactg gtggaggaag
240
gaggtgctgg gagccccaca actcagggcc ccccgacgcc cagtaaggcc actgtacacc
300
cctcctgacc cagaccataa ccagcctccg attgtgcttt tgaccctgtt tccttcaggc
360
accagg
366

<210> 3368
<211> 104
<212> PRT

<213> Homo sapiens

<400> 3368
Met Thr Glu Asn Tyr Ala Thr Glu Val Leu Glu Ala Gly Ile Val Ala
1 5 10 15
Ser Gln Glu His Gly Gly Cys Leu Pro His Phe Arg Pro Leu Ser Val
20 25 30
Lys Asp Val Arg Gly Lys Gly Cys Trp Glu Ser Ile Leu Arg Thr Glu
35 40 45
Gly Gly Val Pro Pro Ala Leu Pro Ser Tyr Trp Trp Arg Lys Glu Val
50 55 60
Leu Gly Ala Pro Gln Leu Arg Ala Pro Arg Arg Pro Val Arg Pro Leu
65 70 75 80
Tyr Thr Pro Pro Asp Pro Asp His Asn Gln Pro Pro Ile Val Leu Leu
85 90 95
Thr Leu Phe Pro Ser Gly Thr Arg
100

<210> 3369
<211> 1405
<212> DNA
<213> Homo sapiens

<400> 3369
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gataaggagc agaaaaatca ggaaaactgt ggtgcaaaga agaataaaaa gaagaggaaa
120
aaggttttat ataatgccaa taaaaatgat gattatgaca acgaggagat cttaacctat
180
gaggaaatgt cactttatca tcagccagca aataggaaga gacctatcat cttgattggt
240
ccacagaact gtggccagaa tgaattgcgt cagaggctca tgaacaaaga aaaggaccgc
300
tttgcatctg cagttcctca tacaacccgg agtaggcgag accaagaagt agccggtaga
360
gattaccact ttgtttcgcg gcaagcattc gaggcagaca tagcagctgg aaagttcatt
420
gagcatggtg aatttgagaa gaatttgtat ggaactagca tagattctgt acggcaagtg
480
atcaactctg gcaaaatatg tcttttaagt cttcgtacac agtcattgaa gactctccgg
540
aattcagatt tgaaaccata tattatcttc attgcacccc cttcacaaga aagacttcgg
600
gcattattgg ccaaagaagg caagaatcca aagcctgaag agttgagaga aatcattgag
660
aagacaagag agatggagca gaacaatggc cactactttg atacggcaat tgtgaattcc
720
gatcttgata aagcctatca ggaattgctt aggttaatta acaaacttga tactgaacct
780
cagtgggtac catccacttg gctgaggtga aagaaacatc cattctgtgg catgttggac
840
ttgatctggc aaaaactgcc aataggagga ctgcccgaca ctgcagcaag attgaggata
900

agatggaagg cagcagtata agctgtagat ctgttcttag atctcttgaa ttagtgagac
960
gacagttccc ttaggcagtt tgtgcatggc atcctttatt ctctatacat ggctttagcg
1020
gttcttgcct cattttggga ttctaaatgg aagctttcaa cagagcattc cattttgtcc
1080
tgttaaaacc ttttgttttc acctaaaccc tttctgctta gttgtatctc tgtgaaaaac
1140
ttgtatacac aagcgtccat gtctcacaca aatattgatg tgattattct taagtgttaa
1200
atcattaaca cttaaatgac ttcattggga atattgagca gagggactgt gcttctatgc
1260
actgggcaag gcagtatttg cttaggaaac taatttagtc atcagagata ctttcctaaa
1320
aaggaaaaat aaaaaacaaa atggtgccac tttgggttga agctactttg ttaggcttga
1380
attcatttat atgtcttttg attct
1405

<210> 3370
<211> 269
<212> PRT
<213> Homo sapiens

<400> 3370
Leu Val Pro Gly Lys Ser Phe Gln Gln Gln Arg Glu Ala Met Lys Gln
1 5 10 15
Thr Ile Glu Glu Asp Lys Glu Gln Lys Asn Gln Glu Asn Cys Gly Ala
20 25 30
Lys Lys Asn Lys Lys Lys Arg Lys Lys Val Leu Tyr Asn Ala Asn Lys
35 40 45
Asn Asp Asp Tyr Asp Asn Glu Glu Ile Leu Thr Tyr Glu Glu Met Ser
50 55 60
Leu Tyr His Gln Pro Ala Asn Arg Lys Arg Pro Ile Ile Leu Ile Gly
65 70 75 80
Pro Gln Asn Cys Gly Gln Asn Glu Leu Arg Gln Arg Leu Met Asn Lys
85 90 95
Glu Lys Asp Arg Phe Ala Ser Ala Val Pro His Thr Thr Arg Ser Arg
100 105 110
Arg Asp Gln Glu Val Ala Gly Arg Asp Tyr His Phe Val Ser Arg Gln
115 120 125
Ala Phe Glu Ala Asp Ile Ala Ala Gly Lys Phe Ile Glu His Gly Glu
130 135 140
Phe Glu Lys Asn Leu Tyr Gly Thr Ser Ile Asp Ser Val Arg Gln Val
145 150 155 160
Ile Asn Ser Gly Lys Ile Cys Leu Leu Ser Leu Arg Thr Gln Ser Leu
165 170 175
Lys Thr Leu Arg Asn Ser Asp Leu Lys Pro Tyr Ile Ile Phe Ile Ala
180 185 190
Pro Pro Ser Gln Glu Arg Leu Arg Ala Leu Leu Ala Lys Glu Gly Lys
195 200 205
Asn Pro Lys Pro Glu Glu Leu Arg Glu Ile Ile Glu Lys Thr Arg Glu
210 215 220
Met Glu Gln Asn Asn Gly His Tyr Phe Asp Thr Ala Ile Val Asn Ser

225 230 235 240
Asp Leu Asp Lys Ala Tyr Gln Glu Leu Leu Arg Leu Ile Asn Lys Leu
245 250 255
Asp Thr Glu Pro Gln Trp Val Pro Ser Thr Trp Leu Arg
260 265

<210> 3371
<211> 790
<212> DNA
<213> Homo sapiens

<400> 3371
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gacagaccag agactccagt caccctcgcc atctgtggaa tcatattctg gctgatcttt
120
ggtttcaaaa gtccggtggc ctggggctgt atggtcccac cccctggggg ggttgaggaa
180
gttgctgtcg tctgaggtac tgccgtacgt gtagtcctgg tccccgcttt tgccctggcc
240
aaagaagcac caagggagca tctggaccac caggctgcac accaaccctt ccccagaccg
300
cgattccgac aagagacggg gcacccttca ttgcaaagag atttccccag atcctttctc
360
cttgatctac caaactttcc agatctttcc aaagctgata tcaatgggca gaatccaaat
420
atccaggtca ccatagaggt ggtcgacggt cctgactctg aagcagataa agatcagcat
480
ccggagaata agcccagctg gtcagtccca tcccccgact ggcgggcctg gtggcagagg
540
tccctgtcct tggccagggc aaacagcggg gaccaggact acaagtacga cagtacctca
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660
acttttgaaa ccaaagatca gccagaatat gattccacag atggcgaggg tgactggagt
720
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780
ggctacgcgt
790

<210> 3372
<211> 198
<212> PRT
<213> Homo sapiens

<400> 3372
Gly Thr Ala Val Arg Val Val Leu Val Pro Ala Phe Ala Leu Ala Lys
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Glu Ala Pro Arg Glu His Leu Asp His Gln Ala Ala His Gln Pro Phe
20 25 30
Pro Arg Pro Arg Phe Arg Gln Glu Thr Gly His Pro Ser Leu Gln Arg
35 40 45
Asp Phe Pro Arg Ser Phe Leu Leu Asp Leu Pro Asn Phe Pro Asp Leu

50 55 60
Ser Lys Ala Asp Ile Asn Gly Gln Asn Pro Asn Ile Gln Val Thr Ile
65 70 75 80
Glu Val Val Asp Gly Pro Asp Ser Glu Ala Asp Lys Asp Gln His Pro
85 90 95
Glu Asn Lys Pro Ser Trp Ser Val Pro Ser Pro Asp Trp Arg Ala Trp
100 105 110
Trp Gln Arg Ser Leu Ser Leu Ala Arg Ala Asn Ser Gly Asp Gln Asp
115 120 125
Tyr Lys Tyr Asp Ser Thr Ser Asp Asp Ser Asn Phe Leu Asn Pro Pro
130 135 140
Arg Gly Trp Asp His Thr Ala Pro Gly His Arg Thr Phe Glu Thr Lys
145 150 155 160
Asp Gln Pro Glu Tyr Asp Ser Thr Asp Gly Glu Gly Asp Trp Ser Leu
165 170 175
Trp Ser Val Cys Ser Val Thr Cys Gly Asn Gly Asn Gln Lys Arg Thr
180 185 190
Arg Ser Cys Gly Tyr Ala
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<210> 3373
<211> 726
<212> DNA
<213> Homo sapiens

<400> 3373
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120
gtgttctggt gcgggccagc gcctgaccgg tgcgggcggc ctcaggagag gagagcttgc
180
tcagtgcgtc acgtagtcag ggctcaggct ggggcccggc tccagagcct ggtcacattc
240
ccaagcttca ttctcttcac ctgtgaattg caggcttccc tggtgtgccc tgcacatgag
300
ggaagacaca cctgaagcac tgggtccctc catggccttg ggccgcagga accgtgggcg
360
cacgagcttg ggaaggacat gtcggaggcc ggcgcctgtg cgggcagaag ctgtgtcctc
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480
agcgcatcgg tggtcttcac gacgtacacc cagaagcacc cgtccatcga ggacgggcct
540
ccgtttgtgg agccgctgct taacttcatc tggttcctgc tgctggctgt ggacgggtgc
600
gtcttgggat cctgcagggg gaggggggctg tgaatgtgcg ggttgtgtgt agacgtggtg
660
tggatagctg tgtgggtgtg tgtgcaagtg tagccatggt gtgggtagcc gtgtgggtat
720
atgcat
726

<210> 3374

<211> 84
<212> PRT
<213> Homo sapiens

<400> 3374
Met Ser Glu Ala Gly Ala Cys Ala Gly Arg Ser Cys Val Leu Gln Pro
1 5 10 15
Phe His His Gln His Val Leu Ile Ser Arg Phe Leu Cys Leu Lys Asn
20 25 30
Lys Ser Ser Ala Ser Val Val Phe Thr Thr Tyr Thr Gln Lys His Pro
35 40 45
Ser Ile Glu Asp Gly Pro Pro Phe Val Glu Pro Leu Leu Asn Phe Ile
50 55 60
Trp Phe Leu Leu Leu Ala Val Asp Gly Cys Val Leu Gly Ser Cys Arg
65 70 75 80
Gly Arg Gly Leu

<210> 3375
<211> 393
<212> DNA
<213> Homo sapiens

<400> 3375
acgcgtgcat acgtgatctc atgtttgcac acatgtgtcc atgcagatgc atgctctcac
60
gcacatgtgc ccacacactc agcactcaca ccccgtcctg caggctcagc cccactcctg
120
agccacctgc ctgggctttg ggggcccagc cggcatgggg agccccaggc tccagctggc
180
ctcgcttggc tctgaaatct aggccaggat gcagagcccg cagtgcggcc agtggagccc
240
ctggtactgt gcgcagcccc cacctggcag ccccttttcc tgtcaaagcc cctcccagcg
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360
cttgcccagc atccccggcc tgcatctcac cag
393

<210> 3376
<211> 103
<212> PRT
<213> Homo sapiens

<400> 3376
Met Phe Ala His Met Cys Pro Cys Arg Cys Met Leu Ser Arg Thr Cys
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Ala His Thr Leu Ser Thr His Thr Pro Ser Cys Arg Leu Ser Pro Thr
20 25 30
Pro Glu Pro Pro Ala Trp Ala Leu Gly Ala Gln Pro Ala Trp Gly Ala
35 40 45
Pro Gly Ser Ser Trp Pro Arg Leu Ala Leu Lys Ser Arg Pro Gly Cys
50 55 60
Arg Ala Arg Ser Ala Ala Ser Gly Ala Pro Gly Thr Val Arg Ser Pro

65 70 75 80
His Leu Ala Ala Pro Phe Pro Val Lys Ala Pro Pro Ser Val Leu Ser
85 90 95
Pro Pro Gly Lys Leu Pro Ala
100

<210> 3377
<211> 5235
<212> DNA
<213> Homo sapiens

<400> 3377
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aggacatggc tgatcagttt tctgacagaa gtgggtaaat ttccgcgttg gtaaatttcc
120
tgacaggaaa tttcggggaa ctaaaaaggc tggaagaaca tgaagatgga gcagtcataa
180
accacccact caaggaccat ctccttcacg accatccaca cgagactcag attgtctgaa
240
ttgagctatc gcaacttaat gctaaaagct ccttaaagct acagatttat gacatagttc
300
cttccaaaat attacatcat aaatcattga gaagattaaa aaaaaacact tgaagaaatt
360
gtagttttaa acatctctgc atatattttg gatagctact aggttacttt aactgtcatt
420
aaggagcaca gacttactga agctttactg gacagaatcc tgggaaatcg atatcattat
480
aaggttatat ttcccagtta gcgggtgaag ggctggagac cttattgcag tcatggcttt
540
cacaaattac agcagtctga atcgagctca gctaaccttt gaatatctgc acacaaattc
600
gtaagtatcc tctaggtgcc actgaggtaa ccagtaactc gttccttgat attatatgga
660
aatcgtttcc ccagaaaatt ttgctttttc acttttgag atgtatccca ctggagtgaa
720
atgtgtcact ggatatcttg agctctgtat tgaagaactg agatcagtga aatacttgtt
780
gctaatccag aagaatctga tttttgttta ttggatcaaa attttctaaa tgcaaacttt
840
agttatttga agtcaatatg ttgagttgtt tcattcaagt gtttatagga atccaacaaa
900
tactgctcta ttggatcgcc aaatgttgga ctattttagt atcaaccgtt tcccctctgt
960
agtgacaacg tcctaaacag ttaggtttat aacaagtgtt tactttctaa caagaaaaca
1020
gaagacattt aaatgacaac tttcaagaag aaaatttta ttttttcaga agttggcatt
1080
atcttcctgg cagattgctc acatccaata ttatttgtat atgctaaaca ggaaacggca
1140
acttgtttat atctctattt agatagtctt tccccaaaat ttccacagaa acatacagtg
1200
ttcatggttc ttgagttcat gaaggagtaa tctaatcact ccaacatggt ctggaatgtt
1260

tcaggtttaa tccatatgcc cactctcttg gaggctgtcc agtagcgtca aaactttagt
1320
gttttaatac attcacctgt tacttttgag atgaagttca cctttcttgg atcacatgca
1380
aaggatgttt aggtctgtga agaaaagaat ttctaggccg ggtgctgtgg ctcacgcctg
1440
taatcccagc actttgggag gccgagaacc actcacgaat tcttgtttgg tgctcttgct
1500
gaactggttg ataatgcaag agatgctgat gccaccagaa tagatattta tgcagaaaga
1560
cgagaggacc ttcgaggagg atttatgctt tgctttttgg atgatggagc aggaatggat
1620
ccaagtgatg ctgccagtgt gatccagttt gggaagtcgg ccaagcgaac acctgagtct
1680
actcagattg ggcagtacgg gaatgggtta aaatcgggct caatgcgcat tgggaaggat
1740
tttatcctgt tcaccaagaa ggaagacacc atgacctgcc tcttcctgtc tcgcacgttt
1800
catgaggaag aaggcattga tgaagtgata gtcccactgc ccacctggaa tgctcggacc
1860
cgggaacctg tcacagacaa tgtagagaaa tttgccattg agacagaact catctataag
1920
tactctccat tccgcactga ggaggaagtg atgacccagt ttatgaagat tcctggggac
1980
agcggaacat tggtgatcat cttcaatctc aaactcatgg ataatggaga gccagaacta
2040
gacataatct caaatccaag agatatccag atggcagaga cgtccccaga gggcacgaag
2100
ccagagcggc gctcgttccg tgcctatgcc gctgtgctct atattgatcc ccggatgagg
2160
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2220
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2280
gcagtgcacg tagcaaggat tgctgaagag aaggcgcggg aggcagagag caaagctcgg
2340
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2400
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<210> 3378
<211> 970
<212> PRT
<213> Homo sapiens

<400> 3378
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35 40 45
Ile Gly Lys Asp Phe Ile Leu Phe Thr Lys Lys Glu Asp Thr Met Thr
50 55 60
Cys Leu Phe Leu Ser Arg Thr Phe His Glu Glu Glu Gly Ile Asp Glu
65 70 75 80
Val Ile Val Pro Leu Pro Thr Trp Asn Ala Arg Thr Arg Glu Pro Val
85 90 95
Thr Asp Asn Val Glu Lys Phe Ala Il- Glu Thr Glu Leu Ile Tyr Lys
100 105 110
Tyr Ser Pro Phe Arg Thr Glu Glu Glu Val Met Thr Gln Phe Met Lys
115 120 125
Ile Pro Gly Asp Ser Gly Thr Leu Val Ile Ile Phe Asn Leu Lys Leu
130 135 140
Met Asp Asn Gly Glu Pro Glu Leu Asp Ile Ile Ser Asn Pro Arg Asp
145 150 155 160
Ile Gln Met Ala Glu Thr Ser Pro Glu Gly Thr Lys Pro Glu Arg Arg

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Ser Phe Arg Ala Tyr Ala Ala Val Leu Tyr Ile Asp Pro Arg Met Arg
            180                 185                 190
Ile Phe Ile His Gly His Lys Val Gln Thr Lys Arg Leu Ser Cys Cys
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Leu Tyr Lys Pro Arg Met Tyr Lys Tyr Thr Ser Ser Arg Phe Lys Thr
    210                 215                 220
Arg Ala Glu Gln Glu Val Arg Ile Ala Val His Val Ala Arg Ile Ala
225                 230                 235                 240
Glu Glu Lys Ala Arg Glu Ala Glu Ser Lys Ala Arg Thr Leu Glu Val
                245                 250                 255
Arg Leu Gly Gly Asp Leu Thr Arg Asp Ser Arg Val Met Leu Arg Gln
            260                 265                 270
Val Gln Asn Arg Ala Ile Thr Leu Arg Arg Glu Ala Asp Val Lys Lys
        275                 280                 285
Arg Ile Lys Glu Ala Lys Gln Arg Ala Leu Lys Glu Pro Lys Glu Leu
    290                 295                 300
Asn Phe Val Phe Gly Val Asn Ile Glu His Arg Asp Leu Asp Gly Met
305                 310                 315                 320
Phe Ile Tyr Asn Cys Ser Arg Leu Ile Lys Met Tyr Glu Lys Val Gly
                325                 330                 335
Pro Gln Leu Glu Gly Gly Met Ala Cys Gly Gly Val Val Gly Val Val
            340                 345                 350
Asp Val Pro Tyr Leu Val Leu Glu Pro Thr His Asn Lys Gln Asp Phe
        355                 360                 365
Ala Asp Ala Lys Glu Tyr Arg His Leu Leu Arg Ala Met Gly Glu His
    370                 375                 380
Leu Ala Gln Tyr Trp Lys Asp Ile Ala Ile Ala Gln Arg Gly Ile Ile
385                 390                 395                 400
Lys Phe Trp Asp Glu Phe Gly Tyr Leu Ser Ala Asn Trp Asn Gln Pro
                405                 410                 415
Pro Ser Ser Glu Leu Arg Tyr Lys Arg Arg Arg Ala Met Glu Ile Pro
            420                 425                 430
Thr Thr Ile Gln Cys Asp Leu Cys Leu Lys Trp Arg Thr Leu Pro Phe
        435                 440                 445
Gln Leu Ser Ser Val Glu Lys Asp Tyr Pro Asp Thr Trp Val Cys Ser
    450                 455                 460
Met Asn Pro Asp Pro Glu Gln Asp Arg Cys Glu Ala Ser Glu Gln Lys
465                 470                 475                 480
Gln Lys Val Pro Leu Gly Thr Phe Arg Lys Asp Met Lys Thr Gln Glu
                485                 490                 495
Glu Lys Gln Lys Gln Leu Thr Glu Lys Ile Arg Gln Gln Gln Glu Lys
            500                 505                 510
Leu Glu Ala Leu Gln Lys Thr Thr Pro Ile Arg Ser Gln Ala Asp Leu
        515                 520                 525
Lys Lys Leu Pro Leu Glu Val Thr Thr Arg Pro Ser Thr Glu Glu Pro
    530                 535                 540
Val Arg Arg Pro Gln Arg Pro Arg Ser Pro Pro Leu Pro Ala Val Ile
545                 550                 555                 560
Arg Asn Ala Pro Ser Arg Pro Pro Ser Leu Pro Thr Pro Arg Pro Ala
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Ser Gln Pro Arg Lys Ala Pro Val Ile Ser Ser Thr Pro Lys Leu Pro
            580                 585                 590
Ala Leu Ala Ala Arg Glu Glu Ala Ser Thr Ser Arg Leu Leu Gln Pro
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Arg Pro Ala Pro Leu Val Gln Gln Leu Ser Pro Ser Leu Leu Pro Asn
625 630 635 640
Ser Lys Ser Pro Arg Glu Val Pro Ser Pro Lys Val Ile Lys Thr Pro
645 650 655
Val Val Lys Lys Thr Glu Ser Pro Ile Lys Leu Ser Pro Ala Thr Pro
660 665 670
Ser Arg Lys Arg Ser Val Ala Val Ser Asp Glu Glu Glu Val Glu Glu
675 680 685
Glu Ala Glu Arg Arg Lys Glu Arg Cys Lys Arg Gly Arg Phe Val Val
690 695 700
Lys Glu Glu Lys Lys Asp Ser Asn Glu Leu Ser Asp Ser Ala Gly Gly
705 710 715 720
Glu Asp Ser Ala Asp Leu Lys Arg Ala Gln Lys Asp Lys Gly Leu His
725 730 735
Val Glu Val Arg Val Asn Arg Glu Trp Tyr Thr Gly Arg Val Thr Ala
740 745 750
Val Glu Val Gly Lys His Val Val Arg Trp Lys Val Lys Phe Asp Tyr
755 760 765
Val Pro Thr Asp Thr Thr Pro Arg Asp Arg Trp Val Glu Lys Gly Ser
770 775 780
Glu Asp Val Arg Leu Met Lys Pro Pro Ser Pro Glu His Gln Ser Leu
785 790 795 800
Asp Thr Gln Gln Glu Gly Gly Glu Glu Glu Val Gly Pro Val Ala Gln
805 810 815
Gln Ala Ile Ala Val Ala Glu Pro Ser Thr Ser Glu Cys Leu Arg Ile
820 825 830
Glu Pro Asp Thr Thr Ala Leu Ser Thr Asn His Glu Thr Ile Asp Leu
835 840 845
Leu Val Gln Ile Leu Arg Asn Cys Leu Arg Tyr Phe Leu Pro Pro Ser
850 855 860
Phe Pro Ile Ser Lys Lys Gln Leu Ser Ala Met Asn Ser Asp Glu Leu
865 870 875 880
Ile Ser Phe Pro Leu Lys Glu Tyr Phe Lys Gln Tyr Glu Val Gly Leu
885 890 895
Gln Asn Leu Cys Asn Ser Tyr Gln Ser Arg Ala Asp Ser Arg Ala Lys
900 905 910
Ala Ser Glu Glu Ser Leu Arg Thr Ser Glu Arg Lys Leu Arg Glu Thr
915 920 925
Glu Glu Lys Leu Gln Lys Leu Arg Thr Asn Ile Val Ala Leu Leu Gln
930 935 940
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945 950 955 960
Tyr Ile Glu Asp Leu Ile Thr Lys Gly Asp
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<210> 3379
<211> 898
<212> DNA
<213> Homo sapiens

<400> 3379

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240
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<210> 3380
<211> 299
<212> PRT
<213> Homo sapiens

<400> 3380
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Thr Asn Gly Asn Arg Pro Thr Ile Pro Gln Pro Trp Glu Leu Arg Val
        35   40   45
Ser Glu Asp Ala Leu Leu Gly Ser Glu Ile Ala Gln Val Thr Gly Asn
    50   55   60
Asp Val Asp Ser Gly Pro Val Leu Trp Tyr Val Leu Ser Pro Ser Gly
65   70   75   80
Pro Gln Asp Pro Phe Ser Val Gly Arg Tyr Gly Gly Arg Val Ser Leu
                85   90   95
Thr Gly Pro Leu Asp Phe Glu Gln Cys Asp Arg Tyr Gln Leu Gln Leu
            100   105   110
Leu Ala His Asp Gly Pro His Glu Gly Arg Ala Xaa Leu Thr Val Leu
        115   120   125
Val Glu Asp Val Asn Asp Asn Ala Pro Ala Phe Ser Gln Ser Leu Tyr

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Gln Val Met Leu Leu Glu His Thr Pro Pro Gly Ser Ala Ile Leu Ser
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Val Ser Ala Thr Asp Arg Asp Ser Gly Ala Asn Gly His Ile Ser Tyr
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His Leu Ala Ser Pro Ala Asp Gly Phe Ser Val Asp Pro Asn Asn Gly
            180                 185                 190
Thr Leu Phe Thr Ile Val Gly Thr Leu Ala Leu Gly His Asp Gly Ser
        195                 200                 205
Gly Ala Val Asp Val Val Leu Glu Ala Arg Asp His Gly Ala Pro Val
    210                 215                 220
Arg Ala Ala Arg Ala Thr Val Asn Val Gln Leu Arg Asp Gln Asn Asp
225                 230                 235                 240
His Ala Pro Ser Phe Thr Leu Phe His Tyr Arg Val Ala Val Thr Glu
                245                 250                 255
Asp Leu Pro Pro Gly Ser Thr Leu Leu Thr Leu Glu Ala Thr Asp Ala
            260                 265                 270
Asp Gly Ser Arg Ser His Ala Ala Val Asp Tyr Ser Ile Ile Ser Gly
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Asn Trp Gly Arg Val Phe Gln Leu Glu Pro Arg
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<210> 3381
<211> 1379
<212> DNA
<213> Homo sapiens

<400> 3381

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<210> 3382
<211> 279
<212> PRT
<213> Homo sapiens

<400> 3382
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Glu Glu Glu Gln Glu Glu Ser Glu Glu Ala Ala Cys Gly Ser Lys Lys
        35   40   45
Arg Val Val Pro Gly Ile Val Tyr Leu Gly His Ile Pro Pro Arg Phe
    50   55   60
Arg Pro Leu His Val Arg Asn Leu Leu Ser Ala Tyr Gly Glu Val Gly
65   70   75   80
Arg Val Phe Phe Gln Ala Glu Asp Arg Phe Val Arg Arg Lys Lys Lys
                85   90   95
Ala Ala Ala Ala Ala Gly Gly Lys Lys Arg Ser Tyr Thr Lys Asp Tyr
            100   105   110
Thr Glu Gly Trp Val Glu Phe Arg Asp Lys Arg Ile Ala Lys Arg Val
        115   120   125
Ala Ala Ser Leu His Asn Thr Pro Met Gly Ala Arg Arg Arg Ser Pro
    130   135   140
Phe Arg Tyr Asp Leu Trp Asn Leu Lys Tyr Leu His Arg Phe Thr Trp
145   150   155   160
Ser His Leu Ser Glu His Leu Ala Phe Glu Arg Gln Val Arg Arg Gln
                165   170   175
Arg Leu Arg Ala Glu Val Ala Gln Ala Lys Arg Glu Thr Asp Phe Tyr
            180   185   190
Leu Gln Ser Val Glu Arg Gly Gln Arg Phe Leu Ala Ala Asp Gly Asp
        195   200   205
Pro Ala Arg Pro Asp Gly Ser Trp Thr Phe Ala Gln Arg Pro Thr Glu

210 215 220
Gln Glu Leu Arg Ala Arg Lys Ala Ala Arg Pro Gly Gly Arg Glu Arg
225 230 235 240
Ala Arg Leu Ala Thr Ala Gln Asp Lys Ala Arg Ser Asn Lys Gly Leu
245 250 255
Leu Ala Arg Ile Phe Gly Ala Pro Pro Pro Ser Glu Ser Met Glu Gly
260 265 270
Pro Ser Leu Val Arg Asp Ser
275

<210> 3383
<211> 309
<212> DNA
<213> Homo sapiens

<400> 3383
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180
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<210> 3384
<211> 94
<212> PRT
<213> Homo sapiens

<400> 3384
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20 25 30
Asn Ala His Phe Leu Thr Ser Phe Val Leu Glu His Arg Ile Thr Ala
35 40 45
Asn Ala His Pro Trp Glu Leu Ser Cys Pro Arg Ser Pro Thr Gln Thr
50 55 60
Leu Gln His Glu Arg Ala Arg Leu Asn Leu Lys Lys Lys Lys Phe Arg
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<210> 3385
<211> 720
<212> DNA
<213> Homo sapiens

<400> 3385

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540
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600
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720

<210> 3386
<211> 188
<212> PRT
<213> Homo sapiens

<400> 3386
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20 25 30
Gln Pro Pro Ala Ser Ala Thr Thr Pro Val Pro Leu Ala Arg Phe Phe
35 40 45
Val Asn Phe Pro Ser Ala Lys Gln Tyr Phe Ser Gln Phe Lys His Met
50 55 60
Glu Asp Pro Leu Glu Met Glu Arg Ser Pro Gln Leu Arg Lys His Ala
65 70 75 80
Cys Arg Val Met Gly Ala Leu Asn Thr Val Val Glu Asn Leu His Asp
85 90 95
Pro Asp Lys Val Ser Ser Val Leu Ala Leu Val Gly Lys Ala His Ala
100 105 110
Leu Lys His Lys Val Glu Pro Val Tyr Phe Lys Ile Leu Ser Gly Val
115 120 125
Ile Leu Glu Val Val Ala Glu Glu Phe Ala Ser Asp Phe Pro Pro Glu
130 135 140
Thr Gln Arg Ala Trp Ala Lys Leu Arg Gly Leu Ile Tyr Ser His Val
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Thr Ala Ala Tyr Lys Glu Val Gly Trp Val Gln Gln Val Pro Asn Ala
165 170 175
Thr Thr Pro Pro Ala Thr Leu Pro Ser Ser Gly Pro

180 185

<210> 3387
<211> 3299
<212> DNA
<213> Homo sapiens

<400> 3387
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420
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1020
cctgggcctg cctgtcagtc aaagcaggaa cacttcttcc tgcataactc gaaacacctt
1080
tccacaggct tcttgtccac agtagagttt aataaaaata ttcactgaaa gacccccccc
1140
acccccatcg gcccaaagct gaataagtta gttagctgtg tccctggtcc tttgcgatgg
1200
tgtgaggcta catcctcccc cagatggcta cgatgttgga gtccgtcagg gcggtgaggt
1260
aggtgaagga ggcattggcc accactgtgt tcaccatggt cttggtcacc acctggccaa
1320
gggcccaggg ctggggccac ttcaggatct gtgtgggggc ctgcagggct gccggcagca
1380

ggggtggctg cttcaggatg ttgctgacgt cgtagagcca cacgttgccc tcctcatccc
1440
cacagagcac aatcccctta tcagggcagg cgctgagcga gaagtaggcc aactcggtgg
1500
acgaccattg cagccgcgcc aggaccacca ctgccactgt ggactggctg ccccggcccc
1560
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1800
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1860
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1980
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2040
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2100
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2160
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2340
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2580
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2760
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2880
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3000

cctgcagctg cgtcaggcgg cacaggagtt tggggtccag gtgctcggaa agcagctcca
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3120
gcattagcag ccgcgccgag agggggccca tggcgaggag gcgcagcccg cgctgaccca
3180
gtcggccacc ccggcgtgtg gcgtcgccct gcgtctcctg gagcccggca ctggcgtccg
3240
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3299

<210> 3388
<211> 153
<212> PRT
<213> Homo sapiens

<400> 3388
Ser Gly Arg Gly Leu Leu Leu Gly Leu Trp Trp Arg Arg Arg Arg Thr
1 5 10 15
Leu Gly Val Trp Thr Gln Arg Arg Arg Glu His Glu Arg Pro Ser Ser
20 25 30
Leu Arg Val Val Leu Ala Leu Arg Gly Arg Glu Glu Val Ser Asp Ala
35 40 45
Gly Cys Gly Gly Pro Arg Ile Thr Ile Asn Lys Asp Thr Lys Val Pro
50 55 60
Asn Ala Cys Leu Phe Thr Ile Asn Lys Glu Asp His Thr Leu Gly Asn
65 70 75 80
Ile Ile Lys Ser Gln Leu Leu Lys Asp Pro Gln Val Leu Phe Ala Gly
85 90 95
Tyr Lys Val Pro His Pro Leu Glu His Lys Ile Ile Ile Arg Val Gln
100 105 110
Thr Thr Pro Asp Tyr Ser Pro Gln Glu Ala Phe Thr Asn Ala Ile Thr
115 120 125
Asp Leu Ile Ser Glu Leu Ser Leu Leu Glu Glu Arg Phe Arg Val Ala
130 135 140
Ile Lys Asp Lys Gln Glu Gly Ile Glu
145 150

<210> 3389
<211> 308
<212> DNA
<213> Homo sapiens

<400> 3389
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aacaaaagta gcgcatcggt ggtcttcacg acgtacaccc agaagcaccc gtccatcgag
120
gacgggcctc cgtttgtgga gccgctgctt aacttcatct ggttcctgct gctggctgtg
180
gacggggaac cttctgacca gcctcatggg ctcctcagag caggaggatg gggaggagag
240
ccccagcgac ggcagcccca tcgagctgga ctgaactggc caggccacgt ggagacacca
300

cggtcgac
308

<210> 3390
<211> 102
<212> PRT
<213> Homo sapiens

<400> 3390
Xaa Val Ser Lys Pro Phe His His Gln His Val Leu Ile Ser Arg Phe
 1   5   10   15
Leu Cys Leu Lys Asn Lys Ser Ser Ala Ser Val Val Phe Thr Thr Tyr
            20   25   30
Thr Gln Lys His Pro Ser Ile Glu Asp Gly Pro Pro Phe Val Glu Pro
        35   40   45
Leu Leu Asn Phe Ile Trp Phe Leu Leu Leu Ala Val Asp Gly Glu Pro
    50   55   60
Ser Asp Gln Pro His Gly Leu Leu Arg Ala Gly Gly Trp Gly Gly Glu
65   70   75   80
Pro Gln Arg Arg Gln Pro His Arg Ala Gly Leu Asn Trp Pro Gly His
                85   90   95
Val Glu Thr Pro Arg Ser
            100

<210> 3391
<211> 1295
<212> DNA
<213> Homo sapiens

<400> 3391
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gaagccctaa gtgacagttc agagcgtctt ttctcctttg gcgtcatcgc agatgttcaa
120
tttgcagact tagaagatgg ctttaatttc caaggaacca ggcggcgata ctacagacat
180
agtcttcttc acttacaggg tgccattgaa gactggaata atgaaagcag catgccctgt
240
tgtgtccttc agcttggaga tatcatcgat ggatataatg cacagtataa tgcatccaaa
300
aagtccctag aacttgttat ggacatgttc aagaggctta aagttccagt tcatcataca
360
tggggaaacc atgaattcta taacttcagt agagagtatt taacacactc taaacttaac
420
actaagtttc tagaagatca gattgtacat catcctgaga ccatgccttc agaagattat
480
tatgcttatc attttgtacc attccctaaa ttccggttca ttttacttga tgcatatgac
540
ttgagtgtct tgggcgtgga tcagtcttct ccaaaatacg agcagtgtat gaagatattg
600
agggagcaca atccaaatac ggaactgaat agtcctcaag gactttctga gccccagttt
660
gtccagttta atggaggatt cagccaagaa cagctaaact ggttgaatga agtgctaaca
720

ttctctgaca caaaccaaga aaaggtggtg attgtgagcc atcttcccat ttacccggac
780
gcctctgaca atgtgtgcct ggcctggaac tacagagatg ccctggcagt catttggtct
840
catgagtgtg tggtgtgttt ctttgctggt cacacccatg atggtggcta ctctgaggat
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ccttttggtg tataccacgt caacctagaa ggagttattg aaacagctcc agacagccaa
960
gcctttggca cagttcatgt ctatcctgac aaaatgatgt tgaaagggag aggcagagtt
1020
ccagatagaa ttatgaatta caagaaagaa agagccttcc attgttagtc taatttattt
1080
taacttgata gaaaatgagc tttgtgtttg tccctcctaa acaaaaaaat aaaaatcctc
1140
tgtctcattg tttagtattc agcttgcata acaaaatgta tttatagttt cagtgtgtga
1200
tggttgataa aatactcaga aatgttattt tggatcatgt atccattgta agttagaaac
1260
aaaccaggga ggaaactgag gcaggggtgt atagt
1295

<210> 3392
<211> 355
<212> PRT
<213> Homo sapiens

<400> 3392
Ile Val Phe Leu Leu Tyr Leu Glu Thr Cys Leu Glu Val Met Asp Asp
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Lys Pro Asn Pro Glu Ala Leu Ser Asp Ser Ser Glu Arg Leu Phe Ser
20 25 30
Phe Gly Val Ile Ala Asp Val Gln Phe Ala Asp Leu Glu Asp Gly Phe
35 40 45
Asn Phe Gln Gly Thr Arg Arg Arg Tyr Tyr Arg His Ser Leu Leu His
50 55 60
Leu Gln Gly Ala Ile Glu Asp Trp Asn Asn Glu Ser Ser Met Pro Cys
65 70 75 80
Cys Val Leu Gln Leu Gly Asp Ile Ile Asp Gly Tyr Asn Ala Gln Tyr
85 90 95
Asn Ala Ser Lys Lys Ser Leu Glu Leu Val Met Asp Met Phe Lys Arg
100 105 110
Leu Lys Val Pro Val His His Thr Trp Gly Asn His Glu Phe Tyr Asn
115 120 125
Phe Ser Arg Glu Tyr Leu Thr His Ser Lys Leu Asn Thr Lys Phe Leu
130 135 140
Glu Asp Gln Ile Val His His Pro Glu Thr Met Pro Ser Glu Asp Tyr
145 150 155 160
Tyr Ala Tyr His Phe Val Pro Phe Pro Lys Phe Arg Phe Ile Leu Leu
165 170 175
Asp Ala Tyr Asp Leu Ser Val Leu Gly Val Asp Gln Ser Ser Pro Lys
180 185 190
Tyr Glu Gln Cys Met Lys Ile Leu Arg Glu His Asn Pro Asn Thr Glu
195 200 205
Leu Asn Ser Pro Gln Gly Leu Ser Glu Pro Gln Phe Val Gln Phe Asn

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    210                 215                 220
Gly Gly Phe Ser Gln Glu Gln Leu Asn Trp Leu Asn Glu Val Leu Thr
225                 230                 235                 240
Phe Ser Asp Thr Asn Gln Glu Lys Val Val Ile Val Ser His Leu Pro
                245                 250                 255
Ile Tyr Pro Asp Ala Ser Asp Asn Val Cys Leu Ala Trp Asn Tyr Arg
            260                 265                 270
Asp Ala Leu Ala Val Ile Trp Ser His Glu Cys Val Val Cys Phe Phe
        275                 280                 285
Ala Gly His Thr His Asp Gly Gly Tyr Ser Glu Asp Pro Phe Gly Val
    290                 295                 300
Tyr His Val Asn Leu Glu Gly Val Ile Glu Thr Ala Pro Asp Ser Gln
305                 310                 315                 320
Ala Phe Gly Thr Val His Val Tyr Pro Asp Lys Met Met Leu Lys Gly
                325                 330                 335
Arg Gly Arg Val Pro Asp Arg Ile Met Asn Tyr Lys Lys Glu Arg Ala
            340                 345                 350
Phe His Cys
        355
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<210> 3393
<211> 510
<212> DNA
<213> Homo sapiens

<400> 3393
nngcgactct gggacccctt gggtcgtggc agcagtggcg gcgatgtttg tcggctcggg
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atgggtccag ganntgttac tccttcttct tttgttgggg tctgggcagg ggccacagca
120
agtcggggcg ggtcaaactt cgagtacttg aaacgggagc actcgctgtc gaagccctac
180
cagggtgtgg gcacaggcag ttcctcactg tggaatctga tgggcaatng catggtgatg
240
acccagtata tccgccttac cccagatatg caaagtaaac agggtgcctt gtggaaccgg
300
gtgccatgtt tcctgagaga ctgggagttg caggtgcact tcaaaatcca tggacaagga
360
aagaagaatc tgcatgggga tggcttggca atctggtaca caaaggatcg gatgcagcca
420
gggcctgtgt ttggaaacat ggacaaattt gtggggctgg gagtatttgt agacacctac
480
cccaatgagg agaagcagcc cttcacgcgt
510

<210> 3394
<211> 170
<212> PRT
<213> Homo sapiens

<400> 3394
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Xaa Arg Leu Trp Asp Pro Leu Gly Arg Gly Ser Ser Gly Gly Asp Val
 1               5                  10                  15
Cys Arg Leu Gly Met Gly Pro Gly Xaa Val Thr Pro Ser Ser Phe Val
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            20                  25                  30
Gly Val Trp Ala Gly Ala Thr Ala Ser Arg Gly Gly Ser Asn Phe Glu
        35                  40                  45
Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro Tyr Gln Gly Val Gly
    50                  55                  60
Thr Gly Ser Ser Ser Leu Trp Asn Leu Met Gly Asn Xaa Met Val Met
65                  70                  75                  80
Thr Gln Tyr Ile Arg Leu Thr Pro Asp Met Gln Ser Lys Gln Gly Ala
                85                  90                  95
Leu Trp Asn Arg Val Pro Cys Phe Leu Arg Asp Trp Glu Leu Gln Val
            100                 105                 110
His Phe Lys Ile His Gly Gln Gly Lys Lys Asn Leu His Gly Asp Gly
        115                 120                 125
Leu Ala Ile Trp Tyr Thr Lys Asp Arg Met Gln Pro Gly Pro Val Phe
    130                 135                 140
Gly Asn Met Asp Lys Phe Val Gly Leu Gly Val Phe Val Asp Thr Tyr
145                 150                 155                 160
Pro Asn Glu Glu Lys Gln Pro Phe Thr Arg
                165                 170
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<210> 3395
<211> 807
<212> DNA
<213> Homo sapiens

<400> 3395

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ntggcactta acggtggtgg ctggttctgc gccggatccg ggagaggggc gggcgccatt
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120
gcggtgcgtg ttgctgcgag tgggacgcgc actggtcggt gccggctcag gagccgggaa
180
aaatctttaa gaatggagtc taaaccttca aggattccaa gaagaatttc tgttcaacct
240
tccagctcct taagtgctag gatgatgtct ggaagcagag gaagtagttt aaatgatacc
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360
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420
cgctcaagat cgcagaacca gcaacgggat catgattcaa aaagacctaa actttcctgt
480
acaaactgta ctacctcagc tgggagaaat gttggaaatg gtttaaacac attatcagat
540
tcatcttgga ggcatagtca agttcctaga tcttcatcaa tggtacttgg atcatttgga
600
acagacttaa tgagagagag gagagatttg gagagaagaa cagattcctc tattagtaat
660
cttatggatt atagtcaccg aagtggtgat ttcacaactt catcatatgt tcaagacaga
720
gttccttcat attcacaagg agcaagacca aaagaaaact caatgagcac tttacagttg
780
aatacatcat ccacaaacca ccaattg
807
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<210> 3396
<211> 205
<212> PRT
<213> Homo sapiens

<400> 3396
Met Glu Ser Lys Pro Ser Arg Ile Pro Arg Arg Ile Ser Val Gln Pro
1 5 10 15
Ser Ser Ser Leu Ser Ala Arg Met Met Ser Gly Ser Arg Gly Ser Ser
20 25 30
Leu Asn Asp Thr Tyr His Ser Arg Asp Ser Ser Phe Arg Leu Asp Ser
35 40 45
Glu Tyr Gln Ser Thr Ser Ala Ser Ala Ser Ala Ser Pro Phe Gln Ser
50 55 60
Ala Trp Tyr Ser Glu Ser Glu Ile Thr Gln Gly Ala Arg Ser Arg Ser
65 70 75 80
Gln Asn Gln Gln Arg Asp His Asp Ser Lys Arg Pro Lys Leu Ser Cys
85 90 95
Thr Asn Cys Thr Thr Ser Ala Gly Arg Asn Val Gly Asn Gly Leu Asn
100 105 110
Thr Leu Ser Asp Ser Ser Trp Arg His Ser Gln Val Pro Arg Ser Ser
115 120 125
Ser Met Val Leu Gly Ser Phe Gly Thr Asp Leu Met Arg Glu Arg Arg
130 135 140
Asp Leu Glu Arg Arg Thr Asp Ser Ser Ile Ser Asn Leu Met Asp Tyr
145 150 155 160
Ser His Arg Ser Gly Asp Phe Thr Thr Ser Ser Tyr Val Gln Asp Arg
165 170 175
Val Pro Ser Tyr Ser Gln Gly Ala Arg Pro Lys Glu Asn Ser Met Ser
180 185 190
Thr Leu Gln Leu Asn Thr Ser Ser Thr Asn His Gln Leu
195 200 205

<210> 3397
<211> 492
<212> DNA
<213> Homo sapiens

<400> 3397
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ggatctcccc ccaggcagcc tcctcagttc tgggacagcc agaggcggcg gcaaccccag
120
ccacagagag acagtggcac ctacgagcag cccagccccc tgatccatga ccgagactct
180
gtgggctccc agccccctct gcctccgggc ctacccccca gccactatga ctcacccaag
240
aacagccaca tccctggaca ttatgacttg cctccagtac ggcatccccc atcacctcan
300
cttcgacgcc aggatcgttg aggagccagg atggtatggc agaggcagca anacctggct
360
gttgctgctc aaggctgggg acagagcata gtgtaccccc gccaggagca gggagtggac
420

cggcaggctg tgaacatgaa caacgcttaa cagagcaagt gatgggagaa taattcatgg
480
cttctaccat gg
492

<210> 3398
<211> 163
<212> PRT
<213> Homo sapiens

<400> 3398
Met Val Glu Ala Met Asn Tyr Ser Pro Ile Thr Cys Ser Val Lys Arg
 1   5   10   15
Cys Ser Cys Ser Gln Pro Ala Gly Pro Leu Pro Ala Pro Gly Arg Gly
            20   25   30
Thr Leu Cys Ser Val Pro Ser Leu Glu Gln Gln Gln Pro Gly Xaa Ala
        35   40   45
Ala Ser Ala Ile Pro Ser Trp Leu Leu Asn Asp Pro Gly Val Glu Xaa
    50   55   60
Glu Val Met Gly Asp Ala Val Leu Glu Ala Ser His Asn Val Gln Gly
65   70   75   80
Cys Gly Cys Ser Trp Val Ser His Ser Gly Arg Gly Val Gly Pro Glu
                85   90   95
Ala Glu Gly Ala Gly Ser Pro Gln Ser Leu Gly His Gly Ser Gly Gly
            100   105   110
Trp Ala Ala Arg Arg Cys His Cys Leu Ser Val Ala Gly Val Ala Ala
        115   120   125
Ala Ser Gly Cys Pro Arg Thr Glu Glu Ala Ala Trp Gly Glu Ile Leu
    130   135   140
Arg Glu Gly Leu Ser Ser Pro Cys Ser Cys Ser Pro Gly Pro Pro Gly
145   150   155   160
Lys Leu Gly

<210> 3399
<211> 5784
<212> DNA
<213> Homo sapiens

<400> 3399
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gggcccggcg tctgcctcga gactgaagac cgataaactc aagccatgga gggattactg
120
cattacatca accctgcaca cgccatttct ctcctaagtg ccctgaatga ggagcgtctc
180
aaaggacagc tgtgtgatgt gctgctgatt gttggagacc aaaagttccg agctcataaa
240
aacgtcttgg ctgccagcag cgaatacttt cagagtttat tcacaaataa ggaaaatgag
300
tcacaaactg tatttcagct tgacttctgt gagccagatg cttttgataa tgttttaaac
360
tacatttatt cttcctctct atttgttgag aagagcagcc ttgctgctgt gcaagaactt
420

ggctatagtc ttgggatttc ctttctgact aacatcgttt ctaaaacacc tcaagccccc
480
tttccaacgt gtcctaatag aaaaaaagtg tttgtagaag atgatgaaaa cagttctcaa
540
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600
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660
accaataagc cacatgtccc aaaaccaata gaaccacttc ataatttgtc attaactgaa
720
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780
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840
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900
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960
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1020
aacttgttgt actattcaaa gttaggctta gtgatcccat ccagtggatc tggttctgga
1080
aaccaaagca ttgacaggag tggcccactt gttaagagtc tcctcagacg gtcattgtcg
1140
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1200
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1260
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1320
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1440
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1620
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1680
gattctgatt tgaataaaga cgaatttggt gagttggagg ggacgagacc aaacaaaaaa
1740
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1860
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1920
ccagcctcta gttcacatgc tgttttggat gaaaaattcc aaagaaagct gattgacata
1980
gtgagagaga gagaaattaa gaaggccctg atcattaagt taaggcgcgg caagcctggt
2040

tttcagggac agagtagctc ccaagcacag caagtcatca agaggaactt gagatctcga
2100
gccaaaggag cttacatttg tacttactgc ggaaaagcgt accgctttct ctctcaattt
2160
aagcagcata taaaaatgca tccaggagaa aaacccccttg gagtaaataa agttgctaaa
2220
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2280
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2520
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2580
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2940
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3120
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5784

<210> 3400
<211> 1069
<212> PRT
<213> Homo sapiens

<400> 3400
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Cys Asp Val Leu Leu Ile Val Gly Asp Gln Lys Phe Arg Ala His Lys
35 40 45
Asn Val Leu Ala Ala Ser Ser Glu Tyr Phe Gln Ser Leu Phe Thr Asn
50 55 60
Lys Glu Asn Glu Ser Gln Thr Val Phe Gln Leu Asp Phe Cys Glu Pro
65 70 75 80
Asp Ala Phe Asp Asn Val Leu Asn Tyr Ile Tyr Ser Ser Ser Leu Phe
85 90 95
Val Glu Lys Ser Ser Leu Ala Ala Val Gln Glu Leu Gly Tyr Ser Leu
100 105 110
Gly Ile Ser Phe Leu Thr Asn Ile Val Ser Lys Thr Pro Gln Ala Pro
115 120 125
Phe Pro Thr Cys Pro Asn Arg Lys Lys Val Phe Val Glu Asp Asp Glu
130 135 140
Asn Ser Ser Gln Lys Arg Ser Val Ile Val Cys Gln Ser Arg Asn Glu
145 150 155 160
Ala Gln Gly Lys Thr Val Ser Gln Asn Gln Pro Asp Val Ser His Thr
165 170 175
Ser Arg Pro Ser Pro Ser Ile Ala Val Lys Ala Asn Thr Asn Lys Pro
180 185 190
His Val Pro Lys Pro Ile Glu Pro Leu His Asn Leu Ser Leu Thr Glu
195 200 205
Lys Ser Trp Pro Lys Asp Ser Ser Val Val Tyr Ala Lys Ser Leu Glu
210 215 220
His Ser Gly Ser Leu Asp Asp Pro Asn Arg Ile Ser Leu Val Lys Arg

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225                 230                 235                 240
Asn Ala Val Leu Pro Ser Lys Pro Leu Gln Asp Arg Glu Ala Met Asp
                245                 250                 255
Asp Lys Pro Gly Val Ser Gly Gln Leu Pro Lys Gly Lys Ala Leu Glu
            260                 265                 270
Leu Ala Leu Lys Arg Pro Arg Pro Pro Val Leu Ser Val Cys Ser Ser
        275                 280                 285
Ser Glu Thr Pro Tyr Leu Leu Lys Glu Thr Asn Lys Gly Asn Gly Gln
    290                 295                 300
Gly Glu Asp Arg Asn Leu Leu Tyr Tyr Ser Lys Leu Gly Leu Val Ile
305                 310                 315                 320
Pro Ser Ser Gly Ser Gly Ser Gly Asn Gln Ser Ile Asp Arg Ser Gly
                325                 330                 335
Pro Leu Val Lys Ser Leu Leu Arg Arg Ser Leu Ser Met Asp Ser Gln
            340                 345                 350
Val Pro Val Tyr Ser Pro Ser Ile Asp Leu Lys Ser Ser Gln Gly Ser
        355                 360                 365
Ser Ser Val Ser Ser Asp Ala Pro Gly Asn Val Leu Cys Ala Leu Ser
    370                 375                 380
Gln Lys Ser Ser Leu Lys Asp Cys Ser Glu Lys Thr Ala Leu Asp Asp
385                 390                 395                 400
Arg Pro Gln Val Leu Gln Pro His Arg Leu Arg Ser Phe Ser Ala Ser
                405                 410                 415
Gln Ser Thr Asp Arg Glu Gly Ala Ser Pro Val Thr Glu Val Arg Ile
            420                 425                 430
Lys Thr Glu Pro Ser Ser Pro Leu Ser Asp Pro Ser Asp Ile Ile Arg
        435                 440                 445
Val Thr Val Gly Asp Ala Ala Thr Thr Ala Ala Ala Ser Ser Ser Ser
    450                 455                 460
Val Thr Arg Asp Leu Ser Leu Lys Thr Glu Asp Asp Gln Lys Asp Met
465                 470                 475                 480
Ser Arg Leu Pro Ala Lys Arg Arg Phe Gln Ala Asp Arg Arg Leu Pro
                485                 490                 495
Phe Lys Lys Leu Lys Val Asn Glu His Gly Ser Pro Val Ser Glu Asp
            500                 505                 510
Asn Phe Glu Glu Gly Ser Ser Pro Thr Leu Leu Asp Ala Asp Phe Pro
        515                 520                 525
Asp Ser Asp Leu Asn Lys Asp Glu Phe Gly Glu Leu Glu Gly Thr Arg
    530                 535                 540
Pro Asn Lys Lys Phe Lys Cys Lys His Cys Leu Lys Ile Phe Arg Ser
545                 550                 555                 560
Thr Ala Gly Leu His Arg His Val Asn Met Tyr His Asn Pro Glu Lys
                565                 570                 575
Pro Tyr Ala Cys Asp Ile Cys His Lys Arg Phe His Thr Asn Phe Lys
            580                 585                 590
Val Trp Thr His Cys Gln Thr Gln His Gly Ile Val Lys Asn Pro Ser
        595                 600                 605
Pro Ala Ser Ser Ser His Ala Val Leu Asp Glu Lys Phe Gln Arg Lys
    610                 615                 620
Leu Ile Asp Ile Val Arg Glu Arg Glu Ile Lys Lys Ala Leu Ile Ile
625                 630                 635                 640
Lys Leu Arg Arg Gly Lys Pro Gly Phe Gln Gly Gln Ser Ser Ser Gln
                645                 650                 655
Ala Gln Gln Val Ile Lys Arg Asn Leu Arg Ser Arg Ala Lys Gly Ala
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660 665 670
Tyr Ile Cys Thr Tyr Cys Gly Lys Ala Tyr Arg Phe Leu Ser Gln Phe
675 680 685
Lys Gln His Ile Lys Met His Pro Gly Glu Lys Pro Leu Gly Val Asn
690 695 700
Lys Val Ala Lys Pro Lys Glu His Ala Pro Leu Ala Ser Pro Val Glu
705 710 715 720
Asn Lys Glu Val Tyr Gln Cys Arg Leu Cys Asn Ala Lys Leu Ser Ser
725 730 735
Leu Leu Glu Gln Gly Ser His Glu Arg Leu Cys Arg Asn Ala Ala Val
740 745 750
Cys Pro Tyr Cys Ser Leu Arg Phe Phe Ser Pro Glu Leu Lys Gln Glu
755 760 765
His Glu Ser Lys Cys Glu Tyr Lys Lys Leu Thr Cys Leu Glu Cys Met
770 775 780
Arg Thr Phe Lys Ser Ser Phe Ser Ile Trp Arg His Gln Val Glu Val
785 790 795 800
His Asn Gln Asn Asn Met Ala Pro Thr Glu Asn Phe Ser Leu Pro Val
805 810 815
Leu Asp His Asn Gly Asp Val Thr Gly Ser Ser Arg Pro Gln Ser Gln
820 825 830
Pro Glu Pro Asn Lys Val Asn His Ile Val Thr Thr Lys Asp Asp Asn
835 840 845
Val Phe Ser Asp Ser Ser Glu Gln Val Asn Phe Asp Ser Glu Asp Ser
850 855 860
Ser Cys Leu Pro Glu Asp Leu Ser Leu Ser Lys Gln Leu Lys Ile Gln
865 870 875 880
Val Lys Glu Glu Pro Val Glu Glu Ala Glu Glu Glu Ala Pro Glu Ala
885 890 895
Ser Thr Ala Pro Lys Glu Ala Gly Pro Ser Lys Glu Ala Ser Leu Trp
900 905 910
Pro Cys Glu Lys Cys Gly Lys Met Phe Thr Val His Lys Gln Leu Glu
915 920 925
Arg His Gln Glu Leu Leu Cys Ser Val Lys Pro Phe Ile Cys His Val
930 935 940
Cys Asn Lys Ala Phe Arg Thr Asn Phe Arg Leu Trp Ser His Phe Gln
945 950 955 960
Ser His Met Ser Gln Ala Ser Glu Glu Ser Ala His Lys Glu Ser Glu
965 970 975
Val Cys Pro Val Pro Thr Asn Ser Pro Ser Pro Pro Pro Leu Pro Pro
980 985 990
Pro Pro Pro Leu Pro Lys Ile Gln Pro Leu Glu Pro Asp Ser Pro Thr
995 1000 1005
Gly Leu Ser Glu Asn Pro Thr Pro Ala Thr Glu Lys Leu Phe Val Pro
1010 1015 1020
Gln Glu Ser Asp Thr Leu Phe Tyr His Ala Pro Pro Leu Ser Ala Ile
1025 1030 1035 1040
Thr Phe Lys Arg Gln Phe Met Cys Lys Leu Cys His Arg Thr Phe Lys
1045 1050 1055
Thr Ala Phe Ser Leu Trp Ser His Glu Gln Thr His Asn
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<210> 3401
<211> 579

<212> DNA
<213> Homo sapiens

<400> 3401
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tctcacttcc aaaagttatt tgatgtgcct tctttaaatg gagtctatcc ccgaatgaat
120
gaagtttata ctaggcttgg agaaatgaac aatgctgtga gaaacctcca agaactctta
180
gaattagata gttcatcctc attgtgtgtg ctagtaagca ctgttggaaa actctgtagg
240
ctgattaatg aagatgtgaa tgagcaggtt atgcaggtat taggacctga agacctccag
300
agcattatct acaaattgga agaacacgag gaatttttcc cagcatttca ggcatttact
360
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420
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480
ttcttaacat tttgtatttt gtaggattga tcttattttg agacaagggt tgtaaaatgt
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579

<210> 3402
<211> 148
<212> PRT
<213> Homo sapiens

<400> 3402
Met Pro His Phe Gln Thr Leu Gln Ala Ile Val Ser His Phe Gln Lys
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Leu Phe Asp Val Pro Ser Leu Asn Gly Val Tyr Pro Arg Met Asn Glu
            20   25   30
Val Tyr Thr Arg Leu Gly Glu Met Asn Asn Ala Val Arg Asn Leu Gln
        35   40   45
Glu Leu Leu Glu Leu Asp Ser Ser Ser Ser Leu Cys Val Leu Val Ser
    50   55   60
Thr Val Gly Lys Leu Cys Arg Leu Ile Asn Glu Asp Val Asn Glu Gln
65   70   75   80
Val Met Gln Val Leu Gly Pro Glu Asp Leu Gln Ser Ile Ile Tyr Lys
                85   90   95
Leu Glu Glu His Glu Glu Phe Phe Pro Ala Phe Gln Ala Phe Thr Asn
            100   105   110
Asp Leu Leu Glu Ile Leu Glu Ile Asp Asp Ser Gly Cys His Cys Thr
        115   120   125
Cys Ser Lys Glu Ile Lys Ser Thr Phe Ile Leu Lys Thr Asn Gln Ile
    130   135   140
Ile Phe Thr Val
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<210> 3403
<211> 1696

<212> DNA
<213> Homo sapiens

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120
accatggccc gaaatgcaga aaaggccatg acggccttag caagatttcg ccaggctcag
180
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240
cctaaagctg agaagtggag acgacagatc attggagaga tctctaaaaa agtggctcag
300
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360
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420
ggaaaagttg gccctaaaat gctggatcat gaaggaaaag aagtcccagg aaaccgaggt
480
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600
tactatggtt acctagatga agatgatggt gttattgtgc ctttggaaca ggaatatgaa
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720
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900
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1320
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1500

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1680
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1696

<210> 3404
<211> 286
<212> PRT
<213> Homo sapiens

<400> 3404
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Gln Ala Gln Leu Glu Glu Gly Lys Val Lys Glu Arg Arg Pro Phe Leu
20 25 30
Ala Ser Glu Cys Thr Glu Leu Pro Lys Ala Glu Lys Trp Arg Arg Gln
35 40 45
Ile Ile Gly Glu Ile Ser Lys Lys Val Ala Gln Ile Gln Asn Ala Gly
50 55 60
Leu Gly Glu Phe Arg Ile Arg Asp Leu Asn Asp Glu Ile Asn Lys Leu
65 70 75 80
Leu Arg Glu Lys Gly His Trp Glu Val Arg Ile Lys Glu Leu Gly Gly
85 90 95
Pro Asp Tyr Gly Lys Val Gly Pro Lys Met Leu Asp His Glu Gly Lys
100 105 110
Glu Val Pro Gly Asn Arg Gly Tyr Lys Tyr Phe Gly Ala Ala Lys Asp
115 120 125
Leu Pro Gly Val Arg Glu Leu Phe Glu Lys Xaa Thr Ser Ser Ser Ser
130 135 140
Gln Xaa Lys Thr Arg Ala Glu Leu Met Lys Ala Ile Asp Phe Glu Tyr
145 150 155 160
Tyr Gly Tyr Leu Asp Glu Asp Asp Gly Val Ile Val Pro Leu Glu Gln
165 170 175
Glu Tyr Glu Lys Lys Leu Arg Ala Glu Leu Val Glu Lys Trp Lys Ala
180 185 190
Glu Arg Glu Ala Arg Leu Ala Arg Gly Glu Lys Glu Glu Glu Glu Glu
195 200 205
Glu Glu Glu Glu Ile Asn Ile Tyr Ala Val Thr Glu Glu Glu Ser Asp
210 215 220
Glu Glu Gly Ser Gln Glu Lys Gly Gly Asp Asp Ser Gln Gln Lys Phe
225 230 235 240
Ile Ala His Val Pro Val Pro Ser Gln Gln Glu Ile Glu Glu Ala Leu
245 250 255
Val Arg Arg Lys Lys Met Glu Leu Leu Gln Lys Tyr Ala Ser Glu Thr
260 265 270
Leu Gln Ala Gln Ser Glu Glu Ala Arg Arg Leu Leu Gly Tyr
275 280 285

<210> 3405
<211> 402

<212> DNA
<213> Homo sapiens

<400> 3405
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agacaagctg gagacagcgc caagatgcgg cgctacgatc gggggcttaa aacactggaa
120
aacctgctcg cctccatccg taagggcaat gccattgacg aagcggacat cccgccgcca
180
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240
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360
ccctctggcc cagttgcaga gccgccagcg cgactacaag ct
402

<210> 3406
<211> 134
<212> PRT
<213> Homo sapiens

<400> 3406
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Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser Ala Lys Met Arg Arg Tyr
            20   25   30
Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu Leu Ala Ser Ile Arg Lys
        35   40   45
Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro Pro Pro Val Ala Ile Gly
    50   55   60
Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser Pro Ala Pro Thr Gln Pro
65   70   75   80
Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro Arg Val Thr Leu Glu Gly
                85   90   95
Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro Gly Leu Ala Lys Pro Gln
            100   105   110
Met Pro Pro Gly Pro Cys Ser Pro Pro Ser Gly Pro Val Ala Glu Pro
        115   120   125
Pro Ala Arg Leu Gln Ala
    130

<210> 3407
<211> 535
<212> DNA
<213> Homo sapiens

<400> 3407
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tttcccggac accatgcctt ctcggcggtg aggcaggtgg cggcaccgac aggcccgggg
120

gggacctttc ccggacaccc aacctcctcg gtggcgaggc aggtggcggc accgacaggc
180
ccggcgggga cctttcccgg ancacctggc ctccttggca agcaggtggc ggcaccaaca
240
ggcccggggg ggacctttcc cggacacctg gcctcctcgg cgaggcaggt ggcagaactg
300
gttccacgtc tgatcttcct tagacaaacc tgccttcaga ggaaattgtg ttcaactgga
360
gaaactggaa aatgtactag atattggctg atatgaagga tatatgtttt aagtatgata
420
attcgatttt ggctctgtag ggaaaggctc ttattttaaa aagatgtgca ctagagaaaa
480
aggaaacagc atgtagcaaa tacatccacg gatgtcctcc tggtttaaaa aaaaa
535

<210> 3408
<211> 131
<212> PRT
<213> Homo sapiens

<400> 3408
Gly Met Arg Gly Asp Gly Glu Glu Pro Pro Arg Thr Ala Pro Ser Arg
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Ser Ala Gly Thr Phe Pro Gly His His Ala Phe Ser Ala Val Arg Gln
20 25 30
Val Ala Ala Pro Thr Gly Pro Gly Gly Thr Phe Pro Gly His Pro Thr
35 40 45
Ser Ser Val Ala Arg Gln Val Ala Ala Pro Thr Gly Pro Ala Gly Thr
50 55 60
Phe Pro Gly Xaa Pro Gly Leu Leu Gly Lys Gln Val Ala Ala Pro Thr
65 70 75 80
Gly Pro Gly Gly Thr Phe Pro Gly His Leu Ala Ser Ser Ala Arg Gln
85 90 95
Val Ala Glu Leu Val Pro Arg Leu Ile Phe Leu Arg Gln Thr Cys Leu
100 105 110
Gln Arg Lys Leu Cys Ser Thr Gly Glu Thr Gly Lys Cys Thr Arg Tyr
115 120 125
Trp Leu Ile
130

<210> 3409
<211> 959
<212> DNA
<213> Homo sapiens

<400> 3409
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120
gagagagagg aaccttgccg gtccgaggca gctctgcgcg tcccctcctg cgcttagcat
180
cctcggccca gcgcggcccg caccgccatg gaggtgctgg agagcgggga gcagggcgtg
240

ctgcagtggg accgcaagct gagcgagctg tcagagcccg gggacggcga ggccctcatg
300
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360
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420
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480
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540
nngagaaatg gtacctgtct acagacttcc cttcaacatc catcaagaca gagccagtta
600
cagacgaacc acccccagga ctcgttccgt ctgtcactct gaccatcaca gccatctcca
660
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720
cagaccatta ttcctaaaat taagctggag cctcatgaag tggatcagtt tctaaacttc
780
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840
tgggtctaca gagagggaat atggcgagag agctgggatg agtttgtacc acagatgttg
900
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959

<210> 3410
<211> 144
<212> PRT
<213> Homo sapiens

<400> 3410
Met Glu Val Leu Glu Ser Gly Glu Gln Gly Val Leu Gln Trp Asp Arg
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Lys Leu Ser Glu Leu Ser Glu Pro Gly Asp Gly Glu Ala Leu Met Tyr
            20   25   30
His Thr His Phe Ser Glu Leu Leu Asp Glu Phe Ser Gln Asn Val Leu
        35   40   45
Gly Gln Leu Leu Asn Asp Pro Phe Leu Ser Glu Lys Ser Val Ser Met
    50   55   60
Glu Val Glu Pro Ser Pro Thr Ser Pro Ala Pro Leu Ile Gln Ala Glu
65   70   75   80
His Ser Tyr Ser Leu Cys Glu Glu Pro Arg Ala Gln Ser Pro Phe Thr
                85   90   95
His Ile Thr Thr Ser Asp Ser Phe Asn Asp Asp Glu Val Glu Ser Xaa
            100   105   110
Arg Asn Gly Thr Cys Leu Gln Thr Ser Leu Gln His Pro Ser Arg Gln
        115   120   125
Ser Gln Leu Gln Thr Asn His Pro Gln Asp Ser Phe Arg Leu Ser Leu
    130   135   140

<210> 3411
<211> 958
<212> DNA
<213> Homo sapiens

<400> 3411
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240
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360
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420
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480
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540
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840
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<211> 185
<212> PRT
<213> Homo sapiens

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Thr Val Gly Lys Leu Lys Thr His Leu Ser Asn Val Tyr Pro Ser Lys
35 40 45
Pro Leu Thr Lys Asp Gln Arg Leu Val Tyr Ser Gly Arg Leu Leu Pro
50 55 60
Asp His Leu Gln Leu Lys Asp Ile Leu Arg Lys Gln Asp Glu Tyr His
65 70 75 80
Met Val His Leu Val Cys Thr Ser Arg Thr Pro Pro Ser Ser Pro Lys
85 90 95
Ser Ser Thr Asn Arg Glu Ser His Glu Ala Leu Ala Ser Ser Ser Asn

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            100                 105                 110
Ser Ser Ser Asp His Ser Gly Ser Thr Thr Pro Ser Ser Gly Gln Glu
        115                 120                 125
Thr Leu Ser Leu Ala Val Gly Ser Ser Ser Glu Gly Leu Arg Gln Arg
    130                 135                 140
Thr Leu Pro Gln Ala Gln Thr Asp Gln Ala Gln Ser His Gln Phe Pro
145                 150                 155                 160
Tyr Val Met Gln Gly Asn Val Asp Asn Gln Phe Pro Gly Gln Ala Ala
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Pro Pro Gly Phe Pro Val Tyr Pro Ala
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<210> 3413
<211> 3344
<212> DNA
<213> Homo sapiens

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180
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240
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360
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420
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480
gacaaaatta aagaagaacc agacaatgct caagagtatg gatgtgtcca acagccaaaa
540
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600
cagcagttga acccaggctt tcagctttct tttgcatcat ctggcccaag tgtgttgctt
660
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720
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1020
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1080

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1200
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1740
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1920
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1980
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2220
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2280
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ccaaatagct gtgggctttc tggaactgct ggctgggttg ctgctggtca tgggcccacc
2700

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3060
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3180
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3240
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3344

<210> 3414
<211> 723
<212> PRT
<213> Homo sapiens

<400> 3414
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Gln Glu Leu Leu Asp Lys Ile Lys Glu Glu Pro Asp Asn Ala Gln Glu
20 25 30
Tyr Gly Cys Val Gln Gln Pro Lys Thr Gln Glu Ser Lys Leu Lys Ile
35 40 45
Gly Gly Val Ser Ser Val Asn Glu Arg Pro Ile Ala Gln Gln Leu Asn
50 55 60
Pro Gly Phe Gln Leu Ser Phe Ala Ser Ser Gly Pro Ser Val Leu Leu
65 70 75 80
Pro Ser Val Pro Ala Val Ala Ile Lys Val Phe Cys Ser Gly Cys Lys
85 90 95
Lys Met Leu Tyr Lys Gly Gln Thr Ala Tyr His Lys Thr Gly Ser Thr
100 105 110
Gln Leu Phe Cys Ser Thr Arg Cys Ile Thr Arg His Ser Ser Pro Ala
115 120 125
Cys Leu Pro Pro Pro Pro Lys Lys Thr Cys Thr Asn Cys Ser Lys Asp
130 135 140
Ile Leu Asn Pro Lys Asp Val Ile Thr Thr Arg Phe Glu Asn Ser Tyr
145 150 155 160
Pro Ser Lys Asp Phe Cys Ser Gln Ser Cys Leu Ser Ser Tyr Glu Leu
165 170 175
Lys Lys Lys Pro Val Val Thr Ile Tyr Thr Lys Ser Ile Ser Thr Lys
180 185 190
Cys Ser Met Cys Gln Lys Asn Ala Asp Thr Arg Phe Glu Val Lys Tyr

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        195                 200                 205
Gln Asn Val Val His Gly Leu Cys Ser Asp Ala Cys Phe Ser Lys Phe
    210                 215                 220
His Ser Thr Asn Asn Leu Thr Thr Asn Cys Cys Glu Asn Cys Gly Ser
225                 230                 235                 240
Tyr Cys Tyr Ser Ser Ser Gly Pro Cys Gln Ser Gln Lys Val Phe Ser
                245                 250                 255
Ser Thr Ser Val Thr Ala Tyr Lys Gln Asn Ser Ala Gln Ile Pro Pro
            260                 265                 270
Tyr Ala Leu Gly Lys Ser Leu Arg Ser Ser Ala Glu Met Ile Glu Asn
        275                 280                 285
Thr Asn Ser Leu Gly Lys Thr Glu Leu Phe Cys Ser Ile Asn Cys Leu
    290                 295                 300
Ser Ala Tyr Arg Val Lys Thr Val Thr Ser Ala Gly Val Gln Val Ser
305                 310                 315                 320
Cys His Ser Cys Lys Thr Ser Ala Ile Pro Gln Tyr His Leu Ala Met
                325                 330                 335
Ser Asp Gly Thr Ile Tyr Ser Phe Cys Ser Ser Ser Cys Val Val Ala
            340                 345                 350
Phe Gln Asn Val Phe Ser Lys Pro Lys Gly Thr Asn Ser Ser Ala Val
        355                 360                 365
Pro Leu Ser Gln Gly Gln Val Val Val Ser Pro Pro Ser Ser Arg Ser
    370                 375                 380
Ala Val Ser Ile Gly Gly Gly Asn Thr Ser Ala Val Ser Pro Ser Ser
385                 390                 395                 400
Ile Arg Gly Ser Ala Ala Ala Ser Leu Gln Pro Leu Gly Glu Gln Ser
                405                 410                 415
Gln Gln Val Ala Leu Thr His Thr Val Val Lys Leu Lys Cys Gln His
            420                 425                 430
Cys Asn His Leu Phe Ala Thr Lys Pro Glu Leu Leu Phe Tyr Lys Gly
        435                 440                 445
Lys Met Phe Leu Phe Cys Gly Lys Asn Cys Ser Asp Glu Tyr Lys Lys
    450                 455                 460
Lys Asn Lys Val Val Ala Met Cys Glu Tyr Cys Lys Ile Glu Lys Ile
465                 470                 475                 480
Val Lys Glu Thr Val Arg Phe Ser Gly Ala Asp Lys Ser Phe Cys Ser
                485                 490                 495
Glu Gly Cys Lys Leu Leu Tyr Lys His Asp Leu Ala Lys Arg Trp Gly
            500                 505                 510
Asn His Cys Lys Met Cys Ser Tyr Cys Ser Gln Thr Ser Pro Asn Leu
        515                 520                 525
Val Gln Asn Arg Leu Glu Gly Lys Leu Glu Glu Phe Cys Cys Glu Asp
    530                 535                 540
Cys Met Ser Lys Phe Thr Val Leu Phe Tyr Gln Met Ala Lys Cys Asp
545                 550                 555                 560
Gly Cys Lys Arg Gln Gly Lys Leu Ser Glu Ser Ile Lys Trp Arg Gly
                565                 570                 575
Asn Ile Lys His Phe Cys Asn Leu Phe Cys Val Leu Glu Phe Cys His
            580                 585                 590
Gln Gln Ile Met Asn Asp Cys Leu Pro Gln Asn Lys Val Asn Ile Ser
        595                 600                 605
Lys Ala Lys Thr Ala Val Thr Glu Leu Pro Ser Ala Arg Thr Asp Thr
    610                 615                 620
Thr Pro Val Ile Thr Ser Val Met Ser Leu Ala Lys Ile Pro Ala Thr
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625 630 635 640
Leu Ser Thr Gly Asn Thr Asn Ser Val Leu Lys Gly Ala Val Thr Lys
645 650 655
Glu Ala Ala Lys Ile Ile Gln Asp Glu Ser Thr Gln Glu Asp Ala Met
660 665 670
Lys Phe Pro Ser Ser Gln Ser Ser Gln Pro Ser Arg Leu Leu Lys Asn
675 680 685
Lys Gly Ile Ser Cys Lys Pro Val Thr Gln Thr Lys Ala Thr Ser Cys
690 695 700
Lys Pro His Thr Gln His Lys Glu Cys Gln Thr Glu Cys Pro Val Arg
705 710 715 720
Ala Val Cys

<210> 3415
<211> 3501
<212> DNA
<213> Homo sapiens

<400> 3415
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120
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180
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240
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360
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2640

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3501

<210> 3416
<211> 259
<212> PRT
<213> Homo sapiens

<400> 3416
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20 25 30
Asn Pro Ala Phe Lys Pro Val Leu Ala Ile Ile Gln Ala Gly Asp Asp
35 40 45
Asn Leu Met Gln Glu Ile Asn Gln Asn Leu Ala Glu Glu Ala Gly Leu
50 55 60
Asn Ile Thr His Ile Cys Leu Pro Pro Asp Ser Ser Glu Ala Glu Ile
65 70 75 80
Ile Asp Glu Ile Leu Lys Ile Asn Glu Asp Thr Arg Val His Gly Leu
85 90 95
Ala Leu Gln Ile Ser Glu Asn Leu Phe Ser Asn Lys Val Leu Asn Ala
100 105 110
Leu Lys Pro Glu Lys Asp Val Asp Gly Val Thr Asp Ile Asn Leu Gly
115 120 125
Lys Leu Val Arg Gly Asp Ala His Glu Cys Phe Val Ser Pro Val Ala

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    130                 135                 140
Lys Ala Val Ile Glu Leu Leu Glu Lys Ser Val Gly Val Asn Leu Asp
145                 150                 155                 160
Gly Lys Lys Ile Leu Val Val Gly Ala His Gly Ser Leu Glu Ala Ala
                165                 170                 175
Leu Gln Cys Leu Phe Gln Arg Lys Gly Ser Met Thr Met Ser Ile Gln
            180                 185                 190
Trp Lys Thr Arg Gln Leu Gln Ser Lys Leu His Glu Ala Asp Ile Val
        195                 200                 205
Val Leu Gly Ser Pro Lys Pro Glu Glu Ile Pro Leu Thr Trp Ile Gln
    210                 215                 220
Pro Gly Thr Thr Val Leu Asn Cys Ser His Asp Phe Leu Ser Gly Lys
225                 230                 235                 240
Val Gly Cys Gly Ser Pro Arg Ile Xaa Ile Leu Val Asp Ser Leu Arg
                245                 250                 255
Lys Met Met
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<210> 3417
<211> 405
<212> DNA
<213> Homo sapiens

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120
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180
attacaatcg attggaacaa gctccagagc ctctcggcat tccagcctgc attgctcttt
240
agtgcacttg aacaacacat tttatattta caggtaaatt tcttgttaga aatgataacc
300
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360
cactatatta atagtgttgc taataaaacg ttatttacat ccgga
405

<210> 3418
<211> 94
<212> PRT
<213> Homo sapiens

<400> 3418
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Leu Glu Arg Arg Cys Ser Pro Asn Leu Ser Arg Glu Val Leu Tyr Glu
            20                  25                  30
Ile Phe Arg Ser Leu His Thr Leu Val Gly Gln Leu Asp Leu Arg Asp
        35                  40                  45
Asp Val Val Lys Ile Thr Ile Asp Trp Asn Lys Leu Gln Ser Leu Ser
    50                  55                  60
Ala Phe Gln Pro Ala Leu Leu Phe Ser Ala Leu Glu Gln His Ile Leu
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65 70 75 80
Tyr Leu Gln Val Asn Phe Leu Leu Glu Met Ile Thr Arg Tyr
85 90

<210> 3419
<211> 418
<212> DNA
<213> Homo sapiens

<400> 3419
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120
aatggggcta cgtcgcgtga cctcacgtgt ggttcctctg agcgtagtgc tttccagggc
180
aaccgtgtca cagtgcagat ggacgcacgg acggcggtga gcctttaacg ccaagcaaca
240
agtcccattg tggacggagg tttgcatttc tcctgggtcc acatctatgg tgcccccata
300
gggcgccttg aggctcgccc cggtcaggct tgccatttct ggggaagagg actgggggg
360
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418

<210> 3420
<211> 105
<212> PRT
<213> Homo sapiens

<400> 3420
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20 25 30
Cys Cys Leu Ala Leu Lys Ala His Arg Arg Pro Cys Val His Leu His
35 40 45
Cys Asp Thr Val Ala Leu Glu Ser Thr Thr Leu Arg Gly Thr Thr Arg
50 55 60
Glu Val Thr Arg Arg Ser Pro Ile Asn Met Lys His Pro Glu Gln Gly
65 70 75 80
Glu Pro Gly Gly Pro Ala Asp Gln Trp Val Pro Arg Arg Glu Trp Ala
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Gly Trp Asp Gly Ser Gly Val Asn Arg
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<210> 3421
<211> 2988
<212> DNA
<213> Homo sapiens

<400> 3421
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120
ggactgcagg ggaagctcca gcttaaaatg taacatgtcc gtcttcccat cctggttcct
180
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300
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360
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420
aaagcgacgg gttcctcgcc tggagcacgt tcccggcctt caaccggctg caaggggatc
480
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540
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600
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660
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720
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1020
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1680

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1740
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1920
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2160
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2280
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2340
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2400
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2700
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2760
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2820
gtgggagaat cacttggact ccaaaggtgg aggttgcagt aagctgaaat catgccactg
2880
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2940
aaagtcctgc cgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa
2988

<210> 3422
<211> 418
<212> PRT
<213> Homo sapiens

<400> 3422
Met Ser Arg His Leu Pro Trp Ile Cys Asp Gln Arg Cys Ser Ser Pro
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Ser Ser Pro Gly Arg Trp Pro Pro Ala Ala Arg Met Trp Leu Pro Arg

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Phe Ser Ser Lys Thr Val Thr Val Leu Leu Leu Ala Gln Thr Thr Cys
        35                  40                  45
Leu Leu Leu Phe Ile Ile Ser Arg Pro Gly Pro Ser Ser Pro Ala Gly
    50                  55                  60
Gly Glu Asp Arg Val His Val Leu Val Leu Ser Ser Trp Arg Ser Gly
65                  70                  75                  80
Ser Ser Phe Leu Gly Gln Leu Phe Ser Gln His Pro Asp Val Phe Tyr
                85                  90                  95
Leu Met Glu Pro Ala Trp His Val Trp Thr Thr Leu Ser Gln Gly Ser
            100                 105                 110
Ala Ala Thr Leu His Met Ala Val Arg Asp Leu Met Arg Ser Ile Phe
        115                 120                 125
Leu Cys Asp Met Asp Val Phe Asp Ala Tyr Met Glu Pro Gly Pro Arg
    130                 135                 140
Arg Gln Ser Ser Leu Phe Gln Trp Glu Asn Ser Arg Ala Leu Cys Ser
145                 150                 155                 160
Ala Pro Ala Cys Asp Ile Ile Pro Gln Asp Glu Ile Ile Pro Arg Ala
                165                 170                 175
His Cys Arg Leu Leu Cys Ser Gln Gln Pro Phe Glu Val Val Glu Lys
            180                 185                 190
Ala Cys Arg Ser Tyr Ser His Val Val Leu Lys Glu Val Arg Phe Phe
        195                 200                 205
Asn Leu Gln Ser Leu Tyr Pro Leu Leu Lys Asp Pro Ser Leu Asn Leu
    210                 215                 220
His Ile Val His Leu Val Arg Asp Pro Arg Ala Val Leu Arg Ser Arg
225                 230                 235                 240
Glu Ala Ala Gly Pro Ile Leu Ala Arg Asp Asn Gly Ile Val Leu Gly
                245                 250                 255
Thr Asn Gly Lys Trp Val Glu Ala Asp Pro His Leu Arg Leu Ile Arg
            260                 265                 270
Glu Val Cys Arg Ser His Val Arg Ile Ala Glu Ala Ala Thr Leu Lys
        275                 280                 285
Pro Pro Pro Phe Leu Arg Gly Arg Tyr Arg Leu Val Arg Phe Glu Asp
    290                 295                 300
Leu Ala Arg Glu Pro Leu Ala Glu Ile Arg Ala Leu Tyr Ala Phe Thr
305                 310                 315                 320
Gly Leu Thr Leu Thr Pro Gln Leu Glu Ala Trp Ile His Asn Ile Thr
                325                 330                 335
His Gly Ser Gly Ile Gly Lys Pro Ile Glu Ala Phe His Thr Ser Ser
            340                 345                 350
Arg Asn Ala Arg Asn Val Ser Gln Ala Trp Arg His Ala Leu Pro Phe
        355                 360                 365
Thr Lys Ile Leu Arg Val Gln Glu Val Cys Ala Gly Ala Leu Gln Leu
    370                 375                 380
Leu Gly Tyr Arg Pro Val Tyr Ser Ala Asp Gln Gln Arg Asp Leu Thr
385                 390                 395                 400
Leu Asp Leu Val Leu Pro Arg Gly Pro Asp His Phe Ser Trp Ala Ser
                405                 410                 415
Pro Asp
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<210> 3423
<211> 1851

<212> DNA
<213> Homo sapiens

<400> 3423
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120
cgttcattgg ccgtggcctc tctagctccg ccccctaggg gggtcgaccc cgtaaccagt
180
gaggcgcggg ccaacctagt gcgacgtgtg ggcgtggcgg gggctggggt ctgcgggcga
240
aggtggtagc ccattggagg tcccgggagc gaagtccagc tgccgttagg cgctgggata
300
gtcgcacgct ggatgcatct acgtccgccg agcccctggg gcgaagaggc cgcgtccgcc
360
ttcagttgtg gccggtgctt cgcccccctga cccttcgccc ccaaagacca gctctaacgt
420
gagcgcctcg gccgccctgc cccagcctcg tacacgccgc cagcctcgcc cagccggtgt
480
ccggagaccc tcgggccgtg tccatttgtg ggcaaagcca gcggggcagg cttggccaga
540
gtgcaccact cggcgccgtc ccaggcccga cgctctgggc gcgcccggaa ccccaggtta
600
atttggagtg gcccctggag tcagtttcct acaccatccg aggccccacc cagcacgagc
660
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720
ctcagcggtg ggcagtccta gtccgaggtg ccaccgtgga aggacagaat ggcagcaaga
780
gcaactcacc accagccttg ggcccagaag catgccctgt ctccctgccc agtcccccgg
840
aagcctccac actcaagggc cctccacctg aggcagatct tcctaggagc cctggaaact
900
tgacggagag agaagagctg gcagggagcc tggcccgggc tattgcaggt ggagacgaga
960
agggggcagc ccaagtggca gccgtcctgg cccagcatcg tgtggccctg agtgttcagc
1020
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1080
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1140
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1200
ggagcctagg tgacatcacc tgccctgatg ctctggccac aggtgttctc agagctcggt
1260
ttcccgccag ccgtgcaacg ctgggtcatc ggacggtgcc tgtgtgtgcc tgagcgcagc
1320
cttgcctctt acggggttcg gcaggatggg gaccctgctt tcctctactt gctgtcagct
1380
cctcgagaag ccccagccac aggacctagc cctcagcacc cccagaagat ggacggggaa
1440
cttggacgct tgtttccccc atcattgggg ctacccccag gcccccagcc agctgcctcc
1500

agcctgccca gtccactcca gcccagctgg tcctgtcctt cctgcacctt catcaatgcc
1560
ccagaccgcc ctggctgtga gatgtgtagc acccagaggc cctgcacttg ggacccccct
1620
gctgcagctt ccacctagca gccaccagag gttacaaggg gagagtggcc cttccctcac
1680
aagtccgaca tctccaggcc cccactgaac tccggggacc tctactgact gcttgctggg
1740
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1800
caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a
1851

<210> 3424
<211> 136
<212> PRT
<213> Homo sapiens

<400> 3424
Met Leu Trp Pro Gln Val Phe Ser Glu Leu Gly Phe Pro Pro Ala Val
1 5 10 15
Gln Arg Trp Val Ile Gly Arg Cys Leu Cys Val Pro Glu Arg Ser Leu
20 25 30
Ala Ser Tyr Gly Val Arg Gln Asp Gly Asp Pro Ala Phe Leu Tyr Leu
35 40 45
Leu Ser Ala Pro Arg Glu Ala Pro Ala Thr Gly Pro Ser Pro Gln His
50 55 60
Pro Gln Lys Met Asp Gly Glu Leu Gly Arg Leu Phe Pro Pro Ser Leu
65 70 75 80
Gly Leu Pro Pro Gly Pro Gln Pro Ala Ala Ser Ser Leu Pro Ser Pro
85 90 95
Leu Gln Pro Ser Trp Ser Cys Pro Ser Cys Thr Phe Ile Asn Ala Pro
100 105 110
Asp Arg Pro Gly Cys Glu Met Cys Ser Thr Gln Arg Pro Cys Thr Trp
115 120 125
Asp Pro Leu Ala Ala Ala Ser Thr
130 135

<210> 3425
<211> 1416
<212> DNA
<213> Homo sapiens

<400> 3425
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120
gaggaggaag tgaggccgcg cggaaggaag gcggcgagcc ccggggcccc gaggccttgg
180
ccgcgtcaca gcacccacat ggcctctgga gtgggcgcgg ccttcgagga actgcctcac
240
gacggcacgt gtgacgagtg cgagcccgac gaggctccgg gggccgagga agtgtgccga
300

gaatgcggct tctgctactg ccgccgccat gccgaggcgc acaggcagaa gttcctcagt
360
caccatctgg ccgaatacgt ccacggctcc caggcctgga ccccgccagc tgacggagag
420
ggggcgggga aggaagaagc ggaggtcaag gtggagcagg agagggagat agaaagcgag
480
gcaggggaag agagtgagtc ggaggaagag agcgagtcag aggaagagag cgagacagag
540
gaagagagtg aggatgagag cgatgaggag agtgaagaag acagcgagga agaaatggag
600
gatgagcaag aaagcgaggc cgaagaagac aaccaagaag aaggggaatc cgaggcggag
660
ggagaaactg aggcagaaag tgaatttgac ccagaaatag aaatggaagc agagagagtg
720
gccaagagga agtgtccgga ccatgggctt gatttgagta cctattgcca ggaagatagg
780
cagctcatct gtgtcctgtg tccagtcatt ggggctcacc agggccacca actctccacc
840
ctagacgaag cctttgaaga attaagaagc aaagactcag gtggactgaa ggccgctatg
900
atcgaattgg tggaaaggtt gaagttcaag agctcagacc ctaaagtaac tcgggaccaa
960
atgaagatgt ttatacagca ggaatttaag aaagttcaga aagtgattgc tgatgaggag
1020
cagaaggccc ttcatctagt ggacatccaa gaggcaatgg ccacagctca tgtgactgag
1080
atactggcag acatccaatc ccacatggat aggttgatga ctcagatggc ccaagccaag
1140
gaacaacttg atacctctaa tgaatcagct gagccaaagg cagagggcga tgaggaagga
1200
cccagtggtg ccagtgaaga agaggacaca tgaaggcttg ctacccccag tgaaaatcat
1260
ccccctcccct tgtgtgtatg tgacagcgtg tatgtaacgg cttctgattt ctgtgaaagc
1320
tgctcagcaa caaacgtact tccaccagat gtgtccccag atccacagca ggcacatatc
1380
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1416

<210> 3426
<211> 410
<212> PRT
<213> Homo sapiens

<400> 3426
Ser Gly Gly Lys Gly Leu Cys Cys Cys Ala Arg Ala Gly Ala Ala Ala
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Ala Pro Gly Pro Ala Ser Arg Arg Gly Ala Val Gln Ala Gly Gly Asp
            20   25   30
Ser Leu Gly Arg Asp Pro Gly Arg Glu Glu Glu Val Arg Pro Arg Gly
        35   40   45
Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro Trp Pro Arg His Ser
    50   55   60
Thr His Met Ala Ser Gly Val Gly Ala Ala Phe Glu Glu Leu Pro His

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65                  70                  75                  80
Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu Ala Pro Gly Ala Glu
                85                  90                  95
Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys Arg Arg His Ala Glu
            100                 105                 110
Ala His Arg Gln Lys Phe Leu Ser His His Leu Ala Glu Tyr Val His
        115                 120                 125
Gly Ser Gln Ala Trp Thr Pro Pro Ala Asp Gly Glu Gly Ala Gly Lys
    130                 135                 140
Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg Glu Ile Glu Ser Glu
145                 150                 155                 160
Ala Gly Glu Glu Ser Glu Ser Glu Glu Glu Ser Glu Ser Glu Glu Glu
                165                 170                 175
Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp Glu Glu Ser Glu
            180                 185                 190
Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln Glu Ser Glu Ala Glu
        195                 200                 205
Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu Gly Glu Thr Glu
    210                 215                 220
Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met Glu Ala Glu Arg Val
225                 230                 235                 240
Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp Leu Ser Thr Tyr Cys
                245                 250                 255
Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys Pro Val Ile Gly Ala
            260                 265                 270
His Gln Gly His Gln Leu Ser Thr Leu Asp Glu Ala Phe Glu Glu Leu
        275                 280                 285
Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala Met Ile Glu Leu Val
    290                 295                 300
Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys Val Thr Arg Asp Gln
305                 310                 315                 320
Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys Val Gln Lys Val Ile
                325                 330                 335
Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val Asp Ile Gln Glu Ala
            340                 345                 350
Met Ala Thr Ala His Val Thr Glu Ile Leu Ala Asp Ile Gln Ser His
        355                 360                 365
Met Asp Arg Leu Met Thr Gln Met Ala Gln Ala Lys Glu Gln Leu Asp
    370                 375                 380
Thr Ser Asn Glu Ser Ala Glu Pro Lys Ala Glu Gly Asp Glu Glu Gly
385                 390                 395                 400
Pro Ser Gly Ala Ser Glu Glu Glu Asp Thr
                405                 410
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<210> 3427
<211> 580
<212> DNA
<213> Homo sapiens

<400> 3427
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ccggatttca atgtcatagt tcccattgtc aatgacatca tcggagaact tgacctgctg
120

gggtctggat tgagacttgg accttctgag cactggcaga tgtactggct tctcttcagg
180
caggattttc tctggacaca actctgaact tagactcttt aaggactctg cactcctgtg
240
cagcatggaa gagttcaaag ttcccatatt gctcatcttc tcacaatctt ctgtttccat
300
ctcctcaaaa ttttgcagag aatacaatga tggccttggc ttgttttctc catccaccga
360
agcccctgtg atattggaca atgccaaaga atccatcgaa tcccgaacac tttgctctgg
420
tttcaggtct gacagacact ccagggaatc ttcataccac tgtgtttcat catgattata
480
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540
gtggctgcca taagcagaat cgcccagtcc atcttgtgac
580

<210> 3428
<211> 132
<212> PRT
<213> Homo sapiens

<400> 3428
Met Asp Ser Leu Ala Leu Ser Asn Ile Thr Gly Ala Ser Val Asp Gly
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Glu Asn Lys Pro Arg Pro Ser Leu Tyr Ser Leu Gln Asn Phe Glu Glu
20 25 30
Met Glu Thr Glu Asp Cys Glu Lys Met Ser Asn Met Gly Thr Leu Asn
35 40 45
Ser Ser Met Leu His Arg Ser Ala Glu Ser Leu Lys Ser Leu Ser Ser
50 55 60
Glu Leu Cys Pro Glu Lys Ile Leu Pro Glu Glu Lys Pro Val His Leu
65 70 75 80
Pro Val Leu Arg Arg Ser Lys Ser Gln Ser Arg Pro Gln Gln Val Lys
85 90 95
Phe Ser Asp Asp Val Ile Asp Asn Gly Asn Tyr Asp Ile Glu Ile Arg
100 105 110
Gln Pro Pro Met Ser Glu Arg Thr Arg Arg Arg Val Tyr Asn Phe Glu
115 120 125
Glu Arg Gly Ser
130

<210> 3429
<211> 634
<212> DNA
<213> Homo sapiens

<400> 3429
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agggaaggga gccggcagct ggatgtggca ggatgatttc tcctgagagt agccctcgcg
120
gtcagcttcc ttttcatact ttcccggcgt tctctccacg agcaggtgca ccagggacct
180

gtccctctgt cctacacggt caccacagtg acgacccaag gcttcccctt gcctacaggc
240
cagcacatcc ctggctgcag tgcccagcag ctcccagcat gctccgtgat gttcagtggg
300
cagcattacc ccctctgctg cctcccgccc ccgcttatcc aggcgtgcac catgcagcag
360
ctgcctgtgc cctatcaggc ctacccccac ctcatctcca gtgaccacta catcctgcac
420
cccccaccac cgggcacaca cccagcagct ccagggtctg tataagaaac cctgtggaag
480
gcccatccct gtcctaggcc acccaggcag gacactccac tgttaaggcc cacagcctca
540
actcctgggc ctctgccaag ctgtgaggca ggtacagggg tactggaagg ttcctgaacc
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ttgaaacact ctattaccaa atgtgaacac gcgt
634

<210> 3430
<211> 122
<212> PRT
<213> Homo sapiens

<400> 3430
Phe Leu Leu Arg Val Ala Leu Ala Val Ser Phe Leu Phe Ile Leu Ser
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Arg Arg Ser Leu His Glu Gln Val His Gln Gly Pro Val Pro Leu Ser
20 25 30
Tyr Thr Val Thr Thr Val Thr Thr Gln Gly Phe Pro Leu Pro Thr Gly
35 40 45
Gln His Ile Pro Gly Cys Ser Ala Gln Gln Leu Pro Ala Cys Ser Val
50 55 60
Met Phe Ser Gly Gln His Tyr Pro Leu Cys Cys Leu Pro Pro Pro Leu
65 70 75 80
Ile Gln Ala Cys Thr Met Gln Gln Leu Pro Val Pro Tyr Gln Ala Tyr
85 90 95
Pro His Leu Ile Ser Ser Asp His Tyr Ile Leu His Pro Pro Pro Pro
100 105 110
Gly Thr His Pro Ala Ala Pro Gly Ser Val
115 120

<210> 3431
<211> 1396
<212> DNA
<213> Homo sapiens

<400> 3431
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ccatcttcac gctggcgccc ccgctgcatt gccactacgg ggccttcccc cctaatgcct
120
ctgcgtggga gcagcgtccc aatgccagcg cgtcacgtcg ccagcgctgc cctagcacgc
180
agcgccgcca gccgtgtcgc caacagtacc aaatcgtcgt gcagcggctt cgccccgccg
240

gacttcaacc attgcctcaa ggattgggac tataatggcc ttcctgtgct caccaccaac
300
gccatcggcc agtgggatct ggtgtgtgac ctgggctggc aggtgatcct ggagcagatc
360
ctcttcatct tgggctttgc ctccggctac ctgttcctgg gttaccccgc agacagattt
420
ggccgtcgcg ggattgtgct gctgaccttg gggctggtgg gcccctgtgg agtaggaggg
480
gctgctgcag gctcctccac aggcgtcatg gccctccgat tcctcttggg ctttctgctt
540
gccggtgttg acctgggtgt ctacctgatg cgcctggagc tgtgcgaccc aacccagagg
600
cttcgggtgg ccctggcagg ggagttggtg ggggtgggag ggcacttcct gttcctgggc
660
ctggcccttg tctctaagga ttggcgattc ctacagcgaa tgatcaccgc tccctgcatc
720
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840
catgggcaga tgctgggggа ggaggcccag gaggccctgc aggacctgga gaatacctgc
900
cctctccctg caacatcctc cttttccttt gcttccctcc tcaactaccg caacatctgg
960
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cagcctgtgg gaggaggagg gagcccatcg gacttctacc tgtgctctct gctggccagc
1080
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1140
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1200
tgggattgtg agcatcctat cttccccaca gtgtgggctc aacaagggaa ccccaacaga
1260
gatctgaacg aggctgccat caccactttc tctgtccttg ggctcttctc ctcccaagct
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1380
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1396

<210> 3432
<211> 296
<212> PRT
<213> Homo sapiens

<400> 3432
Met Ala Leu Arg Phe Leu Leu Gly Phe Leu Leu Ala Gly Val Asp Leu
1 5 10 15
Gly Val Tyr Leu Met Arg Leu Glu Leu Cys Asp Pro Thr Gln Arg Leu
20 25 30
Arg Val Ala Leu Ala Gly Glu Leu Val Gly Val Gly Gly His Phe Leu
35 40 45
Phe Leu Gly Leu Ala Leu Val Ser Lys Asp Trp Arg Phe Leu Gln Arg

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    50                  55                  60
Met Ile Thr Ala Pro Cys Ile Leu Phe Leu Phe Tyr Gly Trp Pro Gly
65                  70                  75                  80
Leu Phe Leu Glu Ser Ala Arg Trp Leu Ile Val Lys Arg Gln Ile Glu
                85                  90                  95
Glu Ala Gln Ser Val Leu Arg Ile Leu Ala Glu Arg Asn Arg Pro His
            100                 105                 110
Gly Gln Met Leu Gly Glu Glu Ala Gln Glu Ala Leu Gln Asp Leu Glu
        115                 120                 125
Asn Thr Cys Pro Leu Pro Ala Thr Ser Ser Phe Ser Phe Ala Ser Leu
    130                 135                 140
Leu Asn Tyr Arg Asn Ile Trp Lys Asn Leu Leu Ile Leu Gly Phe Thr
145                 150                 155                 160
Asn Phe Ile Ala His Ala Ile Arg His Cys Tyr Gln Pro Val Gly Gly
                165                 170                 175
Gly Gly Ser Pro Ser Asp Phe Tyr Leu Cys Ser Leu Leu Ala Ser Gly
            180                 185                 190
Thr Ala Ala Leu Ala Cys Val Phe Leu Gly Val Thr Val Asp Arg Phe
        195                 200                 205
Gly Arg Arg Gly Ile Leu Leu Leu Ser Met Thr Leu Thr Gly Ile Ala
    210                 215                 220
Ser Leu Val Leu Leu Gly Leu Trp Asp Cys Glu His Pro Ile Phe Pro
225                 230                 235                 240
Thr Val Trp Ala Gln Gln Gly Asn Pro Asn Arg Asp Leu Asn Glu Ala
                245                 250                 255
Ala Ile Thr Thr Phe Ser Val Leu Gly Leu Phe Ser Ser Gln Ala Ala
            260                 265                 270
Ala Ile Leu Ser Thr Leu Leu Ala Ala Glu Val Ile Pro Thr Thr Val
        275                 280                 285
Arg Gly Arg Gly Leu Gly Leu Ile
    290                 295
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<210> 3433
<211> 1257
<212> DNA
<213> Homo sapiens

<400> 3433
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tcagtgcccc cttcaccttc acctcgacct ctgccgggag ggagacagcg tccgcagaga
120
ccgagccact cccgttccca caccaggtcg aacttgaaaa gggacgtcgc ccacctgtac
180
cgaggagtcg gctcgcgcta catcatgggg tcaggagaat ccttcatgca gctgcagcag
240
cgtctcctga gagagaagga ggccaagatc aggaaggcct tggacaggct tcgcaagaag
300
aggcacctgc tccgccggca gcggacgagg cgggagttcc ccgtgatctc cgtggtgggg
360
tacaccaact gcggtgagca cgcgcccagg ggaggggcct tccgcggtct ccgtgtcacc
420
ggtgaggact cgcccggggg agggcagggg gtccctgtcg tctcagtggt gccgtacgac
480

agctgcggtg agcacgtgcc caggagaggg ggttcccatg gtcgccgtgt ggggtacacc
540
agctgctgtg agagctcacc caggagacgg gtttcctgtg gtctctgtgt ggggtacagc
600
agccaaggtg aggatgtcat ctaccccatc ctcccatcca gagctttacc accctgtcta
660
taccacaacc tcccctccat ctacaccatc ctcctgtcta gaccatcccc actgccctat
720
ctataccacc accctgtcta cacaatccac ccatctacac catcacctct cctctgtcta
780
taccatcctc ctgtctacac cagcaccact accccatcta taccaccacc ccgtctacat
840
aatccacccg tgtacaccac aatgtccctt tcgtctgcac cgtcctcctg tctacactgg
900
caccactgcc ccagctatac caccaccccg tctacataat ccacccatct gtctacacca
960
tcgcctctcc tctgtctaca ccatccttct gtcaacaccg gcaccactgc cgtatctata
1020
tccacccatc tacaccatca cctcccctgt gtctacacca tcctcccatc cacaccagca
1080
ccaccacccc acctacacca tcccaccatc tacgccattg ccaaatctac acagacgacc
1140
tcactcccat ccacgccttc acacgcacac ccgtccacac caccatctcc cccgtgtccg
1200
cacggcggcc ccgctccatc ggcccgagaa cagcgacggt ggctttgtcc cacgcgt
1257

<210> 3434
<211> 311
<212> PRT
<213> Homo sapiens

<400> 3434
Ala Thr Arg Gly Ala Gly Pro Gln Gln Arg Leu Leu Pro Ser Ala Gln
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Arg Pro Ser Ser Val Pro Pro Ser Pro Ser Pro Arg Pro Leu Pro Gly
            20   25   30
Gly Arg Gln Arg Pro Gln Arg Pro Ser His Ser Arg Ser His Thr Arg
        35   40   45
Ser Asn Leu Lys Arg Asp Val Ala His Leu Tyr Arg Gly Val Gly Ser
    50   55   60
Arg Tyr Ile Met Gly Ser Gly Glu Ser Phe Met Gln Leu Gln Gln Arg
65   70   75   80
Leu Leu Arg Glu Lys Glu Ala Lys Ile Arg Lys Ala Leu Asp Arg Leu
                85   90   95
Arg Lys Lys Arg His Leu Leu Arg Arg Gln Arg Thr Arg Arg Glu Phe
            100   105   110
Pro Val Ile Ser Val Val Gly Tyr Thr Asn Cys Gly Glu His Ala Pro
        115   120   125
Arg Gly Gly Ala Phe Arg Gly Leu Arg Val Thr Gly Glu Asp Ser Pro
    130   135   140
Gly Gly Gly Gln Gly Val Pro Val Val Ser Val Val Pro Tyr Asp Ser
145   150   155   160
Cys Gly Glu His Val Pro Arg Arg Gly Gly Ser His Gly Arg Arg Val

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                165                 170                 175
Gly Tyr Thr Ser Cys Cys Glu Ser Ser Pro Arg Arg Arg Val Ser Cys
            180                 185                 190
Gly Leu Cys Val Gly Tyr Ser Ser Gln Gly Glu Asp Val Ile Tyr Pro
        195                 200                 205
Ile Leu Pro Ser Arg Ala Leu Pro Pro Cys Leu Tyr His Asn Leu Pro
    210                 215                 220
Ser Ile Tyr Thr Ile Leu Leu Ser Arg Pro Ser Pro Leu Pro Tyr Leu
225                 230                 235                 240
Tyr His His Pro Val Tyr Thr Ile His Pro Ser Thr Pro Ser Pro Leu
                245                 250                 255
Leu Cys Leu Tyr His Pro Pro Val Tyr Thr Ser Thr Thr Thr Pro Ser
            260                 265                 270
Ile Pro Pro Pro Arg Leu His Asn Pro Pro Val Tyr Thr Thr Met Ser
        275                 280                 285
Pro Ser Ser Ala Pro Ser Ser Cys Leu His Trp His His Cys Pro Ser
    290                 295                 300
Tyr Thr Thr Thr Pro Ser Thr
305                 310
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<210> 3435
<211> 1225
<212> DNA
<213> Homo sapiens

<400> 3435

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120
gacagcaatg ccgataccta ctgggagagc gatgggtccc agtgccaaca ctgggtacgg
180
cttactatga agaagggcac cattgtcaag aagctgctac tcgcagtgga taccacagat
240
gacaacttta tgccaaagcg ggtggtggtc tatgggggtg aaggggacaa cctgaagaag
300
ctgagtgacg tgagcattga cnngagaccc tcatcggggn atgtctgtgt cctggaggac
360
atgaccgtcc acctcccgat catcgagatc cgcatcgtgg agtgccgaga tgatgggatt
420
gatgttcgtc tccgaggggt caagatcaag tcatctagac agcgggaact agggttgaat
480
gcagacctgt tccagccaac tagtctggtg cgatatccac gcctagaagg caccgaccct
540
gaagtactgt accgcagagc tgtcctcctg cagagattca tcaagatcct cgatagtgtc
600
ctgcaccacc tggtacctgc ctgggaccac acactgggca ccttcagtga gattaagcaa
660
gtgaagcagt tcctactgct gtcccgccag cggccaggcc tggtggctca gtgcctgcgt
720
gactctgaga gcagcaagcc cagcttcatg ccacgcctat acatcaaccg ccgtcttgcc
780
atggaacacc gtgcctgccc ctctcgagac cctgcctgca agaatgcagt cttcacccag
840
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gtatatgaag gcctcaagcc ctctgacaaa tatgaaaagc ccctggacta caggtggccc
900
atgcgctatg accagtggtg ggagtgtaaa tttattgcag aaggcatcat tgaccaaggg
960
ggtggtttcc gggacagcct ggcagatatg tcagaagagc tgtgccctag ctcagcggat
1020
acccccgtgc ccctgccctt ctttgtacgc acagccaacc agggcaatgg cactggtgag
1080
gctcgggaca tgtatgtacc caacccctcc tgccgagact ttgccaagta tgaatggatc
1140
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1200
tttgtgtgga agcagctttc tgcag
1225

<210> 3436
<211> 408
<212> PRT
<213> Homo sapiens

<400> 3436
Xaa His Ser Leu Tyr Asp His Trp Gly Lys Glu Asp Glu Asn Leu Gly
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Ser Val Lys Gln Tyr Val Glu Ser Ile Asp Val Ser Ser Tyr Thr Glu
20 25 30
Glu Phe Asn Val Ser Cys Leu Thr Asp Ser Asn Ala Asp Thr Tyr Trp
35 40 45
Glu Ser Asp Gly Ser Gln Cys Gln His Trp Val Arg Leu Thr Met Lys
50 55 60
Lys Gly Thr Ile Val Lys Lys Leu Leu Leu Ala Val Asp Thr Thr Asp
65 70 75 80
Asp Asn Phe Met Pro Lys Arg Val Val Val Tyr Gly Gly Glu Gly Asp
85 90 95
Asn Leu Lys Lys Leu Ser Asp Val Ser Ile Asp Xaa Arg Pro Ser Ser
100 105 110
Gly Xaa Val Cys Val Leu Glu Asp Met Thr Val His Leu Pro Ile Ile
115 120 125
Glu Ile Arg Ile Val Glu Cys Arg Asp Asp Gly Ile Asp Val Arg Leu
130 135 140
Arg Gly Val Lys Ile Lys Ser Ser Arg Gln Arg Glu Leu Gly Leu Asn
145 150 155 160
Ala Asp Leu Phe Gln Pro Thr Ser Leu Val Arg Tyr Pro Arg Leu Glu
165 170 175
Gly Thr Asp Pro Glu Val Leu Tyr Arg Arg Ala Val Leu Leu Gln Arg
180 185 190
Phe Ile Lys Ile Leu Asp Ser Val Leu His His Leu Val Pro Ala Trp
195 200 205
Asp His Thr Leu Gly Thr Phe Ser Glu Ile Lys Gln Val Lys Gln Phe
210 215 220
Leu Leu Leu Ser Arg Gln Arg Pro Gly Leu Val Ala Gln Cys Leu Arg
225 230 235 240
Asp Ser Glu Ser Ser Lys Pro Ser Phe Met Pro Arg Leu Tyr Ile Asn
245 250 255
Arg Arg Leu Ala Met Glu His Arg Ala Cys Pro Ser Arg Asp Pro Ala

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            260                 265                 270
Cys Lys Asn Ala Val Phe Thr Gln Val Tyr Glu Gly Leu Lys Pro Ser
        275                 280                 285
Asp Lys Tyr Glu Lys Pro Leu Asp Tyr Arg Trp Pro Met Arg Tyr Asp
    290                 295                 300
Gln Trp Trp Glu Cys Lys Phe Ile Ala Glu Gly Ile Ile Asp Gln Gly
305                 310                 315                 320
Gly Gly Phe Arg Asp Ser Leu Ala Asp Met Ser Glu Glu Leu Cys Pro
                325                 330                 335
Ser Ser Ala Asp Thr Pro Val Pro Leu Pro Phe Phe Val Arg Thr Ala
            340                 345                 350
Asn Gln Gly Asn Gly Thr Gly Glu Ala Arg Asp Met Tyr Val Pro Asn
        355                 360                 365
Pro Ser Cys Arg Asp Phe Ala Lys Tyr Glu Trp Ile Gly Gln Leu Met
    370                 375                 380
Gly Ala Ala Leu Arg Gly Lys Glu Phe Leu Val Leu Ala Leu Pro Gly
385                 390                 395                 400
Phe Val Trp Lys Gln Leu Ser Ala
                405
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<210> 3437
<211> 2081
<212> DNA
<213> Homo sapiens

<400> 3437
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120
cacctgctgc accatcgaca aggccaccca gacgcccctg tcctggcaag agctagaagg
180
tgagcgtgcc agttcctgtg cacacaagcg ctcagcatcc tggggcagca cagaccaccg
240
aaaagagatt tccaagttga agcaacaact gcagaggacg aagctgagcc gcagtgggaa
300
agagaaggag cgaggttcac cactcctagg ggaccacgca gtgcggggag cactgagggc
360
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420
gagcctggaa gggctcaacc aagagctgga ggaggtattt gtgaaggagc agggagaaga
480
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540
tggcagctgt gatcatcccc tcctcctcct gagcctggca accttgccag ctctccttcc
600
atgtccttgg catctcccca gcctgtggcc tggccagtca tgaggaacat cggggtgccg
660
ccgaggagct ggcatccacc cccaacgaca aagcctcctc tccaggacac ccagcctttc
720
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780
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840

ccancgtctc caggtcctga cctggccttc ctgacttcct gtcctgacaa gaacaaagtc
900
catttcaacc cgactggctc accttctgcc ccgtcaacct gatgaagccc ctcttccccg
960
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1020
cccaggccac cacctcggaa ggatccggaa gcctccaagg cctccccact gccattcgag
1080
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1380
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1440
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aacgaaggag agaagacgcc acagatttcc ttccctctcc tccaggagac cataagatag
1560
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1620
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1680
gttttcccaa gtggcatttt catctcgctt tcaccctgac taaagattgt cttaagtagc
1740
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1800
gcaaatggcg actctatact ctccgcccgc cccagggctg gatggattag aaaaatgcct
1860
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1920
tttgaagttt gtatattttc cgtactgcag agcttacaca aaattgaaga atgttaatgt
1980
tcgagttttc ttatcttgtg tttagaggtt gtttttgca gatcttggtg ttaatagacc
2040
aaataaataa ataaatattc ccagcaaaaa aaaaaaaaaa a
2081

<210> 3438
<211> 105
<212> PRT
<213> Homo sapiens

<400> 3438
Ala Cys Gln Phe Leu Cys Thr Gln Ala Leu Ser Ile Leu Gly Gln His
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Arg Pro Pro Lys Arg Asp Phe Gln Val Glu Ala Thr Thr Ala Glu Asp
20 25 30
Glu Ala Glu Pro Gln Trp Glu Arg Glu Gly Ala Arg Phe Thr Thr Pro

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        35                  40                  45
Arg Gly Pro Arg Ser Ala Gly Ser Thr Glu Gly Val Pro Ser Gln Leu
    50                  55                  60
Pro Leu Arg Val Pro Cys Leu Ala Thr Gln Pro Leu Pro Ala Gln Glu
65                  70                  75                  80
Pro Gly Arg Ala Gln Pro Arg Ala Gly Gly Gly Ile Cys Glu Gly Ala
                85                  90                  95
Gly Arg Arg Gly Ala Ala Glu Asp Pro
            100                 105
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<210> 3439
<211> 1519
<212> DNA
<213> Homo sapiens

<400> 3439
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ctcaccgcgc ctcgcctcgc tccgccggcg ccgcggcatg ctgggatatg tagtccccac
120
ggggcgccgg gcgccccggg ggagcggggc cggcacccta ggggacgcaa agccccggga
180
aggggccggc ggagggaggc cggagcgggc agcgcggcgg cgccatgtcc gtgaacatgg
240
acgagctcaa gcaccaggtc atgatcaacc agttcgtgct gacggcgggc tgcgcggccg
300
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360
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480
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600
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720
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780
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900
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960
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1020
accacgcagc cttccttcga agacgcacct gcccagccca gcccaggggt gccgtggagg
1080
accaccctgg cggagacatt gctgatccct ggcttggagc tccttggggg ccggcaggcc
1140

tcgaccccca ccctagggaa tgcagagcct ctccgcatgt gtgcgcgtgg ccgtgtctgt
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1260
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1320
cccacccccc cgtcagccag cgttgctgtt ccttgcagag aaaaggattg tgggaaactc
1380
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1500
tccaaaccaa aaaaaaaaa
1519

<210> 3440
<211> 287
<212> PRT
<213> Homo sapiens

<400> 3440
Cys Ala Pro Pro Pro Ile Pro Leu Leu His Pro Pro Thr Ser Leu Thr
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Leu Ser Pro Cys Ser Pro Val Ser Arg Pro Pro Arg Ala Ser Thr Ala
20 25 30
Val Ala Ala Ala Ala Arg Trp Pro Arg Gln Pro Arg His Pro Arg His
35 40 45
Thr Ser Pro Met Pro Pro Pro Ala Ala Leu Arg Pro Pro Ala Gly Pro
50 55 60
Arg Arg Pro Arg Xaa Pro Gly Gly Pro Gln His His Gln Pro Gln Pro
65 70 75 80
Pro Leu Trp Thr Pro Thr Pro Pro Ser Pro Ala Ser Asp Trp Pro Pro
85 90 95
Leu Pro Pro Asn Arg Pro Pro Gln Asn Pro Gly Pro Thr Leu Pro Trp
100 105 110
Arg Gln Arg Asp Lys Gly Gly Pro Ser Pro Leu Pro Glu Ala Arg Thr
115 120 125
Pro Trp Gly Gly Gly Glu Asp Val Ser Ala Gly Pro Leu Xaa Thr Pro
130 135 140
Phe Leu Ser Ala Pro Leu Val Pro Arg Ser Pro Gly Gly Glu Ser Ala
145 150 155 160
Asp Ser Ser Gln Ala Gly Thr Arg Leu Val Pro Glu His Ala Ala Ala
165 170 175
His Thr Gln Gly His Gly Pro Ser Gly Pro Gly Thr Trp Ser Gly Ser
180 185 190
Glu Arg Pro Gly Cys Leu Ala Asp Arg Thr Ser Glu Thr Thr Gln Pro
195 200 205
Ser Phe Glu Asp Ala Pro Ala Gln Pro Ser Pro Gly Val Pro Trp Arg
210 215 220
Thr Thr Leu Ala Glu Thr Leu Leu Ile Pro Gly Leu Glu Leu Leu Gly
225 230 235 240
Gly Arg Gln Ala Ser Thr Pro Thr Leu Gly Asn Ala Glu Pro Leu Arg
245 250 255
Met Cys Ala Arg Gly Arg Val Cys Val Phe Leu Arg Val Ser Leu Phe

260 265 270
Arg Ser Asn Leu Val Pro Gly Ala Ala Gly Leu Cys Met Leu Val
275 280 285

<210> 3441
<211> 2074
<212> DNA
<213> Homo sapiens

<400> 3441
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120
ctcttcgggg acgaggtttc cccactcctg aagcagtaca tcctggagaa ggagagcgct
180
ctcttcagta cagagctctc tgtcctgcac aacttttca gtccttcccc caagaccagg
240
cgccagggcg aggtggtgca gcggctgacg cggatggtgg ggaagaacgt gaagctgtac
300
gacatggtgc tgcagtttct gcgcacgctc ttcctgcgca cgcggaatgt gcactactgc
360
acgctgcggg ctgagctgct catgtccctg cacgacctgg acgtgggtga aatctgcacc
420
gtggacccgt gccacaagtt cacctggtgc ctggacgcct gcatccgaga gcggttcgtg
480
gacagcaaga gggcgcggga gctgcagggg tttctcgatg acgtcaagaa gggccaggag
540
caggtgctgg gggacctgtc catgatcctg tgtgaccct tcgccatcaa cacgctggca
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720
gacagccagg tcttcaagga gcccaagatg gaggtagagc tcatcaccag gttcctcccg
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1020
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1080
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1260
gcagtgaagg agctttactc ccagctcggc gagaagctgg aacagctgga tcaccggaag
1320

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1380
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1440
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1740
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1920
tgcccagcag tgctgccttc agcggccgtg acggggccag ctggacacac ggtgagattt
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2040
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2074

<210> 3442
<211> 374
<212> PRT
<213> Homo sapiens

<400> 3442
Met Val Gly Lys Asn Val Lys Leu Tyr Asp Met Val Leu Gln Phe Leu
1 5 10 15
Arg Thr Leu Phe Leu Arg Thr Arg Asn Val His Tyr Cys Thr Leu Arg
20 25 30
Ala Glu Leu Leu Met Ser Leu His Asp Leu Asp Val Gly Glu Ile Cys
35 40 45
Thr Val Asp Pro Cys His Lys Phe Thr Trp Cys Leu Asp Ala Cys Ile
50 55 60
Arg Glu Arg Phe Val Asp Ser Lys Arg Ala Arg Glu Leu Gln Gly Phe
65 70 75 80
Leu Asp Asp Val Lys Lys Gly Gln Glu Gln Val Leu Gly Asp Leu Ser
85 90 95
Met Ile Leu Cys Asp Pro Phe Ala Ile Asn Thr Leu Ala Leu Ser Thr
100 105 110
Val Arg His Leu Gln Glu Leu Val Gly Gln Glu Thr Leu Pro Arg Asp
115 120 125
Ser Pro Asp Leu Leu Leu Leu Leu Arg Leu Leu Ala Leu Gly Gln Gly
130 135 140
Ala Trp Asp Met Ile Asp Ser Gln Val Phe Lys Glu Pro Lys Met Glu
145 150 155 160
Val Glu Leu Ile Thr Arg Phe Leu Pro Met Leu Met Ser Phe Leu Val

```
                165                 170                 175
Asp Asp Tyr Thr Phe Asn Val Asp Gln Lys Leu Pro Ala Glu Glu Lys
            180                 185                 190
Ala Pro Val Ser Tyr Pro Asn Thr Leu Pro Glu Ser Phe Thr Lys Phe
        195                 200                 205
Leu Gln Glu Gln Arg Met Ala Cys Glu Val Gly Leu Tyr Tyr Val Leu
    210                 215                 220
His Ile Thr Lys Gln Arg Asn Lys Asn Ala Leu Leu Arg Leu Leu Pro
225                 230                 235                 240
Gly Leu Val Glu Thr Phe Gly Asp Leu Ala Phe Gly Asp Ile Phe Leu
                245                 250                 255
His Leu Leu Thr Gly Asn Leu Ala Leu Leu Ala Asp Glu Phe Ala Leu
            260                 265                 270
Glu Asp Phe Cys Ser Ser Leu Phe Asp Gly Phe Phe Leu Thr Ala Ser
        275                 280                 285
Pro Arg Lys Glu Asn Val His Arg His Ala Leu Arg Leu Leu Ile His
    290                 295                 300
Leu His Pro Arg Val Ala Pro Ser Lys Leu Glu Ala Leu Gln Lys Ala
305                 310                 315                 320
Leu Glu Pro Thr Gly Gln Ser Gly Glu Ala Val Lys Glu Leu Tyr Ser
                325                 330                 335
Gln Leu Gly Glu Lys Leu Glu Gln Leu Asp His Arg Lys Pro Ser Pro
            340                 345                 350
Ala Gln Ala Ala Glu Thr Pro Ala Leu Glu Leu Pro Leu Pro Ser Val
        355                 360                 365
Pro Ala Pro Ala Pro Leu
    370
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<210> 3443
<211> 2070
<212> DNA
<213> Homo sapiens

<400> 3443
ctggccgtaa atgccgagga ggacgcctgg ttacgggcac aggtcatctc aacagaagag
60
aacaaaataa aggtatgcta tgttgactat ggttttagtg aaaatgttga aaaaagcaaa
120
gcatacaaat taaacccgaa gttttgttca ctctcatttc aagctacaaa atgtaagctt
180
gcaggcttgg aagtcctaag cgatgaccct gatctagtga aggtggttga atctttaact
240
tgtggaaaga tctttgcagt ggaaatactt gacaaagctg acattccact tgttgttctg
300
tacgatacct caggagaaga tgatatcaat atcaatgcca cctgcttgaa ggctatatgt
360
gacaagtcac tagaggttca cctgcaggtt gacgccatgt acacaaatgt caaaataact
420
aatatttgct ctgatgggac actctactgc caggtgcctt gtaagggtct gaacaagctc
480
agtgaccttc tacgtaagat agaggactac ttccattgca agcacatgac ctctgagtgc
540
tttgtttcat taccctttctg tgggaaaatc tgcctcttcc attgcaaagg aaaatggtta
600

cgagtagaga tcacaaatgt tcacagcagc cgggctcttg atgttcagtt cctggactct
660
ggcactgtga catctgtaaa agtgtcagag ctcagggaaa ttccacctcg gtttctacaa
720
gaaatgattg caataccacc tcaggccatt aagtgctgtt tagcagatct tccacaatct
780
attggcatgt ggacaccaga tgcagtgctg tggttaagag attctgtttt gaattgctcg
840
gactgtagca ttaaggttac aaaagtggat gaaaccagag ggatcgcaca tgtttattta
900
tttaccccta agaacttccc tgaccctcat cgcagtatta atcgccagat tacaaatgca
960
gacttgtgga agcatcagaa ggatgtgttt ttgagtgcca tatccagtgg agctgactct
1020
cccaacagca aaaatggcaa catgcccatg tcgggcaaca ctggagagaa tttcagaaag
1080
aacctcacag atgtcatcaa aaagtccatg gtggaccata cgagcgcttt ctccacagag
1140
gaactgccac ctcctgtcca cttatcaaag ccaggggaac acatggatgt gtatgtgcct
1200
gtggcctgtc acccaggcta cttcgtcatc cagccttggc aggagataca taagttggaa
1260
gttctgatgg aagagatgat tctatattac agcgtgtctg aagagcgcca catagcagtg
1320
gagaaagacc aagtgtatgc tgcaaaagtg gaaaataagt ggcacagggt gcttttaaaa
1380
ggaatcctga ccaatggact ggtatctgtg tatgagctgg attatggcaa acacgaatta
1440
gtcaacataa gaaaagtaca gcccctagtg gacatgttcc gaaagctgcc cttccaagca
1500
gtcacagctc aacttgcagg agtgaagtgc aaccagtggt ctgaggaggc ttctatggtg
1560
tttcgaaatc atgtggagaa gaaacctctg gtggcactgg tgcagacagt cattgaaaat
1620
gctaaccctt gggaccggaa agtagtggtc tacttagtgg acacatcgtt gccagacacc
1680
gatacctgga ttcatgattt tatgtcagag tatctgatag agctttcaaa agttaattaa
1740
tgactgcctc tgaaaccttg acaactaatt cagatttttt agcaataaca aaatgtagta
1800
ggcttaaaaa aaatcttaac tctgctacat ggctctgact gctgtggggg attgaaaaga
1860
atatgcttat gtttgatgaa agatatttaa caagttttgt tttaacagag ttgacttttc
1920
aaagaaaatt gtacttgaat tattactata atattagaat aaaaatgttt atcaatataa
1980
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
2040
aaaaaaaaaa aaaaaaaaaa aaaaaagggg
2070

<210> 3444
<211> 579
<212> PRT

<213> Homo sapiens

<400> 3444

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Leu Ala Val Asn Ala Glu Glu Asp Ala Trp Leu Arg Ala Gln Val Ile
 1               5                  10                  15
Ser Thr Glu Glu Asn Lys Ile Lys Val Cys Tyr Val Asp Tyr Gly Phe
            20                  25                  30
Ser Glu Asn Val Glu Lys Ser Lys Ala Tyr Lys Leu Asn Pro Lys Phe
        35                  40                  45
Cys Ser Leu Ser Phe Gln Ala Thr Lys Cys Lys Leu Ala Gly Leu Glu
    50                  55                  60
Val Leu Ser Asp Asp Pro Asp Leu Val Lys Val Val Glu Ser Leu Thr
65                  70                  75                  80
Cys Gly Lys Ile Phe Ala Val Glu Ile Leu Asp Lys Ala Asp Ile Pro
                85                  90                  95
Leu Val Val Leu Tyr Asp Thr Ser Gly Glu Asp Asp Ile Asn Ile Asn
            100                 105                 110
Ala Thr Cys Leu Lys Ala Ile Cys Asp Lys Ser Leu Glu Val His Leu
        115                 120                 125
Gln Val Asp Ala Met Tyr Thr Asn Val Lys Ile Thr Asn Ile Cys Ser
    130                 135                 140
Asp Gly Thr Leu Tyr Cys Gln Val Pro Cys Lys Gly Leu Asn Lys Leu
145                 150                 155                 160
Ser Asp Leu Leu Arg Lys Ile Glu Asp Tyr Phe His Cys Lys His Met
                165                 170                 175
Thr Ser Glu Cys Phe Val Ser Leu Pro Phe Cys Gly Lys Ile Cys Leu
            180                 185                 190
Phe His Cys Lys Gly Lys Trp Leu Arg Val Glu Ile Thr Asn Val His
        195                 200                 205
Ser Ser Arg Ala Leu Asp Val Gln Phe Leu Asp Ser Gly Thr Val Thr
    210                 215                 220
Ser Val Lys Val Ser Glu Leu Arg Glu Ile Pro Pro Arg Phe Leu Gln
225                 230                 235                 240
Glu Met Ile Ala Ile Pro Pro Gln Ala Ile Lys Cys Cys Leu Ala Asp
                245                 250                 255
Leu Pro Gln Ser Ile Gly Met Trp Thr Pro Asp Ala Val Leu Trp Leu
            260                 265                 270
Arg Asp Ser Val Leu Asn Cys Ser Asp Cys Ser Ile Lys Val Thr Lys
        275                 280                 285
Val Asp Glu Thr Arg Gly Ile Ala His Val Tyr Leu Phe Thr Pro Lys
    290                 295                 300
Asn Phe Pro Asp Pro His Arg Ser Ile Asn Arg Gln Ile Thr Asn Ala
305                 310                 315                 320
Asp Leu Trp Lys His Gln Lys Asp Val Phe Leu Ser Ala Ile Ser Ser
                325                 330                 335
Gly Ala Asp Ser Pro Asn Ser Lys Asn Gly Asn Met Pro Met Ser Gly
            340                 345                 350
Asn Thr Gly Glu Asn Phe Arg Lys Asn Leu Thr Asp Val Ile Lys Lys
        355                 360                 365
Ser Met Val Asp His Thr Ser Ala Phe Ser Thr Glu Glu Leu Pro Pro
    370                 375                 380
Pro Val His Leu Ser Lys Pro Gly Glu His Met Asp Val Tyr Val Pro
385                 390                 395                 400
Val Ala Cys His Pro Gly Tyr Phe Val Ile Gln Pro Trp Gln Glu Ile
```

```
                405                 410                 415
His Lys Leu Glu Val Leu Met Glu Glu Met Ile Leu Tyr Tyr Ser Val
            420                 425                 430
Ser Glu Glu Arg His Ile Ala Val Glu Lys Asp Gln Val Tyr Ala Ala
        435                 440                 445
Lys Val Glu Asn Lys Trp His Arg Val Leu Leu Lys Gly Ile Leu Thr
    450                 455                 460
Asn Gly Leu Val Ser Val Tyr Glu Leu Asp Tyr Gly Lys His Glu Leu
465                 470                 475                 480
Val Asn Ile Arg Lys Val Gln Pro Leu Val Asp Met Phe Arg Lys Leu
                485                 490                 495
Pro Phe Gln Ala Val Thr Ala Gln Leu Ala Gly Val Lys Cys Asn Gln
            500                 505                 510
Trp Ser Glu Glu Ala Ser Met Val Phe Arg Asn His Val Glu Lys Lys
        515                 520                 525
Pro Leu Val Ala Leu Val Gln Thr Val Ile Glu Asn Ala Asn Pro Trp
    530                 535                 540
Asp Arg Lys Val Val Val Tyr Leu Val Asp Thr Ser Leu Pro Asp Thr
545                 550                 555                 560
Asp Thr Trp Ile His Asp Phe Met Ser Glu Tyr Leu Ile Glu Leu Ser
                565                 570                 575
Lys Val Asn
```

<210> 3445
<211> 2086
<212> DNA
<213> Homo sapiens

<400> 3445
nnacgcgtgg cggcagaggg tatccaaggc cggacctggc gcgcaggcgc tgacccgacc
60
tggcagtgag ctggccgcgg ccttggctga gaggccttaa ccccgccggg cggcgcgcgc
120
cctgcatgcg agttgggccg cgggcggggt tggagcctac tcggggcgac tgcgatggac
180
gccttagaag gagagagctt tgcgctgtct ttctcctccg cctctgatgc agaatttgat
240
gctgtggttg gatatttaga ggacattatc atggatgacg agttccagtt attacagaga
300
aatttcatgg acaagtacta cctggagttt gaagacacag aagagaataa actcatctac
360
acacctattt ttaatgaata catttctttg gtagaaaaat acattgaaga acagctgctg
420
cagcggattc ctgagttcaa catggcagcc ttcaccacaa cattacacca tctgttccgt
480
ttgaggcacc ataaggatga agtggctggt gacatattcg acatgctgct caccttcaca
540
gattttctgg cttttaaaga aatgtttttg gactacagag cagaaaaaga aggccgagga
600
ctggacttaa gcagtggctt agtggtgact tcattgtgca aatcatcttc tctgccagct
660
tcccagaaca atctgcggca ctaggtccta cctccagcca atgaatggga tcattctgga
720

tgtcaccagc ccaataggct cagctcatga tgacagaaca catcttggaa agactgactc
780
tgttatgtaa ctcttcattt atgttaagta ttaataggtc aaaaccaaaa tgacctaacc
840
ctcctggacc tatttatcct gaaacacctt cttgtattca ttaaccatag tactcctccc
900
cacctcaagt agacacctct ctcaggagct tctgagtcag acgcctctgg agcgagccct
960
atgtcaggca ctccacctgg ggggcccttc cccagcatac ctgctggtgt gtaagtgtgg
1020
actaacccgc cgccaccacc ctctgttcca gcaggctctg catgaatctt tgtgcacttg
1080
cacctctttt tcacatgggc cacagtttca gtacttcagc ctcagtgggg ttcctgatgt
1140
ttatctaggg tgttactcaa gcccagtttg agattttgga gtctcctgtg atcacatctt
1200
gtctcggctg taggaatcaa cagaaggaga cgtcctctac ataaaagctc catgtgaaaa
1260
gctactccta gtcttaacat ttgcagtcct tgtgtcactg tcttctggtc ctgatgtagt
1320
cccactgttt ctagaagtct cttttaagca ttatttttga aaaaaaaaat atttttatag
1380
atgaatactc aggctaacct agtggatgtg atcttggaac ttccatgatt atccacttaa
1440
agatcaaagt attatatgct gtgtgctttt taggtgtttg ttagtactgt gaaggcaaaa
1500
atgctttcta cattgacatt cattcctatt ttactgggca cctatgaatg tatgctgtgt
1560
gctagaaata gactaaaaca tattcctata gcatgttagt gtgtttgcat gtttgctgaa
1620
aatccttttgt gtataaacca gtttgtaagg ttctctgggt taggtaggga ctctgcagtt
1680
tcttcctgtc aaaatctctc ctaccaagat ggtgttccac tgtccagccc agcatgagta
1740
gcaggtagag cacagcttta ctggctgttt gtatgctttg gtttagtgca atgtgtggta
1800
gattacttat cagaaaacat atatgtcatc tctagaacga agaaaaagca tagtagttca
1860
attcccagtg tgtccctttg attttttttt tttaatagta aaaataagaa tctgtactga
1920
cttttcactt ggccattctg gttttaaagg acaagctaca agctctgtgt ttctgtactg
1980
atgtgtcact tattaaatac ttttgtacca tgagtaaaac ttcaggtgtt tcgcaagaac
2040
caccattctc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa
2086

<210> 3446
<211> 169
<212> PRT
<213> Homo sapiens

<400> 3446
Met Asp Ala Leu Glu Gly Glu Ser Phe Ala Leu Ser Phe Ser Ser Ala

```
 1               5                  10                  15
Ser Asp Ala Glu Phe Asp Ala Val Val Gly Tyr Leu Glu Asp Ile Ile
            20                  25                  30
Met Asp Asp Glu Phe Gln Leu Leu Gln Arg Asn Phe Met Asp Lys Tyr
        35                  40                  45
Tyr Leu Glu Phe Glu Asp Thr Glu Glu Asn Lys Leu Ile Tyr Thr Pro
    50                  55                  60
Ile Phe Asn Glu Tyr Ile Ser Leu Val Glu Lys Tyr Ile Glu Glu Gln
65                  70                  75                  80
Leu Leu Gln Arg Ile Pro Glu Phe Asn Met Ala Ala Phe Thr Thr Thr
                85                  90                  95
Leu His His Leu Phe Arg Leu Arg His His Lys Asp Glu Val Ala Gly
            100                 105                 110
Asp Ile Phe Asp Met Leu Leu Thr Phe Thr Asp Phe Leu Ala Phe Lys
        115                 120                 125
Glu Met Phe Leu Asp Tyr Arg Ala Glu Lys Glu Gly Arg Gly Leu Asp
    130                 135                 140
Leu Ser Ser Gly Leu Val Val Thr Ser Leu Cys Lys Ser Ser Ser Leu
145                 150                 155                 160
Pro Ala Ser Gln Asn Asn Leu Arg His
                165
```

<210> 3447
<211> 936
<212> DNA
<213> Homo sapiens

<400> 3447
acgcgtgaag ggtttgcggg gaagatggag tatcccgcgc cggccacggt gcaggccgcg
60
gacggcggag cggccgggcc ttacagcagc tcggagttgc tggagggcca ggagccggac
120
ggggtgcgct ttgaccgcga gagggcgcgc cgcctgtggg aagccgtgtc cggtgcccag
180
ccggtgggta gagaggaagt ggagcacatg atccagaaga accaatgtct cttcaccaac
240
acccagtgta aggtttgctg cgccttgctt atttctgagt cccagaagct ggcacattac
300
cagagcaaaa aacatgccaa caaagtgaag agatacctag caatccatgg aatggagaca
360
ttaaaggggg aaacgaagaa gctagactca gatcagaaga gcagcagaag caaagacaag
420
aaccagtgct gccccatctg taacatgacc ttttcctccc ctgtcgtggc ccagtcgcac
480
tacctgggga agacccacgc aaagaactta aagctgaagc agcagtccac taaggtggaa
540
gccttgcacc agaatagaga gatgatagac ccagacaagt tctgcagcct ctgccatgca
600
actttcaacg accctgtcat ggctcaacaa cattatgtgg gcaagaaaca cagaaaacag
660
gagaccaagc tcaaactaat ggcacgctat gggcggctgg cggaccctgc tgtcactgac
720
tttccagctg gaaagggcta cccctgcaaa acatgtaaga tagtgctgaa ctccatagaa
780

cagtaccaag ctcatgtcag cggcttcaaa cacaagaacc agtcaccaaa aacagtggca
840
tcatccctgg gccagattcc aatgcaaagg caacccattc agaaagactc aaccaccttg
900
gaagactaga ggtgattctg cccagcatcc catatt
936

<210> 3448
<211> 302
<212> PRT
<213> Homo sapiens

<400> 3448
Thr Arg Glu Gly Phe Ala Gly Lys Met Glu Tyr Pro Ala Pro Ala Thr
1 5 10 15
Val Gln Ala Ala Asp Gly Gly Ala Ala Gly Pro Tyr Ser Ser Ser Glu
20 25 30
Leu Leu Glu Gly Gln Glu Pro Asp Gly Val Arg Phe Asp Arg Glu Arg
35 40 45
Ala Arg Arg Leu Trp Glu Ala Val Ser Gly Ala Gln Pro Val Gly Arg
50 55 60
Glu Glu Val Glu His Met Ile Gln Lys Asn Gln Cys Leu Phe Thr Asn
65 70 75 80
Thr Gln Cys Lys Val Cys Cys Ala Leu Leu Ile Ser Glu Ser Gln Lys
85 90 95
Leu Ala His Tyr Gln Ser Lys Lys His Ala Asn Lys Val Lys Arg Tyr
100 105 110
Leu Ala Ile His Gly Met Glu Thr Leu Lys Gly Glu Thr Lys Lys Leu
115 120 125
Asp Ser Asp Gln Lys Ser Ser Arg Ser Lys Asp Lys Asn Gln Cys Cys
130 135 140
Pro Ile Cys Asn Met Thr Phe Ser Ser Pro Val Val Ala Gln Ser His
145 150 155 160
Tyr Leu Gly Lys Thr His Ala Lys Asn Leu Lys Leu Lys Gln Gln Ser
165 170 175
Thr Lys Val Glu Ala Leu His Gln Asn Arg Glu Met Ile Asp Pro Asp
180 185 190
Lys Phe Cys Ser Leu Cys His Ala Thr Phe Asn Asp Pro Val Met Ala
195 200 205
Gln Gln His Tyr Val Gly Lys Lys His Arg Lys Gln Glu Thr Lys Leu
210 215 220
Lys Leu Met Ala Arg Tyr Gly Arg Leu Ala Asp Pro Ala Val Thr Asp
225 230 235 240
Phe Pro Ala Gly Lys Gly Tyr Pro Cys Lys Thr Cys Lys Ile Val Leu
245 250 255
Asn Ser Ile Glu Gln Tyr Gln Ala His Val Ser Gly Phe Lys His Lys
260 265 270
Asn Gln Ser Pro Lys Thr Val Ala Ser Ser Leu Gly Gln Ile Pro Met
275 280 285
Gln Arg Gln Pro Ile Gln Lys Asp Ser Thr Thr Leu Glu Asp
290 295 300

<210> 3449
<211> 877

<212> DNA
<213> Homo sapiens

<400> 3449
ntgatcttca gcaaccatca ccaccggcta cagctgaagg cagctccggc ctcctccaat
60
ccccccggcg ccccggctct gccgctgcac aattcctccg tgactgccaa ctcccagtcc
120
ccggcccttc tggccggcac caaccccgtt gctgtcgtcg cggatggagg cagttgcccc
180
gcacactacc cggtgcacga gtgcgtcttc aaggggggatg tgaggagact ctcctctctc
240
atccgcacgc acaatatcgg gcagaaagat aatcacggaa atactccttt acaccttgct
300
gtgatgttag gaaataaaga atgtgcccat ttacttttgg ctcacaatgc tccagtcaag
360
gtgaaaaatg ctcagggatg gagccctctg gcggaagcca tcagctatgg agataggcag
420
atgattacag ctcttttgag gaagcttaag cagcaatcca gggaaagtgt tgaagaaaaa
480
cgacctcgat tattaaaagc cctgaaagag ctaggtgact tttatctaga acttcactgg
540
gattttcaaa gctgggtgcc tttactttcc cgaattctgc cttccgatgc atgtaaaata
600
tacaaacaag gtatcaatat caggcttgac acaactctca tagactttac tgacatgaag
660
tgccaacgag gggatctaag cttcattttc aatggggatg cggcgccctc tgaatctttt
720
gtagtattag acaatgaaca aaaagtttat cagcgaatac atcatgaggc tcacatccca
780
ggaatcagag atggaaacag aagaagaggt ggatatttta atgagcagtg atatttactc
840
tgcaacttta tcaacaaaat caatttcttt cacgcgt
877

<210> 3450
<211> 276
<212> PRT
<213> Homo sapiens

<400> 3450
Xaa Ile Phe Ser Asn His His His Arg Leu Gln Leu Lys Ala Ala Pro
 1   5   10   15
Ala Ser Ser Asn Pro Pro Gly Ala Pro Ala Leu Pro Leu His Asn Ser
            20   25   30
Ser Val Thr Ala Asn Ser Gln Ser Pro Ala Leu Leu Ala Gly Thr Asn
        35   40   45
Pro Val Ala Val Val Ala Asp Gly Gly Ser Cys Pro Ala His Tyr Pro
    50   55   60
Val His Glu Cys Val Phe Lys Gly Asp Val Arg Arg Leu Ser Ser Leu
65   70   75   80
Ile Arg Thr His Asn Ile Gly Gln Lys Asp Asn His Gly Asn Thr Pro
                85   90   95
Leu His Leu Ala Val Met Leu Gly Asn Lys Glu Cys Ala His Leu Leu

```
            100                 105                 110
Leu Ala His Asn Ala Pro Val Lys Val Lys Asn Ala Gln Gly Trp Ser
        115                 120                 125
Pro Leu Ala Glu Ala Ile Ser Tyr Gly Asp Arg Gln Met Ile Thr Ala
    130                 135                 140
Leu Leu Arg Lys Leu Lys Gln Gln Ser Arg Glu Ser Val Glu Glu Lys
145                 150                 155                 160
Arg Pro Arg Leu Leu Lys Ala Leu Lys Glu Leu Gly Asp Phe Tyr Leu
                165                 170                 175
Glu Leu His Trp Asp Phe Gln Ser Trp Val Pro Leu Leu Ser Arg Ile
            180                 185                 190
Leu Pro Ser Asp Ala Cys Lys Ile Tyr Lys Gln Gly Ile Asn Ile Arg
        195                 200                 205
Leu Asp Thr Thr Leu Ile Asp Phe Thr Asp Met Lys Cys Gln Arg Gly
    210                 215                 220
Asp Leu Ser Phe Ile Phe Asn Gly Asp Ala Ala Pro Ser Glu Ser Phe
225                 230                 235                 240
Val Val Leu Asp Asn Glu Gln Lys Val Tyr Gln Arg Ile His His Glu
                245                 250                 255
Ala His Ile Pro Gly Ile Arg Asp Gly Asn Arg Arg Arg Gly Gly Tyr
            260                 265                 270
Phe Asn Glu Gln
        275
```

<210> 3451
<211> 595
<212> DNA
<213> Homo sapiens

<400> 3451
gcatttttac agtttgtata tcccattttc aaggcttcag tggggctgct tagacaaaaa
60
cgatcttcag ggtttacaga atgggtcctc ctaaagctct ctgagccccg gccgtaggta
120
gaaatattca gtaagtagtg ccctgccatt gcaggtttgg atgtccttct gccagcaaaa
180
cccagcatga acctctggct tgtggagatg tcttccagct ggaaacctga gtgagcgaag
240
ttgaactgtg agggcggcac aactgagaga agattctgcc tccgaaccct ctgaatgaga
300
gtctgaagga tctgatcttg ggttgcttta cttagtcctt cgtggtattg gtgtgtgtca
360
atgctggagt ccctcagctc cttagctgaa aagagctgaa ggggccttgg aacctggggg
420
agctgcttac tttgcaaggt tttgcccagc tgctgctgcg tagctggatg ggactgtctc
480
tcattaactt cctctctggt gctattttct gttgtgttgg tagctatgag cgctcccatc
540
ccccttttcct cttttgcagg caggggaacc gcttccattt caactttggg gagag
595

<210> 3452
<211> 192
<212> PRT

<213> Homo sapiens

<400> 3452

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Met Glu Ala Val Pro Leu Pro Ala Lys Glu Glu Arg Gly Met Gly Ala
 1               5                  10                  15
Leu Ile Ala Thr Asn Thr Thr Glu Asn Ser Thr Arg Glu Glu Val Asn
            20                  25                  30
Glu Arg Gln Ser His Pro Ala Thr Gln Gln Gln Leu Gly Lys Thr Leu
        35                  40                  45
Gln Ser Lys Gln Leu Pro Gln Val Pro Arg Pro Leu Gln Leu Phe Ser
    50                  55                  60
Ala Lys Glu Leu Arg Asp Ser Ser Ile Asp Thr His Gln Tyr His Glu
65                  70                  75                  80
Gly Leu Ser Lys Ala Thr Gln Asp Gln Ile Leu Gln Thr Leu Ile Gln
                85                  90                  95
Arg Val Arg Arg Gln Asn Leu Leu Ser Val Val Pro Pro Ser Gln Phe
            100                 105                 110
Asn Phe Ala His Ser Gly Phe Gln Leu Glu Asp Ile Ser Thr Ser Gln
        115                 120                 125
Arg Phe Met Leu Gly Phe Ala Gly Arg Arg Thr Ser Lys Pro Ala Met
    130                 135                 140
Ala Gly His Tyr Leu Leu Asn Ile Ser Thr Tyr Gly Arg Gly Ser Glu
145                 150                 155                 160
Ser Phe Arg Arg Thr His Ser Val Asn Pro Glu Asp Arg Phe Cys Leu
                165                 170                 175
Ser Ser Pro Thr Glu Ala Leu Lys Met Gly Tyr Thr Asn Cys Lys Asn
            180                 185                 190
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<210> 3453
<211> 477
<212> DNA
<213> Homo sapiens

<400> 3453

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nnacgcgtga agggtcccgg ccgcggggct ggcgggctga ggggagaaaa gatggcggcg
60
gcggcggcag ctggtgcggc ctccgggctg ccgggtccag tggcacaagg attaaaggaa
120
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<210> 3454
<211> 159
<212> PRT

<213> Homo sapiens

<400> 3454
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Pro Val Ala Gln Gly Leu Lys Glu Ala Leu Val Asp Thr Leu Thr Gly
35 40 45
Ile Leu Ser Pro Val Gln Glu Val Arg Ala Ala Ala Glu Glu Gln Ile
50 55 60
Lys Val Leu Glu Val Thr Glu Glu Phe Gly Val His Leu Ala Glu Leu
65 70 75 80
Thr Val Asp Pro Gln Gly Ala Leu Ala Ile Arg Gln Leu Ala Ser Val
85 90 95
Ile Leu Lys Gln Tyr Val Glu Thr His Trp Cys Ala Gln Ser Glu Lys
100 105 110
Phe Arg Pro Pro Glu Thr Thr Glu Arg Ala Lys Ile Val Ile Arg Glu
115 120 125
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130 135 140
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145 150 155

<210> 3455
<211> 4886
<212> DNA
<213> Homo sapiens

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2280
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2340

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4886

<210> 3456
<211> 117
<212> PRT
<213> Homo sapiens

<400> 3456
Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
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Lys Lys Gln Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn
20 25 30
Pro Pro Cys Pro Arg Leu Asn Gly Val Leu Met Glu Val Glu Glu Pro
35 40 45
Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Met
50 55 60
Tyr Phe Glu Leu Pro Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr
65 70 75 80
Ser Phe Glu Glu Glu His Ile Ser Phe Ala Leu Tyr Val Asp Asn Arg
85 90 95
Phe Phe Thr Leu Thr Val Thr Ser Leu His Leu Val Phe Gln Met Gly
100 105 110
Val Ile Phe Pro Gln

115

<210> 3457
<211> 646
<212> DNA
<213> Homo sapiens

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120
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420
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480
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540
aaccctccag gccttctcct gccacaggct ctgtctctgt cccgtcgctg tgcctcctgc
600
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646

<210> 3458
<211> 61
<212> PRT
<213> Homo sapiens

<400> 3458
Thr Arg Asp Phe Val Ser Met Ser Arg Cys Pro Cys Ala Cys Val Cys
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Arg Cys Val Xaa Val Pro Gly Cys Val Cys Ala Cys Val Cys Val Asp
            20   25   30
Ile Cys Ala Cys Leu Phe Thr His Arg Trp Glu Cys Arg Val Cys Ile
        35   40   45
Leu Cys Xaa Cys Thr Cys Thr Gln Ala Xaa Ala Gly Lys
    50   55   60

<210> 3459
<211> 592
<212> DNA
<213> Homo sapiens

<400> 3459
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120
gaccctactt cactgcaggg ggctcagccc agtctgcctc aggcagaaca agggtctggg
180
ggtggctgtg gggggctgtg gatgggtccc agtgggcctg ctgccactcc caccacatgg
240
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300
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360
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480
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592

<210> 3460
<211> 115
<212> PRT
<213> Homo sapiens

<400> 3460
Met Gly Pro Ser Gly Pro Ala Ala Thr Pro Thr Thr Trp Asp Leu Pro
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Ser Gly Pro Ala Arg Ile Pro Val Leu Pro Cys Ser Pro Gln Leu Pro
            20   25   30
Gly Pro Ser Leu Cys Ala Ala Ser Val Cys Leu Leu Gln Asn Lys His
        35   40   45
His Ala Pro Ser Trp Ala Glu Ala Pro Ala Asp Ser Pro Arg Ala Leu
    50   55   60
Gln Ala Cys Pro Val Leu Cys Gln Ala Gly Pro Gly His Val Pro Ala
65   70   75   80
Pro Gly Ala Gly Leu Gln Arg Gly Gln Trp Ser Ala Leu Lys Thr Val
                85   90   95
Ile Pro Ala Arg Pro Ala Leu Pro Cys Ser Ala Arg Gly Gln Phe Glu
            100   105   110
Leu Lys Leu
        115

<210> 3461
<211> 474
<212> DNA
<213> Homo sapiens

<400> 3461
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120
agctttgcgt ccgtggcaga tgtcagctcc agtcgcagcc gcaccttccg gatggccctg
180

ctggaagcca gcatcggggt ggctgggatg ctggcaagcc tcctcggggg ccactggctc
240
cgggcccagg gttatgccaa ccccttctgg ctggccttgg ccttgctgat agccatgact
300
ctctatgcag ctttctgctt tggtgagacc ttaaaggagc caaagtccac ccggctcttc
360
acgttccgtc accaccgatc cattgtccag ctctatgtgg ctcccgcccc agagaagtcc
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474

<210> 3462
<211> 101
<212> PRT
<213> Homo sapiens

<400> 3462
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Leu Leu Gly Gly His Trp Leu Arg Ala Gln Gly Tyr Ala Asn Pro Phe
            20   25   30
Trp Leu Ala Leu Ala Leu Leu Ile Ala Met Thr Leu Tyr Ala Ala Phe
        35   40   45
Cys Phe Gly Glu Thr Leu Lys Glu Pro Lys Ser Thr Arg Leu Phe Thr
    50   55   60
Phe Arg His His Arg Ser Ile Val Gln Leu Tyr Val Ala Pro Ala Pro
65   70   75   80
Glu Lys Ser Arg Lys His Leu Ala Leu Tyr Ser Leu Ala Ile Phe Val
                85   90   95
Val Ile Thr Val His
            100

<210> 3463
<211> 1734
<212> DNA
<213> Homo sapiens

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120
cagcagcggc agggcaagca ccatcctaat tatctcatgg ctaatgaacg catgaacctc
180
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240
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300
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360
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420
cttccaggac ttaagacacc agtaggtaga ggaagagcct ggcttcgttt ggcattaatg
480

caaaagaaac tttcagaata tatgaaagct ttgatcaata agaaagaact tctcagtgaa
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720
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1620
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<210> 3464
<211> 434
<212> PRT
<213> Homo sapiens

<400> 3464
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20 25 30
Glu Leu Pro Glu Arg Arg Arg Arg Gln Gln Arg Gln Gly Lys His His

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        35                  40                  45
Pro Asn Tyr Leu Met Ala Asn Glu Arg Met Asn Leu Met Asn Met Ala
    50                  55                  60
Lys Leu Ser Ile Lys Gly Leu Ile Glu Ser Ala Leu Asn Leu Gly Arg
65                  70                  75                  80
Thr Leu Asp Ser Asp Tyr Ala Pro Leu Gln Gln Phe Phe Val Val Met
                85                  90                  95
Glu His Cys Leu Lys His Gly Leu Lys Ala Lys Lys Thr Phe Leu Gly
            100                 105                 110
Gln Asn Lys Ser Phe Trp Gly Pro Leu Glu Leu Val Glu Lys Leu Val
        115                 120                 125
Pro Glu Ala Ala Glu Ile Thr Ala Ser Val Lys Asp Leu Pro Gly Leu
    130                 135                 140
Lys Thr Pro Val Gly Arg Gly Arg Ala Trp Leu Arg Leu Ala Leu Met
145                 150                 155                 160
Gln Lys Lys Leu Ser Glu Tyr Met Lys Ala Leu Ile Asn Lys Lys Glu
                165                 170                 175
Leu Leu Ser Glu Phe Tyr Glu Pro Asn Ala Leu Met Met Glu Glu Glu
            180                 185                 190
Gly Ala Ile Ile Ala Gly Leu Leu Val Gly Leu Asn Val Ile Asp Ala
        195                 200                 205
Asn Phe Cys Met Lys Gly Glu Asp Leu Asp Ser Gln Val Gly Val Ile
    210                 215                 220
Asp Phe Ser Met Tyr Leu Lys Asp Gly Asn Ser Ser Lys Gly Thr Glu
225                 230                 235                 240
Gly Asp Gly Gln Ile Thr Ala Ile Leu Asp Gln Lys Asn Tyr Val Glu
                245                 250                 255
Glu Leu Asn Arg His Leu Asn Ala Thr Val Asn Asn Leu Gln Ala Lys
            260                 265                 270
Val Asp Ala Leu Glu Lys Ser Asn Thr Lys Leu Thr Glu Glu Leu Ala
        275                 280                 285
Val Ala Asn Asn Arg Ile Ile Thr Leu Gln Glu Glu Met Glu Arg Val
    290                 295                 300
Lys Glu Glu Ser Ser Tyr Ile Leu Glu Ser Asn Arg Lys Gly Pro Lys
305                 310                 315                 320
Gln Asp Arg Thr Ala Glu Gly Gln Ala Leu Ser Glu Ala Arg Lys His
                325                 330                 335
Leu Lys Glu Glu Thr Gln Leu Arg Leu Asp Val Glu Lys Glu Leu Glu
            340                 345                 350
Met Gln Ile Ser Met Arg Gln Glu Met Glu Leu Ala Met Lys Met Leu
        355                 360                 365
Glu Lys Asp Val Cys Glu Lys Gln Asp Ala Leu Val Ser Leu Arg Gln
    370                 375                 380
Gln Leu Asp Asp Leu Arg Ala Leu Lys His Glu Leu Ala Phe Lys Leu
385                 390                 395                 400
Gln Ser Ser Asp Leu Gly Val Lys Gln Lys Ser Glu Leu Asn Ser Arg
                405                 410                 415
Leu Glu Glu Lys Thr Asn Gln Met Ala Ala Thr Ile Lys Gln Leu Glu
            420                 425                 430
Gln Arg
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<210> 3465
<211> 2904

<212> DNA
<213> Homo sapiens

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120
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180
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240
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300
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360
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<211> 315
<212> PRT
<213> Homo sapiens

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Gly Arg His Arg Lys Leu Pro Glu Asn Trp Thr Asp Thr Arg Glu Thr
35 40 45
Leu Leu Glu Gly Met Leu Phe Ser Leu Lys Tyr Leu Gly Met Thr Leu
50 55 60
Val Glu Gln Pro Lys Gly Glu Glu Leu Ser Ala Ala Ala Ile Lys Arg
65 70 75 80
Ile Val Ala Thr Ala Lys Ala Ser Gly Lys Lys Leu Gln Lys Val Thr
85 90 95
Leu Lys Val Ser Pro Arg Gly Ile Ile Leu Thr Asp Asn Leu Thr Asn
100 105 110
Gln Leu Ile Glu Asn Val Ser Ile Tyr Arg Ile Ser Tyr Cys Thr Ala
115 120 125
Asp Lys Met His Asp Lys Val Phe Ala Tyr Ile Ala Gln Ser Gln His
130 135 140
Asn Gln Ser Leu Glu Cys His Ala Phe Leu Cys Thr Lys Arg Lys Met
145 150 155 160
Ala Gln Ala Val Thr Leu Thr Val Ala Gln Ala Phe Lys Val Ala Phe
165 170 175
Glu Phe Trp Gln Val Ser Lys Glu Glu Lys Glu Lys Arg Asp Lys Ala
180 185 190
Ser Gln Glu Gly Gly Asp Val Leu Gly Ala Arg Gln Asp Cys Thr Pro
195 200 205
Pro Leu Lys Ser Leu Val Ala Thr Gly Asn Leu Leu Asp Leu Glu Glu
210 215 220
Thr Ala Lys Ala Pro Leu Ser Thr Val Ser Ala Asn Thr Thr Asn Met
225 230 235 240
Asp Glu Val Pro Arg Pro Gln Ala Leu Ser Gly Ser Ser Val Val Trp
245 250 255
Glu Leu Asp Asp Gly Leu Asp Glu Ala Phe Ser Arg Leu Ala Gln Ser
260 265 270
Arg Thr Asn Pro Gln Val Leu Asp Thr Gly Leu Thr Ala Gln Asp Met
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His Tyr Ala Gln Cys Leu Ser Pro Val Asp Trp Asp Lys Pro Asp Ser
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Ser Gly Thr Glu Gln Asp Asp Leu Phe Ser Phe
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<210> 3467
<211> 638
<212> DNA
<213> Homo sapiens

<400> 3467
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ggtctgaggt gaaggtccta ggagcatcag ttctctgttg ggatcaaggt tgctgggaca
180

gagcttgatc cctgtcaact gctaaaacaa tccaggacaa tccaatagta gagctgaatt
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420
accaacgttt cctccctgtg gagccaagaa gacagggaca tgaccggagc ttgaggggcg
480
gaacgctttc agaagggaag ggtccattat cctggaagat ctggtgctga aacctgccat
540
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638

<210> 3468
<211> 88
<212> PRT
<213> Homo sapiens

<400> 3468
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Tyr Asp Phe Pro Pro Leu Cys Met Ser Gly Leu His Asp Phe Gln Phe
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Trp Leu Cys Tyr Thr Ser Cys Tyr Gln Gln Asn Arg Val Ser Leu Gly
35 40 45
Gln Ser Cys Gly Tyr Thr Ser Val Ser Gln Asp Phe Leu Cys Gln Arg
50 55 60
Ala Val Lys Leu Arg Thr Lys Val Ile Lys Ile Gln Leu Tyr Tyr Trp
65 70 75 80
Ile Val Leu Asp Cys Phe Ser Ser
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<210> 3469
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<212> DNA
<213> Homo sapiens

<400> 3469
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240
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300
gttattattg tatctgaatt gggtgataag acatttttta tagcagccat catggcaatg
360

cgctataacc gcctgaccgt gctggctggt gcaatgcttg ccttgggact aatgacatgc
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gaatttcaac gaaccaaact tttaaatgga ccgggagatg ttgaaacggg tacaagcata
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720
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<210> 3470
<211> 322
<212> PRT
<213> Homo sapiens

<400> 3470
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Pro Asp Glu Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala
        35                  40                  45
Gln Gln Leu Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala
    50                  55                  60
Arg Val Glu Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys
65                  70                  75                  80
Glu Asp Pro Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val
                85                  90                  95
Ala Ala Ile Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe
            100                 105                 110
Phe Ile Ala Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu
        115                 120                 125
Ala Gly Ala Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu
    130                 135                 140
Phe Gly Tyr Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val
145                 150                 155                 160
Ser Thr Val Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly
                165                 170                 175
Leu Lys Met Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln
            180                 185                 190
Ala Glu Leu Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu
        195                 200                 205
Asn Gly Pro Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln
    210                 215                 220
Lys Lys Trp Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr
225                 230                 235                 240
Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile
                245                 250                 255
Val Leu Ala Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr
            260                 265                 270
Val Gly His Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met
        275                 280                 285
Ile Ala Gln Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile
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<210> 3471
<211> 2335
<212> DNA
<213> Homo sapiens

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<210> 3472
<211> 631
<212> PRT
<213> Homo sapiens

<400> 3472
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Lys Val Cys Val Ser Val Val Ser Glu Lys Cys Arg Ile Asp Thr Glu
35 40 45
Ile Leu Pro Ser Leu Phe Met Arg Cys Thr Thr Asp Leu Asn Arg Lys
50 55 60
Asp Lys Phe Pro Ala Ile Thr His Leu Lys Phe Leu Ala Arg Asp Met
65 70 75 80
Ser Glu Gln Val Leu Leu Cys Ala Ser Ser Gln Thr Ser Ser Ile Val
85 90 95
Glu Cys Trp Ser Leu Arg Lys Glu Gly Leu Pro Val Asn Asn Ile Phe
100 105 110
Gln Gln Ile Ser Pro Val Val Gly Asp Lys Gln Pro Thr Ile Leu Lys
115 120 125
Trp Arg Ile Leu Ser Ala Thr Asn Asp Leu Asp Arg Val Ser Ala Val
130 135 140
Ala Leu Pro Lys Leu Pro Ile Ser Leu Thr Asn Thr Asp Leu Lys Val
145 150 155 160
Ala Ser Asp Thr Gln Phe Tyr Pro Gly Leu Gly Leu Ala Leu Ala Phe
165 170 175
His Asp Gly Ser Val His Ile Val His Arg Leu Ser Leu Gln Thr Met
180 185 190
Ala Val Phe Tyr Ser Ser Ala Ala Pro Arg Pro Val Asp Glu Pro Ala
195 200 205
Met Lys Arg Pro Arg Thr Ala Gly Pro Ala Val His Leu Lys Ala Met
210 215 220
Gln Leu Ser Trp Thr Ser Leu Ala Leu Val Gly Ile Asp Ser His Gly

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Lys Leu Ser Val Leu Arg Leu Ser Pro Ser Met Gly His Pro Leu Glu
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Val Gly Leu Ala Leu Arg His Leu Leu Phe Leu Leu Glu Tyr Cys Met
            260                 265                 270
Val Thr Gly Tyr Asp Trp Trp Asp Ile Leu Leu His Val Gln Pro Ser
        275                 280                 285
Met Val Gln Ser Leu Val Glu Lys Leu His Glu Glu Tyr Thr Arg Gln
    290                 295                 300
Thr Ala Ala Leu Gln Gln Val Leu Ser Thr Arg Ile Leu Ala Met Lys
305                 310                 315                 320
Ala Ser Leu Cys Lys Leu Ser Pro Cys Thr Val Thr Arg Val Cys Asp
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Tyr His Thr Lys Leu Phe Leu Ile Ala Ile Ser Ser Thr Leu Lys Ser
            340                 345                 350
Leu Leu Arg Pro His Phe Leu Asn Thr Pro Asp Lys Ser Pro Gly Asp
        355                 360                 365
Arg Leu Thr Glu Ile Cys Thr Lys Ile Thr Asp Val Asp Ile Asp Lys
    370                 375                 380
Val Met Ile Asn Leu Lys Thr Glu Glu Phe Val Leu Asp Met Asn Thr
385                 390                 395                 400
Leu Gln Ala Leu Gln Gln Leu Leu Gln Trp Val Gly Asp Phe Val Leu
                405                 410                 415
Tyr Leu Leu Ala Ser Leu Pro Asn Gln Gly Ser Leu Leu Arg Pro Gly
            420                 425                 430
His Ser Phe Leu Arg Asp Gly Thr Ser Leu Gly Met Leu Arg Glu Leu
        435                 440                 445
Met Val Val Ile Arg Ile Trp Gly Leu Leu Lys Pro Ser Cys Leu Pro
    450                 455                 460
Val Tyr Thr Ala Thr Ser Asp Thr Gln Asp Ser Met Ser Leu Leu Phe
465                 470                 475                 480
Arg Leu Leu Thr Lys Leu Trp Ile Cys Cys Arg Asp Glu Gly Pro Ala
                485                 490                 495
Ser Glu Pro Asp Glu Ala Leu Val Asp Glu Cys Cys Leu Leu Pro Ser
            500                 505                 510
Gln Leu Leu Ile Pro Ser Leu Asp Trp Leu Pro Ala Ser Asp Gly Leu
        515                 520                 525
Val Ser Arg Leu Gln Pro Lys Gln Pro Leu Arg Leu Gln Phe Gly Arg
    530                 535                 540
Ala Pro Thr Leu Pro Gly Ser Ala Ala Thr Leu Gln Leu Asp Gly Leu
545                 550                 555                 560
Ala Arg Ala Pro Gly Gln Pro Lys Ile Asp His Leu Arg Arg Leu His
                565                 570                 575
Leu Gly Ala Cys Pro Thr Glu Glu Cys Lys Ala Cys Thr Arg Cys Gly
            580                 585                 590
Cys Val Thr Met Leu Lys Ser Pro Asn Arg Thr Thr Ala Val Lys Gln
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Trp Glu Gln Arg Trp Ile Lys Asn Cys Leu Cys Gly Gly Leu Trp Trp
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Arg Val Pro Leu Ser Tyr Pro
625                 630
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<210> 3473
<211> 1660

<212> DNA
<213> Homo sapiens

<400> 3473
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cgcacagccg tggagcagtg gcatagcctg aggtcccgag ctgagtgtga ccgcgtgtct
1560
cctgcctccc tggaggtgac ctgagggctg cagggaaggc agctttcatt tgtttaaaaa
1620
aaaaaagacg gaaaaaaatg tgtcacatac tattacatcc
1660

<210> 3474
<211> 474
<212> PRT
<213> Homo sapiens

<400> 3474
Met Ala Tyr Ile Gln Leu Glu Pro Leu Asn Glu Gly Phe Leu Ser Arg
1 5 10 15
Ile Ser Gly Leu Leu Leu Cys Arg Trp Thr Cys Arg His Cys Cys Gln
20 25 30
Lys Cys Tyr Glu Ser Ser Cys Cys Gln Ser Ser Glu Asp Glu Val Glu
35 40 45
Ile Leu Gly Pro Phe Pro Ala Gln Thr Pro Pro Trp Leu Met Ala Ser
50 55 60
Arg Ser Ser Asp Lys Asp Gly Asp Ser Val His Thr Ala Ser Glu Val
65 70 75 80
Pro Leu Thr Pro Arg Thr Asn Ser Pro Asp Gly Arg Arg Ser Ser Ser
85 90 95
Asp Thr Ser Lys Ser Thr Tyr Ser Leu Thr Arg Arg Ile Ser Ser Leu
100 105 110
Glu Ser Arg Arg Pro Ser Ser Pro Leu Ile Asp Ile Lys Pro Ile Glu
115 120 125
Phe Gly Val Leu Ser Ala Lys Lys Glu Pro Ile Gln Pro Ser Val Leu
130 135 140
Arg Arg Thr Tyr Asn Pro Asp Asp Tyr Phe Arg Lys Phe Glu Pro His
145 150 155 160
Leu Tyr Ser Leu Asp Ser Asn Ser Asp Asp Val Asp Ser Leu Thr Asp
165 170 175
Glu Glu Ile Leu Ser Lys Tyr Gln Leu Gly Met Leu His Phe Ser Thr
180 185 190
Gln Tyr Asp Leu Leu His Asn His Leu Thr Val Arg Val Ile Glu Ala
195 200 205
Arg Asp Leu Pro Pro Pro Ile Ser His Asp Gly Ser Arg Gln Asp Met
210 215 220
Ala His Ser Asn Pro Tyr Val Lys Ile Cys Leu Leu Pro Asp Gln Lys
225 230 235 240
Asn Ser Lys Gln Thr Gly Val Lys Arg Lys Thr Gln Lys Pro Val Phe
245 250 255
Glu Glu Arg Tyr Thr Phe Glu Ile Pro Phe Leu Glu Ala Gln Arg Arg
260 265 270
Thr Leu Leu Leu Thr Val Val Asp Phe Asp Lys Phe Ser Arg His Cys
275 280 285
Val Ile Gly Lys Val Ser Val Pro Leu Cys Glu Val Asp Leu Val Lys
290 295 300
Gly Gly His Trp Trp Lys Ala Leu Ile Pro Ser Ser Gln Asn Glu Val
305 310 315 320
Glu Leu Gly Glu Leu Leu Leu Ser Leu Asn Tyr Leu Pro Ser Ala Gly

```
                325                 330                 335
Arg Leu Asn Val Asp Val Ile Arg Ala Lys Gln Leu Leu Gln Thr Asp
            340                 345                 350
Val Ser Gln Gly Ser Asp Pro Phe Val Lys Ile Gln Leu Val His Gly
        355                 360                 365
Leu Lys Leu Val Lys Thr Lys Lys Thr Ser Phe Leu Arg Gly Thr Ile
    370                 375                 380
Asp Pro Phe Tyr Asn Glu Ser Phe Ser Phe Lys Val Pro Gln Glu Glu
385                 390                 395                 400
Leu Glu Asn Ala Ser Leu Val Phe Thr Val Phe Gly His Asn Met Lys
                405                 410                 415
Ser Ser Asn Asp Phe Ile Gly Arg Ile Val Ile Gly Gln Tyr Ser Ser
            420                 425                 430
Gly Pro Ser Glu Thr Asn His Trp Arg Arg Met Leu Asn Thr His Arg
        435                 440                 445
Thr Ala Val Glu Gln Trp His Ser Leu Arg Ser Arg Ala Glu Cys Asp
    450                 455                 460
Arg Val Ser Pro Ala Ser Leu Glu Val Thr
465                 470
```

<210> 3475
<211> 514
<212> DNA
<213> Homo sapiens

<400> 3475
acgcgtctgg agggctggtt cttctgcacg cccgcccgca agctgctctg gctggtgctg
60
cagcccttct tctactcact acggccgctc tgcgtccacc ccaaggccgt gacccgcatg
120
gaggtgctca acacgctggt gcagctggcg gccgacctgg ccatctttgc cctttggggg
180
ctcaagcccg tggtctacct gctggccagc tccttcctgg gcctgggcct gcaccccatc
240
tcgggccact tcgtggccga gcactacatg ttcctcaagg gccacgagac ctactcctac
300
tatgggcctc tcaactggat caccttcaat gtgggctacc acgtggagca ccacgacttc
360
cccagcatcc cgggctacaa cctgccgctg gtgcggaaga tcgcgcccga gtactacgac
420
cacctgccgc agcaccactc ctgggtgaag gtgctctggg attttgtgtt tgaggactcc
480
ctggggccct atgccagggt gaagcgggtg taca
514

<210> 3476
<211> 171
<212> PRT
<213> Homo sapiens

<400> 3476
```
Thr Arg Leu Glu Gly Trp Phe Phe Cys Thr Pro Ala Arg Lys Leu Leu
 1               5                  10                  15
Trp Leu Val Leu Gln Pro Phe Phe Tyr Ser Leu Arg Pro Leu Cys Val
```

```
            20                  25                  30
His Pro Lys Ala Val Thr Arg Met Glu Val Leu Asn Thr Leu Val Gln
        35                  40                  45
Leu Ala Ala Asp Leu Ala Ile Phe Ala Leu Trp Gly Leu Lys Pro Val
    50                  55                  60
Val Tyr Leu Leu Ala Ser Ser Phe Leu Gly Leu Gly Leu His Pro Ile
65                  70                  75                  80
Ser Gly His Phe Val Ala Glu His Tyr Met Phe Leu Lys Gly His Glu
                85                  90                  95
Thr Tyr Ser Tyr Tyr Gly Pro Leu Asn Trp Ile Thr Phe Asn Val Gly
            100                 105                 110
Tyr His Val Glu His His Asp Phe Pro Ser Ile Pro Gly Tyr Asn Leu
        115                 120                 125
Pro Leu Val Arg Lys Ile Ala Pro Glu Tyr Tyr Asp His Leu Pro Gln
    130                 135                 140
His His Ser Trp Val Lys Val Leu Trp Asp Phe Val Phe Glu Asp Ser
145                 150                 155                 160
Leu Gly Pro Tyr Ala Arg Val Lys Arg Val Tyr
                165                 170
```

<210> 3477
<211> 356
<212> DNA
<213> Homo sapiens

<400> 3477
gcgcgcctcg gctgcctgcc cggcggtctc cgggtcctcg tccagaccgg ccaccggagc
60
ttgacctcct gcatcgaccc ttccatggga cttaatgaag agcagaaaga atttcaaaaa
120
gtggcctttg actttgctgc ccgagagatg gctccaaata tggcagagtg ggaccagaag
180
gtaggcgttt ttcttgtgct tagacgttct aacaacagat gtctcaggca gacctttatc
240
tttgtctccc gataatgtaa ttgttaaatg tctcctccac ttaccaactc ttactgcaag
300
tgagaatacc ggtagtggat gatttttcct agaaggcatc ctgatcatct tgtaca
356

<210> 3478
<211> 116
<212> PRT
<213> Homo sapiens

<400> 3478
```
Met Ile Arg Met Pro Ser Arg Lys Asn His Pro Leu Pro Val Phe Ser
 1               5                  10                  15
Leu Ala Val Arg Val Gly Lys Trp Arg Arg His Leu Thr Ile Thr Leu
            20                  25                  30
Ser Gly Asp Lys Asp Lys Gly Leu Pro Glu Thr Ser Val Val Arg Thr
        35                  40                  45
Ser Lys His Lys Lys Asn Ala Tyr Leu Leu Val Pro Leu Cys His Ile
    50                  55                  60
Trp Ser His Leu Ser Gly Ser Lys Val Lys Gly His Phe Leu Lys Phe
```

65 70 75 80
Phe Leu Leu Phe Ile Lys Ser His Gly Arg Val Asp Ala Gly Gly Gln
85 90 95
Ala Pro Val Ala Gly Leu Asp Glu Asp Pro Glu Thr Ala Gly Gln Ala
100 105 110
Ala Glu Ala Arg
115

<210> 3479
<211> 797
<212> DNA
<213> Homo sapiens

<400> 3479
nctttccaac ccagcctgaa ggggaaagcc acctcggagg acaccctcaa tctaaggaga
60
taccccggct ctgacaggat catgctgcag aagtggcaga aaagggacat cagcaatttt
120
gagtatctca tgtacctcaa caccgcggct gggagaacct gcaatgacta catgcagtac
180
ccagtgttcc cctgggtcct cgcagactac acctcagaga cattgaactt ggcaaatccg
240
aagattttcc gggatctttc aaagcccatg ggggctcaga ccaaggaaag gaagctgaaa
300
tttatccaga ggtttaaaga agttgagaaa actgaaggag acatgactgc ccagtgccac
360
tactacaccc actactcctc ggccatcatc gtggcctcct acctggtccg gatgccaccc
420
ttcacccagg ccttctgcgc tctgcaggtg agctgctgcc actctctgta cacacacaca
480
cacacacaca cacacacata cgcctgtatc acaagactaa gacctgtgct tgaacaaaga
540
caggatgcct ctgctaaaaa cttagtcatt agccagtgat tcccagttga cattggctcc
600
aggattctgg ctcaccagcc aaggcaggct gttcttcctc agttacacct gcacatctgc
660
ccaacaaagt cttgcaaaat gattctaaaa aataagaaat gagacatgaa aaaaatgatt
720
taacataaat aagatttagt ggaaaaagaa aaagcaggaa acttggagac tagaaaggca
780
ggcggtcaag gattaga
797

<210> 3480
<211> 192
<212> PRT
<213> Homo sapiens

<400> 3480
Xaa Phe Gln Pro Ser Leu Lys Gly Lys Ala Thr Ser Glu Asp Thr Leu
1 5 10 15
Asn Leu Arg Arg Tyr Pro Gly Ser Asp Arg Ile Met Leu Gln Lys Trp
20 25 30
Gln Lys Arg Asp Ile Ser Asn Phe Glu Tyr Leu Met Tyr Leu Asn Thr

```
        35                  40                  45
Ala Ala Gly Arg Thr Cys Asn Asp Tyr Met Gln Tyr Pro Val Phe Pro
    50                  55                  60
Trp Val Leu Ala Asp Tyr Thr Ser Glu Thr Leu Asn Leu Ala Asn Pro
65                  70                  75                  80
Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly Ala Gln Thr Lys Glu
                85                  90                  95
Arg Lys Leu Lys Phe Ile Gln Arg Phe Lys Glu Val Glu Lys Thr Glu
            100                 105                 110
Gly Asp Met Thr Ala Gln Cys His Tyr Tyr Thr His Tyr Ser Ser Ala
        115                 120                 125
Ile Ile Val Ala Ser Tyr Leu Val Arg Met Pro Pro Phe Thr Gln Ala
    130                 135                 140
Phe Cys Ala Leu Gln Val Ser Cys Cys His Ser Leu Tyr Thr His Thr
145                 150                 155                 160
His Thr His Thr His Thr Tyr Ala Cys Ile Thr Arg Leu Arg Pro Val
                165                 170                 175
Leu Glu Gln Arg Gln Asp Ala Ser Ala Lys Asn Leu Val Ile Ser Gln
            180                 185                 190
```

<210> 3481
<211> 1794
<212> DNA
<213> Homo sapiens

<400> 3481
nncaacgtgg tcaccacctc acgaactata agaagcgtgt ggcagccttg gaagccacgc
60
aaaagcccag cacttcccag agccagggac tgacacaaca gaaagtctgc aagcaatgcc
120
atgaggtcct gaccagaggg tcttctgcca atgcctccaa gtggtcacca cctcagctct
180
gcagaccctg cggtgctggg agccaccatg gagagtaggt gctacggctg cgctgtcaag
240
ttcaccctct tcaagaagga gtacggctgt aagaattgtg gcaggngctt ctgttcaggc
300
tgcctaagct tcagtgcagc agtgcctcgg actgggaaca cccaacagaa agtctgcaag
360
caatgccatg aggtcctgac cagagggtct tctgccaatg cctccaagtg gtcaccacct
420
cagaactata agaagcgtgt ggcagccttg gaagccaagc aaaagcccag cacttcccag
480
agccagggac tgacacgaca agaccagatg attgctgagc gcctagcacg actccgccag
540
gagaacaagc ccaagttagt cccctcacag gcagagatag aggcacggct ggctgcccta
600
aaggatgaac gtcagggttc catcccttcc acccaggaaa tggaggcacg acttgcagcg
660
ttgcagggca gagttctacc ttctcaaacc ccccagcccg gcacatcaca caccggacac
720
caggacccaa gcccagcaga cacaggatct gctaacgcag ctggcagctg aggtggctat
780
cgatgaaagc tggaaaggag gaggcccagc tgcctctctc cagaatgatc tcaaccaggg
840

tggcccaggg agcactaatt ccaagaggca ggccacttgg ttcttggaga aggagaagag
900
cagactgctg gctgaggcag cacttgagtt gcgggaggag aacacgaggc aggaacggat
960
tctggccctg gccaagcgac tagccatgct gcggggacag gaccccgaga gagtgaccct
1020
ccaggactat cgcctcccag acagtgatga cgacgaggat gaggagacag ccatccaaag
1080
agtcctgcag cagctcactg aagaagcttc cctggatgag gcaagtggct ttaacatccc
1140
tgcagagcag gcttctcgac cctggacgca accccgcggg gcagagcctg aggcccagga
1200
tgtggacccc aggcctgagg ctgaggaaga ggagctcccc tggtgctgca tctgcaatga
1260
ggatgccacc ctacgctgcg ctggctgcga tggggacctc ttctgtgccc gctgcttccg
1320
agagggccat gatgcctttg agcttaaaga gcaccagaca tctgcctact ctcctccacg
1380
tgcaggccaa gagcactgaa gacaccctgg tcctcccgga agggcagtcc cacaggcagc
1440
ggcacccatt tctgggcccc gccacaggac gtccgatggg agagcttgtc tggctctact
1500
gatgatggat aggccccttc ctgagccttg gtgtccctgg aatgaggaaa gattctccat
1560
tcgagagaat gactgggagg gaagaagtcg gggccctcct attagaagcc cagactggaa
1620
gtgagaggca tgatggggag agaccagact gaatctacgg gtgagccctg taacctggct
1680
ctagggcaca ggcccctccc ctggcactta gtgggtctaa taaagtatgt tgattcattg
1740
ggaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa
1794

<210> 3482
<211> 206
<212> PRT
<213> Homo sapiens

<400> 3482
Met Pro Pro Ser Gly His His Leu Ser Ser Ala Asp Pro Ala Val Leu
 1   5   10   15
Gly Ala Thr Met Glu Ser Arg Cys Tyr Gly Cys Ala Val Lys Phe Thr
            20   25   30
Leu Phe Lys Lys Glu Tyr Gly Cys Lys Asn Cys Gly Arg Xaa Phe Cys
        35   40   45
Ser Gly Cys Leu Ser Phe Ser Ala Ala Val Pro Arg Thr Gly Asn Thr
    50   55   60
Gln Gln Lys Val Cys Lys Gln Cys His Glu Val Leu Thr Arg Gly Ser
65   70   75   80
Ser Ala Asn Ala Ser Lys Trp Ser Pro Pro Gln Asn Tyr Lys Lys Arg
                85   90   95
Val Ala Ala Leu Glu Ala Lys Gln Lys Pro Ser Thr Ser Gln Ser Gln
            100   105   110
Gly Leu Thr Arg Gln Asp Gln Met Ile Ala Glu Arg Leu Ala Arg Leu

```
        115                 120                 125
Arg Gln Glu Asn Lys Pro Lys Leu Val Pro Ser Gln Ala Glu Ile Glu
    130                 135                 140
Ala Arg Leu Ala Ala Leu Lys Asp Glu Arg Gln Gly Ser Ile Pro Ser
145                 150                 155                 160
Thr Gln Glu Met Glu Ala Arg Leu Ala Ala Leu Gln Gly Arg Val Leu
                165                 170                 175
Pro Ser Gln Thr Pro Gln Pro Gly Thr Ser His Thr Gly His Gln Asp
            180                 185                 190
Pro Ser Pro Ala Asp Thr Gly Ser Ala Asn Ala Ala Gly Ser
        195                 200                 205
```

<210> 3483
<211> 477
<212> DNA
<213> Homo sapiens

<400> 3483
ncggccgcgg cgcggaacgg cgcctcccgc cccaccatgg gcaacagcgc gagccgcaac
60
gacttcgagt gggtctacac cgaccagccg cacacgcagc ggcgcaagga gatactggcc
120
aagtacccgg ccatcaaggc cctgatgcgg ccagacccgc gcctcaagtg ggcggggctg
180
gtgctggtgc tggtgcagat gctggcctgc tggctggtgc gcgggctggc ctggcgctgg
240
ctgctgttct gggcctacgc ctttggtggc tgcgtgaacc actcgctgac gctggccatc
300
cacgacatct cgcacaacgc ggccttcggc acgggccgtg cggcacgcaa ccgctggctg
360
gccgtgttcg ccaacctgcc cgtgggtgtg ccctacgccg cctccttcaa gaagtaccac
420
gtggaccacc accgctacct gggcggcgac ggactggacg tggacgtgcc cacgcgt
477

<210> 3484
<211> 147
<212> PRT
<213> Homo sapiens

<400> 3484
```
Met Gly Asn Ser Ala Ser Arg Asn Asp Phe Glu Trp Val Tyr Thr Asp
 1               5                  10                  15
Gln Pro His Thr Gln Arg Arg Lys Glu Ile Leu Ala Lys Tyr Pro Ala
            20                  25                  30
Ile Lys Ala Leu Met Arg Pro Asp Pro Arg Leu Lys Trp Ala Gly Leu
        35                  40                  45
Val Leu Val Leu Val Gln Met Leu Ala Cys Trp Leu Val Arg Gly Leu
    50                  55                  60
Ala Trp Arg Trp Leu Leu Phe Trp Ala Tyr Ala Phe Gly Gly Cys Val
65                  70                  75                  80
Asn His Ser Leu Thr Leu Ala Ile His Asp Ile Ser His Asn Ala Ala
                85                  90                  95
Phe Gly Thr Gly Arg Ala Ala Arg Asn Arg Trp Leu Ala Val Phe Ala
```

```
            100                 105                 110
Asn Leu Pro Val Gly Val Pro Tyr Ala Ala Ser Phe Lys Lys Tyr His
        115                 120                 125
Val Asp His His Arg Tyr Leu Gly Gly Asp Gly Leu Asp Val Asp Val
    130                 135                 140
Pro Thr Arg
145
```

<210> 3485
<211> 812
<212> DNA
<213> Homo sapiens

<400> 3485
tatttattta tagtcacaaa aactgttcag gaagaaatgt tatgaaaaga acatttttac
60
tgcatgctta aaacatttaa ttttctatta tacagttaaa catttgcttg aattcagtga
120
gtctaaaaaa tcttattgtt ctcaggttag cagttagttg agcagagtcc attggtgaag
180
caatctagtt attggcaaat tctaacacat ggtaaggtgt gggggaaagg atttaaaata
240
acagaaaaat gtaagtacaa acatacataa cagcaaaata aaactcactt taacaaaaat
300
ttatttaaaa tgttaccccc atatttcctc aatgaccaac ttgtttcagt tttatctccc
360
cctcatccgg ttattttatg tctttttggg aggaagggag atgagggttt ttgtttttta
420
acaaaatcac tggcttttta aaaagtgtta ctgcagtcat ttataagatg catgttatgt
480
ggaagtgata cctgagttgt ttgcatgggc aatggaagag gcagcagctc tgaaaggagt
540
atgagtccag aaaaaaatcc ttcaggaacc ttcaagattg aagaaagaac ttcttttaac
600
attaaagacc aagtattatt ggccagagtc tcttctgaga ttgtgagttt ttcattaact
660
ccttgtgtaa aagtcagtaa aatatcaatg atatcattct gaattttctg ttcatcacta
720
tccaaacgac ctgagagggg gatagagcac aggagcatat gtaaagtaac aagcgctgaa
780
ggaacacgca tgtccttaaa ctcaaaggat cc
812

<210> 3486
<211> 117
<212> PRT
<213> Homo sapiens

<400> 3486
```
Met Arg Val Pro Ser Ala Leu Val Thr Leu His Met Leu Leu Cys Ser
 1               5                  10                  15
Ile Pro Leu Ser Gly Arg Leu Asp Ser Asp Glu Gln Lys Ile Gln Asn
            20                  25                  30
Asp Ile Ile Asp Ile Leu Leu Thr Phe Thr Gln Gly Val Asn Glu Lys
```

```
        35                  40                  45
Leu Thr Ile Ser Glu Glu Thr Leu Ala Asn Asn Thr Trp Ser Leu Met
    50                  55                  60
Leu Lys Glu Val Leu Ser Ser Ile Leu Lys Val Pro Glu Gly Phe Phe
65                  70                  75                  80
Ser Gly Leu Ile Leu Leu Ser Glu Leu Leu Pro Leu Pro Leu Pro Met
                85                  90                  95
Gln Thr Thr Gln Val Ser Leu Pro His Asn Met His Leu Ile Asn Asp
            100                 105                 110
Cys Ser Asn Thr Phe
        115
```

<210> 3487
<211> 772
<212> DNA
<213> Homo sapiens

<400> 3487
nnattgtatc aaaatcctag atttgaataa cttattattt taaataatca gtaactaaaa
60
ccaagcaatc catcacacaa agaggggaaa gggtaatatt ctgagttata aatttttttac
120
cctgtctgat aaaaatagaa gcctgaaagt ttaaattttt cctggattta aatttaaaga
180
taaatttgtt tttcagtgaa atatcctcaa tagcaatttt accaaagagg ccttcttctg
240
aaggccacct ctgaaataat tagaggataa atgtcaatgg catgatatta agatattact
300
tggccaggcg tggtcgtcac gcgtgtaatc ccagcacttt gggaggccga ggcaggtgga
360
tcacgaggtc aagaaatcga gaccagcctg gctaacacag tgaaaccccg tctcattctg
420
agcttcttga caccttttaa tccagtcact gaaattagca tctgcaccta gaaagaaaaa
480
actgactata acatcactca tctgcacaac ctattaatca gcaaatactt actgaatacc
540
tactacatcc caggcagtgt tctaggcact ggggagtcgg cagcgaacaa aacctgtctt
600
aacagacctt atcaccaact ctactatagt tataaacata ccaatagttt aacatttagt
660
tgttaatcat gaaacatttt gatttttaa aaattttaac tacagtcaac cttaatttca
720
cagatacaaa taatctgcat ttcccccaat cccgctgctc ttagagaagc tt
772

<210> 3488
<211> 59
<212> PRT
<213> Homo sapiens

<400> 3488
Asp Ile Thr Trp Pro Gly Val Val Val Thr Arg Val Ile Pro Ala Leu
 1   5   10   15
Trp Glu Ala Glu Ala Gly Gly Ser Arg Gly Gln Glu Ile Glu Thr Ser

```
            20                  25                  30
Leu Ala Asn Thr Val Lys Pro Arg Leu Ile Leu Ser Phe Leu Thr Pro
        35                  40                  45
Phe Asn Pro Val Thr Glu Ile Ser Ile Cys Thr
    50                  55
```

<210> 3489
<211> 288
<212> DNA
<213> Homo sapiens

<400> 3489
tagctaacac tccactatgg gagcccatct cctcccaggg ccagggagac cagggagacc
60
agggagacca ggtctggccc ccaactctaa ggctcatctt agaggcgaga ttcaggccca
120
gcccagggtg ccccatgagg cctggtggtt ggaggcagag ggtatccctt gcccaaattc
180
gtgccacatt cacagtcact gggaaagcta cggggatggg ccgggcgcgg tggctcacac
240
ctgtaatccc agcactttgg agagccccaa gacgacggat cacgagtc
288

<210> 3490
<211> 90
<212> PRT
<213> Homo sapiens

<400> 3490
```
Met Gly Ala His Leu Leu Pro Gly Pro Gly Arg Pro Gly Arg Pro Gly
 1               5                  10                  15
Arg Pro Gly Leu Ala Pro Asn Ser Lys Ala His Leu Arg Gly Glu Ile
            20                  25                  30
Gln Ala Gln Pro Arg Val Pro His Glu Ala Trp Trp Leu Glu Ala Glu
        35                  40                  45
Gly Ile Pro Cys Pro Asn Ser Cys His Ile His Ser His Trp Glu Ser
    50                  55                  60
Tyr Gly Asp Gly Pro Gly Ala Val Ala His Thr Cys Asn Pro Ser Thr
65                  70                  75                  80
Leu Glu Ser Pro Lys Thr Thr Asp His Glu
                85                  90
```

<210> 3491
<211> 568
<212> DNA
<213> Homo sapiens

<400> 3491
gggaaccgac gtccctctgt ggtgaaattc cacccttca cgccgtgcat cgccgtagcc
60
gacaaggaca gcatctgctt ttgggactgg gagaaagggg agaagctgga ttatttccac
120
aatgggaacc ctcggtacac gagggtcact gccatggagt atctgaatgg ccaggactgc
180

tcgcttctgc tgacggccac agacgatggt gccatcaggg tctggaagaa ttttgctgat
240
ttggaaaaga acccagagat ggtgaccgcg tggcaggggc tctcggacat gctgccaacg
300
acgcgaggag ctgggatggt ggtggactgg gagcaggaga ccggcctcct catgagctca
360
ggagacgtgc ggatcgtccg gatctgggac acagaccgtg agatgaaggt gcaggacatc
420
cctacgggcg cagacagctg tgtgacgagt ctgtcctgtg attcccaccg ctcactcatc
480
gtggctggcc tcggtgacgg ctccatccgc gtctacgaca gaaggatggc actcagcgaa
540
tgccgcgtca tgacgtaccg ggagcaca
568

<210> 3492
<211> 189
<212> PRT
<213> Homo sapiens

<400> 3492
Gly Asn Arg Arg Pro Ser Val Val Lys Phe His Pro Phe Thr Pro Cys
1 5 10 15
Ile Ala Val Ala Asp Lys Asp Ser Ile Cys Phe Trp Asp Trp Glu Lys
20 25 30
Gly Glu Lys Leu Asp Tyr Phe His Asn Gly Asn Pro Arg Tyr Thr Arg
35 40 45
Val Thr Ala Met Glu Tyr Leu Asn Gly Gln Asp Cys Ser Leu Leu Leu
50 55 60
Thr Ala Thr Asp Asp Gly Ala Ile Arg Val Trp Lys Asn Phe Ala Asp
65 70 75 80
Leu Glu Lys Asn Pro Glu Met Val Thr Ala Trp Gln Gly Leu Ser Asp
85 90 95
Met Leu Pro Thr Thr Arg Gly Ala Gly Met Val Val Asp Trp Glu Gln
100 105 110
Glu Thr Gly Leu Leu Met Ser Ser Gly Asp Val Arg Ile Val Arg Ile
115 120 125
Trp Asp Thr Asp Arg Glu Met Lys Val Gln Asp Ile Pro Thr Gly Ala
130 135 140
Asp Ser Cys Val Thr Ser Leu Ser Cys Asp Ser His Arg Ser Leu Ile
145 150 155 160
Val Ala Gly Leu Gly Asp Gly Ser Ile Arg Val Tyr Asp Arg Arg Met
165 170 175
Ala Leu Ser Glu Cys Arg Val Met Thr Tyr Arg Glu His
180 185

<210> 3493
<211> 2244
<212> DNA
<213> Homo sapiens

<400> 3493
nggggggggat atccatgcag cgatcaggat gaaagaggtg attcaggaca accaagtaat
60

aaggaactgt ttggagatga cagtgaggac gagggagctt cacatcatag tggtagtgat
120
aatcactctg aaagatcaga caatagatca gaagcttctg agcgttctga ccatgaggac
180
aatgacccct cagatgtaga tcagcacagt ggatcagaag cccctaatga tgatgaagac
240
gaaggtcata gatcggatgg agggagccat cattcagaag cagaaggttc tgaaaaagca
300
cattcagatg atgaaaaatg gggcagagaa gataaaagtg accagtcaga tgatgaaaag
360
atacaaaatt ctgatgatga ggagagggca caaggatctg atgaagataa gctgcagaat
420
tctgacgatg atgagaaaat gcagaacaca gatgatgagg agaggcctca gctttccgat
480
gatgagagac aacagctatc tgaggaggaa aaggctaatt ctgatgatga acggccggta
540
gcttctgata atgatgatga gaaacagaat tctgatgatg aagaacaacc acagctgtct
600
gatgaagaga aaatgcaaaa ttctgatgat gaaaggccac aggccccaga tgaagaacac
660
aggcattcag atgatgaaga ggaacaggat cataaatcag aatccgcaag aggcagtgat
720
agtgaagatg aagttttacg aatgaaacgc aagaatgcga ttgcatctga ttcagaagcg
780
gatagtgaca ctgaggtgcc aaaagataat agtggaacca tggatttatt tggaggtgca
840
gatgatatct cttcagggag tgatggagaa gacaaaccac ctactccagg acagcctgtt
900
gatgaaaatg gattgcctca ggatcaacag gaagaggagc caattcctga gaccagaata
960
gaagtagaaa tacccaaagt aaacactgat ttaggaaacg acttatattt tgttaaactg
1020
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1080
gaagatgaag aaatgctgga tgaagaaggt agaaccaggt taaaattaaa ggtagaaaat
1140
actataagat ggaggatacg ccgagatgaa gaaggaaatg aaattaaaga aagcaatgct
1200
cggatagtca agtggtcaga tggaagcatg tccctgcatt taggcaatga agtgtttgat
1260
gtgtacaaag ccccactgca gggcgaccac aatcatcttt ttataagaca aggtactggt
1320
ctacagggac aagcagtctt taaagcgaaa ctcaccttca gacctcactc tacggacagt
1380
gccacacata gaaagatgac tctgtcactt gcagataggt gttcaaagac acagaagatt
1440
agaatcttgc caatggctgg tcgtgatcct gaatgccaac gcacagaaat gattaagaaa
1500
gaagaagaac gtttgagggc ttccatacgt agggaatctc agcagcgccg aatgagagag
1560
aaacagcacc agcgggggct gagcgccagt tacctggaac ctgatcgata cgatgaggag
1620
gaggaaggcg aggagtccat cagcttggct gccattaaaa accgatataa agggggcatt
1680

cgagaggaac gagccagaat ctattcatca gacagtgatg agggatcaga agaagataaa
1740
gctcaaagat tactcaaagc aaagaaactt accagtgatg aggaaggtga accttccgga
1800
aagagaaaag cagaagatga tgataaagca aataaaaagc ataagaagta tgtgatcagc
1860
gatgaagagg aagaagatga tgattgaagt atgaaatatg aaaacatttt atatatttta
1920
ttgtacagtt ataaatatgt aaacatgagt tattttgatt gaaatgaatc gatttgcttt
1980
tgtgtaattt taattgtaat aaaacaattt aaaagcaagt ctctatgttt aagaaatcta
2040
cttttccggc caggcgcggt ggctcatgcc tgtaatccca gcacttcggg aggccgaggc
2100
aggtggatca caaggtcgtg gtggcgggtg cctgtagtcg cagctactcg ggaggctgag
2160
gcgggggaat tggttgaacc caggaggcag aggttgcagt tagccgagat cgcgccactg
2220
cactccagcc tggcgacaga gcta
2244

<210> 3494
<211> 628
<212> PRT
<213> Homo sapiens

<400> 3494
Xaa Gly Gly Tyr Pro Cys Ser Asp Gln Asp Glu Arg Gly Asp Ser Gly
1 5 10 15
Gln Pro Ser Asn Lys Glu Leu Phe Gly Asp Asp Ser Glu Asp Glu Gly
20 25 30
Ala Ser His His Ser Gly Ser Asp Asn His Ser Glu Arg Ser Asp Asn
35 40 45
Arg Ser Glu Ala Ser Glu Arg Ser Asp His Glu Asp Asn Asp Pro Ser
50 55 60
Asp Val Asp Gln His Ser Gly Ser Glu Ala Pro Asn Asp Asp Glu Asp
65 70 75 80
Glu Gly His Arg Ser Asp Gly Gly Ser His His Ser Glu Ala Glu Gly
85 90 95
Ser Glu Lys Ala His Ser Asp Asp Glu Lys Trp Gly Arg Glu Asp Lys
100 105 110
Ser Asp Gln Ser Asp Asp Glu Lys Ile Gln Asn Ser Asp Asp Glu Glu
115 120 125
Arg Ala Gln Gly Ser Asp Glu Asp Lys Leu Gln Asn Ser Asp Asp Asp
130 135 140
Glu Lys Met Gln Asn Thr Asp Asp Glu Glu Arg Pro Gln Leu Ser Asp
145 150 155 160
Asp Glu Arg Gln Gln Leu Ser Glu Glu Glu Lys Ala Asn Ser Asp Asp
165 170 175
Glu Arg Pro Val Ala Ser Asp Asn Asp Asp Glu Lys Gln Asn Ser Asp
180 185 190
Asp Glu Glu Gln Pro Gln Leu Ser Asp Glu Glu Lys Met Gln Asn Ser
195 200 205
Asp Asp Glu Arg Pro Gln Ala Pro Asp Glu Glu His Arg His Ser Asp

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    210                 215                 220
Asp Glu Glu Glu Gln Asp His Lys Ser Glu Ser Ala Arg Gly Ser Asp
225                 230                 235                 240
Ser Glu Asp Glu Val Leu Arg Met Lys Arg Lys Asn Ala Ile Ala Ser
                245                 250                 255
Asp Ser Glu Ala Asp Ser Asp Thr Glu Val Pro Lys Asp Asn Ser Gly
            260                 265                 270
Thr Met Asp Leu Phe Gly Gly Ala Asp Asp Ile Ser Ser Gly Ser Asp
        275                 280                 285
Gly Glu Asp Lys Pro Pro Thr Pro Gly Gln Pro Val Asp Glu Asn Gly
    290                 295                 300
Leu Pro Gln Asp Gln Gln Glu Glu Glu Pro Ile Pro Glu Thr Arg Ile
305                 310                 315                 320
Glu Val Glu Ile Pro Lys Val Asn Thr Asp Leu Gly Asn Asp Leu Tyr
                325                 330                 335
Phe Val Lys Leu Pro Asn Phe Leu Ser Val Glu Pro Arg Pro Phe Asp
            340                 345                 350
Pro Gln Tyr Tyr Glu Asp Glu Phe Glu Asp Glu Glu Met Leu Asp Glu
        355                 360                 365
Glu Gly Arg Thr Arg Leu Lys Leu Lys Val Glu Asn Thr Ile Arg Trp
    370                 375                 380
Arg Ile Arg Arg Asp Glu Glu Gly Asn Glu Ile Lys Glu Ser Asn Ala
385                 390                 395                 400
Arg Ile Val Lys Trp Ser Asp Gly Ser Met Ser Leu His Leu Gly Asn
                405                 410                 415
Glu Val Phe Asp Val Tyr Lys Ala Pro Leu Gln Gly Asp His Asn His
            420                 425                 430
Leu Phe Ile Arg Gln Gly Thr Gly Leu Gln Gly Gln Ala Val Phe Lys
        435                 440                 445
Ala Lys Leu Thr Phe Arg Pro His Ser Thr Asp Ser Ala Thr His Arg
    450                 455                 460
Lys Met Thr Leu Ser Leu Ala Asp Arg Cys Ser Lys Thr Gln Lys Ile
465                 470                 475                 480
Arg Ile Leu Pro Met Ala Gly Arg Asp Pro Glu Cys Gln Arg Thr Glu
                485                 490                 495
Met Ile Lys Lys Glu Glu Glu Arg Leu Arg Ala Ser Ile Arg Arg Glu
            500                 505                 510
Ser Gln Gln Arg Arg Met Arg Glu Lys Gln His Gln Arg Gly Leu Ser
        515                 520                 525
Ala Ser Tyr Leu Glu Pro Asp Arg Tyr Asp Glu Glu Glu Glu Gly Glu
    530                 535                 540
Glu Ser Ile Ser Leu Ala Ala Ile Lys Asn Arg Tyr Lys Gly Gly Ile
545                 550                 555                 560
Arg Glu Glu Arg Ala Arg Ile Tyr Ser Ser Asp Ser Asp Glu Gly Ser
                565                 570                 575
Glu Glu Asp Lys Ala Gln Arg Leu Leu Lys Ala Lys Lys Leu Thr Ser
            580                 585                 590
Asp Glu Glu Gly Glu Pro Ser Gly Lys Arg Lys Ala Glu Asp Asp Asp
        595                 600                 605
Lys Ala Asn Lys Lys His Lys Lys Tyr Val Ile Ser Asp Glu Glu Glu
    610                 615                 620
Glu Asp Asp Asp
625
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<210> 3495
<211> 1085
<212> DNA
<213> Homo sapiens

<400> 3495
cgggggccag ggtgccggca ggggcgtccg gggcgctctg accggcctcg cccgcccccc
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cgcagacaca agatggtgaa ggagacccag tactatgaca tcctgggcgt gaagcccagc
120
gcgtccccgg aggagatcaa gaaggcctat cggaagctgg cgctcaagta ccacccggac
180
aagaacccgg atgagggcga gaagtttaaa ctcatatccc aggcatatga agtgctttca
240
gatccaaaga aaagggatgt ttatgaccaa ggcggagagc aggcaattaa agaaggaggc
300
tcaggcagcc ccagcttctc ttcacccatg gacatctttg acatgttctt tggtggtggt
360
ggacggatgg ctagagagag aagaggcaag aatgttgtac accagttatc tgtaactctt
420
gaagatctat ataatggagt cacgaagaaa ttggccctcc agaaaaatgt aatttgtgag
480
aaatgtgaag gtgttggtgg gaagaaggga tcggtggaga agtgcccgct gtgcaagggg
540
cgggggatgc agatccacat ccagcagatc gggccgggca tggtacagca gatccagacc
600
gtgtgcatcg agtgcaaggg ccagggtgag cgcatcaacc ccaaggaccg ctgcgagagc
660
tgcagcgggg ccaaggtgat ccgtgagaag aagattatcg aggtacatgt tgaaaaaggt
720
atgaaagatg ggcaaaagat actatttcat ggagaaggag atcaggagcc tgagctggag
780
cctggtgatg tcataattgt gcttgatcag aaggatcata gtgtctttca gagacgaggc
840
catgacttga tcatgaaaat gaaaattcag ctttctgaag ctctttgtgg cttcaagaag
900
acgataaaaa cattggacaa tcgaattctt gttattacat ccaaagcagg tgaggtgata
960
aagcacgggg acctgagatg cgtgcgcgat gaaggaatgc ccatctacaa agcacccctg
1020
gaaaaaggga ttctgatcat acagttttta gtaatctttc ctganaaaca ctggctttct
1080
ctgga
1085

<210> 3496
<211> 337
<212> PRT
<213> Homo sapiens

<400> 3496
Met Val Lys Glu Thr Gln Tyr Tyr Asp Ile Leu Gly Val Lys Pro Ser
1 5 10 15
Ala Ser Pro Glu Glu Ile Lys Lys Ala Tyr Arg Lys Leu Ala Leu Lys

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            20                  25                  30
Tyr His Pro Asp Lys Asn Pro Asp Glu Gly Glu Lys Phe Lys Leu Ile
        35                  40                  45
Ser Gln Ala Tyr Glu Val Leu Ser Asp Pro Lys Lys Arg Asp Val Tyr
    50                  55                  60
Asp Gln Gly Gly Glu Gln Ala Ile Lys Glu Gly Gly Ser Gly Ser Pro
65                  70                  75                  80
Ser Phe Ser Ser Pro Met Asp Ile Phe Asp Met Phe Phe Gly Gly Gly
                85                  90                  95
Gly Arg Met Ala Arg Glu Arg Arg Gly Lys Asn Val Val His Gln Leu
            100                 105                 110
Ser Val Thr Leu Glu Asp Leu Tyr Asn Gly Val Thr Lys Lys Leu Ala
        115                 120                 125
Leu Gln Lys Asn Val Ile Cys Glu Lys Cys Glu Gly Val Gly Gly Lys
    130                 135                 140
Lys Gly Ser Val Glu Lys Cys Pro Leu Cys Lys Gly Arg Gly Met Gln
145                 150                 155                 160
Ile His Ile Gln Gln Ile Gly Pro Gly Met Val Gln Gln Ile Gln Thr
                165                 170                 175
Val Cys Ile Glu Cys Lys Gly Gln Gly Glu Arg Ile Asn Pro Lys Asp
            180                 185                 190
Arg Cys Glu Ser Cys Ser Gly Ala Lys Val Ile Arg Glu Lys Lys Ile
        195                 200                 205
Ile Glu Val His Val Glu Lys Gly Met Lys Asp Gly Gln Lys Ile Leu
    210                 215                 220
Phe His Gly Glu Gly Asp Gln Glu Pro Glu Leu Glu Pro Gly Asp Val
225                 230                 235                 240
Ile Ile Val Leu Asp Gln Lys Asp His Ser Val Phe Gln Arg Arg Gly
                245                 250                 255
His Asp Leu Ile Met Lys Met Lys Ile Gln Leu Ser Glu Ala Leu Cys
            260                 265                 270
Gly Phe Lys Lys Thr Ile Lys Thr Leu Asp Asn Arg Ile Leu Val Ile
        275                 280                 285
Thr Ser Lys Ala Gly Glu Val Ile Lys His Gly Asp Leu Arg Cys Val
    290                 295                 300
Arg Asp Glu Gly Met Pro Ile Tyr Lys Ala Pro Leu Glu Lys Gly Ile
305                 310                 315                 320
Leu Ile Ile Gln Phe Leu Val Ile Phe Pro Xaa Lys His Trp Leu Ser
                325                 330                 335
Leu
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<210> 3497
<211> 1638
<212> DNA
<213> Homo sapiens

<400> 3497
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gtggcaactt tgttgctata attttatgca gcagataaag gtagacgttc ctccccaaag
120
tttttagtat atccttctaa aaagttttcc tgagaatttt tagtttggcc tctcaagttt
180

ccttatttta ccttttctta aattacctcc ctccttcctt agtgaaatga gccttccttc
240
agcatacgca acttatcctt attgcttttt tcatacccaa ttttttgttt tatctctttc
300
agccaactgg gtcctgaagt agctgaaatg cgaaaaaggc agcagtccca aaatgaagga
360
acacctgctg tgtctcaagc tcctggaaac cagaggccca acaacacctg ttgcttttgt
420
tggtgctgtt gttgcagctg ctcctgcctc actgtgagga atgaagaaag aggggaaaat
480
gcgggaagac ccacacacac tacaaaaatg gagagtatcc aggtcctaga ggaatgccaa
540
aaccccactg cagaggaagt cttgtcctgg tctcaaaatt ttgacaagat gatgaaggcc
600
ccagcaggaa gaaacctttt cagagagttc ctccgaacag aatacagtga agagaaccta
660
cttttctggc ttgcttgtga agacttaaag aaggagcaga acaaaaaagt aattgaagaa
720
aaggctagga tgatatatga agattacatt tctatactat caccaaaaga ggtcagtctt
780
gattctcgag ttagagaggt gatcaataga aatctgttgg atcccaatcc tcacatgtat
840aacttcagat atatacttta atgcacagag attcttttcc aaggtttttg 900
aactctcaaa tttataagtc atttgttgaa agtactgctg gctcttcttc tgaatcttaa
960
tgttcattta aaaacaatca ttttggaggg ctgagatggg aaataaaagt agttaaataa
1020
catcagaaac tgagttcctg gagaactaca gtttagcatt cctcaggcta ctgtgaaaac
1080
acaaccgtta tggtctttgt ctccattttt atcaaggttt tccatggtta agtttggaga
1140
aaataccaca caaaacaatg aattgccaaa ttgtttgttt tattcaagac tcattctact
1200
tgcaagcaaa gtgtatttgt agtcctatga acagtctcct cgtgtatctc cagagactgc
1260
atgtgcaaag taaaatgctt catttgccac atagttgttg taatatttaa tccagtagca
1320
taacttatat ctgtatttaa ggacttttgt gcaatatggt cttaagaaat aattgccaaa
1380
aaaatcggcc atggtttgca ttttttaaca taatctaaga cagaaaaaaa gcaatttta
1440
ctatgtaaca atggtattca acattctata tactgtgttt agtacactaa ttttgaagcc
1500
aatatttctg tacatgaaaa agagctattt atctctgttt gttggaaaat cctaatgggg
1560
attcctctgg ttgttcactg ccaaaactgt ggcattttca ttacaggaga gtttactatg
1620
ctaaaagcaa aaaacaaa
1638

<210> 3498
<211> 210
<212> PRT
<213> Homo sapiens

<400> 3498
Met Arg Lys Arg Gln Gln Ser Gln Asn Glu Gly Thr Pro Ala Val Ser
1 5 10 15
Gln Ala Pro Gly Asn Gln Arg Pro Asn Asn Thr Cys Cys Phe Cys Trp
20 25 30
Cys Cys Cys Cys Ser Cys Ser Cys Leu Thr Val Arg Asn Glu Glu Arg
35 40 45
Gly Glu Asn Ala Gly Arg Pro Thr His Thr Thr Lys Met Glu Ser Ile
50 55 60
Gln Val Leu Glu Glu Cys Gln Asn Pro Thr Ala Glu Glu Val Leu Ser
65 70 75 80
Trp Ser Gln Asn Phe Asp Lys Met Met Lys Ala Pro Ala Gly Arg Asn
85 90 95
Leu Phe Arg Glu Phe Leu Arg Thr Glu Tyr Ser Glu Glu Asn Leu Leu
100 105 110
Phe Trp Leu Ala Cys Glu Asp Leu Lys Lys Glu Gln Asn Lys Lys Val
115 120 125
Ile Glu Glu Lys Ala Arg Met Ile Tyr Glu Asp Tyr Ile Ser Ile Leu
130 135 140
Ser Pro Lys Glu Val Ser Leu Asp Ser Arg Val Arg Glu Val Ile Asn
145 150 155 160
Arg Asn Leu Leu Asp Pro Asn Pro His Met Tyr Glu Asp Ala Gln Leu
165 170 175
Gln Ile Tyr Thr Leu Met His Arg Asp Ser Phe Pro Arg Phe Leu Asn
180 185 190
Ser Gln Ile Tyr Lys Ser Phe Val Glu Ser Thr Ala Gly Ser Ser Ser
195 200 205
Glu Ser
210

<210> 3499
<211> 732
<212> DNA
<213> Homo sapiens

<400> 3499
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60
gtcctgattc gtcctcacag ccctgacctg gcagaagctt cactcctgcc cccagccccc
120
tgccacgggc ggcgtcccag cctggcacag aggtattgtg attcccanaa tggccaagnc
180
aacagactcn aacctcagga tngttctatt ttcgcccaga agcaataatt ttttttttcct
240
tctggaaagc cctttcaaga tagtgatgtt gatgtggggg cacggcggtc gccgggtaca
300
tggaggtacc ggggtcacag cagcgcaagc accgggaagc agggagcccc tggtcctgac
360
tgggcctgta tttttcatgt tgttcttcag ccctctcggc atggtccgga ggcgacggca
420
gctcctcagt cccctcccac tcctgctgtt ccccctggac atggggcaca cgactcagga
480
ccaggccaga ggcaaaggca aggagcaggc agtacgccag caagagtccc tgtccacggg
540

agcccatctt cctgccgggc cctccgtccc gccggccgct cctcccgcgc cgcccctaga
600
gcatctcccg ccggccaagc ctcctcccgg ccanggtccg gggcgatgca cagactcggt
660
gaaggaaaca gagcagggga aaaggtcttc cggaggacgg cagtgcagaa gaggagggtg
720
gggggcggta cg
732

<210> 3500
<211> 168
<212> PRT
<213> Homo sapiens

<400> 3500
Phe Phe Phe Pro Ser Gly Lys Pro Phe Gln Asp Ser Asp Val Asp Val
1 5 10 15
Gly Ala Arg Arg Ser Pro Gly Thr Trp Arg Tyr Arg Gly His Ser Ser
20 25 30
Ala Ser Thr Gly Lys Gln Gly Ala Pro Gly Pro Asp Trp Ala Cys Ile
35 40 45
Phe His Val Val Leu Gln Pro Ser Arg His Gly Pro Glu Ala Thr Ala
50 55 60
Ala Pro Gln Ser Pro Pro Thr Pro Ala Val Pro Pro Gly His Gly Ala
65 70 75 80
His Asp Ser Gly Pro Gly Gln Arg Gln Arg Gln Gly Ala Gly Ser Thr
85 90 95
Pro Ala Arg Val Pro Val His Gly Ser Pro Ser Ser Cys Arg Ala Leu
100 105 110
Arg Pro Ala Gly Arg Ser Ser Arg Ala Ala Pro Arg Ala Ser Pro Ala
115 120 125
Gly Gln Ala Ser Ser Arg Pro Xaa Ser Gly Ala Met His Arg Leu Gly
130 135 140
Glu Gly Asn Arg Ala Gly Glu Lys Val Phe Arg Arg Thr Ala Val Gln
145 150 155 160
Lys Arg Arg Val Gly Gly Gly Thr
165

<210> 3501
<211> 691
<212> DNA
<213> Homo sapiens

<400> 3501
nnagtagcaa ccgccggaat ggcgaaagca acaacaatca aagaagcctt agcgagatgg
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gaagagaaaa ctggccagag gccatctgaa gccaaagaga taaaacttta tgcccagatt
120
ccccctatag agaagatgga tgcatccttg tccatgcttg ctaattgcga gaagctttca
180
ctgtctacaa actgcattga aaaaattgcc aacctgaatg gcttaaaaaa cttgaggata
240
ttatctttag gaagaaacaa cataaagaac ttaaatggac tggaggcagt aggggacaca
300

ttagaagaac tgtggatctc ctacaatttt attgagaagt tgaaagggat ccacataatg
360
aagaaattga agattctcta catgtctaat aacctggtaa aagactgggc tgagtttgtg
420
aagctggcag aactgccatg cctcgaagac ctggtgtttg taggcaatcc cttggaagag
480
aaacattctg ctgagaataa ctggattgaa gaagcaacca agagagtgcc caaactgaaa
540
aagctggatg gtactccagt aattaaaggg gatgaggaag aagacaacta atgccacgct
600
ttccactgtg tgttaactta tttaaatgtc ataagaacaa tagataaatt ttatataatt
660
gtctatttta aaaaaaaaaa aaaaaaaaaa a
691

<210> 3502
<211> 196
<212> PRT
<213> Homo sapiens

<400> 3502
Xaa Val Ala Thr Ala Gly Met Ala Lys Ala Thr Thr Ile Lys Glu Ala
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Leu Ala Arg Trp Glu Glu Lys Thr Gly Gln Arg Pro Ser Glu Ala Lys
            20   25   30
Glu Ile Lys Leu Tyr Ala Gln Ile Pro Pro Ile Glu Lys Met Asp Ala
        35   40   45
Ser Leu Ser Met Leu Ala Asn Cys Glu Lys Leu Ser Leu Ser Thr Asn
    50   55   60
Cys Ile Glu Lys Ile Ala Asn Leu Asn Gly Leu Lys Asn Leu Arg Ile
65   70   75   80
Leu Ser Leu Gly Arg Asn Asn Ile Lys Asn Leu Asn Gly Leu Glu Ala
                85   90   95
Val Gly Asp Thr Leu Glu Glu Leu Trp Ile Ser Tyr Asn Phe Ile Glu
            100   105   110
Lys Leu Lys Gly Ile His Ile Met Lys Lys Leu Lys Ile Leu Tyr Met
        115   120   125
Ser Asn Asn Leu Val Lys Asp Trp Ala Glu Phe Val Lys Leu Ala Glu
    130   135   140
Leu Pro Cys Leu Glu Asp Leu Val Phe Val Gly Asn Pro Leu Glu Glu
145   150   155   160
Lys His Ser Ala Glu Asn Asn Trp Ile Glu Glu Ala Thr Lys Arg Val
                165   170   175
Pro Lys Leu Lys Lys Leu Asp Gly Thr Pro Val Ile Lys Gly Asp Glu
            180   185   190
Glu Glu Asp Asn
        195

<210> 3503
<211> 857
<212> DNA
<213> Homo sapiens

<400> 3503

gcggcgccca ggtggagcgc gtcgggcccc tggatccggg gaaacggcca aggttgcggg
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agtctcttca ctctcgtctc aaagccattt tgtgccgctg ccgctgcctc tacggccata
120
aatgcccaga gattagcgga gaagctccga gcccagaaac gggaacaaga cacaaagaag
180
gagccggtgt ccacaaacgc tgttcagcgg agagtgcaag aaatagtgcg gttcacacgg
240
cagctgcagc gagtccaccc caacgtgctt gctaaggcac tgacccgagg aattctccac
300
caggacaaga accttgtggt catcaataag ccctacggtc tccctgtgca tggtggccct
360
ggggtccagc tctgcatcac tgatgtacta cctatcctgg caaagatgct tcatggccac
420
aaggcagagc ccttgcatct gtgccaccgg ctggacaagg aaaccacagg tgtaatggtg
480
ttggcttggg acaaggacat ggcacatcaa gtccaagagt tgtttagaac ccgtcaggtg
540
gtgaagaagt actgggccat cactgtgcat gtccccatgc cctcagcagg agtcgtggac
600
atccccattg tggagaagga ggggcaaggc cagcagcaac accccagaat gacattgtcc
660
ccgagctccc gcatggacga tgggaaaatg gtgaaagtgc ggcgcagccg gaatgcgcaa
720
gttgctgtaa ctcagtacca ggtgctcagc agcactctct cctccgccct cgtggagctc
780
cagcccatca ctggaataaa acatcagctt cgagttcact tgtcttttgg attggattgt
840
ccaatccttg gtgatca
857

<210> 3504
<211> 285
<212> PRT
<213> Homo sapiens

<400> 3504
Ala Ala Pro Arg Trp Ser Ala Ser Gly Pro Trp Ile Arg Gly Asn Gly
1 5 10 15
Gln Gly Cys Gly Ser Leu Phe Thr Leu Val Ser Lys Pro Phe Cys Ala
20 25 30
Ala Ala Ala Ala Ser Thr Ala Ile Asn Ala Gln Arg Leu Ala Glu Lys
35 40 45
Leu Arg Ala Gln Lys Arg Glu Gln Asp Thr Lys Lys Glu Pro Val Ser
50 55 60
Thr Asn Ala Val Gln Arg Arg Val Gln Glu Ile Val Arg Phe Thr Arg
65 70 75 80
Gln Leu Gln Arg Val His Pro Asn Val Leu Ala Lys Ala Leu Thr Arg
85 90 95
Gly Ile Leu His Gln Asp Lys Asn Leu Val Val Ile Asn Lys Pro Tyr
100 105 110
Gly Leu Pro Val His Gly Gly Pro Gly Val Gln Leu Cys Ile Thr Asp
115 120 125
Val Leu Pro Ile Leu Ala Lys Met Leu His Gly His Lys Ala Glu Pro

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    130                 135                 140
Leu His Leu Cys His Arg Leu Asp Lys Glu Thr Thr Gly Val Met Val
145                 150                 155                 160
Leu Ala Trp Asp Lys Asp Met Ala His Gln Val Gln Glu Leu Phe Arg
                165                 170                 175
Thr Arg Gln Val Val Lys Lys Tyr Trp Ala Ile Thr Val His Val Pro
            180                 185                 190
Met Pro Ser Ala Gly Val Val Asp Ile Pro Ile Val Glu Lys Glu Gly
        195                 200                 205
Gln Gly Gln Gln Gln His Pro Arg Met Thr Leu Ser Pro Ser Ser Arg
    210                 215                 220
Met Asp Asp Gly Lys Met Val Lys Val Arg Arg Ser Arg Asn Ala Gln
225                 230                 235                 240
Val Ala Val Thr Gln Tyr Gln Val Leu Ser Ser Thr Leu Ser Ser Ala
                245                 250                 255
Leu Val Glu Leu Gln Pro Ile Thr Gly Ile Lys His Gln Leu Arg Val
            260                 265                 270
His Leu Ser Phe Gly Leu Asp Cys Pro Ile Leu Gly Asp
        275                 280                 285
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<210> 3505
<211> 1612
<212> DNA
<213> Homo sapiens

<400> 3505
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120
cttgtcgcat ccctgggctc tgcggagaag gaacccgagc agcccccggc cctgtggagg
180
aaggttgtgg acttcctgct gaaggccatc atgcgcacca tgtggttcgc cggcggcttc
240
caccgggtgg ccgtgaaggg gcggcaggcg ctgcccaccg aggcggccat cctcacgctc
300
gcgcctcact cgtcctactt cgacgccatc cctgtgacca tgacgatgtc ctccatcgtg
360
atgaagacag agagcagaga catcccgatc tggggaactc tgatccagta tatacggcct
420
gtgttcgtgt cccggtcaga ccaggattct cgcaggaaaa cagtagaaga aatcaagaga
480
cgggcgcagt ccaacggaaa gtggccacag ataatgattt ttccagaagg aacttgtaca
540
aacaggacct gcctaattac cttcaaacct ggtgcattca tccctggagc gcccgtccac
600
cctggggttt tacgatatcc aaataaactg gacaccatca catggacgtg gcaaggacct
660
ggagcgctgg aaatcctgtg gctcacgctg tgtcagtttc acaaccaagt ggaaatcgag
720
ttccttcctg tgtacagccc ttctgaggag gagaagagga accccgcgct gtatgccagc
780
aacgtgcggc gagtcatggc cgaggccttg ggtgtctccg tgactgacta cacgttcgag
840

gactgccagc tggccctggc ggaaggacag ctccgtctcc ccgctgacac ttgcctttta
900
gaatttgcca ggctcgtgcg gggcctcggg ctaaaaccag aaaagcttga aaaagatctg
960
gacagatact cagaaagagc caggatgaag ggaggagaga agataggtat tgcggagttt
1020
gccgcctccc tggaagtccc cgtttctgac ttgctggaag acatgttttc actgttcgac
1080
gagagcggca gcggcgaggt ggacctgcga gagtgtgtgg ttgccctgtc tgtcgtctgc
1140
tggccggccc ggaccctgga caccatccag ctggctttca agatgtacgg agcgcaagag
1200
gacggcagcg tcggcgaagg tgacctgtcc tgcatcctca agacggccct gggggtggca
1260
gagctcactg tgaccgacct attccgagcc attgaccaag aggagaaggg gaagatcaca
1320
ttcgctgact tccacaggtt tgcagaaatg taccctgcct tcgcagagga atacctgtac
1380
ccggatcaga cacatttcga aagctgtgca gagacctcac ctgcgccaat cccaaacggc
1440
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1500
ctggattagg acccagggtt gcggagagac gcggcccctc ccgcgtggac atcaccgcca
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1612

<210> 3506
<211> 502
<212> PRT
<213> Homo sapiens

<400> 3506
Val His Glu Leu His Leu Ser Ala Leu Gln Lys Ala Gln Val Ala Leu
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Met Thr Leu Thr Leu Phe Pro Val Arg Leu Leu Val Ala Ala Ala Met
20 25 30
Met Leu Leu Ala Trp Pro Leu Ala Leu Val Ala Ser Leu Gly Ser Ala
35 40 45
Glu Lys Glu Pro Glu Gln Pro Pro Ala Leu Trp Arg Lys Val Val Asp
50 55 60
Phe Leu Leu Lys Ala Ile Met Arg Thr Met Trp Phe Ala Gly Gly Phe
65 70 75 80
His Arg Val Ala Val Lys Gly Arg Gln Ala Leu Pro Thr Glu Ala Ala
85 90 95
Ile Leu Thr Leu Ala Pro His Ser Ser Tyr Phe Asp Ala Ile Pro Val
100 105 110
Thr Met Thr Met Ser Ser Ile Val Met Lys Thr Glu Ser Arg Asp Ile
115 120 125
Pro Ile Trp Gly Thr Leu Ile Gln Tyr Ile Arg Pro Val Phe Val Ser
130 135 140
Arg Ser Asp Gln Asp Ser Arg Arg Lys Thr Val Glu Glu Ile Lys Arg
145 150 155 160
Arg Ala Gln Ser Asn Gly Lys Trp Pro Gln Ile Met Ile Phe Pro Glu

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                165                 170                 175
Gly Thr Cys Thr Asn Arg Thr Cys Leu Ile Thr Phe Lys Pro Gly Ala
            180                 185                 190
Phe Ile Pro Gly Ala Pro Val His Pro Gly Val Leu Arg Tyr Pro Asn
        195                 200                 205
Lys Leu Asp Thr Ile Thr Trp Thr Trp Gln Gly Pro Gly Ala Leu Glu
    210                 215                 220
Ile Leu Trp Leu Thr Leu Cys Gln Phe His Asn Gln Val Glu Ile Glu
225                 230                 235                 240
Phe Leu Pro Val Tyr Ser Pro Ser Glu Glu Glu Lys Arg Asn Pro Ala
                245                 250                 255
Leu Tyr Ala Ser Asn Val Arg Arg Val Met Ala Glu Ala Leu Gly Val
            260                 265                 270
Ser Val Thr Asp Tyr Thr Phe Glu Asp Cys Gln Leu Ala Leu Ala Glu
        275                 280                 285
Gly Gln Leu Arg Leu Pro Ala Asp Thr Cys Leu Leu Glu Phe Ala Arg
    290                 295                 300
Leu Val Arg Gly Leu Gly Leu Lys Pro Glu Lys Leu Glu Lys Asp Leu
305                 310                 315                 320
Asp Arg Tyr Ser Glu Arg Ala Arg Met Lys Gly Gly Glu Lys Ile Gly
                325                 330                 335
Ile Ala Glu Phe Ala Ala Ser Leu Glu Val Pro Val Ser Asp Leu Leu
            340                 345                 350
Glu Asp Met Phe Ser Leu Phe Asp Glu Ser Gly Ser Gly Glu Val Asp
        355                 360                 365
Leu Arg Glu Cys Val Val Ala Leu Ser Val Val Cys Trp Pro Ala Arg
    370                 375                 380
Thr Leu Asp Thr Ile Gln Leu Ala Phe Lys Met Tyr Gly Ala Gln Glu
385                 390                 395                 400
Asp Gly Ser Val Gly Glu Gly Asp Leu Ser Cys Ile Leu Lys Thr Ala
                405                 410                 415
Leu Gly Val Ala Glu Leu Thr Val Thr Asp Leu Phe Arg Ala Ile Asp
            420                 425                 430
Gln Glu Glu Lys Gly Lys Ile Thr Phe Ala Asp Phe His Arg Phe Ala
        435                 440                 445
Glu Met Tyr Pro Ala Phe Ala Glu Glu Tyr Leu Tyr Pro Asp Gln Thr
    450                 455                 460
His Phe Glu Ser Cys Ala Glu Thr Ser Pro Ala Pro Ile Pro Asn Gly
465                 470                 475                 480
Phe Cys Ala Asp Phe Ser Pro Glu Asn Ser Asp Ala Gly Arg Lys Pro
                485                 490                 495
Val Arg Lys Lys Leu Asp
            500
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<210> 3507
<211> 885
<212> DNA
<213> Homo sapiens

<400> 3507
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120

cgagcccgct ccccggcatc cgtgctcaag tcccactcgc tgtagtcatt gttgatgctg
180
acctgggcca tggccccgag agccttcttc ctgcaaggtc tgtgggttct gccttacaac
240
cacatgcctc agggagctga gcaacaccca cctgtttggg gctgttagct taggactctt
300
ctcaacctgc tctttctccc tgatgggctg tgccagaggc ggttgctatg tgaggtggcc
360
atcgctgtct acacctttgg cacctgcatt gccttcctaa tcatcattgg cgaccagcag
420
gacaagatta tagctgtgat ggcgaaagag ccggaggggg ccagcggccc ttggtacaca
480
gaccgcaagt tcaccatcag cctcactgcc ttcctcttca tcctgccctt ctccatcccc
540
agggagattg gtttccagaa atatgccagc ttcctgagcg tcgtgggtac ctggtacgtc
600
acagccatcg ttatcatcaa gtacatctgg ccagataaag agatgacccc agggaacatc
660
ctgaccaggc cggcttcctg gatggctgtg ttcaatgcca tgcccaccat ctgcttcgga
720
tttcagtgcc acgtcagcag tgtgcccgtc ttcaacagca tgcagcagcc tgaagtgaag
780
acctggggtg gagtggtgac agctgccatg gtcatagccc tcgctgtcta catggggaca
840
ggcatctgtg gcttcctgac ctttggagct gctgtggatc ctgac
885

<210> 3508
<211> 199
<212> PRT
<213> Homo sapiens

<400> 3508
Leu Arg Thr Leu Leu Asn Leu Leu Phe Leu Pro Asp Gly Leu Cys Gln
1 5 10 15
Arg Arg Leu Leu Cys Glu Val Ala Ile Ala Val Tyr Thr Phe Gly Thr
20 25 30
Cys Ile Ala Phe Leu Ile Ile Ile Gly Asp Gln Gln Asp Lys Ile Ile
35 40 45
Ala Val Met Ala Lys Glu Pro Glu Gly Ala Ser Gly Pro Trp Tyr Thr
50 55 60
Asp Arg Lys Phe Thr Ile Ser Leu Thr Ala Phe Leu Phe Ile Leu Pro
65 70 75 80
Leu Ser Ile Pro Arg Glu Ile Gly Phe Gln Lys Tyr Ala Ser Phe Leu
85 90 95
Ser Val Val Gly Thr Trp Tyr Val Thr Ala Ile Val Ile Ile Lys Tyr
100 105 110
Ile Trp Pro Asp Lys Glu Met Thr Pro Gly Asn Ile Leu Thr Arg Pro
115 120 125
Ala Ser Trp Met Ala Val Phe Asn Ala Met Pro Thr Ile Cys Phe Gly
130 135 140
Phe Gln Cys His Val Ser Ser Val Pro Val Phe Asn Ser Met Gln Gln
145 150 155 160
Pro Glu Val Lys Thr Trp Gly Gly Val Val Thr Ala Ala Met Val Ile

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                165                 170                 175
Ala Leu Ala Val Tyr Met Gly Thr Gly Ile Cys Gly Phe Leu Thr Phe
            180                 185                 190
Gly Ala Ala Val Asp Pro Asp
        195
```

<210> 3509
<211> 331
<212> DNA
<213> Homo sapiens

<400> 3509
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gccctggtgc atgtcaaggc cgagtacttc cgctccctgg cccactacca cgtagccatg
120
gccctctgcg acggctcccc gaccgaggga gagctcccca cgcacgagca ggtcttcctg
180
agccccccac ctcctttaag cccccgaggg cctgggttgc cccagaagtt ggaggagcgc
240
aggcagcttg gtaaggcgcc catgggtgga gtgccctggg gctcagatgg tcaccaacgg
300
tggcagggtg tcccccacca ccctcacgcg t
331

<210> 3510
<211> 110
<212> PRT
<213> Homo sapiens

<400> 3510

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Leu Val His Arg Thr Met Ala Gln Pro Pro Val His Asp Tyr Val Pro
 1               5                  10                  15
Val Ser Trp Thr Ala Leu Val His Val Lys Ala Glu Tyr Phe Arg Ser
            20                  25                  30
Leu Ala His Tyr His Val Ala Met Ala Leu Cys Asp Gly Ser Pro Thr
        35                  40                  45
Glu Gly Glu Leu Pro Thr His Glu Gln Val Phe Leu Ser Pro Pro Pro
    50                  55                  60
Pro Leu Ser Pro Arg Gly Pro Gly Leu Pro Gln Lys Leu Glu Glu Arg
65                  70                  75                  80
Arg Gln Leu Gly Lys Ala Pro Met Gly Gly Val Pro Trp Gly Ser Asp
                85                  90                  95
Gly His Gln Arg Trp Gln Gly Val Pro His His Pro His Ala
            100                 105                 110
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<210> 3511
<211> 3319
<212> DNA
<213> Homo sapiens

<400> 3511
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60

agcacggggt ggtgtgtggg ggaagccgcc cccggcagca ggatgaaacg aggaggaaga
120
gatagtgacc gtaattcatc agaagaagga actgcagaga aatccaagaa actgaggact
180
acaaatgagc attctcagac ttgtgattgg ggtaatctcc ttcaggacat tattctccaa
240
gtatttaaat atttgcctct tcttgaccgg gctcatgctt cacaagtttg ccgcaactgg
300
aaccaggtat ttcacatgcc tgacttgtgg agatgttttg aatttgaact gaatcagcca
360
gctacatctt atttgaaagc tacccatcca gagctgatca aacagattat taaaagacat
420
tcaaaccatc tacaatatgt cagcttcaag gtggacagca gcaaggaatc agctgaagca
480
gcttgtgata tactatcgca acttgtgaat tgctctttaa aaacacttgg acttatttca
540
actgctcgac caagctttat ggatttacca aagtctcact ttatctctgc actgacagtt
600
gtgttcgtaa actccaaatc cctgtcttcg cttaagatag atgatactcc agtagatgat
660
ccatctctca aagtactagt ggccaacaat agtgatacac tcaagctgtt gaaaatgagc
720
agctgtcctc atgtctctcc agcaggtatc ctttgtgtgg ctgatcagtg tcacggctta
780
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840
gaaaaacatg ttcgattaga acatttgcgc attgatgtag tcagtgagaa tcctggacag
900
acacacttcc atactattca gaagagtagc tgggatgctt tcatcagaca ttcacccaaa
960
gtgaacttag tgatgtattt ttttttatat gaagaagaat ttgacccctt ctttcgctat
1020
gaaatacctg ccacccatct gtactttggg agatcagtaa gcaaagatgt gcttggccgt
1080
gtgggaatga catgccctag actggttgaa ctagtagtgt gtgcaaatgg attacggcca
1140
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1260
ctatctcaat tatccattat ggaagaagta ctaattcctg accaaaagta tagtttggag
1320
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1380
acttggtaaa aactgcatga tgaatagcac cttaatttca agcaaatgta ttataattaa
1440
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1500
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1560
aaattccact tgtttcctta gtgtaatagc agtcatatct ccgaattttt tttaatgtgg
1620
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1680

cctatatgtt ataatatcca agaagtacta ataggttttc tgaaatgtta tattctctat
1740
gcattaaaaa aaaaatgtaa acttgacatt ttagggtctt cagttacaca tacacctgtt
1800
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1860
atctaatgga aaagattgga tgaatgttct caaatgttac aaagctgttt aaagaaaaag
1920
gtatatataa gtaatcagaa cacttagaag actgatagat gtcacacagt ggtattatag
1980
aaggataata cagagccaag atcaaattaa aagacaataa atggaacaga agggaggcag
2040
tgtttagctt tgtataaact tttaggtttg ctctgtaatc tgctaaacca tatacattct
2100
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2160
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2220
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2280
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2340
ctcacttttc tattttggaa ttacatagtt atgtaagtaa aatttttaaa aatcataaag
2400
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2460
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2520
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2580
acattttata ttactttcat atgaataaaa gtaatccatg cattgtagag tctataaaat
2640
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2700
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2760
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2820
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2880
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2940
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3060
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3120
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3180
tttataagca aaatgcatag tacttaattt gtttatactg taaagtatat gttaaatgct
3240
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3300

aaaaaaaaaa aaaaaaaaa
3319

<210> 3512
<211> 462
<212> PRT
<213> Homo sapiens

<400> 3512
Xaa Arg Ala Arg Gly Ala Ser Cys Glu Ser Arg Gly Thr Cys Ser Arg
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Arg Arg Pro Arg Ser Thr Gly Trp Cys Val Gly Glu Ala Ala Pro Gly
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Ser Arg Met Lys Arg Gly Gly Arg Asp Ser Asp Arg Asn Ser Ser Glu
35 40 45
Glu Gly Thr Ala Glu Lys Ser Lys Lys Leu Arg Thr Thr Asn Glu His
50 55 60
Ser Gln Thr Cys Asp Trp Gly Asn Leu Leu Gln Asp Ile Ile Leu Gln
65 70 75 80
Val Phe Lys Tyr Leu Pro Leu Leu Asp Arg Ala His Ala Ser Gln Val
85 90 95
Cys Arg Asn Trp Asn Gln Val Phe His Met Pro Asp Leu Trp Arg Cys
100 105 110
Phe Glu Phe Glu Leu Asn Gln Pro Ala Thr Ser Tyr Leu Lys Ala Thr
115 120 125
His Pro Glu Leu Ile Lys Gln Ile Ile Lys Arg His Ser Asn His Leu
130 135 140
Gln Tyr Val Ser Phe Lys Val Asp Ser Ser Lys Glu Ser Ala Glu Ala
145 150 155 160
Ala Cys Asp Ile Leu Ser Gln Leu Val Asn Cys Ser Leu Lys Thr Leu
165 170 175
Gly Leu Ile Ser Thr Ala Arg Pro Ser Phe Met Asp Leu Pro Lys Ser
180 185 190
His Phe Ile Ser Ala Leu Thr Val Val Phe Val Asn Ser Lys Ser Leu
195 200 205
Ser Ser Leu Lys Ile Asp Asp Thr Pro Val Asp Asp Pro Ser Leu Lys
210 215 220
Val Leu Val Ala Asn Asn Ser Asp Thr Leu Lys Leu Leu Lys Met Ser
225 230 235 240
Ser Cys Pro His Val Ser Pro Ala Gly Ile Leu Cys Val Ala Asp Gln
245 250 255
Cys His Gly Leu Arg Glu Leu Ala Leu Asn Tyr His Leu Leu Ser Asp
260 265 270
Glu Leu Leu Leu Ala Leu Ser Ser Glu Lys His Val Arg Leu Glu His
275 280 285
Leu Arg Ile Asp Val Val Ser Glu Asn Pro Gly Gln Thr His Phe His
290 295 300
Thr Ile Gln Lys Ser Ser Trp Asp Ala Phe Ile Arg His Ser Pro Lys
305 310 315 320
Val Asn Leu Val Met Tyr Phe Phe Leu Tyr Glu Glu Glu Phe Asp Pro
325 330 335
Phe Phe Arg Tyr Glu Ile Pro Ala Thr His Leu Tyr Phe Gly Arg Ser
340 345 350
Val Ser Lys Asp Val Leu Gly Arg Val Gly Met Thr Cys Pro Arg Leu

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        355                 360                 365
Val Glu Leu Val Val Cys Ala Asn Gly Leu Arg Pro Leu Asp Glu Glu
    370                 375                 380
Leu Ile Arg Ile Ala Glu Arg Cys Lys Asn Leu Ser Ala Ile Gly Leu
385                 390                 395                 400
Gly Glu Cys Glu Val Ser Cys Ser Ala Phe Val Glu Phe Val Lys Met
                405                 410                 415
Cys Gly Gly Arg Leu Ser Gln Leu Ser Ile Met Glu Glu Val Leu Ile
            420                 425                 430
Pro Asp Gln Lys Tyr Ser Leu Glu Gln Ile His Trp Glu Val Ser Lys
        435                 440                 445
His Leu Gly Arg Val Trp Phe Pro Asp Met Met Pro Thr Trp
    450                 455                 460
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<210> 3513
<211> 2103
<212> DNA
<213> Homo sapiens

<400> 3513
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cagctggagc gaggggaaga tccctgggtc ctggacagga agggggctaa gaagagccag
120
ggcctgtgga gtgactactc agaatatgaa cccaagggag agagtcaaaa tacagacttg
180
agtccgaagc cattaatttc agagcaaaca gtgattctgg ggaaaacacc cttggggagg
240
attgatcaag aaaataatga aacaaagcaa agcttctgtt tgagtccgaa ctctgttgac
300
caccgtgaag ttcaggtctt aagccaaagc atgccactca ctccgcacca ggcagtgcct
360
agtggagaga ggccctacat gtgtgttgag tgtgggaagt gctttggccg gagttcccac
420
ctccttcagc atcagcgtat ccacactgga gagaagccct atgtgtgcag tgtatgtggg
480
aaggccttca gccagagctc agtccttagt aaacacagga gaattcacac aggtgagaag
540
ccctatgagt gtaatgagtg tggaaaagcc tttagagtga gctcagatct tgctcagcat
600
cacaagatac atacaggaga gaagcctcac gaatgtcttg agtgtcggaa agccttcact
660
caactctcac atctcattca gcaccagcgg atccacacgg gagaaaggcc atatgtgtgt
720
ccgttgtgtg ggaaagcctt caaccatagc actgttctgc ggagccacca gagggtacac
780
actggggaga agcctcacag gtgcaatgag tgtgggaaaa ccttcagtgt gaagaggaca
840
ctgctgcagc accagaggat ccacaccggg gagaagccct acacgtgcag cgagtgtggg
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960
ccctatgagt gcagtgagtg tgggaagacc ttcagccacc gctccacact gatgaatcac
1020

gagcggatcc acaccgagga aaagccctat gcatgctacg aatgtgggaa ggccttcgtt
1080
cagcactcac acctgatcca gcaccagaga gtccacactg gggagaagcc ctatgtgtgt
1140
ggtgaatgtg ggcacgcctt cagtgcacgc cggtctctga tccagcatga gagaatccac
1200
acaggtgaaa agcccttcca gtgcacagaa tgtggcaaag ctntcagcct gaaagcaact
1260
ctgattgtgc acctgaggac ccacacgggc gagaagccat atgagtgcaa tagctgcggg
1320
aaggccttca gccagtactc agtgctcatc cagcaccagc ggatccacac aggcgagaag
1380
ccctatgagt gcggggagtg tgggcgtgcc ttcaaccagc atggccacct aatccagcac
1440
cagaaagtgc acagaaagtt gtgacccatg gctgacacaa gaatccattc tcacagaaac
1500
tgcatgtgga accacaagca gccttcagcc caagagaagt ctctgttaac tctataggaa
1560
gcttttcttt ggcgattcag tgtcacaaaa taactccaga aagaagcact tagcgtgctg
1620
ttcctgtgga aaaacttcag agactacctg ttttattttc ctcaacatct tgaagttatg
1680
ttggagagta atcatacaat tgtagagaat tttggtaaaa aacagccata attctttaac
1740
attagtttat ttgaactaag ggaatttaag gcataagaac cattatccca ataaaatctt
1800
acattccaaa taaagttctt tttctaagaa cattacatgc ccttcctaaa tatcaattaa
1860
ccatactaat tattgcactt aaaatttgaa agtcggacta ttttcagtat tctcttaaaa
1920
gactaaagta ttgtatggat aaagtgatat aaaaagatat tttcatcaag catcatgtaa
1980
aatggttgga aatcctaagt gtgtggattt ccatcctaag tgtgtggagt cctgttttgt
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atgaaacaag gaaaaagctt atatattagt gagaaattac ataaatttaa aaaaaaaaaa
2100
aaa
2103

<210> 3514
<211> 484
<212> PRT
<213> Homo sapiens

<400> 3514
Gly Asn Val Val Ser Leu Gly Leu Pro Gly Ser Lys Pro Asp Ile Ile
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Ser Gln Leu Glu Arg Gly Glu Asp Pro Trp Val Leu Asp Arg Lys Gly
20 25 30
Ala Lys Lys Ser Gln Gly Leu Trp Ser Asp Tyr Ser Glu Tyr Glu Pro
35 40 45
Lys Gly Glu Ser Gln Asn Thr Asp Leu Ser Pro Lys Pro Leu Ile Ser
50 55 60
Glu Gln Thr Val Ile Leu Gly Lys Thr Pro Leu Gly Arg Ile Asp Gln

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65                  70                  75                  80
Glu Asn Asn Glu Thr Lys Gln Ser Phe Cys Leu Ser Pro Asn Ser Val
                85                  90                  95
Asp His Arg Glu Val Gln Val Leu Ser Gln Ser Met Pro Leu Thr Pro
            100                 105                 110
His Gln Ala Val Pro Ser Gly Glu Arg Pro Tyr Met Cys Val Glu Cys
        115                 120                 125
Gly Lys Cys Phe Gly Arg Ser Ser His Leu Leu Gln His Gln Arg Ile
    130                 135                 140
His Thr Gly Glu Lys Pro Tyr Val Cys Ser Val Cys Gly Lys Ala Phe
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Ser Gln Ser Ser Val Leu Ser Lys His Arg Arg Ile His Thr Gly Glu
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Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe Arg Val Ser Ser
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Asp Leu Ala Gln His His Lys Ile His Thr Gly Glu Lys Pro His Glu
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Cys Leu Glu Cys Arg Lys Ala Phe Thr Gln Leu Ser His Leu Ile Gln
    210                 215                 220
His Gln Arg Ile His Thr Gly Glu Arg Pro Tyr Val Cys Pro Leu Cys
225                 230                 235                 240
Gly Lys Ala Phe Asn His Ser Thr Val Leu Arg Ser His Gln Arg Val
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His Thr Gly Glu Lys Pro His Arg Cys Asn Glu Cys Gly Lys Thr Phe
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Ser Val Lys Arg Thr Leu Leu Gln His Gln Arg Ile His Thr Gly Glu
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Lys Pro Tyr Thr Cys Ser Glu Cys Gly Lys Ala Phe Ser Asp Arg Ser
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Val Leu Ile Gln His His Asn Val His Thr Gly Glu Lys Pro Tyr Glu
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Cys Ser Glu Cys Gly Lys Thr Phe Ser His Arg Ser Thr Leu Met Asn
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His Glu Arg Ile His Thr Glu Glu Lys Pro Tyr Ala Cys Tyr Glu Cys
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Gly Lys Ala Phe Val Gln His Ser His Leu Ile Gln His Gln Arg Val
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His Thr Gly Glu Lys Pro Tyr Val Cys Gly Glu Cys Gly His Ala Phe
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Ser Ala Arg Arg Ser Leu Ile Gln His Glu Arg Ile His Thr Gly Glu
385                 390                 395                 400
Lys Pro Phe Gln Cys Thr Glu Cys Gly Lys Ala Xaa Ser Leu Lys Ala
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Thr Leu Ile Val His Leu Arg Thr His Thr Gly Glu Lys Pro Tyr Glu
            420                 425                 430
Cys Asn Ser Cys Gly Lys Ala Phe Ser Gln Tyr Ser Val Leu Ile Gln
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His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Gly Glu Cys
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<210> 3515
<211> 5003
<212> DNA
<213> Homo sapiens

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<210> 3516
<211> 547
<212> PRT
<213> Homo sapiens

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Asp Gln Ile Gln Thr Leu Met Leu Gln Asn Arg Thr Leu Leu Glu Gln
35 40 45
Asn Met Glu Ser Lys Asp Leu Phe His Val Glu Gln Arg Gln Tyr Ile
50 55 60
Asp Lys Leu Asn Glu Leu Arg Arg Gln Lys Glu Lys Leu Glu Glu Lys
65 70 75 80
Ile Met Asp Gln Tyr Lys Phe Tyr Asp Pro Ser Pro Pro Arg Arg Arg
85 90 95
Gly Asn Trp Ile Thr Leu Lys Met Arg Lys Leu Ile Lys Ser Lys Lys
100 105 110
Asp Ile Asn Arg Glu Arg Gln Lys Ser Leu Thr Leu Thr Pro Thr Arg
115 120 125
Ser Asp Ser Ser Glu Gly Phe Leu Gln Leu Pro His Gln Asp Ser Gln
130 135 140
Asp Ser Ser Ser Val Gly Ser Asn Ser Leu Glu Asp Gly Gln Thr Leu
145 150 155 160
Gly Thr Lys Lys Ser Ser Thr Met Asn Asp Leu Val Gln Ser Met Val
165 170 175
Leu Ala Gly Gln Trp Thr Gly Ser Thr Glu Asn Leu Glu Val Pro Asp
180 185 190
Asp Ile Ser Thr Gly Lys Arg Arg Lys Glu Leu Gly Ala Met Ala Phe
195 200 205
Ser Thr Thr Ala Ile Asn Phe Ser Thr Val Asn Ser Ser Ala Gly Phe
210 215 220
Arg Ser Lys Gln Leu Val Asn Asn Lys Asp Thr Thr Ser Phe Glu Asp
225 230 235 240
Ile Ser Pro Gln Gly Val Ser Asp Asp Ser Ser Thr Gly Ser Arg Val
245 250 255
His Ala Ser Arg Pro Ala Ser Leu Asp Ser Gly Arg Thr Ser Thr Ser
260 265 270
Asn Ser Asn Asn Asn Ala Ser Leu His Glu Val Lys Ala Gly Ala Val

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        275                 280                 285
Asn Asn Gln Ser Arg Pro Gln Ser His Ser Ser Gly Glu Phe Ser Leu
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Leu His Asp His Glu Ala Trp Ser Ser Ser Gly Ser Ser Pro Ile Gln
305                 310                 315                 320
Tyr Leu Lys Arg Gln Thr Arg Ser Ser Pro Val Leu Gln His Lys Ile
                325                 330                 335
Ser Glu Thr Leu Glu Ser Arg His His Lys Ile Lys Thr Gly Ser Pro
            340                 345                 350
Gly Ser Glu Val Val Thr Leu Gln Gln Phe Leu Glu Glu Ser Asn Lys
        355                 360                 365
Leu Thr Ser Val Gln Ile Lys Ser Ser Ser Gln Glu Asn Leu Leu Asp
    370                 375                 380
Glu Val Met Lys Ser Leu Ser Val Ser Ser Asp Phe Leu Gly Lys Asp
385                 390                 395                 400
Lys Pro Val Ser Cys Gly Leu Ala Arg Ser Val Ser Gly Lys Thr Pro
                405                 410                 415
Gly Asp Phe Tyr Asp Arg Arg Thr Thr Lys Pro Glu Phe Leu Arg Pro
            420                 425                 430
Gly Pro Arg Lys Thr Glu Asp Thr Tyr Phe Ile Ser Ser Ala Gly Lys
        435                 440                 445
Pro Thr Pro Gly Thr Gln Gly Lys Ile Lys Leu Val Lys Glu Ser Ser
    450                 455                 460
Leu Ser Arg Gln Ser Lys Asp Ser Asn Pro Tyr Ala Thr Leu Pro Arg
465                 470                 475                 480
Ala Ser Ser Val Ile Ser Thr Ala Glu Gly Thr Thr Arg Arg Thr Ser
                485                 490                 495
Ile His Asp Phe Leu Thr Lys Asp Ser Arg Leu Pro Ile Ser Val Asp
            500                 505                 510
Ser Pro Pro Ala Ala Ala Asp Ser Asn Thr Thr Ala Ala Ser Asn Val
        515                 520                 525
Asp Lys Val Gln Glu Ser Arg Asn Ser Lys Ser Arg Ser Arg Glu Gln
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Gln Ser Ser
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<210> 3517
<211> 342
<212> DNA
<213> Homo sapiens

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240
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342

<210> 3518
<211> 99
<212> PRT
<213> Homo sapiens

<400> 3518
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20 25 30
Ile Val Ala Ser Phe Val Leu Ala Gly Glu Thr Glu Ala Thr Ala Leu
35 40 45
Gln Arg Met Pro Asp Arg Pro Thr Ser Arg Pro Leu Leu Val Arg Ala
50 55 60
Ser Leu Ser Pro Ser Gly Leu Gly Ala Cys Asp Thr Ala Leu Arg Pro
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Thr Arg Ser Trp Gly Ala Cys Trp Gln Trp Leu Gly His Ser Cys Ser
85 90 95
Gly Gln Gly

<210> 3519
<211> 2207
<212> DNA
<213> Homo sapiens

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<210> 3520
<211> 303
<212> PRT
<213> Homo sapiens

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Val Val Asn Leu Pro Pro Ala Gln Leu Ser Ser Ser Asp Glu Glu Thr
35 40 45
Arg Glu Glu Leu Ala Arg Ile Gly Leu Val Pro Pro Pro Glu Glu Phe
50 55 60
Ala Asn Gly Val Leu Leu Ala Thr Pro Leu Ala Gly Pro Gly Pro Ser
65 70 75 80
Pro Thr Thr Val Pro Ser Pro Ala Ser Gly Lys Pro Ser Ser Glu Pro
85 90 95
Pro Pro Ala Pro Glu Ser Ala Ala Asp Ser Gly Val Glu Glu Ala Asp
100 105 110
Thr Arg Ser Ser Ser Asp Pro His Leu Glu Thr Thr Ser Thr Ile Ser
115 120 125
Thr Val Ser Ser Met Ser Thr Leu Ser Ser Glu Ser Gly Glu Leu Thr
130 135 140
Asp Thr His Thr Ser Phe Ala Asp Gly His Thr Phe Leu Leu Glu Lys
145 150 155 160
Pro Pro Val Pro Pro Lys Pro Lys Leu Lys Ser Pro Leu Gly Lys Gly
165 170 175
Pro Val Thr Phe Arg Asp Pro Leu Leu Lys Gln Ser Ser Asp Ser Glu
180 185 190
Leu Met Ala Gln Gln His His Ala Ala Ser Ala Gly Leu Ala Ser Ala
195 200 205
Ala Gly Pro Ala Arg Pro Arg Tyr Leu Phe Gln Arg Arg Ser Lys Leu
210 215 220
Trp Gly Asp Pro Val Glu Ser Arg Gly Leu Pro Gly Pro Glu Asp Asp
225 230 235 240
Lys Pro Thr Val Ile Ser Glu Leu Ser Ser Arg Leu Gln Gln Leu Asn
245 250 255
Lys Asp Thr Arg Ser Leu Gly Glu Glu Pro Val Gly Gly Leu Gly Ser
260 265 270
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275 280 285
Leu Ser Ser Leu Gly Leu Gly Gly Trp Tyr Val Asp Ala Thr Ser
290 295 300

<210> 3521
<211> 638
<212> DNA
<213> Homo sapiens

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120
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240

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<210> 3522
<211> 181
<212> PRT
<213> Homo sapiens

<400> 3522
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Gln His Ala Asp Gln Gly Pro Pro Gly Pro His Leu Asp Leu His Gln
        35   40   45
Asp Leu Gln Ala Glu Pro Leu Arg Pro Ala Gly Leu Gly Gly Gly Leu
    50   55   60
Leu Arg Cys Gly Leu Pro Ser Glu Gln Arg Ala Ala Gly Glu Ala Arg
65   70   75   80
Gly Leu His Leu Leu Gln Asp Pro Thr Pro Gly Arg Leu Cys Gln Ala
                85   90   95
Pro Ala Gly Pro Pro Gly Gly Gly His Gly Pro Ala Gly Arg Gly Gln
            100   105   110
Pro Ser Arg His Arg Pro Gly Glu Pro Gln Gly Gly Arg Gly Gly Xaa
        115   120   125
Pro Asp Pro Ser Thr Pro Ser Val Arg Gly Ser Gln Arg Thr Ala Ser
    130   135   140
Pro Gly Arg Ala Ser Pro Gly Gly Cys Pro Glu Ala Thr Gly Trp Cys
145   150   155   160
Cys Arg His Thr Arg Ser Ala Pro Thr Pro Leu Leu Pro Pro Cys Pro
                165   170   175
Ser Pro Ala Ser Ser
            180

<210> 3523
<211> 2614
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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Gln Asp Ala Thr Asp Pro Phe Val Ala Phe His Ile Asn Lys Gly Leu
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Leu Leu Cys Ala Val Leu Leu Ser Ala Val Gln Ala Gln Ala Gly Trp
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Leu Gln His Asp Phe Gly His Leu Ser Val Phe Ser Thr Ser Lys Trp
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Asn His Leu Leu His His Phe Val Ile Gly His Leu Lys Gly Ala Pro
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Ala Ser Trp Trp Asn His Met His Phe Gln His His Ala Lys Pro Asn
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Cys Phe Arg Lys Asp Pro Asp Ile Asn Met His Pro Phe Phe Phe Ala
225                 230                 235                 240
Leu Gly Lys Ile Leu Ser Val Glu Leu Gly Lys Gln Lys Lys Lys Tyr
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Met Pro Tyr Asn His Gln His Lys Tyr Phe Phe Leu Ile Gly Pro Pro
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Ala Leu Leu Pro Leu Tyr Phe Gln Trp Tyr Ile Phe Tyr Phe Val Ile
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Gln Arg Lys Lys Trp Val Asp Leu Val Trp Met Ile Thr Phe Tyr Val
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Arg Phe Phe Leu Thr Tyr Val Pro Leu Leu Gly Leu Lys Ala Phe Leu
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Gly Leu Phe Phe Ile Val Arg Phe Leu Glu Ser Asn Trp Phe Val Trp
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Val Thr Gln Met Asn His Ile Pro Met His Ile Asp His Asp Arg Asn
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Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys Asn Val His Lys
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Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
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His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Lys Val Ala
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Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
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Lys Pro Leu Leu Ser Ala Phe Ala Asp Ile Ile His Ser Leu Lys Glu
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<213> Homo sapiens

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35 40 45
Glu Thr Phe Ile Gly Gly Gln Lys Leu Xaa Ala Asp Ala Asn Phe Ser
50 55 60
Asp Trp Ile Lys Arg Cys Gln Glu Ala Gln Asn Gly Ser Glu Ser Glu
65 70 75 80
Val Val Met Glu Pro Ala Leu Glu Gly Thr Gly Lys Glu Gly Lys Lys
85 90 95
Ala Ser Ser Arg Lys Arg Thr Leu Ala Glu Pro Pro Ala Lys Gly Leu
100 105 110
Leu Gln Pro Val Lys Leu Ser Arg Ala Glu Leu Tyr Lys Glu Pro Thr

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Ser Leu Leu Arg Leu Gln Val Glu Glu Leu Leu Lys Glu Val Arg Leu
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Ser Glu Lys Lys Lys Asp Arg Ile Asp Ala Phe Leu Arg Glu Val Asn
                165                 170                 175
Gln Arg Val Val Arg Val Pro Ser Val Pro Glu Thr Glu Leu Thr Asp
            180                 185                 190
Gln Ala Trp Leu Pro Ala Gly Val Arg Val Pro Leu His Gln Val Pro
        195                 200                 205
Tyr Ala Val Lys Gly Cys Phe Arg Phe Leu Pro Pro Ala Gln Val Thr
    210                 215                 220
Val Val Gly Ser Tyr Leu Leu Gly Thr Cys Ile Arg Pro Asp Ile Asn
225                 230                 235                 240
Val Asp Val Ala Leu Thr Met Pro Arg Glu Ile Leu Gln Asp Lys Asp
                245                 250                 255
Gly Leu Asn Gln Arg Tyr Phe Arg Lys Arg Ala Leu Tyr Leu Ala His
            260                 265                 270
Leu Ala His His Leu Ala Gln Asp Pro Leu Phe Gly Ser Val Cys Phe
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<212> DNA
<213> Homo sapiens

<400> 3527

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<213> Homo sapiens

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Val Trp Gln Glu Gly Thr Gly Gln Thr Pro Ala Lys Gln Ala Val Arg
195 200 205
Phe Arg Ala Trp Asn Gly Gln Ile Phe Glu Ala Gly Gly Gln Phe Arg
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Pro Glu Val Ser Met Asp Gly Cys Lys Val Gln Asp Gly Arg Trp His

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<212> DNA
<213> Homo sapiens

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<400> 3530
Met Ala Ser Val Ser Lys Cys Pro Ser Pro Met Pro Pro Ala Pro Trp
1 5 10 15
Thr Thr Ala Trp Arg Pro Ala Thr Leu Pro Pro Arg Ser Pro Ser His
20 25 30
Cys Xaa Ser Pro Val Ala Gly Val Ala His Arg Phe His Ser Thr Cys
35 40 45
Gly Lys Asn Val Thr Leu Glu Glu Asp Gly Thr Arg Ala Val Arg Ala
50 55 60
Ala Gly Tyr Ala His Gly Leu Val Phe Ser Thr Lys Glu Leu Arg Ala
65 70 75 80
Glu Glu Val Phe Glu Val Lys Val Glu Glu Leu Asp Glu Lys Trp Ala
85 90 95
Gly Ser Leu Arg Leu Gly Leu Thr Thr Leu Ala Pro Gly Glu Met Gly
100 105 110
Pro Gly Ala Gly Gly Gly Gly Pro Gly Leu Pro Pro Ser Leu Pro Glu
115 120 125
Leu Arg Thr Lys Thr Thr Trp Met Val Ser Ser Cys Glu Val Arg Arg
130 135 140
Asp Gly Gln Leu Gln Arg Met Asn Tyr Gly Arg Asn Leu Glu Arg Leu
145 150 155 160
Gly Val Lys Trp Leu Ala Pro Gly Thr Gly Glu Gly Leu Gly Val Glu
165 170 175
Val Ala Gly Arg Gly Gly Leu Asn Ile Val Arg Pro Cys Pro Thr Ser
180 185 190
Val Leu Gly Gly Glu Pro Cys Gly Cys Ser Ser Gly Gly Arg
195 200 205

<210> 3531
<211> 879
<212> DNA
<213> Homo sapiens

<400> 3531
nggatcctca gacttaggaa gggacgctct gaagatattt atagaattta cagccacgat
60
ggcaccgatt ctccccctga tgctgatgag gtggttatcg tcctcaacaa cttcaaaagc
120
aaaattatta aagtgaaggt tcagaagaag gcagatatgg tgaacgaaga cttgctgagt
180

gatggaacga gtgagaatga atctggattt tgggattcct tcaaatgggg ctttacagga
240
cagaagactg aggaagtgaa gcaagataaa gatgacataa ttaatatttt ctccgttgca
300
tctggtcatc tctacgaaag atttcttcgc ataatgatgc tatccgtgct gaagaatacc
360
aagactcctg tgaaattctg gttcttgaag aattacttgt cccccacatt taaggagttt
420
ataccttaca tggcaaatga atacaatttc cagtatgagc ttgttcagta caaatggccc
480
cggtggcttc atcaacaaac tgaaaaacag cgtatcatct ggggttacaa gatcctcttc
540
ctggatgtac ttttcccact agttgttgac aagttcctgt ttgtggatgc tgatcagatt
600
gtacgaacag atctgaaaga gttaagagat ttcaatttgg atggtgctcc ttatggttac
660
actcctttct gtgacagccg aagagaaatg gacggctaca ggttctggaa gtcagggtac
720
tgggccagtc atttagccgg gcgaaagtat catatcaggt actgaaaaga agcactccta
780
acactgttac ggggttttcc ttaaaattga ttttgtgtgg ttaaaattgt gaataggtaa
840
tacattggta tggttgaaaa ataaaaatga taaaaaata
879

<210> 3532
<211> 254
<212> PRT
<213> Homo sapiens

<400> 3532
Xaa Ile Leu Arg Leu Arg Lys Gly Arg Ser Glu Asp Ile Tyr Arg Ile
 1   5   10   15
Tyr Ser His Asp Gly Thr Asp Ser Pro Pro Asp Ala Asp Glu Val Val
            20   25   30
Ile Val Leu Asn Asn Phe Lys Ser Lys Ile Ile Lys Val Lys Val Gln
        35   40   45
Lys Lys Ala Asp Met Val Asn Glu Asp Leu Leu Ser Asp Gly Thr Ser
    50   55   60
Glu Asn Glu Ser Gly Phe Trp Asp Ser Phe Lys Trp Gly Phe Thr Gly
65   70   75   80
Gln Lys Thr Glu Glu Val Lys Gln Asp Lys Asp Asp Ile Ile Asn Ile
                85   90   95
Phe Ser Val Ala Ser Gly His Leu Tyr Glu Arg Phe Leu Arg Ile Met
            100   105   110
Met Leu Ser Val Leu Lys Asn Thr Lys Thr Pro Val Lys Phe Trp Phe
        115   120   125
Leu Lys Asn Tyr Leu Ser Pro Thr Phe Lys Glu Phe Ile Pro Tyr Met
    130   135   140
Ala Asn Glu Tyr Asn Phe Gln Tyr Glu Leu Val Gln Tyr Lys Trp Pro
145   150   155   160
Arg Trp Leu His Gln Gln Thr Glu Lys Gln Arg Ile Ile Trp Gly Tyr
                165   170   175
Lys Ile Leu Phe Leu Asp Val Leu Phe Pro Leu Val Val Asp Lys Phe

```
            180                 185                 190
Leu Phe Val Asp Ala Asp Gln Ile Val Arg Thr Asp Leu Lys Glu Leu
        195                 200                 205
Arg Asp Phe Asn Leu Asp Gly Ala Pro Tyr Gly Tyr Thr Pro Phe Cys
    210                 215                 220
Asp Ser Arg Arg Glu Met Asp Gly Tyr Arg Phe Trp Lys Ser Gly Tyr
225                 230                 235                 240
Trp Ala Ser His Leu Ala Gly Arg Lys Tyr His Ile Arg Tyr
                245                 250
```

<210> 3533
<211> 1151
<212> DNA
<213> Homo sapiens

<400> 3533
gaattcggca cgagggcttc tataggagag ctttagaatg aagtcattta gaggagcagg
60
cgaatcctaa ccgcatctct ctctttagct ggactgaacc caaacatgaa tgtcaacagc
120
atggacatga ccggtggctt gtcggtgaag gacccatccc agtcccagtc acgcctcccc
180
cagtggacgc accccaactc catggataac ttgcccagtg ccgcttcccc cctggagcag
240
aaccctagca agcatggtgc tatccctgga ggtctaagca ttgggcctcc aggtaagtcc
300
tccattgatg actcctatgg ccggtacgat ttaatccaga acagtgagtc accagccagt
360
cctcccgtag ctgttcccca tagctggtca cgtgccaaat ctgacagtga taaaatctca
420
aatggctcta gcatcaactg gcccccagaa ttccatccgg gagttccatg gaaaggactg
480
cagaatattg accctgagaa tgaccctgac gtcactcctg gcagtgtccc cactgggcct
540
accatcaaca ccaccatcca ggatgtcaac cgctacctcc tcaagagtgg agggtcctcc
600
ccgccatcat ctcagaatgc cacgctgcct tcttcgagtg cctggccact cagtgcctcc
660
ggctacagta gctctttcag cagcattgca tccgcaccta gtgttgcagg taaactgtca
720
gacatcaaat cgacgtggtc ctctggccct acctcccaca cgcaagcctc tctgtctcat
780
gaactatgga aggtgcccag aaacagtact gcacccacga ggccacctcc agggttaacc
840
aatcccaagc cctcctccac ctggggtgcc agccccctcg gctggaccag ctcctactcc
900
tcgggttctg cctggagcac cgacacctca ggaagaacca gcagctggct cgttcttcga
960
aacctcactc cccaggtgca atatggtgcc cctgcatcac tgagcatgat ccagggaggg
1020
ttcccgcttg gcccccaatg cagatgaggc tgtctggtgg ggcaggatag ttgggggttc
1080
ttggtcaggg tccataagtg acgctgcatg ggaggagatg agcaagtgcc aggattggct
1140

ccagcagcgg c
1151

<210> 3534
<211> 313
<212> PRT
<213> Homo sapiens

<400> 3534
Met Asn Val Asn Ser Met Asp Met Thr Gly Gly Leu Ser Val Lys Asp
1 5 10 15
Pro Ser Gln Ser Gln Ser Arg Leu Pro Gln Trp Thr His Pro Asn Ser
20 25 30
Met Asp Asn Leu Pro Ser Ala Ala Ser Pro Leu Glu Gln Asn Pro Ser
35 40 45
Lys His Gly Ala Ile Pro Gly Gly Leu Ser Ile Gly Pro Pro Gly Lys
50 55 60
Ser Ser Ile Asp Asp Ser Tyr Gly Arg Tyr Asp Leu Ile Gln Asn Ser
65 70 75 80
Glu Ser Pro Ala Ser Pro Pro Val Ala Val Pro His Ser Trp Ser Arg
85 90 95
Ala Lys Ser Asp Ser Asp Lys Ile Ser Asn Gly Ser Ser Ile Asn Trp
100 105 110
Pro Pro Glu Phe His Pro Gly Val Pro Trp Lys Gly Leu Gln Asn Ile
115 120 125
Asp Pro Glu Asn Asp Pro Asp Val Thr Pro Gly Ser Val Pro Thr Gly
130 135 140
Pro Thr Ile Asn Thr Thr Ile Gln Asp Val Asn Arg Tyr Leu Leu Lys
145 150 155 160
Ser Gly Gly Ser Ser Pro Pro Ser Ser Gln Asn Ala Thr Leu Pro Ser
165 170 175
Ser Ser Ala Trp Pro Leu Ser Ala Ser Gly Tyr Ser Ser Ser Phe Ser
180 185 190
Ser Ile Ala Ser Ala Pro Ser Val Ala Gly Lys Leu Ser Asp Ile Lys
195 200 205
Ser Thr Trp Ser Ser Gly Pro Thr Ser His Thr Gln Ala Ser Leu Ser
210 215 220
His Glu Leu Trp Lys Val Pro Arg Asn Ser Thr Ala Pro Thr Arg Pro
225 230 235 240
Pro Pro Gly Leu Thr Asn Pro Lys Pro Ser Ser Thr Trp Gly Ala Ser
245 250 255
Pro Leu Gly Trp Thr Ser Ser Tyr Ser Ser Gly Ser Ala Trp Ser Thr
260 265 270
Asp Thr Ser Gly Arg Thr Ser Ser Trp Leu Val Leu Arg Asn Leu Thr
275 280 285
Pro Gln Val Gln Tyr Gly Ala Pro Ala Ser Leu Ser Met Ile Gln Gly
290 295 300
Gly Phe Pro Leu Gly Pro Gln Cys Arg
305 310

<210> 3535
<211> 723
<212> DNA
<213> Homo sapiens

<400> 3535
tccggacaaa gctctcagta tcctgggtgc cattgtttct tctactcagc cgtgtttttt
60
ctactgagac agacaaaccc tcagcccagg acagcagagg ccgtgggagt tcaggccaac
120
cggcagacct gctacaggtt ctctctgctg gtgaccaccc accccacaac cactcaagaa
180
gcctcatcaa aacattgttg gagaaaactg ggtgcccacg gaggagaaac ggaatgcaag
240
gagattgcaa tctgtgcttt gaaccagatg cactattact aatagctgga ggaaattttg
300
aagatcagct tagagaagaa gtggtccaga gagtttctct tctccttctc tattacatta
360
ttcatcagga agagatctgt tcttcaaagc tcaacatgag taataaagag tataaatttt
420
acctacacag cctactgagc ctcaggcagg atgaagattc ctctttcctt tcacagaatg
480
agacagaaga tatcttggct ttcaccaggc agtactttga cacttctcaa agccagtgta
540
tggaaaccaa aacgctgcag aaaaaatctg gaatagtgag cagtgaaggt gctaatgaaa
600
gtacgcttcc tcagttggca gccatgatca ttactttgtc cctccagggt gtttgtctgg
660
gacaaggaaa cttgccttcc ccagactact ttacagaata tattttcagt tccttgaatc
720
gta
723

<210> 3536
<211> 163
<212> PRT
<213> Homo sapiens

<400> 3536
Met Gln Gly Asp Cys Asn Leu Cys Phe Glu Pro Asp Ala Leu Leu Leu
1 5 10 15
Ile Ala Gly Gly Asn Phe Glu Asp Gln Leu Arg Glu Glu Val Val Gln
20 25 30
Arg Val Ser Leu Leu Leu Leu Tyr Tyr Ile Ile His Gln Glu Glu Ile
35 40 45
Cys Ser Ser Lys Leu Asn Met Ser Asn Lys Glu Tyr Lys Phe Tyr Leu
50 55 60
His Ser Leu Leu Ser Leu Arg Gln Asp Glu Asp Ser Ser Phe Leu Ser
65 70 75 80
Gln Asn Glu Thr Glu Asp Ile Leu Ala Phe Thr Arg Gln Tyr Phe Asp
85 90 95
Thr Ser Gln Ser Gln Cys Met Glu Thr Lys Thr Leu Gln Lys Lys Ser
100 105 110
Gly Ile Val Ser Ser Glu Gly Ala Asn Glu Ser Thr Leu Pro Gln Leu
115 120 125
Ala Ala Met Ile Ile Thr Leu Ser Leu Gln Gly Val Cys Leu Gly Gln
130 135 140
Gly Asn Leu Pro Ser Pro Asp Tyr Phe Thr Glu Tyr Ile Phe Ser Ser

145 150 155 160
Leu Asn Arg

<210> 3537
<211> 714
<212> DNA
<213> Homo sapiens

<400> 3537
ttttttttttt ttttttttttt ttttttttttt ttttttttttt agcaatatat atatataatt
60
tatttacatt cacgcccgat aaaaccccta tgtgccccgg cggccgggca aggctgtgta
120
cataaggcca agagtaagtg cgtgaatgca cttaagacaa agtcaggaca cgagcttcac
180
atgacaggcc ccgcgtgggc gaccagccag ccctggggac gggcacgcca cgccacacac
240
acactcacca ctgtacagcc tgggactccc attgcatatt cacaggcccc gccgggcagg
300
gcacctcaag gctgggggag gggcaggggc agggaggagc cgtggggtgt ccctgggtgg
360
gtggagaggg cagcatgtga gaggcaaatg tgcaccaaca ctgggcgtga gacgtgagca
420
gcctcaggtg tacggcatga gatgtgtgtg gttggggggt gtctgcgtga cccgggaggg
480
gggtgtgtgt gagatgagca cacgaggcat gcgtggcacg tgctcgtgtg gtggtcgcgt
540
gcctgaatcc aggggctacc ccctgtccgg ctgtggccct cggtcctgca gggttggaag
600
aagggtcctt cagacgtgcc cctacccagc aggcacagaa atgtttgcat aaggtccagc
660
tcaggcagga gctctggggc cctggcccag gcccagtgtg tgcgtgcatg gcca
714

<210> 3538
<211> 154
<212> PRT
<213> Homo sapiens

<400> 3538
Met His Ala His Thr Gly Pro Gly Pro Gly Pro Gln Ser Ser Cys Leu
1 5 10 15
Ser Trp Thr Leu Cys Lys His Phe Cys Ala Cys Trp Val Gly Ala Arg
20 25 30
Leu Lys Asp Pro Ser Ser Asn Pro Ala Gly Pro Arg Ala Thr Ala Gly
35 40 45
Gln Gly Val Ala Pro Gly Phe Arg His Ala Thr Thr Thr Arg Ala Arg
50 55 60
Ala Thr His Ala Ser Cys Ala His Leu Thr His Thr Pro Leu Pro Gly
65 70 75 80
His Ala Asp Thr Pro Gln Pro His Thr Ser His Ala Val His Leu Arg
85 90 95
Leu Leu Thr Ser His Ala Gln Cys Trp Cys Thr Phe Ala Ser His Met

```
            100                 105                 110
Leu Pro Ser Pro Pro Thr Gln Gly His Pro Thr Ala Pro Pro Cys Pro
        115                 120                 125
Cys Pro Ser Pro Ser Leu Glu Val Pro Cys Pro Ala Gly Pro Val Asn
    130                 135                 140
Met Gln Trp Glu Ser Gln Ala Val Gln Trp
145                 150
```

<210> 3539
<211> 818
<212> DNA
<213> Homo sapiens

<400> 3539
ngcgcgccag gggaagttgc ccagcttggc tctggaagaa ccgagggtcg tctgattctg
60
ggcaatgggg gtgcctgtgg tcccagctgc tcgggaggct gaggcggaat tgcttgagcg
120
cgggggggcgg aggttgcagt gagccgagat cgcgcaggta cgctccagtc tgggcgacaa
180
gagcgaaact cgatatcaaa aaaaaaaaaa acgtcctgat cccagagcct cttcacgcgt
240
cccctaccac agcacttcag agaagcaggt ctttaatcag tgtgtctaga tgcagctgct
300
gactgtcacc cctaccccgc ctctctccca gtctgcggac ggccagtcac ccccattgcc
360
cagaatcaga cgaccctcgg ttcttccaga gccaagctgg gcaacttccc ctggcaagcc
420
ttcaccagta tccacggccg tgggggcggg gccctgctgg gggacagatg gatcctcact
480
gctgcccaca ccgtctaccc caaggacagt gtttctctca ggaagaacca gagtgtgaat
540
gtgttcttgg gccacacagc catagatgag atgctgaaac tggggaacca ccctgtccac
600
cgtgtcgttg tgcaccccga ctaccgtcag aatgagtccc ataactttag cggggacatc
660
gccctcctgg agctgcagca cagcatcccc ctgggcccca acgtcctccc ggtctgtctg
720
cccgataatg agaccctcta ccgcagcggc ttgttgggct acgtcagtgg gtttggcatg
780
gagatgggct ggctaactac tgagctgaag tactcgag
818

<210> 3540
<211> 180
<212> PRT
<213> Homo sapiens

<400> 3540
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Ser Val Cys Leu Asp Ala Ala Ala Asp Cys His Pro Tyr Pro Ala Ser
 1               5                  10                  15
Leu Pro Val Cys Gly Arg Pro Val Thr Pro Ile Ala Gln Asn Gln Thr
            20                  25                  30
Thr Leu Gly Ser Ser Arg Ala Lys Leu Gly Asn Phe Pro Trp Gln Ala
```

```
        35                  40                  45
Phe Thr Ser Ile His Gly Arg Gly Gly Gly Ala Leu Leu Gly Asp Arg
    50                  55                  60
Trp Ile Leu Thr Ala Ala His Thr Val Tyr Pro Lys Asp Ser Val Ser
65                  70                  75                  80
Leu Arg Lys Asn Gln Ser Val Asn Val Phe Leu Gly His Thr Ala Ile
                85                  90                  95
Asp Glu Met Leu Lys Leu Gly Asn His Pro Val His Arg Val Val Val
            100                 105                 110
His Pro Asp Tyr Arg Gln Asn Glu Ser His Asn Phe Ser Gly Asp Ile
        115                 120                 125
Ala Leu Leu Glu Leu Gln His Ser Ile Pro Leu Gly Pro Asn Val Leu
    130                 135                 140
Pro Val Cys Leu Pro Asp Asn Glu Thr Leu Tyr Arg Ser Gly Leu Leu
145                 150                 155                 160
Gly Tyr Val Ser Gly Phe Gly Met Glu Met Gly Trp Leu Thr Thr Glu
                165                 170                 175
Leu Lys Tyr Ser
            180
```

<210> 3541
<211> 722
<212> DNA
<213> Homo sapiens

<400> 3541
tctctccgac ggcgtgcagg tggccatttc aagacccgta ctaggtagat ggtcaattag
60
agttcccagg gtttgaagcc tgtaactgct gccgccgctc aagccctcca gagcattgct
120
acggctgctg cccttgtact actacctcca aatacgttct tgctggtagt ggcggcagca
180
ggaccaatta cctcttttttt gctctccctc gagaagctcc agatggcgtc ttccgtgggc
240
aacgtggccg acagcacaga accaacgaaa cgtatgcttt ccttccaagg gttagctgag
300
ttggcacatc gagaatatca ggcaggagat tttgaggcag ctgagagaca ctgcatgcag
360
ctctggagac aagagccaga caatactggt gtgcttttat tactttcatc tatacacttc
420
cagtgtcgaa ggctggacag atctgctcac tttagcactc tggcaattaa acagaacccc
480
cttctggcag aagcttattc gaatttgggg aatgtgtaca aggaaagagg gcagttgcag
540
gaggcaattg agcattatcg acatgcattg cgtctcaaac ctgatttcat cgatggttat
600
attaacgctg cagccgcctt ggtagcagcg ggtgacatgg aaggggcagt acaagcttac
660
gtctctgcac tccagcctgg gtgacaaagt gaggccctgt ctcaaaaaaa aaaaaaaaaa
720
aa
722

<210> 3542

<211> 153
<212> PRT
<213> Homo sapiens

<400> 3542
Met Ala Ser Ser Val Gly Asn Val Ala Asp Ser Thr Glu Pro Thr Lys
1 5 10 15
Arg Met Leu Ser Phe Gln Gly Leu Ala Glu Leu Ala His Arg Glu Tyr
20 25 30
Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His Cys Met Gln Leu Trp
35 40 45
Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu Leu Leu Ser Ser Ile
50 55 60
His Phe Gln Cys Arg Arg Leu Asp Arg Ser Ala His Phe Ser Thr Leu
65 70 75 80
Ala Ile Lys Gln Asn Pro Leu Leu Ala Glu Ala Tyr Ser Asn Leu Gly
85 90 95
Asn Val Tyr Lys Glu Arg Gly Gln Leu Gln Glu Ala Ile Glu His Tyr
100 105 110
Arg His Ala Leu Arg Leu Lys Pro Asp Phe Ile Asp Gly Tyr Ile Asn
115 120 125
Ala Ala Ala Ala Leu Val Ala Ala Gly Asp Met Glu Gly Ala Val Gln
130 135 140
Ala Tyr Val Ser Ala Leu Gln Pro Gly
145 150

<210> 3543
<211> 1206
<212> DNA
<213> Homo sapiens

<400> 3543
nntcagagtt ttgagttaag agctcaccat ttaatataca aattagtatg tcagaatctc
60
cagctaatga aagtatttta tgaatgctgt ccttaagacc gagtaacagc attgtgttca
120
gtttggttgt tgctcaggat gtgtaatagt ttctcttcag ccataagcca cgcctggtag
180
atattaattg agtggagaga tcttgcacct cttccagtta tgcatttgtg gtttgtcgtc
240
tgatttggag cacttggaag atcactgttt tgtgttctac gacccaattg agaggattat
300
gtggagctaa gttttaccaa tcaggatcat ccttccttgt gggttagcag gcagttataa
360
gattgcaaaa tgggtctccg gattcacttt gttgttgacc cacatggttg gtgctgcatg
420
ggtttgattg tctttgtttg gttatacaat attgttttaa ttcccaaaat tgtcctcttt
480
cctcactatg aagaaggaca tattccaggc atattaataa taatattcta tggcatttcc
540
atattctgtc tggttgcctt agtgagggcc tccataactg atccaggaag actccctgag
600
aaccccaaga tcccacatgg agaaagggag ttctgggaat tatgtaacaa gtgtaatttg
660

atgagaccaa agcgttccca tcactgtagc cgctgcggcc actgtgtgag gagaatggat
720
catcactgtc catggattaa caattgtgtt ggtgaagata atcattggct ctttctgcag
780
ttgtgtttct acactgaact tcttacttgc tacgcactga tgttttcttt ctgccactat
840
tactattttc ttccactaaa aaagcgtaat ttggacctct ttgtttttag acatgaattg
900
gccataatga gactagcagc ctttatgggc attactatgt tagttggaat aactggactc
960
ttttacactc aactaattgg catcatcaca ccttgcagtc tcatcctact caagtgtggc
1020
tctgtatcca acaacagtct tggagatctc atgaagattt ctgaaacttt tgctctgagg
1080
ataccttcct ttgtggttat gtgccctgaa aactccagcc tccgtgtctt caattcagtg
1140
aaactactac tctgcttgga ttccccctctt atacaatggt ctaccaagtg actgcaaaca
1200
gaaatc
1206

<210> 3544
<211> 273
<212> PRT
<213> Homo sapiens

<400> 3544
Met Gly Leu Arg Ile His Phe Val Val Asp Pro His Gly Trp Cys Cys
 1   5   10   15
Met Gly Leu Ile Val Phe Val Trp Leu Tyr Asn Ile Val Leu Ile Pro
            20   25   30
Lys Ile Val Leu Phe Pro His Tyr Glu Glu Gly His Ile Pro Gly Ile
        35   40   45
Leu Ile Ile Ile Phe Tyr Gly Ile Ser Ile Phe Cys Leu Val Ala Leu
    50   55   60
Val Arg Ala Ser Ile Thr Asp Pro Gly Arg Leu Pro Glu Asn Pro Lys
65   70   75   80
Ile Pro His Gly Glu Arg Glu Phe Trp Glu Leu Cys Asn Lys Cys Asn
                85   90   95
Leu Met Arg Pro Lys Arg Ser His His Cys Ser Arg Cys Gly His Cys
            100   105   110
Val Arg Arg Met Asp His His Cys Pro Trp Ile Asn Asn Cys Val Gly
        115   120   125
Glu Asp Asn His Trp Leu Phe Leu Gln Leu Cys Phe Tyr Thr Glu Leu
    130   135   140
Leu Thr Cys Tyr Ala Leu Met Phe Ser Phe Cys His Tyr Tyr Tyr Phe
145   150   155   160
Leu Pro Leu Lys Lys Arg Asn Leu Asp Leu Phe Val Phe Arg His Glu
                165   170   175
Leu Ala Ile Met Arg Leu Ala Ala Phe Met Gly Ile Thr Met Leu Val
            180   185   190
Gly Ile Thr Gly Leu Phe Tyr Thr Gln Leu Ile Gly Ile Ile Thr Pro
        195   200   205
Cys Ser Leu Ile Leu Leu Lys Cys Gly Ser Val Ser Asn Asn Ser Leu

```
    210                 215                 220
Gly Asp Leu Met Lys Ile Ser Glu Thr Phe Ala Leu Arg Ile Pro Ser
225                 230                 235                 240
Phe Val Val Met Cys Pro Glu Asn Ser Ser Leu Arg Val Phe Asn Ser
                245                 250                 255
Val Lys Leu Leu Leu Cys Leu Asp Ser Pro Leu Ile Gln Trp Ser Thr
            260                 265                 270
Lys
```

<210> 3545
<211> 3657
<212> DNA
<213> Homo sapiens

<400> 3545
cctaggctgt tggagactga gtgagtgaat gtgtggagag tactaggctt ggcacaggcc
60
agagcaggtg ctcaggaggt ctggcccatc atctggctcc ggctgaccct tgccctcacc
120
ctggcagacc ctggctgggc atccatcagc aggggtgtgc tggtgtgtga cgagtgctgc
180
agcgtgcacc ggagcctggg acgccacatc tccattgtca agcaccttcg ccacagcgcc
240
tggcctccca cgctgctgca gatggtgcac acgcttgcca gcaacggggc caactccatc
300
tgggagcact ccctgctgga ccccgcacaa gtgcagagcg gccggcgtaa agccaacccc
360
caagacaaag tccaccccat caagtcagag ttcatcaggg ccaagtacca gatgctggca
420
tttgtgcaca agcttccctg ccgggacgat gatggagtca ccgccaaaga cctcagcaag
480
caactacact cgagcgtgcg gacaggcaac ctggagacat gtctgcgcct gctctccctg
540
ggtgcccagg ccaacttctt ccacccagag aagggcacca cacctctgca cgtggctgcc
600
aaggcaggac agacactgca ggccgagctg cttgtagtgt atggggctga ccctggctcc
660
cctgatgtta atggccgcac acccattgac tatgccaggc aggcggggca ccatgagctg
720
gcggaaaggc tggttgagtg ccaatatgag ctcactgacc ggctggcctt ctacctctgt
780
ggacgcaagc cggatcacaa gaatgggcat tacatcatcc cacagatggc tgacagatct
840
cggcaaaagt gcatgtctca gagccttgac ttatccgaat tggccaaagc tgctaagaag
900
aagctgcagg cgctcagcaa ccggcttttt gaggaactcg ccatggacgt gtatgacgag
960
gtggatcgaa gagaaaatga tgcagtgtgg ctggctaccc aaaaccacag cactctggtg
1020
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<210> 3546
<211> 792
<212> PRT
<213> Homo sapiens

<400> 3546
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Leu Ala Asp Pro Gly Trp Ala Ser Ile Ser Arg Gly Val Leu Val Cys
35 40 45
Asp Glu Cys Cys Ser Val His Arg Ser Leu Gly Arg His Ile Ser Ile
50 55 60
Val Lys His Leu Arg His Ser Ala Trp Pro Pro Thr Leu Leu Gln Met
65 70 75 80
Val His Thr Leu Ala Ser Asn Gly Ala Asn Ser Ile Trp Glu His Ser
85 90 95
Leu Leu Asp Pro Ala Gln Val Gln Ser Gly Arg Arg Lys Ala Asn Pro
100 105 110
Gln Asp Lys Val His Pro Ile Lys Ser Glu Phe Ile Arg Ala Lys Tyr
115 120 125
Gln Met Leu Ala Phe Val His Lys Leu Pro Cys Arg Asp Asp Asp Gly

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Val Thr Ala Lys Asp Leu Ser Lys Gln Leu His Ser Ser Val Arg Thr
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Gly Asn Leu Glu Thr Cys Leu Arg Leu Leu Ser Leu Gly Ala Gln Ala
                165                 170                 175
Asn Phe Phe His Pro Glu Lys Gly Thr Thr Pro Leu His Val Ala Ala
            180                 185                 190
Lys Ala Gly Gln Thr Leu Gln Ala Glu Leu Leu Val Val Tyr Gly Ala
        195                 200                 205
Asp Pro Gly Ser Pro Asp Val Asn Gly Arg Thr Pro Ile Asp Tyr Ala
    210                 215                 220
Arg Gln Ala Gly His His Glu Leu Ala Glu Arg Leu Val Glu Cys Gln
225                 230                 235                 240
Tyr Glu Leu Thr Asp Arg Leu Ala Phe Tyr Leu Cys Gly Arg Lys Pro
                245                 250                 255
Asp His Lys Asn Gly His Tyr Ile Ile Pro Gln Met Ala Asp Arg Ser
            260                 265                 270
Arg Gln Lys Cys Met Ser Gln Ser Leu Asp Leu Ser Glu Leu Ala Lys
        275                 280                 285
Ala Ala Lys Lys Lys Leu Gln Ala Leu Ser Asn Arg Leu Phe Glu Glu
    290                 295                 300
Leu Ala Met Asp Val Tyr Asp Glu Val Asp Arg Arg Glu Asn Asp Ala
305                 310                 315                 320
Val Trp Leu Ala Thr Gln Asn His Ser Thr Leu Val Thr Glu Arg Ser
                325                 330                 335
Ala Val Pro Phe Leu Pro Val Asn Pro Glu Tyr Ser Ala Thr Arg Asn
            340                 345                 350
Gln Gly Arg Gln Lys Leu Ala Arg Phe Asn Ala Arg Glu Phe Ala Thr
        355                 360                 365
Leu Ile Ile Asp Ile Leu Ser Glu Ala Lys Arg Arg Gln Gln Gly Lys
    370                 375                 380
Ser Leu Ser Ser Pro Thr Asp Asn Leu Glu Leu Ser Leu Arg Ser Gln
385                 390                 395                 400
Ser Asp Leu Asp Asp Gln His Asp Tyr Asp Ser Val Ala Ser Asp Glu
                405                 410                 415
Asp Thr Asp Gln Glu Pro Leu Arg Ser Thr Gly Ala Thr Arg Ser Asn
            420                 425                 430
Arg Ala Arg Ser Met Asp Ser Ser Asp Leu Ser Asp Gly Ala Val Thr
        435                 440                 445
Leu Gln Glu Tyr Leu Glu Leu Lys Lys Ala Leu Ala Thr Ser Glu Ala
    450                 455                 460
Lys Val Gln Gln Leu Met Lys Val Asn Ser Ser Leu Ser Asp Glu Leu
465                 470                 475                 480
Arg Arg Leu Gln Arg Glu His Phe Ala Pro Ile Ile His Lys Leu Gln
                485                 490                 495
Ala Glu Asn Leu Gln Leu Arg Gln Pro Pro Gly Pro Val Pro Thr Pro
            500                 505                 510
Pro Leu Pro Ser Glu Arg Ala Glu His Thr Pro Met Ala Pro Gly Gly
        515                 520                 525
Ser Thr His Arg Arg Asp Arg Gln Ala Phe Ser Met Tyr Glu Pro Gly
    530                 535                 540
Ser Ala Leu Lys Pro Phe Gly Gly Pro Pro Gly Asp Glu Leu Thr Thr
545                 550                 555                 560
Arg Leu Gln Pro Phe His Ser Thr Glu Leu Glu Asp Asp Ala Ile Tyr
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565 570 575
Ser Val His Val Pro Ala Gly Leu Tyr Arg Ile Arg Lys Gly Val Ser
580 585 590
Ala Ser Ala Val Pro Phe Thr Pro Ser Ser Pro Leu Leu Ser Cys Ser
595 600 605
Gln Glu Gly Ser Arg His Thr Ser Lys Leu Ser Arg His Gly Ser Gly
610 615 620
Ala Asp Ser Asp Tyr Glu Asn Thr Gln Ser Gly Asp Pro Leu Leu Gly
625 630 635 640
Leu Glu Gly Lys Arg Phe Leu Glu Leu Gly Lys Glu Glu Asp Phe His
645 650 655
Pro Glu Leu Glu Ser Leu Asp Gly Asp Leu Asp Pro Gly Leu Pro Ser
660 665 670
Thr Glu Asp Val Ile Leu Lys Thr Glu Gln Val Thr Lys Asn Ile Gln
675 680 685
Glu Leu Leu Arg Ala Ala Gln Glu Phe Lys His Asp Ser Phe Val Pro
690 695 700
Cys Ser Glu Lys Ile His Leu Ala Val Thr Glu Met Ala Ser Leu Phe
705 710 715 720
Pro Lys Arg Pro Ala Leu Glu Pro Val Arg Ser Ser Leu Arg Leu Leu
725 730 735
Asn Ala Ser Ala Tyr Arg Leu Gln Ser Glu Cys Arg Lys Thr Val Pro
740 745 750
Pro Glu Pro Gly Ala Pro Val Asp Phe Gln Leu Leu Thr Gln Gln Val
755 760 765
Ile Gln Cys Ala Tyr Asp Ile Ala Lys Ala Ala Lys Gln Leu Val Thr
770 775 780
Ile Thr Thr Arg Glu Lys Lys Gln
785 790

<210> 3547
<211> 1039
<212> DNA
<213> Homo sapiens

<400> 3547
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gaaggtggag tgtttacttt tggagctgga gggtatggtc agttgggcca taattctacc
120
agtcatgaaa taaacccaag gaaagttttt gaacttatgg gaagcattgt cactgagatt
180
gcttgtggac ggcagcacac ttctgctttt gttccttcat caggacgaat ttactctttt
240
gggcttggtg gtaatgggca gctgggaacc ggttcaacaa gcaacaggaa aagccccttt
300
actgtaaaag gaaattggta cccctataat gggcagtgtc taccagatat tgattctgaa
360
gaatatttct gtgtaaaaag aattttctca gggggagatc aaagcttttc acattactct
420
agtccccaga actgtgggcc accagatgac ttcagatgtc ccaatccgac aaagcagatc
480
tggacagtga atgaagctct aattcagaaa tggctgagct atccttctgg aaggtttcct
540

gtggagatag ccaatgagat agatggaacg ttttcttcct ctggttgcct aaatggaagt
600
tttttagctg ttagcaatga tgatcactat agaacaggta ccagattttc aggggttgat
660
atgaatgctg ctaggctttt attccacaaa cttatacaac ctgatcatcc gcagatatct
720
cagcaggtgg cagctagttt ggaaaagaat cttattccta aactgactag ctccttacct
780
gatgttgaag cattgaggtt ttatcttact ctaccagaat gtcccctgat gagtgattcc
840
aacaatttca taacaatagc aattcccttt ggtacagctc ttgtgaacct agaaaaggca
900
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1039

<210> 3548
<211> 346
<212> PRT
<213> Homo sapiens

<400> 3548
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Ala Leu Thr Lys Glu Gly Gly Val Phe Thr Phe Gly Ala Gly Gly Tyr
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Gly Gln Leu Gly His Asn Ser Thr Ser His Glu Ile Asn Pro Arg Lys
35 40 45
Val Phe Glu Leu Met Gly Ser Ile Val Thr Glu Ile Ala Cys Gly Arg
50 55 60
Gln His Thr Ser Ala Phe Val Pro Ser Ser Gly Arg Ile Tyr Ser Phe
65 70 75 80
Gly Leu Gly Gly Asn Gly Gln Leu Gly Thr Gly Ser Thr Ser Asn Arg
85 90 95
Lys Ser Pro Phe Thr Val Lys Gly Asn Trp Tyr Pro Tyr Asn Gly Gln
100 105 110
Cys Leu Pro Asp Ile Asp Ser Glu Glu Tyr Phe Cys Val Lys Arg Ile
115 120 125
Phe Ser Gly Gly Asp Gln Ser Phe Ser His Tyr Ser Ser Pro Gln Asn
130 135 140
Cys Gly Pro Pro Asp Asp Phe Arg Cys Pro Asn Pro Thr Lys Gln Ile
145 150 155 160
Trp Thr Val Asn Glu Ala Leu Ile Gln Lys Trp Leu Ser Tyr Pro Ser
165 170 175
Gly Arg Phe Pro Val Glu Ile Ala Asn Glu Ile Asp Gly Thr Phe Ser
180 185 190
Ser Ser Gly Cys Leu Asn Gly Ser Phe Leu Ala Val Ser Asn Asp Asp
195 200 205
His Tyr Arg Thr Gly Thr Arg Phe Ser Gly Val Asp Met Asn Ala Ala
210 215 220
Arg Leu Leu Phe His Lys Leu Ile Gln Pro Asp His Pro Gln Ile Ser

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225                 230                 235                 240
Gln Gln Val Ala Ala Ser Leu Glu Lys Asn Leu Ile Pro Lys Leu Thr
                245                 250                 255
Ser Ser Leu Pro Asp Val Glu Ala Leu Arg Phe Tyr Leu Thr Leu Pro
            260                 265                 270
Glu Cys Pro Leu Met Ser Asp Ser Asn Asn Phe Ile Thr Ile Ala Ile
        275                 280                 285
Pro Phe Gly Thr Ala Leu Val Asn Leu Glu Lys Ala Pro Leu Lys Val
    290                 295                 300
Leu Glu Asn Trp Trp Ser Val Leu Glu Pro Pro Leu Phe Leu Lys Ile
305                 310                 315                 320
Val Glu Leu Phe Lys Glu Val Val Val His Leu Leu Lys Leu Tyr Lys
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Ile Gly Ile Pro Pro Ser Glu Arg Ile Ile
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<210> 3549
<211> 2542
<212> DNA
<213> Homo sapiens

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agatatgaga aaattcatgg aagaagtaag gaaaaggaga gagctagtct agataaaaaa
180
agagataaag actacagaag gaaagagatc ttgccttttg aaaagatgaa ggaacaaagg
240
ttgagagaac atttagttcg ttttgaaagg ctgcgacgag caatggaact tcgaagacga
300
agagagattg cagagagaga gcgtcgagag cgagaacgca ttagaataat tcgtgaacgg
360
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420
gagagagaga gaatggaacg cgaacgcttg gaaagggaac gcattcgtat tgaacaggaa
480
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cagcttcgtt atgaacaaga aaaaaggaat tccttgaaac gcccacgtga tgtagatcat
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660
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720
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780
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840
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900
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960

acggtgatta ttcatgacag gcctgatatc actcatccta gacatcctcg agaggcaggg
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gaaacaagag ttgaaaggcc agaacgatct gggagagaag tatcagggca cagtgtgaga
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2160
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2280
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2340
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2520
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2542

<210> 3550
<211> 500
<212> PRT
<213> Homo sapiens

<400> 3550
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His Cys Arg Pro Ser Arg Arg Gly Arg Tyr Glu Lys Ile His Gly Arg
35 40 45
Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp Lys Lys Arg Asp Lys Asp
50 55 60
Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu Lys Met Lys Glu Gln Arg
65 70 75 80
Leu Arg Glu His Leu Val Arg Phe Glu Arg Leu Arg Arg Ala Met Glu
85 90 95
Leu Arg Arg Arg Arg Glu Ile Ala Glu Arg Glu Arg Arg Glu Arg Glu
100 105 110
Arg Ile Arg Ile Ile Arg Glu Arg Glu Glu Arg Glu Arg Leu Gln Arg
115 120 125
Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln Lys Leu Glu Arg Glu Arg
130 135 140
Met Glu Arg Glu Arg Leu Glu Arg Glu Arg Ile Arg Ile Glu Gln Glu
145 150 155 160
Arg Arg Lys Glu Ala Glu Arg Ile Ala Arg Glu Arg Glu Glu Leu Arg
165 170 175
Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln Glu Lys Arg Asn Ser Leu
180 185 190
Lys Arg Pro Arg Asp Val Asp His Arg Arg Asp Asp Pro Tyr Trp Ser
195 200 205
Glu Asn Lys Lys Leu Ser Leu Asp Thr Asp Ala Arg Phe Gly His Gly
210 215 220
Ser Asp Tyr Ser Arg Gln Gln Asn Arg Phe Asn Asp Phe Asp His Arg
225 230 235 240
Glu Arg Gly Arg Phe Pro Glu Ser Ser Ala Val Gln Ser Ser Ser Phe
245 250 255
Glu Arg Arg Asp Arg Phe Val Gly Gln Ser Glu Gly Lys Lys Ala Arg
260 265 270
Pro Thr Ala Arg Arg Glu Asp Pro Ser Phe Glu Arg Tyr Pro Lys Asn
275 280 285
Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro Pro Pro Arg Asn Glu Leu
290 295 300
Arg Glu Ser Asp Arg Arg Glu Val Arg Gly Glu Arg Asp Glu Arg Arg
305 310 315 320
Thr Val Ile Ile His Asp Arg Pro Asp Ile Thr His Pro Arg His Pro
325 330 335
Arg Glu Ala Gly Pro Asn Pro Ser Arg Pro Thr Ser Trp Lys Ser Asp
340 345 350
Gly Ser Met Ser Thr Asp Lys Arg Glu Thr Arg Val Glu Arg Pro Glu
355 360 365
Arg Ser Gly Arg Glu Val Ser Gly His Ser Val Arg Gly Ala Pro Pro

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    370                 375                 380
Gly Asn Arg Ser Ser Ala Ser Gly Tyr Gly Ser Arg Glu Gly Asp Arg
385                 390                 395                 400
Gly Val Ile Thr Asp Arg Gly Gly Gly Ser Gln His Tyr Pro Glu Glu
                405                 410                 415
Arg His Val Val Glu Arg His Gly Arg Asp Thr Ser Gly Pro Arg Lys
            420                 425                 430
Glu Trp His Gly Pro Pro Ser Gln Gly Pro Ser Tyr His Asp Thr Arg
        435                 440                 445
Arg Met Gly Asp Gly Arg Ala Gly Ala Gly Met Ile Thr Gln His Ser
    450                 455                 460
Ser Asn Ala Ser Pro Ile Asn Arg Ile Val Gln Ile Ser Gly Asn Ser
465                 470                 475                 480
Met Pro Arg Gly Ser Gly Ser Gly Phe Lys Pro Phe Lys Gly Gly Pro
                485                 490                 495
Pro Arg Arg Phe
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<210> 3551
<211> 545
<212> DNA
<213> Homo sapiens

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120
tttcttgtga ctggctataa attccatgca gtgctggaat gtgcttctca cagttagagt
180
gctgagcacc tgttttattt cacactccct tgattcctgg ggtaaatccc atctccgcag
240
catgggctcc agttaaattc attagtggtc cagatgtgtg tcccctgtca gctggccaag
300
taaccccact gtttatcgac aggttctcag gaatcagata gctcgcagtc ggccaagaag
360
gacatgctgg ctgccttgaa gtccaggcag gaagctctgg aggaaaccct gcgtcagagg
420
ctggaggaac tgaagaagct gtgtctccga gaagctgtaa gcctttccta gctcatcccg
480
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540
gtcat
545

<210> 3552
<211> 55
<212> PRT
<213> Homo sapiens

<400> 3552
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Ala Lys Lys Asp Met Leu Ala Ala Leu Lys Ser Arg Gln Glu Ala Leu
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Glu Glu Thr Leu Arg Gln Arg Leu Glu Glu Leu Lys Lys Leu Cys Leu
35 40 45
Arg Glu Ala Val Ser Leu Ser
50 55

<210> 3553
<211> 1412
<212> DNA
<213> Homo sapiens

<400> 3553
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120
gatgaccagc tcaacatcct gcccatctcc tcccacgttg ccaccatgga ggccctgcct
180
ccccagactc cggatgagag tcttggtcct tctgatctgg agctgaggga gttgaaggag
240
agcttgcagg acacccagcc tgtgggtgtg ttggtggact gctgtaagac tctagaccag
300
gccaaagctg tcttgaaatt tatcgagggc atctctgaaa agaccctgag gagtactgtt
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420
gcggtggcat ttgggtactc caatatcttt gttacctccc caagccctga taacctccat
480
actctgtttg aatttgtatt taaaggattt gatgctctgc aatatcagga acatctggat
540
tatgagatta tccagtctct aaatcctgaa tttaacaaag cagtgatcat agtgaatgta
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caggctgaac tagttgtgat tgatgaagct gccgccatcc ccctcccctt ggtgaagagc
720
ctacttggcc cctaccttgt tttcatggca tccaccatca atggctatga gggcactggc
780
cggtcactgt ccctcaagct aattcagcag ctccgtcaac agagcgccca gagccaggtc
840
agcaccactg ctgagaataa gaccacgacg acagccagat tggcatcagc gcggacactg
900
catgaggttt ccctccagga gtcaatccga tacgcccctg gggatgcagt ggagaagtgg
960
ctgaatgact tgctgtgcct ggattgcctc aacatcactc ggatagtctc aggctgcccc
1020
ttgcctgaag cttgtgaact gtactatgtt aatagagata ccctcttttg ctaccacaag
1080
gcctctgaag ttttcctcca acggcttatg gccctctacg tggcttctca ctacaagaac
1140
tctcccaatg atctccagat gctctccgat gcaccttctc accatctctt ctgccttctg
1200
cctcctgtgc cccccaccca gaatgccctt ccaaaagtgc ttgctgttat ccaggtatag
1260

gaacagaggc gtccttgtgg cagtgatttg gggaaccact gaggcatcag gaattagtgg
1320
cttaataact gcattgtggg agttttgaaa ctgtggagtc ctggtctgga accaaggggc
1380
tgggtctgct gagacaggtg actagggtgc ac
1412

<210> 3554
<211> 419
<212> PRT
<213> Homo sapiens

<400> 3554
Tyr Thr Val Thr Met Asp Val His Ser Arg Tyr Arg Thr Glu Ala His
1 5 10 15
Gln Asp Val Val Gly Arg Phe Asn Glu Arg Phe Ile Leu Ser Leu Ala
20 25 30
Ser Cys Lys Lys Cys Leu Val Ile Asp Asp Gln Leu Asn Ile Leu Pro
35 40 45
Ile Ser Ser His Val Ala Thr Met Glu Ala Leu Pro Pro Gln Thr Pro
50 55 60
Asp Glu Ser Leu Gly Pro Ser Asp Leu Glu Leu Arg Glu Leu Lys Glu
65 70 75 80
Ser Leu Gln Asp Thr Gln Pro Val Gly Val Leu Val Asp Cys Cys Lys
85 90 95
Thr Leu Asp Gln Ala Lys Ala Val Leu Lys Phe Ile Glu Gly Ile Ser
100 105 110
Glu Lys Thr Leu Arg Ser Thr Val Ala Leu Thr Ala Ala Arg Gly Arg
115 120 125
Gly Lys Ser Ala Ala Leu Gly Leu Ala Ile Ala Gly Ala Val Ala Phe
130 135 140
Gly Tyr Ser Asn Ile Phe Val Thr Ser Pro Ser Pro Asp Asn Leu His
145 150 155 160
Thr Leu Phe Glu Phe Val Phe Lys Gly Phe Asp Ala Leu Gln Tyr Gln
165 170 175
Glu His Leu Asp Tyr Glu Ile Ile Gln Ser Leu Asn Pro Glu Phe Asn
180 185 190
Lys Ala Val Ile Ile Val Asn Val Phe Arg Glu His Arg Gln Thr Ile
195 200 205
Gln Tyr Ile His Pro Ala Asp Ala Val Lys Leu Gly Gln Ala Glu Leu
210 215 220
Val Val Ile Asp Glu Ala Ala Ala Ile Pro Leu Pro Leu Val Lys Ser
225 230 235 240
Leu Leu Gly Pro Tyr Leu Val Phe Met Ala Ser Thr Ile Asn Gly Tyr
245 250 255
Glu Gly Thr Gly Arg Ser Leu Ser Leu Lys Leu Ile Gln Gln Leu Arg
260 265 270
Gln Gln Ser Ala Gln Ser Gln Val Ser Thr Thr Ala Glu Asn Lys Thr
275 280 285
Thr Thr Thr Ala Arg Leu Ala Ser Ala Arg Thr Leu His Glu Val Ser
290 295 300
Leu Gln Glu Ser Ile Arg Tyr Ala Pro Gly Asp Ala Val Glu Lys Trp
305 310 315 320
Leu Asn Asp Leu Leu Cys Leu Asp Cys Leu Asn Ile Thr Arg Ile Val

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                325                 330                 335
Ser Gly Cys Pro Leu Pro Glu Ala Cys Glu Leu Tyr Tyr Val Asn Arg
            340                 345                 350
Asp Thr Leu Phe Cys Tyr His Lys Ala Ser Glu Val Phe Leu Gln Arg
        355                 360                 365
Leu Met Ala Leu Tyr Val Ala Ser His Tyr Lys Asn Ser Pro Asn Asp
    370                 375                 380
Leu Gln Met Leu Ser Asp Ala Pro Ser His His Leu Phe Cys Leu Leu
385                 390                 395                 400
Pro Pro Val Pro Pro Thr Gln Asn Ala Leu Pro Lys Val Leu Ala Val
                405                 410                 415
Ile Gln Val
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<210> 3555
<211> 1038
<212> DNA
<213> Homo sapiens

<400> 3555
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ctggtggggt cggaccaggc cccgggccgg gacaagaaca tccccgccgg gctgcagtcc
120
atgaaccagg cgttgcagag gcgcttcgcc aaggggggtgc agtacaacat gaagatagtg
180
atccggggag acaggaacac gggcaagaca gcgctgtggc accgcctgca gggccggccg
240
ttcgtggagg agtacatccc cacacaggag atccaggtca ccagcatcca ctggagctac
300
aagaccacgg atgacatcgt gaaggttgaa gtctgggatg tagtagacaa aggaaaatgc
360
aaaaagcgag gcgacggctt aaagatggag aacgaccccc aggaggcgga gtctgaaatg
420
gccctggatg ctgagttcct ggacgtgtac aagaactgca acggggtggt catgatgttc
480
gacattacca agcagtggac cttcaattac attctccggg agcttccaaa agtgcccacc
540
cacgtgccag tgtgcgtgct ggggaactac cgggacatgg gcgagcaccg agtcatcnnc
600
tgccggacgn acgtgcgtga cttcatcgac aacctggaca gacctccagg ttcctcctac
660
ttccgctatg ctgagtcttc catgaagaac agcttcggcc taaagtacct tcataagttc
720
ttcaatatcc catttttgca gcttcagagg gagacgctgt tgcggcagct ggagacgaac
780
cagctggaca tggacgccac gctggaggag ctgtcggtgc agcaggagac ggaggaccag
840
aactacggca tcttcctgga gatgatggag gctcgcagcc gtggccatgc gtccccactg
900
gcggccaacg ggcagagccc atccccgggc tcccagtcac cagtggtgcc tgcaggcgct
960
gtgtccacgg ggagctccag ccccggcaca gcccagcccg ccccacagct gcccctcaat
1020

ggttgcccca ccatcctc
1038

<210> 3556
<211> 333
<212> PRT
<213> Homo sapiens

<400> 3556
Met Phe Ser Ala Leu Lys Lys Leu Val Gly Ser Asp Gln Ala Pro Gly
1 5 10 15
Arg Asp Lys Asn Ile Pro Ala Gly Leu Gln Ser Met Asn Gln Ala Leu
20 25 30
Gln Arg Arg Phe Ala Lys Gly Val Gln Tyr Asn Met Lys Ile Val Ile
35 40 45
Arg Gly Asp Arg Asn Thr Gly Lys Thr Ala Leu Trp His Arg Leu Gln
50 55 60
Gly Arg Pro Phe Val Glu Glu Tyr Ile Pro Thr Gln Glu Ile Gln Val
65 70 75 80
Thr Ser Ile His Trp Ser Tyr Lys Thr Thr Asp Asp Ile Val Lys Val
85 90 95
Glu Val Trp Asp Val Val Asp Lys Gly Lys Cys Lys Lys Arg Gly Asp
100 105 110
Gly Leu Lys Met Glu Asn Asp Pro Gln Glu Ala Glu Ser Glu Met Ala
115 120 125
Leu Asp Ala Glu Phe Leu Asp Val Tyr Lys Asn Cys Asn Gly Val Val
130 135 140
Met Met Phe Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg
145 150 155 160
Glu Leu Pro Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn
165 170 175
Tyr Arg Asp Met Gly Glu His Arg Val Ile Xaa Cys Arg Thr Xaa Val
180 185 190
Arg Asp Phe Ile Asp Asn Leu Asp Arg Pro Pro Gly Ser Ser Tyr Phe
195 200 205
Arg Tyr Ala Glu Ser Ser Met Lys Asn Ser Phe Gly Leu Lys Tyr Leu
210 215 220
His Lys Phe Phe Asn Ile Pro Phe Leu Gln Leu Gln Arg Glu Thr Leu
225 230 235 240
Leu Arg Gln Leu Glu Thr Asn Gln Leu Asp Met Asp Ala Thr Leu Glu
245 250 255
Glu Leu Ser Val Gln Gln Glu Thr Glu Asp Gln Asn Tyr Gly Ile Phe
260 265 270
Leu Glu Met Met Glu Ala Arg Ser Arg Gly His Ala Ser Pro Leu Ala
275 280 285
Ala Asn Gly Gln Ser Pro Ser Pro Gly Ser Gln Ser Pro Val Val Pro
290 295 300
Ala Gly Ala Val Ser Thr Gly Ser Ser Ser Pro Gly Thr Ala Gln Pro
305 310 315 320
Ala Pro Gln Leu Pro Leu Asn Gly Cys Pro Thr Ile Leu
325 330

<210> 3557
<211> 486

<212> DNA
<213> Homo sapiens

<400> 3557
tcagtgacaa ggaggacgtt tgggcacagc ggcattgcag tgcacacgtg gtatgcatgt
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ccggcattga tcaagtccat ctgggctatg gccataagcc aacaccagtt ctatctggac
120
agaaagcaga gtaagtccaa aatccatgca gcacgcagcc tgagtgagat cgccatcgac
180
ctgaccgaga cggggacgct gaagacctcg aagctggcca acatgggtag caaggggaag
240
atcatcagcg gcagcagcgg cagcctgctg tcttcaggat ctggtgccag gagacactgc
300
attctactcc caggttctca ggaatcagat agctcgcagt cggccaagaa ggacatgctg
360
gctgccttga agtccaggca ggaagctctg gaggaaaccc tgcgtcagag gctggaggaa
420
ctgaagaagc tgtgtctccg agaagctgag ctcacgggca agctgccagt agaatatccc
480
ctggat
486

<210> 3558
<211> 162
<212> PRT
<213> Homo sapiens

<400> 3558
Ser Val Thr Arg Arg Thr Phe Gly His Ser Gly Ile Ala Val His Thr
 1   5   10   15
Trp Tyr Ala Cys Pro Ala Leu Ile Lys Ser Ile Trp Ala Met Ala Ile
            20   25   30
Ser Gln His Gln Phe Tyr Leu Asp Arg Lys Gln Ser Lys Ser Lys Ile
        35   40   45
His Ala Ala Arg Ser Leu Ser Glu Ile Ala Ile Asp Leu Thr Glu Thr
    50   55   60
Gly Thr Leu Lys Thr Ser Lys Leu Ala Asn Met Gly Ser Lys Gly Lys
65   70   75   80
Ile Ile Ser Gly Ser Ser Gly Ser Leu Leu Ser Ser Gly Ser Gly Ala
                85   90   95
Arg Arg His Cys Ile Leu Leu Pro Gly Ser Gln Glu Ser Asp Ser Ser
            100   105   110
Gln Ser Ala Lys Lys Asp Met Leu Ala Ala Leu Lys Ser Arg Gln Glu
        115   120   125
Ala Leu Glu Glu Thr Leu Arg Gln Arg Leu Glu Glu Leu Lys Lys Leu
    130   135   140
Cys Leu Arg Glu Ala Glu Leu Thr Gly Lys Leu Pro Val Glu Tyr Pro
145   150   155   160
Leu Asp

<210> 3559
<211> 673

<212> DNA
<213> Homo sapiens

<400> 3559
gaaggagcga gcgggggcgc gaggcgttta cctggaggca gcggcttggg cgcgcagagc
60
ggccgcggct cccccgcacc tgcggccatg gatgaggagc gcgccctcta catcgtccgg
120
gccggcgaag caggggctat cgagcgggtc ctgagggatt acagcgacaa gcatagggct
180
actttcaaat ttgaatcaac agatgaagat aaaagaaaga aactctgtga aggcatattt
240
aaagtcctta taaaggacat cccaacaaca tgtcaagtgt cctgcctgga agtactccgc
300
attctctcca gagacaaaaa ggttttagtt cctgtgacaa ctaaggaaaa tatgcagata
360
ctgctgcgac tagccaagct aaatgagtta gatgattctt tggagaaagt atcagagttc
420
ccagttattg tggagtcatt aaaatgtctg tgtaatatag tgttcaacag tcagatggca
480
cagcagctca gcctggaact taatcttgct gcaaagctct gtaacctcct gagaaagtgc
540
aaggaccgga aatttatcaa tgacattaag tgctttgact tgcgcttgct cttccttctg
600
tcacttttgc acaccgacat caggtcacaa ttgcgctatg agctccaggg actaccgctg
660
ctaacgcaga tcg
673

<210> 3560
<211> 195
<212> PRT
<213> Homo sapiens

<400> 3560
Met Asp Glu Glu Arg Ala Leu Tyr Ile Val Arg Ala Gly Glu Ala Gly
 1   5   10   15
Ala Ile Glu Arg Val Leu Arg Asp Tyr Ser Asp Lys His Arg Ala Thr
            20   25   30
Phe Lys Phe Glu Ser Thr Asp Glu Asp Lys Arg Lys Lys Leu Cys Glu
        35   40   45
Gly Ile Phe Lys Val Leu Ile Lys Asp Ile Pro Thr Thr Cys Gln Val
    50   55   60
Ser Cys Leu Glu Val Leu Arg Ile Leu Ser Arg Asp Lys Lys Val Leu
65   70   75   80
Val Pro Val Thr Thr Lys Glu Asn Met Gln Ile Leu Leu Arg Leu Ala
                85   90   95
Lys Leu Asn Glu Leu Asp Asp Ser Leu Glu Lys Val Ser Glu Phe Pro
            100   105   110
Val Ile Val Glu Ser Leu Lys Cys Leu Cys Asn Ile Val Phe Asn Ser
        115   120   125
Gln Met Ala Gln Gln Leu Ser Leu Glu Leu Asn Leu Ala Ala Lys Leu
    130   135   140
Cys Asn Leu Leu Arg Lys Cys Lys Asp Arg Lys Phe Ile Asn Asp Ile

145 150 155 160
Lys Cys Phe Asp Leu Arg Leu Leu Phe Leu Leu Ser Leu Leu His Thr
165 170 175
Asp Ile Arg Ser Gln Leu Arg Tyr Glu Leu Gln Gly Leu Pro Leu Leu
180 185 190
Thr Gln Ile
195

<210> 3561
<211> 523
<212> DNA
<213> Homo sapiens

<400> 3561
acgcgtgcct gtaggcagac gaggggccag tgggcagagc agacatgaat gccccctgaa
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ggctcacaga gctgactcag aagggccatt gtcacacact ggtaagagct gattctgagg
120
ggagggcatg agacgcctat tgcagagctg ctcaccagaa ggtcacagga atttagaaga
180
gaagctccta cctgcccccg atcatgcacg tggccactga ggatgccaga cgaggtgatg
240
ctggtctcat agagaatgta cccgaaggac tgtccatttc ccccattgac tggcaggttc
300
tccatgttga tgggcttttc agacttgatt ggctgcgtac agaagagatg gaggggtggg
360
caggctcagg aggagtgggg tcacagacag actctgcttg ggggctggca catggggtgg
420
aagcggaggt ttggtgggtg ttttctactt tgacttctca ttgcactaaa catacaactc
480
tccagggtga cggggaagag gagtggggca aaggggtgtg cac
523

<210> 3562
<211> 106
<212> PRT
<213> Homo sapiens

<400> 3562
Met His Val Ala Thr Glu Asp Ala Arg Arg Gly Asp Ala Gly Leu Ile
1 5 10 15
Glu Asn Val Pro Glu Gly Leu Ser Ile Ser Pro Ile Asp Trp Gln Val
20 25 30
Leu His Val Asp Gly Leu Phe Arg Leu Asp Trp Leu Arg Thr Glu Glu
35 40 45
Met Glu Gly Trp Ala Gly Ser Gly Gly Val Gly Ser Gln Thr Asp Ser
50 55 60
Ala Trp Gly Leu Ala His Gly Val Glu Ala Glu Val Trp Trp Val Phe
65 70 75 80
Ser Thr Leu Thr Ser His Cys Thr Lys His Thr Thr Leu Gln Gly Asp
85 90 95
Gly Glu Glu Glu Trp Gly Lys Gly Val Cys
100 105

<210> 3563
<211> 359
<212> DNA
<213> Homo sapiens

<400> 3563
nnacgcgtag tcgaactgcc cgcgctcgag cgcctccttg tggtcggtcc ccgtccgggt
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cgaagccagg ggcgcgcggc gatgtgagcc atgagcgcga cgtggacgct gtcgccggag
120
cccctgccgc cgtcgacggg gcccccagtg ggcgcgggcc tggacgcgga gcagcgcacg
180
gtgttcgcct tcgtgctctg cctgctcgtg gtgctggtgc tgttgatggt gcgctgcgtg
240
cgcatcctgc tcgaccccta cagccgcatg cccgcctcgt cctggaccga ccacaaggag
300
gcgctcgagc gcgggcagtt cgactacgcg ttggtgtgag gggcgcggcg ccccctagg
359

<210> 3564
<211> 82
<212> PRT
<213> Homo sapiens

<400> 3564
Met Ser Ala Thr Trp Thr Leu Ser Pro Glu Pro Leu Pro Pro Ser Thr
 1   5   10   15
Gly Pro Pro Val Gly Ala Gly Leu Asp Ala Glu Gln Arg Thr Val Phe
            20   25   30
Ala Phe Val Leu Cys Leu Leu Val Val Leu Val Leu Leu Met Val Arg
        35   40   45
Cys Val Arg Ile Leu Leu Asp Pro Tyr Ser Arg Met Pro Ala Ser Ser
    50   55   60
Trp Thr Asp His Lys Glu Ala Leu Glu Arg Gly Gln Phe Asp Tyr Ala
65   70   75   80
Leu Val

<210> 3565
<211> 580
<212> DNA
<213> Homo sapiens

<400> 3565
acgcgtcgtg ggtgggaaaa gggatgccag gacaccagaa gagcaataca aaacagctcc
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cgtgagcagg cacaggagac cttccgcgcc gccggccggg cgaccccgca ggaagtagga
120
aggacgagcg cgcacttcaa gtcccagaag cccccgtttc ctggagcccg cgccgtgccg
180
cgctacgccc gccgggagcc gggcagagcg gccaagatgt cgcagcccaa gaaaagaaag
240
cttgagtcgg ggggcggcgc cgaaggaggg gagggaactg aagaggaaga tggcgcggag
300

cgggaggcgg ccctggagcg accccggacg actaagcggg aacgggacca gctgtactac
360
gagtgctact cggacgtttc ggtccacgag gagatgatcg cggaccgcgt ccgcaccgat
420
gcctaccgct gggtttccct tcggaactgg gcagcactgc gaggcaagac ggtactggac
480
gtgggcgcgg gcaccggcat tctgagcatc ttctgtgccc aggccggggc ccggcgcgtg
540
tacgcggtag aggccagcgc catctggcaa caggcccggg
580

<210> 3566
<211> 193
<212> PRT
<213> Homo sapiens

<400> 3566
Thr Arg Arg Gly Trp Glu Lys Gly Cys Gln Asp Thr Arg Arg Ala Ile
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Gln Asn Ser Ser Arg Glu Gln Ala Gln Glu Thr Phe Arg Ala Ala Gly
20 25 30
Arg Ala Thr Pro Gln Glu Val Gly Arg Thr Ser Ala His Phe Lys Ser
35 40 45
Gln Lys Pro Pro Phe Pro Gly Ala Arg Ala Val Pro Arg Tyr Ala Arg
50 55 60
Arg Glu Pro Gly Arg Ala Ala Lys Met Ser Gln Pro Lys Lys Arg Lys
65 70 75 80
Leu Glu Ser Gly Gly Gly Ala Glu Gly Gly Glu Gly Thr Glu Glu Glu
85 90 95
Asp Gly Ala Glu Arg Glu Ala Ala Leu Glu Arg Pro Arg Thr Thr Lys
100 105 110
Arg Glu Arg Asp Gln Leu Tyr Tyr Glu Cys Tyr Ser Asp Val Ser Val
115 120 125
His Glu Glu Met Ile Ala Asp Arg Val Arg Thr Asp Ala Tyr Arg Trp
130 135 140
Val Ser Leu Arg Asn Trp Ala Ala Leu Arg Gly Lys Thr Val Leu Asp
145 150 155 160
Val Gly Ala Gly Thr Gly Ile Leu Ser Ile Phe Cys Ala Gln Ala Gly
165 170 175
Ala Arg Arg Val Tyr Ala Val Glu Ala Ser Ala Ile Trp Gln Gln Ala
180 185 190
Arg

<210> 3567
<211> 2811
<212> DNA
<213> Homo sapiens

<400> 3567
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ccttgcagaa gagccagaag gaagctgaac tgacccgtga actggagaaa cagaaggaaa
120

ataagcaggt ggaagagatc ctccgtctgg agaaagaaat cgaggacctg cagcgcatga
180
aggagcagca ggagctgtcg ctgaccgagg cttccctgca gaagctgcag gagcggcggg
240
accaggagct ccgcaggctg gaggaggaga tttttgcacc tgaaaaaggc agccatagtt
300
ttccagaagc aactcagagg tcagattgct cggagagttt acagacaatt gctggcagag
360
aaaagggagc aagaagaaaa gaagaaacag gaagaggaag aaaagaagaa acgggaggaa
420
gaagaaagag aaagagagag agagcgaaga gaagccgagc tccgcgccca gcaggaagaa
480
gaaacgagga agcagcaaga actcgaagcc ttgcagaaga gccagaagga agctgaactg
540
acccgtgaac tggagaaaca gaaggaaaat aagcaggtgg aagagatcct ccgtctggag
600
aaagaaatcg aggacctgca gcgcatgaag gagcagcagg agctgtcgct gaccgaggct
660
tccctgcaga agctgcagga gcggcgggac caggagctcc gcaggctgga ggaggaagcg
720
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780
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840
gcatgcgagg agaagcccaa cttcaacttc agccagccct acccagagga ggaggtcgat
900
gagggcttcg aagccgacga cgacgccttc aaggactccc ccaaccccag cgagcacggc
960
cactcagacc agcgaacaag tggcatccgg accagcgatg actcttcaga ggaggaccca
1020
tacatgaacg acacggtggt gcccaccagc cccagtgcgg acagcacggt gctgctcgcc
1080
ccatcagtgc aggactccgg gagcctacac aactcctcca gcggcgagtc cacctactgc
1140
atgccccaga acgctgggga cttgccctcc ccagacggcg actacgacta cgaccaggat
1200
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1320
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1380
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1440
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1500
cgctggtgcg tcctcaagga tgaaaccttc ttgtggttcc gctccaagca ggaggccctc
1560
aagcaaggct ggctccacaa aaaaggggggg ggctcctcca cgctgtccag gagaaattgg
1620
aagaagcgct ggtttgtcct ccgccagtcc aagctgatgt actttgaaaa cgacagcgag
1680
gagaagctca agggcaccgt agaagtgcga acggcaaaag agatcataga taacaccacc
1740

aaggagaatg ggatcgacat cattatggcc gataggactt tccacctgat tgcagagtcc
1800
ccagaagatg ccagccagtg gttcagcgtg ctgagtcagg tccacgcgtc cacggaccag
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1980
atcatcacgg ccaaccgggt gctgcactgc aacgccgaca cgccggagga gatgcaccac
2040
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2100
gtgagaggat ggttgcacaa agaggtgaag aacagtccaa agatgtcttc actgaaactg
2160
aagaaacggt ggtttgtact cacccacaat tccctggatt actacaagag ttcagagaag
2220
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2280
gagaagatat tcaaagagac aggctactgg aacgtcaccg tgtacgggcg caagcactgt
2340
taccggctct acaccaagct gctcaacgag gccacccggt ggtccagtgt cagtcaaaac
2400
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2460
gagaactgcc tgaactcgga tgtggtggaa cagatttaca agcggaaccc gatccttcga
2520
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2580
aacttgctca aagacaaagg ctataccacc cttcaggatg aggccatcaa gatattcaat
2640
tccctgcagc aactggagtc catgtctgac ccaattccaa taatccaggg catcctacag
2700
acagggcatg acctgcgacc tctgcgggac gagctgtact gccagcttat caaacagacc
2760
aacaaagtgc cccaccccgg cagtgtgggc aacctgtaca gctggcagat c
2811

<210> 3568
<211> 869
<212> PRT
<213> Homo sapiens

<400> 3568
Pro Arg Leu Pro Cys Arg Ser Cys Arg Ser Gly Gly Thr Arg Ser Ser
1 5 10 15
Ala Gly Trp Arg Arg Arg Phe Leu His Leu Lys Lys Ala Ala Ile Val
20 25 30
Phe Gln Lys Gln Leu Arg Gly Gln Ile Ala Arg Arg Val Tyr Arg Gln
35 40 45
Leu Leu Ala Glu Lys Arg Glu Gln Glu Glu Lys Lys Lys Gln Glu Glu
50 55 60
Glu Glu Lys Lys Lys Arg Glu Glu Glu Glu Arg Glu Arg Glu Arg Glu
65 70 75 80
Arg Arg Glu Ala Glu Leu Arg Ala Gln Gln Glu Glu Glu Thr Arg Lys

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                85                  90                  95
Gln Gln Glu Leu Glu Ala Leu Gln Lys Ser Gln Lys Glu Ala Glu Leu
            100                 105                 110
Thr Arg Glu Leu Glu Lys Gln Lys Glu Asn Lys Gln Val Glu Glu Ile
        115                 120                 125
Leu Arg Leu Glu Lys Glu Ile Glu Asp Leu Gln Arg Met Lys Glu Gln
    130                 135                 140
Gln Glu Leu Ser Leu Thr Glu Ala Ser Leu Gln Lys Leu Gln Glu Arg
145                 150                 155                 160
Arg Asp Gln Glu Leu Arg Arg Leu Glu Glu Glu Ala Cys Arg Ala Ala
                165                 170                 175
Gln Glu Phe Leu Glu Ser Leu Asn Phe Asp Glu Ile Asp Glu Cys Val
            180                 185                 190
Arg Asn Ile Glu Arg Ser Leu Ser Gly Gly Ser Glu Phe Ser Ser Glu
        195                 200                 205
Leu Ala Glu Ser Ala Cys Glu Glu Lys Pro Asn Phe Asn Phe Ser Gln
    210                 215                 220
Pro Tyr Pro Glu Glu Glu Val Asp Glu Gly Phe Glu Ala Asp Asp Asp
225                 230                 235                 240
Ala Phe Lys Asp Ser Pro Asn Pro Ser Glu His Gly His Ser Asp Gln
                245                 250                 255
Arg Thr Ser Gly Ile Arg Thr Ser Asp Asp Ser Ser Glu Glu Asp Pro
            260                 265                 270
Tyr Met Asn Asp Thr Val Val Pro Thr Ser Pro Ser Ala Asp Ser Thr
        275                 280                 285
Val Leu Leu Ala Pro Ser Val Gln Asp Ser Gly Ser Leu His Asn Ser
    290                 295                 300
Ser Ser Gly Glu Ser Thr Tyr Cys Met Pro Gln Asn Ala Gly Asp Leu
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Pro Ser Pro Asp Gly Asp Tyr Asp Tyr Asp Gln Asp Asp Tyr Glu Asp
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Ser Gln Trp Ser Pro Asp Tyr Arg Cys Ser Val Gly Thr Tyr Asn Ser
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Asp Ser Glu Glu Asp Phe Asp Ser Arg Phe Asp Thr Asp Asp Glu Leu
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Ser Tyr Arg Arg Asp Ser Val Tyr Ser Cys Val Thr Leu Pro Tyr Phe
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His Ser Phe Leu Tyr Met Lys Gly Gly Leu Met Asn Ser Trp Lys Arg
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Arg Trp Cys Val Leu Lys Asp Glu Thr Phe Leu Trp Phe Arg Ser Lys
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Gln Glu Ala Leu Lys Gln Gly Trp Leu His Lys Lys Gly Gly Gly Ser
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Ser Thr Leu Ser Arg Arg Asn Trp Lys Lys Arg Trp Phe Val Leu Arg
465                 470                 475                 480
Gln Ser Lys Leu Met Tyr Phe Glu Asn Asp Ser Glu Glu Lys Leu Lys
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        595                 600                 605
Glu Met His His Trp Ile Thr Leu Leu Gln Arg Ser Lys Gly Asp Thr
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Val Lys Asn Ser Pro Lys Met Ser Ser Leu Lys Leu Lys Lys Arg Trp
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Val Pro Pro Asp Glu Lys Ile Phe Lys Glu Thr Gly Tyr Trp Asn Val
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Thr Val Tyr Gly Arg Lys His Cys Tyr Arg Leu Tyr Thr Lys Leu Leu
705                 710                 715                 720
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                725                 730                 735
Lys Ala Pro Ile Asp Thr Pro Thr Gln Gln Leu Ile Gln Asp Ile Lys
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Glu Asn Cys Leu Asn Ser Asp Val Val Glu Gln Ile Tyr Lys Arg Asn
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Pro Ile Leu Arg Tyr Thr His His Pro Leu His Ser Pro Leu Leu Pro
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Leu Pro Tyr Gly Asp Ile Asn Leu Asn Leu Leu Lys Asp Lys Gly Tyr
785                 790                 795                 800
Thr Thr Leu Gln Asp Glu Ala Ile Lys Ile Phe Asn Ser Leu Gln Gln
                805                 810                 815
Leu Glu Ser Met Ser Asp Pro Ile Pro Ile Ile Gln Gly Ile Leu Gln
            820                 825                 830
Thr Gly His Asp Leu Arg Pro Leu Arg Asp Glu Leu Tyr Cys Gln Leu
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Ile Lys Gln Thr Asn Lys Val Pro His Pro Gly Ser Val Gly Asn Leu
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<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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Arg Ala Pro Ser Pro Pro Trp Pro Pro Gln Gly Pro Leu Ser Pro Gly
35 40 45
Pro Gly Ser Leu Pro Leu Ser Ile Ala Arg Val Gln Thr Pro Pro Trp
50 55 60
His Pro Pro Gly Ala Pro Ser Pro Gly Leu Leu Gln Asp Ser Asp Ser
65 70 75 80
Leu Ser Gly Ser Tyr Leu Asp Pro Asn Tyr Gln Ser Ile Lys Trp Gln
85 90 95
Pro His Gln Gln Asn Lys Trp Ala Thr Leu Tyr Asp Ala Asn Tyr Lys
100 105 110
Glu Leu Pro Met Leu Thr Tyr Arg Val Asp Ala Asp Lys Gly Phe Asn
115 120 125
Phe Ser Val Gly Asp Asp Ala Phe Val Cys Gln Lys Lys Asn His Phe
130 135 140
Gln Val Thr Val Tyr Ile Gly Met Leu Gly Glu Pro Lys Tyr Val Lys
145 150 155 160
Thr Pro Glu Gly Leu Lys Pro Leu Asp Cys Phe Tyr Leu Lys Leu His
165 170 175
Gly Val Lys Leu Glu Ala Leu Asn Gln Ser Ile Asn Ile Glu Gln Ser
180 185 190
Gln Ser Asp Arg Ser Lys Arg Pro Phe Asn Pro Val Thr Val Asn Leu
195 200 205
Pro Pro Glu Gln Val Thr Lys Val Thr Val Gly Arg Leu His Phe Ser
210 215 220
Glu Thr Thr Ala Asn Asn Met Arg Lys Lys Gly Lys Pro Asn Pro Asp
225 230 235 240
Gln Arg Tyr Phe Met Leu Val Val Ala Leu Gln Ala His Ala Gln Asn
245 250 255
Gln Asn Tyr Thr Leu Ala Ala Gln Ile Ser Glu Arg Ile Ile Val Arg
260 265 270
Ala Ser Asn Pro Gly Gln Phe Glu Ser Asp Ser Asp Val Leu Trp Gln
275 280 285
Arg Ala Gln Val Pro Asp Thr Val Phe His His Gly Arg Val Gly Ile
290 295 300
Asn Thr Asp Arg Pro Asp Glu Ala Leu Val Val His Gly Asn Val Lys
305 310 315 320
Val Met Gly Ser Leu Met His Pro Ser Asp Leu Arg Ala Lys Glu His
325 330 335
Val Gln Glu Val Asp Thr Thr Glu Gln Leu Lys Arg Ile Ser Arg Met

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            340                 345                 350
Arg Leu Val His Tyr Arg Tyr Lys Pro Glu Phe Ala Ala Ser Ala Gly
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Ile Glu Ala Thr Ala Pro Glu Thr Gly Val Ile Ala Gln Glu Val Lys
    370                 375                 380
Glu Ile Leu Pro Glu Ala Val Lys Asp Thr Gly Asp Met Val Phe Ala
385                 390                 395                 400
Asn Gly Lys Thr Ile Glu Asn Phe Leu Val Val Asn Lys Glu Arg Ile
                405                 410                 415
Phe Met Glu Asn Val Gly Ala Val Lys Glu Leu Cys Lys Leu Thr Asp
            420                 425                 430
Asn Leu Glu Thr Arg Ile Asp Glu Leu Glu Arg Trp Ser His Lys Leu
        435                 440                 445
Ala Lys Leu Arg Arg Leu Asp Ser Leu Lys Ser Thr Gly Ser Ser Gly
    450                 455                 460
Ala Phe Ser His Ala Gly Ser Gln Phe Ser Arg Ala Gly Ser Val Pro
465                 470                 475                 480
His Lys Lys Arg Pro Pro Lys Val Ala Ser Lys Ser Ser Ser Val Val
                485                 490                 495
Pro Asp Gln Ala Cys Ile Ser Gln Arg Phe Leu Gln Gly Thr Ile Ile
            500                 505                 510
Ala Leu Val Val Val Met Ala Phe Ser Val Val Ser Met Ser Thr Leu
        515                 520                 525
Tyr Val Leu Ser Leu Arg Thr Glu Glu Asp Leu Val Asp Thr Asp Gly
    530                 535                 540
Ser Phe Ala Val Ser Thr Ser Cys Leu Leu Ala Leu Leu Arg Pro Gln
545                 550                 555                 560
Pro Pro Gly Gly Ser Glu Ala Leu Cys Pro Trp Ser Ser Gln Ser Phe
                565                 570                 575
Gly Thr Thr Gln Leu Arg Gln Ser Pro Leu Thr Thr Gly Leu Pro Gly
            580                 585                 590
Ile Gln Pro Ser Leu Leu Leu Val Thr Thr Ser Leu Thr Ser Ser Ala
        595                 600                 605
Pro Gly Ser Ala Val Arg Thr Leu Asp Met Cys Ser Ser His Pro Cys
    610                 615                 620
Pro Val Ile Cys Cys Ser Ser Pro Thr Thr Asn Pro Thr Thr Gly Pro
625                 630                 635                 640
Ser Leu Gly Pro Ser Phe Asn Pro Gly His Val Leu Ser Pro Ser Pro
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Ser Pro Ser Thr Asn Arg Ser Gly Pro Ser Gln Met Ala Leu Leu Pro
            660                 665                 670
Val Thr Asn Ile Arg Ala Lys Ser Trp Gly Leu Ser Val Asn Gly Ile
        675                 680                 685
Asp His Ser Lys His His Lys Ser Leu Glu Pro Leu Ala Ser Pro Ala
    690                 695                 700
Val Pro Phe Pro Gly Gly Gln Gly Lys Ala Lys Asn Ser Pro Ser Leu
705                 710                 715                 720
Gly Phe His Gly Arg Ala Arg Arg Gly Ala Leu Gln Ser Ser Val Gly
                725                 730                 735
Pro Ala Glu Pro Thr Trp Ala Gln Gly Gln Ser Ala Ser Leu Leu Ala
            740                 745                 750
Glu Pro Val Pro Ser Leu Thr Ser Ile Gln Val Leu Glu Asn Ser Met
        755                 760                 765
Ser Ile Thr Ser Gln Tyr Cys Ala Pro Gly Asp Ala Cys Arg Pro Gly
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    770                 775                 780
Asn Phe Thr Tyr His Ile Pro Val Ser Ser Gly Thr Pro Leu His Leu
785                 790                 795                 800
Ser Leu Thr Leu Gln Met Asn Ser Ser Ser Pro Val Ser Val Val Leu
                805                 810                 815
Cys Ser Leu Arg Ser Lys Glu Glu Pro Cys Glu Glu Gly Ser Leu Pro
            820                 825                 830
Gln Ser Leu His Thr His Gln Asp Thr Gln Gly Thr Ser His Arg Trp
        835                 840                 845
Pro Ile Thr Ile Leu Ser Phe Arg Glu Phe Thr Tyr His Phe Arg Val
    850                 855                 860
Ala Leu Leu Gly Gln Ala Asn Cys Ser Ser Glu Ala Leu Ala Gln Pro
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<211> 528
<212> DNA
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<210> 3572
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<213> Homo sapiens

<400> 3572
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            20                  25                  30
Ser Tyr Phe Leu Phe Val Ile Phe Thr Ala Tyr Ala Met Leu Pro Leu
        35                  40                  45
Gly Met Arg Asp Ala Ala Val Ala Gly Leu Ala Ser Ser Leu Ser His
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    50                  55                  60
Leu Leu Val Leu Gly Leu Tyr Leu Gly Pro Gln Pro Asp Ser Arg Pro
65                  70                  75                  80
Ala Leu Leu Pro Gln Val Ser Thr Gln Val Ala Gln Ala Ala Leu Arg
                85                  90                  95
Thr Ala Leu Pro Arg Ala Ser Arg Leu Leu Leu Gly Gly Cys
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<212> DNA
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<210> 3574
<211> 361
<212> PRT
<213> Homo sapiens

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35 40 45
Thr Cys Val Phe Asn Lys Pro Gly Gly His Thr Ala Ser His Thr His
50 55 60
Thr Leu Thr Ala Thr Asn Pro Arg Ser His Ala His Ala Asp Ala Pro
65 70 75 80
Cys Gly Thr Cys Thr His Asn His Thr Cys Val Gln Ser Gly Arg His
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Thr His Thr Cys Ile Glu Ala Ser Leu Trp Thr Pro Ser Ala Ser His
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Arg Gly Gly Ser Pro Ala Val Phe Asp Trp Phe Phe Glu Ala Ala Cys
115 120 125
Pro Ala Ser Val Gln Glu Asp Pro Pro Ile Leu Arg Gln Phe Pro Pro
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Asp Phe Arg Asp Gln Glu Ala Met Gln Met Val Pro Lys Phe Cys Phe
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Pro Phe Asp Val Glu Arg Gly Pro Pro Ser Pro Ala Val Gln His Phe
165 170 175
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180 185 190
Arg Leu Arg Ala Gly Thr Gln Ser Cys Leu Cys Ile Leu Ser His Leu
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Gly Ser Gly Val Thr Val Ser Ser Gly Gln Gly Ile Pro Pro Pro Thr
260 265 270
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275 280 285
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<212> DNA
<213> Homo sapiens

<400> 3575
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240
cactagaagg caccatgtaa cttgctggat ttggagtgtg acttcttctt ctgggagcag
300
gagaagtatg tggagtaatc ttgggggaat gaagagggga agacccagca gacaacgaca
360
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420
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480
caaagatgaa ggaaataatt ttatcttgtt ttgttgtaga aaaagctctg attaaagcaa
540
atgtaaagtt tctttttttca aatgtactta tttccaaata tgttagcaga tttactgcaa
600
gaatagtctc ctccatatca aggtttacat caggaaattt aatagcaaga gtgaccaaaa
660
atttaataaa ttaatggaag agtgggaagt aacagaattg tggctcttta taaaattatg
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769

<210> 3576
<211> 205
<212> PRT
<213> Homo sapiens

<400> 3576
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Ser Thr Thr Lys Gln Asp Lys Ile Ile Ser Phe Ile Phe Ala Leu Thr
35 40 45
Ile Pro Lys Met Met Phe Leu Pro Asn Glu Cys Leu His Phe Ile Phe
50 55 60
Gln Thr Cys Ser Leu Lys Pro Ile Ile Ala Pro Leu Arg Asn Ile Phe
65 70 75 80
Thr Ser Ser Ser Gly Met Ser Leu Ser Ala Gly Ser Ser Pro Leu His
85 90 95
Ser Pro Lys Ile Thr Pro His Thr Ser Pro Ala Pro Arg Arg Arg Ser

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            100                 105                 110
His Thr Pro Asn Pro Ala Ser Tyr Met Val Pro Ser Ser Ala Ser Thr
        115                 120                 125
Ser Val Asn Asn Pro Val Ser Gln Thr Pro Ser Ser Gly Gln Val Ile
    130                 135                 140
Gln Lys Glu Thr Val Gly Gly Thr Thr Tyr Phe Tyr Thr Asp Thr Thr
145                 150                 155                 160
Pro Ala Pro Leu Thr Gly Met Val Phe Pro Asn Tyr His Ile Tyr Pro
                165                 170                 175
Pro Thr Ala Pro His Val Ala Tyr Met Gln Pro Lys Ala Asn Ala Pro
            180                 185                 190
Ser Phe Phe Met Ala Asp Glu Leu Arg Gln Glu Leu Ile
        195                 200                 205
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<210> 3577
<211> 1225
<212> DNA
<213> Homo sapiens

<400> 3577
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120
gtgattgggg agagcatgta cggggacttt gaggaagctt ttgaccatct gcagaacaga
180
ctgatcgcca ccaagaaccc agaagaaatc agaggcgggg gacttctcaa gtacagcaac
240
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300
atgtgctcca ggttcttcat cgacttcccg gacatccttg aacagcagag gaagttggag
360
acttaccttc aaaaccactt cgctgaagaa gagagaagca agtacgacta cctcatgatc
420
cttcgcaggg tggtgaacga gagcaccgtg tgtctcatgg ggcatgaacg caggcagact
480
ctgaacctca tctccctcct ggccttgcgt gtgctgggcg gaacaaaaca tcatccccca
540
gtgccaccaa ggtcacctgt tactaccagc ggtcccctta gtcagtgatg gcaacttcag
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caactactac gttgcccatc ctccagtcac ctacagccag ccttacccta cctggctgcc
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ctgtaactaa ccttgagacc tgagggtttc cacagtggga accccaatag ggctagggct
720
ctcaggtagg ggagctcctt ctagatgtag gcatttgact tttaaagggg aactcagctc
780
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1020

agtgctaagc tacttgtttt ctcacttgag cccgggtagg ctgtgttggc cctcacttgg
1080
gattctcagc agttacatga aagttgtgct gataatctct tctcttgtac caattttagt
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1225

<210> 3578
<211> 195
<212> PRT
<213> Homo sapiens

<400> 3578
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Ile Ser Glu His Phe His Pro Thr Val Ile Gly Glu Ser Met Tyr Gly
35 40 45
Asp Phe Glu Glu Ala Phe Asp His Leu Gln Asn Arg Leu Ile Ala Thr
50 55 60
Lys Asn Pro Glu Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Ser Asn
65 70 75 80
Leu Leu Val Arg Asp Phe Arg Pro Thr Asp Gln Glu Glu Ile Lys Thr
85 90 95
Leu Glu Arg Tyr Met Cys Ser Arg Phe Phe Ile Asp Phe Pro Asp Ile
100 105 110
Leu Glu Gln Gln Arg Lys Leu Glu Thr Tyr Leu Gln Asn His Phe Ala
115 120 125
Glu Glu Glu Arg Ser Lys Tyr Asp Tyr Leu Met Ile Leu Arg Arg Val
130 135 140
Val Asn Glu Ser Thr Val Cys Leu Met Gly His Glu Arg Arg Gln Thr
145 150 155 160
Leu Asn Leu Ile Ser Leu Leu Ala Leu Arg Val Leu Gly Gly Thr Lys
165 170 175
His His Pro Pro Val Pro Pro Arg Ser Pro Val Thr Thr Ser Gly Pro
180 185 190
Leu Ser Gln
195

<210> 3579
<211> 755
<212> DNA
<213> Homo sapiens

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attttggaga tacacttctg gtcagaactc aggtgagata atcttgcaat actccaaatg
120
cagatactcc agccacccgc aaggttccag gaaaggacaa tgtcctgcga gaaaatcagg
180

aggcctccac ttcctgggcc acttgagaag ttcctgggca tgtcactaca tgttggttga
240
ctcagccatt tctcatgctg ttttgtttct tgcggtggcc acttaacccc aaagaatgaa
300
gggaggatcc acagtgaaag tgcctgagtt tctctatgag accagatgct gtcgaaacca
360
aacatctttt cctttgctct atgggaacat tttagggttt gttttgcaca gctggtttcc
420
agactagaag attaacaagt ttgggtccac ccctaagaat cagtggctgt cttttaaggt
480
gaggagtgtg ggcttaactg aggtcctttg agggagctat aaaggagaaa caacctggga
540
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600
aatggtaaat atatgcttta agctctacct ttaaacttgt atgttattca ggcatctctt
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720
ccaaatttac ttctcttcag tttaattgtc catgg
755

<210> 3580
<211> 121
<212> PRT
<213> Homo sapiens

<400> 3580
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Ser Leu Trp Ile Leu Pro Ser Phe Phe Gly Val Lys Trp Pro Pro Gln
20 25 30
Glu Thr Lys Gln His Glu Lys Trp Leu Ser Gln Pro Thr Cys Ser Asp
35 40 45
Met Pro Arg Asn Phe Ser Ser Gly Pro Gly Ser Gly Gly Leu Leu Ile
50 55 60
Phe Ser Gln Asp Ile Val Leu Ser Trp Asn Leu Ala Gly Gly Trp Ser
65 70 75 80
Ile Cys Ile Trp Ser Ile Ala Arg Leu Ser His Leu Ser Ser Asp Gln
85 90 95
Lys Cys Ile Ser Lys Ile Ile Thr Ser Thr Lys Thr Ile Ile Asp Cys
100 105 110
Glu Gln Thr Phe Ser Val Thr Ser Arg
115 120

<210> 3581
<211> 2132
<212> DNA
<213> Homo sapiens

<400> 3581
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120

ggcgcctgct ggacttgtac tcggcgggcg agcagcgcgt gtacgaggcg cgggaccgcg
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240
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300
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360
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420
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1740

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1980
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2100
tttttaaaaa aaaaaaaaaa aaaaaaaaaa aa
2132

<210> 3582
<211> 138
<212> PRT
<213> Homo sapiens

<400> 3582
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Pro Arg Thr Gly Cys Thr Thr Ala Ser Ala Cys Ser Thr Gly Thr Cys
20 25 30
Ala Ala Pro Gly Val Ala Pro Arg Gly Ala Cys Trp Thr Cys Thr Arg
35 40 45
Arg Ala Ser Ser Ala Cys Thr Arg Arg Gly Thr Ala Ala Ala Trp Ser
50 55 60
Ser Arg Pro Arg Pro Ser Thr Thr Ala Thr Ser Arg Cys Ser Ser Ala
65 70 75 80
Arg Trp Arg Arg Arg Thr Arg Gly Cys Thr Pro Ala Thr Cys Thr Ile
85 90 95
Thr Thr Ala Thr Ser Thr Arg Ala Trp Pro Ser Ala Trp Arg Ser Pro
100 105 110
Thr Ala Pro Arg Pro Pro Pro Pro Thr Gly Thr Ala Arg Arg Arg Cys
115 120 125
Trp Arg Trp Arg Ala Ala His Pro Arg Phe
130 135

<210> 3583
<211> 1554
<212> DNA
<213> Homo sapiens

<400> 3583
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120
ctccgaaatg ggatcgcgga agacttaaag ggccaggctg attttttttt cctactgcag
180
gtctctgagg ctgtggttgc tacagggtca ccacgagctt ggcttacttg tctcatcctt
240

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300
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1554

<210> 3584
<211> 356
<212> PRT
<213> Homo sapiens

<400> 3584
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Ser Thr Leu Asp Gly Ala Ala Ala Arg Ala Phe Tyr Glu Ala Leu Ile
        35                  40                  45
Gly Asp Glu Ser Ser Ala Pro Asp Ser Gln Arg Ser Gln Thr Glu Pro
    50                  55                  60
Ala Arg Glu Arg Lys Arg Lys Lys Arg Arg Ile Met Lys Ala Pro Ala
65                  70                  75                  80
Ala Glu Ala Val Ala Glu Gly Ala Ser Gly Arg His Gly Gln Gly Arg
                85                  90                  95
Ser Leu Glu Ala Glu Asp Lys Met Thr His Arg Ile Leu Arg Ala Ala
            100                 105                 110
Gln Glu Gly Asp Leu Pro Glu Leu Arg Arg Leu Leu Glu Pro His Glu
        115                 120                 125
Ala Gly Gly Ala Gly Gly Asn Ile Asn Ala Arg Asp Ala Phe Trp Trp
    130                 135                 140
Thr Pro Leu Met Cys Ala Ala Arg Ala Gly Gln Gly Ala Ala Val Ser
145                 150                 155                 160
Tyr Leu Leu Gly Arg Gly Ala Ala Trp Val Gly Val Cys Glu Leu Ser
                165                 170                 175
Gly Arg Asp Ala Ala Gln Leu Ala Glu Glu Ala Gly Phe Pro Glu Val
            180                 185                 190
Ala Arg Met Val Arg Glu Ser His Gly Glu Thr Arg Ser Pro Glu Asn
        195                 200                 205
Arg Ser Pro Thr Pro Ser Leu Gln Tyr Cys Glu Asn Cys Asp Thr His
    210                 215                 220
Phe Gln Asp Ser Asn His Arg Thr Ser Thr Ala His Leu Leu Ser Leu
225                 230                 235                 240
Ser Gln Gly Pro Gln Pro Pro Asn Leu Pro Leu Gly Val Pro Ile Ser
                245                 250                 255
Ser Pro Gly Phe Lys Leu Leu Leu Arg Gly Gly Trp Glu Pro Gly Met
            260                 265                 270
Gly Leu Gly Pro Arg Gly Glu Gly Arg Ala Asn Pro Ile Pro Thr Val
        275                 280                 285
Leu Lys Arg Asp Gln Glu Gly Leu Gly Tyr Arg Ser Ala Pro Gln Pro
    290                 295                 300
Arg Val Thr His Phe Pro Ala Trp Asp Thr Arg Ala Val Ala Gly Arg
305                 310                 315                 320
Glu Arg Pro Pro Arg Val Ala Thr Leu Ser Trp Arg Glu Glu Arg Arg
                325                 330                 335
Arg Glu Glu Lys Asp Arg Ala Trp Glu Arg Asp Leu Arg Thr Tyr Met
            340                 345                 350
Asn Leu Glu Phe
        355
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<210> 3585
<211> 2782
<212> DNA
<213> Homo sapiens

<400> 3585
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120

gtgggcgggg ccccttgggc cgtcgccacc actgtagtca tgtacccacc gccgccgccg
180
ccgcctcatc gggacttcat ctcggtgacg ctgagctttg gcgagagcta tgacaacagc
240
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300
aatatgattc tcttcctcct tgcctttctg cttttctgtg gactcctctt ctacatcaac
360
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1380
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1980
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2640
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2760
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2782

<210> 3586
<211> 663
<212> PRT
<213> Homo sapiens

<400> 3586
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Arg Ser Cys Trp Arg Lys Trp Lys Gln Leu Ser Arg Leu Gln Arg Asn
35 40 45
Met Ile Leu Phe Leu Leu Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe
50 55 60
Tyr Ile Asn Leu Ala Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu
65 70 75 80
Glu Glu Gln Lys Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn

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                85                  90                  95
Pro Pro Val Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn
            100                 105                 110
Leu Pro Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly
        115                 120                 125
Pro Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly
    130                 135                 140
Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro Arg
145                 150                 155                 160
Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly Ala Val
                165                 170                 175
Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg Ala Glu Val
            180                 185                 190
Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln Gly Thr Pro Val
        195                 200                 205
His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp Val Phe Leu His Ala
    210                 215                 220
Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly His Asp Glu Leu Lys Pro
225                 230                 235                 240
Val Ser Arg Ser Phe Ser Glu Trp Phe Gly Leu Gly Leu Thr Leu Ile
                245                 250                 255
Asp Ala Leu Asp Thr Met Trp Ile Leu Gly Leu Arg Lys Glu Phe Glu
            260                 265                 270
Glu Ala Arg Lys Trp Val Ser Lys Lys Leu His Phe Glu Lys Asp Val
        275                 280                 285
Asp Val Asn Leu Phe Glu Ser Thr Ile Arg Ile Leu Gly Gly Leu Leu
    290                 295                 300
Ser Ala Tyr His Leu Ser Gly Asp Ser Leu Phe Leu Arg Lys Ala Glu
305                 310                 315                 320
Asp Phe Gly Asn Arg Leu Met Pro Ala Phe Arg Thr Pro Ser Lys Ile
                325                 330                 335
Pro Tyr Ser Asp Val Asn Ile Gly Thr Gly Val Ala His Pro Pro Arg
            340                 345                 350
Trp Thr Ser Asp Ser Thr Val Ala Glu Val Thr Ser Ile Gln Leu Glu
        355                 360                 365
Phe Arg Glu Leu Ser Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala
    370                 375                 380
Val Glu Lys Val Thr Gln His Ile His Gly Leu Ser Gly Lys Lys Asp
385                 390                 395                 400
Gly Leu Val Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe Thr His
                405                 410                 415
Leu Gly Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr Tyr Glu Tyr
            420                 425                 430
Leu Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu Thr Gln Leu Leu
        435                 440                 445
Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg Thr His Leu Leu Arg
    450                 455                 460
His Ser Glu Pro Ser Lys Leu Thr Phe Val Gly Glu Leu Ala His Gly
465                 470                 475                 480
Arg Phe Ser Ala Lys Met Asp His Leu Val Cys Phe Leu Pro Gly Thr
                485                 490                 495
Leu Ala Leu Gly Val Tyr His Gly Leu Pro Ala Ser His Met Glu Leu
            500                 505                 510
Ala Gln Glu Leu Met Glu Thr Cys Tyr Gln Met Asn Arg Gln Met Glu
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        515                 520                 525
Thr Gly Leu Ser Pro Glu Ile Val His Phe Asn Leu Tyr Pro Gln Pro
    530                 535                 540
Gly Arg Arg Asp Val Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu
545                 550                 555                 560
Arg Pro Glu Thr Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly
                565                 570                 575
Asp Arg Lys Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser
            580                 585                 590
Arg Phe Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val
        595                 600                 605
Gln Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe
    610                 615                 620
Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp Pro
625                 630                 635                 640
Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala His Pro
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Leu Pro Ile Trp Thr Pro Ala
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<210> 3587
<211> 3148
<212> DNA
<213> Homo sapiens

<400> 3587
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120
tccagggcct catctgcttc aaagccaaag tcttcctcaa ccttaatctg caccggggcc
180
agctctggag tcagcgcatt tcctgctcgg cgtccatccc gtggcactcg ccgcctcttc
240
cgcccactgg gcccctcacc gggggctggg ctgccgggtt ctgggggtgc aggagtcctt
300
ctgggcgggg acagtgtctc tttctctgga ggctcattct ccgcattgcc tggggtgggg
360
gcatccgtgc cctggctgcc ctcatcctcc agcacaatgg tgaactggct ggcccggtag
420
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480
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660
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720
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780
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840

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900
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1020
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1080
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1140
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1200
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1320
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1980
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2160
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2220
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2280
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2340
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2400
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2460

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2520
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2580
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2760
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2820
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3120
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3148

<210> 3588
<211> 499
<212> PRT
<213> Homo sapiens

<400> 3588
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Glu Asp Val Gln Glu Glu Thr Gln Leu Asp Leu Ser Gly Asp Ser Val
35 40 45
Lys Thr Ile Ala Lys Leu Trp Asp Ser Lys Met Phe Ala Glu Ile Met
50 55 60
Met Lys Ile Glu Glu Tyr Ile Ser Lys Gln Ala Lys Ala Ser Glu Val
65 70 75 80
Met Gly Pro Val Glu Ala Ala Pro Glu Tyr Arg Val Ile Val Asp Ala
85 90 95
Asn Asn Leu Thr Val Glu Ile Glu Asn Glu Leu Asn Ile Ile His Lys
100 105 110
Phe Ile Arg Asp Lys Tyr Ser Lys Arg Phe Pro Glu Leu Glu Ser Leu
115 120 125
Val Pro Asn Ala Leu Asp Tyr Ile Arg Thr Val Lys Glu Leu Gly Asn
130 135 140
Ser Leu Asp Lys Cys Lys Asn Asn Glu Asn Leu Gln Gln Ile Leu Thr
145 150 155 160
Asn Ala Thr Ile Met Val Val Ser Val Thr Ala Ser Thr Thr Gln Gly
165 170 175
Gln Gln Leu Ser Glu Glu Glu Leu Glu Arg Leu Glu Glu Ala Cys Asp

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            180                 185                 190
Met Ala Leu Glu Leu Asn Ala Ser Lys His Arg Ile Tyr Glu Tyr Val
        195                 200                 205
Glu Ser Arg Met Ser Phe Ile Ala Pro Asn Leu Ser Ile Ile Ile Gly
    210                 215                 220
Ala Ser Thr Ala Ala Lys Ile Met Gly Val Ala Gly Gly Leu Thr Asn
225                 230                 235                 240
Leu Ser Lys Met Pro Ala Cys Asn Ile Met Leu Leu Gly Ala Gln Arg
                245                 250                 255
Lys Thr Leu Ser Gly Phe Ser Ser Thr Ser Val Leu Pro His Thr Gly
            260                 265                 270
Tyr Ile Tyr His Ser Asp Ile Val Gln Ser Leu Pro Pro Asp Leu Arg
        275                 280                 285
Arg Lys Ala Ala Arg Leu Val Ala Ala Lys Cys Thr Leu Ala Ala Arg
    290                 295                 300
Val Asp Ser Phe His Glu Ser Thr Glu Gly Lys Val Gly Tyr Glu Leu
305                 310                 315                 320
Lys Asp Glu Ile Glu Arg Lys Phe Asp Lys Trp Gln Glu Pro Pro Pro
                325                 330                 335
Val Lys Gln Val Lys Pro Leu Pro Ala Pro Leu Asp Gly Gln Arg Lys
            340                 345                 350
Lys Arg Gly Gly Arg Arg Tyr Arg Lys Met Lys Glu Arg Leu Gly Leu
        355                 360                 365
Thr Glu Ile Arg Lys Gln Ala Asn Arg Met Ser Phe Gly Glu Ile Glu
    370                 375                 380
Glu Asp Ala Tyr Gln Glu Asp Leu Gly Phe Ser Leu Gly His Leu Gly
385                 390                 395                 400
Lys Ser Gly Ser Gly Arg Val Arg Gln Thr Gln Val Asn Glu Ala Thr
                405                 410                 415
Lys Ala Arg Ile Ser Lys Thr Leu Gln Arg Thr Leu Gln Lys Gln Ser
            420                 425                 430
Val Val Tyr Gly Gly Lys Ser Thr Ile Arg Asp Arg Ser Ser Gly Thr
        435                 440                 445
Ala Ser Ser Val Ala Phe Thr Pro Leu Gln Gly Leu Glu Ile Val Asn
    450                 455                 460
Pro Gln Ala Ala Glu Lys Lys Val Ala Glu Ala Asn Gln Lys Tyr Phe
465                 470                 475                 480
Ser Ser Met Ala Glu Phe Leu Lys Val Lys Gly Glu Lys Ser Gly Leu
                485                 490                 495
Met Ser Thr
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<210> 3589
<211> 675
<212> DNA
<213> Homo sapiens

<400> 3589
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120
aatagttctt gacccaggtc cctccatgaa cctcgaagct gacccagcca taggggggat
180

accttcattt cagtcccagc agcctccccc aaccagtcag ggtccctgaa gagcatctgg
240
ctctccacaa gacaatagac aggaagggga cccagtggcc cccccaagct tagctaatgt
300
gagtgaagaa ccaggcagaa cccaggcagc agatgggata ggagtttcca agccagtgct
360
tggggatagg ccctcccaat tcagaaacaa agcaaggccc tggccacagc caggaaggat
420
tgtaagggcc ttcctgagca gacacaaagg agccctgagc tgctgggggt gatgaggagc
480
ggaggcaggg ccaggcagag ggtctgcaaa gaattacact ggaaaggtgg aaggggaca
540
ttgggtctag tggtttggcc tgtggagagc tgtcaggaga ggggaggatg aggttggtgg
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660
gaggcagcca cgcgt
675

<210> 3590
<211> 117
<212> PRT
<213> Homo sapiens

<400> 3590
Met Leu Pro Thr Arg Pro Pro Asn Thr Leu Ala Ser Gly Val Ser Thr
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Asn Leu Ile Leu Pro Ser Pro Asp Ser Ser Pro Gln Ala Lys Pro Leu
            20   25   30
Asp Pro Met Ser Pro Phe His Leu Ser Ser Val Ile Leu Cys Arg Pro
        35   40   45
Ser Ala Trp Pro Cys Leu Arg Ser Ser Ser Pro Pro Ala Ala Gln Gly
    50   55   60
Ser Phe Val Ser Ala Gln Glu Gly Pro Tyr Asn Pro Ser Trp Leu Trp
65   70   75   80
Pro Gly Pro Cys Phe Val Ser Glu Leu Gly Gly Pro Ile Pro Lys His
                85   90   95
Trp Leu Gly Asn Ser Tyr Pro Ile Cys Cys Leu Gly Ser Ala Trp Phe
            100   105   110
Phe Thr His Ile Ser
        115

<210> 3591
<211> 669
<212> DNA
<213> Homo sapiens

<400> 3591
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cgcggaaggg cccccgcctc cctaggctgg cagaggaagc aggttaattg gaaggcctgc
120
cgatggtctt catcaggggt gattcctaat gaaaaaatac gaaatattgg aatctcagct
180

cacattgatt ctgggaaaac tacattaaca gaacgagtcc tttactacac tggcagaatt
240
gcaaagatgc atgaggtgaa aggtaaagat ggagttggtg ctgtcatgga ttccatggaa
300
ctagagagac aaagaggaat cactattcag tcagcagcca cttacaccat gtggaaagat
360
gtcaatatta acattataga tactcctggg catgtggact tcacaataga agtggaaagg
420
gccctgagag tgttggatgg tgcagtcctt gttctctgtg ctgttggagg ggtacagtgc
480
cagaccatga ctgtcaatcg tcagatgaag cgctacaacg ttccgtttct aacttttatt
540
aacaaattgg accgaatggg ctccaaccca gccagggccc tgcagcaaat gaggtctaaa
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ctaaatcata atgcagcgtt tatgcagata cccatgggtt tggagggtaa ttttaaaggt
660
attgtagat
669

<210> 3592
<211> 223
<212> PRT
<213> Homo sapiens

<400> 3592

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Ala	Ala	Leu	Gly	Arg	Gly	Arg	Ala	Pro	Ala	Ser	Leu	Gly	Trp	Gln	Arg
		20					25					30			
Lys	Gln	Val	Asn	Trp	Lys	Ala	Cys	Arg	Trp	Ser	Ser	Ser	Gly	Val	Ile
	35					40					45				
Pro	Asn	Glu	Lys	Ile	Arg	Asn	Ile	Gly	Ile	Ser	Ala	His	Ile	Asp	Ser
50					55					60					
Gly	Lys	Thr	Thr	Leu	Thr	Glu	Arg	Val	Leu	Tyr	Tyr	Thr	Gly	Arg	Ile
65				70					75						80
Ala	Lys	Met	His	Glu	Val	Lys	Gly	Lys	Asp	Gly	Val	Gly	Ala	Val	Met
			85					90						95	
Asp	Ser	Met	Glu	Leu	Glu	Arg	Gln	Arg	Gly	Ile	Thr	Ile	Gln	Ser	Ala
		100					105					110			
Ala	Thr	Tyr	Thr	Met	Trp	Lys	Asp	Val	Asn	Ile	Asn	Ile	Ile	Asp	Thr
	115					120					125				
Pro	Gly	His	Val	Asp	Phe	Thr	Ile	Glu	Val	Glu	Arg	Ala	Leu	Arg	Val
130					135					140					
Leu	Asp	Gly	Ala	Val	Leu	Val	Leu	Cys	Ala	Val	Gly	Gly	Val	Gln	Cys
145				150					155						160
Gln	Thr	Met	Thr	Val	Asn	Arg	Gln	Met	Lys	Arg	Tyr	Asn	Val	Pro	Phe
			165					170					175		
Leu	Thr	Phe	Ile	Asn	Lys	Leu	Asp	Arg	Met	Gly	Ser	Asn	Pro	Ala	Arg
		180					185					190			
Ala	Leu	Gln	Gln	Met	Arg	Ser	Lys	Leu	Asn	His	Asn	Ala	Ala	Phe	Met
	195					200					205				
Gln	Ile	Pro	Met	Gly	Leu	Glu	Gly	Asn	Phe	Lys	Gly	Ile	Val	Asp	
210					215					220					

<210> 3593
<211> 1005
<212> DNA
<213> Homo sapiens

<400> 3593
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120
ccctcaagca acggatcccc atggcgcttg ttgggcgcgt tgtgcctgca gcggccacct
180
gtagtctcca agccgttgac cccattgcag gaagagatgg cgtctctact gcagcagatt
240
gagatagaga gaagcctgta ttcagaccac gagcttcgtg ctctggatga aaaccagcga
300
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360
caagatttgg aagatatgtg ggagcagaaa tttctacagt tcaaacttgg agctcgcata
420
acagaagctg atgaaaagaa tgaccgaaca tccctgaaca ggaagctaga caggaacctt
480
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540
tggcagcctg gggagaccct tcgaggaaca gctgaacgaa ccctggccac actctcagaa
600
aacaacatgg aagccaagtt cctaggaaat gcaccctgtg ggcactacac attcaagttc
660
ccccaggcaa tgcggacaga gagtaacctc ggagccaagg tgttcttctt caaagcactg
720
ctattaactg gagacttttc ccaggctggg aataagggcc atcatgtgtg ggtcactaag
780
gatgagctgg gtgactattt gaaaccaaaa tacctggccc aagttaggag gtttgtttca
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gagaaataaa cgagtctatt actgaaaaaa aaaaaaaaaa aaaaa
1005

<210> 3594
<211> 282
<212> PRT
<213> Homo sapiens

<400> 3594
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20 25 30
Arg Ser Leu Ala Leu Ala Ala Ala Pro Ser Ser Asn Gly Ser Pro Trp
35 40 45
Arg Leu Leu Gly Ala Leu Cys Leu Gln Arg Pro Pro Val Val Ser Lys

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    50                  55                  60
Pro Leu Thr Pro Leu Gln Glu Glu Met Ala Ser Leu Leu Gln Gln Ile
65                  70                  75                  80
Glu Ile Glu Arg Ser Leu Tyr Ser Asp His Glu Leu Arg Ala Leu Asp
                85                  90                  95
Glu Asn Gln Arg Leu Ala Lys Lys Lys Ala Asp Leu His Asp Glu Glu
            100                 105                 110
Asp Glu Gln Asp Ile Leu Leu Ala Gln Asp Leu Glu Asp Met Trp Glu
        115                 120                 125
Gln Lys Phe Leu Gln Phe Lys Leu Gly Ala Arg Ile Thr Glu Ala Asp
    130                 135                 140
Glu Lys Asn Asp Arg Thr Ser Leu Asn Arg Lys Leu Asp Arg Asn Leu
145                 150                 155                 160
Val Leu Leu Val Arg Glu Lys Phe Gly Asp Gln Asp Val Trp Ile Leu
                165                 170                 175
Pro Gln Ala Glu Trp Gln Pro Gly Glu Thr Leu Arg Gly Thr Ala Glu
            180                 185                 190
Arg Thr Leu Ala Thr Leu Ser Glu Asn Asn Met Glu Ala Lys Phe Leu
        195                 200                 205
Gly Asn Ala Pro Cys Gly His Tyr Thr Phe Lys Phe Pro Gln Ala Met
    210                 215                 220
Arg Thr Glu Ser Asn Leu Gly Ala Lys Val Phe Phe Phe Lys Ala Leu
225                 230                 235                 240
Leu Leu Thr Gly Asp Phe Ser Gln Ala Gly Asn Lys Gly His His Val
                245                 250                 255
Trp Val Thr Lys Asp Glu Leu Gly Asp Tyr Leu Lys Pro Lys Tyr Leu
            260                 265                 270
Ala Gln Val Arg Arg Phe Val Ser Asp Leu
        275                 280
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<210> 3595
<211> 1903
<212> DNA
<213> Homo sapiens

<400> 3595

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180
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240
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300
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360
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420
tccggcatcc ctgccggcat caacatcccc aactacgatg atctgaggca gacggaaggc
480
tttaagaacg tgtcgctggg gaatgtgctg gctgtggcct acgccacgca gcgggagaag
540
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660
gacgaaaaag gagcattcaa ctttgaccag gaaacagtga tcaacccaga gacgggcgag
720
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780
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1440
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1560
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1620
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1800
gacagctagg gttcaaaacg ttctcaccaa atccaatgct cctcacatat taattttata
1860
accagacaaa taaatattag agacaaccac catcaaaaaa aaa
1903

<210> 3596
<211> 496
<212> PRT
<213> Homo sapiens

<400> 3596
Phe Gln Val Thr Arg Gly Asp Tyr Ala Pro Ile Leu Gln Lys Val Val

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Glu Gln Leu Glu Lys Ala Lys Ala Tyr Ala Ala Asn Ser His Gln Gly
            20                  25                  30
Gln Met Leu Ala Gln Tyr Ile Glu Ser Phe Thr Gln Gly Ser Ile Glu
        35                  40                  45
Ala His Lys Arg Gly Ser Arg Phe Trp Ile Gln Asp Lys Gly Pro Ile
    50                  55                  60
Val Glu Ser Tyr Ile Gly Phe Ile Glu Ser Tyr Arg Asp Pro Phe Gly
65                  70                  75                  80
Ser Arg Gly Glu Phe Glu Gly Phe Val Ala Val Val Asn Lys Ala Met
                85                  90                  95
Ser Ala Lys Phe Glu Arg Leu Val Ala Ser Ala Glu Gln Leu Leu Lys
            100                 105                 110
Glu Leu Pro Trp Pro Pro Thr Phe Glu Lys Asp Lys Phe Leu Thr Pro
        115                 120                 125
Asp Phe Thr Ser Leu Asp Val Leu Thr Phe Ala Gly Ser Gly Ile Pro
    130                 135                 140
Ala Gly Ile Asn Ile Pro Asn Tyr Asp Asp Leu Arg Gln Thr Glu Gly
145                 150                 155                 160
Phe Lys Asn Val Ser Leu Gly Asn Val Leu Ala Val Ala Tyr Ala Thr
                165                 170                 175
Gln Arg Glu Lys Leu Thr Phe Leu Glu Glu Asp Asp Lys Asp Leu Tyr
            180                 185                 190
Ile Leu Trp Lys Gly Pro Ser Phe Asp Val Gln Val Gly Leu His Glu
        195                 200                 205
Leu Leu Gly His Gly Ser Gly Lys Leu Phe Val Gln Asp Glu Lys Gly
    210                 215                 220
Ala Phe Asn Phe Asp Gln Glu Thr Val Ile Asn Pro Glu Thr Gly Glu
225                 230                 235                 240
Gln Ile Gln Ser Trp Tyr Arg Ser Gly Glu Thr Trp Asp Ser Lys Phe
                245                 250                 255
Ser Thr Ile Ala Ser Ser Tyr Glu Glu Cys Arg Ala Glu Ser Val Gly
            260                 265                 270
Leu Tyr Leu Cys Leu His Pro Gln Val Leu Glu Ile Phe Gly Phe Glu
        275                 280                 285
Gly Ala Asp Ala Glu Asp Val Ile Tyr Val Asn Trp Leu Asn Met Val
    290                 295                 300
Arg Ala Gly Leu Leu Ala Leu Glu Phe Tyr Thr Pro Glu Ala Phe Asn
305                 310                 315                 320
Trp Arg Gln Ala His Met Gln Ala Arg Phe Val Ile Leu Arg Val Leu
                325                 330                 335
Leu Glu Ala Gly Glu Gly Leu Val Thr Ile Thr Pro Thr Thr Gly Ser
            340                 345                 350
Asp Gly Arg Pro Asp Ala Arg Val Arg Leu Asp Arg Ser Lys Ile Arg
        355                 360                 365
Ser Val Gly Lys Pro Ala Leu Glu Arg Phe Leu Arg Arg Leu Gln Val
    370                 375                 380
Leu Lys Ser Thr Gly Asp Val Ala Gly Gly Arg Ala Leu Tyr Glu Gly
385                 390                 395                 400
Tyr Ala Thr Val Thr Asp Ala Pro Pro Glu Cys Phe Leu Thr Leu Arg
                405                 410                 415
Asp Thr Val Leu Leu Arg Lys Glu Ser Arg Lys Leu Ile Val Gln Pro
            420                 425                 430
Asn Thr Arg Leu Glu Gly Asn Gly Ser Asp Val Gln Leu Leu Glu Tyr
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435 440 445
Glu Ala Ser Ala Ala Gly Leu Ile Arg Ser Phe Ser Glu Arg Phe Pro
450 455 460
Glu Asp Gly Pro Glu Leu Glu Glu Ile Leu Thr Gln Leu Ala Thr Ala
465 470 475 480
Asp Ala Arg Phe Trp Lys Gly Pro Ser Glu Ala Pro Ser Gly Gln Ala
485 490 495

<210> 3597
<211> 1090
<212> DNA
<213> Homo sapiens

<400> 3597
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120
gaaaatggtg ttctgctgtg tgatttgatt aataagctta aacctggcgt cattaagaag
180
atcaatagac tgtctacacc aatagcagga ttggataata taaacgtttt cttgaaagct
240
tgtgaacaga ttggattgaa agaagcccag cttttccatc ctggagatct acaggattta
300
tcaaatcgag tcactgtcaa gcaagaagag actgacagga gagtgaaaaa tgttttgata
360
acattgtact ggctgggaag aaaagcacaa agcaacccgt actataatgg tccccatctt
420
aatttgaaag cgtttgagaa tcttttagga caagcactga cgaaggcact cgaagactcc
480
agcttcctga aaagaagtgg cagggacagt ggctacggtg acatctggtg tcctgaacgt
540
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600
tctttgggct cgaggtcatt gacaagctgc tcctctgata tcacgttgag agggggggcgt
660
gaaggttttg aaagtgacac agattcggaa tttacattca agatgcagga ttataataaa
720
gatgatatgt cgtatcgaag gatttcggct gttgagccaa agactgcgtt acccttcaat
780
cgtttttttac ccaacaaaag tagacagcca tcctatgtac cagcacctct gagaaagaaa
840
aagccagaca aacatgagga taacagaaga agttgggcaa gcccggttta tacagaagca
900
gatggaacat tttcaaggag taagtccatg agtgatgtca gcgcagaaga tgttcaaaac
960
ttgcgtcagc tgcgttacga ggagatgcag aaaataaaat cacaattaaa agaacaagat
1020
cagaaatggc aggatgacct tgcaaaatgg aaagatcgtc gaaaaagtta cacttcagat
1080
ctgcagaaga
1090

<210> 3598

<211> 159
<212> PRT
<213> Homo sapiens

<400> 3598
Arg Ser Leu Thr Ser Cys Ser Ser Asp Ile Thr Leu Arg Gly Gly Arg
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Glu Gly Phe Glu Ser Asp Thr Asp Ser Glu Phe Thr Phe Lys Met Gln
20 25 30
Asp Tyr Asn Lys Asp Asp Met Ser Tyr Arg Arg Ile Ser Ala Val Glu
35 40 45
Pro Lys Thr Ala Leu Pro Phe Asn Arg Phe Leu Pro Asn Lys Ser Arg
50 55 60
Gln Pro Ser Tyr Val Pro Ala Pro Leu Arg Lys Lys Lys Pro Asp Lys
65 70 75 80
His Glu Asp Asn Arg Arg Ser Trp Ala Ser Pro Val Tyr Thr Glu Ala
85 90 95
Asp Gly Thr Phe Ser Arg Ser Lys Ser Met Ser Asp Val Ser Ala Glu
100 105 110
Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile
115 120 125
Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala
130 135 140
Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys
145 150 155

<210> 3599
<211> 691
<212> DNA
<213> Homo sapiens

<400> 3599
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120
aggagctggt cggggtccct ggtggggtgg ctggctcccc gtcccttgtc cgtgccgata
180
gagcatctgc tgggagccaa gaactgctgc aggcacgggg ggcagtgggt gaggcgtgca
240
gtcccagccg tcctgagctt agtgggagcc tcgagccttc atcatgcagt gtatttgttt
300
ctgttgtgat ccagctgatc cattgatcag tggggttggg gacgcttctg ttctgctcat
360
ttattgctgt gtaacaaacc acctctaagt gagggcttta aaacaagatc gttcatttct
420
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480
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540
cagacaatga gggctttggc ggctggggct ccccagcgac acccttcacc tcgtggcctc
600
caggtagcct gtccacctgc caagaacaca cacacccagc cccacaggtc acccctcacc
660

tgctgctgct cctctctctc cctgcacgcg t
691

<210> 3600
<211> 98
<212> PRT
<213> Homo sapiens

<400> 3600
Met Gly Ser Cys Tyr Lys Thr Lys Lys Phe Leu Leu Ser Leu Ala Glu
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Asn Lys Leu Gly Pro Cys Met Leu Leu Ala Leu Arg Gly Asn Gln Thr
20 25 30
Met Val Glu Val Arg Ser Trp Ser Gly Ser Leu Val Gly Trp Leu Ala
35 40 45
Pro Arg Pro Leu Ser Val Pro Ile Glu His Leu Leu Gly Ala Lys Asn
50 55 60
Cys Cys Arg His Gly Gly Gln Trp Val Arg Arg Ala Val Pro Ala Val
65 70 75 80
Leu Ser Leu Val Gly Ala Ser Ser Leu His His Ala Val Tyr Leu Phe
85 90 95
Leu Leu

<210> 3601
<211> 2963
<212> DNA
<213> Homo sapiens

<400> 3601
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gtgtgcactg ctgtttactt agtatttttc tttaactaga tttatttta aacaaggctt
120
tgtccaagga catttggctc gcaggcacag agctgattaa ctcgttatgt atcttttgat
180
aataaggcag cgatcattaa gaaaaacgtg tagccaatga aataacatgt tctgggcccc
240
accactggac tgggaggtgc agcgcatcca agcagaggct gcctcctgcc ctccacgcct
300
gctgctctcg caggcagggg ctctgctgct tacagcagtg cggccatctc ggcttctctc
360
cacatcgtct gtcacgcgct ggtccccacc atacctctcg ccaccccgtg cctctgtccc
420
cgtgcggcct gaggagctcc agctttccct gccagcggtg ctctgggagt ggggacgtga
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tgcagggcga gcatgatgca acggggcacc ccagaccctt ccctcccgtg gggggagggg
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tgtggcacgc agaggggcag agggcgggga cactggcccc gtgggggaag aaggtgctgt
600
cacagccgtt actgtccccc gtgggacccc agcctggagc cccccatcct ttggctcctg
660
cctgtggcca ctcagctctc aggtggccac atgcacatcc cctgctcctt ccctgcgcac
720

ctgccctgcc cagtggcctt tctggtccca gctactgaaa ccggtgagct gctccagggt
780
gaggctgctt tctggctcct ggtgtatttg gacacagata ggcccttagt gtccagaggc
840
gccccatgca gccctcatgg tcagcaggac acccaggata gacccccctcc acgcagcacc
900
tgggccctgg gagcggctgc ttttaggatg ccacctgttc ctgggcgcct tgtttttagc
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1020
tctcctctct gtggcaggta catgtcccag agcaagcaca cggaggcccg ggagctcatg
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1140
atgctggtcc tggagtccct ggagaaggcg gaagtggagg tggctgacga gctgctggaa
1200
aatctggcta aagtgttcag cctgatggac cccaactctc ctgagcgcgt gacctttgtg
1260
tccagagccc tgaagtggtc cagtgggggc tccgggaagc tgggccaccc ccggctgcac
1320
cagctgctgg ccctcaccct gtggaaagaa caaaactatt gtgagtcgag gtatcatttt
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1440
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1980
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2100
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2340

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2400
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2520
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2580
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2640
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2700
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2760
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2820
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2880
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2940
aaaaaaaaaa aaaaaaaaaa aaa
2963

<210> 3602
<211> 299
<212> PRT
<213> Homo sapiens

<400> 3602
Pro Glu Asp Glu Arg Gly Ser Ala Val Ala Arg Ala Arg Gly Arg Gly
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Ser Arg Ser Pro Leu Cys Gly Arg Tyr Met Ser Gln Ser Lys His Thr
            20   25   30
Glu Ala Arg Glu Leu Met Tyr Ser Gly Ala Leu Leu Phe Phe Ser His
        35   40   45
Gly Gln Gln Asn Ser Ala Ala Asp Leu Ser Met Leu Val Leu Glu Ser
    50   55   60
Leu Glu Lys Ala Glu Val Glu Val Ala Asp Glu Leu Leu Glu Asn Leu
65   70   75   80
Ala Lys Val Phe Ser Leu Met Asp Pro Asn Ser Pro Glu Arg Val Thr
                85   90   95
Phe Val Ser Arg Ala Leu Lys Trp Ser Ser Gly Gly Ser Gly Lys Leu
            100   105   110
Gly His Pro Arg Leu His Gln Leu Leu Ala Leu Thr Leu Trp Lys Glu
        115   120   125
Gln Asn Tyr Cys Glu Ser Arg Tyr His Phe Leu His Ser Ala Asp Gly
    130   135   140
Glu Gly Cys Ala Asn Met Leu Val Glu Tyr Ser Thr Ser Arg Gly Phe
145   150   155   160
Arg Ser Glu Val Asp Met Phe Val Ala Gln Ala Val Leu Gln Phe Leu
                165   170   175
Cys Leu Lys Asn Lys Ser Ser Ala Ser Val Val Phe Thr Thr Tyr Thr
            180   185   190
Gln Lys His Pro Ser Ile Glu Asp Gly Pro Pro Phe Val Glu Pro Leu

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        195                 200                 205
Leu Asn Phe Ile Trp Phe Leu Leu Leu Ala Val Asp Gly Gly Lys Leu
    210                 215                 220
Thr Val Phe Thr Val Leu Cys Glu Gln Tyr Gln Pro Ser Leu Arg Arg
225                 230                 235                 240
Asp Pro Met Tyr Asn Glu Tyr Leu Asp Arg Ile Gly Gln Leu Phe Phe
                245                 250                 255
Gly Val Pro Pro Lys Gln Thr Ser Ser Tyr Gly Gly Leu Leu Gly Asn
            260                 265                 270
Leu Leu Thr Ser Leu Met Gly Ser Ser Glu Gln Glu Asp Gly Glu Glu
        275                 280                 285
Ser Pro Ser Asp Gly Ser Pro Ile Glu Leu Asp
    290                 295
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<210> 3603
<211> 1082
<212> DNA
<213> Homo sapiens

<400> 3603
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120
agagagccga tgatttttaa atgtgtgttt gtgggtgaaa tggctgcgca ggtcggagcg
180
gtgcgcgtag tacgggcggt ggcggcgcag gaggagccgg acaaagaggg gaaggagaaa
240
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360
cgtcgcagcc gccaacatcc tgggccgctg ccgccaacga atgcagcccc aactgtccca
420
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480
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600
accaccgcgg ccccgatggt gatcccagct cctgcggaac cgatctcaag cacaaggaca
660
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720
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780
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840
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900
gacaaataaa tagcacttca ggacttaata aggagtcctt caggtatctg aaagatgaac
960
agctgtgccg attaaatttg ggtatgcaag aatatcgggt accccaggga gtacaaacac
1020

cttttatgac tcaccaggaa cattctattc gtagaaattt cttaaaaaca ggtactaaat
1080
tt
1082

<210> 3604
<211> 146
<212> PRT
<213> Homo sapiens

<400> 3604
Met Lys Met Val Lys Pro Arg Glu Pro Met Ile Phe Lys Cys Val Phe
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Val Gly Glu Met Ala Ala Gln Val Gly Ala Val Arg Val Val Arg Ala
20 25 30
Val Ala Ala Gln Glu Glu Pro Asp Lys Glu Gly Lys Glu Lys Pro His
35 40 45
Ala Gly Val Ser Pro Arg Gly Val Lys Arg Gln Arg Arg Ser Ser Ser
50 55 60
Gly Gly Ser Gln Glu Lys Arg Gly Arg Pro Ser Gln Glu Pro Pro Leu
65 70 75 80
Ala Pro Pro His Arg Arg Arg Arg Ser Arg Gln His Pro Gly Pro Leu
85 90 95
Pro Pro Thr Asn Ala Ala Pro Thr Val Pro Gly Pro Val Glu Pro Leu
100 105 110
Leu Leu Pro Pro Pro Pro Pro Pro Ser Leu Ala Pro Ala Gly Pro Ala
115 120 125
Val Ala Ala Pro Leu Pro Ala Pro Ser Thr Arg Pro Ser Ser Pro Ser
130 135 140
Arg Leu
145

<210> 3605
<211> 2004
<212> DNA
<213> Homo sapiens

<400> 3605
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120
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180
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240
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300
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360
acctttgtgt ccagagccct gaagtggtcc agtgggggct ccgggaagct gggccacccc
420
cggctgcacc agctgctggc cctcaccctg tggaaagaac aaaactattg tgagtcgagg
480

tatcattttc tgcactcagc ggacggggag ggctgtgcca acatgctggt ggagtattcc
540
acgtcccgcg gcttccgcag cgaggtggac atgttcgtgg ctcaggccgt gctacagttt
600
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660
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720
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780
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900
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1320
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1860
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1920
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1980
ctaccgggca aaaaaaaaaa aaaa
2004

<210> 3606

<211> 324
<212> PRT
<213> Homo sapiens

<400> 3606
Xaa Arg Arg Arg Trp Pro Ser Arg Arg Ala Pro Ala Thr Ala Ala Gln
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Pro Arg Gly Val Gln Arg Val Glu Gly Lys Leu Arg Ala Ser Val Glu
20 25 30
Lys Gly Asp Tyr Tyr Glu Ala His Gln Met Tyr Arg Thr Leu Phe Phe
35 40 45
Arg Tyr Met Ser Gln Ser Lys His Thr Glu Ala Arg Glu Leu Met Tyr
50 55 60
Ser Gly Ala Leu Leu Phe Phe Ser His Gly Gln Gln Asn Ser Ala Ala
65 70 75 80
Asp Leu Ser Met Leu Val Leu Glu Ser Leu Glu Lys Ala Glu Val Glu
85 90 95
Val Ala Asp Glu Leu Leu Glu Asn Leu Ala Lys Val Phe Ser Leu Met
100 105 110
Asp Pro Asn Ser Pro Glu Arg Val Thr Phe Val Ser Arg Ala Leu Lys
115 120 125
Trp Ser Ser Gly Gly Ser Gly Lys Leu Gly His Pro Arg Leu His Gln
130 135 140
Leu Leu Ala Leu Thr Leu Trp Lys Glu Gln Asn Tyr Cys Glu Ser Arg
145 150 155 160
Tyr His Phe Leu His Ser Ala Asp Gly Glu Gly Cys Ala Asn Met Leu
165 170 175
Val Glu Tyr Ser Thr Ser Arg Gly Phe Arg Ser Glu Val Asp Met Phe
180 185 190
Val Ala Gln Ala Val Leu Gln Phe Leu Cys Leu Lys Asn Lys Ser Ser
195 200 205
Ala Ser Val Val Phe Thr Thr Tyr Thr Gln Lys His Pro Ser Ile Glu
210 215 220
Asp Gly Pro Pro Phe Val Glu Pro Leu Leu Asn Phe Ile Trp Phe Leu
225 230 235 240
Leu Leu Ala Val Asp Gly Gly Lys Leu Thr Val Phe Thr Val Leu Cys
245 250 255
Glu Gln Tyr Gln Pro Ser Leu Arg Arg Asp Pro Met Tyr Asn Glu Tyr
260 265 270
Leu Asp Arg Ile Gly Gln Leu Phe Phe Gly Val Pro Pro Lys Gln Thr
275 280 285
Ser Ser Tyr Gly Gly Leu Leu Gly Asn Leu Leu Thr Ser Leu Met Gly
290 295 300
Ser Ser Glu Gln Glu Asp Gly Glu Glu Ser Pro Ser Asp Gly Ser Pro
305 310 315 320
Ile Glu Leu Asp

<210> 3607
<211> 1726
<212> DNA
<213> Homo sapiens

<400> 3607

nacgcgtcgt gggagttggt ggaccccaca ccggacttgc aggcactgtt tgttcagttt
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120
accctgtgtg ctgggatatg cagctatgaa gggaagggtg gaatgtgttc catccgtctc
180
agcgaacccc ttttgaagtt gaggccaaga aaggatcttg tagagaccct cctgcatgaa
240
atgatacatg cctatttatt tgtcactaat aacgacaaag accgagaagg gcatggtcca
300
gaattttgta aacatatgca tcgcatcaac agcctgactg gagccaatat aacggtatac
360
catacttttc acgatgaggt ggatgagtat cggcgacact ggtggcgctg caatgggccg
420
tgccagcaca ggccaccgta ttacggctat gtcaaacgag ctactaacag ggaaccctct
480
gctcatgact attggtgggc tgagcaccag aaaacctgtg gaggcactta cataaaaatc
540
aaggaaccag agaattactc aaaaaaaggc aaaggaaagg caaaactagg aaaggaacca
600
gtattggccg cagagaataa agataaaccc aacagaggtg aggcccagct agtaatccct
660
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720
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780
gctgtaagac ctaattctaa aatcaaggtg aaatttgaac agaatggttc aagtaaaaat
840
tctcatctgg tctcccctgc tgttagtaac agtcaccaaa atgttctaag caactacttt
900
cctagagtat catttgccaa ccaaaaggct ttcagaggtg tgaatggatc tccaaggata
960
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1020
tcatcttcta agatatccct aagaaattct tcaaaagtaa cggaatcagc atctgtgatg
1080
ccatcccagg atgtgagtgg gtctgaagat acattcccaa ataaacgacc taggctagaa
1140
gataagactg tttttgacaa tttttttatc aagaaagagc aaataaaaag cagtggtaat
1200
gatccaaagt atagtacaac cacagctcag aattccagca gttcatccag tcagagcaaa
1260
atggttaatt gcccagtttg tcagaatgaa gttctgggag tctcagatta atgagcactt
1320
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1380
gtttcaaagt ctcaagtacc acctgtatta tctcactaat gtgctatgtc agccagtcag
1440
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1500
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1560
gtgctacatt cactcttgcc ttaggtatac tgtaacccag gttctgcctg tcgtgtataa
1620

ttttagata cttttgttct ttcttgctct taaggatttt aaaaacctgt taatcttttt
1680
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1726

<210> 3608
<211> 436
<212> PRT
<213> Homo sapiens

<400> 3608
Xaa Ala Ser Trp Glu Leu Val Asp Pro Thr Pro Asp Leu Gln Ala Leu
1 5 10 15
Phe Val Gln Phe Asn Asp Gln Phe Phe Trp Gly Gln Leu Glu Ala Val
20 25 30
Glu Val Lys Trp Ser Val Arg Met Thr Leu Cys Ala Gly Ile Cys Ser
35 40 45
Tyr Glu Gly Lys Gly Gly Met Cys Ser Ile Arg Leu Ser Glu Pro Leu
50 55 60
Leu Lys Leu Arg Pro Arg Lys Asp Leu Val Glu Thr Leu Leu His Glu
65 70 75 80
Met Ile His Ala Tyr Leu Phe Val Thr Asn Asn Asp Lys Asp Arg Glu
85 90 95
Gly His Gly Pro Glu Phe Cys Lys His Met His Arg Ile Asn Ser Leu
100 105 110
Thr Gly Ala Asn Ile Thr Val Tyr His Thr Phe His Asp Glu Val Asp
115 120 125
Glu Tyr Arg Arg His Trp Trp Arg Cys Asn Gly Pro Cys Gln His Arg
130 135 140
Pro Pro Tyr Tyr Gly Tyr Val Lys Arg Ala Thr Asn Arg Glu Pro Ser
145 150 155 160
Ala His Asp Tyr Trp Trp Ala Glu His Gln Lys Thr Cys Gly Gly Thr
165 170 175
Tyr Ile Lys Ile Lys Glu Pro Glu Asn Tyr Ser Lys Lys Gly Lys Gly
180 185 190
Lys Ala Lys Leu Gly Lys Glu Pro Val Leu Ala Ala Glu Asn Lys Asp
195 200 205
Lys Pro Asn Arg Gly Glu Ala Gln Leu Val Ile Pro Phe Ser Gly Lys
210 215 220
Gly Tyr Val Leu Gly Glu Thr Ser Asn Leu Pro Ser Pro Gly Lys Leu
225 230 235 240
Ile Thr Ser His Ala Ile Asn Lys Thr Gln Asp Leu Leu Asn Gln Asn
245 250 255
His Ser Ala Asn Ala Val Arg Pro Asn Ser Lys Ile Lys Val Lys Phe
260 265 270
Glu Gln Asn Gly Ser Ser Lys Asn Ser His Leu Val Ser Pro Ala Val
275 280 285
Ser Asn Ser His Gln Asn Val Leu Ser Asn Tyr Phe Pro Arg Val Ser
290 295 300
Phe Ala Asn Gln Lys Ala Phe Arg Gly Val Asn Gly Ser Pro Arg Ile
305 310 315 320
Ser Val Thr Val Gly Asn Ile Pro Lys Asn Ser Val Ser Ser Ser Ser
325 330 335
Gln Arg Arg Val Ser Ser Ser Lys Ile Ser Leu Arg Asn Ser Ser Lys

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            340                 345                 350
Val Thr Glu Ser Ala Ser Val Met Pro Ser Gln Asp Val Ser Gly Ser
        355                 360                 365
Glu Asp Thr Phe Pro Asn Lys Arg Pro Arg Leu Glu Asp Lys Thr Val
    370                 375                 380
Phe Asp Asn Phe Phe Ile Lys Lys Glu Gln Ile Lys Ser Ser Gly Asn
385                 390                 395                 400
Asp Pro Lys Tyr Ser Thr Thr Thr Ala Gln Asn Ser Ser Ser Ser Ser
                405                 410                 415
Ser Gln Ser Lys Met Val Asn Cys Pro Val Cys Gln Asn Glu Val Leu
            420                 425                 430
Gly Val Ser Asp
        435
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<210> 3609
<211> 1286
<212> DNA
<213> Homo sapiens

<400> 3609
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120
tgcgtcaacc agtgggagca gctgaggggg ccgggtggca acgaggatgg gccacagaag
180
ctggacttgg aagctgatgc tgagccccaa gacctcgaga gtacgaacct cttggagagt
240
gaagctccca gggactattt cctcaagttt gcctatattg tggatttgga cagcgacaca
300
gcagacaagt tcctgcagct gntttggaac caaaggtgtc aagagggtgc tgtgtcctat
360
caannctacc ccttgtcgcc cacccgcttc acccattgtg agcaggtgct gggcgagggt
420
gccctggacc gaggcaccta ctactgggag gtggagatta tcgagggctg ggtcagcatg
480
ggggtcatgg ccgcagactt ctccccacaa gagccctacg accgcggccg gctgggccgc
540
aacgcccact cctgctgcct gcagtggaat ggacgcagct tctccgtctg gtttcatggg
600
ctggaggctc ccctgcccca ccccttctcg cccacggttg gggtctgcct ggaatacgct
660
gaccgtgcct tggccttcta tgctgtacgg gacggcaaga tgagcctcct gcggaggctg
720
aaggcctccc ggccccgccg gggtggcatc ccggcctccc ccattgaccc cttccagagc
780
cgcctggaca gtcactttgc ggggctcttc acccacagac tcaagcctgc cttcttcctg
840
gagagtgtgg acgcccactt gcagatcggg cccctcaaga agtcctgcat atccgtgctg
900
aagaggaggt gatgccgggc acgggcgctc ctgctgccgt ctctgctcca ggaagctgcc
960
tcctctgggc cctctccttc gtctgggaag gcaccagcat gagtcccaca cacccagcct
1020

tctcatttct agaggcttcc acctttttat acactcagcc ttccctctcc caggcaggag
1080
gacccccaga ccctgttccc ctgcagacct cacttctggg agacagagct acagctggga
1140
cagctccaag ctaccctaac ccctcctttc ccaggtttct agaatagtgt ctggcatgta
1200
gtagatgctc aataaacact tgtcgagggg cccgatctgc aagtggggtc cgtcgaccgg
1260
ccgctaattt agtagtagta gtaggc
1286

<210> 3610
<211> 268
<212> PRT
<213> Homo sapiens

<400> 3610
Met Leu Ala Val Ala Cys Val Asn Gln Trp Glu Gln Leu Arg Gly Pro
1 5 10 15
Gly Gly Asn Glu Asp Gly Pro Gln Lys Leu Asp Leu Glu Ala Asp Ala
20 25 30
Glu Pro Gln Asp Leu Glu Ser Thr Asn Leu Leu Glu Ser Glu Ala Pro
35 40 45
Arg Asp Tyr Phe Leu Lys Phe Ala Tyr Ile Val Asp Leu Asp Ser Asp
50 55 60
Thr Ala Asp Lys Phe Leu Gln Leu Xaa Trp Asn Gln Arg Cys Gln Glu
65 70 75 80
Gly Ala Val Ser Tyr Gln Xaa Tyr Pro Leu Ser Pro Thr Arg Phe Thr
85 90 95
His Cys Glu Gln Val Leu Gly Glu Gly Ala Leu Asp Arg Gly Thr Tyr
100 105 110
Tyr Trp Glu Val Glu Ile Ile Glu Gly Trp Val Ser Met Gly Val Met
115 120 125
Ala Ala Asp Phe Ser Pro Gln Glu Pro Tyr Asp Arg Gly Arg Leu Gly
130 135 140
Arg Asn Ala His Ser Cys Cys Leu Gln Trp Asn Gly Arg Ser Phe Ser
145 150 155 160
Val Trp Phe His Gly Leu Glu Ala Pro Leu Pro His Pro Phe Ser Pro
165 170 175
Thr Val Gly Val Cys Leu Glu Tyr Ala Asp Arg Ala Leu Ala Phe Tyr
180 185 190
Ala Val Arg Asp Gly Lys Met Ser Leu Leu Arg Arg Leu Lys Ala Ser
195 200 205
Arg Pro Arg Arg Gly Gly Ile Pro Ala Ser Pro Ile Asp Pro Phe Gln
210 215 220
Ser Arg Leu Asp Ser His Phe Ala Gly Leu Phe Thr His Arg Leu Lys
225 230 235 240
Pro Ala Phe Phe Leu Glu Ser Val Asp Ala His Leu Gln Ile Gly Pro
245 250 255
Leu Lys Lys Ser Cys Ile Ser Val Leu Lys Arg Arg
260 265

<210> 3611
<211> 816

<212> DNA
<213> Homo sapiens

<400> 3611
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agctacaaag ggatcttcca gtatgactac catgataaag tgaagccaag aaagatattc
120
caatggagac agttggaaaa cctgtacttc agagaaaaga agttttccgt ggaagttcat
180
gacccacgca gggcttcagt gacaaggagg acgtttgggc acagcggcat tgcagtgcac
240
acgtggtatg catgtccggc attgatcaag tccatctggg ctatggccat aagccaacac
300
cagttctatc tggacagaaa gcagagtaag tccaaaatcc atgcagcacg cagcctgagt
360
gagatcgcca tcgacctgac cgagacgggg acgctgaaga cctcgaagct ggccaacatg
420
ggtagcaagg ggaagatcat cagcggcagc agcggcagcc tgctgtcttc aggttctcag
480
gaatcagata gctcgcagtc ggccaagaag gacatgctgg ctgccttgaa gtccaggcag
540
gaagctctgg aggaaaccct gcgtcagagg ctggaggaac tgaagaagct gtgtctccga
600
gaagctgagc tcacgggcaa gctgccagta gaatatcccc tggatccagg ggaggaacca
660
cccattgttc ggagaagaat aggaacagcc ttcaaactgg atgaacagaa aatcctgccc
720
aaaggagagg aagctgaact ggaacgcctg gaacgagagt ttgccattca gtcccagatt
780
acggaggccg cccgccgcct agccagtgac cccaac
816

<210> 3612
<211> 272
<212> PRT
<213> Homo sapiens

<400> 3612
Tyr Gly Val His Tyr Tyr Ala Val Lys Asp Lys Gln Gly Ile Pro Trp
 1   5   10   15
Trp Leu Gly Leu Ser Tyr Lys Gly Ile Phe Gln Tyr Asp Tyr His Asp
            20   25   30
Lys Val Lys Pro Arg Lys Ile Phe Gln Trp Arg Gln Leu Glu Asn Leu
        35   40   45
Tyr Phe Arg Glu Lys Lys Phe Ser Val Glu Val His Asp Pro Arg Arg
    50   55   60
Ala Ser Val Thr Arg Arg Thr Phe Gly His Ser Gly Ile Ala Val His
65   70   75   80
Thr Trp Tyr Ala Cys Pro Ala Leu Ile Lys Ser Ile Trp Ala Met Ala
                85   90   95
Ile Ser Gln His Gln Phe Tyr Leu Asp Arg Lys Gln Ser Lys Ser Lys
            100   105   110
Ile His Ala Ala Arg Ser Leu Ser Glu Ile Ala Ile Asp Leu Thr Glu

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        115                 120                 125
Thr Gly Thr Leu Lys Thr Ser Lys Leu Ala Asn Met Gly Ser Lys Gly
    130                 135                 140
Lys Ile Ile Ser Gly Ser Ser Gly Ser Leu Leu Ser Ser Gly Ser Gln
145                 150                 155                 160
Glu Ser Asp Ser Ser Gln Ser Ala Lys Lys Asp Met Leu Ala Ala Leu
                165                 170                 175
Lys Ser Arg Gln Glu Ala Leu Glu Glu Thr Leu Arg Gln Arg Leu Glu
            180                 185                 190
Glu Leu Lys Lys Leu Cys Leu Arg Glu Ala Glu Leu Thr Gly Lys Leu
        195                 200                 205
Pro Val Glu Tyr Pro Leu Asp Pro Gly Glu Glu Pro Pro Ile Val Arg
    210                 215                 220
Arg Arg Ile Gly Thr Ala Phe Lys Leu Asp Glu Gln Lys Ile Leu Pro
225                 230                 235                 240
Lys Gly Glu Glu Ala Glu Leu Glu Arg Leu Glu Arg Glu Phe Ala Ile
                245                 250                 255
Gln Ser Gln Ile Thr Glu Ala Ala Arg Arg Leu Ala Ser Asp Pro Asn
            260                 265                 270
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<210> 3613
<211> 659
<212> DNA
<213> Homo sapiens

<400> 3613
acgcgtaaag ttgcctttca agctctggcc tccgggcacg cgatgctccg cggcgggctg
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actcagggct gccttgggcc tccctgccac cctcctggaa atgatgcaag tcctgactgt
120
cacctggatc cctgcagccc agcctggaat gcgtctggat taggggaaag acgagaaacg
180
acactccagg tgttgcacgg cccaccaaag cgggaagata gggcagttgc tcagaccaaa
240
tactgtatct agtgcttctg ctcctatctt caatcgtggg gttcttttta atgcaaagtg
300
tcacaaggcc aggaattccc atgtgtgctc agttggccca cagcatcatt gtgcctagga
360
aactgcttca atttatcaag tcctctgggc tgggaatctc actgaattcc aaacggcgga
420
aagaggaaac tttcccaacc cgatgtgggt gtgacgcgag ccaggggccc cagggacact
480
gtcccagagc acaccgtccc cctttaacag caactggagc ttggattcgc tcttatattg
540
tacagtcctt tcgaccattg ccctggagca cccgcacacg cgcacgcatc tccggccgcg
600
ctcacacaca ctcatacaca cgcacgcaaa cgcggtcgga gaagagcccc ccccccccc
659

<210> 3614
<211> 123
<212> PRT
<213> Homo sapiens

<400> 3614
Met Gln Ser Val Thr Arg Pro Gly Ile Pro Met Cys Ala Gln Leu Ala
1 5 10 15
His Ser Ile Ile Val Pro Arg Lys Leu Leu Gln Phe Ile Lys Ser Ser
20 25 30
Gly Leu Gly Ile Ser Leu Asn Ser Lys Arg Arg Lys Glu Glu Thr Phe
35 40 45
Pro Thr Arg Cys Gly Cys Asp Ala Ser Gln Gly Pro Gln Gly His Cys
50 55 60
Pro Arg Ala His Arg Pro Pro Leu Thr Ala Thr Gly Ala Trp Ile Arg
65 70 75 80
Ser Tyr Ile Val Gln Ser Phe Arg Pro Leu Pro Trp Ser Thr Arg Thr
85 90 95
Arg Ala Arg Ile Ser Gly Arg Ala His Thr His Ser Tyr Thr Arg Thr
100 105 110
Gln Thr Arg Ser Glu Lys Ser Pro Pro Pro Pro
115 120

<210> 3615
<211> 1388
<212> DNA
<213> Homo sapiens

<400> 3615
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agccggtacc ggcaaccacg ggcagctctc agggaatctc cgtcgtgagg ccagaggctc
120
cagtccccgc gagtccagat gcctgtccag cctccaagca aagacacaga agagatggaa
180
gcagagggtg attctgctgc tgagatgaat ggggaggagg aagagagtga ggaggagcgg
240
agcggcagcc agacagagtc agaagaggag agctccgaga tggatgatga ggactatgag
300
cgacgccgca gcgagtgtgt cagtgagatg ctggacctag agaagcagtt ctcggagcta
360
aaggagaagt tgttcaggga acgactgagt cagctgcggt tgcggctgga ggaagtgggg
420
gctgagagag cccctgaata cacggagccc cttgggggggc tgcagcggag cctcaagatt
480
cgcattcagg tggcagggat ctacaagggc ttctgtctgg atgtgatcag gaataagtac
540
gaatgtgagc tgcagggagc caaacagcac ctggagagtg agaagctgct gctctatgac
600
acgctgcagg gggagctgca ggagcggatc cagaggctgg aggaggaccg ccagagcctg
660
gacctcagct ctgaatggtg ggacgacaaa ctgcacgcca gaggcagctc caggtcttgg
720
gactccctgc cgcccagcaa gaggaagaag gcacctctgg tttctggccc atacatcgtg
780
tacatgcttc aagagatcgg catcctggag gactggacag ccatcaaaaa ggctagggca
840
gctgtgtccc ctcagaagag aaaatcggat gacaggcgga cccacaggcc cctcagggtc
900

tgcccagcca ggctcctgtg gtgctgctgg gccctcccac tccatctggc actggcctgg
960
actcctcctc tgccctcctc gaggcctgca cagctgtggc cgtggagctg acctgaccag
1020
gcaaggctgc tgtctccatc cctgagccgc ctgccacctc ccactcctga agatccatct
1080
cttggggctc ccctgacaga gaagacagcc gaagtcaaag ccacatcctc ttgctgatgt
1140
tggatgcagg ctgtccggcc tcagggccag ggagccagtt tccactgtgc gggaactctg
1200
agtcagacgt gattatctgg gggtctgtcc accctggctg gatctggagg caagatgcca
1260
ggcccccccag gtgttctcag ggcagttctt ggtgtctgct tctcagattc caaggactgg
1320
aattaaaacc tttcctggga ctctggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
1380
aaaaaaaa
1388

<210> 3616
<211> 290
<212> PRT
<213> Homo sapiens

<400> 3616
Met Pro Val Gln Pro Pro Ser Lys Asp Thr Glu Glu Met Glu Ala Glu
1 5 10 15
Gly Asp Ser Ala Ala Glu Met Asn Gly Glu Glu Glu Glu Ser Glu Glu
20 25 30
Glu Arg Ser Gly Ser Gln Thr Glu Ser Glu Glu Glu Ser Ser Glu Met
35 40 45
Asp Asp Glu Asp Tyr Glu Arg Arg Arg Ser Glu Cys Val Ser Glu Met
50 55 60
Leu Asp Leu Glu Lys Gln Phe Ser Glu Leu Lys Glu Lys Leu Phe Arg
65 70 75 80
Glu Arg Leu Ser Gln Leu Arg Leu Arg Leu Glu Glu Val Gly Ala Glu
85 90 95
Arg Ala Pro Glu Tyr Thr Glu Pro Leu Gly Gly Leu Gln Arg Ser Leu
100 105 110
Lys Ile Arg Ile Gln Val Ala Gly Ile Tyr Lys Gly Phe Cys Leu Asp
115 120 125
Val Ile Arg Asn Lys Tyr Glu Cys Glu Leu Gln Gly Ala Lys Gln His
130 135 140
Leu Glu Ser Glu Lys Leu Leu Leu Tyr Asp Thr Leu Gln Gly Glu Leu
145 150 155 160
Gln Glu Arg Ile Gln Arg Leu Glu Glu Asp Arg Gln Ser Leu Asp Leu
165 170 175
Ser Ser Glu Trp Trp Asp Asp Lys Leu His Ala Arg Gly Ser Ser Arg
180 185 190
Ser Trp Asp Ser Leu Pro Pro Ser Lys Arg Lys Lys Ala Pro Leu Val
195 200 205
Ser Gly Pro Tyr Ile Val Tyr Met Leu Gln Glu Ile Gly Ile Leu Glu
210 215 220
Asp Trp Thr Ala Ile Lys Lys Ala Arg Ala Ala Val Ser Pro Gln Lys

225 230 235 240
Arg Lys Ser Asp Asp Arg Arg Thr His Arg Pro Leu Arg Val Cys Pro
245 250 255
Ala Arg Leu Leu Trp Cys Cys Trp Ala Leu Pro Leu His Leu Ala Leu
260 265 270
Ala Trp Thr Pro Pro Leu Pro Ser Ser Arg Pro Ala Gln Leu Trp Pro
275 280 285
Trp Ser
290

<210> 3617
<211> 804
<212> DNA
<213> Homo sapiens

<400> 3617
nnccaacctg catgagattc agtttggccg aaccttccag catcagcttc gagattctgg
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ggctttaaca gcaagggaga ggtgcatggg atcaatggga cccaatgggg ccagactctg
120
aggatgggat ggtagtagtg aaggacatag gatgggggta gagtgtggag acttttttgaa
180
atagtataga tgaatgccct gaggggactg tgaacaagct ctgcccctct taggaaatca
240
atggggaatc aactaaatta aataaaaaat ggggtcaaga ttaagaggca gggtcaccca
300
gggaatggtt taggtcctgg catctttgaa ggggttggaa gggctggcag gaggcactga
360
gggccctggg ccctgggcca ggtggtgaat tacagcgact cacggacagc agaagagatc
420
tgtgagagca gctccaagat gatcaccttc atcgacctgg caggccacca taagtaccta
480
cacaccacca tctttggcct cacatcatac tgccccgact gcgccctgct cctcgtcagt
540
gccaacactg ggattgctgg caccacaagg gaacatctgg ggctggccct ggccctgaaa
600
gtgccccttct tcatcgtggt cagcaagatc gacctatgtg ccaagaccac agtggagagg
660
acagtacgcc agctggagcg ggtcctcaag cagcctggct gccacaaggt ccccatgctg
720
gtcacctctg aggatgatgc cgtcactgct gcccagcagt ttgctcagtc acccaatgtc
780
acccccatct tcacattgtc cagt
804

<210> 3618
<211> 148
<212> PRT
<213> Homo sapiens

<400> 3618
Gly Pro Trp Ala Leu Gly Gln Val Val Asn Tyr Ser Asp Ser Arg Thr
1 5 10 15
Ala Glu Glu Ile Cys Glu Ser Ser Ser Lys Met Ile Thr Phe Ile Asp

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            20                  25                  30
Leu Ala Gly His His Lys Tyr Leu His Thr Thr Ile Phe Gly Leu Thr
        35                  40                  45
Ser Tyr Cys Pro Asp Cys Ala Leu Leu Leu Val Ser Ala Asn Thr Gly
    50                  55                  60
Ile Ala Gly Thr Thr Arg Glu His Leu Gly Leu Ala Leu Ala Leu Lys
65                  70                  75                  80
Val Pro Phe Phe Ile Val Val Ser Lys Ile Asp Leu Cys Ala Lys Thr
                85                  90                  95
Thr Val Glu Arg Thr Val Arg Gln Leu Glu Arg Val Leu Lys Gln Pro
            100                 105                 110
Gly Cys His Lys Val Pro Met Leu Val Thr Ser Glu Asp Asp Ala Val
        115                 120                 125
Thr Ala Ala Gln Gln Phe Ala Gln Ser Pro Asn Val Thr Pro Ile Phe
    130                 135                 140
Thr Leu Ser Ser
145
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<210> 3619
<211> 948
<212> DNA
<213> Homo sapiens

<400> 3619
acgcgtcggc agaggtggct tcgtcccgcg gagtccaggc ttcagctcct ggcttctctt
60
ctttcctcct agagatcaga tgtcggaact ccagctgagg gcatgtctta ctgggcacgc
120
aggtgtcctc tcttgagaag aactgtccat accatggtgg tggtaaggct ttcaccagtt
180
ctcaggatgc ccatagggat gggtgaagcc tgcctggcct gtggtgcttt ccagtggccg
240
tcatctcatt agggccccac agtggcatta ggatgcacct ctcggcggtg ttcaacgccc
300
tcctggtgtc ggtgctggca gcggtcctgt ggaagcatgt gcggctgcgt gagcatgcag
360
ccacactgga ggaggagctg gccctcagcc gacaggccac agagccagcc ccagcactga
420
ggatcgacta cccgaaggca ctgcagatcc tgatggaggg cggcacacac atggtgtgca
480
cgggccgcac gcacacagac cgcatctgcc gcttcaagtg gctctgctac tccaacgagg
540
ctgaggagtt catcttcttc catggcaaca cctctgtcat gctgcccaac ctgggctccc
600
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<211> 159
<212> PRT
<213> Homo sapiens

<400> 3620
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Ser Ser Ser Ser Met Ala Thr Pro Leu Ser Cys Cys Pro Thr Trp Ala
35 40 45
Pro Gly Ala Ser Ser Gln Pro Cys Ser Thr Tyr Pro Pro Trp Arg Thr
50 55 60
Thr Thr Leu Ser Thr Ser Thr Ser Trp Ser Cys Leu Leu Leu Pro Cys
65 70 75 80
Ala Ser Cys Pro Ser Arg Cys Ser Cys Gln Thr Trp Pro Ser Ser Pro
85 90 95
Thr Ala Ser Thr Pro Thr Thr Ser Cys Thr Ser Phe Met Thr Thr Cys
100 105 110
Cys His Ser Ser Thr Pro Cys Gly Ser Phe Pro Ala Trp Pro Thr Arg
115 120 125
His Gly Ser Ser Ser Trp Arg Ala Gly Ala Arg Val His Thr Ser Thr
130 135 140
Ser Thr Ser Cys Ser Ala Pro Ser Ser Leu Ser Cys Gly His Ser
145 150 155

<210> 3621
<211> 2934
<212> DNA
<213> Homo sapiens

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180
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360
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420
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480
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agtggctttg acccaaatat tcgtgacagc aggggcagaa caggccttca ccttgcagca
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1980
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2040
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2160

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2340
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2934

<210> 3622
<211> 228
<212> PRT
<213> Homo sapiens

<400> 3622
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            20   25   30
Glu Ser Gly Phe Asp Pro Asn Ile Arg Asp Ser Arg Gly Arg Thr Gly
        35   40   45
Leu His Leu Ala Ala Ala Arg Gly Asn Val Asp Ile Cys Gln Leu Leu
    50   55   60
His Lys Phe Gly Ala Asp Leu Leu Ala Thr Asp Tyr Gln Gly Asn Thr
65   70   75   80
Ala Leu His Leu Cys Gly His Val Asp Thr Ile Gln Phe Leu Val Ser
                85   90   95
Asn Gly Leu Lys Ile Asp Ile Cys Asn His Gln Gly Ala Thr Pro Leu
            100   105   110
Val Leu Ala Lys Arg Arg Gly Val Asn Lys Asp Val Ile Arg Leu Leu
        115   120   125
Glu Ser Leu Glu Glu Gln Glu Val Lys Gly Phe Asn Arg Gly Thr His
    130   135   140
Ser Lys Leu Glu Thr Met Gln Thr Ala Glu Ser Glu Ser Ala Met Glu
145   150   155   160
Ser His Ser Leu Leu Asn Pro Asn Leu Gln Gln Gly Glu Gly Val Leu

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                165                 170                 175
Ser Ser Phe Arg Thr Thr Trp Gln Glu Phe Val Glu Asp Leu Gly Phe
            180                 185                 190
Trp Arg Val Leu Leu Leu Ile Phe Val Ile Ala Leu Leu Ser Leu Gly
        195                 200                 205
Ile Ala Tyr Tyr Val Ser Gly Val Leu Pro Phe Val Glu Asn Gln Pro
    210                 215                 220
Glu Leu Val His
225
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<210> 3623
<211> 586
<212> DNA
<213> Homo sapiens

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240
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300
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586

<210> 3624
<211> 159
<212> PRT
<213> Homo sapiens

<400> 3624
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            20                  25                  30
Arg Asp Ile Thr Lys Glu Glu Ile Ser Lys Phe Ser Lys Ala Glu Trp
        35                  40                  45
Glu Lys Lys Arg Met Asp Lys Ala Ile Gly Tyr Ser Phe Ala Ile Val
    50                  55                  60
Gly Ile Asn Ile Thr Asp Leu Ala Tyr Asn Leu Leu Val Ser Gly Ala
65                  70                  75                  80
Leu Lys Thr His Phe Tyr Asn Ile Ala Pro Glu Ala Pro Thr Leu Ser
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                85                  90                  95
His Phe Gln Gln Thr Phe Cys Tyr Leu Met His Glu Phe His Lys Phe
            100                 105                 110
Trp Ile Glu Glu Asp Pro Met Asp Ile Met Glu Phe Asn Arg Val Arg
        115                 120                 125
Glu Lys Phe Arg Lys Arg Ile Ile Lys Gln Leu Gln Asn Pro Asp Met
    130                 135                 140
Ala Leu Cys Pro His Phe Ala Ala Ser Glu Gly Leu Ile Asn Met
145                 150                 155
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<210> 3625
<211> 4799
<212> DNA
<213> Homo sapiens

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120
ttcttagagt taaaaccata aataagagga tttaaaccac taaaatgaca cgtgccaaca
180
tcttcattca gccagacctg gtaaattcta tcaaaactag acagttaaat aagaaccacg
240
ttataaaaat attagccaaa aaaagactat tagataattc tgcaaactca aatatgaaac
300
tgtgctaaac aaaatatgtg caaaggtaca caagcataga gccacgttgg gggttatgct
360
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420
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480
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540
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600
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720
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780
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<210> 3626
<211> 551
<212> PRT
<213> Homo sapiens

<400> 3626
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20 25 30
Trp Gly Pro Ser Ser Ser Leu Met Ser Glu Ile Ala Asp Leu Thr Tyr
35 40 45
Asn Val Val Ala Phe Ser Glu Ile Met Ser Met Ile Trp Lys Arg Leu
50 55 60
Asn Asp His Gly Lys Asn Trp Arg His Val Tyr Lys Ala Met Thr Leu
65 70 75 80
Met Glu Tyr Leu Ile Lys Thr Gly Ser Glu Arg Val Ser Gln Gln Cys
85 90 95
Lys Glu Asn Met Tyr Ala Val Gln Thr Leu Lys Asp Phe Gln Tyr Val
100 105 110
Asp Arg Asp Gly Lys Asp Gln Gly Val Asn Val Arg Glu Lys Ala Lys
115 120 125
Gln Leu Val Ala Leu Leu Arg Asp Glu Asp Arg Leu Arg Glu Glu Arg
130 135 140
Ala His Ala Leu Lys Thr Lys Glu Lys Leu Ala Gln Thr Ala Thr Ala
145 150 155 160
Ser Ser Ala Ala Val Gly Ser Gly Pro Pro Pro Glu Ala Glu Gln Ala
165 170 175
Trp Pro Gln Ser Ser Gly Glu Glu Glu Leu Gln Leu Gln Leu Ala Leu
180 185 190
Ala Met Ser Lys Glu Glu Ala Asp Gln Glu Glu Arg Ile Arg Arg Gly
195 200 205
Asp Asp Leu Arg Leu Gln Met Ala Ile Glu Glu Ser Lys Arg Glu Thr
210 215 220
Gly Gly Lys Glu Glu Ser Ser Leu Met Asp Leu Ala Asp Val Phe Thr
225 230 235 240
Ala Pro Ala Pro Ala Pro Thr Thr Asp Pro Trp Gly Gly Pro Ala Pro
245 250 255
Met Ala Ala Ala Val Pro Thr Ala Ala Pro Thr Ser Asp Pro Trp Gly

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            260                 265                 270
Gly Pro Pro Val Pro Pro Ala Ala Asp Pro Trp Gly Gly Pro Ala Pro
        275                 280                 285
Thr Pro Ala Ser Gly Asp Pro Trp Arg Pro Ala Ala Pro Ala Gly Pro
    290                 295                 300
Ser Val Asp Pro Trp Gly Gly Thr Pro Ala Pro Ala Ala Gly Glu Gly
305                 310                 315                 320
Pro Thr Pro Asp Pro Trp Gly Ser Ser Asp Gly Gly Val Pro Val Ser
                325                 330                 335
Gly Pro Ser Ala Ser Asp Pro Trp Thr Pro Ala Pro Ala Phe Ser Asp
            340                 345                 350
Pro Trp Gly Gly Ser Pro Ala Lys Pro Ser Thr Asn Gly Thr Thr Thr
        355                 360                 365
Ala Gly Gly Phe Asp Thr Glu Pro Asp Glu Phe Ser Asp Phe Asp Arg
    370                 375                 380
Leu Arg Thr Ala Leu Pro Thr Ser Gly Ser Ser Ala Gly Glu Leu Glu
385                 390                 395                 400
Leu Leu Ala Gly Glu Val Pro Ala Arg Ser Pro Gly Ala Phe Asp Met
                405                 410                 415
Ser Gly Val Arg Gly Ser Leu Ala Glu Ala Val Gly Ser Pro Pro Pro
            420                 425                 430
Ala Ala Thr Pro Thr Pro Thr Pro Pro Thr Arg Lys Thr Pro Glu Ser
        435                 440                 445
Phe Leu Gly Pro Asn Ala Ala Leu Val Asp Leu Asp Ser Leu Val Ser
    450                 455                 460
Arg Pro Gly Pro Thr Pro Pro Gly Ala Lys Ala Ser Asn Pro Phe Leu
465                 470                 475                 480
Pro Gly Gly Gly Pro Ala Thr Gly Pro Ser Val Thr Asn Pro Phe Gln
                485                 490                 495
Pro Ala Pro Pro Ala Thr Leu Thr Leu Asn Gln Leu Arg Leu Ser Pro
            500                 505                 510
Val Pro Pro Val Pro Gly Ala Pro Pro Thr Tyr Ile Ser Pro Leu Gly
        515                 520                 525
Gly Gly Pro Gly Leu Pro Pro Met Met Pro Pro Gly Pro Pro Ala Pro
    530                 535                 540
Asn Thr Asn Pro Phe Leu Leu
545                 550
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<210> 3627
<211> 1760
<212> DNA
<213> Homo sapiens

<400> 3627
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120
aaaccaaaca tcataaattt tgacaccagt ctgccgacat cacatacata cctaggtgct
180
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240
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300

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360
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<210> 3628
<211> 440
<212> PRT

<213> Homo sapiens

<400> 3628

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Asp Gln Asp Ser Lys Glu Ala Lys Lys Pro Asn Ile Ile Asn Phe Asp
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Thr Ser Leu Pro Thr Ser His Thr Tyr Leu Gly Ala Asp Met Glu Glu
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Phe His Gly Arg Thr Leu His Asp Asp Asp Ser Cys Gln Val Ile Pro
65                  70                  75                  80
Val Leu Pro Gln Val Met Met Ile Leu Ile Pro Gly Gln Thr Leu Pro
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Leu Gln Leu Phe His Pro Gln Glu Val Ser Met Val Arg Asn Leu Ile
            100                 105                 110
Gln Lys Asp Arg Thr Phe Ala Val Leu Ala Tyr Ser Asn Val Gln Glu
        115                 120                 125
Arg Glu Ala Gln Phe Gly Thr Thr Ala Glu Ile Tyr Ala Tyr Arg Glu
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Glu Gln Asp Phe Gly Ile Glu Ile Val Lys Val Lys Ala Ile Gly Arg
145                 150                 155                 160
Gln Arg Phe Lys Val Leu Glu Leu Arg Thr Gln Ser Asp Gly Ile Gln
                165                 170                 175
Gln Ala Lys Val Gln Ile Leu Pro Glu Cys Val Leu Pro Ser Thr Met
            180                 185                 190
Ser Ala Val Gln Leu Glu Ser Leu Asn Lys Cys Gln Ile Phe Pro Ser
        195                 200                 205
Lys Pro Val Ser Arg Glu Asp Gln Cys Ser Tyr Lys Trp Trp Gln Lys
    210                 215                 220
Tyr Gln Lys Arg Lys Phe His Cys Ala Asn Leu Thr Ser Trp Pro Arg
225                 230                 235                 240
Trp Leu Tyr Ser Leu Tyr Asp Ala Glu Thr Leu Met Asp Arg Ile Lys
                245                 250                 255
Lys Gln Leu Arg Glu Trp Asp Glu Asn Leu Lys Asp Asp Ser Leu Pro
            260                 265                 270
Ser Asn Pro Ile Asp Phe Ser Tyr Arg Val Ala Ala Cys Leu Pro Ile
        275                 280                 285
Asp Asp Val Leu Arg Ile Gln Leu Leu Lys Ile Gly Ser Ala Ile Gln
    290                 295                 300
Arg Leu Arg Cys Glu Leu Asp Ile Met Asn Lys Cys Thr Ser Leu Cys
305                 310                 315                 320
Cys Lys Gln Cys Gln Glu Thr Glu Ile Thr Thr Lys Asn Glu Ile Phe
                325                 330                 335
Ser Leu Ser Leu Cys Gly Pro Met Ala Ala Tyr Val Asn Pro His Gly
            340                 345                 350
Tyr Val His Glu Thr Leu Thr Val Tyr Lys Ala Cys Asn Leu Asn Leu
        355                 360                 365
Ile Gly Arg Pro Ser Thr Glu His Ser Trp Phe Pro Gly Tyr Ala Trp
    370                 375                 380
Thr Val Ala Gln Cys Lys Ile Cys Ala Ser His Ile Gly Trp Lys Phe
385                 390                 395                 400
Thr Ala Thr Lys Lys Asp Met Ser Pro Gln Lys Phe Trp Gly Leu Thr
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<210> 4398
<211> 354
<212> PRT
<213> Homo sapiens

<400> 4398
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35 40 45
Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Asp Ala Asp
50 55 60
Ser Ser Glu Arg Ile Ile Ala Pro Met Arg Trp Gly Leu Val Pro Ser
65 70 75 80
Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu Gln Phe Asn Thr Thr Asn
85 90 95
Cys Arg Ser Asp Thr Val Met Glu Lys Arg Ser Phe Lys Val Pro Leu
100 105 110
Gly Lys Gly Arg Arg Cys Val Val Leu Ala Asp Gly Phe Tyr Glu Trp
115 120 125
Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln Pro Tyr Phe Ile Tyr Phe
130 135 140
Pro Gln Ile Lys Thr Glu Lys Ser Gly Ser Ile Gly Ala Ala Asp Ser
145 150 155 160
Pro Glu Asn Trp Glu Lys Val Trp Asp Asn Trp Arg Leu Leu Thr Met
165 170 175
Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro Glu Gly Gly Asp Val Leu
180 185 190
Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser Cys Lys Gly Leu Ser Asp
195 200 205
Ile His His Arg Met Pro Ala Ile Leu Asp Gly Glu Glu Ala Val Ser

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    210                 215                 220
Lys Trp Leu Asp Phe Gly Glu Val Ser Thr Gln Glu Ala Leu Lys Leu
225                 230                 235                 240
Ile His Pro Thr Glu Asn Ile Thr Phe His Ala Val Ser Ser Val Val
                245                 250                 255
Asn Asn Ser Arg Asn Asn Thr Pro Glu Cys Leu Ala Pro Val Asp Leu
            260                 265                 270
Val Val Lys Lys Glu Leu Arg Ala Ser Gly Ser Ser Gln Arg Met Leu
        275                 280                 285
Gln Trp Leu Ala Thr Lys Ser Pro Lys Lys Glu Asp Ser Lys Thr Pro
    290                 295                 300
Gln Lys Glu Glu Ser Asp Val Pro Gln Trp Ser Ser Gln Phe Leu Gln
305                 310                 315                 320
Lys Ser Pro Leu Pro Thr Lys Arg Gly Thr Ala Gly Leu Leu Glu Gln
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Ser Gln
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<210> 4399
<211> 723
<212> DNA
<213> Homo sapiens

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120
cagaagctgc ttctgcagaa agaggctttg gatgagcagc tggttcaggt caaggaggcc
180
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240
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300
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360
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420
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480
gaggagaaaa tcaagaacct cacgcgggaa aacgtggaaa tgaaagaaaa gctgtcagcg
540
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aag
723

<210> 4400

<211> 241
<212> PRT
<213> Homo sapiens

<400> 4400
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20 25 30
Leu Gly Val Gln Ala Gly Gln Thr Gln Lys Leu Leu Leu Gln Lys Glu
35 40 45
Ala Leu Asp Glu Gln Leu Val Gln Val Lys Glu Ala Glu Arg His His
50 55 60
Ser Ser Pro Lys Arg Glu Leu Pro Pro Gly Ile Gly Asp Met Val Glu
65 70 75 80
Leu Met Gly Val Gln Asp Gln His Met Asp Glu Arg Asp Val Arg Arg
85 90 95
Phe Gln Leu Lys Ile Ala Glu Leu Asn Ser Val Ile Arg Lys Leu Glu
100 105 110
Asp Arg Asn Thr Leu Leu Ala Asp Glu Arg Asn Glu Leu Leu Lys Arg
115 120 125
Ser Arg Glu Thr Glu Val Gln Leu Lys Pro Leu Val Glu Lys Asn Lys
130 135 140
Arg Met Asn Lys Lys Asn Glu Asp Leu Leu Gln Ser Ile Gln Arg Met
145 150 155 160
Glu Glu Lys Ile Lys Asn Leu Thr Arg Glu Asn Val Glu Met Lys Glu
165 170 175
Lys Leu Ser Ala Gln Ala Ser Leu Lys Arg His Thr Ser Leu Asn Asp
180 185 190
Leu Ser Leu Thr Arg Asp Glu Gln Glu Ile Glu Phe Leu Arg Leu Gln
195 200 205
Val Leu Glu Gln Gln His Val Ile Asp Asp Leu Ser Leu Glu Arg Glu
210 215 220
Arg Leu Leu Arg Ser Lys Arg His Arg Gly Lys Ser Leu Lys Pro Pro
225 230 235 240
Lys

<210> 4401
<211> 1131
<212> DNA
<213> Homo sapiens

<400> 4401
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agaaaggtga tccaaggaat cacatgtgag aaaaacagtg ctctagcaaa gggatcctcg
180
aatcaaaggc atcgagaata tttttaaata ctaatgcctt tttgctattt ccggggaaag
240
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cctgcagatt ggccttaaga gaaggacgga gccacatact gctgacggcc cagaactggc
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agagagaagg ttgccatggc tgctgttgac agtttctacc tcttgtacag ggaaatcgcc
420
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480
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ctggggagca gagcagactt gatcaagcag tatggaagat gggccgttgt cagcggtgca
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720
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780
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1131

<210> 4402
<211> 252
<212> PRT
<213> Homo sapiens

<400> 4402
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Thr Ala Arg Lys Ser Ile Thr Val Ile Cys Asp Phe Tyr Ser Leu Ile
35 40 45
Arg Leu His Phe Ile Pro Arg Leu Gly Ser Arg Ala Asp Leu Ile Lys
50 55 60
Gln Tyr Gly Arg Trp Ala Val Val Ser Gly Ala Thr Asp Gly Ile Gly
65 70 75 80
Lys Ala Tyr Ala Glu Glu Leu Ala Ser Arg Gly Leu Asn Ile Ile Leu
85 90 95
Ile Ser Arg Asn Glu Glu Lys Leu Gln Val Val Ala Lys Asp Ile Ala
100 105 110
Asp Thr Tyr Lys Val Glu Thr Asp Ile Ile Val Ala Asp Phe Ser Ser
115 120 125
Gly Arg Glu Ile Tyr Leu Pro Ile Arg Glu Ala Leu Lys Asp Lys Asp
130 135 140
Val Gly Ile Leu Val Asn Asn Val Gly Val Phe Tyr Pro Tyr Pro Gln

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145                 150                 155                 160
Tyr Phe Thr Gln Leu Ser Glu Asp Lys Leu Trp Asp Ile Ile Asn Val
                165                 170                 175
Asn Ile Ala Ala Ala Ser Leu Met Val His Val Val Leu Pro Gly Met
            180                 185                 190
Val Glu Arg Lys Lys Gly Ala Ile Val Thr Ile Ser Ser Gly Leu Leu
        195                 200                 205
Leu Gln Pro Thr Pro Gln Leu Ala Ala Phe Ser Ala Ser Lys Ala Tyr
    210                 215                 220
Leu Asp His Phe Ser Arg Ala Leu Gln Tyr Glu Tyr Ala Ser Lys Gly
225                 230                 235                 240
Ile Phe Val Gln Ser Leu Xaa Pro Phe Tyr Val Ala
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<210> 4403
<211> 4237
<212> DNA
<213> Homo sapiens

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1020

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4237

<210> 4404
<211> 779
<212> PRT
<213> Homo sapiens

<400> 4404
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Gly Met Met Pro Asn Gly Gln Asp Met Ser Thr Met Glu Ser Gly Pro
35 40 45
Asn Asn His Gly Asn Phe Gln Gly Asp Ser Asn Phe Asn Arg Met Trp
50 55 60
Gln Pro Glu Trp Gly Met His Gln Gln Pro Pro His Pro Pro Pro Asp
65 70 75 80
Gln Pro Trp Met Pro Pro Thr Pro Gly Pro Met Asp Ile Val Pro Pro
85 90 95
Ser Glu Asp Ser Asn Ser Gln Asp Ser Gly Glu Phe Ala Pro Asp Asn
100 105 110
Arg His Ile Phe Asn Gln Asn Asn His Asn Phe Gly Gly Pro Pro Asp
115 120 125
Asn Phe Ala Val Gly Pro Val Asn Gln Phe Asp Tyr Gln His Gly Ala
130 135 140
Ala Phe Gly Pro Pro Gln Gly Gly Phe His Pro Pro Tyr Trp Gln Pro
145 150 155 160
Gly Pro Pro Gly Pro Pro Ala Pro Pro Gln Asn Arg Arg Glu Arg Pro
165 170 175
Ser Ser Phe Arg Asp Arg Gln Arg Ser Pro Ile Ala Leu Pro Val Lys
180 185 190
Gln Glu Pro Pro Gln Ile Asp Ala Val Lys Arg Arg Thr Leu Pro Ala
195 200 205
Trp Ile Arg Glu Gly Leu Glu Lys Met Glu Arg Glu Lys Gln Lys Lys
210 215 220
Leu Glu Lys Glu Arg Met Glu Gln Gln Arg Ser Gln Leu Ser Lys Lys
225 230 235 240
Lys Lys Lys Ala Thr Glu Asp Ala Glu Gly Gly Asp Gly Pro Arg Leu
245 250 255
Pro Gln Arg Ser Lys Phe Asp Ser Asp Glu Glu Glu Glu Asp Thr Glu
260 265 270
Asn Val Glu Ala Ala Ser Ser Gly Lys Val Thr Arg Ser Pro Ser Pro
275 280 285
Val Pro Gln Glu Glu His Ser Asp Pro Glu Met Thr Glu Glu Glu Lys
290 295 300
Glu Tyr Gln Met Met Leu Leu Thr Lys Met Leu Leu Thr Glu Ile Leu
305 310 315 320
Leu Asp Val Thr Asp Glu Glu Ile Tyr Tyr Val Ala Lys Asp Ala His
325 330 335
Arg Lys Ala Thr Lys Ala Pro Ala Lys Gln Leu Ala Gln Ser Ser Ala
340 345 350
Leu Ala Ser Leu Thr Gly Leu Gly Gly Leu Gly Gly Tyr Gly Ser Gly
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Asp Ser Glu Asp Glu Arg Ser Asp Arg Gly Ser Glu Ser Ser Asp Thr

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Asp Asp Glu Glu Leu Arg His Arg Ile Arg Gln Lys Gln Glu Ala Phe
385                 390                 395                 400
Trp Arg Lys Glu Lys Glu Gln Gln Leu Leu His Asp Lys Gln Met Glu
                405                 410                 415
Glu Glu Lys Gln Gln Thr Glu Arg Val Thr Lys Glu Met Asn Glu Phe
            420                 425                 430
Ile His Lys Glu Gln Asn Ser Leu Ser Leu Leu Glu Ala Arg Glu Ala
        435                 440                 445
Asp Gly Asp Val Val Asn Glu Lys Lys Arg Thr Pro Asn Glu Thr Thr
    450                 455                 460
Ser Val Leu Glu Pro Lys Lys Glu His Lys Glu Lys Glu Lys Gln Gly
465                 470                 475                 480
Arg Ser Arg Ser Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Asn Ser
                485                 490                 495
Arg Thr Ser Ser Thr Ser Ser Thr Val Ser Ser Ser Ser Tyr Ser Ser
            500                 505                 510
Ser Ser Gly Ser Ser Arg Thr Ser Ser Arg Ser Ser Ser Pro Lys Arg
        515                 520                 525
Lys Lys Arg His Ser Arg Ser Arg Ser Pro Thr Ile Lys Ala Arg Arg
    530                 535                 540
Ser Arg Ser Arg Ser Tyr Ser Arg Arg Ile Lys Ile Glu Ser Asn Arg
545                 550                 555                 560
Ala Arg Val Lys Ile Arg Asp Arg Arg Arg Ser Asn Arg Asn Ser Ile
                565                 570                 575
Glu Arg Glu Arg Arg Arg Asn Arg Ser Pro Ser Arg Glu Arg Arg Arg
            580                 585                 590
Ser Arg Ser Arg Ser Arg Asp Arg Arg Thr Asn Arg Ala Ser Arg Ser
        595                 600                 605
Arg Ser Arg Asp Arg Arg Lys Ile Asp Asp Gln Arg Gly Asn Leu Ser
    610                 615                 620
Gly Asn Ser His Lys His Lys Gly Glu Ala Lys Glu Gln Glu Arg Lys
625                 630                 635                 640
Lys Glu Arg Ser Arg Ser Ile Asp Lys Asp Arg Lys Lys Lys Asp Lys
                645                 650                 655
Glu Arg Glu Arg Glu Gln Asp Lys Arg Lys Glu Lys Gln Lys Arg Glu
            660                 665                 670
Glu Lys Asp Phe Lys Phe Ser Ser Gln Asp Asp Arg Leu Lys Arg Lys
        675                 680                 685
Arg Glu Ser Glu Arg Thr Phe Ser Arg Ser Gly Ser Ile Ser Val Lys
    690                 695                 700
Ile Ile Arg His Asp Ser Arg Gln Asp Ser Lys Lys Ser Thr Thr Lys
705                 710                 715                 720
Asp Ser Lys Lys His Ser Gly Ser Asp Ser Ser Gly Arg Ser Ser Ser
                725                 730                 735
Glu Ser Pro Gly Ser Ser Lys Glu Lys Lys Ala Lys Lys Pro Lys His
            740                 745                 750
Ser Arg Ser Arg Ser Val Glu Lys Ser Gln Arg Ser Gly Lys Lys Ala
        755                 760                 765
Ser Arg Lys His Lys Ser Lys Ser Arg Ser Arg
    770                 775
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<210> 4405
<211> 918

<212> DNA
<213> Homo sapiens

<400> 4405
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120
aggaccagat cttttgagag ctgagggttg agggcattga gccaacacac agatttgtcg
180
cctctgtccc cgaagacacc tgcaccctcc atgcggagcc aagatgggga atggaactga
240
ggaagattat aactttgtct tcaagggtac tatcgtggtg cagtgggggc cctcctggtg
300
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360
gaccatgctg aagccacgat cgtcgtcatg ctcgtgggta acaaaagtga cctcagccag
420
gcccgggaag tgcccactga ggaggcccga atgttcgctg aaaacaatgg actgctcttc
480
ctggagacct cagccctgga ctctaccaat gttgagctag cctttgagac tgtcctgaaa
540
gaaatctttg cgaaggtgtc caagcagaga cagaacagca tccggaccaa tgccatcact
600
ctgggcagtg cccaggctgg acaggagcct ggccctgggg agaagagggc ctgttgcatc
660
agcctctgac cttggccagc accacctgcc cccactggct ttttggtgcc ccttgtcccc
720
acttcagccc caggaccttt ccttgccctt tggttccaga tatcagactg ttccctgttc
780
acagcaccct cagggtctta aggtcttcat gccctatcac aaatacctct tttatctgtc
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900
aaaaaaaaaa aaaaaaaa
918

<210> 4406
<211> 138
<212> PRT
<213> Homo sapiens

<400> 4406
Leu Cys Leu Gln Gly Tyr Tyr Arg Gly Ala Val Gly Ala Leu Leu Val
1 5 10 15
Phe Asp Leu Thr Lys His Gln Thr Tyr Ala Val Val Glu Arg Trp Leu
20 25 30
Lys Glu Leu Tyr Asp His Ala Glu Ala Thr Ile Val Val Met Leu Val
35 40 45
Gly Asn Lys Ser Asp Leu Ser Gln Ala Arg Glu Val Pro Thr Glu Glu
50 55 60
Ala Arg Met Phe Ala Glu Asn Asn Gly Leu Leu Phe Leu Glu Thr Ser
65 70 75 80
Ala Leu Asp Ser Thr Asn Val Glu Leu Ala Phe Glu Thr Val Leu Lys

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                85                  90                  95
Glu Ile Phe Ala Lys Val Ser Lys Gln Arg Gln Asn Ser Ile Arg Thr
            100                 105                 110
Asn Ala Ile Thr Leu Gly Ser Ala Gln Ala Gly Gln Glu Pro Gly Pro
        115                 120                 125
Gly Glu Lys Arg Ala Cys Cys Ile Ser Leu
    130                 135
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<210> 4407
<211> 974
<212> DNA
<213> Homo sapiens

<400> 4407
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120
ttctctgtag tccttgagca gccatttgac caaataaatt taattttata atcaataaaa
180
gtcaaaagaa taccttttga agatagggga tcacccattt atacctctaa atgttaacct
240
caatgcacat tttggaggat atttgcaaga tttattattc atttgatgtt ttcttaaagg
300
atgtttgatg taggtggaca gagatctgag agaaagaagt ggattcactg ctttgaagga
360
gttacatgca ttatattttg tgctgcactt agtgcctatg acatggtcct cgtggaagac
420
gaagaagtga atagaatgca tgaaagcctt cacctgttca acagtatctg taatcacaag
480
tatttttcaa caacctccat tgtcctgttc ctcaacaaaa aagatatctt tcaagaaaag
540
gtaaccaagg tgcatcttag tatctgcttt ccagaataca ctgggccaaa tacatttgaa
600
gatgcaggaa actacatcaa gaaccagttt ctagacctga atttaaaaaa agaagataag
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gaaatttatt cccacatgac ctgtgctact gacacccaaa atgtcaagtt tgtgtttgac
720
gcagttacag atataataat caaagagaat ctaaaagact gtgggctttt ctaatcaact
780
attttctctt ccactcttgc tcatgtatgc ttttcaaaat ataaaagaaa aggtgctgta
840
tgacgtgttt agtttgaata gacattaact tatctagaca tataactagc attgtaaagc
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960
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974

<210> 4408
<211> 158
<212> PRT
<213> Homo sapiens

<400> 4408
Arg Met Phe Asp Val Gly Gly Gln Arg Ser Glu Arg Lys Lys Trp Ile
1 5 10 15
His Cys Phe Glu Gly Val Thr Cys Ile Ile Phe Cys Ala Ala Leu Ser
20 25 30
Ala Tyr Asp Met Val Leu Val Glu Asp Glu Glu Val Asn Arg Met His
35 40 45
Glu Ser Leu His Leu Phe Asn Ser Ile Cys Asn His Lys Tyr Phe Ser
50 55 60
Thr Thr Ser Ile Val Leu Phe Leu Asn Lys Lys Asp Ile Phe Gln Glu
65 70 75 80
Lys Val Thr Lys Val His Leu Ser Ile Cys Phe Pro Glu Tyr Thr Gly
85 90 95
Pro Asn Thr Phe Glu Asp Ala Gly Asn Tyr Ile Lys Asn Gln Phe Leu
100 105 110
Asp Leu Asn Leu Lys Lys Glu Asp Lys Glu Ile Tyr Ser His Met Thr
115 120 125
Cys Ala Thr Asp Thr Gln Asn Val Lys Phe Val Phe Asp Ala Val Thr
130 135 140
Asp Ile Ile Ile Lys Glu Asn Leu Lys Asp Cys Gly Leu Phe
145 150 155

<210> 4409
<211> 4217
<212> DNA
<213> Homo sapiens

<400> 4409
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120
gagaacgccc ggcgccgggg taccctgaa cctgaagaag ctgggcggcg gggtgggaag
180
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300
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360
cagatctgcg accagtgcgg caagcgcttc ctgctggaga gcgagctgct gctgcacagg
420
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480
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780

cagttcatgt gccagtggtg tggcaaggat ttcaacatga agcagtactt cgacgaacac
840
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agccgcccca acatgaagag acaccgcaga actcacacag gcgagaagcc ctatccatgt
960
gatgtgtgtg gccagcggtt ccgcttctcg aacatgctca aggcccacaa ggagaagtgc
1020
ttccgcgtca gccacaccct ggccggcgac ggcgtccccg ctgccccagg cctgccccca
1080
acccagcccc aggcgcacgc actgcccctg ctcccggggc tgccccagac cctgccgccc
1140
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1260
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2400

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2520
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2580
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2760
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4020

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4080
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4140
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4200
aaaaaaaaaa aaaaaaa
4217

<210> 4410
<211> 405
<212> PRT
<213> Homo sapiens

<400> 4410
Glu Ser Ser Glu Glu Glu Glu Gly Glu Glu Gly Glu Ala Gly Gly Lys
1 5 10 15
Gln Gly Pro Arg Gly Ser Arg Ser Ser Arg Ala Asp Pro Pro Pro His
20 25 30
Ser His Met Ala Thr Arg Ser Arg Glu Asn Ala Arg Arg Arg Gly Thr
35 40 45
Pro Glu Pro Glu Glu Ala Gly Arg Arg Gly Gly Lys Arg Pro Lys Pro
50 55 60
Pro Pro Gly Val Ala Ser Ala Ser Ala Arg Gly Pro Pro Ala Thr Asp
65 70 75 80
Gly Leu Gly Ala Lys Val Lys Leu Glu Glu Lys Gln His His Pro Cys
85 90 95
Gln Lys Cys Pro Arg Val Phe Asn Asn Arg Trp Tyr Leu Glu Lys His
100 105 110
Met Asn Val Thr His Ser Arg Met Gln Ile Cys Asp Gln Cys Gly Lys
115 120 125
Arg Phe Leu Leu Glu Ser Glu Leu Leu Leu His Arg Gln Thr Asp Cys
130 135 140
Glu Arg Asn Ile Gln Cys Val Thr Cys Gly Lys Ala Phe Lys Lys Leu
145 150 155 160
Trp Ser Leu His Glu His Asn Lys Ile Val His Gly Tyr Ala Glu Lys
165 170 175
Lys Phe Ser Cys Glu Ile Cys Glu Lys Lys Phe Tyr Thr Met Ala His
180 185 190
Val Arg Lys His Met Val Ala His Thr Lys Asp Met Pro Phe Thr Cys
195 200 205
Glu Thr Cys Gly Lys Ser Phe Lys Arg Ser Met Ser Leu Lys Val His
210 215 220
Ser Leu Gln His Ser Gly Glu Lys Pro Phe Arg Cys Glu Asn Cys Asp
225 230 235 240
Glu Arg Phe Gln Tyr Lys Tyr Gln Leu Arg Ser His Met Ser Ile His
245 250 255
Ile Gly His Lys Gln Phe Met Cys Gln Trp Cys Gly Lys Asp Phe Asn
260 265 270
Met Lys Gln Tyr Phe Asp Glu His Met Lys Thr His Thr Gly Glu Lys
275 280 285
Pro Phe Ile Cys Glu Ile Cys Gly Lys Ser Phe Thr Ser Arg Pro Asn
290 295 300
Met Lys Arg His Arg Arg Thr His Thr Gly Glu Lys Pro Tyr Pro Cys

305 310 315 320
Asp Val Cys Gly Gln Arg Phe Arg Phe Ser Asn Met Leu Lys Ala His
325 330 335
Lys Glu Lys Cys Phe Arg Val Ser His Thr Leu Ala Gly Asp Gly Val
340 345 350
Pro Ala Ala Pro Gly Leu Pro Pro Thr Gln Pro Gln Ala His Ala Leu
355 360 365
Pro Leu Leu Pro Gly Leu Pro Gln Thr Leu Pro Pro Pro Pro His Leu
370 375 380
Pro Pro Pro Pro Pro Leu Phe Pro Thr Thr Ala Ser Pro Gly Gly Arg
385 390 395 400
Met Asn Ala Asn Asn
405

<210> 4411
<211> 484
<212> DNA
<213> Homo sapiens

<400> 4411
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120
caaaagagga gtttagggtg gctatggtgc aggggcagct gtatgcttca cctcaaatgt
180
tactgtcttc tctctccatc aaggaggaag ggcccaggct ggggttagga gggctagggg
240
cccaggctgt gtgtcccctt ttttcctcct ggtgccctgc ccccccacgc tgtcatctcc
300
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360
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420
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480
atcc
484

<210> 4412
<211> 113
<212> PRT
<213> Homo sapiens

<400> 4412
Met Val Gln Gly Gln Leu Tyr Ala Ser Pro Gln Met Leu Leu Ser Ser
1 5 10 15
Leu Ser Ile Lys Glu Glu Gly Pro Arg Leu Gly Leu Gly Gly Leu Gly
20 25 30
Ala Gln Ala Val Cys Pro Leu Phe Ser Ser Trp Cys Pro Ala Pro Pro
35 40 45
Arg Cys His Leu Pro Gln Trp Gln Trp Gly Phe Ile Thr Gly Ser Ser
50 55 60
Gly Pro Leu Pro Met Ala Gly Gly Val Pro Gly Gly Pro Asn Gln Ala

65 70 75 80
Ala Pro Ala Ser Arg Gln Arg Val Gly Phe Leu Gly Gln Pro Gln Ser
85 90 95
Cys Gln Arg Gln His Val Ser Leu His Arg Ser His Gln Ala Pro Leu
100 105 110
Asp

<210> 4413
<211> 1097
<212> DNA
<213> Homo sapiens

<400> 4413
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120
agcagcctgg cactcttcag agatgatacg ggtgtcaaat atggcttggt gggattggag
180
cccaccaagg tgccttgaat gtggagcgct tccgggagtt ggcaggtgct ggcagacaca
240
gcggtcacca gtggcagaca ctactgggaa gtgacagtga agcgctccca gcagttccgg
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360
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420
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720
caattcagtg ttgggtcctc tgtgcaatat catgatcatc ttcctcatcc cctaccttgt
780
gaaagctagg catacagcca aaccctcctt ttccccaccc accaactact gccaatttcc
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960
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1080
aaaaaaaaaa aaaaaaa
1097

<210> 4414

<211> 65
<212> PRT
<213> Homo sapiens

<400> 4414
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Lys Arg Leu Gly Val Ala Ser Thr Glu Arg Gln Arg Gly Val Ser Phe
20 25 30
Lys Leu Glu Glu Lys Thr Ala His Ser Ser Leu Ala Leu Phe Arg Asp
35 40 45
Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro Thr Lys Val
50 55 60
Pro
65

<210> 4415
<211> 775
<212> DNA
<213> Homo sapiens

<400> 4415
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120
attattgaat acacaaaagg aatgttaccg ttacttgttc atagtcaaag gtgaagttaa
180
aaaaaaaggg aagttaaata actgaagtaa tggtttgccc aaatagcaaa cgtaggatac
240
aggcgtgggc aaagagcagc tactgaagct catgaggagg atgctggata tagggtaggt
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360
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480
tgtctgaatc catttctctt ggggtaggag gaggtaatga acattaacgt tctgcatctc
540
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600
ccataagtaa tgatactcca ggcctgtaaa gcatttttca ttgtcccaca ttgcagctaa
660
atgagtataa actcgacagt gttctgattt cacaacatat gcatttatga caactgctaa
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775

<210> 4416
<211> 100
<212> PRT
<213> Homo sapiens

<400> 4416
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20 25 30
Arg Leu Arg Cys Arg Thr Leu Met Phe Ile Thr Ser Ser Tyr Pro Lys
35 40 45
Arg Asn Gly Phe Arg His Val Leu Ser Gln Gln Glu Ile Asp Phe Phe
50 55 60
Leu Asn Tyr Leu Ile Leu Leu Pro Asn Ile Thr Glu Val Met Arg Ser
65 70 75 80
Leu Val Thr Phe Gly Cys Cys Ala Leu Lys Glu Pro Gly Leu Glu Phe
85 90 95
Val Gly Val Ile
100

<210> 4417
<211> 980
<212> DNA
<213> Homo sapiens

<400> 4417
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360
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<211> 263
<212> PRT
<213> Homo sapiens

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Glu Val Met Arg Glu Met Thr Lys Lys Leu Tyr Ser Gln Tyr Glu Glu
35 40 45
Lys Leu Gln Glu Glu Gln Arg Lys His Ser Ala Glu Lys Glu Ala Leu
50 55 60
Leu Glu Glu Thr Asn Ser Phe Leu Lys Ala Ile Glu Glu Ala Asn Lys
65 70 75 80
Lys Met Gln Ala Ala Glu Ile Ser Leu Glu Glu Lys Asp Gln Arg Ile
85 90 95
Gly Glu Leu Asp Arg Leu Ile Glu Arg Met Glu Lys Glu Arg His Gln
100 105 110
Leu Gln Leu Gln Leu Leu Glu His Glu Thr Glu Met Ser Gly Glu Leu
115 120 125
Thr Asp Ser Asp Lys Glu Arg Tyr Gln Gln Leu Glu Glu Ala Ser Ala
130 135 140
Ser Leu Arg Glu Arg Ile Arg His Leu Asp Asp Met Val His Cys Gln
145 150 155 160
Gln Lys Lys Val Lys Gln Met Val Glu Glu Ile Glu Ser Leu Lys Lys
165 170 175
Lys Val Gln Gln Lys Gln Leu Leu Ile Leu Gln Leu Leu Glu Lys Ile
180 185 190
Ser Phe Leu Glu Gly Glu Asn Asn Glu Leu Gln Ser Arg Leu Asp Tyr
195 200 205
Leu Thr Glu Thr Gln Ala Lys Thr Glu Val Glu Thr Arg Glu Ile Gly
210 215 220
Val Gly Cys Asp Leu Leu Pro Ser Pro Thr Gly Arg Thr Arg Glu Ile
225 230 235 240
Val Met Pro Ser Arg Asn Tyr Thr Pro Tyr Thr Arg Val Leu Glu Leu
245 250 255
Ser Ser Lys Lys Thr Leu Thr
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<211> 369
<212> DNA
<213> Homo sapiens

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<210> 4420
<211> 91
<212> PRT
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Trp Cys Asp Leu Gly Ser Leu Gln Pro Pro Pro Pro Gln Leu Lys Gln
35 40 45
Leu Ser Cys Pro Ser His Pro Ser Xaa Asn Tyr Arg Pro Val Pro Pro
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His Pro Ala Asn Phe Cys Ile Phe Ser Arg Asp Gly Val Ser Pro Tyr
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Trp Pro Gly Arg Ser Gln Thr Pro Gly Pro Met
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<210> 4421
<211> 1356
<212> DNA
<213> Homo sapiens

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360
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1356

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<211> 58
<212> PRT
<213> Homo sapiens

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<210> 4423
<211> 2673
<212> DNA
<213> Homo sapiens

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<211> 768
<212> PRT
<213> Homo sapiens

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35 40 45
Lys Ala Leu Gly Lys Asn Arg Ser Ala Asp Phe Asn Pro Asp Phe Val
50 55 60
Phe Thr Glu Lys Glu Gly Thr Tyr Asp Gly Ser Trp Ala Leu Ala Asp
65 70 75 80
Val Met Ser Gln Leu Lys Lys Lys Arg Ala Ala Thr Thr Leu Asp Glu
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Lys Ile Glu Lys Val Arg Lys Lys Arg Lys Thr Glu Asp Lys Glu Ala
100 105 110
Lys Ser Gly Lys Leu Glu Lys Glu Lys Glu Ala Lys Glu Gly Ser Glu

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Thr Lys Ala Asp Thr Leu Lys Val Lys Asp Arg Lys Lys Lys Lys Lys
                165                 170                 175
Lys Gly Gln Glu Ala Gly Gly Phe Phe Glu Asp Ala Ser Gln Tyr Asp
            180                 185                 190
Glu Asn Leu Ser Phe Gln Asp Met Asn Leu Ser Arg Pro Leu Leu Lys
        195                 200                 205
Ala Ile Thr Ala Met Gly Phe Lys Gln Pro Thr Pro Ile Gln Lys Ala
    210                 215                 220
Cys Ile Pro Val Gly Leu Leu Gly Lys Asp Ile Cys Ala Cys Ala Ala
225                 230                 235                 240
Thr Gly Thr Gly Lys Thr Ala Ala Phe Ala Leu Pro Val Leu Glu Arg
                245                 250                 255
Leu Ile Tyr Lys Pro Arg Gln Ala Pro Val Thr Arg Val Leu Val Leu
            260                 265                 270
Val Pro Thr Arg Glu Leu Gly Ile Gln Val His Ser Val Thr Arg Gln
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Leu Ala Gln Phe Cys Asn Ile Thr Thr Cys Leu Ala Val Gly Gly Leu
    290                 295                 300
Asp Val Lys Ser Gln Glu Ala Ala Leu Arg Ala Ala Pro Asp Ile Leu
305                 310                 315                 320
Ile Ala Thr Pro Gly Arg Leu Ile Asp His Leu His Asn Cys Pro Ser
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Phe His Leu Ser Ser Ile Glu Val Leu Ile Leu Asp Glu Ala Asp Arg
            340                 345                 350
Met Leu Asp Glu Tyr Phe Glu Glu Gln Met Lys Glu Ile Ile Arg Met
        355                 360                 365
Cys Ser His His Arg Gln Thr Met Leu Phe Ser Ala Thr Met Thr Asp
    370                 375                 380
Glu Val Lys Asp Leu Ala Ser Val Ser Leu Lys Asn Pro Val Arg Ile
385                 390                 395                 400
Phe Val Asn Ser Asn Thr Asp Val Ala Pro Phe Leu Arg Gln Glu Phe
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Ile Arg Ile Arg Pro Asn Arg Glu Gly Asp Arg Glu Ala Ile Val Ala
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Ala Leu Leu Thr Arg Thr Phe Thr Asp His Val Met Leu Phe Thr Gln
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Thr Lys Lys Gln Ala His Arg Met His Ile Leu Leu Gly Leu Met Gly
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Leu Gln Val Gly Glu Leu His Gly Asn Leu Ser Gln Thr Gln Arg Leu
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Glu Ala Leu Arg Arg Phe Lys Asp Glu Gln Ile Asp Ile Leu Val Ala
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Thr Asp Val Ala Ala Arg Gly Leu Asp Ile Glu Gly Val Lys Thr Val
            500                 505                 510
Ile Asn Phe Thr Met Pro Asn Thr Ile Lys His Tyr Val His Arg Val
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Gly Arg Thr Ala Arg Ala Gly Arg Ala Gly Arg Ser Val Ser Leu Val
    530                 535                 540
Gly Glu Asp Glu Arg Lys Met Leu Lys Glu Ile Val Lys Ala Ala Lys
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Leu Glu Ala Glu Glu Lys Glu Met Gln Gln Ser Glu Ala Gln Ile Asn
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Thr Ala Lys Arg Leu Leu Glu Lys Gly Lys Glu Ala Val Val Gln Glu
    610                 615                 620
Pro Glu Arg Ser Trp Phe Gln Thr Lys Glu Glu Arg Lys Lys Glu Lys
625                 630                 635                 640
Ile Ala Lys Ala Leu Gln Glu Phe Asp Leu Ala Leu Arg Gly Lys Lys
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Lys Arg Lys Lys Phe Met Lys Asp Ala Lys Lys Lys Gly Glu Met Thr
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Ala Glu Glu Arg Ser Gln Phe Glu Ile Leu Lys Ala Gln Met Phe Ala
        675                 680                 685
Glu Arg Leu Ala Lys Arg Asn Arg Arg Ala Lys Arg Ala Arg Ala Met
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Pro Glu Glu Glu Pro Val Arg Gly Pro Ala Lys Lys Gln Lys Gln Gly
705                 710                 715                 720
Lys Lys Ser Val Phe Asp Glu Glu Leu Thr Asn Thr Ser Lys Lys Ala
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Leu Lys Gln Tyr Arg Ala Gly Pro Ser Phe Glu Glu Arg Lys Gln Leu
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Gly Leu Pro His Gln Arg Arg Gly Gly Asn Phe Lys Ser Lys Ser Arg
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<212> DNA
<213> Homo sapiens

<400> 4425

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<213> Homo sapiens

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Thr Lys Arg Lys Ala Ile Ala Ala Glu Asp Pro Ser Leu Asp Phe Arg
    50                  55                  60
Asn Asn Pro Thr Lys Glu Asp Leu Gly Lys Leu Gln Pro Leu Val Ala
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Ser Tyr Leu Cys Ser Asp Val Thr Ser Val Pro Ser Lys Glu Ser Leu
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Lys Leu Gln Gly Val Phe Ser Lys Gln Thr Val Leu Lys Ser His Pro
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Leu Leu Ser Gln Ser Tyr Glu Leu Arg Ala Glu Leu Leu Gly Arg Gln
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Pro Val Leu Glu Phe Ser Leu Glu Asn Leu Arg Thr Met Asn Thr Ser
    130                 135                 140
Gly Gln Thr Ala Leu Pro Gln Ala Pro Val Asn Gly Leu Ala Lys Lys
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Leu Thr Lys Ser Ser Thr His Ser Asp His Asp Asn Ser Thr Ser Leu
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Asn Gly Gly Lys Arg Ala Leu Thr Ser Ser Ala Leu His Gly Gly Glu
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Met Gly Gly Ser Glu Ser Gly Asp Leu Lys Gly Gly Met Thr Asn Cys
        195                 200                 205
Thr Leu Pro His Arg Ser Leu Asp Val Glu His Thr Thr Leu Tyr Ser
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Asn Asn Ser Thr Ala Asn Lys Ser Phe Val Asn Ser Met Glu Gln Pro
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Ala Leu Gln Gly Ser Ser Arg Leu Ser Pro Gly Thr Asp Ser Ser Ser
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Asn Leu Gly Gly Val Lys Leu Glu Gly Lys Lys Ser Pro Leu Ser Ser
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Ile Leu Phe Ser Ala Leu Asp Ser Asp Thr Arg Ile Thr Ala Leu Leu
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Arg Arg Gln Ala Asp Ile Glu Ser Arg Ala Arg Arg Leu Gln Lys Arg
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Leu Gln Val Val Gln Ala Lys Gln Val Glu Arg His Ile Gln His Gln
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Leu Gly Gly Phe Leu Glu Lys Thr Leu Ser Lys Leu Pro Asn Leu Glu
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Ser Leu Arg Pro Arg Ser Gln Leu Met Leu Thr Arg Lys Ala Glu Ala
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Ala Leu Arg Lys Ala Ala Ser Glu Thr Thr Thr Ser Glu Gly Leu Ser
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Asn Phe Leu Lys Ser Asn Ser Ile Ser Glu Glu Leu Glu Arg Phe Thr
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Ala Ser Gly Ile Ala Asn Leu Arg Cys Ser Glu Gln Ala Phe Asp Ser
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Asp Val Thr Asp Ser Ser Ser Gly Gly Glu Ser Asp Ile Glu Glu Glu
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Glu Leu Thr Arg Ala Asp Pro Glu Gln Arg His Val Pro Leu Arg Arg
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Arg Ser Glu Trp Lys Trp Ala Ala Asp Arg Ala Ala Ile Val Ser Arg
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Pro Leu Ser Ser Glu Val Lys Thr Asp His Gly Thr Asp Lys Leu Ile
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His Ile Ser Glu Ser Leu Ser Thr Lys Ser Cys Gly Ala Leu Arg Pro
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Pro Gly Asp Ser Ser Asp Ala Glu Glu Gln Leu His Lys Lys Gln Arg
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Thr Arg Pro Val Leu Ser Cys Lys Lys Arg Arg Leu Val Arg Pro Asn
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Pro Gly Cys Asp Val Asn Pro Ser Cys Ala Leu Cys Gly Ser Gly Ser
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Asp Asp Val Pro Thr Ser Leu His Phe Gln Ser Met Leu Lys Ser Gln
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Trp Gln Asn Lys Pro Phe Asp Lys Ile Lys Pro Pro Lys Lys Leu Ser
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Leu Lys His Arg Ala Pro Met Pro Gly Ser Leu Pro Asp Ser Ala Arg
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Ser His His Gln Thr Arg Pro Asp Arg Thr His Arg Gln His Leu Asp
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Asp Val Gly Ala Val Pro Met Val Glu Arg Val Thr Ala Pro Lys Ala
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Glu Arg Leu Leu Asn Pro Pro Pro Pro Val His Asp Pro Asn His Ser
    770                 775                 780
Lys Met Arg Leu Arg Asp His Ser Ser Glu Arg Ser Glu Val Leu Lys
785                 790                 795                 800
His His Thr Asp Met Ser Ser Ser Ser Tyr Leu Ala Ala Thr His His
                805                 810                 815
Pro Pro His Ser Pro Leu Val Arg Gln Leu Ser Thr Ser Ser Asp Ser
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Pro Ala Pro Ala Ser Ser Ser Ser Gln Val Thr Ala Ser Thr Ser Gln
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Gln Pro Val Arg Arg Arg Arg Gly Glu Ser Ser Phe Asp Ile Asn Asn
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Ser Leu Lys Gly Ser Pro Asp Glu Glu Asn Glu Glu Ile Glu Asp Leu
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Ser Asp Ala Ala Phe Ala Ala Leu His Ala Lys Cys Glu Glu Met Glu
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Arg Ala Arg Trp Leu Trp Thr Thr Ser Val Pro Pro Gln Arg Arg Gly
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Ser Arg Ser Tyr Arg Ser Ser Asp Gly Arg Thr Thr Pro Gln Leu Gly
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Ser Ala Asn Pro Ser Thr Pro Gln Pro Ala Ser Pro Asp Val Ser Ser
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Ser His Ser Leu Ser Glu Tyr Ser His Gly Gln Ser Pro Arg Ser Pro
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Ile Ser Pro Glu Leu His Ser Ala Pro Leu Thr Pro Val Ala Arg Asp
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Thr Leu Arg His Leu Ala Ser Glu Asp Thr Arg Cys Ser Thr Pro Glu
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Leu Gly Leu Asp Glu Gln Ser Val Gln Pro Trp Glu Arg Arg Thr Phe
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Pro Leu Ala His Ser Pro Gln Ala Glu Cys Glu Asp Gln Leu Asp Ala
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Gln Glu Arg Ala Ala Arg Cys Thr Arg Arg Thr Ser Gly Ser Lys Thr
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Xaa Pro Gly Asp Arg Gly Ser Ala His Leu Ala Ser His Cys Pro Pro
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<211> 4474
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<213> Homo sapiens

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<212> PRT
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Val Ala Val Val Arg Ile Asn Ser Pro Asn Ser Lys Val Asn Thr Leu
50 55 60
Ser Lys Glu Leu His Ser Glu Phe Ser Glu Val Met Asn Glu Ile Trp
65 70 75 80
Ala Ser Asp Gln Ile Arg Ser Ala Val Leu Ile Ser Ser Lys Pro Gly
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Cys Phe Ile Ala Gly Ala Asp Ile Asn Met Leu Ala Ala Cys Lys Thr
100 105 110
Leu Gln Glu Val Thr Gln Leu Ser Gln Glu Ala Gln Arg Ile Val Glu
115 120 125
Lys Leu Glu Lys Ser Thr Lys Pro Ile Val Ala Ala Ile Asn Gly Ser
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Cys Leu Gly Gly Gly Leu Glu Val Ala Ile Ser Cys Gln Tyr Arg Ile
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Ala Thr Lys Asp Arg Lys Thr Val Leu Gly Thr Pro Glu Val Leu Leu

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Gly Val Pro Ala Ala Leu Asp Met Met Leu Thr Gly Arg Ser Ile Arg
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Ala Asp Arg Ala Lys Lys Met Gly Leu Val Asp Gln Leu Val Glu Pro
    210                 215                 220
Leu Gly Pro Gly Leu Lys Pro Pro Glu Glu Arg Thr Ile Glu Tyr Leu
225                 230                 235                 240
Glu Glu Val Ala Ile Thr Phe Ala Lys Gly Leu Ala Asp Lys Lys Ile
                245                 250                 255
Ser Pro Lys Arg Asp Lys Gly Leu Val Glu Lys Leu Thr Ala Tyr Ala
            260                 265                 270
Met Thr Ile Pro Phe Val Arg Gln Gln Val Tyr Lys Lys Val Glu Glu
        275                 280                 285
Lys Val Arg Lys Gln Thr Lys Gly Leu Tyr Pro Ala Pro Leu Lys Ile
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Ile Asp Val Val Lys Thr Gly Ile Glu Gln Gly Ser Asp Ala Gly Tyr
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Leu Cys Glu Ser Gln Lys Phe Gly Glu Leu Val Met Thr Lys Glu Ser
                325                 330                 335
Lys Ala Leu Met Gly Leu Tyr His Gly Gln Val Leu Cys Lys Lys Asn
            340                 345                 350
Lys Phe Gly Ala Pro Gln Lys Asp Val Lys His Leu Ala Ile Leu Gly
        355                 360                 365
Ala Gly Leu Met Gly Ala Gly Ile Ala Gln Val Ser Val Asp Lys Gly
    370                 375                 380
Leu Lys Thr Ile Leu Lys Asp Ala Thr Leu Thr Ala Leu Asp Arg Gly
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Gln Gln Gln Val Phe Lys Gly Leu Asn Asp Lys Val Lys Lys Lys Ala
                405                 410                 415
Leu Thr Ser Phe Glu Arg Asp Ser Ile Phe Ser Asn Leu Thr Gly Gln
            420                 425                 430
Leu Asp Tyr Gln Gly Phe Glu Lys Ala Asp Met Val Ile Glu Ala Val
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Phe Glu Asp Leu Ser Leu Lys His Arg Val Leu Lys Glu Val Glu Ala
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Val Ile Pro Asp His Cys Ile Phe Ala Ser Asn Thr Ser Ala Leu Pro
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Ile Ser Glu Ile Ala Ala Val Ser Lys Arg Pro Glu Lys Val Ile Gly
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Met His Tyr Phe Ser Pro Val Asp Lys Met Gln Leu Leu Glu Ile Ile
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Gly Leu Lys Gln Gly Lys Val Ile Ile Val Val Lys Asp Gly Pro Gly
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Phe Tyr Thr Thr Arg Cys Leu Ala Pro Met Met Ser Glu Val Ile Arg
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Ile Leu Gln Glu Gly Val Asp Pro Lys Lys Leu Asp Ser Leu Thr Thr
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Ser Phe Gly Phe Pro Val Gly Ala Ala Thr Leu Val Asp Glu Val Gly
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Val Asp Val Ala Lys His Val Ala Glu Asp Leu Gly Lys Val Phe Gly
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Glu Gly Val Lys Arg Lys Asp Leu Asn Ser Asp Met Asp Ser Ile Leu
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Ala Ser Leu Lys Leu Pro Pro Lys Ser Glu Val Ser Ser Asp Glu Asp
660 665 670
Ile Gln Phe Arg Leu Val Thr Arg Phe Val Asn Glu Ala Val Met Cys
675 680 685
Leu Gln Glu Gly Ile Leu Ala Thr Pro Ala Glu Gly Asp Ile Gly Ala
690 695 700
Val Phe Gly Leu Gly Phe Pro Pro Cys Leu Gly Gly Pro Phe Arg Phe
705 710 715 720
Val Asp Leu Tyr Gly Ala Gln Lys Ile Val Asp Arg Leu Lys Lys Tyr
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Leu Arg Arg Val Met Pro Ile Asn Gly Thr Pro Ile Gly Arg Leu Arg
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Ser Ala Leu Pro Gln Val Asn Thr Arg Arg Glu Ser Leu Asn Arg Gln
        35   40   45
Ala Pro Gln Pro Arg Arg Lys Pro Ser Phe Gln Thr Val Gly Ile Pro
    50   55   60
Phe Ile Pro Trp His Arg Glu Pro Lys Gly Met Gln Thr Asp Pro Gly
65   70   75   80
Arg Ala Leu His Ser Gln Thr Leu Ala Arg Thr Arg Arg Leu Gly Ala
                85   90   95
Pro Arg Arg Ala Leu Pro Pro Arg Pro Pro Pro Pro Ala Asp Ser Pro
            100   105   110
Leu Cys Glu Leu Asn His Leu Gly Ala Met Cys Arg Gly Arg Ala Ser
        115   120   125
Ala Ser Glu Val Leu Gly Gly Pro Val Thr Ala Ser Arg Phe Tyr Gly
    130   135   140
Xaa Pro Pro Pro Val Ser Trp
145   150

<210> 4431
<211> 507
<212> DNA
<213> Homo sapiens

<400> 4431
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ctgggtgacc gacccatccc cgtcaccttc aagagggcca tcgcagcgct ctccttctgg
120
cagaaggtca ggctggcttg gggcctgtgc ttcctgtcag accccatcag gtagggctgc
180
ccccgggacc ctggccggcc tgcagggtgg tctgtgggag gctccaggcc ctcctgtgca
240
ggtccaagcg cagccaatcc tcactcaagg ccttccctgc cctttccttc cgccacaaat
300
cccaaacaaa cgtgctgtgg tccctgcccg gtgtccacag tgccagcccc accctcccag
360

cccgttgccc atccctgcgg ggctgcagcc atccctctcc acagcaagga tgacgtggaa
420
cgctgcaagc agaaggccta ctggagcaga tgatggccga gatgattggc gagttcccag
480
acctgcaccg caccatcgtt tttggag
507

<210> 4432
<211> 57
<212> PRT
<213> Homo sapiens

<400> 4432
Gly Gly Glu Phe Arg Glu Ala Phe Lys Glu Ala Ser Lys Val Pro Phe
1 5 10 15
Cys Lys Phe His Leu Gly Asp Arg Pro Ile Pro Val Thr Phe Lys Arg
20 25 30
Ala Ile Ala Ala Leu Ser Phe Trp Gln Lys Val Arg Leu Ala Trp Gly
35 40 45
Leu Cys Phe Leu Ser Asp Pro Ile Arg
50 55

<210> 4433
<211> 447
<212> DNA
<213> Homo sapiens

<400> 4433
ntgtacaaca cctcgtcgcc gagggagatg gtggcccagt tcctcctcgt ggacggcaac
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gtgaccaaca tcaccaccgt cagcctctgg gaagaattct cctccagcga cctcgcagat
120
ctccgcttcc tggacatgag ccagaaccag ttccagtacc tgccagacgg cttcctgagg
180
aaaatgcctt ccctctccca cctgaacctc caccagaatt gcctgatgac gcttcacatt
240
cgggagcacg agcccccggg agcgctcacc gagctggacc tgagccacaa ccagctgtcg
300
gagctgcacc tggctccggg gctggccagc tgcctgggca gcctgcgctt gttcaacctg
360
agctccaacc agctcctggg cgtccccct ggcctcttcg ccaatgctag gaacatcact
420
acacttgaca tgagccacaa tcagatc
447

<210> 4434
<211> 149
<212> PRT
<213> Homo sapiens

<400> 4434
Xaa Tyr Asn Thr Ser Ser Pro Arg Glu Met Val Ala Gln Phe Leu Leu
1 5 10 15
Val Asp Gly Asn Val Thr Asn Ile Thr Thr Val Ser Leu Trp Glu Glu

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            20                  25                  30
Phe Ser Ser Ser Asp Leu Ala Asp Leu Arg Phe Leu Asp Met Ser Gln
        35                  40                  45
Asn Gln Phe Gln Tyr Leu Pro Asp Gly Phe Leu Arg Lys Met Pro Ser
    50                  55                  60
Leu Ser His Leu Asn Leu His Gln Asn Cys Leu Met Thr Leu His Ile
65                  70                  75                  80
Arg Glu His Glu Pro Pro Gly Ala Leu Thr Glu Leu Asp Leu Ser His
                85                  90                  95
Asn Gln Leu Ser Glu Leu His Leu Ala Pro Gly Leu Ala Ser Cys Leu
            100                 105                 110
Gly Ser Leu Arg Leu Phe Asn Leu Ser Ser Asn Gln Leu Leu Gly Val
        115                 120                 125
Pro Pro Gly Leu Phe Ala Asn Ala Arg Asn Ile Thr Thr Leu Asp Met
    130                 135                 140
Ser His Asn Gln Ile
145
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<210> 4435
<211> 783
<212> DNA
<213> Homo sapiens

<400> 4435
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120
gtggacctgc tcctgggagg cgacctgcgc taccatctgc agcagaatgt gcatttcaca
180
gaggggactg tgaaactcta catctgtgag ctggcactgg ccctggagta tcttcagagg
240
taccacatca tccacagaga catcaagcca gacaatatcc tgctggatga acacggacat
300
gttcacatta cagacttcaa catagcgacg gtagtgaaag gagcagaaag ggcttcctcc
360
atggctggca ccaagcccta catggctcca gaagtattcc aggtgtacat ggacagaggc
420
cccggatact cgtaccctgt cgactggtgg tccctgggca tcacagccta tgagctgctg
480
cggggctgga ggccgtacga aatccactcg gtcacgccca tcgatgaaat cctcaacatg
540
ttcaaggtgg agcgtgtcca ctactcctcc acgtggtgca aggggatggt ggccctgcta
600
aggaagctcc tgaccaagga tcctgagagc cgcgtgtcca gccttcatga catacagagc
660
gtgccctact tggccgacat gaactgggac gcggtgttca agaaggcact gatgcccggc
720
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780
cta
783

<210> 4436

<211> 261
<212> PRT
<213> Homo sapiens

<400> 4436
Xaa Ala Arg Asp Glu Val Arg Asn Val Phe Arg Glu Leu Gln Ile Met
1 5 10 15
Gln Gly Leu Glu His Pro Phe Val Val Asn Leu Trp Tyr Ser Phe Gln
20 25 30
Asp Glu Glu Asp Met Phe Met Val Val Asp Leu Leu Leu Gly Gly Asp
35 40 45
Leu Arg Tyr His Leu Gln Gln Asn Val His Phe Thr Glu Gly Thr Val
50 55 60
Lys Leu Tyr Ile Cys Glu Leu Ala Leu Ala Leu Glu Tyr Leu Gln Arg
65 70 75 80
Tyr His Ile Ile His Arg Asp Ile Lys Pro Asp Asn Ile Leu Leu Asp
85 90 95
Glu His Gly His Val His Ile Thr Asp Phe Asn Ile Ala Thr Val Val
100 105 110
Lys Gly Ala Glu Arg Ala Ser Ser Met Ala Gly Thr Lys Pro Tyr Met
115 120 125
Ala Pro Glu Val Phe Gln Val Tyr Met Asp Arg Gly Pro Gly Tyr Ser
130 135 140
Tyr Pro Val Asp Trp Trp Ser Leu Gly Ile Thr Ala Tyr Glu Leu Leu
145 150 155 160
Arg Gly Trp Arg Pro Tyr Glu Ile His Ser Val Thr Pro Ile Asp Glu
165 170 175
Ile Leu Asn Met Phe Lys Val Glu Arg Val His Tyr Ser Ser Thr Trp
180 185 190
Cys Lys Gly Met Val Ala Leu Leu Arg Lys Leu Leu Thr Lys Asp Pro
195 200 205
Glu Ser Arg Val Ser Ser Leu His Asp Ile Gln Ser Val Pro Tyr Leu
210 215 220
Ala Asp Met Asn Trp Asp Ala Val Phe Lys Lys Ala Leu Met Pro Gly
225 230 235 240
Phe Val Pro Asn Lys Gly Arg Leu Asn Cys Asp Pro Thr Phe Glu Leu
245 250 255
Glu Glu Met Ile Leu
260

<210> 4437
<211> 620
<212> DNA
<213> Homo sapiens

<400> 4437
nnctgcaggg tgtacgtggt ggggacagcc cacttcagcg acgacagcaa gagggacgtt
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gtgaagacca tccgggaggt gcagcctgac gtggtggtcg tggagctctg ccaatatcgt
120
gtgtccatgc tgaagatgga cgagagcacg ctgctgcggg aggcccagga gctcagcctg
180
gagaagctgc agcaggccgt gaggcagaac gggctcatgt cggggctgat gcagatgctg
240

ctgctgaagg tgtctgcaca catcaccgag cagctgggca tggccccagg tggcgagttc
300
agggaggcct tcaaggaggc cagcaaggtg cctttctgca agttccacct gggtgaccga
360
cccatccccg tcaccttcaa gagggccatc gcagcgctct ccttctggca gaaggtcagg
420
ctggcttggg gcctgtgctt cctgtcagac cccatcagca aggatgacgt ggaacgctgc
480
aagcagaagg acctactgga gcagatgatg gccgagatga ttggcgagtt cccagacctg
540
caccgcacca tcgtctcgga gcgcgacgtc tacctaacct acatgctgcg ccaggccgcg
600
cggcgcctcg agctgcctcg
620

<210> 4438
<211> 206
<212> PRT
<213> Homo sapiens

<400> 4438
Xaa Cys Arg Val Tyr Val Val Gly Thr Ala His Phe Ser Asp Asp Ser
1 5 10 15
Lys Arg Asp Val Val Lys Thr Ile Arg Glu Val Gln Pro Asp Val Val
20 25 30
Val Val Glu Leu Cys Gln Tyr Arg Val Ser Met Leu Lys Met Asp Glu
35 40 45
Ser Thr Leu Leu Arg Glu Ala Gln Glu Leu Ser Leu Glu Lys Leu Gln
50 55 60
Gln Ala Val Arg Gln Asn Gly Leu Met Ser Gly Leu Met Gln Met Leu
65 70 75 80
Leu Leu Lys Val Ser Ala His Ile Thr Glu Gln Leu Gly Met Ala Pro
85 90 95
Gly Gly Glu Phe Arg Glu Ala Phe Lys Glu Ala Ser Lys Val Pro Phe
100 105 110
Cys Lys Phe His Leu Gly Asp Arg Pro Ile Pro Val Thr Phe Lys Arg
115 120 125
Ala Ile Ala Ala Leu Ser Phe Trp Gln Lys Val Arg Leu Ala Trp Gly
130 135 140
Leu Cys Phe Leu Ser Asp Pro Ile Ser Lys Asp Asp Val Glu Arg Cys
145 150 155 160
Lys Gln Lys Asp Leu Leu Glu Gln Met Met Ala Glu Met Ile Gly Glu
165 170 175
Phe Pro Asp Leu His Arg Thr Ile Val Ser Glu Arg Asp Val Tyr Leu
180 185 190
Thr Tyr Met Leu Arg Gln Ala Ala Arg Arg Leu Glu Leu Pro
195 200 205

<210> 4439
<211> 2121
<212> DNA
<213> Homo sapiens

<400> 4439

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tcccagatat ttgacgtaag aatttgtttt gaaaaagttt ggtaattaat ataaaactac
120
tctaaaatta acttttattg ttagagacac atctttagaa aagtttgtaa atatcaacat
180
ttaccatctt attttttcct ttgagaccaa gcatcacaga ccaaaagcca caaagtttac
240
aataatttat tattgttgca tgacatttgc cagtaaaata aattatagaa actatagagt
300
ctttataaac tattttgtat atcatattca cttcctaatg cttactgcag taactgtatg
360
aaatttaatt agattacgtt ttagcattag tcagaagatt taaaaaatat gtaaaatgtt
420
ttcacagtac tttggattta taaaagaccc cattatttta acttttgtgc aacctgtttg
480
aaatgtataa aaaacctttt acaaaccaaa aggtggcgta aggttttact gagttgctga
540
agacatctta ctttcttgaa tttctactta acatccatgt ggtgcacttt ttcaggcatt
600
gtaataagtg caaataaata atcaattatt gatttctaaa aatctatacc aatagacaat
660
actcaggctt ggaaatattt tgaacactca gatataaaaa ttcagtaaac aatttatgca
720
tggtattttc tctccctgtc ctccctctcc ctcctccctt cccctatcta tttggttaaa
780
aaaaaaaaag ttcaacttcg atttaagtcc tagggcctga caaagtgacc ctggataaat
840
gtcatctcca gccatctgtt ttctttagtt ctcattacat ctgtccaggc tcttctatca
900
gcatcaatcc tttcctgcag ggacggaaga gttttcaaat ccttgctgaa agcattttgt
960
tctcctctgt aacagcacag ggcatgaaat tgtttggagt ctttgtaacc agtctgttca
1020
gtcctggtcc ctttccagtc ccggtccctt tccagcctct ggagtcctga cagaagagaa
1080
gcttgtaagg tagcagcaaa atgctgcatc tgttagaatc tcacaaactc acttggtctt
1140
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1200
gaatatttcc gcagtttcag aaactggaaa agcttgtctt ttgtcctctt cttcaaggcc
1260
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1440
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1560
tcatctgaag agaaattttt gcgtagaatt ggaagattcg gttatgggta tggcccttat
1620

cagccagttc cagaacaacc actataccca caaccatacc aaccacaata ccaacaatat
1680
acctttttaat atcatcagta actgcaggac atgattatgg aggtttgact ggcaaatacg
1740
acttctacat ccatattctc atctttcata ccatatcaca ctactaccac tttttgaaga
1800
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1860
caggatactt cccttcctaa ttatcatttg attagatact tgcaatttaa actgttaagc
1920
tgtgttcact gctgtttctg aataatagaa attcattcct ctccaaaagc aataaatttc
1980
aagcacattt tccaatacct gtggcatcac actactacca ctttttgaag aatcatcaaa
2040
gggcaatgca aatgaaaaac attataattt actgtatact ctttgtttca ggatacttgc
2100
cttttcaatt gtcacttgat g
2121

<210> 4440
<211> 82
<212> PRT
<213> Homo sapiens

<400> 4440
Met Asp Gly Leu Thr Arg Ser Asp Val Asp Met Met Met Ala Trp Trp
1 5 10 15
Leu Arg Phe Ala Phe Ile Asp Val Gly Ile Phe Arg Asn Ser Ala Pro
20 25 30
Arg Leu Ser Met Ile Gly Ala Asp Ser Ser Glu Glu Lys Phe Leu Arg
35 40 45
Arg Ile Gly Arg Phe Gly Tyr Gly Tyr Gly Pro Tyr Gln Pro Val Pro
50 55 60
Glu Gln Pro Leu Tyr Pro Gln Pro Tyr Gln Pro Gln Tyr Gln Gln Tyr
65 70 75 80
Thr Phe

<210> 4441
<211> 2055
<212> DNA
<213> Homo sapiens

<400> 4441
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gtcgtgggag ctgggagagg agggaaagag gggaagagtc gtgggagctg gcagaggagg
120
gaaaggggga gccgaacgtg aagggcgaag ggcggggcgg ggcaggagag tcggggtata
180
gagcaggcag gtgttaatgg catgggaagg aagagtaaga agtggggcaa gaaggtgtcg
240
cggtacgagg ggaaggtgag actcaagaag gtgccggcta agaagctggt gccggcgtgg
300

aaggagaagg tgctgtgggc cctgctggca gtgctcctgg cgtcgtggag gctgtgggcg
360
atcaaggatt tccaggaatg cacctggcag gttgtcctga acgagtttaa gagggtaggc
420
gagagtggtg tgagcgacag cttctttgag caagagcccg tggacacagt gagcagcttg
480
tttcacatgc tggtggactc acccatcgac ccgagcgaga aatacctggg cttcccttac
540
tacctgaaga tcaactactc ctgcgaggaa aagccctctg aggacctggt gcgcatgggc
600
cacctgacgg ggctaaagcc cctggtgctg gtcaccttcc agtccccagt caacttctac
660
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720
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780
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840
ccccagtact ttgtgggtgt ctcatcgagg cccttgtggc acactgtgga ccagtcacct
900
gtgcttatcc tgggaggcat tcccaatgag aagtacgtcc tgatgactga caccagcttc
960
aaggacttct ctctcgtgga ggtgaacggt gtggggcaga tgctgagcat tgacagttgc
1020
tgggtgggct ccttctactg cccccattct ggcttcacag ccaccatcta tgacactatt
1080
gccaccgaga gcaccctctt cattcggcag aaccagctgg tctactattt tacaggcacc
1140
tataccacac tctatgagag aaaccgcggc agtggtgagt gtgctgtggc tggacccacg
1200
cctggggagg gcaccctggt gaacccctcc actgaaggca gttggattcg tgtcctggcc
1260
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1320
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1380
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1440
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ttcctgatga tcctagggac agagtcctac accagcactg caatggcccc caagggcatc
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1860
atcggggcac cccaggaggg ctgaccccag ctcacctggc cctgccttcc ccctgcagct
1920

ggtgtacctt atgaacaacc agaagggcca gctggtcaag aggctcgtgc ccgtggagca
1980
gcttctgatg tatcaacagc acaccagcca ctatgacttg gagcggaaag ggtgagaaga
2040
caccggacca tgaca
2055

<210> 4442
<211> 517
<212> PRT
<213> Homo sapiens

<400> 4442
Met Gly Arg Lys Ser Lys Lys Trp Gly Lys Lys Val Ser Arg Tyr Glu
1 5 10 15
Gly Lys Val Arg Leu Lys Lys Val Pro Ala Lys Lys Leu Val Pro Ala
20 25 30
Trp Lys Glu Lys Val Leu Trp Ala Leu Leu Ala Val Leu Leu Ala Ser
35 40 45
Trp Arg Leu Trp Ala Ile Lys Asp Phe Gln Glu Cys Thr Trp Gln Val
50 55 60
Val Leu Asn Glu Phe Lys Arg Val Gly Glu Ser Gly Val Ser Asp Ser
65 70 75 80
Phe Phe Glu Gln Glu Pro Val Asp Thr Val Ser Ser Leu Phe His Met
85 90 95
Leu Val Asp Ser Pro Ile Asp Pro Ser Glu Lys Tyr Leu Gly Phe Pro
100 105 110
Tyr Tyr Leu Lys Ile Asn Tyr Ser Cys Glu Glu Lys Pro Ser Glu Asp
115 120 125
Leu Val Arg Met Gly His Leu Thr Gly Leu Lys Pro Leu Val Leu Val
130 135 140
Thr Phe Gln Ser Pro Val Asn Phe Tyr Arg Trp Lys Ile Glu Gln Leu
145 150 155 160
Gln Ile Gln Met Glu Ala Ala Pro Phe Arg Ser Lys Gly Gly Pro Gly
165 170 175
Gly Gly Gly Arg Asp Arg Asn Leu Ala Gly Met Asn Ile Asn Gly Phe
180 185 190
Leu Lys Arg Asp Arg Asp Asn Asn Ile Gln Phe Thr Val Gly Glu Glu
195 200 205
Leu Phe Asn Leu Met Pro Gln Tyr Phe Val Gly Val Ser Ser Arg Pro
210 215 220
Leu Trp His Thr Val Asp Gln Ser Pro Val Leu Ile Leu Gly Gly Ile
225 230 235 240
Pro Asn Glu Lys Tyr Val Leu Met Thr Asp Thr Ser Phe Lys Asp Phe
245 250 255
Ser Leu Val Glu Val Asn Gly Val Gly Gln Met Leu Ser Ile Asp Ser
260 265 270
Cys Trp Val Gly Ser Phe Tyr Cys Pro His Ser Gly Phe Thr Ala Thr
275 280 285
Ile Tyr Asp Thr Ile Ala Thr Glu Ser Thr Leu Phe Ile Arg Gln Asn
290 295 300
Gln Leu Val Tyr Tyr Phe Thr Gly Thr Tyr Thr Thr Leu Tyr Glu Arg
305 310 315 320
Asn Arg Gly Ser Gly Glu Cys Ala Val Ala Gly Pro Thr Pro Gly Glu

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                325                 330                 335
Gly Thr Leu Val Asn Pro Ser Thr Glu Gly Ser Trp Ile Arg Val Leu
            340                 345                 350
Ala Ser Glu Cys Ile Lys Lys Leu Cys Pro Val Tyr Phe His Ser Asn
        355                 360                 365
Gly Ser Glu Tyr Ile Met Ala Leu Thr Thr Gly Lys His Glu Gly Tyr
    370                 375                 380
Val His Phe Gly Thr Ile Arg Val Thr Thr Cys Ser Ile Ile Trp Ser
385                 390                 395                 400
Glu Tyr Ile Ala Gly Glu Tyr Thr Leu Leu Leu Leu Val Glu Ser Gly
                405                 410                 415
Tyr Gly Asn Ala Ser Lys Arg Phe Gln Val Val Ser Tyr Asn Thr Ala
            420                 425                 430
Ser Asp Asp Leu Glu Leu Leu Tyr His Ile Pro Glu Phe Ile Pro Glu
        435                 440                 445
Ala Arg Gly Leu Glu Phe Leu Met Ile Leu Gly Thr Glu Ser Tyr Thr
    450                 455                 460
Ser Thr Ala Met Ala Pro Lys Gly Ile Phe Cys Asn Pro Tyr Asn Asn
465                 470                 475                 480
Leu Ile Phe Ile Trp Gly Asn Phe Leu Leu Gln Arg Ser Gly Thr Ser
                485                 490                 495
Trp Arg Ala Ala Thr Gly Ser Thr Ser Cys Ser Leu Pro Arg Ala Gly
            500                 505                 510
Arg Cys Thr Ser Ala
        515
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<210> 4443
<211> 692
<212> DNA
<213> Homo sapiens

<400> 4443
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ccagggtaag gtctgggccc ctgctgctga catcccccac atgtcagtct gcctgctagt
120
gggattgact aactcatcaa cgtggagttt aatgcccaac caagtgcaga ccacgctcct
180
gttttgcgtc accctctgcg aagcttcctg caaacttgac tccctgccca gtgccccccag
240
ccccaaggct ggtctccagg aggtaaggcc cgccctgcag gcaacaccgg tgcttgggct
300
cctgctgagc agttctttcc tgcgagtaac agaaccaggg agggaggtgg gctgtggcct
360
cccctgcccc tacagtcatc tcctgcagct cccaccatgc tggactcatc agcagcagag
420
caagtgaccc gactgacgct gaagctcttg ggacagaagc tggagcaaga acggcagaac
480
gtggaagggg gacctgaggg ctccacctcg agccaggaaa tgaggaccgg ccggacgatg
540
ccctgcagac tgctctgaag agaaggaggg accttctgca gagactccgg gaacaacacc
600
tcctggacga gctctctcgg gcccaggcct ggagcgggcc aagcagagga gccctcgagt
660

cagccctgcc cccagagctg ccccccacgc gt
692

<210> 4444
<211> 108
<212> PRT
<213> Homo sapiens

<400> 4444
Met Ser Val Cys Leu Leu Val Gly Leu Thr Asn Ser Ser Thr Trp Ser
1 5 10 15
Leu Met Pro Asn Gln Val Gln Thr Thr Leu Leu Phe Cys Val Thr Leu
20 25 30
Cys Glu Ala Ser Cys Lys Leu Asp Ser Leu Pro Ser Ala Pro Ser Pro
35 40 45
Lys Ala Gly Leu Gln Glu Val Arg Pro Ala Leu Gln Ala Thr Pro Val
50 55 60
Leu Gly Leu Leu Leu Ser Ser Ser Phe Leu Arg Val Thr Glu Pro Gly
65 70 75 80
Arg Glu Val Gly Cys Gly Leu Pro Cys Pro Tyr Ser His Leu Leu Gln
85 90 95
Leu Pro Pro Cys Trp Thr His Gln Gln Gln Ser Lys
100 105

<210> 4445
<211> 901
<212> DNA
<213> Homo sapiens

<400> 4445
ggatccactg cctctgtgcc tgcctgtact gccgatgctc cagtggataa ctcagcatcc
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cagccaaggc ccaatgccac tgaagatgga cctgcccccc ggggacccag gagtcctacc
120
actcagctgt ccccaggagt gcccagaccc tcattcttat ccaggaccta ggagccctac
180
ccctggcctt ccctcatcag ccgtaaatga tgatttactg ctgttaccat catcactgcc
240
ttcagtgacc aagggccttc caaggtgcca gctctggaac gaaggatgcc cttgggaggt
300
gatgatactc aggtacacgg gtgctcaaca gattgcttcc tcctatcctc agacggtctt
360
tgcatgcatg cagccattgg cactcccatt gtgtggaagg aaaccagccc agggtcacac
420
agctggtcag cagcaacata gctggtctca aatctaaggt gcctgaccat gcctccatga
480
gggaccgcct ccaagggagg ttgatcctgg ctttggggag cctttcctgg gctgcacgaa
540
taacctccat tgttcgagac cccaaactct gctcacatct tcctttccct gtctctgctt
600
gggctatgat cacggtgact ctagcaaccc ttcatggaca ttataatact ctctgccatt
660
cacttttggt ctaatctgac ttcaaccccc acttacttgg tctctccttt tacaaccaac
720

atggcaaaac cccatctcca caaaaattgg ataatttgat aattatcatt attgggtttc
780
tgagacgtta cacatttaac attctcttct gcacaagttg cctttgtgtg agtatactaa
840
ctttctgtag aggtatactt gtaatcacaa ataagaataa attatataaa acaaaaaaaa
900
a
901

<210> 4446
<211> 140
<212> PRT
<213> Homo sapiens

<400> 4446
Met Leu Gln Trp Ile Thr Gln His Pro Ser Gln Gly Pro Met Pro Leu
1 5 10 15
Lys Met Asp Leu Pro Pro Gly Asp Pro Gly Val Leu Pro Leu Ser Cys
20 25 30
Pro Gln Glu Cys Pro Asp Pro His Ser Tyr Pro Gly Pro Arg Ser Pro
35 40 45
Thr Pro Gly Leu Pro Ser Ser Ala Val Asn Asp Asp Leu Leu Leu Leu
50 55 60
Pro Ser Ser Leu Pro Ser Val Thr Lys Gly Leu Pro Arg Cys Gln Leu
65 70 75 80
Trp Asn Glu Gly Cys Pro Trp Glu Val Met Ile Leu Arg Tyr Thr Gly
85 90 95
Ala Gln Gln Ile Ala Ser Ser Tyr Pro Gln Thr Val Phe Ala Cys Met
100 105 110
Gln Pro Leu Ala Leu Pro Leu Cys Gly Arg Lys Pro Ala Gln Gly His
115 120 125
Thr Ala Gly Gln Gln Gln His Ser Trp Ser Gln Ile
130 135 140

<210> 4447
<211> 951
<212> DNA
<213> Homo sapiens

<400> 4447
agatgtccaa agagcagcgg ctgcccaggc cttgtgcagc gggcagcgag cagcccaggg
60
agccaggccc cagacaccgc actcagggcc atggccgaca ggggcccgtg gagggtgggg
120
gtggtgggct atggccgcct cggacagtcc cttgtgtccc gccttctggc tcagggatca
180
gaactgggcc tagaacttgt ttttgtgtgg aaccgtgacc ctggacgaat ggcagggagt
240
gtgccccctg ccctgcagct cgaagacctc actacacttg aggaaaggca ccctgacctt
300
gtggtagaag tggcccatcc aaaaataatc catgaatctg gggtacaaat cctccgtcat
360
gcaaaccttc tgagccttcg tgtcaccatg gccacacacc ccgatggctt ccggcttgag
420

ggacccctgg ctgcagccca cagccctggg ccttgcactg tgctctacga aggccctgtc
480
cgtgggctct gcccctttgc cccgcgaaat tccaacacca tggcggcggc tgccctggct
540
gcccccagcc tgggcttcga tggggtgatt ggggtgctcg tggctgatac cagcctcacg
600
gacatgcacg tggtggatgt agagctgagc ggaccccggg gccccacggg ccgaagcttt
660
gctgtgcaca cccgcagaga gaaccctgcc gagccaggcg cggtcaccgg ctccgccacc
720
gtcacggcct tctggcggag cctcctggcc tgctgccagc tcccctccag gccggggatc
780
catctctgct gagaagcctc ctccctcccg agacaagatc atctgcctgg cctctcacca
840
ccaccatccc acccctgccc tgccccactt ccccagggtc tcccttctga ctcagtaaag
900
atcaccgctg cctcccccca caaaaaaaaa aaaaaaaaaa aaaaaaaaaa a
951

<210> 4448
<211> 263
<212> PRT
<213> Homo sapiens

<400> 4448
Arg Cys Pro Lys Ser Ser Gly Cys Pro Gly Leu Val Gln Arg Ala Ala
1 5 10 15
Ser Ser Pro Gly Ser Gln Ala Pro Asp Thr Ala Leu Arg Ala Met Ala
20 25 30
Asp Arg Gly Pro Trp Arg Val Gly Val Val Gly Tyr Gly Arg Leu Gly
35 40 45
Gln Ser Leu Val Ser Arg Leu Leu Ala Gln Gly Ser Glu Leu Gly Leu
50 55 60
Glu Leu Val Phe Val Trp Asn Arg Asp Pro Gly Arg Met Ala Gly Ser
65 70 75 80
Val Pro Pro Ala Leu Gln Leu Glu Asp Leu Thr Thr Leu Glu Glu Arg
85 90 95
His Pro Asp Leu Val Val Glu Val Ala His Pro Lys Ile Ile His Glu
100 105 110
Ser Gly Val Gln Ile Leu Arg His Ala Asn Leu Leu Ser Leu Arg Val
115 120 125
Thr Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu Gly Pro Leu Ala
130 135 140
Ala Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr Glu Gly Pro Val
145 150 155 160
Arg Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn Thr Met Ala Ala
165 170 175
Ala Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val
180 185 190
Leu Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu
195 200 205
Leu Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr
210 215 220
Arg Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr

225 230 235 240
Val Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser
245 250 255
Arg Pro Gly Ile His Leu Cys
260

<210> 4449
<211> 1365
<212> DNA
<213> Homo sapiens

<400> 4449
ncaattgatg atatttatca ttgtgcccag tttctacaaa taaaagatgg gtggattatt
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ttctcgatgg aggacaaaac ctccaactgt agaagttcta gaaagtatag ataaggaaat
120
tcaagcattg gaagaattta gggaaaaaaa tcagagatta caaaaattat gggttggaag
180
attaattctg tattcctcag ttctctatct gtttacatgc ttaattgtat atttgtggta
240
tcttcctgat gaatttacag caagacttgc catgacactc ccatttttg cttttccatt
300
gatcatctgg agcataagaa cagtaattat tttcttcttt tccaagagaa cagaaagaaa
360
taatgaagca ttggatgatt taaaatccca gaggaaaaaa atacttgaag aagtcatgga
420
aaaagaaact tacaagacgg ctaaattaat tcttgaaagg tttgatccgt actcaaagaa
480
agcaaaggag tgtgagccgc catctgctgg agcagctgta actgcaagac ctggacaaga
540
gattcgtcag cgaactgcag ctcaaagaaa cctttctcaa caccagcaag ccctaaccag
600
ggccctcctc cacaagttcc agtatctcct ggaccaccaa aggacagttc tgcccctggt
660
ggacccccag aaaggactgt tactccagcc ctatcatcaa atgtgttacc aagacatctt
720
ggatcccctg ctacttcagt gcctggaatg ggtcttcatc ctccaggtcc acctttagca
780
agacctattc tcccccgaga acgaggtgct ttggatagaa ttgttgaata tttggttggt
840
gatggtccac aaaacaggta tgcacttata tgtcagcagt gtttttctca taatggcatg
900
gctttgaagg aagaatttga atacattgct tttcgatgtg cctactgttt tttcttgaac
960
cctgcaagaa aaaccagacc tcaggctcca agacttcctg agtttagttt tgagaagagg
1020
caggtggtgg aaggttcaag ttcagttggt cccttgccat caggaagtgt gctttcatca
1080
gacaaccagt ttaatgaaga atctttagaa cacgatgttc ttgatgataa tacagagcag
1140
acagatgaca aaataccagc tacagaacag acaaaccaag tgattgaaaa agcatctgac
1200
tcagaggaac cagaggagaa acaagagact gagaatgagg aagcctcagt gattgaaacc
1260

aactccacag ttcctggagc tgattctatt cctgatcctg aactaagtgg agaatctttg
1320
acggcagagt agtaaatgct tccacgtgcc ttcaactgga aaaaa
1365

<210> 4450
<211> 194
<212> PRT
<213> Homo sapiens

<400> 4450
Met Gly Leu His Pro Pro Gly Pro Pro Leu Ala Arg Pro Ile Leu Pro
1 5 10 15
Arg Glu Arg Gly Ala Leu Asp Arg Ile Val Glu Tyr Leu Val Gly Asp
20 25 30
Gly Pro Gln Asn Arg Tyr Ala Leu Ile Cys Gln Gln Cys Phe Ser His
35 40 45
Asn Gly Met Ala Leu Lys Glu Glu Phe Glu Tyr Ile Ala Phe Arg Cys
50 55 60
Ala Tyr Cys Phe Phe Leu Asn Pro Ala Arg Lys Thr Arg Pro Gln Ala
65 70 75 80
Pro Arg Leu Pro Glu Phe Ser Phe Glu Lys Arg Gln Val Val Glu Gly
85 90 95
Ser Ser Ser Val Gly Pro Leu Pro Ser Gly Ser Val Leu Ser Ser Asp
100 105 110
Asn Gln Phe Asn Glu Glu Ser Leu Glu His Asp Val Leu Asp Asp Asn
115 120 125
Thr Glu Gln Thr Asp Asp Lys Ile Pro Ala Thr Glu Gln Thr Asn Gln
130 135 140
Val Ile Glu Lys Ala Ser Asp Ser Glu Glu Pro Glu Glu Lys Gln Glu
145 150 155 160
Thr Glu Asn Glu Glu Ala Ser Val Ile Glu Thr Asn Ser Thr Val Pro
165 170 175
Gly Ala Asp Ser Ile Pro Asp Pro Glu Leu Ser Gly Glu Ser Leu Thr
180 185 190
Ala Glu

<210> 4451
<211> 1637
<212> DNA
<213> Homo sapiens

<400> 4451
nntcctggag gacccaggac tgaccaagtc cccggcctca gcaggcgatc atgttggcag
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gcttggatct tctcgctctg tgaccagcct gggccacaca ctggtggaat ctgctctcac
120
gaggccttcc ctgcccagtc cccacaggac ctcacctagg gtggaggaga gcaacagcaa
180
gctcctggag tcagagagga agctgcagga ggagcgacac cgcaccgtgg tcttggagca
240
acatctggag aagatacgcc tggagccagg gaaggcatca gcctcccaga gagcagctcc
300

caggaccaaa acagctccgc tcctggatgt atgctgtgta cggggccttg gctgtgatgg
360
gcacaatggg cccttggtac ctgctgctgc tgcttggtca ctgtgtgggc ctctatgtgg
420
cctcgctttt gggccagccc tggctctgtc ttggccttgg cttggccagc ctggcctcct
480
tcaagatgga ccccctaatc tcttggcaga gcgggtttgt aacaggcact tttgatcttc
540
aagaggtgct gtttcatggg ggcagcagct tcacagtgct gcgttgcacc agctttgcac
600
tggagagctg tgcccaccct gaccgccact nactccttag ctgacctgct caagtacaac
660
ttctacctgc ccttcttctt cttcgggccc atcatgacct ttgatcgctt ccatgctcag
720
gtgagccagg tggagccagt gagacgcgag ggtgagctgt ggcacatccg agcccaggca
780
ggcctaagcg tggtggccat catggccgtc gacatcttct ttcacttctt ctacatcctc
840
actatcccca gcgacctcaa gttcgccaac cgcctcccag acagtgccct cgctggccta
900
gcctattcaa acctggtgta tgactgggtg aaggcggccg tcctctttgg tgttgtcaac
960
actgtggcat gcctcgacca cctggaccca ccccagcctc ccaagtgcat caccgcactc
1020
tacgtctttg cggaaacgca ctttgaccgt ggcatcaacg actggctttg caaatatgtg
1080
tataaccaca ttggtgggga gcattccgct gtgatcccag agctggcagc cacagtggcc
1140
acatttgcca tcaccacact gtggcttggg ccttgtgaca ttgtctacct gtggtcattc
1200
cttaactgct ttggcctcaa ctttgagctc tggatgcaaa aactggcaga gtgggggccc
1260
ctagcacgaa ttgaggcctc tctgtcagtg cagatgtccc gtagggtccg ggccctgttt
1320
ggagccatga acttctgggc catcatcatg tacaaccttg tgagcctgaa cagcctcaaa
1380
ttcacagagc tggttgcccg gcgcctgcta ctcacagggt tcccccagac cacgctgtcc
1440
atcctgtttg tcacctactg tggcgtccag ctggtaaagg agcgtgagcg aaccttggca
1500
ctggaggagg agcagaagca ggacaaagag aagccggagt aggagggagc gggtagaggg
1560
atgggctctg ctcagctatt cttgggccag atggggcctg accgatagaa taaaagactt
1620
ttctacaaca aaaaaaa
1637

<210> 4452
<211> 328
<212> PRT
<213> Homo sapiens

<400> 4452
Met Gly Ala Ala Ala Ser Gln Cys Cys Val Ala Pro Ala Leu His Trp

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 1               5                  10                  15
Arg Ala Val Pro Thr Leu Thr Ala Thr Xaa Ser Leu Ala Asp Leu Leu
            20                  25                  30
Lys Tyr Asn Phe Tyr Leu Pro Phe Phe Phe Phe Gly Pro Ile Met Thr
        35                  40                  45
Phe Asp Arg Phe His Ala Gln Val Ser Gln Val Glu Pro Val Arg Arg
    50                  55                  60
Glu Gly Glu Leu Trp His Ile Arg Ala Gln Ala Gly Leu Ser Val Val
65                  70                  75                  80
Ala Ile Met Ala Val Asp Ile Phe Phe His Phe Phe Tyr Ile Leu Thr
                85                  90                  95
Ile Pro Ser Asp Leu Lys Phe Ala Asn Arg Leu Pro Asp Ser Ala Leu
            100                 105                 110
Ala Gly Leu Ala Tyr Ser Asn Leu Val Tyr Asp Trp Val Lys Ala Ala
        115                 120                 125
Val Leu Phe Gly Val Val Asn Thr Val Ala Cys Leu Asp His Leu Asp
    130                 135                 140
Pro Pro Gln Pro Pro Lys Cys Ile Thr Ala Leu Tyr Val Phe Ala Glu
145                 150                 155                 160
Thr His Phe Asp Arg Gly Ile Asn Asp Trp Leu Cys Lys Tyr Val Tyr
                165                 170                 175
Asn His Ile Gly Gly Glu His Ser Ala Val Ile Pro Glu Leu Ala Ala
            180                 185                 190
Thr Val Ala Thr Phe Ala Ile Thr Thr Leu Trp Leu Gly Pro Cys Asp
        195                 200                 205
Ile Val Tyr Leu Trp Ser Phe Leu Asn Cys Phe Gly Leu Asn Phe Glu
    210                 215                 220
Leu Trp Met Gln Lys Leu Ala Glu Trp Gly Pro Leu Ala Arg Ile Glu
225                 230                 235                 240
Ala Ser Leu Ser Val Gln Met Ser Arg Arg Val Arg Ala Leu Phe Gly
                245                 250                 255
Ala Met Asn Phe Trp Ala Ile Ile Met Tyr Asn Leu Val Ser Leu Asn
            260                 265                 270
Ser Leu Lys Phe Thr Glu Leu Val Ala Arg Arg Leu Leu Leu Thr Gly
        275                 280                 285
Phe Pro Gln Thr Thr Leu Ser Ile Leu Phe Val Thr Tyr Cys Gly Val
    290                 295                 300
Gln Leu Val Lys Glu Arg Glu Arg Thr Leu Ala Leu Glu Glu Glu Gln
305                 310                 315                 320
Lys Gln Asp Lys Glu Lys Pro Glu
                325
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<210> 4453
<211> 685
<212> DNA
<213> Homo sapiens

<400> 4453
tttttttttt tttttttttt tttttttttt tttttccagt gtggaaactt actttattcc
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agccatgatt atcctagttg tcaccttgca cacctgccat ccggtgccat ctcctggctg
120
gcacatctat acccactctg gctctgaaag gcttgtcaac caaaaatggg cagctggggc
180

taaggcatat ttaaacaaag gctccaaagg acccctttca cttgggtcta gcatccagcc
240
tctctctcag caaaggcagg attgtggtcc cttgtgtttt ctgaacaggg cccagggcag
300
ccaaggcatg ccatcactgc agcactcaac cctctggtca cagtggagtc gccggtccag
360
cctgaaatat tactacagag gagaaagacc cattcttgct atgttgctct atcttccacg
420
tccaaaaaca gtcctatgta gcttcagctg ctccgaaatc aggtcacaga acagcaggag
480
acattccttt ggcaaaaaag gacacgcttt tgtcctgtat cttatactgg taagtgaagc
540
tctgatcccg gtggactgcg ggctgcgatg gtctcctcca caggatcctc agctacagag
600
acagagaaga atgaaagagg agcagccacc ccaggacctg ctccactggg aaccccaccc
660
taccttctct gtgcccttca cgcgt
685

<210> 4454
<211> 207
<212> PRT
<213> Homo sapiens

<400> 4454
Met Ile Ile Leu Val Val Thr Leu His Thr Cys His Pro Val Pro Ser
1 5 10 15
Pro Gly Trp His Ile Tyr Thr His Ser Gly Ser Glu Arg Leu Val Asn
20 25 30
Gln Lys Trp Ala Ala Gly Ala Lys Ala Tyr Leu Asn Lys Gly Ser Lys
35 40 45
Gly Pro Leu Ser Leu Gly Ser Ser Ile Gln Pro Leu Ser Gln Gln Arg
50 55 60
Gln Asp Cys Gly Pro Leu Cys Phe Leu Asn Arg Ala Gln Gly Ser Gln
65 70 75 80
Gly Met Pro Ser Leu Gln His Ser Thr Leu Trp Ser Gln Trp Ser Arg
85 90 95
Arg Ser Ser Leu Lys Tyr Tyr Tyr Arg Gly Glu Arg Pro Ile Leu Ala
100 105 110
Met Leu Leu Tyr Leu Pro Arg Pro Lys Thr Val Leu Cys Ser Phe Ser
115 120 125
Cys Ser Glu Ile Arg Ser Gln Asn Ser Arg Arg His Ser Phe Gly Lys
130 135 140
Lys Gly His Ala Phe Val Leu Tyr Leu Ile Leu Val Ser Glu Ala Leu
145 150 155 160
Ile Pro Val Asp Cys Gly Leu Arg Trp Ser Pro Pro Gln Asp Pro Gln
165 170 175
Leu Gln Arg Gln Arg Arg Met Lys Glu Glu Gln Pro Pro Gln Asp Leu
180 185 190
Leu His Trp Glu Pro His Pro Thr Phe Ser Val Pro Phe Thr Arg
195 200 205

<210> 4455
<211> 882

<212> DNA
<213> Homo sapiens

<400> 4455
nacgcgtgcc tcagtaccaa cgggctcggc agcagcccgg gcagtgccgg gcacatgaac
60
ggattaagcc acagcccggg gaacccgtcg accattccca tgaaggacca cgatgccatc
120
aagctgttca ttgggcagat cccccgcaac ctggatgaga aggacctcaa gcccctcttc
180
gaggagtttg gcaaaatcta cgagcttacg gttctgaagg acaggttcac aggcatgcac
240
aaaggctgcg ccttcctcac ctactgcgag cgtgagtcag cgctgaaggc ccagagcgcg
300
ctgcacgagc agaagactct gcccgggatg aaccggccga tccaggtgaa gcctgcggac
360
agcgagagcc gaggagatag tagctgcctg cgccagcccc cttcacatag aaaactcttc
420
gtgggcatgc tcaacaagca acagtccgag gacgacgtgc gccgcctttt cgaggccttt
480
gggaacatcg aggagtgcac catcctgcgc gggcccgacg gcaacagcaa ggggtgcgcc
540
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600
cagaccatgc cgggagcctc gtccagtctg gtggtcaagt tcgccgacac cgacaaggag
660
cgcacgatgc ggcgaatgca gcagatggct ggccagatgg gcatgttcaa ccccatggcc
720
atccctttcg gggcctacgg cgcctacgct caggcactga tgcagcagca agcggccctg
780
atggcatcag tcgcgcaggg cggctacctg aaccccatgg ctgccttcgc tgccgcccag
840
atgcagcaga tggcggccct caacatgaat ggcctggcgg cc
882

<210> 4456
<211> 261
<212> PRT
<213> Homo sapiens

<400> 4456
Met Lys Asp His Asp Ala Ile Lys Leu Phe Ile Gly Gln Ile Pro Arg
 1   5   10   15
Asn Leu Asp Glu Lys Asp Leu Lys Pro Leu Phe Glu Glu Phe Gly Lys
            20   25   30
Ile Tyr Glu Leu Thr Val Leu Lys Asp Arg Phe Thr Gly Met His Lys
        35   40   45
Gly Cys Ala Phe Leu Thr Tyr Cys Glu Arg Glu Ser Ala Leu Lys Ala
    50   55   60
Gln Ser Ala Leu His Glu Gln Lys Thr Leu Pro Gly Met Asn Arg Pro
65   70   75   80
Ile Gln Val Lys Pro Ala Asp Ser Glu Ser Arg Gly Asp Ser Ser Cys
                85   90   95
Leu Arg Gln Pro Pro Ser His Arg Lys Leu Phe Val Gly Met Leu Asn

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           100                 105                 110
Lys Gln Gln Ser Glu Asp Asp Val Arg Arg Leu Phe Glu Ala Phe Gly
       115                 120                 125
Asn Ile Glu Glu Cys Thr Ile Leu Arg Gly Pro Asp Gly Asn Ser Lys
   130                 135                 140
Gly Cys Ala Phe Val Lys Tyr Ser Ser His Ala Glu Ala Gln Ala Ala
145                 150                 155                 160
Ile Asn Ala Leu His Gly Ser Gln Thr Met Pro Gly Ala Ser Ser Ser
                165                 170                 175
Leu Val Val Lys Phe Ala Asp Thr Asp Lys Glu Arg Thr Met Arg Arg
            180                 185                 190
Met Gln Gln Met Ala Gly Gln Met Gly Met Phe Asn Pro Met Ala Ile
        195                 200                 205
Pro Phe Gly Ala Tyr Gly Ala Tyr Ala Gln Ala Leu Met Gln Gln Gln
    210                 215                 220
Ala Ala Leu Met Ala Ser Val Ala Gln Gly Gly Tyr Leu Asn Pro Met
225                 230                 235                 240
Ala Ala Phe Ala Ala Ala Gln Met Gln Gln Met Ala Ala Leu Asn Met
                245                 250                 255
Asn Gly Leu Ala Ala
            260
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<210> 4457
<211> 1491
<212> DNA
<213> Homo sapiens

<400> 4457
nggctggcag gtgcacatca gcttaaagct gatgcaacag tcctctctct acgcatccaa
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tgagaccatg ctgaccctct tctacgaaga cagcaaactg taccaggtgc ccggtggagc
120
tatgcgggga catcggggca ccccaggagg gctgacccca gctcacctgg ccctgccttc
180
cccctgcagc tggtgtacct tatgaacaac cagaagggcc agctggtcaa gaggctcgtg
240
cccgtggagc agcttctgat gtatcaacag cacaccagcc actatgactt ggagcggaaa
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360
agcctgccca gtccgcagag atacacgcgc caggagcgct accgggcgcg gccgccgcgc
420
gtcctggagc gctcgggctt ccacaacgag aactcgctcg ccatctacca gggcctggtc
480
tactacctgc tgtggctgca ctccgtgtac gacaaggatt actacttctt cttggcgagc
540
aattggcgaa gcgcgggcgg cgtgtccata gaaatggaca gctacgaaaa gatctacaac
600
ctcgagtccg cgtacgagct gccggagcgc attttcctgg acaagggcac tgagtacagc
660
ttcgccatct tcctgtcggc gcagggccac tcgttccgga cgcagtcaga actcggtctg
720
cgcgggacca gagtggagcc cgaagggcgg ggcgagggct accagaatct gggagcctgg
780

ggggcgggga caccatcgga ggggcggggc ctgtctgtgg acgtgggcgt ggtgctggcc
840
gaccccggct gcatcgaggc ctcggtgaag caggaggtcc tgattaatcg caactcggtg
900
ctattttcga ttacgctcaa ggataaaaag ctttgctatg accaaggcat tagtggacat
960
caccttatgg agacttccat gacggtcaat gtgaggtcca agcctggagg ggagggcaag
1020
cgcctggcct tcgacatcac ctacacgctg gaatacagcc gcctgaagaa caaacactac
1080
tttgactgcg ttaacgtgaa cccggagatg ccctgctttc tcttccggga cagtgtctat
1140
gttctgctgg tggtgggtgg cgggcccaca ctggacagcc tcaaggacta cagtgaggac
1200
gaaatctacc gcttcaacag ccccctggac aagaccaaca gccttatctg gaccacgagg
1260
accacaagga ccaccaaaga ctcagccttt cacatcatgt cccacgagag cccaggcatc
1320
gagtggctct gtctggagaa tgccccatgc tatgacaatg ttccccaagg catctttgcc
1380
cctgaattct tcttcaaggt gttggtgagc aataggtgag ccaggcaagt ggcccaggtg
1440
cgggtcaggg gctgcccatg gaatgcctgg cttctcctct aatcctggat c
1491

<210> 4458
<211> 405
<212> PRT
<213> Homo sapiens

<400> 4458
Met Asn Asn Gln Lys Gly Gln Leu Val Lys Arg Leu Val Pro Val Glu
1 5 10 15
Gln Leu Leu Met Tyr Gln Gln His Thr Ser His Tyr Asp Leu Glu Arg
20 25 30
Lys Gly Gly Tyr Leu Met Leu Ser Phe Ile Asp Phe Cys Pro Phe Ser
35 40 45
Val Met Arg Leu Arg Ser Leu Pro Ser Pro Gln Arg Tyr Thr Arg Gln
50 55 60
Glu Arg Tyr Arg Ala Arg Pro Pro Arg Val Leu Glu Arg Ser Gly Phe
65 70 75 80
His Asn Glu Asn Ser Leu Ala Ile Tyr Gln Gly Leu Val Tyr Tyr Leu
85 90 95
Leu Trp Leu His Ser Val Tyr Asp Lys Asp Tyr Tyr Phe Phe Leu Ala
100 105 110
Ser Asn Trp Arg Ser Ala Gly Gly Val Ser Ile Glu Met Asp Ser Tyr
115 120 125
Glu Lys Ile Tyr Asn Leu Glu Ser Ala Tyr Glu Leu Pro Glu Arg Ile
130 135 140
Phe Leu Asp Lys Gly Thr Glu Tyr Ser Phe Ala Ile Phe Leu Ser Ala
145 150 155 160
Gln Gly His Ser Phe Arg Thr Gln Ser Glu Leu Gly Leu Arg Gly Thr
165 170 175
Arg Val Glu Pro Glu Gly Arg Gly Glu Gly Tyr Gln Asn Leu Gly Ala

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            180                 185                 190
Trp Gly Ala Gly Thr Pro Ser Glu Gly Arg Gly Leu Ser Val Asp Val
        195                 200                 205
Gly Val Val Leu Ala Asp Pro Gly Cys Ile Glu Ala Ser Val Lys Gln
    210                 215                 220
Glu Val Leu Ile Asn Arg Asn Ser Val Leu Phe Ser Ile Thr Leu Lys
225                 230                 235                 240
Asp Lys Lys Leu Cys Tyr Asp Gln Gly Ile Ser Gly His His Leu Met
                245                 250                 255
Glu Thr Ser Met Thr Val Asn Val Arg Ser Lys Pro Gly Gly Glu Gly
            260                 265                 270
Lys Arg Leu Ala Phe Asp Ile Thr Tyr Thr Leu Glu Tyr Ser Arg Leu
        275                 280                 285
Lys Asn Lys His Tyr Phe Asp Cys Val Asn Val Asn Pro Glu Met Pro
    290                 295                 300
Cys Phe Leu Phe Arg Asp Ser Val Tyr Val Leu Leu Val Val Gly Gly
305                 310                 315                 320
Gly Pro Thr Leu Asp Ser Leu Lys Asp Tyr Ser Glu Asp Glu Ile Tyr
                325                 330                 335
Arg Phe Asn Ser Pro Leu Asp Lys Thr Asn Ser Leu Ile Trp Thr Thr
            340                 345                 350
Arg Thr Thr Arg Thr Thr Lys Asp Ser Ala Phe His Ile Met Ser His
        355                 360                 365
Glu Ser Pro Gly Ile Glu Trp Leu Cys Leu Glu Asn Ala Pro Cys Tyr
    370                 375                 380
Asp Asn Val Pro Gln Gly Ile Phe Ala Pro Glu Phe Phe Phe Lys Val
385                 390                 395                 400
Leu Val Ser Asn Arg
                405
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<210> 4459
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 4459
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60
aaggcaacac cgagggaggc ccagcaccac agtccatggc agacacatgg ttcagacttg
120
gccgattgat ctaagaaact ttattgctca gaaccttccc tccctgggca atggaaagag
180
ctttggagac cagcccatgg ggacagagtc agaggcactg ggtgtaaaaa aagagcgagc
240
gtgtggcaca tttggtccat tgtcatgtgt gggtatggca ggaggagggg gtaatctaga
300
agccccacat ctagggcctt ctagggaccc agatatgccc ccttaggcaa ggctcacatg
360
ccaaagcaaa gcagatgagg tcagcctggc ttgggttgag ggctcagtgc ctcttagcct
420
tgccctgggg ttcttggacc ttccggaaac tgagccacat caggctcacg ttgatagcat
480
aggtggtgat acaaacaatg cagaaatcat agagcacgaa gaacaggatc caggccaggt
540

agacagaacc agcgagagac accagggagc tcagcagcat caggacagag gcccagcgtg
600
tccgcaggca acctaacaat agctgtagtg tgtagaagat gcaaccgaat atgctgttgg
660
attgattgag gatgctgtcc tgtcccagca catgctccac cagcccgaaa cccctgcccc
720
acctggagga gaagacgcgc gaacagctga tggcggtgcc cacgtcgcag agcgcgcggt
780
aatcccggtc ccgggcgcgc gccgccttca cgtgcagcgc gtagagcgag agcactaagc
840
ccgtcaggca aagagcgagc cgcacccagc cagggctccc ccaggtgctg cccattatct
900
ccaggttccg cccgaggcgc ccgcggagaa aaccagccac ggagcagggg ccgggcggcg
960
aatggccgcg cccctcctgg ccctctgact cggcgattgg ccggccgtgc tcgcactcca
1020
cgacccaaat ggctgttcca gggcgctagt caagcgggcg agttaggaaa acagcgaaga
1080
atgccgggac tagtgaagcg ggtaagggac gtgc
1114

<210> 4460
<211> 121
<212> PRT
<213> Homo sapiens

<400> 4460
Trp Arg Cys Pro Arg Arg Arg Ala Arg Gly Asn Pro Gly Pro Gly Arg
 1   5   10   15
Ala Pro Pro Ser Arg Ala Ala Arg Arg Ala Arg Ala Leu Ser Pro Ser
            20   25   30
Gly Lys Glu Arg Ala Ala Pro Ser Gln Gly Ser Pro Arg Cys Cys Pro
        35   40   45
Leu Ser Pro Gly Ser Ala Arg Gly Ala Arg Gly Glu Asn Gln Pro Arg
    50   55   60
Ser Arg Gly Arg Ala Ala Asn Gly Arg Ala Pro Pro Gly Pro Leu Thr
65   70   75   80
Arg Arg Leu Ala Gly Arg Ala Arg Thr Pro Arg Pro Lys Trp Leu Phe
                85   90   95
Gln Gly Ala Ser Gln Ala Gly Glu Leu Gly Lys Gln Arg Arg Met Pro
            100   105   110
Gly Leu Val Lys Arg Val Arg Asp Val
        115   120

<210> 4461
<211> 488
<212> DNA
<213> Homo sapiens

<400> 4461
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aatctgatct tcatctgggg caacttcctc ctgcagagct ctaacaagga aaacttcatc
120

tacctggcag acttccccaa ggaactgtcc atcaaataca tggccagatc gttccgtggg
180
gctgtggcta ttgtcacaga gacggaggag gtgggctgcc ccgcccttct ccccattccc
240
tctctgccca cccccaaacc ccaggggccc ctctttcccc cgtcacagta aaggagccaa
300
gggaaggggg caccctcggg gaccctgaga aagggcagtg aagctccatt tataactgaa
360
actcctggaa ctcagggtaa gtgtcagctc caaagtcacg cagaccggag ctatgatccg
420
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480
catttaaa
488

<210> 4462
<211> 96
<212> PRT
<213> Homo sapiens

<400> 4462
Thr Glu Ser Tyr Thr Ser Thr Ala Met Ala Pro Lys Gly Ile Phe Cys
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Asn Pro Tyr Asn Asn Leu Ile Phe Ile Trp Gly Asn Phe Leu Leu Gln
20 25 30
Ser Ser Asn Lys Glu Asn Phe Ile Tyr Leu Ala Asp Phe Pro Lys Glu
35 40 45
Leu Ser Ile Lys Tyr Met Ala Arg Ser Phe Arg Gly Ala Val Ala Ile
50 55 60
Val Thr Glu Thr Glu Glu Val Gly Cys Pro Ala Leu Leu Pro Ile Pro
65 70 75 80
Ser Leu Pro Thr Pro Lys Pro Gln Gly Pro Leu Phe Pro Pro Ser Gln
85 90 95

<210> 4463
<211> 2662
<212> DNA
<213> Homo sapiens

<400> 4463
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120
cctcccatgg gccatttgct ccctggaggc cctcgcgtct tgctgagccc ggggagttag
180
gatgacgcga gcggtgaggg aacccggaac aattccttca cagaacaatt gaggcgaggc
240
ctttgggagt actttgtggg acggaccctg gcgggccctg ccagacgcac agggatggcg
300
gcggaggcgg ccgatttggg gctgggggcc gccgtccccg tggagctgag gcgggagcga
360
cgcatggtgt gcgtggagta cccgggagtg gtgcgtgatg tggctaagat gctgccgact
420

ctgggcggtg aggaaggcgt ctcccggatc tacgcagacc ccaccaagag gctggagctg
480
tacttccggc ccaaggaccc atactgccac ccagtgtgcg ccaaccgctt cagtaccagc
540
agcctgctgc tccgcatcag gaagagaacg aggcggcaga aaggggtgct gggcactgag
600
gcccactccg aggtcacatt tgacatggag atccttggca tcatctccac catttacaaa
660
tttcagggga tgtctgactt ccagtacttg gctgtgcata cggaagcagg cggcaagcat
720
acgtcaatgt atgacaaggt gctcatgctc cggcccgaga aggaggcctt tttccaccag
780
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840
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aatctgattg gcctgagcag agcccggcgc ccccacaatg ccatctttgt caactttgag
960
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1080
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1260
atccgttgtg gaatgaaaca cggttacgcc cccagtgact tgccggtcaa agcaaagcgc
1320
agcacctaca actacagcct ccccatcacc gtcaagaaga catccagcca gcttgtcacc
1380
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1440
tccagcaagt acaagctcaa ggactctgtc tacatcttcc gggaaggggc cttgccaccc
1500
tatcggcaga tgttctacca gttatgcgac ttgaatgtgg aagagttgca gaagatcatt
1560
caccgcaatg acggggcaga gaattcctgc acagaacggg atgggtggtg cctccccaag
1620
accagcgacg agctcaggga caccatgtcc ctcatgatcc ggcagaccat ccgctccaag
1680
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1740
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1800
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1860
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1920
ctccccattg ccacccacag tgcccggaat ggccctagga ggccctctga ggagagctag
1980
agtcccagca aagggtgcag ctgaccctag cactggctgt gacatgctgc ttggtgctgc
2040

ctctggtcct gaggggttag ggacatcccc aaagggtata ccctggctct gccacccatg
2100
aaccagccca gcatccagcc agtgagtggg cacccaatgc ctctcaggat gagaccagta
2160
aatgccggag gtggagctgg gcagctgtgg agccccaggc cacaggccag tctcgcttgg
2220
ctctcatgac tgtggtggtg gagatagcgt ggggagcctc gcccatggtc tcacgtggca
2280
agaagtgcct ttagctctgg atcccaaccg tttggcacag ctttggccac agccaggccc
2340
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2400
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2460
atattccttc attcattcct tcattcattc agtgacatgc tggcagtgct ggcctgtgcc
2520
cccctcacat gtggtcgggt tgggtgaggg cagctaggaa gactccaggg gctgggtcag
2580
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2640
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2662

<210> 4464
<211> 519
<212> PRT
<213> Homo sapiens

<400> 4464
Met Ala Ala Glu Ala Ala Asp Leu Gly Leu Gly Ala Ala Val Pro Val
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Glu Leu Arg Arg Glu Arg Arg Met Val Cys Val Glu Tyr Pro Gly Val
20 25 30
Val Arg Asp Val Ala Lys Met Leu Pro Thr Leu Gly Gly Glu Glu Gly
35 40 45
Val Ser Arg Ile Tyr Ala Asp Pro Thr Lys Arg Leu Glu Leu Tyr Phe
50 55 60
Arg Pro Lys Asp Pro Tyr Cys His Pro Val Cys Ala Asn Arg Phe Ser
65 70 75 80
Thr Ser Ser Leu Leu Leu Arg Ile Arg Lys Arg Thr Arg Arg Gln Lys
85 90 95
Gly Val Leu Gly Thr Glu Ala His Ser Glu Val Thr Phe Asp Met Glu
100 105 110
Ile Leu Gly Ile Ile Ser Thr Ile Tyr Lys Phe Gln Gly Met Ser Asp
115 120 125
Phe Gln Tyr Leu Ala Val His Thr Glu Ala Gly Gly Lys His Thr Ser
130 135 140
Met Tyr Asp Lys Val Leu Met Leu Arg Pro Glu Lys Glu Ala Phe Phe
145 150 155 160
His Gln Glu Leu Pro Leu Tyr Ile Pro Pro Pro Ile Phe Ser Arg Leu
165 170 175
Asp Ala Pro Val Asp Tyr Phe Tyr Arg Pro Glu Thr Gln His Arg Glu
180 185 190
Gly Tyr Asn Asn Pro Pro Ile Ser Gly Glu Asn Leu Ile Gly Leu Ser

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        195                 200                 205
Arg Ala Arg Arg Pro His Asn Ala Ile Phe Val Asn Phe Glu Asp Glu
    210                 215                 220
Glu Val Pro Lys Gln Pro Leu Glu Ala Ala Ala Gln Thr Trp Arg Arg
225                 230                 235                 240
Val Cys Thr Asn Pro Val Asp Arg Lys Val Glu Glu Glu Leu Arg Lys
                245                 250                 255
Leu Phe Asp Ile Arg Pro Ile Trp Ser Arg Asn Ala Val Lys Ala Asn
            260                 265                 270
Ile Ser Val His Pro Asp Lys Leu Lys Val Leu Leu Pro Phe Ile Ala
        275                 280                 285
Tyr Tyr Met Ile Thr Gly Pro Trp Arg Ser Leu Trp Ile Arg Phe Gly
    290                 295                 300
Tyr Asp Pro Arg Lys Asn Pro Asp Ala Lys Ile Tyr Gln Val Leu Asp
305                 310                 315                 320
Phe Arg Ile Arg Cys Gly Met Lys His Gly Tyr Ala Pro Ser Asp Leu
                325                 330                 335
Pro Val Lys Ala Lys Arg Ser Thr Tyr Asn Tyr Ser Leu Pro Ile Thr
            340                 345                 350
Val Lys Lys Thr Ser Ser Gln Leu Val Thr Met His Asp Leu Lys Gln
        355                 360                 365
Gly Leu Gly Arg Ser Gly Thr Ser Gly Ala Arg Lys Pro Ala Ser Ser
    370                 375                 380
Lys Tyr Lys Leu Lys Asp Ser Val Tyr Ile Phe Arg Glu Gly Ala Leu
385                 390                 395                 400
Pro Pro Tyr Arg Gln Met Phe Tyr Gln Leu Cys Asp Leu Asn Val Glu
                405                 410                 415
Glu Leu Gln Lys Ile Ile His Arg Asn Asp Gly Ala Glu Asn Ser Cys
            420                 425                 430
Thr Glu Arg Asp Gly Trp Cys Leu Pro Lys Thr Ser Asp Glu Leu Arg
        435                 440                 445
Asp Thr Met Ser Leu Met Ile Arg Gln Thr Ile Arg Ser Lys Arg Pro
    450                 455                 460
Ala Leu Phe Ser Ser Ser Ala Lys Ala Asp Gly Gly Lys Glu Gln Leu
465                 470                 475                 480
Thr Tyr Glu Ser Gly Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Glu
                485                 490                 495
Glu Glu Glu Asp Phe Lys Pro Ser Asp Gly Ser Glu Asn Glu Met Glu
            500                 505                 510
Thr Glu Ile Leu Asp Tyr Val
        515
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<210> 4465
<211> 1291
<212> DNA
<213> Homo sapiens

<400> 4465
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120
ngcgccgtgg ggctagtgga cgccgtgaag gccaccgacc agtactgcgc ccgcctccgc
180

caggccggct cggccgcgcc ccggccaccg cgggcccagc agccacagca gccatcccaa
240
gagaagttct acagcatggc tgccagatca agctactctt agaaattccg gagaagatct
300
ggagctcgat ggaagcctct cagtgtctcc acgccacacn agctctacct gctctgctgc
360
cacctccaca gcctgctcca gctggattct tctagttccc gatacagtcc cgtcctctcc
420
cggtttccta tactcatccg gcaggtggcg gccgccagcc acttccggtc aactattctg
480
catgaaagca agatgttgct caaatgccaa ggtgtgtctg accaagctgt ggccgaggcc
540
ctgtgctcta taatgctctt agaagagagt tctcctcgcc aagccctcac agacttcctg
600
ctggccagaa aggcaactat tcagaaactt ctcaaccagc cacaccatgg tgctggtatc
660
aaggctcaga tttgctcatt agtggagttg ctggccacca ctctgaagca agctcatgcc
720
cttttctaca ctttgccaga aggactgctg ccagatccag ccctgccatg tggcttgctc
780
ttctctactc tggagaccat cacaggccag catcctgccg gaaagggcac tggtgtcctg
840
caggaagaga tgaaactctg cagctggttt aaacacctgc cagcatccat cgtcgagttc
900
cagccaacac tccgaaccct tgcacatccc atcagtcagg aatacctgaa agacacgctg
960
cagaaatgga tccacatgtg taatgaagac attaaaaatg ggatcaccaa cctgctcatg
1020
tacgtgaaga gcatgaaggg tctcgcggga atccgggacg ccatgtggga gttacttacc
1080
agtgagtcca ccaatcacag ctgggatgtg ctatgtaccc gcnttctgga gaagccgctc
1140
ttgttctggg aagatatgat gcagcaactg ttccttgacc gattacagac tctgacaaaa
1200
gaaggctttg actccatctc cagtagtncc aaggagctct tggtttcang tttgcaggaa
1260
cttgaaagca gcaccagcaa ctcccacttc a
1291

<210> 4466
<211> 93
<212> PRT
<213> Homo sapiens

<400> 4466
Gly Leu Glu Arg Gln Val Arg Ala Glu Ile Glu His Lys Lys Glu Glu
1 5 10 15
Leu Arg Gln Met Val Gly Glu Arg Tyr Arg Asp Leu Ile Glu Ala Xaa
20 25 30
Asp Thr Ile Gly Gln Met Arg Arg Xaa Ala Val Gly Leu Val Asp Ala
35 40 45
Val Lys Ala Thr Asp Gln Tyr Cys Ala Arg Leu Arg Gln Ala Gly Ser
50 55 60
Ala Ala Pro Arg Pro Pro Arg Ala Gln Gln Pro Gln Gln Pro Ser Gln

65 70 75 80
Glu Lys Phe Tyr Ser Met Ala Ala Arg Ser Ser Tyr Ser
85 90

<210> 4467
<211> 1142
<212> DNA
<213> Homo sapiens

<400> 4467
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tcccagctgg agtcccctgt ggtgttttgt cacaatgacc tgctctgcaa gaatatcatc
120
tatgacagca tcaaaggtca cgtgcggttc attgactatg aatatgctgg ctacaactac
180
caagcttttg acattggcaa ccatttcaat gagtttgcag gcgtgaatga ggtggattac
240
tgcctgtacc cggcgcggga gacccagctg cagtggctgc actactacct gcaggcacaa
300
aaggggatgg ccgtgacccc cagggaggtg caaaggctct acgtgcaagt caacaagttt
360
gccctggcgt ctcacttctt ctgggctctc tgggccctca tccagaacca gtactccacc
420
atcgactttg atttcctcag gtacgcagtg atccgattca accagtactt caaggtgaag
480
cctcaagcgt cagccttgga gatgccaaag tgaccagcca ccccatccct cccctaccca
540
tctgtctggc cagacctgtt ctccagagct caattctgca ctctgggatc cacacccttg
600
gacagggtgg gagaggggac acatgggtgt ccagggagaa ggctctgtcc ctgccgccag
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accccagtgg ttgccactga agacctcatt ctcctgtctg gaggggctga taggaccccc
720
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780
accataacca cccctgggaa acacatcatt cccagcctca ggccctgctg gaattggggc
840
tgccttatat gtgtgtttac cccttcctgg cctggggaag gaggcgggga gggctccttt
900
ctacctccag tgccctgagc ctccagtccg tctcccccctg catgccccat gtgggaggtg
960
ctgagctcca aaccagcatc acaccaactc tgacacatgg atgtacctat cttggtgatg
1020
ggtgggggcc aagaattgag catgacatct tccccagcag ccacctcctc tgagatccct
1080
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1140
gt
1142

<210> 4468
<211> 170
<212> PRT

<213> Homo sapiens

<400> 4468
Xaa Asp Val Pro Lys Val Glu Val Leu Glu Arg Glu Leu Ala Trp Leu
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Lys Glu His Leu Ser Gln Leu Glu Ser Pro Val Val Phe Cys His Asn
20 25 30
Asp Leu Leu Cys Lys Asn Ile Ile Tyr Asp Ser Ile Lys Gly His Val
35 40 45
Arg Phe Ile Asp Tyr Glu Tyr Ala Gly Tyr Asn Tyr Gln Ala Phe Asp
50 55 60
Ile Gly Asn His Phe Asn Glu Phe Ala Gly Val Asn Glu Val Asp Tyr
65 70 75 80
Cys Leu Tyr Pro Ala Arg Glu Thr Gln Leu Gln Trp Leu His Tyr Tyr
85 90 95
Leu Gln Ala Gln Lys Gly Met Ala Val Thr Pro Arg Glu Val Gln Arg
100 105 110
Leu Tyr Val Gln Val Asn Lys Phe Ala Leu Ala Ser His Phe Phe Trp
115 120 125
Ala Leu Trp Ala Leu Ile Gln Asn Gln Tyr Ser Thr Ile Asp Phe Asp
130 135 140
Phe Leu Arg Tyr Ala Val Ile Arg Phe Asn Gln Tyr Phe Lys Val Lys
145 150 155 160
Pro Gln Ala Ser Ala Leu Glu Met Pro Lys
165 170

<210> 4469
<211> 409
<212> DNA
<213> Homo sapiens

<400> 4469
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ctgaacgttg cattctgtcc tgatgacact cactttgttt ccagatccca gtgttggtca
120
ggcctgggat ggccaagaca gttggaaagc aggagatgga caacttgaag gcattgcaca
180
gtgctttaga ggcctcctgc gagccttggt tttgaagctt taacaggcct ccctcccatc
240
tggaaatagg tagctgtgtc tgagactcct ggagaacaat taatatgagg gccaggcaga
300
tcacaatttc aggaaaatgg ctaccctgtg aggagagaaa gccacccaat gatgctgata
360
cctggccatt tcctgtaccg aggcatggng ttgggggggtc tgaagttag
409

<210> 4470
<211> 55
<212> PRT
<213> Homo sapiens

<400> 4470
Ile Tyr Asp Ala Gln His Ala Asn Leu Ala Gly Thr Leu Ser Gly His

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Ala Ser Trp Val Leu Asn Val Ala Phe Cys Pro Asp Asp Thr His Phe
            20                  25                  30
Val Ser Arg Ser Gln Cys Trp Ser Gly Leu Gly Trp Pro Arg Gln Leu
        35                  40                  45
Glu Ser Arg Arg Trp Thr Thr
    50                  55
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<210> 4471
<211> 1771
<212> DNA
<213> Homo sapiens

<400> 4471
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agtttcctct tctggaaatt ggggaatctt catgtcacct tcttgacagc atttgccagg
120
catccagcag gcgcttaata aatggccaag tcattgtttg ggtttctaaa taaggctctc
180
ctaatggccg ggtctggcca cggtcccagt gtccctgggc agccctccga ggggccggca
240
cagggcgcac tataaatgag cggctgcgca cgcaggggca ctgcaacgcg gaggagcagg
300
atggagatcc ctgtgcctgt gcagccgtct tggctgcgcc gcgcctcggc cccgttgccc
360
ggactttcgg cgcccggacg cctctttgac cagcgcttcg gcgaggggct gctggaggcc
420
gagctggctg cgctctgccc caccacgctc gccccctact acctgcgcgc acccagcgtg
480
gcgctgcccg tcgcccaggt gccgacggac cccggccact tttcggtgct gctagacgtg
540
aagcacttct cgccggagga aattgctgtc aaggtggtgg gcgaacacgt ggaggtgcac
600
gcgcgccacg aggagcgccc ggatgagcac ggattcgtcg cgcgcgagtt ccaccgtcgc
660
taccgcctgc cgcctggcgt ggatccggct gccgtgacgt ccgcgctgtc ccccgagggc
720
gtcctgtcca tccaggccgc accagcgtcg gcccaggccc caccgccagc cgcagccaag
780
taggaggggg ctgggccgcg cccgcacccc gggagcctcc tcaggctccc tctattaaag
840
ccgatctgac tccgcccagc cagatgtccc gagtgcgcca aggactgtcc tctcacccac
900
tcctggattc tgccctgacc tccatcctgg acactgcctt gataacatag acccttccac
960
tgacaccctc gctcttcacc ccctccagc tttccgaccc cacaccgaca actccccggc
1020
ttccagaccc taccagcact accctaaccc tcagccgaca gtctcagccc caccgaccca
1080
ctttcttggc atatagcccc acttaagacc cctcctctac ttccttctga gtcctctaca
1140
aagacatccg ggtactacat ttccatccct tccctatttt gacaccaaat tatggtgtag
1200

acagccctcc cccaacccca ggccagtcag gcacaatccc cccacccccc aaacgtcctg
1260
gactgcacag acctcccact ccagaccatc caggcctggt tcccaagacc cgatccttcc
1320
cctgcaacca gacagtctac aactgccccc tccagcccat tttctgccgt gaaaccccag
1380
ccagccacac cagactctgg aacccttttt cgactgcccc aactcttgga caccaggcca
1440
actagaacac ccaacaccaa actgtacaga ctctcccacc ccaacctccc cagactctgc
1500
acggatgtcc taggcccccc ccccaactct aaccagaccc catcccccta agtccctttg
1560
tcttgacccc caagtcttca accagatatc ctcggcaacc cacctcccac cctcctcctc
1620
ttctccttca agacccaact gagcacccgc tctgattccc cacagccttt ctccctgcca
1680
ccactccctt agtctttccc aggcttactc tcccaataaa tgtgctagag ctctgccaaa
1740
aaaagaaaaa aaagtcgacg cggccggaat t
1771

<210> 4472
<211> 160
<212> PRT
<213> Homo sapiens

<400> 4472
Met Glu Ile Pro Val Pro Val Gln Pro Ser Trp Leu Arg Arg Ala Ser
1 5 10 15
Ala Pro Leu Pro Gly Leu Ser Ala Pro Gly Arg Leu Phe Asp Gln Arg
20 25 30
Phe Gly Glu Gly Leu Leu Glu Ala Glu Leu Ala Ala Leu Cys Pro Thr
35 40 45
Thr Leu Ala Pro Tyr Tyr Leu Arg Ala Pro Ser Val Ala Leu Pro Val
50 55 60
Ala Gln Val Pro Thr Asp Pro Gly His Phe Ser Val Leu Leu Asp Val
65 70 75 80
Lys His Phe Ser Pro Glu Glu Ile Ala Val Lys Val Val Gly Glu His
85 90 95
Val Glu Val His Ala Arg His Glu Glu Arg Pro Asp Glu His Gly Phe
100 105 110
Val Ala Arg Glu Phe His Arg Arg Tyr Arg Leu Pro Pro Gly Val Asp
115 120 125
Pro Ala Ala Val Thr Ser Ala Leu Ser Pro Glu Gly Val Leu Ser Ile
130 135 140
Gln Ala Ala Pro Ala Ser Ala Gln Ala Pro Pro Pro Ala Ala Ala Lys
145 150 155 160

<210> 4473
<211> 1255
<212> DNA
<213> Homo sapiens

<400> 4473

gccggcgcga tgccccgccc cttcgatagc tcatctttgc gcgccgcagt cgcgcggagc
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ccggcttccg acgtgcagcc tggcagtgca gtgagctgtc tggccttttg tccttgatcc
120
ttggttaagg aaatgaccaa ccagtacggt attctcttca aacaagagca agcccatgat
180
gatgccattt ggtcagttgc ttgggggaca aacaagaagg aaaactctga gacagtggtc
240
acaggctccc tagatgacct ggtgaaggtc tggaaatggc gtgatgagag gctggaccta
300
cagtggagtc tggagggaca tcagctggga gtggtgtctg tggacatcag ccacaccctt
360
cccattgctg cctccagttc tctagatgct catattcgac tctgggactt ggaaaatggc
420
aaacagatga agtctataga tgcaggaccg gtggatgcct ggactttggc attctctccg
480
gactcccagc atctggcaac aggaactcac atggggaaag tgaacatttt tggtgtggaa
540
agtggaaaaa aagaatactc tttggacact agaggaaaat tcatccttag tattgcatat
600
agtcctgatg gaaaatacct ggccagcgga gccatagatg gaatcatcaa tatttttgat
660
attgcaactg gaaaacttct gcataccctg gaaggccatg ccatgcccat tcgctccttg
720
acctttttccc cggactccca gctccttgtc actgcttcag atgatggcta catcaagatc
780
tatgatgtac aacatgccaa tttggctggc acgctgagcg gccatgcctc ctgggtgctg
840
aacgttgcat tctgtcctga tgacactcac tttgtttcca gttcgtctga caaaagtgta
900
aaagtttggg atgttggaac gaggacttgt gttcacacct tctttgatca ccaggatcag
960
gtctggggag taaaatacaa tggaaatggt tcaaaaattg tgtctgttgg agatgaccag
1020
gaaattcaca tctatgattg tccaatttaa acatcaaagt ctccaggctt atgctgcaaa
1080
gagaatgtac ggattgatca tgacattcct taccttctta ggcttgttta aaagaaatat
1140
agcatttatt gtagcaaaga cttaaatttt gtagatacaa tatgaatctt ttcatgtttt
1200
attggaaatg ctgttcatac tttaacataa agctttctta atgcaaaaaa aaaaa
1255

<210> 4474
<211> 305
<212> PRT
<213> Homo sapiens

<400> 4474
Met Thr Asn Gln Tyr Gly Ile Leu Phe Lys Gln Glu Gln Ala His Asp
1 5 10 15
Asp Ala Ile Trp Ser Val Ala Trp Gly Thr Asn Lys Lys Glu Asn Ser
20 25 30
Glu Thr Val Val Thr Gly Ser Leu Asp Asp Leu Val Lys Val Trp Lys

```
        35                  40                  45
Trp Arg Asp Glu Arg Leu Asp Leu Gln Trp Ser Leu Glu Gly His Gln
    50                  55                  60
Leu Gly Val Val Ser Val Asp Ile Ser His Thr Leu Pro Ile Ala Ala
65                  70                  75                  80
Ser Ser Ser Leu Asp Ala His Ile Arg Leu Trp Asp Leu Glu Asn Gly
                85                  90                  95
Lys Gln Met Lys Ser Ile Asp Ala Gly Pro Val Asp Ala Trp Thr Leu
            100                 105                 110
Ala Phe Ser Pro Asp Ser Gln His Leu Ala Thr Gly Thr His Met Gly
        115                 120                 125
Lys Val Asn Ile Phe Gly Val Glu Ser Gly Lys Lys Glu Tyr Ser Leu
    130                 135                 140
Asp Thr Arg Gly Lys Phe Ile Leu Ser Ile Ala Tyr Ser Pro Asp Gly
145                 150                 155                 160
Lys Tyr Leu Ala Ser Gly Ala Ile Asp Gly Ile Ile Asn Ile Phe Asp
                165                 170                 175
Ile Ala Thr Gly Lys Leu Leu His Thr Leu Glu Gly His Ala Met Pro
            180                 185                 190
Ile Arg Ser Leu Thr Phe Ser Pro Asp Ser Gln Leu Leu Val Thr Ala
        195                 200                 205
Ser Asp Asp Gly Tyr Ile Lys Ile Tyr Asp Val Gln His Ala Asn Leu
    210                 215                 220
Ala Gly Thr Leu Ser Gly His Ala Ser Trp Val Leu Asn Val Ala Phe
225                 230                 235                 240
Cys Pro Asp Asp Thr His Phe Val Ser Ser Ser Ser Asp Lys Ser Val
                245                 250                 255
Lys Val Trp Asp Val Gly Thr Arg Thr Cys Val His Thr Phe Phe Asp
            260                 265                 270
His Gln Asp Gln Val Trp Gly Val Lys Tyr Asn Gly Asn Gly Ser Lys
        275                 280                 285
Ile Val Ser Val Gly Asp Asp Gln Glu Ile His Ile Tyr Asp Cys Pro
    290                 295                 300
Ile
305
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<210> 4475
<211> 475
<212> DNA
<213> Homo sapiens

<400> 4475
acgcgtgaac ccgtgagctt gggaggggat atcgtccaag cgaggtctct ctgatcccgc
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tggtgtccag actccttctg gagttccaat cccacccctg gcacactgtc catctctggc
120
tggtctgtcg tgaagctgga gagccgtgca aggcgacaga gccttctgtg tggcccgtcc
180
tggcgctctg gggcaagggc tgacttgagc tgcttcgtct gctcatctgc tgtctgccag
240
ctgccctcag acctcctcct gggtgcagcc cgttcccact tgagagggag gtggtcttca
300
ctttaggggg taggcacatc cctgtttgcg ccttgccccg acagcctcgt caatgcccag
360

ccacttctga gggctggagg gacaggaact tcctttcttc ccccttttctg tctcctcgcg
420
tgggtacaaa agcacgtctg tagtccatgt gtgtgaagag aggacgcatt ctaga
475

<210> 4476
<211> 106
<212> PRT
<213> Homo sapiens

<400> 4476
Met Cys Leu Pro Pro Lys Val Lys Thr Thr Ser Leu Ser Ser Gly Asn
1 5 10 15
Gly Leu His Pro Gly Gly Gly Leu Arg Ala Ala Gly Arg Gln Gln Met
20 25 30
Ser Arg Arg Ser Ser Ser Ser Gln Pro Leu Pro Gln Ser Ala Arg Thr
35 40 45
Gly His Thr Glu Gly Ser Val Ala Leu His Gly Ser Pro Ala Ser Arg
50 55 60
Gln Thr Ser Gln Arg Trp Thr Val Cys Gln Gly Trp Asp Trp Asn Ser
65 70 75 80
Arg Arg Ser Leu Asp Thr Ser Gly Ile Arg Glu Thr Ser Leu Gly Arg
85 90 95
Tyr Pro Leu Pro Ser Ser Arg Val His Ala
100 105

<210> 4477
<211> 1153
<212> DNA
<213> Homo sapiens

<400> 4477
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tccatgtggt agagtgtcag tttgtcaaat accccaagtg cggcacatgc ttaccagctc
120
taggccaggg cagatgggat atgacgaatg gactgccagc tggatacaag gatgctcacc
180
aagcaccaag ttctcacaag ttatttttatg tgactttgca ggaactgagg cattatatct
240
gaggacacca ggggaaaagt gtggcatctc agggaaatac agccctgggc tgtgtctaca
300
cacaccatga gagtgctgat gggggcgcaa tagtcttgaa aatgtataaa gtgtccagga
360
atggaagtgc tctttgattc attattattt tcttccttca tattcccctc ccagagtctc
420
ctatctagga catcagcatt ctcacacaag cctaatggct tatctgagta agcagggctt
480
agaaattcac tttcttgata ctcagtcttg ccttctaaac actccttgat cttgcctacc
540
tctccccttt tccacatgtc ttttcctgta ggaacacttt ctccatttat tcctgcctat
600
ccaattcttc cctatatttc ctggaccagc taaagtccag tgtttccaga gacttttgaa
660

agtcaactta cacttttcc ttcttcattc acaaagctct tcttccctgg gccctggtat
720
gtatgccttt ctctcctact gtctaatagc acctcgtaaa ttgtcaatga acttttctaa
780
ggggtattct tgaattccca actagattgt gagcttctgg aagacaaggc tatgtctttg
840
attgttgtct cccctaccac agcccagtac tttagttaca gaaaataata aatatttact
900
gattgattga ctttcctctt gtccactagc tttaggtttg ggggccaaat tctaccctgg
960
attttgaaaa attcaaactg tgaacaccac aatgttatag agcatatgag gtagtagcca
1020
gcatgaagga tgttttcttc ctgagaaaca gtgtcaaggg ctggaggaag agggcaaaat
1080
agcagactca gagggcaaat aaattttggt attacttggt cacacaaggt tatacaggtg
1140
ttttcttgta gga
1153

<210> 4478
<211> 118
<212> PRT
<213> Homo sapiens

<400> 4478
Met Trp Lys Arg Gly Glu Val Gly Lys Ile Lys Glu Cys Leu Glu Gly
1 5 10 15
Lys Thr Glu Tyr Gln Glu Ser Glu Phe Leu Ser Pro Ala Tyr Ser Asp
20 25 30
Lys Pro Leu Gly Leu Cys Glu Asn Ala Asp Val Leu Asp Arg Arg Leu
35 40 45
Trp Glu Gly Asn Met Lys Glu Glu Asn Asn Asn Glu Ser Lys Ser Thr
50 55 60
Ser Ile Pro Gly His Phe Ile His Phe Gln Asp Tyr Cys Ala Pro Ile
65 70 75 80
Ser Thr Leu Met Val Cys Val Asp Thr Ala Gln Gly Cys Ile Ser Leu
85 90 95
Arg Cys His Thr Phe Pro Leu Val Ser Ser Asp Ile Met Pro Gln Phe
100 105 110
Leu Gln Ser His Ile Lys
115

<210> 4479
<211> 2158
<212> DNA
<213> Homo sapiens

<400> 4479
nngcggcggc ctgcggcggg ttcggtgggc ccaatcccgg ggcggtgcgg ctgtttcggg
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cgcgggcccc gcttttccgc accctgctcc ggcctcgact acggcgagcc tgagcgcggc
120
ggcggcccac gcgcagcaca gggagagatg agcagcacca gcagtaagag ggctccgacc
180

acggcaaccc agaggctgaa gcaggactac cttcgcatta agaaagaccc ggtgccttac
240
atctgtgccg agcccctccc ttcgaatatt ctcgagtggc actatgtcgt ccgaggccca
300
gagatgaccc cttatgaagg tggctattac catggaaaac taatttttcc cagagaattt
360
cctttcaaac ctcccagtat ctatatgatc actcccaacg ggaggtttaa gtgcaacacc
420
aggctgtgtc tttctatcac ggatttccac ccggacacgt ggaacccggc ctggtctgtc
480
tccaccatcc tgactgggct cctgagcttc atggtggaga agggccccac cctgggcagt
540
atagagacgt cggacttcac gaaaagacaa ctggcagtgc agagtttagc atttaatttg
600
aaagataaag tcttttgtga attatttcct gaagtcgtgg aggagattaa acaaaaacag
660
aaagcacaag acgaactcag tagcagaccc cagactctcc ccttgccaga cgtggttcca
720
gacggggaga cgcacctcgt ccagaacggg attcagctgc tcaacgggca tgcgccgggg
780
gccgtcccaa acctcgcagg gctccagcag gccaaccggc accacggact cctgggtggc
840
gccctggcga acttgtttgt gatagttggg tttgcagcct ttgcttacac ggtcaagtac
900
gtgctgagga gcatcgcgca ggagtgaggc ccaggcgccg agacccaagg cgccactgag
960
ggcaccgcgc accagagcgt gacctcggca ggctggacac actgcccagc acaggcagac
1020
ccaccaggct cctaggttta gcttttaaaa acctgaaagg ggaagcaaaa accaaaatgt
1080
gtgactgggc tttggaggag actggagcct cagccctgtc ctggccacgg gccgctgggg
1140
ctggtgtggg tgggccttgt gtgctggatt tgtagcttat cttccgtgtt gtctttggac
1200
ctgttttagt aaacccgttt ttcattttat tagatgtggt cacttagaaa tgcaaacttg
1260
ctgccgaccg cgggctgctc ctgcgttctt ggagctcctg gcgcgtttct cggagctccc
1320
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1380
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1440
tccataagtc ggggtttggt ctcagcattt acaaatgtgt ttacagtcag aatgaaacac
1500
attccttcta gaaagtgctt gggggttttt gctgccctgg aagccaggag cctgctcact
1560
ccaaccacaa gtcgcccttg actgcggcgg ccgcgagcgg ggcgggggct gccggtgccc
1620
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1680
tgcagagcct tttctctgaa ttccttatgt ccggtgggcc agaagcccgt cctcctatgc
1740
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1800

cacatcccgt gccccctgcg ctggccttca cagtaggtaa tggctccggc ccgggtgttc
1860
gctgtccacg gaacatggca gaggggcacc ccggcccgga aagacgccag agccagcagg
1920
ggctgtttcg ggccgcgtgg ctccccgggt ctcggccgtc tcccctcttc tgcgtctgtt
1980
ccgtgacttc gcctgggtgg gatgtaccgc aggtgcatcg cgtcgaggtg gggcacggcc
2040
gccggcaaga aacccaccct gtccggaggc gggcgtgaga caagcccagc ccgcacgcgc
2100
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2158

<210> 4480
<211> 308
<212> PRT
<213> Homo sapiens

<400> 4480
Xaa Arg Arg Pro Ala Ala Gly Ser Val Gly Pro Ile Pro Gly Arg Cys
1 5 10 15
Gly Cys Phe Gly Arg Gly Pro Arg Phe Ser Ala Pro Cys Ser Gly Leu
20 25 30
Asp Tyr Gly Glu Pro Glu Arg Gly Gly Gly Pro Arg Ala Ala Gln Gly
35 40 45
Glu Met Ser Ser Thr Ser Ser Lys Arg Ala Pro Thr Thr Ala Thr Gln
50 55 60
Arg Leu Lys Gln Asp Tyr Leu Arg Ile Lys Lys Asp Pro Val Pro Tyr
65 70 75 80
Ile Cys Ala Glu Pro Leu Pro Ser Asn Ile Leu Glu Trp His Tyr Val
85 90 95
Val Arg Gly Pro Glu Met Thr Pro Tyr Glu Gly Gly Tyr Tyr His Gly
100 105 110
Lys Leu Ile Phe Pro Arg Glu Phe Pro Phe Lys Pro Pro Ser Ile Tyr
115 120 125
Met Ile Thr Pro Asn Gly Arg Phe Lys Cys Asn Thr Arg Leu Cys Leu
130 135 140
Ser Ile Thr Asp Phe His Pro Asp Thr Trp Asn Pro Ala Trp Ser Val
145 150 155 160
Ser Thr Ile Leu Thr Gly Leu Leu Ser Phe Met Val Glu Lys Gly Pro
165 170 175
Thr Leu Gly Ser Ile Glu Thr Ser Asp Phe Thr Lys Arg Gln Leu Ala
180 185 190
Val Gln Ser Leu Ala Phe Asn Leu Lys Asp Lys Val Phe Cys Glu Leu
195 200 205
Phe Pro Glu Val Val Glu Glu Ile Lys Gln Lys Gln Lys Ala Gln Asp
210 215 220
Glu Leu Ser Ser Arg Pro Gln Thr Leu Pro Leu Pro Asp Val Val Pro
225 230 235 240
Asp Gly Glu Thr His Leu Val Gln Asn Gly Ile Gln Leu Leu Asn Gly
245 250 255
His Ala Pro Gly Ala Val Pro Asn Leu Ala Gly Leu Gln Gln Ala Asn
260 265 270
Arg His His Gly Leu Leu Gly Gly Ala Leu Ala Asn Leu Phe Val Ile

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        275                 280                 285
Val Gly Phe Ala Ala Phe Ala Tyr Thr Val Lys Tyr Val Leu Arg Ser
    290                 295                 300
Ile Ala Gln Glu
305
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<210> 4481
<211> 320
<212> DNA
<213> Homo sapiens

<400> 4481
ggcacccctg tggggatggg ctgtgcctgg aggctggggg gctgcatctg gacagcctct
60
gggtggggcc tcggaacctc ctgctgtgca gccagaaaac aggactcggc ctgtccaccc
120
acgtggggag gggaccccgg gctgggcttc gtaggggctt caaggacccc tgacttctgg
180
ggtgtgcctg acagcagggg aggccccaga gctggccttg gccatgtcca gtccctaatt
240
gacctttgtc ccttccttcc cctgcctctc tgtgcgtcgc tggactcgcc acgggagttc
300
tcacgaatgg gcacccaatt
320

<210> 4482
<211> 101
<212> PRT
<213> Homo sapiens

<400> 4482

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Met Gly Cys Ala Trp Arg Leu Gly Gly Cys Ile Trp Thr Ala Ser Gly
 1               5                  10                  15
Trp Gly Leu Gly Thr Ser Cys Cys Ala Ala Arg Lys Gln Asp Ser Ala
            20                  25                  30
Cys Pro Pro Thr Trp Gly Gly Asp Pro Gly Leu Gly Phe Val Gly Ala
        35                  40                  45
Ser Arg Thr Pro Asp Phe Trp Gly Val Pro Asp Ser Arg Gly Gly Pro
    50                  55                  60
Arg Ala Gly Leu Gly His Val Gln Ser Leu Ile Asp Leu Cys Pro Phe
65                  70                  75                  80
Leu Pro Leu Pro Leu Cys Ala Ser Leu Asp Ser Pro Arg Glu Phe Ser
                85                  90                  95
Arg Met Gly Thr Gln
            100
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<210> 4483
<211> 1852
<212> DNA
<213> Homo sapiens

<400> 4483
nnggttgcgg cgtgccggga gctgagttat agctgtgact tctgccctgc caggccgcac
60

acaagctggc tgacccggtt tgtaaaaatg gaatttcaag cagtagtgat ggcagtaggt
120
ggaggatctc ggatgacaga cctaacttcc agcattccca aacctctgct tccagttggg
180
aacaaacctt taatttggta cccattgaac ctgcttgagc gtgttggatt tgaagaagtc
240
attgtggtta caaccaggga tgttcaaaag gctctatgtg cagaattcaa gatgaaaatg
300
aagccagata ttgtgtgtat tcctgatgac gctgacatgg gaactgcaga ttctttgcgc
360
tacatatatc caaaacttaa gacagatgtg ctggtgctga gctgtgatct gataacagac
420
gttgccttac atgaggttgt ggacctgttt agagcttatg atgcatcact tgctatgttg
480
atgagaaaag gccaagatag catagaacct gttcccggtc aaaaggggaa aaaaaaagca
540
gtggagcagc gtgacttcat tggagtggac agcacaggaa agaggctgct cttcatggct
600
aatgaagcag acttggatga agagctggtc attaagggat ccatcctaca gaagcatcct
660
agaatacgtt tccacacggg tcttgtggat gcccacctct actgtttgaa aaaatacatc
720
gtggatttcc taatggaaaa tgggtcaata acttctatcc ggagtgaact gattccatat
780
ttagtgagaa aacagttttc ctcagcttcc tcacaacagg gacaagaaga aaaagaggag
840
gatctaaaga aaaaggagct gaagtcctta gatatctaca gttttataaa agaagccaat
900
acactgaacc tggctcccta tgatgcctgc tggaatgcct gtcgaggaga caggtgggaa
960
gacttgtcca gatcacaggt gcgctgctat gtccacatca tgaaagaggg gctctgctct
1020
cgagtgagca cactgggact ctacatggaa gcaaacagac aggtgcccaa attgctgtct
1080
gctctctgtc cagaagaacc accagtccat tcgtcagccc agattgtcag caaacacctg
1140
gttggagttg acagcctcat tgggccagag acacagattg gagagaagtc atccattaag
1200
cgctcagtca ttggctcatc ctgtctcata aaagatagag tgactattac caattgcctt
1260
ctcatgaact cagtcactgt ggaggaagga agcaatatcc aaggcagtgt catctgcaac
1320
aatgctgtga tcgagaaggg tgcagacatc aaggactgct tgattggaag tggccagagg
1380
attgaagcca aagctaaacg agtgaatgag gtgatcgtgg ggaatgacca gctcatggag
1440
atctgagttc tgagcaagtc agactccttc cttttggcct ccaaagccac agatgttggc
1500
cggcccacct gtttaactct gtatttattt cccaataaag aagggcttcc aaaggcatgc
1560
tggagacttg tggagcagtc caaagctcca tgtcaggtgg gctccaggtg tacacagtgt
1620
atgttcatgt gtcatgtggt aaagatcatc tggagcaagt gtgtgggaca ggacagatac
1680

agtggcctaa ctcttgtgtg ccaagatgta tcggtggggc agcagctgtc caatgtaaag
1740
ctcctaggaa ggctactttc tgactggctg acccaaccca gtcctgaaag tatccctcac
1800
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1852

<210> 4484
<211> 452
<212> PRT
<213> Homo sapiens

<400> 4484
Met Glu Phe Gln Ala Val Val Met Ala Val Gly Gly Gly Ser Arg Met
1 5 10 15
Thr Asp Leu Thr Ser Ser Ile Pro Lys Pro Leu Leu Pro Val Gly Asn
20 25 30
Lys Pro Leu Ile Trp Tyr Pro Leu Asn Leu Leu Glu Arg Val Gly Phe
35 40 45
Glu Glu Val Ile Val Val Thr Thr Arg Asp Val Gln Lys Ala Leu Cys
50 55 60
Ala Glu Phe Lys Met Lys Met Lys Pro Asp Ile Val Cys Ile Pro Asp
65 70 75 80
Asp Ala Asp Met Gly Thr Ala Asp Ser Leu Arg Tyr Ile Tyr Pro Lys
85 90 95
Leu Lys Thr Asp Val Leu Val Leu Ser Cys Asp Leu Ile Thr Asp Val
100 105 110
Ala Leu His Glu Val Val Asp Leu Phe Arg Ala Tyr Asp Ala Ser Leu
115 120 125
Ala Met Leu Met Arg Lys Gly Gln Asp Ser Ile Glu Pro Val Pro Gly
130 135 140
Gln Lys Gly Lys Lys Lys Ala Val Glu Gln Arg Asp Phe Ile Gly Val
145 150 155 160
Asp Ser Thr Gly Lys Arg Leu Leu Phe Met Ala Asn Glu Ala Asp Leu
165 170 175
Asp Glu Glu Leu Val Ile Lys Gly Ser Ile Leu Gln Lys His Pro Arg
180 185 190
Ile Arg Phe His Thr Gly Leu Val Asp Ala His Leu Tyr Cys Leu Lys
195 200 205
Lys Tyr Ile Val Asp Phe Leu Met Glu Asn Gly Ser Ile Thr Ser Ile
210 215 220
Arg Ser Glu Leu Ile Pro Tyr Leu Val Arg Lys Gln Phe Ser Ser Ala
225 230 235 240
Ser Ser Gln Gln Gly Gln Glu Glu Lys Glu Glu Asp Leu Lys Lys Lys
245 250 255
Glu Leu Lys Ser Leu Asp Ile Tyr Ser Phe Ile Lys Glu Ala Asn Thr
260 265 270
Leu Asn Leu Ala Pro Tyr Asp Ala Cys Trp Asn Ala Cys Arg Gly Asp
275 280 285
Arg Trp Glu Asp Leu Ser Arg Ser Gln Val Arg Cys Tyr Val His Ile
290 295 300
Met Lys Glu Gly Leu Cys Ser Arg Val Ser Thr Leu Gly Leu Tyr Met
305 310 315 320
Glu Ala Asn Arg Gln Val Pro Lys Leu Leu Ser Ala Leu Cys Pro Glu

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                325                 330                 335
Glu Pro Pro Val His Ser Ser Ala Gln Ile Val Ser Lys His Leu Val
            340                 345                 350
Gly Val Asp Ser Leu Ile Gly Pro Glu Thr Gln Ile Gly Glu Lys Ser
        355                 360                 365
Ser Ile Lys Arg Ser Val Ile Gly Ser Ser Cys Leu Ile Lys Asp Arg
    370                 375                 380
Val Thr Ile Thr Asn Cys Leu Leu Met Asn Ser Val Thr Val Glu Glu
385                 390                 395                 400
Gly Ser Asn Ile Gln Gly Ser Val Ile Cys Asn Asn Ala Val Ile Glu
                405                 410                 415
Lys Gly Ala Asp Ile Lys Asp Cys Leu Ile Gly Ser Gly Gln Arg Ile
            420                 425                 430
Glu Ala Lys Ala Lys Arg Val Asn Glu Val Ile Val Gly Asn Asp Gln
        435                 440                 445
Leu Met Glu Ile
    450
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<210> 4485
<211> 513
<212> DNA
<213> Homo sapiens

<400> 4485
ggatccacgt cagcccgaca tcgctgcttt atagccatgt tcacgtgtca tatgcgtctc
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agggtaccca aaatcacagg gccaactcac ggggctccta ccactctagc cagtcatggg
120
gtcaggaata ccccaccctc atccaaaatg tgtactcccc caacctttg tgttcagacc
180
cacaggcctt atagcgccct gtgcgtgccc cagcatttcc ctgcctagtg gggctccagg
240
cgggcagggt gacctccttc cccaggcagt tccacacctg atcccaaaag tcagttctaa
300
tgaagtggat tcattcaaat actggtggtt ctggttggcc cgggtaagtg agggcacaga
360
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<212> PRT
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<400> 4486
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<212> PRT
<213> Homo sapiens

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            20                  25                  30
Leu Leu Ala Cys Gly Asp Val Glu Gly Lys Phe Asp Ile Leu Phe Asn
        35                  40                  45
Arg Val Gln Ala Ile Gln Lys Lys Ser Gly Asn Phe Asp Leu Leu Leu
    50                  55                  60
Cys Val Gly Asn Phe Phe Gly Ser Thr Gln Asp Ala Glu Trp Glu Glu
65                  70                  75                  80
Tyr Lys Thr Gly Ile Lys Lys Ala Pro Ile Gln Thr Tyr Val Leu Gly
                85                  90                  95
Ala Asn Asn Gln Glu Thr Val Lys Tyr Phe Gln Asp Ala Asp Gly Cys
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Gln Asn Pro Pro Gly Leu Pro Ser Ile Ala Val Cys Trp Phe Val Gly
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Cys Leu Cys Gly Ser Lys Leu Val Ile Asp Trp His Asn Tyr Gly Tyr
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Ser Ile Met Gly Leu Val His Gly Pro Asn His Pro Leu Val Leu Leu
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Ala Lys Trp Tyr Glu Lys Phe Phe Gly Arg Leu Ser His Leu Asn Leu

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Ser Pro Phe Arg Ala Arg Ser Glu Pro Glu Asp Pro Val Thr Glu Arg
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Ser Ala Phe Thr Glu Arg Asp Ala Gly Ser Gly Leu Val Thr Arg Leu
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Arg Glu Arg Pro Ala Leu Leu Val Ser Ser Thr Ser Trp Thr Glu Asp
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Glu Asp Phe Ser Ile Leu Leu Ala Ala Leu Glu Lys Phe Glu Gln Leu
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Thr Leu Asp Gly His Asn Leu Pro Ser Leu Val Cys Val Ile Thr Gly
225                 230                 235                 240
Lys Gly Pro Leu Arg Glu Tyr Tyr Ser Arg Leu Ile His Gln Lys His
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Phe Gln His Ile Gln Val Cys Thr Pro Trp Leu Glu Ala Glu Asp Tyr
            260                 265                 270
Pro Leu Leu Leu Gly Ser Ala Asp Leu Gly Val Cys Leu His Thr Ser
        275                 280                 285
Ser Ser Gly Leu Asp Leu Pro Met Lys Val Val Asp Met Phe Gly Cys
    290                 295                 300
Cys Leu Pro Val Cys Ala Val Asn Phe Lys Cys Leu His Glu Leu Val
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Lys His Glu Glu Asn Gly Leu Val Phe Glu Asp Ser Glu Glu Leu Ala
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Ala Gln Leu Gln Met Leu Phe Ser Asn Phe Pro Asp Pro Ala Gly Lys
            340                 345                 350
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<212> DNA
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<210> 4492
<211> 674
<212> PRT

<213> Homo sapiens

<400> 4492

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Lys Val Phe Tyr Leu Asp Leu Pro Ser Val Thr Ile Ser Glu Lys Leu
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Gln Thr Leu Gly Arg Ile Ser Pro Val Pro Ser Pro Glu Ser Ala Tyr
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225                 230                 235                 240
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Thr Glu Gln Lys Glu Lys Val Glu Leu Gln His Ile Ser Gln Lys Asp
    370                 375                 380
Cys Gln Glu Asp Asp Thr Thr Val Lys Glu Gln Asn Phe Leu Tyr Lys
385                 390                 395                 400
Glu Thr Gln Glu Thr Glu Lys Lys Leu Leu Phe Ile Ser Glu Pro Ile
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                405                 410                 415
Pro His Pro Ser Asn Glu Leu Arg Gly Leu Asn Glu Lys Met Ser Asn
            420                 425                 430
Lys Cys Ser Met Leu Ser Thr Ala Glu Asp Asp Ile Arg Gln Asn Phe
        435                 440                 445
Thr Gln Leu Pro Leu His Lys Asn Lys Gln Glu Cys Ile Leu Asp Ile
    450                 455                 460
Ser Glu His Thr Leu Ser Glu Asn Asp Leu Glu Glu Leu Arg Val Asp
465                 470                 475                 480
His Tyr Lys Cys Asn Ile Gln Ala Ser Val His Val Ser Asp Phe Ser
                485                 490                 495
Thr Asp Asn Ser Gly Ser Gln Pro Lys Gln Lys Ser Asp Thr Val Leu
            500                 505                 510
Phe Pro Ala Lys Asp Leu Lys Glu Lys Asp Leu His Ser Ile Phe Thr
        515                 520                 525
His Asp Ser Gly Leu Ile Thr Ile Asn Ser Ser Gln Glu His Leu Thr
    530                 535                 540
Val Gln Ala Lys Ala Pro Phe His Thr Pro Pro Glu Glu Pro Asn Glu
545                 550                 555                 560
Cys Asp Phe Lys Asn Met Asp Ser Leu Pro Ser Gly Lys Ile His Arg
                565                 570                 575
Lys Val Lys Ile Ile Leu Gly Arg Asn Arg Lys Glu Asn Leu Glu Pro
            580                 585                 590
Asn Ala Glu Phe Asp Lys Arg Thr Glu Phe Ile Thr Gln Glu Glu Asn
        595                 600                 605
Arg Ile Cys Ser Ser Pro Val Gln Ser Leu Leu Asp Leu Phe Gln Thr
    610                 615                 620
Ser Glu Glu Lys Ser Glu Phe Leu Gly Phe Thr Ser Tyr Thr Glu Lys
625                 630                 635                 640
Ser Gly Ile Cys Asn Val Leu Asp Ile Trp Glu Glu Glu Asn Ser Asp
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Asn Leu Leu Thr Ala Phe Phe Ser Ser Pro Ser Thr Ser Thr Phe Thr
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Gly Phe
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<210> 4493
<211> 1829
<212> DNA
<213> Homo sapiens

<400> 4493
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120
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240
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300
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360

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420
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480
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540
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660
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720
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840
cacacagatg acaaattata tttgaaatcg ttggaaaata aattcagatc aaaatgcctt
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960
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1020
agaaactatt tttgtgtttg aaagtgaaac caacatccag atctatagca gagtccttat
1080
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1140
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1320
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1740
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1829

<210> 4494
<211> 111
<212> PRT

<213> Homo sapiens

<400> 4494
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Asp Leu Ile Ser Glu Glu Thr Asp Pro Lys Ile Ile Thr Ala Gly Asn
35 40 45
Leu Val His Leu Ala Leu Arg Phe Lys Cys Asn Gln Asn Cys Pro Gln
50 55 60
Gly Pro Ala Ile Lys Ala Leu Ser Leu Ser Thr Phe Trp Tyr Leu Val
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Arg Glu Leu Phe Thr Val Arg Lys Cys Gly Lys Ile Ala Leu Cys Val
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Cys Val Cys Val Cys Val Cys Val Cys Asn Leu Leu Gly Trp Gly
100 105 110

<210> 4495
<211> 3623
<212> DNA
<213> Homo sapiens

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120
catgttctgc tgttaatggc tctggtggga aagacagcct gtgggttctc cctgatgtct
180
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300
tacactgagg accaagctga tccatgccag cccaacccct gtgaacacgg tggggactgc
360
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3623

<210> 4496
<211> 560
<212> PRT
<213> Homo sapiens

<400> 4496
Met Phe Ala Arg Met Ser Asp Leu His Val Leu Leu Leu Met Ala Leu
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Val Gly Lys Thr Ala Cys Gly Phe Ser Leu Met Ser Leu Leu Glu Ser
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Leu Asp Pro Asp Trp Thr Pro Asp Gln Tyr Asp Tyr Ser Tyr Glu Asp
35 40 45
Tyr Asn Gln Glu Glu Asn Thr Ser Ser Thr Leu Thr His Ala Glu Asn
50 55 60
Pro Asp Trp Tyr Tyr Thr Glu Asp Gln Ala Asp Pro Cys Gln Pro Asn
65 70 75 80
Pro Cys Glu His Gly Gly Asp Cys Leu Val His Gly Ser Thr Phe Thr

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                85                  90                  95
Cys Ser Cys Leu Ala Pro Phe Ser Gly Asn Lys Cys Gln Lys Val Gln
            100                 105                 110
Asn Thr Cys Lys Asp Asn Pro Cys Gly Arg Gly Gln Cys Leu Ile Thr
        115                 120                 125
Gln Ser Pro Pro Tyr Tyr Arg Cys Val Cys Lys His Pro Tyr Thr Gly
    130                 135                 140
Pro Ser Cys Ser Gln Val Val Pro Val Cys Arg Pro Asn Pro Cys Gln
145                 150                 155                 160
Asn Gly Ala Thr Cys Ser Arg His Lys Arg Arg Ser Lys Phe Thr Cys
                165                 170                 175
Ala Cys Pro Asp Gln Phe Lys Gly Lys Phe Cys Glu Ile Gly Ser Asp
            180                 185                 190
Asp Cys Tyr Val Gly Asp Gly Tyr Ser Tyr Arg Gly Lys Met Asn Arg
        195                 200                 205
Thr Val Asn Gln His Ala Cys Leu Tyr Trp Asn Ser His Leu Leu Leu
    210                 215                 220
Gln Glu Asn Tyr Asn Met Phe Met Glu Asp Ala Glu Thr His Gly Ile
225                 230                 235                 240
Gly Glu His Asn Phe Cys Arg Asn Pro Asp Ala Asp Glu Lys Pro Trp
                245                 250                 255
Cys Phe Ile Lys Val Thr Asn Asp Lys Val Lys Trp Glu Tyr Cys Asp
            260                 265                 270
Val Ser Ala Cys Ser Ala Gln Asp Val Ala Tyr Pro Glu Glu Ser Pro
        275                 280                 285
Thr Glu Pro Ser Thr Lys Leu Pro Gly Phe Asp Ser Cys Gly Lys Thr
    290                 295                 300
Glu Ile Ala Glu Arg Lys Ile Lys Arg Ile Tyr Gly Gly Phe Lys Ser
305                 310                 315                 320
Thr Ala Gly Lys His Pro Trp Gln Ala Ser Leu Gln Ser Ser Leu Pro
                325                 330                 335
Leu Thr Ile Ser Met Pro Gln Gly His Phe Cys Gly Gly Ala Leu Ile
            340                 345                 350
His Pro Cys Trp Val Leu Thr Ala Ala His Cys Thr Asp Ile Lys Thr
        355                 360                 365
Arg His Leu Lys Val Val Leu Gly Asp Gln Asp Leu Lys Lys Glu Glu
    370                 375                 380
Phe His Glu Gln Ser Phe Arg Val Glu Lys Ile Phe Lys Tyr Ser His
385                 390                 395                 400
Tyr Asn Glu Arg Asp Glu Ile Pro His Asn Asp Ile Ala Leu Leu Lys
                405                 410                 415
Leu Lys Pro Val Asp Gly His Cys Ala Leu Glu Ser Lys Tyr Val Lys
            420                 425                 430
Thr Val Cys Leu Pro Asp Gly Ser Phe Pro Ser Gly Ser Glu Cys His
        435                 440                 445
Ile Ser Gly Trp Gly Val Thr Glu Thr Gly Lys Gly Ser Arg Gln Leu
    450                 455                 460
Leu Asp Ala Lys Val Lys Leu Ile Ala Asn Thr Leu Cys Asn Ser Arg
465                 470                 475                 480
Gln Leu Tyr Asp His Met Ile Asp Asp Ser Met Ile Cys Ala Gly Asn
                485                 490                 495
Leu Gln Lys Pro Gly Gln Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro
            500                 505                 510
Leu Thr Cys Glu Lys Asp Gly Thr Tyr Tyr Val Tyr Gly Ile Val Ser
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515 520 525
Trp Gly Leu Glu Cys Gly Lys Arg Pro Gly Val Tyr Thr Gln Val Thr
530 535 540
Lys Phe Leu Asn Trp Ile Lys Ala Thr Ile Lys Ser Glu Ser Gly Phe
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<210> 4497
<211> 840
<212> DNA
<213> Homo sapiens

<400> 4497
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120
ggagatgaga gccccccatc cagccctgga aacccagttc agggacagtg tggtgaagaa
180
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300
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360
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420
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480
caggccttga agctcaaccc ccaggaccac cggttatttg gaaatcgttc cttctgccat
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720
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<210> 4498
<211> 280
<212> PRT
<213> Homo sapiens

<400> 4498
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Gln Lys Glu Arg Lys Arg Gln Glu Arg Leu Glu Gln Tyr Cys Gly Glu
20 25 30
Pro Lys Ala Ser Thr Thr Ser Asp Gly Asp Glu Ser Pro Pro Ser Ser
35 40 45
Pro Gly Asn Pro Val Gln Gly Gln Cys Gly Glu Glu Glu Asp Ser Leu

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    50                  55                  60
Asp Leu Ser Ser Thr Phe Val Ser Leu Ala Leu Arg Lys Val Gly Asp
65                  70                  75                  80
Trp Pro Leu Ser Ala Arg Arg Glu Lys Gly Leu Asn Gln Glu Pro Gln
                85                  90                  95
Gly Arg Gly Leu Ala Leu Gln Lys Met Gly Gln Glu Glu Glu Ser Pro
            100                 105                 110
Pro Arg Glu Glu Arg Pro Gln Gln Ser Pro Lys Ala Ser Pro Gly Leu
        115                 120                 125
Leu Ala Ala Ala Leu Gln Gln Ser Gln Glu Leu Ala Lys Leu Gly Thr
    130                 135                 140
Ser Phe Ala Gln Asn Gly Phe Tyr His Glu Ala Val Val Leu Phe Thr
145                 150                 155                 160
Gln Ala Leu Lys Leu Asn Pro Gln Asp His Arg Leu Phe Gly Asn Arg
                165                 170                 175
Ser Phe Cys His Glu Arg Leu Gly Gln Pro Ala Trp Ala Leu Ala Asp
            180                 185                 190
Ala Gln Val Ala Leu Thr Leu Arg Pro Gly Trp Pro Arg Gly Leu Phe
        195                 200                 205
Arg Leu Gly Lys Ala Leu Met Gly Leu Gln Arg Phe Arg Glu Ala Ala
    210                 215                 220
Ala Val Phe Gln Glu Thr Leu Arg Gly Gly Ser Gln Pro Asp Ala Ala
225                 230                 235                 240
Arg Glu Leu Arg Ser Cys Leu Leu His Leu Thr Leu Gln Gly Gln Arg
                245                 250                 255
Gly Gly Ile Cys Ala Pro Pro Leu Ser Pro Gly Ala Leu Gln Pro Leu
            260                 265                 270
Pro His Ala Glu Leu Ala Pro Ser
        275                 280
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<210> 4499
<211> 562
<212> DNA
<213> Homo sapiens

<400> 4499
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attgcggagg atgggaccat gacctccctc tgcggggact ggttgcaggg tcttcaccgg
180
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240
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300
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360
ctccgttaga atacgagctc cgtgtcggtt ttattcgcta ttgtatcctc agtaccaagg
420
gcctggcatg gcatggggtc ctgtgcccct gggagaagtc acagggccgg aagagcagtg
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540

cagtggtttg tccgctgcca cg
562

<210> 4500
<211> 91
<212> PRT
<213> Homo sapiens

<400> 4500
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Lys Val Thr Pro Ala His Ser Pro Ala Asp Ala Glu Met Gly Ala Arg
20 25 30
His Gly Leu Ser Pro Leu Asn Val Ile Ala Glu Asp Gly Thr Met Thr
35 40 45
Ser Leu Cys Gly Asp Trp Leu Gln Gly Leu His Arg Phe Val Ala Arg
50 55 60
Glu Lys Ile Met Ser Val Leu Ser Glu Arg Gly Leu Phe Arg Gly Leu
65 70 75 80
Gln Asn His Pro Met Val Leu Pro Ile Cys Arg
85 90

<210> 4501
<211> 1866
<212> DNA
<213> Homo sapiens

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120
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<211> 267
<212> PRT
<213> Homo sapiens

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        35   40   45
Ala Ala Pro Gly Gln Arg Leu Pro Glu Ser Leu Arg Ala Thr Tyr Arg
    50   55   60
Glu Gly Phe Tyr Asn Glu Tyr Met Gln Arg Val Phe Lys Tyr Leu Gly

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Glu Gln Gly Val Arg Pro Arg Asp Leu Ser Ala Ile Tyr Glu Ala Ile
85 90 95
Pro Leu Ser Pro Gly Met Ser Asp Leu Leu Gln Phe Val Ala Lys Gln
100 105 110
Gly Ala Cys Phe Glu Val Ile Leu Ile Ser Asp Ala Asn Thr Phe Gly
115 120 125
Val Glu Ser Ser Leu Arg Ala Ala Gly His His Ser Leu Phe Arg Arg
130 135 140
Ile Leu Ser Asn Pro Ser Gly Pro Asp Ala Arg Gly Leu Leu Ala Leu
145 150 155 160
Arg Pro Phe His Thr His Ser Cys Ala Arg Cys Pro Ala Asn Met Cys
165 170 175
Lys His Lys Val Leu Ser Asp Tyr Leu Arg Glu Arg Ala His Asp Gly
180 185 190
Val His Phe Glu Arg Leu Phe Tyr Val Gly Asp Gly Ala Asn Asp Phe
195 200 205
Cys Pro Met Gly Leu Leu Ala Gly Gly Asp Val Ala Phe Pro Arg Arg
210 215 220
Gly Tyr Pro Met His Arg Leu Ile Gln Glu Ala Gln Lys Ala Glu Pro
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<211> 1983
<212> DNA
<213> Homo sapiens

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gtg
1983

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<213> Homo sapiens

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35 40 45
Lys Lys Ile Ile Glu Thr Lys Met Leu Met Gly Glu Val Met Arg Glu
50 55 60
Ala Ala Phe Ser Leu Ala Glu Ala Lys Phe Thr Ala Gly Asp Phe Ser
65 70 75 80
Thr Thr Val Ile Gln Asn Val Asn Lys Ala Gln Val Lys Ile Arg Ala
85 90 95
Lys Lys Asp Asn Val Ala Gly Val Thr Leu Pro Val Phe Glu His Tyr
100 105 110
His Glu Gly Thr Asp Ser Tyr Glu Leu Thr Gly Leu Ala Arg Gly Gly
115 120 125
Glu Gln Leu Ala Lys Leu Lys Arg Asn Tyr Ala Lys Ala Val Glu Leu
130 135 140
Leu Val Glu Leu Ala Ser Leu Gln Thr Ser Phe Val Thr Leu Asp Glu
145 150 155 160
Ala Ile Lys Ile Thr Asn Arg Arg Val Asn Ala Ile Glu His Gly Glu
165 170 175
Tyr Val Ile Ile Pro Arg Ile Glu Arg Thr Leu Ala Tyr Ile Ile Thr
180 185 190
Glu Leu Asp Glu Arg Glu Arg Glu Glu Phe Tyr Arg Leu Lys Lys Ile
195 200 205
Gln Glu Lys Lys Lys Ile Leu Lys Glu Lys Ser Glu Lys Asp Leu Glu
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Glu Glu Lys Asp Glu Asp Leu Leu Phe Glu
245 250

<210> 4505
<211> 379
<212> DNA
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<210> 4506
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<212> PRT
<213> Homo sapiens

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35 40 45
Pro Thr Pro Ser Ala Gln Gly Gln Ala Ala Leu Arg Gln Thr Cys Pro
50 55 60
His Leu Arg Glu Ser Gly Pro Leu Ser Val Arg His Val Ala Leu Leu
65 70 75 80
Ala Leu Glu Thr Ala Ser His Pro Ser Gly Pro His Thr Asn Gln Ala
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100 105 110
Ser Ser Thr Asp Ser Leu Ile Lys Ile
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<210> 4507
<211> 3664
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

<400> 4508
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Phe Gly Phe Val Thr Phe Glu Asn Ile Asp Asp Ala Lys Asp Ala Met
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Met Ala Met Asn Gly Lys Ser Val Asp Gly Arg Gln Ile Arg Val Asp
65                  70                  75                  80
Gln Ala Gly Lys Ser Ser Asp Asn Arg Ser Arg Gly Tyr Arg Gly Gly
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Ser Ala Gly Gly Arg Gly Phe Phe Arg Gly Gly Arg Gly Arg Gly Arg
            100                 105                 110
Gly Phe Ser Arg Gly Gly Gly Asp Arg Gly Tyr Gly Gly Asn Arg Phe
        115                 120                 125
Glu Ser Arg Ser Gly Gly Tyr Gly Gly Ser Arg Asp Tyr Tyr Ser Ser
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Arg Asp Ser Tyr Asp Ser Tyr Ala Thr His Asn Glu
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His Asp Leu Arg Asn Ile Phe Gln Arg Phe Gly Glu Ile Val Asp Ile
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Asp Ile Lys Lys Val Asn Gly Val Pro Gln Tyr Ala Phe Leu Gln Tyr

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Gly Leu Ser Ser Gln Leu Lys Ser Asp Pro Val Asp Pro Asp Lys Glu
    1730                1735                1740
Pro Glu Lys Glu Asp Val Ser Ala Ser Gly Pro Ser Pro Glu Ala Thr
1745                1750                1755                1760
Gln Leu Ala Lys Gln Met Glu Leu Glu Gln Ala Val Glu His Ile Ala
                1765                1770                1775
Lys Leu Ala Glu Ala Ser Ala Ser Ala Ala Tyr Lys Ala Asp Ala Pro
            1780                1785                1790
Glu Gly Leu Ala Pro Glu Asp Arg Asp Lys Pro Ala His Gln Ala Ser
```

1795 1800 1805
Glu Thr Glu Leu Ala Ala Ala Ile Gly Ser Ile Ile Asn Asp Ile Ser
1810 1815 1820
Gly Glu Pro Glu Asn Phe Pro Ala Pro Pro Pro Tyr Pro Gly Glu Ser
1825 1830 1835 1840
Gln Thr Asp Leu Gln Pro Pro Ala Gly Ala Gln Ala Leu Gln Pro Ser
1845 1850 1855
Glu Glu Gly Met Glu Thr Asp Glu Ala Val Ser Gly Ile Leu Glu Thr
1860 1865 1870
Glu Ala Ala Thr Glu Ser Ser Arg Pro Pro Val Asn Ala Pro Asp Pro
1875 1880 1885
Ser Ala Gly Pro Thr Asp Thr Lys Glu Ala Arg Gly Asn Ser Ser Glu
1890 1895 1900
Thr Ser His Ser Val Pro Glu Ala Lys Gly Ser Lys Glu Val Glu Val
1905 1910 1915 1920
Thr Leu Val Arg Lys Asp Lys Gly Arg Gln Lys Thr Thr Arg Ser Arg
1925 1930 1935
Arg Lys Arg Asn Thr Asn Lys Lys Val Val Ala Pro Val Glu Ser His
1940 1945 1950
Val Pro Glu Ser Asn Gln Ala Gln Gly Glu Ser Pro Ala Ala Asn Glu
1955 1960 1965
Gly Thr Thr Val Gln His Pro Glu Ala Pro Gln Glu Glu Lys Gln Ser
1970 1975 1980
Glu Lys Pro His Ser Thr Pro Pro Gln Ser Cys Thr Ser Asp Leu Ser
1985 1990 1995 2000
Lys Ile Pro Ser Thr Glu Asn Ser Ser Gln Glu Ile Ser Val Glu Glu
2005 2010 2015
Arg Thr Pro Thr Lys Ala Ser Val Pro Pro Asp Leu Pro Pro Pro Pro
2020 2025 2030
Gln Pro Ala Pro Val Asp Glu Glu Pro Gln Ala Arg Phe Arg Val His
2035 2040 2045
Ser Ile Ile Glu Ser Asp Pro Val Thr Pro Pro Ser Asp Pro Ser Ile
2050 2055 2060
Pro Ile Pro Thr Leu Pro Ser Val Thr Ala Ala Lys Leu Ser Pro Pro
2065 2070 2075 2080
Val Ala Ser Gly Gly Ile Pro His Gln Ser Pro Pro Thr Lys Val Thr
2085 2090 2095
Glu Trp Ile Thr Arg Gln Glu Glu Pro Arg Ala Gln Ser Thr Pro Ser
2100 2105 2110
Pro Ala Leu Pro Pro Asp Thr Lys Ala Ser Asp Val Asp Thr Ser Ser
2115 2120 2125
Ser Thr Leu Arg Lys Ile Leu Met Asp Pro Lys Tyr Val Ser Ala Thr
2130 2135 2140
Ser Val Thr Ser Thr Ser Val Thr Thr Ala Ile Ala Glu Pro Val Ser
2145 2150 2155 2160
Ala Ala Pro Cys Leu His Glu Ala Pro Pro Pro Pro Val Asp Ser Lys
2165 2170 2175
Lys Pro Leu Glu Glu Lys Thr Ala Pro Pro Val Thr Asn Asn Ser Glu
2180 2185 2190
Ile Gln Ala Ser Glu Val Leu Val Ala Ala Asp Lys Glu Lys Val Ala
2195 2200 2205
Pro Val Ile Ala Pro Lys Ile Thr Ser Val Ile Ser Arg Met Pro Val
2210 2215 2220
Ser Ile Asp Leu Glu Asn Ser Gln Lys Ile Thr Leu Ala Lys Pro Ala

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2225                2230                2235                2240
Pro Gln Thr Leu Thr Gly Leu Val Ser Ala Leu Thr Gly Leu Val Asn
                2245                2250                2255
Val Ser Leu Val Pro Val Asn Ala Leu Lys Gly Pro Val Lys Gly Ser
            2260                2265                2270
Val Thr Thr Leu Lys Ser Leu Val Ser Thr Pro Ala Gly Pro Val Asn
        2275                2280                2285
Val Leu Lys Gly Pro Val Asn Val Leu Thr Gly Pro Val Asn Val Leu
    2290                2295                2300
Thr Thr Pro Val Asn Ala Thr Val Gly Thr Val Asn Ala Ala Pro Gly
2305                2310                2315                2320
Thr Val Asn Ala Ala Ala Ser Ala Val Asn Ala Thr Ala Ser Ala Val
                2325                2330                2335
Thr Val Thr Ala Gly Ala Val Thr Ala Ala Ser Gly Gly Val Thr Ala
            2340                2345                2350
Thr Thr Gly Thr Val Thr Met Ala Gly Ala Val Ile Ala Pro Ser Thr
        2355                2360                2365
Lys Cys Lys Gln Arg Ala Ser Ala Asn Glu Asn Ser Arg Phe His Pro
    2370                2375                2380
Gly Ser Met Pro Val Ile Asp Asp Arg Pro Ala Asp Ala Gly Ser Gly
2385                2390                2395                2400
Ala Gly Leu Arg Val Asn Thr Ser Glu Gly Val Val Leu Leu Ser Tyr
                2405                2410                2415
Ser Gly Gln Lys Thr Glu Gly Pro Gln Arg Ile Ser Ala Lys Ile Ser
            2420                2425                2430
Gln Ile Pro Pro Ala Ser Ala Met Asp Ile Glu Phe Gln Gln Ser Val
        2435                2440                2445
Ser Lys Ser Gln Val Lys Pro Asp Ser Val Thr Ala Ser Gln Pro Pro
    2450                2455                2460
Ser Lys Gly Pro Gln Ala Pro Ala Gly Tyr Ala Asn Val Ala Thr His
2465                2470                2475                2480
Ser Thr Leu Val Leu Thr Ala Gln Thr Tyr Asn Ala Ser Pro Val Ile
                2485                2490                2495
Ser Ser Val Lys Ala Asp Arg Pro Ser Leu Glu Lys Pro Glu Pro Ile
            2500                2505                2510
His Leu Ser Val Ser Thr Pro Val Thr Gln Gly Gly Thr Val Lys Val
        2515                2520                2525
Leu Thr Gln Gly Ile Asn Thr Pro Pro Val Leu Val His Asn Gln Leu
    2530                2535                2540
Val Leu Thr Pro Ser Ile Val Thr Thr Asn Lys Lys Leu Ala Asp Pro
2545                2550                2555                2560
Val Thr Leu Lys Ile Glu Thr Lys Val Leu Gln Pro Ala Asn Leu Gly
                2565                2570                2575
Ser Thr Leu Thr Pro His His Pro Pro Ala Leu Pro Ser Lys Leu Pro
            2580                2585                2590
Thr Glu Val Asn His Val Pro Ser Gly Pro Ser Ile Pro Ala Asp Arg
        2595                2600                2605
Thr Val Ser His Leu Ala Ala Ala Lys Leu Asp Ala His Ser Pro Arg
    2610                2615                2620
Pro Ser Gly Pro Gly Pro Ser Ser Phe Pro Arg Ala Ser His Pro Ser
2625                2630                2635                2640
Ser Thr Ala Ser Thr Ala Leu Ser Thr Asn Ala Thr Val Met Leu Ala
                2645                2650                2655
Ala Gly Ile Pro Val Pro Gln Phe Ile Ser Ser Ile His Pro Glu Gln
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            2660                2665                2670
Ser Val Ile Met Pro Pro His Ser Ile Thr Gln Thr Val Ser Leu Ser
        2675                2680                2685
His Leu Ser Gln Gly Glu Val Arg Met Asn Thr Pro Thr Leu Pro Ser
    2690                2695                2700
Ile Thr Tyr Ser Ile Arg Pro Glu Ala Leu His Ser Pro Arg Ala Pro
2705                2710                2715                2720
Leu Gln Pro Gln Gln Ile Glu Val Arg Ala Pro Gln Arg Ala Ser Thr
                2725                2730                2735
Pro Gln Pro Ala Pro Ala Gly Val Pro Ala Leu Ala Ser Gln His Pro
            2740                2745                2750
Pro Glu Glu Glu Val His Tyr His Leu Pro Val Ala Arg Ala Thr Ala
        2755                2760                2765
Pro Val Gln Ser Glu Val Leu Val Met Gln Ser Glu Tyr Arg Leu His
    2770                2775                2780
Pro Tyr Thr Val Pro Arg Asp Val Arg Ile Met Val His Pro His Val
2785                2790                2795                2800
Thr Ala Val Ser Glu Gln Pro Arg Ala Ala Asp Gly Val Val Lys Val
                2805                2810                2815
Pro Pro Ala Ser Lys Ala Pro Gln Gln Pro Gly Lys Glu Ala Ala Lys
            2820                2825                2830
Thr Pro Asp Ala Lys Ala Ala Pro Thr Pro Thr Pro Ala Pro Val Pro
        2835                2840                2845
Val Pro Val Pro Leu Pro Ala Pro Ala Pro Ala Pro His Gly Glu Ala
    2850                2855                2860
Arg Ile Leu Thr Val Thr Pro Ser Asn Gln Leu Gln Gly Leu Pro Leu
2865                2870                2875                2880
Thr Pro Pro Val Val Val Thr His Gly Val Gln Ile Val His Ser Ser
                2885                2890                2895
Gly Glu Leu Phe Gln Glu Tyr Arg Tyr Gly Asp Ile Arg Thr Tyr His
            2900                2905                2910
Pro Pro Ala Gln Leu Thr His Thr Gln Phe Pro Ala Ala Ser Ser Val
        2915                2920                2925
Gly Leu Pro Ser Arg Thr Lys Thr Ala Ala Gln Gly Pro Pro Pro Glu
    2930                2935                2940
Gly Glu Pro Leu Gln Pro Pro Gln Pro Val Gln Ser Thr Gln Pro Ala
2945                2950                2955                2960
Gln Pro Ala Pro Pro Cys Pro Pro Ser Gln Leu Gly Gln Pro Gly Gln
                2965                2970                2975
Pro Pro Ser Ser Lys Met Pro Gln Val Ser Gln Glu Ala Lys Gly Thr
            2980                2985                2990
Gln Thr Gly Val Glu Gln Pro Arg Leu Pro Ala Gly Pro Ala Asn Arg
        2995                3000                3005
Pro Pro Glu Pro His Thr Gln Val Gln Arg Ala Gln Ala Glu Thr Gly
    3010                3015                3020
Pro Thr Ser Phe Pro Ser Pro Val Ser Val Ser Met Lys Pro Asp Leu
3025                3030                3035                3040
Pro Val Ser Leu Pro Thr Gln Thr Ala Pro Lys Gln Pro Leu Phe Val
                3045                3050                3055
Pro Thr Thr Ser Gly Pro Ser Thr Pro Pro Gly Leu Val Leu Pro His
            3060                3065                3070
Thr Glu Phe Gln Pro Ala Pro Lys Gln Asp Ser Ser Pro His Leu Thr
        3075                3080                3085
Ser Gln Arg Pro Val Asp Met Val Gln Leu Leu Lys Lys Tyr Pro Ile
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    3090                3095                3100
Val Trp Gln Gly Leu Leu Ala Leu Lys Asn Asp Thr Ala Ala Val Gln
3105                3110                3115                3120
Leu His Phe Val Ser Gly Asn Asn Val Leu Ala His Arg Ser Leu Pro
                3125                3130                3135
Leu Ser Glu Gly Gly Pro Pro Leu Arg Ile Ala Gln Arg Met Arg Leu
            3140                3145                3150
Glu Ala Thr Gln Leu Glu Gly Val Ala Arg Arg Met Thr Leu Ala Ser
        3155                3160                3165
Ala Ser Val Glu Thr Asp Tyr Cys Leu Leu Leu Ala Leu Pro Cys Gly
    3170                3175                3180
Arg Asp Gln Glu Asp Val Val Ser Gln Thr Glu Ser Leu Lys Ala Ala
3185                3190                3195                3200
Phe Ile Thr Tyr Leu Gln Ala Lys Gln Ala Ala Gly Ile Ile Asn Val
                3205                3210                3215
Pro Asn Pro Gly Ser Asn Gln Pro Ala Tyr Val Leu Gln Ile Phe Pro
            3220                3225                3230
Pro Cys Glu Phe Ser Glu Ser His Leu Ser Arg Leu Ala Pro Asp Leu
        3235                3240                3245
Leu Ala Ser Ile Ser Asn Ile Ser Pro His Leu Met Ile Val Ile Ala
    3250                3255                3260
Ser Val
3265

<210> 4511
<211> 1375
<212> DNA
<213> Homo sapiens

<400> 4511
gctggtcgga ccaggtctct tcccatcact attgaaatgc taaaagttcc agacgatgaa
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gaagaagagg agcaaacctg tccatccaca ttcagtgaag aaatgacacc tacctcagtc
120
attcctaaat taccacagtg tctacgggag gaagaagaga aggagagcga ctctgattca
180
gaaggtccca ttcagtaccg agatgaagaa gatgaagatg aaagctatca gagtgcactc
240
gccaacaaag tgaagaggaa agacacactg gcaatgaagt tgaaccacag acccagtgaa
300
ccagagttga acctgaattc ttggccttgt aaaagcaagg aggagtggaa tgaaatacgg
360
caccagattg gaaacacact gatccggcga ctgagtcaaa gaccaacacc agaagaacta
420
gaacaacgca atatattgca acctaaaaat gaagctgatc gtcaggcaga aaaacgagaa
480
attaaacgtc ggctcactag aaagctcagt caaaggccaa ctgtcgctga actccttgcc
540
aggaagattc tgaggtttaa tgaatatgta gaggtaacag atgctcaaga ttatgaccgg
600
cgagccgaca aaccttggac caaactgacc cctgctgaca aggctgccat aagaaaagaa
660
ttaaatgaat ttaaaagctc cgagatggag gttcatgaag agagcaaaca ttttacacgc
720
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taccatcgtc catgatgcca aaggttgaga gaggaatcaa catggctgct ttgctgcttc
780
cttctccaaa gtgacatatg gagggaactt tagcacttcc cagcacagcc agaattgcat
840
cctctgggat cttctgaggt ggacagcact ttgaatgtag catttcactg gaacagagtc
900
ttatgtgctg caccgggggc aaaacaacac tttgtcagtg cttttgaacc tttcaatatt
960
gtagcatgct tgaggagttt ttcccttact ggccaccaaa gttctgaacc acttgcaggt
1020
tccaggtttt actggctgca ccacacccct tcccctagat gactgcctgt gcagagacac
1080
agtttgcacc attagcctta cctgccctgc cctgattgtg agacccaaat gtgtaggctc
1140
taaattccag ccatcaaatc caattcctgg tggggaaaac cttctggaga cccccaacct
1200
tctgataaaa gagtctctac ctccagggaa agccttctta ccacactggc atatcagatg
1260
aaagcattgc actgtacctc tcgtaacaca gcaatacagt cctcttgagg cactcaagcc
1320
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1375

<210> 4512
<211> 244
<212> PRT
<213> Homo sapiens

<400> 4512
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Pro Asp Asp Glu Glu Glu Glu Glu Gln Thr Cys Pro Ser Thr Phe Ser
20 25 30
Glu Glu Met Thr Pro Thr Ser Val Ile Pro Lys Leu Pro Gln Cys Leu
35 40 45
Arg Glu Glu Glu Glu Lys Glu Ser Asp Ser Asp Ser Glu Gly Pro Ile
50 55 60
Gln Tyr Arg Asp Glu Glu Asp Glu Asp Glu Ser Tyr Gln Ser Ala Leu
65 70 75 80
Ala Asn Lys Val Lys Arg Lys Asp Thr Leu Ala Met Lys Leu Asn His
85 90 95
Arg Pro Ser Glu Pro Glu Leu Asn Leu Asn Ser Trp Pro Cys Lys Ser
100 105 110
Lys Glu Glu Trp Asn Glu Ile Arg His Gln Ile Gly Asn Thr Leu Ile
115 120 125
Arg Arg Leu Ser Gln Arg Pro Thr Pro Glu Glu Leu Glu Gln Arg Asn
130 135 140
Ile Leu Gln Pro Lys Asn Glu Ala Asp Arg Gln Ala Glu Lys Arg Glu
145 150 155 160
Ile Lys Arg Arg Leu Thr Arg Lys Leu Ser Gln Arg Pro Thr Val Ala
165 170 175
Glu Leu Leu Ala Arg Lys Ile Leu Arg Phe Asn Glu Tyr Val Glu Val
180 185 190
Thr Asp Ala Gln Asp Tyr Asp Arg Arg Ala Asp Lys Pro Trp Thr Lys

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        195                 200                 205
Leu Thr Pro Ala Asp Lys Ala Ala Ile Arg Lys Glu Leu Asn Glu Phe
    210                 215                 220
Lys Ser Ser Glu Met Glu Val His Glu Glu Ser Lys His Phe Thr Arg
225                 230                 235                 240
Tyr His Arg Pro
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<210> 4513
<211> 545
<212> DNA
<213> Homo sapiens

<400> 4513
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tgcatcaccg agtccacgca cacttgcctt gcagcttcat gtcagagagc agctgagcag
120
tcagcacctg cacccggggg ttgggccctg gggcttcctt cccagtccag cctctcagct
180
cctgtctgtg gcttagcacg tgcaccacag agccaaccag atcctctgta aacttttgga
240
cttctctggc cttcacggga ccttctgtgg cagaaatcat tttcataatc atgagactct
300
tctcctcgga gtttcctttc aacaggtggg acatggatgc tgtgaactgc tcctgggaca
360
cgttctcact gggtcccttc gccttccctg tcaggtcgac cctccgcatg ccatcataca
420
gcctggtgac catctctggg ggaagagctt ccccgacgtg gttctgtagt gccttcagag
480
agaaggattt ggatgagaca ttcgggctgt ttttatctga tgacagagca tcaaacaatt
540
gatca
545

<210> 4514
<211> 122
<212> PRT
<213> Homo sapiens

<400> 4514
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Met Val Thr Arg Leu Tyr Asp Gly Met Arg Arg Val Asp Leu Thr Gly
 1               5                  10                  15
Lys Ala Lys Gly Pro Ser Glu Asn Val Ser Gln Glu Gln Phe Thr Ala
            20                  25                  30
Ser Met Ser His Leu Leu Lys Gly Asn Ser Glu Glu Lys Ser Leu Met
        35                  40                  45
Ile Met Lys Met Ile Ser Ala Thr Glu Gly Pro Val Lys Ala Arg Glu
    50                  55                  60
Val Gln Lys Phe Thr Glu Asp Leu Val Gly Ser Val Val His Val Leu
65                  70                  75                  80
Ser His Arg Gln Glu Leu Arg Gly Trp Thr Gly Lys Glu Ala Pro Gly
                85                  90                  95
Pro Asn Pro Arg Val Gln Val Leu Thr Ala Gln Leu Leu Ser Asp Met
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100 105 110
Lys Leu Gln Gly Lys Cys Ala Trp Thr Arg
115 120

<210> 4515
<211> 3207
<212> DNA
<213> Homo sapiens

<400> 4515
ncaaacaacc actgggaggc actgtttccc ccccatcccg ccctgggcag ggcacgtccc
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actcccccccg cgcggttgct gggaacccgg aggccgcccg ggcggagcgc ggagggcgcg
120
tcggaacctg gccggggccc tccacccgcg ccgtggtccc ggtggttgcg ccccgtggcg
180
agcgacgccg acaactttgc gatggagttt gtgcgggcgc tgtggctggg cctggcgctg
240
gcgctggggc cggggtccgc ggggggccac cctcagccgt gcggcgtcct ggcgcgcctc
300
gggggctccg tgcgcctggg cgccctcctg ccccgcgcgc ctctcgcccg cgcccgcgcc
360
cgcgccgccc tggcccgggc cgccctggcg ccgcggctgc cgcacaacct gagcttggag
420
ctggtggtcg ccgcgccccc cgcccgcgac cccgcctcgc tgacccgcgg cctgtgccag
480
gcgctggtgc ctccgggcgt ggcggccctg ctcgcctttc ccgaggctcg gcccgagctg
540
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600
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720
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780
cgggctggcc ggcccccaca gctggtcctg gacctaagcc ggcgggacac gggagatgca
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1080
catgacattg tgcaactggt ggcccgggcg ctgggcagtg cggcccaggt gcagccgaag
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1260
gtgtgggtga caggcagctc ccaggtacac atgtctcggc actttaaggt gtggagcctt
1320

cgccgggacc cacggggcgc cccggcctgg gccacggtgg gcagctggcg gtacggccag
1380
ctggacttgg aaccgggagg tgcctctgca tggcccccgc ccccgcaggg tgcccaggtc
1440
cggcccaagc tgcgtgtggt aacgctgttg gaacacccat ttgtgtttgc ccgtgatcca
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1680
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1740
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1800
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1980
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2040
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2100
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2880
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2940

cccagaccca ccaccccacc agctcgcccc gaagccggcc gcggggtgca ggaggttccc
3000
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3060
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3120
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3180
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3207

<210> 4516
<211> 901
<212> PRT
<213> Homo sapiens

<400> 4516
Met Glu Phe Val Arg Ala Leu Trp Leu Gly Leu Ala Leu Ala Leu Gly
1 5 10 15
Pro Gly Ser Ala Gly Gly His Pro Gln Pro Cys Gly Val Leu Ala Arg
20 25 30
Leu Gly Gly Ser Val Arg Leu Gly Ala Leu Leu Pro Arg Ala Pro Leu
35 40 45
Ala Arg Ala Arg Ala Arg Ala Ala Leu Ala Arg Ala Ala Leu Ala Pro
50 55 60
Arg Leu Pro His Asn Leu Ser Leu Glu Leu Val Val Ala Ala Pro Pro
65 70 75 80
Ala Arg Asp Pro Ala Ser Leu Thr Arg Gly Leu Cys Gln Ala Leu Val
85 90 95
Pro Pro Gly Val Ala Ala Leu Leu Ala Phe Pro Glu Ala Arg Pro Glu
100 105 110
Leu Leu Gln Leu His Phe Leu Ala Ala Ala Thr Glu Thr Pro Val Leu
115 120 125
Ser Leu Leu Arg Arg Glu Ala Arg Ala Pro Leu Gly Ala Pro Asn Pro
130 135 140
Phe His Leu Gln Leu His Trp Ala Ser Pro Leu Glu Thr Leu Leu Asp
145 150 155 160
Val Leu Val Ala Val Leu Gln Ala His Ala Trp Glu Asp Val Gly Leu
165 170 175
Ala Leu Cys Arg Thr Gln Asp Pro Gly Gly Leu Val Ala Leu Trp Thr
180 185 190
Ser Arg Ala Gly Arg Pro Pro Gln Leu Val Leu Asp Leu Ser Arg Arg
195 200 205
Asp Thr Gly Asp Ala Gly Leu Arg Ala Arg Leu Ala Pro Met Ala Ala
210 215 220
Pro Val Gly Gly Glu Ala Pro Val Pro Ala Ala Val Leu Leu Gly Cys
225 230 235 240
Asp Ile Ala Arg Ala Arg Arg Val Leu Glu Ala Val Pro Pro Gly Pro
245 250 255
His Trp Leu Leu Gly Thr Pro Leu Pro Pro Lys Ala Leu Pro Thr Ala
260 265 270
Gly Leu Pro Pro Gly Leu Leu Ala Leu Gly Glu Val Ala Arg Pro Pro
275 280 285
Leu Glu Ala Ala Ile His Asp Ile Val Gln Leu Val Ala Arg Ala Leu

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    290                 295                 300
Gly Ser Ala Ala Gln Val Gln Pro Lys Arg Ala Leu Leu Pro Ala Pro
305                 310                 315                 320
Val Asn Cys Gly Asp Leu Gln Pro Ala Gly Pro Glu Ser Pro Gly Arg
                325                 330                 335
Phe Leu Ala Arg Phe Leu Ala Asn Thr Ser Phe Gln Gly Arg Thr Gly
            340                 345                 350
Pro Val Trp Val Thr Gly Ser Ser Gln Val His Met Ser Arg His Phe
        355                 360                 365
Lys Val Trp Ser Leu Arg Arg Asp Pro Arg Gly Ala Pro Ala Trp Ala
    370                 375                 380
Thr Val Gly Ser Trp Arg Tyr Gly Gln Leu Asp Leu Glu Pro Gly Gly
385                 390                 395                 400
Ala Ser Ala Trp Pro Pro Pro Pro Gln Gly Ala Gln Val Arg Pro Lys
                405                 410                 415
Leu Arg Val Val Thr Leu Leu Glu His Pro Phe Val Phe Ala Arg Asp
            420                 425                 430
Pro Asp Glu Asp Gly Gln Cys Pro Ala Gly Gln Leu Cys Leu Asp Pro
        435                 440                 445
Gly Thr Asn Asp Ser Ala Thr Leu Asp Ala Leu Phe Ala Ala Leu Ala
    450                 455                 460
Asn Gly Ser Ala Pro Arg Ala Leu Arg Lys Cys Cys Tyr Gly Tyr Cys
465                 470                 475                 480
Ile Asp Leu Leu Glu Arg Leu Ala Glu Asp Thr Pro Phe Asp Phe Glu
                485                 490                 495
Leu Tyr Leu Val Gly Asp Gly Lys Tyr Gly Ala Leu Arg Asp Gly Arg
            500                 505                 510
Trp Thr Gly Leu Val Gly Asp Leu Leu Ala Gly Arg Ala His Met Ala
        515                 520                 525
Val Thr Ser Phe Ser Ile Asn Ser Ala Arg Ser Gln Val Val Asp Phe
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Thr Ser Pro Phe Phe Ser Thr Ser Leu Gly Ile Met Val Arg Ala Arg
545                 550                 555                 560
Asp Thr Ala Ser Pro Ile Gly Ala Phe Met Trp Pro Leu His Trp Ser
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Thr Trp Leu Gly Val Phe Ala Ala Leu His Leu Thr Ala Leu Phe Leu
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Thr Val Tyr Glu Trp Arg Ser Pro Tyr Gly Leu Thr Pro Arg Gly Arg
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Asn Arg Ser Thr Val Phe Ser Tyr Ser Ser Ala Leu Asn Leu Cys Tyr
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Ala Ile Leu Phe Arg Arg Thr Val Ser Ser Lys Thr Pro Lys Cys Pro
625                 630                 635                 640
Thr Gly Arg Leu Leu Met Asn Leu Trp Ala Ile Phe Cys Leu Leu Val
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Leu Ser Ser Tyr Thr Ala Asn Leu Ala Ala Val Met Val Gly Asp Lys
            660                 665                 670
Thr Phe Glu Glu Leu Ser Gly Ile His Asp Pro Lys Leu His His Pro
        675                 680                 685
Ala Gln Gly Phe Arg Phe Gly Thr Val Trp Glu Ser Ser Ala Glu Ala
    690                 695                 700
Tyr Ile Lys Lys Ser Phe Pro Asp Met His Ala His Met Arg Arg His
705                 710                 715                 720
Ser Ala Pro Thr Thr Pro Arg Gly Val Ala Met Leu Thr Ser Asp Pro
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725 730 735
Pro Lys Leu Asn Ala Phe Ile Met Asp Lys Ser Leu Leu Asp Tyr Glu
740 745 750
Val Ser Ile Asp Ala Asp Cys Lys Leu Leu Thr Val Gly Lys Pro Phe
755 760 765
Ala Ile Glu Gly Tyr Gly Ile Gly Leu Pro Gln Asn Ser Pro Leu Thr
770 775 780
Ser Asn Leu Ser Glu Phe Ile Ser Arg Tyr Lys Ser Ser Gly Phe Ile
785 790 795 800
Asp Leu Leu His Asp Lys Trp Tyr Lys Met Val Pro Cys Gly Lys Arg
805 810 815
Val Phe Ala Val Thr Glu Thr Leu Gln Met Ser Ile Tyr His Phe Ala
820 825 830
Gly Leu Phe Val Leu Leu Cys Leu Gly Leu Gly Ser Ala Leu Leu Ser
835 840 845
Ser Leu Gly Glu His Ala Phe Phe Arg Leu Ala Leu Pro Arg Ile Arg
850 855 860
Lys Gly Ser Arg Leu Gln Tyr Trp Leu His Thr Ser Gln Lys Ile His
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Glu Ala Glu Pro Arg
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<210> 4517
<211> 2275
<212> DNA
<213> Homo sapiens

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240
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420
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1080
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2100
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2160
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2275

<210> 4518

<211> 650
<212> PRT
<213> Homo sapiens

<400> 4518

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Val Ser Ser Leu Leu Leu Gln Glu Glu Glu Pro Leu Ala Gly Gly Lys
        35                  40                  45
Pro Gly Ala Asp Gly Gly Ser Leu Glu Ala Val Arg Leu Gly Pro Ser
    50                  55                  60
Ser Gly Leu Leu Val Asp Trp Leu Glu Met Leu Asp Pro Glu Val Val
65                  70                  75                  80
Ser Ser Cys Pro Asp Leu Gln Leu Arg Leu Leu Phe Ser Arg Arg Lys
                85                  90                  95
Gly Lys Gly Gln Ala Gln Val Pro Ser Phe Arg Pro Tyr Leu Leu Thr
            100                 105                 110
Leu Phe Thr His Gln Ser Ser Trp Pro Thr Leu His Gln Cys Ile Arg
        115                 120                 125
Val Leu Leu Gly Lys Ser Arg Glu Gln Arg Phe Asp Pro Ser Ala Ser
    130                 135                 140
Leu Asp Phe Leu Trp Ala Cys Ile His Val Pro Arg Ile Trp Gln Gly
145                 150                 155                 160
Arg Asp Gln Arg Thr Pro Gln Lys Arg Arg Glu Glu Leu Val Leu Arg
                165                 170                 175
Val Gln Gly Pro Glu Leu Ile Ser Leu Val Glu Leu Ile Leu Ala Glu
            180                 185                 190
Ala Glu Thr Arg Ser Gln Asp Gly Asp Thr Ala Ala Cys Ser Leu Ile
        195                 200                 205
Gln Ala Arg Leu Pro Leu Leu Leu Ser Cys Cys Cys Gly Asp Asp Glu
    210                 215                 220
Ser Val Arg Lys Val Thr Glu His Leu Ser Gly Cys Ile Gln Gln Trp
225                 230                 235                 240
Gly Asp Ser Val Leu Gly Arg Arg Cys Arg Asp Leu Leu Leu Gln Leu
                245                 250                 255
Tyr Leu Gln Arg Pro Glu Leu Arg Val Pro Val Pro Glu Val Leu Leu
            260                 265                 270
His Ser Glu Gly Ala Ala Ser Ser Ser Val Cys Lys Leu Asp Gly Leu
        275                 280                 285
Ile His Arg Phe Ile Thr Leu Leu Ala Asp Thr Ser Asp Ser Arg Ala
    290                 295                 300
Leu Glu Asn Arg Gly Ala Asp Ala Ser Met Ala Cys Arg Lys Leu Ala
305                 310                 315                 320
Val Ala His Pro Leu Leu Leu Leu Arg His Leu Pro Met Ile Ala Ala
                325                 330                 335
Leu Leu His Gly Arg Thr His Leu Asn Phe Gln Glu Phe Arg Gln Gln
            340                 345                 350
Asn His Leu Ser Cys Phe Leu His Val Leu Gly Leu Leu Glu Leu Leu
        355                 360                 365
Gln Pro His Val Phe Arg Ser Glu His Gln Gly Ala Leu Trp Asp Cys
    370                 375                 380
Leu Leu Ser Phe Ile Arg Leu Leu Leu Asn Tyr Arg Lys Ser Ser Arg
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385 390 395 400
His Leu Ala Ala Phe Ile Asn Lys Phe Val Gln Phe Ile His Lys Tyr
405 410 415
Ile Thr Tyr Asn Ala Pro Ala Ala Ile Ser Phe Leu Gln Lys His Ala
420 425 430
Asp Pro Leu His Asp Leu Ser Phe Asp Asn Ser Asp Leu Val Met Leu
435 440 445
Lys Ser Leu Leu Ala Gly Leu Ser Leu Pro Ser Arg Asp Asp Arg Thr
450 455 460
Asp Arg Gly Leu Asp Glu Glu Gly Glu Glu Glu Ser Ser Ala Gly Ser
465 470 475 480
Leu Pro Leu Val Ser Val Ser Leu Phe Thr Pro Leu Thr Ala Ala Glu
485 490 495
Met Ala Pro Tyr Met Lys Arg Leu Ser Arg Gly Gln Thr Val Glu Gly
500 505 510
Glu Ser Gly Pro Ala Ser Pro Thr Pro Asp Leu Leu Glu Val Leu Ser
515 520 525
Asp Ile Asp Glu Met Ser Arg Arg Arg Pro Glu Ile Leu Ser Phe Phe
530 535 540
Ser Thr Asn Leu Gln Arg Leu Met Ser Ser Ala Glu Glu Cys Cys Arg
545 550 555 560
Asn Leu Ala Phe Ser Leu Ala Leu Arg Ser Met Gln Asn Ser Pro Ser
565 570 575
Ile Ala Ala Ala Phe Leu Pro Thr Phe Met Tyr Cys Leu Gly Ser Gln
580 585 590
Asp Phe Glu Val Val Gln Thr Ala Leu Arg Asn Leu Pro Glu Tyr Ala
595 600 605
Leu Leu Cys Gln Glu His Ala Ala Val Leu Leu His Arg Ala Phe Leu
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Val Gly Met Tyr Gly Gln Met Asp Pro Ser Ala Gln Ile Ser Glu Ala
625 630 635 640
Leu Arg Ile Leu His Met Glu Ala Val Met
645 650

<210> 4519
<211> 2326
<212> DNA
<213> Homo sapiens

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120
acagacaact atccggctta cggccagggg agcccctgca gctgcacaga accagtttct
180
tatgtatctg gcggtaattg ggaaagcttc tgagaaagtc catggggccg atgtatggga
240
gatgaatgtg gtcccggagg catccaaacg agggctgtgt ggtgtgctca tgtggaggga
300
tggactacac tgcatactaa ctgtaagcag gccgagagac ccaataacca gcagaattgt
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420

tgtcagcccg tgatttcaaa aagcctagag aaacctcttg agtgcattaa gggggaagaa
480
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720
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840
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1080
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1140
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1260
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1320
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1380
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1920
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gaaggtgagt cgccagcttc agacgccatc taggttcgtt tcaaaagtta gtgtgcatct
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2220
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2326

<210> 4520
<211> 617
<212> PRT
<213> Homo sapiens

<400> 4520
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20 25 30
Thr Asn Cys Lys Gln Ala Glu Arg Pro Asn Asn Gln Gln Asn Cys Phe
35 40 45
Lys Val Cys Asp Trp His Lys Glu Leu Tyr Asp Trp Arg Leu Gly Pro
50 55 60
Trp Asn Gln Cys Gln Pro Val Ile Ser Lys Ser Leu Glu Lys Pro Leu
65 70 75 80
Glu Cys Ile Lys Gly Glu Glu Gly Ile Gln Val Arg Glu Ile Ala Cys
85 90 95
Ile Gln Lys Asp Lys Asp Ile Pro Ala Glu Asp Ile Ile Cys Glu Tyr
100 105 110
Phe Glu Pro Lys Pro Leu Leu Glu Gln Ala Cys Leu Ile Pro Cys Gln
115 120 125
Gln Asp Cys Ile Val Ser Glu Phe Ser Ala Trp Ser Glu Cys Ser Lys
130 135 140
Thr Cys Gly Ser Gly Leu Gln His Arg Thr Arg His Val Val Ala Pro
145 150 155 160
Pro Gln Phe Gly Gly Ser Gly Cys Pro Asn Leu Thr Glu Phe Gln Val
165 170 175
Cys Gln Ser Ser Pro Cys Glu Ala Glu Glu Leu Arg Tyr Ser Leu His
180 185 190
Val Gly Pro Trp Ser Thr Cys Ser Met Pro His Ser Arg Gln Val Arg
195 200 205
Gln Ala Arg Arg Arg Gly Lys Asn Lys Glu Arg Glu Lys Asp Arg Ser
210 215 220
Lys Gly Val Lys Asp Pro Glu Ala Arg Glu Leu Ile Lys Lys Lys Arg
225 230 235 240
Asn Arg Asn Arg Gln Asn Arg Gln Glu Asn Lys Tyr Trp Asp Ile Gln
245 250 255
Ile Gly Tyr Gln Thr Arg Glu Val Met Cys Ile Asn Lys Thr Gly Lys
260 265 270
Ala Ala Asp Leu Ser Phe Cys Gln Gln Glu Lys Leu Pro Met Thr Phe
275 280 285
Gln Ser Cys Val Ile Thr Lys Glu Cys Gln Val Ser Glu Trp Ser Glu

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Trp Ser Pro Cys Ser Lys Thr Cys His Asp Met Val Ser Pro Ala Gly
305                 310                 315                 320
Thr Arg Val Arg Thr Arg Thr Ile Arg Gln Phe Pro Ile Gly Ser Glu
                325                 330                 335
Lys Glu Cys Pro Glu Phe Glu Glu Lys Glu Pro Cys Leu Ser Gln Gly
            340                 345                 350
Asp Gly Val Val Pro Cys Ala Thr Tyr Gly Trp Arg Thr Thr Glu Trp
        355                 360                 365
Thr Glu Cys Arg Val Asp Pro Leu Leu Ser Gln Gln Asp Lys Arg Arg
    370                 375                 380
Gly Asn Gln Thr Ala Leu Cys Gly Gly Gly Ile Gln Thr Arg Glu Val
385                 390                 395                 400
Tyr Cys Val Gln Ala Asn Glu Asn Leu Leu Ser Gln Leu Ser Thr His
                405                 410                 415
Lys Asn Lys Glu Ala Ser Lys Pro Met Asp Leu Lys Leu Cys Thr Gly
            420                 425                 430
Pro Ile Pro Asn Thr Thr Gln Leu Cys His Ile Pro Cys Pro Thr Glu
        435                 440                 445
Cys Glu Val Ser Pro Trp Ser Ala Trp Gly Pro Cys Thr Tyr Glu Asn
    450                 455                 460
Cys Asn Asp Pro Gln Gly Lys Lys Gly Phe Lys Leu Arg Lys Arg Arg
465                 470                 475                 480
Ile Thr Asn Glu Pro Thr Gly Gly Ser Gly Leu Thr Gly Asn Cys Pro
                485                 490                 495
His Leu Leu Glu Ala Ile Pro Cys Glu Glu Pro Ala Cys Tyr Asp Trp
            500                 505                 510
Lys Ala Val Arg Leu Gly Asp Cys Glu Pro Asp Asn Gly Lys Glu Cys
        515                 520                 525
Gly Pro Gly Thr Gln Val Gln Glu Val Val Cys Ile Asn Ser Asp Gly
    530                 535                 540
Glu Glu Val Asp Arg Gln Leu Cys Arg Asp Ala Ile Phe Pro Ile Pro
545                 550                 555                 560
Val Ala Cys Asp Ala Pro Cys Pro Lys Asp Cys Val Leu Ser Thr Trp
                565                 570                 575
Ser Thr Trp Ser Ser Cys Ser His Thr Cys Ser Gly Lys Thr Thr Glu
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Gly Lys Gln Ile Arg Ala Arg Ser Ile Leu Ala Tyr Ala Gly Glu Glu
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Gly Glu Ser Pro Ala Ser Asp Ala Ile
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<210> 4521
<211> 1071
<212> DNA
<213> Homo sapiens

<400> 4521
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120
ttataccaat ataaacaatt actcaggaaa aaaagaaaat aaaaacttgc aagggctaaa
180

ataacttgct taccaccaaa gatgcttgct ctaagaactg tgaagggatt caagaggaaa
240
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360
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420
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540
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960
attaatatat caaacaaata aagattaata agaatttgga atttgtatga aatggcaaag
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1071

<210> 4522
<211> 189
<212> PRT
<213> Homo sapiens

<400> 4522
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His Thr Glu Thr Ala Ser Ser Phe Gln Pro Ser Pro Phe Ser Ala Asp
35 40 45
Phe Glu Leu Gln Ile Ser Leu Leu Tyr Leu Glu Ser Pro Ile Ser Leu
50 55 60
Gln Glu Phe Ala Leu Ser Phe Ile Ile Ile Leu Val Tyr Val Leu Asp
65 70 75 80
Trp Ala Ala Ile Thr Arg Cys His Arg Leu Ser Gly Leu Asn Asn Lys
85 90 95
His Ser Tyr Pro Thr Val Thr Glu Ala Glu Lys Pro Gly Val Lys Val
100 105 110
Pro Ala Trp Ser Asp Ser Val Leu Glu Ala Gly Lys Ser Lys Met Glu
115 120 125
Ala Leu Val Gly Leu Val Ser Gly Arg Ala Ser Leu Cys Phe Gln Asp

130 135 140
Gly Ala Leu Ser Leu His Leu Pro Glu Gly Arg Asn Ala Val Ser Leu
145 150 155 160
Gln His Arg Arg Asn Thr Ser Glu Lys Lys Ser Ser Arg Lys Val Glu
165 170 175
Asn Lys Glu Met Glu Tyr Ile Tyr Glu Asn Tyr Tyr Ile
180 185

<210> 4523
<211> 1022
<212> DNA
<213> Homo sapiens

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120
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aaccgagacc cccgggaatg gaaggctcat ttcttggagg ctgtggatga tgctttcaag
420
acaatggatg tggatatggc cgaggaacat gccagggccc agatgagggc ccagatgaat
480
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720
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1020
aa
1022

<210> 4524
<211> 262
<212> PRT

<213> Homo sapiens

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35 40 45
Glu Ala Leu Arg Lys Met Gly Leu Arg Pro Gly Val Arg His Pro Phe
50 55 60
Leu Gly Asp Leu Arg Lys Leu Ile Thr Asp Asp Phe Val Lys Gln Lys
65 70 75 80
Tyr Leu Glu Tyr Lys Lys Ile Pro Asn Ser Asn Pro Pro Glu Tyr Glu
85 90 95
Phe Leu Trp Gly Leu Arg Ala Arg His Glu Thr Ser Lys Met Arg Val
100 105 110
Leu Arg Phe Ile Ala Gln Asn Gln Asn Arg Asp Pro Arg Glu Trp Lys
115 120 125
Ala His Phe Leu Glu Ala Val Asp Asp Ala Phe Lys Thr Met Asp Val
130 135 140
Asp Met Ala Glu Glu His Ala Arg Ala Gln Met Arg Ala Gln Met Asn
145 150 155 160
Ile Gly Asp Glu Ala Leu Ile Gly Arg Trp Ser Trp Asp Asp Ile Gln
165 170 175
Val Glu Leu Leu Thr Trp Asp Glu Asp Gly Asp Phe Gly Asp Ala Trp
180 185 190
Ala Arg Ile Pro Phe Ala Phe Trp Ala Arg Tyr His Gln Tyr Ile Leu
195 200 205
Asn Ser Asn Arg Ala Asn Arg Arg Ala Thr Trp Arg Ala Gly Val Ser
210 215 220
Ser Gly Thr Asn Gly Gly Ala Ser Thr Ser Val Leu Asp Gly Pro Ser
225 230 235 240
Thr Ser Ser Thr Ile Arg Thr Arg Asn Ala Ala Arg Ala Gly Ala Ser
245 250 255
Phe Phe Ser Trp Ile Gln
260

<210> 4525
<211> 1731
<212> DNA
<213> Homo sapiens

<400> 4525
nngaaccatg gcattctcca ggctctgacc acagaagctt atgaatggga gccacgtgtt
60
gtgagtacag aggtggtcag agcccaagaa gaatgggaag ctgtggacac catccagcca
120
gagacaggga gccaagctag ctcagagcag cctgggcagc taatctcctt cagtgaggcc
180
ctgcagcact tccagactgt ggacctttcc cccttcaaga aaagaatcca gccaactatt
240
cgaaggactg ggctcgccgc cctccgacac tacctcttcg ggcctccaaa gctccaccag
300

cgccttcggg aagaaaggga cttggtcctg accattgctc agtgtggcct ggatagccaa
360
gacccagtgc atggccgagt cctccagacc atctataaga agctgaccgg ctccaagttt
420
gactgtgccc ttcatggaaa ccactgggag gacctgggct ttcagggagc gaatccagcc
480
acagacctga gaggcgcagg cttccttgcc ctcctgcatc tgctctacct agtgatggac
540
tcaaagacct tgccgatggc gcaggagatt ttccgcctgt ctcgtcacca catccagcaa
600
ttccctttct gtttgatgtc cgtgaacatc acccacattg ccatccaggc cttgagagag
660
gagtgtctct ccagagagtg taatcggcag cagaaggtca tccccgtggt gaacagcttc
720
tatgccgcca cattcctcca cctcgcacat gtctggagga cacagcggaa gaccatctca
780
gactcgggct ttgtcctcaa aggtgtgctc tttcttctgg ggaggcctag gctgaatgca
840
cagtgtccca ggtccagaga gcccaaggtg gttgctagac tggttttggc tgcagttctt
900
ccccatccac actttctcaa attccagctt accaaaatct ccatcaccca ccccctggag
960
tctgctagtt ctcctttctc tgccctgact gtcgcccttt tctggtctta tacttatgac
1020
aagcatatat tctgatcaaa aattgggagc cagggtccaa tagttggact attcaaagtt
1080
gcaattgtgc agacaaggta gagtgtgtgg tccctgtggc tgtagctggc tccctagcct
1140
acctctctgg tgatctctcc atctgaggct ccttcacttt ctctccatgg gataggggtt
1200
gggggtactc cctagagctg ctaggcttga ggccttgact gttgtgtcac ccagagcccc
1260
ctcaagcctt ctgctcccca attctctctg ttgcagagtt ggaagtattg gccaagaaga
1320
gcccacggcg ggctgctcaa gaccctggag ctgtacttgg ccagggtgtc aaagggacag
1380
gcctccttgt tgggagcaca gaagtgctat gggccagaag ccctccctt caaggatctc
1440
accttcacag gtgagagtga cctgcagtct cactcatccg aaggcgtatg gctgatctga
1500
cctccgagat gaatggaggc ttaaaggctg agctgcaggg gctttcaggg ggtcagtgga
1560
gccatgtcag gagcctggcc aggccgcacc ccttgctgtc tcagcagatg ggatatagga
1620
agctcctggg cttagctgtg ggaagccaag taccctcacc ggcatgggac atgaggggca
1680
gctagacttc acccccttcc cgcagacctg cctccagagc aaggagaatt c
1731

<210> 4526
<211> 344
<212> PRT
<213> Homo sapiens

<400> 4526
Xaa Asn His Gly Ile Leu Gln Ala Leu Thr Thr Glu Ala Tyr Glu Trp
1 5 10 15
Glu Pro Arg Val Val Ser Thr Glu Val Val Arg Ala Gln Glu Glu Trp
20 25 30
Glu Ala Val Asp Thr Ile Gln Pro Glu Thr Gly Ser Gln Ala Ser Ser
35 40 45
Glu Gln Pro Gly Gln Leu Ile Ser Phe Ser Glu Ala Leu Gln His Phe
50 55 60
Gln Thr Val Asp Leu Ser Pro Phe Lys Lys Arg Ile Gln Pro Thr Ile
65 70 75 80
Arg Arg Thr Gly Leu Ala Ala Leu Arg His Tyr Leu Phe Gly Pro Pro
85 90 95
Lys Leu His Gln Arg Leu Arg Glu Glu Arg Asp Leu Val Leu Thr Ile
100 105 110
Ala Gln Cys Gly Leu Asp Ser Gln Asp Pro Val His Gly Arg Val Leu
115 120 125
Gln Thr Ile Tyr Lys Lys Leu Thr Gly Ser Lys Phe Asp Cys Ala Leu
130 135 140
His Gly Asn His Trp Glu Asp Leu Gly Phe Gln Gly Ala Asn Pro Ala
145 150 155 160
Thr Asp Leu Arg Gly Ala Gly Phe Leu Ala Leu Leu His Leu Leu Tyr
165 170 175
Leu Val Met Asp Ser Lys Thr Leu Pro Met Ala Gln Glu Ile Phe Arg
180 185 190
Leu Ser Arg His His Ile Gln Gln Phe Pro Phe Cys Leu Met Ser Val
195 200 205
Asn Ile Thr His Ile Ala Ile Gln Ala Leu Arg Glu Glu Cys Leu Ser
210 215 220
Arg Glu Cys Asn Arg Gln Gln Lys Val Ile Pro Val Val Asn Ser Phe
225 230 235 240
Tyr Ala Ala Thr Phe Leu His Leu Ala His Val Trp Arg Thr Gln Arg
245 250 255
Lys Thr Ile Ser Asp Ser Gly Phe Val Leu Lys Gly Val Leu Phe Leu
260 265 270
Leu Gly Arg Pro Arg Leu Asn Ala Gln Cys Pro Arg Ser Arg Glu Pro
275 280 285
Lys Val Val Ala Arg Leu Val Leu Ala Ala Val Leu Pro His Pro His
290 295 300
Phe Leu Lys Phe Gln Leu Thr Lys Ile Ser Ile Thr His Pro Leu Glu
305 310 315 320
Ser Ala Ser Ser Pro Phe Ser Ala Leu Thr Val Ala Leu Phe Trp Ser
325 330 335
Tyr Thr Tyr Asp Lys His Ile Phe
340

<210> 4527
<211> 885
<212> DNA
<213> Homo sapiens

<400> 4527
nnttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttg cagagacatg
60

gctgcattta ttgttcccag cccggcgaga aggtgttccc agaaaggttc cttgggtcac
120
ctgcccaccc agccttggct ctgggctgcc atgtccccac gggggcagga gagaggcaca
180
agtcacagtc aggcaaggga gcctcagcgt cctgggcggt ggctgttggg gtccctccag
240
tcttcacctg ggaccctcgg ccaggctggg acagcatcca ggaggcgagg ctgcatggtc
300
cagcggtggg tgcaggtggc aacaggtcgg cgggctgtgc aggttccaaa aggagctctc
360
gggttggcac tgggtgagac cagccccggg gccagcaggg gaatgagcgg tggagcaggg
420
ggttgctggg cactggggtg ggccccatct cctgtccttc cctcatggct gctggaaggg
480
ccgcctccct ggctcagcat catctcagat tccgggactc aaacaccgtc tcctcgtcgc
540
tgtccagcga ggccatctcc gtggggtcct cagtgttggc gaggaggccg tatcgcctcc
600
gctgaggctt cttcaaccta aacgcccgga tcaggaagta gagcgcggtc aggccgcaga
660
agcccaggat cacgtagaag gagcgcgtca gcgccgagcc cgacgccccc ggcggacgcg
720
tgtgcgtgct gttgtgtggc gcgcccggct ggctcccgtt cgtcacggcc ggcggcggcg
780
acaacgtgac ctggcggggg cagcggcgag cctcttcggc accgcacggc agcgccgcca
840
gcagcagcgc cagcaggagc agcagcagcg gcggctgcag cacgc
885

<210> 4528
<211> 206
<212> PRT
<213> Homo sapiens

<400> 4528
Xaa Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe
1 5 10 15
Cys Arg Asp Met Ala Ala Phe Ile Val Pro Ser Pro Ala Arg Arg Cys
20 25 30
Ser Gln Lys Gly Ser Leu Gly His Leu Pro Thr Gln Pro Trp Leu Trp
35 40 45
Ala Ala Met Ser Pro Arg Gly Gln Glu Arg Gly Thr Ser His Ser Gln
50 55 60
Ala Arg Glu Pro Gln Arg Pro Gly Arg Trp Leu Leu Gly Ser Leu Gln
65 70 75 80
Ser Ser Pro Gly Thr Leu Gly Gln Ala Gly Thr Ala Ser Arg Arg Arg
85 90 95
Gly Cys Met Val Gln Arg Trp Val Gln Val Ala Thr Gly Arg Arg Ala
100 105 110
Val Gln Val Pro Lys Gly Ala Leu Gly Leu Ala Leu Gly Glu Thr Ser
115 120 125
Pro Gly Ala Ser Arg Gly Met Ser Gly Gly Ala Gly Gly Cys Trp Ala
130 135 140
Leu Gly Trp Ala Pro Ser Pro Val Leu Pro Ser Trp Leu Leu Glu Gly

```
145                 150                 155                 160
Pro Pro Pro Trp Leu Ser Ile Ile Ser Asp Ser Gly Thr Gln Thr Pro
                165                 170                 175
Ser Pro Arg Arg Cys Pro Ala Arg Pro Ser Pro Trp Gly Pro Gln Cys
            180                 185                 190
Trp Arg Gly Gly Arg Ile Ala Ser Ala Glu Ala Ser Ser Thr
        195                 200                 205
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<210> 4529
<211> 546
<212> DNA
<213> Homo sapiens

<400> 4529
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gtggccgccg cctaagctgc agccgccgga gccgcagaaa caagaggccg agccgtgtcg
120
aagatggagg agaaaccctc agggcccatc ccggacatgc tggccactgc agagcccagc
180
tccagtgaga ccgacaagga ggtgttgtcc ccggctgtgc cagctgcagc ccctcctcc
240
tccatgtcgg aggagccagg ccctgagcag gcagccacac cgccagtggg gaacgtggag
300
gggctggagg gatgcagcag ggctcctccc cagccccaga cagctgccag tctggccccg
360
gacccagccc tggcctgacc agcatagtct ccgggaccag cgaggacctg cggcctccca
420
gacgacgccc acctccaggg aagcaaatcc cttgctccag ccctggctgc tgcctcagtt
480
ttcccagcgt ccgtgacctg gcacagcatc tgcgaaccca ctgcccgccg agccctatgc
540
agtctc
546

<210> 4530
<211> 84
<212> PRT
<213> Homo sapiens

<400> 4530

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Met Glu Glu Lys Pro Ser Gly Pro Ile Pro Asp Met Leu Ala Thr Ala
 1               5                  10                  15
Glu Pro Ser Ser Ser Glu Thr Asp Lys Glu Val Leu Ser Pro Ala Val
            20                  25                  30
Pro Ala Ala Ala Pro Ser Ser Ser Met Ser Glu Glu Pro Gly Pro Glu
        35                  40                  45
Gln Ala Ala Thr Pro Pro Val Gly Asn Val Glu Gly Leu Glu Gly Cys
    50                  55                  60
Ser Arg Ala Pro Pro Gln Pro Gln Thr Ala Ala Ser Leu Ala Pro Asp
65                  70                  75                  80
Pro Ala Leu Ala
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<210> 4531
<211> 1414
<212> DNA
<213> Homo sapiens

<400> 4531
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60
gccggtccct tgcagggcgg tggggcccgg gccctggacc tactccgggg cctgccgcgt
120
gtgagcctgg ccaacttaaa gccgaatccc ggctccaaga aaccggagag aagaccaaga
180
ggtcggagaa gaggtagaaa atgtggcaga ggccataaag gagaaaggca aagaggaacc
240
cggccccgct tgggctttga gggaggccag actccatttt acatccgaat cccaaaatac
300
gggtttaacg aaggacatag tttcagacgc cagtataagc ctttgagtct caatagactg
360
cagtatctta ttgatttggg tcgtgttgat cctagtcaac ctattgactt aacccagctt
420
gtcaatggga gaggtgtgac catccagcca cttaaaaggg attatggtgt ccagctggtt
480
gaggagggtg ctgacacctt tacggcaaaa gttaatattg aagtacagtt ggcttcagaa
540
ctagctattg ctgccattga aaaaaatggt ggtgttgtta ctacagcctt ctatgatcca
600
agaagtctgg acattgtatg caaacctgtt ccattctttc ttcgtggaca acccattcca
660
aaaagaatgc ttccaccaga agaactggta ccatattaca ctgatgcaaa gaaccgtggg
720
tacctggcgg atcctgccaa atttcctgaa gcacgacttg aactcgccag gaagtatggt
780
tatatcttac ctgatatcac taaagatgaa ctcttcaaaa tgctctgtac taggaaggat
840
ccaaggcaga ttttctttgg tcttgctcca ggatgggtgg tgaatatggc cgataagaaa
900
atcctaaaac ctacagatga aaatctcctt aagtattata cctcatgaat tcccgtccaa
960
ggaagcagag ttgttaaaga gtactggaat aggggctgaa ggatctatat tcccttattg
1020
cattttcctt atgtataatt ttccagatgg tgatgttact tttcagtgta ctcatatgtc
1080
tcattttcat ctaaaattaa atggcaggaa acaaggactg catagagaaa ctgagtctgt
1140
gtgggttctg tctcaaagat acaaactccc tgatagtcta tggaaggaaa atgacaacta
1200
ttttagaata tttctagttt gttttttcag tgatcttttc atccaggcct tgttactgtt
1260
acagatcaga atgaaatgca caagtggaat gggattgacc tgtaggcctg ctctgccgag
1320
atgagagcag atggaatgag ttggtgaccc ctcttaatct gtagcctcag ggaaacacgg
1380
ctacccaatg ccaagatggt aaaccctcac gcgt
1414

<210> 4532
<211> 296
<212> PRT
<213> Homo sapiens

<400> 4532
Met Ala Gly Pro Leu Gln Gly Gly Gly Ala Arg Ala Leu Asp Leu Leu
1 5 10 15
Arg Gly Leu Pro Arg Val Ser Leu Ala Asn Leu Lys Pro Asn Pro Gly
20 25 30
Ser Lys Lys Pro Glu Arg Arg Pro Arg Gly Arg Arg Arg Gly Arg Lys
35 40 45
Cys Gly Arg Gly His Lys Gly Glu Arg Gln Arg Gly Thr Arg Pro Arg
50 55 60
Leu Gly Phe Glu Gly Gly Gln Thr Pro Phe Tyr Ile Arg Ile Pro Lys
65 70 75 80
Tyr Gly Phe Asn Glu Gly His Ser Phe Arg Arg Gln Tyr Lys Pro Leu
85 90 95
Ser Leu Asn Arg Leu Gln Tyr Leu Ile Asp Leu Gly Arg Val Asp Pro
100 105 110
Ser Gln Pro Ile Asp Leu Thr Gln Leu Val Asn Gly Arg Gly Val Thr
115 120 125
Ile Gln Pro Leu Lys Arg Asp Tyr Gly Val Gln Leu Val Glu Glu Gly
130 135 140
Ala Asp Thr Phe Thr Ala Lys Val Asn Ile Glu Val Gln Leu Ala Ser
145 150 155 160
Glu Leu Ala Ile Ala Ala Ile Glu Lys Asn Gly Gly Val Val Thr Thr
165 170 175
Ala Phe Tyr Asp Pro Arg Ser Leu Asp Ile Val Cys Lys Pro Val Pro
180 185 190
Phe Phe Leu Arg Gly Gln Pro Ile Pro Lys Arg Met Leu Pro Pro Glu
195 200 205
Glu Leu Val Pro Tyr Tyr Thr Asp Ala Lys Asn Arg Gly Tyr Leu Ala
210 215 220
Asp Pro Ala Lys Phe Pro Glu Ala Arg Leu Glu Leu Ala Arg Lys Tyr
225 230 235 240
Gly Tyr Ile Leu Pro Asp Ile Thr Lys Asp Glu Leu Phe Lys Met Leu
245 250 255
Cys Thr Arg Lys Asp Pro Arg Gln Ile Phe Phe Gly Leu Ala Pro Gly
260 265 270
Trp Val Val Asn Met Ala Asp Lys Lys Ile Leu Lys Pro Thr Asp Glu
275 280 285
Asn Leu Leu Lys Tyr Tyr Thr Ser
290 295

<210> 4533
<211> 968
<212> DNA
<213> Homo sapiens

<400> 4533
acgcgtgccc agcacatgtg tgcacacgca gatgcaggag agaacacaca ccaccgtctc
60

tttgcacacg tgtgcccctg tccggacgcc ggggctgagg ccgatcgcgt cgggcagcgg
120
gcgcggcggc cccgcgcagc catggactgg ctcatgggga agtccaaagc caagcccaat
180
ggcaagaagc ccgctgcgga ggagaggaag gcctacctgg agcctgagca caccaaggcc
240
aggatcaccg acttccagtt caaggagctg gtggtgctgc cccgggagat cgacctcaac
300
gagtggctgg ccagcaacac aacaacattt ttccaccaca tcaacctgca gtatagcaca
360
atctcggagt tctgcacagg agagacgtgt cagacgatgg ccgtgtgcaa cacacagtac
420
tactggtatg acgagcgggg gaagaaggtc aagtgcacgg ccccacagta cgttgacttc
480
gtcatgagct ccgtgcagaa gctggtgacg gatgaggacg tgttccccac aaaatacggc
540
agagaattcc ccagctcctt tgagtccctg gtgaggaaga tctgcagaca cctgttccac
600
gtgctggcac acatctactg ggcccacttc aaggagacgc tggccctgga gctgcacgga
660
cacttgaaca cgctctacgt ccacttcatc ctctttgctc gggagttcaa cctgctggac
720
cccaaagaga ccgccatcat ggacgacctc accgaggtgc tatgcagcgg ggccggcggg
780
gtccacagtg ggggcagtgg ggatggggcc ggcagcgggg gcccgggagc acagaaccac
840
gtgaaggaga gatgagcccc ccgggccgga caggggcaca cgtgtgcaaa gagacggtgg
900
tgtgtgttct ctcctgcatc tgcgtgtgca cacatgtgct gggccctctc agacctcacc
960
acacgcgt
968

<210> 4534
<211> 284
<212> PRT
<213> Homo sapiens

<400> 4534
Thr Arg Ala Gln His Met Cys Ala His Ala Asp Ala Gly Glu Asn Thr
1 5 10 15
His His Arg Leu Phe Ala His Val Cys Pro Cys Pro Asp Ala Gly Ala
20 25 30
Glu Ala Asp Arg Val Gly Gln Arg Ala Arg Arg Pro Arg Ala Ala Met
35 40 45
Asp Trp Leu Met Gly Lys Ser Lys Ala Lys Pro Asn Gly Lys Lys Pro
50 55 60
Ala Ala Glu Glu Arg Lys Ala Tyr Leu Glu Pro Glu His Thr Lys Ala
65 70 75 80
Arg Ile Thr Asp Phe Gln Phe Lys Glu Leu Val Val Leu Pro Arg Glu
85 90 95
Ile Asp Leu Asn Glu Trp Leu Ala Ser Asn Thr Thr Thr Phe Phe His
100 105 110
His Ile Asn Leu Gln Tyr Ser Thr Ile Ser Glu Phe Cys Thr Gly Glu

```
        115                 120                 125
Thr Cys Gln Thr Met Ala Val Cys Asn Thr Gln Tyr Tyr Trp Tyr Asp
    130                 135                 140
Glu Arg Gly Lys Lys Val Lys Cys Thr Ala Pro Gln Tyr Val Asp Phe
145                 150                 155                 160
Val Met Ser Ser Val Gln Lys Leu Val Thr Asp Glu Asp Val Phe Pro
                165                 170                 175
Thr Lys Tyr Gly Arg Glu Phe Pro Ser Ser Phe Glu Ser Leu Val Arg
            180                 185                 190
Lys Ile Cys Arg His Leu Phe His Val Leu Ala His Ile Tyr Trp Ala
        195                 200                 205
His Phe Lys Glu Thr Leu Ala Leu Glu Leu His Gly His Leu Asn Thr
    210                 215                 220
Leu Tyr Val His Phe Ile Leu Phe Ala Arg Glu Phe Asn Leu Leu Asp
225                 230                 235                 240
Pro Lys Glu Thr Ala Ile Met Asp Asp Leu Thr Glu Val Leu Cys Ser
                245                 250                 255
Gly Ala Gly Gly Val His Ser Gly Gly Ser Gly Asp Gly Ala Gly Ser
            260                 265                 270
Gly Gly Pro Gly Ala Gln Asn His Val Lys Glu Arg
        275                 280
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<210> 4535
<211> 473
<212> DNA
<213> Homo sapiens

<400> 4535
cgacttttt ttttttttt ttttgagatg gagtctcgtt ctgtcaccca ggctggagtg
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cagtggcatg atcacagctc actgcaacct ctgcctccca ggttcaagca gttctctngc
120
ctcagcctcc cgagtagctg ggattacagg cgtccgccac cacgcccggc taatttttgt
180
atttttagta gaaacggggt ttcaccatct cggccaggct ggtcttgaac tcctgacctc
240
atgatccatc cgccttggcc tcccaaagtg ctgggattac aggcatgagc taccgcgccc
300
ggccttggct gcagattaac gggaatacct cccttgggct tcctaggtga cactgtgata
360
ttcggtatga cctcccttgc tctattcctt ggaagaagta caggcactgg tcaagagtgc
420
ccgggaccca cattgcctgg ttttgaatcc cagcacctcc acatgttacg cgt
473

<210> 4536
<211> 75
<212> PRT
<213> Homo sapiens

<400> 4536
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Arg Leu Phe Phe Phe Phe Phe Phe Glu Met Glu Ser Arg Ser Val Thr
 1               5                  10                  15
Gln Ala Gly Val Gln Trp His Asp His Ser Ser Leu Gln Pro Leu Pro
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```
            20                  25                  30
Pro Arg Phe Lys Gln Phe Ser Xaa Leu Ser Leu Pro Ser Ser Trp Asp
        35                  40                  45
Tyr Arg Arg Pro Pro Pro Arg Pro Ala Asn Phe Cys Ile Phe Ser Arg
    50                  55                  60
Asn Gly Val Ser Pro Ser Arg Pro Gly Trp Ser
65                  70                  75

<210> 4537
<211> 2811
<212> DNA
<213> Homo sapiens

<400> 4537
naagcttggc acgagggaaa tgaagcctgt gatttggact ccacagtgtc tgctcttgcc
60
ctggcttttt acctagcaaa gacaactgag gctgaggaag tctttgtgcc agttttaaat
120
ataaaacgtt ctgaactacc tctgcgaggt gacattgtct tctttcttca gaaggttcat
180
attccagaga gtatcttgat ttttcgggat gagattgacc tccatgcatt ataccaggct
240
ggccaactca ccctcatcct tgtcgaccat catatcttat ccaaaagtga cacagcccta
300
gaggagngca gtagcagagg tgctagacca tcgacccatc gagccgaaac actgccctcc
360
ctgnnccatg tttcagttga gctggtgggg tcctgtgcta ccctggtgac cgagagaatc
420
ctgcaggggg caccagagat cttggacagg caaactgcag cccttctgca tggaaccatc
480
atcctggact gtgtcaacat ggaccttaaa attggaaagg caaccccaaa ggacagcaaa
540
tatgtggaga aactagaggc ccttttccca gacctaccca agagaaatga tatatttgat
600
tccctacaaa aggcaaagtt tgatgtatca ggactgacca ctgagcagat gctgagaaaa
660
gaccagaaga ctatctatag acaaggcgtc aaggtggcca ttagtgcaat atatatggat
720
ttggaggcct ttctgcagag gtctaacctc cttgcagatc tccatgcttt ctgccaggct
780
cacagctatg atgtcctggt tgccatgact atctttttca acactcacaa tgagccagtg
840
cggcagttgg ctattttctg tccccatgtg gcactccaaa caacgatctg tgaagtcctg
900
gaacgctccc actctccacc cctgaagctg acccctgcct caagtaccca ccctaacctc
960
catgcctatc ttcaaggcaa cacccaggtc tctcgaaaga aacttctgcc cctgctccag
1020
gaagccctgt cagcatattt tgactccatg aagatccctt caggacagcc tgagacagca
1080
gatgtgtcca gggagcaagt ggacaaggaa ttggacaggg caagtaactc cctgatttct
1140
ggactgagtc aagatgagga ggaccctccg ctgcccccga cgcccatgaa cagcttggtg
1200
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gatgagtgcc ctctagatca ggggctgcct aaactctctg ctgaggccgt cttcgagaag
1260
tgcagtcaga tctcactgtc acagtctacc acagcctccc tgtccaagaa gtgactgttg
1320
agaggcgagg aggtagtggg tgaggctacc tgactcactt caaatgcatg ttttgagatg
1380
tttggagatt cagcaattct gtcttcattg ctccaggatc tggtatactg ttctcataaa
1440
actgagagga gaaaaaaagt gaaagaaagc agctgcttta agaatggttt tccacctttt
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1560
tatttgccag gggcacgatg tgacatatct gcagtcccag cacagtggga caaaaagaat
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ttagacccca aaagtgtcct cggcatggat cttgaacaga accagtatct gtcatggaac
1680
tgaacattca tcgatggtct ccatgtattc atttattcac ttgttcattc aagtatttat
1740
tgaatacctg cctcaagcta gagagaaaag agagtgcgct ttggaaattt attccagttt
1800
tcagcctaca gcagattatc agctcggtga cttttctttc tgccaccatt taggtgatgg
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gtttgggaac agattagagg ccattgtctt ctgtcctgat caggtggcct ggctgtttct
1980
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2160
ccttgctcac attaaaagga agcatggagt tctaatgctc ccataaacta tgtattttgg
2220
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2280
gtgttccctg gtattctgtg atctgcctct tgctgccatt ctttctctcc tctgcttctc
2340
tgtatttttc ttctgttatc cctgggggtg ctcaggttca cttgattgtc tgtatttctg
2400
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2460
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2520
ttttttaacg caacccttte ccctttttcc taccccacag ctctgttcca tgtaagttgc
2580
caacagtttc actgaacagt ggggtatgtg atggttttgg catgacatct tcagtatgag
2640
ggggacagtt tgacttcact ttgagggtgt gatgtctgta gctatgtgga aggtaaaaat
2700
agtggtgtga tcatgaacca aaggaattta tgttttgtaa cttgggtact ttattttgca
2760
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2811

<210> 4538
<211> 437
<212> PRT
<213> Homo sapiens

<400> 4538
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Ser Ala Leu Ala Leu Ala Phe Tyr Leu Ala Lys Thr Thr Glu Ala Glu
20 25 30
Glu Val Phe Val Pro Val Leu Asn Ile Lys Arg Ser Glu Leu Pro Leu
35 40 45
Arg Gly Asp Ile Val Phe Phe Leu Gln Lys Val His Ile Pro Glu Ser
50 55 60
Ile Leu Ile Phe Arg Asp Glu Ile Asp Leu His Ala Leu Tyr Gln Ala
65 70 75 80
Gly Gln Leu Thr Leu Ile Leu Val Asp His His Ile Leu Ser Lys Ser
85 90 95
Asp Thr Ala Leu Glu Glu Xaa Ser Ser Arg Gly Ala Arg Pro Ser Thr
100 105 110
His Arg Ala Glu Thr Leu Pro Ser Leu Xaa His Val Ser Val Glu Leu
115 120 125
Val Gly Ser Cys Ala Thr Leu Val Thr Glu Arg Ile Leu Gln Gly Ala
130 135 140
Pro Glu Ile Leu Asp Arg Gln Thr Ala Ala Leu Leu His Gly Thr Ile
145 150 155 160
Ile Leu Asp Cys Val Asn Met Asp Leu Lys Ile Gly Lys Ala Thr Pro
165 170 175
Lys Asp Ser Lys Tyr Val Glu Lys Leu Glu Ala Leu Phe Pro Asp Leu
180 185 190
Pro Lys Arg Asn Asp Ile Phe Asp Ser Leu Gln Lys Ala Lys Phe Asp
195 200 205
Val Ser Gly Leu Thr Thr Glu Gln Met Leu Arg Lys Asp Gln Lys Thr
210 215 220
Ile Tyr Arg Gln Gly Val Lys Val Ala Ile Ser Ala Ile Tyr Met Asp
225 230 235 240
Leu Glu Ala Phe Leu Gln Arg Ser Asn Leu Leu Ala Asp Leu His Ala
245 250 255
Phe Cys Gln Ala His Ser Tyr Asp Val Leu Val Ala Met Thr Ile Phe
260 265 270
Phe Asn Thr His Asn Glu Pro Val Arg Gln Leu Ala Ile Phe Cys Pro
275 280 285
His Val Ala Leu Gln Thr Thr Ile Cys Glu Val Leu Glu Arg Ser His
290 295 300
Ser Pro Pro Leu Lys Leu Thr Pro Ala Ser Ser Thr His Pro Asn Leu
305 310 315 320
His Ala Tyr Leu Gln Gly Asn Thr Gln Val Ser Arg Lys Lys Leu Leu
325 330 335
Pro Leu Leu Gln Glu Ala Leu Ser Ala Tyr Phe Asp Ser Met Lys Ile
340 345 350
Pro Ser Gly Gln Pro Glu Thr Ala Asp Val Ser Arg Glu Gln Val Asp
355 360 365
Lys Glu Leu Asp Arg Ala Ser Asn Ser Leu Ile Ser Gly Leu Ser Gln

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    370                 375                 380
Asp Glu Glu Asp Pro Pro Leu Pro Pro Thr Pro Met Asn Ser Leu Val
385                 390                 395                 400
Asp Glu Cys Pro Leu Asp Gln Gly Leu Pro Lys Leu Ser Ala Glu Ala
                405                 410                 415
Val Phe Glu Lys Cys Ser Gln Ile Ser Leu Ser Gln Ser Thr Thr Ala
            420                 425                 430
Ser Leu Ser Lys Lys
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<210> 4539
<211> 331
<212> DNA
<213> Homo sapiens

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120
tcacctggaa actccagcaa gagcagaggc aggtggagga gctgaggatg cagcttcaga
180
agcagaaaag gaataactgt tcagagaaga agccgctgcc tttcctggct gcctccatca
240
agcaagaaga ggctgtctcc agctgtcctt ttgcatccca agtacctgtg aaaagacaaa
300
gcagcagctc aaagtgtcac ccaccggctt g
331

<210> 4540
<211> 99
<212> PRT
<213> Homo sapiens

<400> 4540
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Met Gly Ala Leu Phe Leu Leu Ser Trp Met Gly Trp Thr Pro Arg Lys
 1               5                  10                  15
Thr Arg Ser Leu Gly Glu Asn Gln Arg Val Ile Asn Glu Leu Thr Trp
            20                  25                  30
Lys Leu Gln Gln Glu Gln Arg Gln Val Glu Glu Leu Arg Met Gln Leu
        35                  40                  45
Gln Lys Gln Lys Arg Asn Asn Cys Ser Glu Lys Lys Pro Leu Pro Phe
    50                  55                  60
Leu Ala Ala Ser Ile Lys Gln Glu Glu Ala Val Ser Ser Cys Pro Phe
65                  70                  75                  80
Ala Ser Gln Val Pro Val Lys Arg Gln Ser Ser Ser Ser Lys Cys His
                85                  90                  95
Pro Pro Ala
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<210> 4541
<211> 452
<212> DNA
<213> Homo sapiens

<400> 4541
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cacaggcaga tccagggatg taactgcttc agcaagaact gttgcgaatc ccttcgctgt
120
tccagtctga gaaccataaa aaatcttcac tccagacaca aagatgtctt tctcttgaag
180
ggagacataa ccatttgtca tcaaatcctg agctgctttt ggaacagatt tttcctgtaa
240
gttcttgccc tgcgtcttga tgacaatctg gacacaaatc caaaggctaa tgctaacagc
300
aaagcccaaa taaatgtaaa acctgtttat ccacaatgat attaaaggtg agaagaggtc
360
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420
ctggagagcc cgatgattcg cactggtact gc
452

<210> 4542
<211> 128
<212> PRT
<213> Homo sapiens

<400> 4542
Met Asp Pro Ser Ala Asp Thr Trp Asp Leu Phe Ser Pro Leu Ile Ser
1 5 10 15
Leu Trp Ile Asn Arg Phe Tyr Ile Tyr Leu Gly Phe Ala Val Ser Ile
20 25 30
Ser Leu Trp Ile Cys Val Gln Ile Val Ile Lys Thr Gln Gly Lys Asn
35 40 45
Leu Gln Glu Lys Ser Val Pro Lys Ala Ala Gln Asp Leu Met Thr Asn
50 55 60
Gly Tyr Val Ser Leu Gln Glu Lys Asp Ile Phe Val Ser Gly Val Lys
65 70 75 80
Ile Phe Tyr Gly Ser Gln Thr Gly Thr Ala Lys Gly Phe Ala Thr Val
85 90 95
Leu Ala Glu Ala Val Thr Ser Leu Asp Leu Pro Val Ala Ile Ile Asn
100 105 110
Leu Lys Glu Tyr Asp Pro Asp Asp His Leu Ile Glu Glu Val Thr Ser
115 120 125

<210> 4543
<211> 815
<212> DNA
<213> Homo sapiens

<400> 4543
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agggaggagg gagagcgagt cactgcaggt ccctggcctg cggctccgcc gtggctgcct
120
gaggccccgc gcaccaatgc tttgcacttt gcctcgcccg acaccctgcg ggccagagct
180

cctctgccgc ccaccgggct aacccttccg ggcctcacca ctcccgagtg gctctgctta
240
tccggccact gactccggct cctcggaagc agggccaccc tcctgaaatg gcttggaacg
300
gggctttcca ctggtgccct ccccagacga ttgcttgtaa tgggccagtg cctcgccagg
360
gacacagcgg cagccccctg tagcttgtgg ctgttcagaa acaagtccag cccaggtagg
420
gcagagggct ctgactgggg acccaagaag ggctggctgt gccgccaccg ctgccccgtc
480
accatcactg tgctgaagag ctcgaggctg ggcccacccg cgccggcccc acgttcctcc
540
ccgggctcag gtcagggcca gggagtgacc agaaggtgct gaccctgtgg cctgactggc
600
ccagagctca cccctgaaca tgagcaagcg caaagaaacc cccatccctg ctcccaaaaa
660
agggcgcccc caaggccatt ttgaaggtgg ggggaagccc ggattccgag aaaccgcaac
720
cagccgtcta cctcaggaag ctcgctaggg aggagcgcat tctatgtgac taatgcggac
780
tggcctgcac cgcctacgga gagaagacaa cgcgt
815

<210> 4544
<211> 150
<212> PRT
<213> Homo sapiens

<400> 4544
Met Val Thr Gly Gln Arg Trp Arg His Ser Gln Pro Phe Leu Gly Pro
 1   5   10   15
Gln Ser Glu Pro Ser Ala Leu Pro Gly Leu Asp Leu Phe Leu Asn Ser
            20   25   30
His Lys Leu Gln Gly Ala Ala Ala Val Ser Leu Ala Arg His Trp Pro
        35   40   45
Ile Thr Ser Asn Arg Leu Gly Arg Ala Pro Val Glu Ser Pro Val Pro
    50   55   60
Ser His Phe Arg Arg Val Ala Leu Leu Pro Arg Ser Arg Ser Gln Trp
65   70   75   80
Pro Asp Lys Gln Ser His Ser Gly Val Val Arg Pro Gly Arg Val Ser
                85   90   95
Pro Val Gly Gly Arg Gly Ala Leu Ala Arg Arg Val Ser Gly Glu Ala
            100   105   110
Lys Cys Lys Ala Leu Val Arg Gly Ala Ser Gly Ser His Gly Gly Ala
        115   120   125
Ala Gly Gln Gly Pro Ala Val Thr Arg Ser Pro Ser Ser Leu Cys Leu
    130   135   140
Ala Leu Val Ser Thr Gly
145   150

<210> 4545
<211> 3568
<212> DNA
<213> Homo sapiens

<400> 4545
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tcaaagagtc agtcagaaga acaggaagag cctgctaaaa ctgatcaggc tgtcagcaaa
120
gacagaaatg cagaggagaa aaagcgttta tctcttcagc gagaaaagat tatcgcaagg
180
gtgagtattg ataacaggac ccgggcatta gttcaggcat taagaagaac aactgaccca
240
aagctctgca ttactagggt tgaagaactg acttttcatc ttctagaatt tcctgaagga
300
aaaggagtgg ctgtcaagga aagaattatt ccatatttat tacgactgag acaaattaag
360
gatgaaactc ttcaggctgc agttagagaa attttggccc taattggcta tgtggatcca
420
gtgaaaggga gaggaatccg aattctctca attgatggtg gaggaacaag gggcgtggtt
480
gctctccaga ccctacgaaa attagttgaa cttactcaga agccagttca tcagctcttt
540
gattacattt gtggtgtaag cacaggtgcc atattagctt tcatgttggg gttgtttcat
600
atgcccttgg atgaatgtga ggaactttat cgaaaattag gatcagatgt attttcacaa
660
aatgtcattg ttggaacagt aaaaatgagt tggagccatg cattttatga cagtcaaaca
720
tgggaaaaca ttcttaagga taggatggga tctgcactga tgattgaaac agcaagaaac
780
cccacatgtc ctaaggtagc tgctgtaagt accatagtaa atagagggat aacacccaaa
840
gcttttgtgt tcagaaacta tggtcatttt cctggaatca actctcatta tttgggaggc
900
tgtcagtata aaatgtggca ggccattaga gcctcatctg ctgctccagg ctactttgca
960
gaatatgcat tgggaaatga tcttcatcaa gatggaggtt tgcttctgaa taacccttcg
1020
gcattagcta tgcatgagtg taaatgtctt tggccagatg tgccgttaga gtgcatagta
1080
tccctgggca ctggacgtta tgagagtgat gtgagaaaca cggtaacata cacaagcttg
1140
aaaactaaac tttctaatgt tatcaacagt gctacagata cagaagaagt ccatataatg
1200
cttgatggcc tgttacctcc tgacacctat tttagattca atcctgtaat gtgtgaaaac
1260
atacctctag atgaaagtcg aaatgaaaag ctggatcagc tgcagttgga agggttgaaa
1320
tacatagaaa gaaatgaaca aaaaatgaaa aaagttgcaa aaatattaag tcaagaaaaa
1380
acaactctgc agaaaattaa tgattggata aaattaaaaa ctgatatgta tgaaggactt
1440
ccattctttt caaaattgtg atgagtatat gcttatgttc tcataaatga aggtctgttt
1500
agaagatcaa ccacattcaa taaggaattg tggggttcga catgagttaa ctttgaaata
1560

cgtatgaatt ctggagaatc ctgaaaaaga cggtgcttca accagcttgc atagcacaga
1620
gaatattctt ggttacagaa ttcatatggg aactaggctt ttaagatgtt aataattagc
1680
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1740
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1920
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1980
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2100
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2160
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2220
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2280
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2340
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2400
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2700
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2940
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3000
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3060
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3120
aagaaattat attcaggcat attaagcatt gagtgtcatt attattgatg tataatggat
3180

tcccatccaa cattatggtg tgattttaaa agaagagcca ggaaatcaaa agtattttct
3240
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3300
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3360
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3420
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3480
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3568

<210> 4546
<211> 380
<212> PRT
<213> Homo sapiens

<400> 4546
Glu Arg Ile Ile Pro Tyr Leu Leu Arg Leu Arg Gln Ile Lys Asp Glu
1 5 10 15
Thr Leu Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly Tyr Val
20 25 30
Asp Pro Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp Gly Gly
35 40 45
Gly Thr Arg Gly Val Val Ala Leu Gln Thr Leu Arg Lys Leu Val Glu
50 55 60
Leu Thr Gln Lys Pro Val His Gln Leu Phe Asp Tyr Ile Cys Gly Val
65 70 75 80
Ser Thr Gly Ala Ile Leu Ala Phe Met Leu Gly Leu Phe His Met Pro
85 90 95
Leu Asp Glu Cys Glu Glu Leu Tyr Arg Lys Leu Gly Ser Asp Val Phe
100 105 110
Ser Gln Asn Val Ile Val Gly Thr Val Lys Met Ser Trp Ser His Ala
115 120 125
Phe Tyr Asp Ser Gln Thr Trp Glu Asn Ile Leu Lys Asp Arg Met Gly
130 135 140
Ser Ala Leu Met Ile Glu Thr Ala Arg Asn Pro Thr Cys Pro Lys Val
145 150 155 160
Ala Ala Val Ser Thr Ile Val Asn Arg Gly Ile Thr Pro Lys Ala Phe
165 170 175
Val Phe Arg Asn Tyr Gly His Phe Pro Gly Ile Asn Ser His Tyr Leu
180 185 190
Gly Gly Cys Gln Tyr Lys Met Trp Gln Ala Ile Arg Ala Ser Ser Ala
195 200 205
Ala Pro Gly Tyr Phe Ala Glu Tyr Ala Leu Gly Asn Asp Leu His Gln
210 215 220
Asp Gly Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met His Glu
225 230 235 240
Cys Lys Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val Ser Leu
245 250 255
Gly Thr Gly Arg Tyr Glu Ser Asp Val Arg Asn Thr Val Thr Tyr Thr

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            260                 265                 270
Ser Leu Lys Thr Lys Leu Ser Asn Val Ile Asn Ser Ala Thr Asp Thr
        275                 280                 285
Glu Glu Val His Ile Met Leu Asp Gly Leu Leu Pro Pro Asp Thr Tyr
    290                 295                 300
Phe Arg Phe Asn Pro Val Met Cys Glu Asn Ile Pro Leu Asp Glu Ser
305                 310                 315                 320
Arg Asn Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys Tyr Ile
                325                 330                 335
Glu Arg Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu Ser Gln
            340                 345                 350
Glu Lys Thr Thr Leu Gln Lys Ile Asn Asp Trp Ile Lys Leu Lys Thr
        355                 360                 365
Asp Met Tyr Glu Gly Leu Pro Phe Phe Ser Lys Leu
    370                 375                 380
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<210> 4547
<211> 2211
<212> DNA
<213> Homo sapiens

<400> 4547
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120
cacagttcga cgaatcggca tggtgctatc ttctaccttc tctgagctcg gcggctggga
180
ctggaggaca gcggtggcgg aggcgactag cggcggcggg agcggcgccg agaggccgtg
240
cgggacgcgg gcgccaggac cggccgaacg cagaggttga ttcttcacca cactgaaacc
300
attaggaaaa atccttgtgg ttaacagcag aggcttcaga gtgtaacctg tactcgggcc
360
tagaaattat ttaaaatggc gactgatacg tctcaaggtg aactcgtcca tcctaaggca
420
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480
gatagcacca tgccgattcg tcgaactgtg aattctaccc gggaaactcc tcccaaaagc
540
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660
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720
aaggatgaga aagatcagtc taaagaaaag gagaagaaag tgaaaaaaac aattccttcc
780
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840
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900
agtggtgcat cagtggttgc tattcgaaaa tacatcatcc ataagtatcc ttctctggag
960

ctggagagaa ggggttatct ccttaaacaa gcactgaaaa gagaattaaa tagaggagtc
1020
atcaaacagg tattacacaa tgttaaagga aaaggtgctt ctggaagttt tgttgtggtt
1080
cagaaatcaa gaaaaacacc tcagaaatcc agaaacagaa agaataggag ctctgcagtg
1140
gatccagaac cacaagtaaa attggaggat gtcctcccac tggcctttac tcgcctttgt
1200
gaacctaaag aagcttccta cagtctcatc aggaaatatg tgtctcagta ttatcctaag
1260
cttagagtgg acatcaggcc tcagctgttg aagaacgctc tgcagagagc agtagagagg
1320
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1500
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1560
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1620
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1800
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1920
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1980
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2040
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2100
aggtcagtgt gcatttgttt agttttgatg cttttcaaat tacattattt tcctccccta
2160
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2211

<210> 4548
<211> 515
<212> PRT
<213> Homo sapiens

<400> 4548
Arg Thr Val Asn Ser Thr Arg Glu Thr Pro Pro Lys Ser Lys Leu Ala
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Glu Gly Glu Glu Glu Lys Pro Glu Pro Asp Ile Ser Ser Glu Glu Ser
 20 25 30
Val Ser Thr Val Glu Glu Gln Glu Asn Glu Thr Pro Pro Ala Thr Ser

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        35                  40                  45
Ser Glu Ala Glu Gln Pro Lys Gly Glu Pro Glu Asn Glu Glu Lys Glu
    50                  55                  60
Glu Asn Lys Ser Ser Glu Glu Thr Lys Lys Asp Glu Lys Asp Gln Ser
65                  70                  75                  80
Lys Glu Lys Glu Lys Lys Val Lys Lys Thr Ile Pro Ser Trp Ala Thr
                85                  90                  95
Leu Ser Ala Ser Gln Leu Ala Arg Ala Gln Lys Gln Thr Pro Met Ala
            100                 105                 110
Ser Ser Pro Arg Pro Lys Met Asp Ala Ile Leu Thr Glu Ala Ile Lys
        115                 120                 125
Ala Cys Phe Gln Lys Ser Gly Ala Ser Val Val Ala Ile Arg Lys Tyr
    130                 135                 140
Ile Ile His Lys Tyr Pro Ser Leu Glu Leu Glu Arg Arg Gly Tyr Leu
145                 150                 155                 160
Leu Lys Gln Ala Leu Lys Arg Glu Leu Asn Arg Gly Val Ile Lys Gln
                165                 170                 175
Val Leu His Asn Val Lys Gly Lys Gly Ala Ser Gly Ser Phe Val Val
            180                 185                 190
Val Gln Lys Ser Arg Lys Thr Pro Gln Lys Ser Arg Asn Arg Lys Asn
        195                 200                 205
Arg Ser Ser Ala Val Asp Pro Glu Pro Gln Val Lys Leu Glu Asp Val
    210                 215                 220
Leu Pro Leu Ala Phe Thr Arg Leu Cys Glu Pro Lys Glu Ala Ser Tyr
225                 230                 235                 240
Ser Leu Ile Arg Lys Tyr Val Ser Gln Tyr Tyr Pro Lys Leu Arg Val
                245                 250                 255
Asp Ile Arg Pro Gln Leu Leu Lys Asn Ala Leu Gln Arg Ala Val Glu
            260                 265                 270
Arg Gly Gln Leu Glu Gln Ile Thr Gly Lys Gly Ala Ser Gly Thr Phe
        275                 280                 285
Gln Leu Lys Lys Ser Gly Glu Lys Pro Leu Leu Gly Gly Ser Leu Met
    290                 295                 300
Glu Tyr Ala Ile Leu Ser Ala Ile Ala Ala Met Asn Glu Pro Lys Thr
305                 310                 315                 320
Cys Ser Thr Thr Ala Leu Lys Lys Tyr Val Leu Glu Asn His Pro Gly
                325                 330                 335
Thr Asn Ser Asn Tyr Gln Met His Leu Leu Lys Lys Thr Leu Gln Lys
            340                 345                 350
Cys Glu Lys Asn Gly Trp Met Glu Gln Ile Ser Gly Lys Gly Phe Ser
        355                 360                 365
Gly Thr Phe Gln Leu Cys Phe Pro Tyr Tyr Pro Ser Pro Gly Val Leu
    370                 375                 380
Phe Pro Lys Lys Glu Pro Asp Asp Ser Arg Asp Glu Asp Glu Asp Glu
385                 390                 395                 400
Asp Glu Ser Ser Glu Glu Asp Ser Glu Asp Glu Glu Pro Pro Pro Lys
                405                 410                 415
Arg Arg Leu Gln Lys Lys Thr Pro Ala Lys Ser Pro Gly Lys Ala Ala
            420                 425                 430
Ser Val Lys Gln Arg Gly Ser Lys Pro Ala Pro Lys Val Ser Ala Ala
        435                 440                 445
Gln Arg Gly Lys Ala Arg Pro Leu Pro Lys Lys Ala Pro Pro Lys Ala
    450                 455                 460
Lys Thr Pro Ala Lys Lys Thr Arg Pro Ser Ser Thr Val Ile Lys Lys
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465                 470                 475                 480
Pro Ser Gly Gly Ser Ser Lys Lys Pro Ala Thr Ser Ala Arg Lys Glu
                485                 490                 495
Val Lys Leu Pro Gly Lys Gly Lys Ser Thr Met Lys Lys Ser Phe Arg
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Val Lys Lys
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<210> 4549
<211> 2927
<212> DNA
<213> Homo sapiens

<400> 4549
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120
ggggagacca acttgaagtt cagacaggcc ctgatggtca cccacaaaga actggccact
180
ataaagaaga tggcgtcctt tcaaggcaca gtgacgtgtg aggcgcctaa cagtcggatg
240
caccacttcg tggggtgcct ggaatggaat gacaagaaat actccctgga cattggcaac
300
ctcctcctcc gaggctgcag gattcgcaac acagacacct gctatggact ggtcatttat
360
gctgatggat acatgtttgt aggttttgac acaaaaatta tgaagaactg tggcaagatc
420
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480
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540
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660
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720
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780
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840
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900
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960
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1020
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1080
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1140
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1200

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1260
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1320
gcccaggaga ccctgcggac actgtgcctg gcctacaggg aggtggctga ggacatttac
1380
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2160
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2280
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2340
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2640
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2700
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2760
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2820

aggagctacg tgccaaggtg aggtgggcct gggcctgggg tcctcatctg gtacattcca
2880
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2927

<210> 4550
<211> 908
<212> PRT
<213> Homo sapiens

<400> 4550
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Pro Ala Asp Met Leu Leu Leu Ala Ser Thr Glu Pro Ser Ser Leu Cys
20 25 30
Tyr Val Glu Thr Val Asp Ile Asp Gly Glu Thr Asn Leu Lys Phe Arg
35 40 45
Gln Ala Leu Met Val Thr His Lys Glu Leu Ala Thr Ile Lys Lys Met
50 55 60
Ala Ser Phe Gln Gly Thr Val Thr Cys Glu Ala Pro Asn Ser Arg Met
65 70 75 80
His His Phe Val Gly Cys Leu Glu Trp Asn Asp Lys Lys Tyr Ser Leu
85 90 95
Asp Ile Gly Asn Leu Leu Leu Arg Gly Cys Arg Ile Arg Asn Thr Asp
100 105 110
Thr Cys Tyr Gly Leu Val Ile Tyr Ala Asp Gly Tyr Met Phe Val Gly
115 120 125
Phe Asp Thr Lys Ile Met Lys Asn Cys Gly Lys Ile His Leu Lys Arg
130 135 140
Thr Lys Leu Asp Leu Leu Met Asn Lys Leu Val Val Val Ile Phe Ile
145 150 155 160
Ser Val Val Leu Val Cys Leu Val Leu Ala Phe Gly Phe Gly Phe Ser
165 170 175
Val Lys Glu Phe Lys Asp His His Tyr Tyr Leu Ser Gly Val His Gly
180 185 190
Ser Ser Val Ala Ala Glu Ser Phe Phe Val Phe Trp Ser Phe Leu Ile
195 200 205
Leu Leu Ser Val Thr Ile Pro Met Ser Met Phe Ile Leu Ser Glu Phe
210 215 220
Ile Tyr Leu Gly Asn Ser Val Phe Ile Asp Trp Asp Val Gln Met Tyr
225 230 235 240
Tyr Lys Pro Gln Asp Val Pro Ala Lys Ala Arg Ser Thr Ser Leu Asn
245 250 255
Asp His Leu Gly Gln Val Glu Tyr Ile Phe Ser Asp Lys Thr Gly Thr
260 265 270
Leu Thr Gln Asn Ile Leu Thr Phe Asn Lys Cys Cys Ile Ser Gly Arg
275 280 285
Val Tyr Gly Glu Pro Leu Pro Leu Glu Gln Val Arg Arg Arg Glu Ala
290 295 300
Ala Leu Pro Gln Cys Gly Pro Ala Ala Pro Arg Ala Asp Gln Arg Gly
305 310 315 320
Arg Gly Arg Ala Gly Val Leu Ala Pro Ala Gly His Leu Pro His Gly
325 330 335
Asp Asp Gln Leu Leu Tyr Gln Ala Ala Ser Pro Asp Glu Gly Ala Leu

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            340                 345                 350
Val Thr Ala Ala Arg Asn Phe Gly Tyr Val Phe Leu Ser Arg Thr Gln
        355                 360                 365
Asp Thr Val Thr Ile Met Glu Leu Gly Glu Glu Arg Val Tyr Gln Val
    370                 375                 380
Leu Ala Ile Met Asp Phe Asn Ser Thr Arg Lys Arg Met Ser Val Leu
385                 390                 395                 400
Val Arg Lys Pro Glu Gly Ala Ile Cys Leu Tyr Thr Lys Gly Ala Asp
                405                 410                 415
Thr Val Ile Phe Glu Arg Leu His Arg Arg Gly Ala Met Glu Phe Ala
            420                 425                 430
Thr Glu Glu Ala Leu Ala Ala Phe Ala Gln Glu Thr Leu Arg Thr Leu
        435                 440                 445
Cys Leu Ala Tyr Arg Glu Val Ala Glu Asp Ile Tyr Glu Asp Trp Gln
    450                 455                 460
Gln Arg His Gln Glu Ala Ser Leu Leu Leu Gln Asn Arg Ala Gln Ala
465                 470                 475                 480
Leu Gln Gln Val Tyr Asn Glu Met Glu Gln Asp Leu Arg Leu Leu Gly
                485                 490                 495
Ala Thr Ala Ile Glu Asp Arg Leu Gln Asp Gly Val Pro Glu Thr Ile
            500                 505                 510
Lys Cys Leu Lys Lys Ser Asn Ile Lys Ile Trp Val Leu Thr Gly Asp
        515                 520                 525
Lys Gln Glu Thr Ala Val Asn Ile Gly Phe Ala Cys Glu Leu Leu Ser
    530                 535                 540
Glu Asn Met Leu Ile Leu Glu Glu Lys Glu Ile Ser Arg Ile Leu Glu
545                 550                 555                 560
Thr Tyr Trp Glu Asn Ser Asn Asn Leu Leu Thr Arg Glu Ser Leu Ser
                565                 570                 575
Gln Val Lys Leu Ala Leu Val Ile Asn Gly Asp Phe Leu Asp Lys Leu
            580                 585                 590
Leu Val Ser Leu Arg Lys Glu Pro Arg Ala Leu Ala Gln Asn Val Asn
        595                 600                 605
Met Asp Glu Ala Trp Gln Glu Leu Gly Gln Ser Arg Arg Asp Phe Leu
    610                 615                 620
Tyr Ala Arg Arg Leu Ser Leu Leu Cys Arg Arg Phe Gly Leu Pro Leu
625                 630                 635                 640
Ala Ala Pro Pro Ala Gln Asp Ser Arg Ala Arg Arg Ser Ser Glu Val
                645                 650                 655
Leu Gln Glu Arg Ala Phe Val Asp Leu Ala Ser Lys Cys Gln Ala Val
            660                 665                 670
Ile Cys Cys Arg Val Thr Pro Lys Gln Lys Ala Leu Ile Val Ala Leu
        675                 680                 685
Val Lys Lys Tyr His Gln Val Val Thr Leu Ala Ile Gly Asp Gly Ala
    690                 695                 700
Asn Asp Ile Asn Met Ile Lys Thr Ala Asp Val Gly Val Gly Leu Ala
705                 710                 715                 720
Gly Gln Glu Gly Met Gln Ala Val Gln Asn Ser Asp Phe Val Leu Gly
                725                 730                 735
Gln Phe Cys Phe Leu Gln Arg Leu Leu Leu Val His Gly Arg Trp Ser
            740                 745                 750
Tyr Val Arg Ile Cys Lys Phe Leu Arg Tyr Phe Phe Tyr Lys Ser Met
        755                 760                 765
Ala Ser Met Met Val Gln Val Trp Phe Ala Cys Tyr Asn Gly Phe Thr
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    770                 775                 780
Gly Gln Asp Val Ser Ala Glu Gln Ser Leu Glu Lys Pro Glu Leu Tyr
785                 790                 795                 800
Val Val Gly Gln Lys Asp Glu Leu Phe Asn Tyr Trp Val Phe Val Gln
                805                 810                 815
Ala Ile Ala His Gly Val Thr Thr Ser Leu Val Asn Phe Phe Met Thr
            820                 825                 830
Leu Trp Ile Ser Arg Asp Thr Ala Gly Pro Ala Ser Phe Ser Asp His
        835                 840                 845
Gln Ser Phe Ala Val Val Val Ala Leu Ser Cys Leu Leu Ser Ile Thr
    850                 855                 860
Met Glu Val Ile Leu Ile Ile Lys Tyr Trp Thr Ala Leu Cys Val Ala
865                 870                 875                 880
Thr Ile Leu Leu Ser Leu Gly Phe Tyr Ala Ile Met Thr Thr Thr Thr
                885                 890                 895
Gln Ser Phe Trp Leu Phe Arg Met Pro Thr Ser Ala
            900                 905
```

<210> 4551
<211> 361
<212> DNA
<213> Homo sapiens

<400> 4551
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120
caggcagggg tggctttgcc tgtctcagag caggcctcag cagcacactg tccagtacca
180
ggcatcagtg agggtccaag aacttgcagc cagcagggac gacagggcag ggcccccagg
240
agagacccca cacagcgcac atgggagagt ggatgccaaa ggtgggcagc ggggagggcg
300
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360
c
361

<210> 4552
<211> 100
<212> PRT
<213> Homo sapiens

<400> 4552
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Met Glu Gly Pro Ser Val Arg Val Arg Thr Gly Gly Arg Gly Ser Arg
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Ala Leu Gln Gly Gln Ala Gly Val Ala Leu Pro Val Ser Glu Gln Ala
            20                  25                  30
Ser Ala Ala His Cys Pro Val Pro Gly Ile Ser Glu Gly Pro Arg Thr
        35                  40                  45
Cys Ser Gln Gln Gly Arg Gln Gly Arg Ala Pro Arg Arg Asp Pro Thr
    50                  55                  60
Gln Arg Thr Trp Glu Ser Gly Cys Gln Arg Trp Ala Ala Gly Arg Ala
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65 70 75 80
Pro Ala Lys Gln Ser Leu Cys Gly Val Pro His Ala Ala Glu Val Ser
85 90 95
Val Arg Cys Trp
100

<210> 4553
<211> 2970
<212> DNA
<213> Homo sapiens

<400> 4553
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120
tgcaattgtg gcactggcac ttatttcagt gaagaaaaac tttgtggttc tatggcattc
180
atcatttgac aaatgcaagc atcttcctta tcaatcagct cctattgaac ttactagcac
240
tgactgtgga atccttaagg gcccattaca tttctgaaga agaaagctaa gatgaaggac
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360
gataaaaaag tggattgtcc acggttatgt acgtgtgaaa tcaggccttg gtttacaccc
420
agatccattt atatggaagc atctacagtg gattgtaatg atttaggtct tttaactttc
480
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540
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600
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660
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720
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780
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840
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900
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960
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1020
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1080
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1140
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1200
gctgtggata acctgccaga tttaagaaaa atagaagcta ctaacaaccc tagattgtct
1260

tacattcacc ccaatgcatt tttcagactc cccaagctgg aatcactcat gctgaacagc
1320
aatgctctca gtgccctgta ccatggtacc attgagtctc tgccaaacct caaggaaatc
1380
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1440
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1680
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2100
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2340
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2640
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2700
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2760
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2820
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2970

<210> 4554
<211> 705
<212> PRT
<213> Homo sapiens

<400> 4554
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20 25 30
Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met Glu Ala Ser
35 40 45
Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro Ala Arg Leu
50 55 60
Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn Ile Ala Lys
65 70 75 80
Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly Leu Asp Leu
85 90 95
Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val Lys Lys Met
100 105 110
Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu Thr Glu Leu
115 120 125
Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu Leu Tyr Ile
130 135 140
Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe Ile Gly Leu
145 150 155 160
His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu Gln Met Ile
165 170 175
Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile Leu Met Ile
180 185 190
Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe Lys Pro Leu
195 200 205
Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu Thr Glu Ile
210 215 220
Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser Ile Ser Phe
225 230 235 240
Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu Gln Lys Val
245 250 255
Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile Asn Arg Ile
260 265 270
Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu Leu Gly Ile
275 280 285
Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala Val Asp Asn
290 295 300
Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro Arg Leu Ser
305 310 315 320
Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu Glu Ser Leu
325 330 335
Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly Thr Ile Glu

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Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn Pro Ile Arg
        355                 360                 365
Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr Asn Ile Arg
    370                 375                 380
Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro Glu Phe Gln
385                 390                 395                 400
Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met Glu Ile Cys
                405                 410                 415
Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu Asn Val Glu
            420                 425                 430
Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala Glu Pro Gln
        435                 440                 445
Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu Leu Pro Asn
    450                 455                 460
Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr Leu Asp Ile
465                 470                 475                 480
Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys Ile Ala Thr
                485                 490                 495
Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys Val Asp Gly
            500                 505                 510
Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys Ile Arg Asp
        515                 520                 525
Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser Ser Lys Ile
    530                 535                 540
Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr Glu Asn Ser
545                 550                 555                 560
His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys Val Tyr Asn
                565                 570                 575
Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys Ile Asp Ile
            580                 585                 590
Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn Val Thr Thr
        595                 600                 605
Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn Asn Thr Thr
    610                 615                 620
Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile Gly Val Ile
625                 630                 635                 640
Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp Gly Gly His
                645                 650                 655
Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala Leu Gly Glu
            660                 665                 670
Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys Glu Lys Ser
        675                 680                 685
Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro Thr Asn Met
    690                 695                 700
Ser
705
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<210> 4555
<211> 1128
<212> DNA
<213> Homo sapiens

<400> 4555

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240
gaaagtgtgg agacaggcct gaagctggcc ctgtgtggaa cggtgctgga ccacctggtc
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360
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480
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1128

<210> 4556
<211> 67
<212> PRT
<213> Homo sapiens

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Leu Asp Thr Pro Gly Val Leu Ala Pro Arg Ile Glu Ser Val Glu Thr
20 25 30
Gly Leu Lys Leu Ala Leu Cys Gly Thr Val Leu Asp His Leu Val Gly
35 40 45
Glu Glu Thr Met Ala Asp Tyr Leu Leu Tyr Thr Leu Asn Lys His Gln
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Arg Phe Gly

65

<210> 4557
<211> 446
<212> DNA
<213> Homo sapiens

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<210> 4558
<211> 148
<212> PRT
<213> Homo sapiens

<400> 4558
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35 40 45
Glu Thr Ser Arg Ala Phe Leu Pro Pro Pro Ser Asp Val Arg Val Arg
50 55 60
Ser Cys Leu Tyr His Trp Ser Ala Thr Ala His Leu Pro Pro Leu Ser
65 70 75 80
Lys Lys Pro Pro Cys Thr Ile Ser His Leu Arg Pro Leu Leu Gly Leu
85 90 95
Pro Pro Pro Ser Asp Leu His Ile Pro Ser Ala Ala Thr Leu Gly Pro
100 105 110
Cys Met His Trp Pro Pro Pro Ser Asp Ala Pro Cys Thr Ile Ser Leu
115 120 125
Ala Leu Asp Ala Leu Leu Gly Leu Pro Pro Pro Ser Asp His His Ile
130 135 140
Thr Ser Thr Arg
145

<210> 4559
<211> 919

<212> DNA
<213> Homo sapiens

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240
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919

<210> 4560
<211> 126
<212> PRT
<213> Homo sapiens

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            20   25   30
Pro Cys Asp Pro Asp Arg Asp Gln Arg Tyr Leu Thr Thr Tyr Asn Gln
        35   40   45
Gly Tyr Phe Glu Asn Ile Pro Lys Gly Leu Asp Gln Glu Gly Trp Thr
    50   55   60
Arg Gly Gly Ile Gln Pro Gln Met Pro Gly Gly Tyr Ala Leu Ser Gln
65   70   75   80
Pro Val Ser Cys Met Glu Ala Thr Pro Asn Pro Met Glu Ser Leu Arg

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                85                  90                  95
His Leu His Pro His Val Gly Arg Thr Leu Thr Ser Ala Asp Pro Phe
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Tyr Gln Asn Thr Pro His Ser Ser Arg Cys Val Ala His Ser
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<210> 4561
<211> 4172
<212> DNA
<213> Homo sapiens

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1260

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4172

<210> 4562
<211> 1182
<212> PRT
<213> Homo sapiens

<400> 4562
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Ala Gln Asn His Pro Ile Tyr Leu Ala Thr Gly Thr Ser Ala Gln Gln

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Leu Asp Ala Thr Phe Ser Thr Asn Ala Ser Leu Glu Ile Phe Glu Leu
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Asp Leu Ser Asp Pro Ser Leu Asp Met Lys Ser Cys Ala Thr Phe Ser
    50                  55                  60
Ser Ser His Arg Tyr His Lys Leu Ile Trp Gly Pro Tyr Lys Met Asp
65                  70                  75                  80
Ser Lys Gly Asp Val Ser Gly Val Leu Ile Ala Gly Gly Glu Asn Gly
                85                  90                  95
Asn Ile Ile Leu Tyr Asp Pro Ser Lys Ile Ile Ala Gly Asp Lys Glu
            100                 105                 110
Val Val Ile Ala Gln Asn Asp Lys His Thr Gly Pro Val Arg Ala Leu
        115                 120                 125
Asp Val Asn Ile Phe Gln Thr Asn Leu Val Ala Ser Gly Ala Asn Glu
    130                 135                 140
Ser Glu Ile Tyr Ile Trp Asp Leu Asn Asn Phe Ala Thr Pro Met Thr
145                 150                 155                 160
Pro Gly Ala Lys Thr Gln Pro Pro Glu Asp Ile Ser Cys Ile Ala Trp
                165                 170                 175
Asn Arg Gln Val Gln His Ile Leu Ala Ser Ala Ser Pro Ser Gly Arg
            180                 185                 190
Ala Thr Val Trp Asp Leu Arg Glu Asn Glu Pro Ile Ile Lys Val Ser
        195                 200                 205
Asp His Ser Asn Arg Met His Cys Ser Gly Leu Ala Trp His Pro Asp
    210                 215                 220
Val Ala Thr Gln Met Val Leu Ala Ser Glu Asp Asp Arg Leu Pro Val
225                 230                 235                 240
Ile Gln Met Trp Asp Leu Arg Phe Ala Ser Ser Pro Leu Arg Val Leu
                245                 250                 255
Glu Asn His Ala Arg Gly Ile Leu Ala Ile Ala Trp Ser Met Ala Asp
            260                 265                 270
Pro Glu Leu Leu Leu Ser Cys Gly Lys Asp Ala Lys Ile Leu Cys Ser
        275                 280                 285
Asn Pro Asn Thr Gly Glu Val Leu Tyr Glu Leu Pro Thr Asn Thr Gln
    290                 295                 300
Trp Cys Phe Asp Ile Gln Trp Cys Pro Arg Asn Pro Ala Val Leu Ser
305                 310                 315                 320
Ala Ala Ser Phe Asp Gly Arg Ile Ser Val Tyr Ser Ile Met Gly Gly
                325                 330                 335
Ser Thr Asp Gly Leu Arg Gln Lys Gln Val Asp Lys Leu Ser Ser Ser
            340                 345                 350
Phe Gly Asn Leu Asp Pro Phe Gly Thr Gly Gln Pro Leu Pro Pro Leu
        355                 360                 365
Gln Ile Pro Gln Gln Thr Ala Gln His Ser Ile Val Leu Pro Leu Lys
    370                 375                 380
Lys Pro Pro Lys Trp Ile Arg Arg Pro Val Gly Ala Ser Phe Ser Phe
385                 390                 395                 400
Gly Gly Lys Leu Val Thr Phe Glu Asn Val Arg Met Pro Ser His Gln
                405                 410                 415
Gly Ala Glu Gln Gln Gln Gln His His Val Phe Ile Ser Gln Val
            420                 425                 430
Val Thr Glu Lys Glu Phe Leu Ser Arg Ser Asp Gln Leu Gln Gln Ala
        435                 440                 445
Val Gln Ser Gln Gly Phe Ile Asn Tyr Cys Gln Lys Lys Ile Asp Ala
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Ser Gln Thr Glu Phe Glu Lys Asn Val Trp Ser Phe Leu Lys Val Asn
465                 470                 475                 480
Phe Glu Asp Asp Ser Arg Gly Lys Tyr Leu Glu Leu Leu Gly Tyr Arg
                485                 490                 495
Lys Glu Asp Leu Glu Lys Xaa Gln Asp Ile Lys Glu Glu Lys Glu Glu
            500                 505                 510
Ser Glu Phe Leu Pro Ser Ser Gly Gly Thr Phe Asn Ile Ser Val Ser
        515                 520                 525
Gly Asp Ile Asp Gly Leu Ile Thr Gln Ala Leu Leu Thr Gly Asn Phe
    530                 535                 540
Glu Ser Ala Val Asp Leu Cys Leu His Asp Asn Arg Met Ala Asp Ala
545                 550                 555                 560
Ile Ile Leu Ala Ile Ala Gly Gly Gln Glu Leu Leu Ala Arg Thr Gln
                565                 570                 575
Lys Lys Tyr Phe Ala Lys Ser Gln Ser Lys Ile Thr Arg Leu Ile Thr
            580                 585                 590
Ala Val Val Met Lys Asn Trp Lys Glu Ile Val Glu Ser Cys Asp Leu
        595                 600                 605
Lys Asn Trp Arg Glu Ala Leu Ala Ala Val Leu Thr Tyr Ala Lys Pro
    610                 615                 620
Asp Glu Phe Ser Ala Leu Cys Asp Leu Leu Gly Thr Arg Leu Glu Asn
625                 630                 635                 640
Glu Gly Asp Ser Leu Leu Gln Thr Gln Ala Cys Leu Cys Tyr Ile Cys
                645                 650                 655
Ala Gly Asn Val Glu Lys Leu Val Ala Cys Trp Thr Lys Ala Gln Asp
            660                 665                 670
Gly Ser His Pro Leu Ser Leu Gln Asp Leu Ile Glu Lys Val Val Ile
        675                 680                 685
Leu Arg Lys Ala Val Gln Leu Thr Gln Ala Met Asp Thr Ser Thr Val
    690                 695                 700
Gly Val Leu Leu Ala Ala Lys Met Ser Gln Tyr Ala Asn Leu Leu Ala
705                 710                 715                 720
Ala Gln Gly Ser Ile Ala Ala Ala Leu Ala Phe Leu Pro Asp Asn Thr
                725                 730                 735
Asn Gln Pro Asn Ile Met Gln Leu Arg Asp Arg Leu Cys Arg Ala Gln
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Gly Glu Pro Val Ala Gly His Glu Ser Pro Lys Ile Pro Tyr Glu Lys
        755                 760                 765
Gln Gln Leu Pro Lys Gly Arg Pro Gly Pro Val Ala Gly His His Gln
    770                 775                 780
Met Pro Arg Val Gln Thr Gln Gln Tyr Tyr Pro His Gly Glu Asn Pro
785                 790                 795                 800
Pro Pro Pro Gly Phe Ile Met His Gly Asn Val Asn Pro Asn Ala Ala
                805                 810                 815
Gly Gln Leu Pro Thr Ser Pro Gly His Met His Thr Gln Val Pro Pro
            820                 825                 830
Tyr Pro Gln Pro Gln Pro Tyr Gln Pro Ala Gln Pro Tyr Pro Phe Gly
        835                 840                 845
Thr Gly Gly Ser Ala Met Tyr Arg Pro Gln Gln Pro Val Ala Pro Pro
    850                 855                 860
Thr Ser Asn Ala Tyr Pro Asn Thr Pro Tyr Ile Ser Ser Ala Ser Ser
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Tyr Thr Gly Gln Ser Gln Leu Tyr Ala Ala Gln His Gln Ala Ser Ser
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Tyr Ala Leu Pro Pro Gly Thr Thr Gly Thr Leu Pro Ala Ala Ser Glu
    930                 935                 940
Leu Pro Ala Ser Gln Arg Thr Gly Pro Gln Asn Gly Trp Asn Asp Pro
945                 950                 955                 960
Pro Ala Leu Asn Arg Val Pro Lys Lys Lys Lys Met Pro Glu Asn Phe
                965                 970                 975
Met Pro Pro Val Pro Ile Thr Ser Pro Ile Met Asn Pro Leu Gly Asp
            980                 985                 990
Pro Gln Ser Gln Met Leu Gln Gln Gln Pro Ser Ala Pro Val Pro Leu
        995                 1000                1005
Ser Ser Gln Ser Ser Phe Pro Gln Pro His Leu Pro Gly Gly Gln Pro
    1010                1015                1020
Phe His Gly Val Gln Gln Pro Leu Gly Gln Thr Gly Met Pro Pro Ser
1025                1030                1035                1040
Phe Ser Lys Pro Asn Ile Glu Gly Ala Pro Gly Ala Pro Ile Gly Asn
                1045                1050                1055
Thr Phe Gln His Val Gln Ser Leu Pro Thr Lys Lys Ile Thr Lys Lys
            1060                1065                1070
Pro Ile Pro Asp Glu His Leu Ile Leu Lys Thr Thr Phe Glu Asp Leu
        1075                1080                1085
Ile Gln Arg Cys Leu Ser Ser Ala Thr Asp Pro Gln Thr Lys Arg Lys
    1090                1095                1100
Leu Asp Asp Ala Ser Lys Arg Leu Glu Phe Leu Tyr Asp Lys Leu Arg
1105                1110                1115                1120
Glu Gln Thr Leu Ser Pro Thr Ile Thr Ser Gly Leu His Asn Ile Ala
                1125                1130                1135
Arg Ser Ile Glu Thr Arg Asn Tyr Ser Glu Gly Leu Thr Met His Thr
            1140                1145                1150
His Ile Val Ser Thr Ser Asn Phe Ser Glu Thr Ser Ala Phe Met Pro
        1155                1160                1165
Val Leu Lys Val Val Leu Thr Gln Ala Asn Lys Leu Gly Val
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<210> 4563
<211> 2037
<212> DNA
<213> Homo sapiens

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300
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1740
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1800
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1860
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1920

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1980
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2037

<210> 4564
<211> 354
<212> PRT
<213> Homo sapiens

<400> 4564
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20 25 30
Asp Glu Asp Gly Leu Val Val Leu Val Phe Asn Lys Lys Glu Thr Glu
35 40 45
Ile Arg Ser Gln Gln Gln Gln Leu Val Glu Ser Leu His Lys Val Leu
50 55 60
Gly Gly Asn Gln Thr Leu Thr Val Asn Val Glu Gly Thr Lys Thr Leu
65 70 75 80
Pro Asp Asp Gln Thr Glu Val Val Ile Tyr Val Val Glu Arg Ser Pro
85 90 95
Asn Gly Thr Ser Arg Arg Val Pro Ala Thr Thr Leu Tyr Ala His Phe
100 105 110
Glu Gln Ala Asn Ile Lys Thr Gln Leu Gln Gln Leu Gly Val Thr Leu
115 120 125
Ser Met Thr Arg Thr Glu Leu Ser Pro Ala Gln Ile Arg Gln Leu Leu
130 135 140
Gln Asn Pro Pro Ala Gly Val Asp Pro Ile Ile Trp Glu Gln Ala Lys
145 150 155 160
Val Asp Asn Pro Asp Ser Glu Lys Leu Ile Pro Val Pro Met Val Gly
165 170 175
Phe Lys Glu Leu Leu Arg Arg Leu Lys Val Gln Asp Gln Met Thr Lys
180 185 190
Gln His Gln Thr Arg Leu Asp Ile Ile Ser Glu Asp Ile Ser Glu Leu
195 200 205
Gln Lys Asn Gln Thr Thr Ser Val Ala Lys Ile Ala Gln Tyr Lys Arg
210 215 220
Lys Leu Met Asp Leu Ser His Arg Thr Leu Gln Val Leu Ile Lys Gln
225 230 235 240
Glu Ile Gln Arg Lys Ser Gly Tyr Ala Ile Gln Ala Asp Glu Glu Gln
245 250 255
Leu Arg Val Gln Leu Asp Thr Ile Gln Gly Glu Leu Asn Ala Pro Thr
260 265 270
Gln Phe Lys Gly Arg Leu Asn Glu Leu Met Ser Gln Ile Arg Met Gln
275 280 285
Asn His Phe Gly Ala Val Arg Ser Glu Glu Arg Tyr Tyr Ile Asp Ala
290 295 300
Asp Leu Leu Arg Glu Ile Lys Gln His Leu Lys Gln Gln Gln Glu Gly
305 310 315 320
Leu Ser His Leu Ile Ser Ile Ile Lys Asp Asp Leu Glu Asp Ile Lys
325 330 335
Leu Val Glu His Gly Leu Asn Glu Thr Ile His Ile Arg Gly Gly Val

340 345 350
Phe Ser

<210> 4565
<211> 2344
<212> DNA
<213> Homo sapiens

<400> 4565
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120
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180
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240
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300
cccaactctt tggatcagtt caagagcaaa ttgcgtagcc tgagttactc tgagattcta
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420
ctgagggaga agatccagcc cgagatcctt gagctgatca agcagcagcg cctgaaccgg
480
ctctgtgagg gcagcagctt ccgaaagatt gggaaccgcc gaaggcaaga acggttctgg
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720
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900
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1020
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1140
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1200
gtgctctgcc cactccatca ccatgaagcc tgggattggg ccacgaggaa caaacagcag
1260
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1320

acctttttcct cctgagcctg ctctctgatc agctggatcc ccacgtgagc aacagctggc
1380
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1440
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1560
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1680
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1740
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1800
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1860
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1920
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1980
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2100
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2160
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2220
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2280
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2340
aaaa
2344

<210> 4566
<211> 247
<212> PRT
<213> Homo sapiens

<400> 4566
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Asn Ser Leu Asp Gln Phe Lys Ser Lys Leu Arg Ser Leu Ser Tyr Ser
            20   25   30
Glu Ile Leu Arg Leu Arg Gln Ser Glu Arg Met Ser Gln Asp Asp Phe
        35   40   45
Gln Ser Pro Pro Ile Val Glu Leu Arg Glu Lys Ile Gln Pro Glu Ile
    50   55   60
Leu Glu Leu Ile Lys Gln Gln Arg Leu Asn Arg Leu Cys Glu Gly Ser
65   70   75   80
Ser Phe Arg Lys Ile Gly Asn Arg Arg Arg Gln Glu Arg Phe Trp Tyr

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                85                  90                  95
Cys Arg Leu Ala Leu Asn His Lys Val Leu His Tyr Gly Asp Leu Asp
            100                 105                 110
Asp Asn Pro Gln Gly Glu Val Thr Phe Glu Ser Leu Gln Glu Lys Ile
        115                 120                 125
Pro Val Ala Asp Ile Lys Ala Ile Val Thr Gly Lys Asp Cys Pro His
    130                 135                 140
Met Lys Glu Lys Ser Ala Leu Lys Gln Asn Lys Glu Val Leu Glu Leu
145                 150                 155                 160
Ala Phe Ser Ile Leu Tyr Asp Pro Asp Glu Thr Leu Asn Phe Ile Ala
                165                 170                 175
Pro Asn Lys Tyr Glu Tyr Cys Ile Trp Ile Asp Gly Leu Ser Ala Leu
            180                 185                 190
Leu Gly Lys Asp Met Ser Ser Glu Leu Thr Lys Ser Asp Leu Asp Thr
        195                 200                 205
Leu Leu Ser Met Glu Met Lys Leu Arg Leu Leu Asp Leu Glu Asn Ile
    210                 215                 220
Gln Ile Pro Glu Ala Pro Pro Pro Ile Pro Lys Glu Pro Ser Ser Tyr
225                 230                 235                 240
Asp Phe Val Tyr His Tyr Gly
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<210> 4567
<211> 1211
<212> DNA
<213> Homo sapiens

<400> 4567
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120
cagtctgttc aacaagtggg accccagggc cttctgtatg ttcagcaaag agagcttgca
180
gtgacctccc caaaggatgg ctccatctcc attctgggtt ctgatgatgc cactacttgt
240
cacattgtgg tcctgaggca cacaggtaat ggggccacct gcttgacaca ttgtgacgga
300
accgacacca aagctgaggt ccccttgatc atgaactcca taaaatcctt ttctgaccac
360
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420
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480
gacaggcaag aagatgacat tcacttagtg acattatgtg tgacagaatt aaatgaccgg
540
gaagaaaacg aaaaccactt tccagtaata tatggcattg ctgtcaacat taagactgca
600
gagatttaca gagcatcctt tcaagatcgg ggtccggagg agcagcttcg tgctgcgcga
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720
ggaccgtact cctggacacc atttccacat gtggatttct ggttgcacca agatgacaag
780

caaatactag agaatctttc cacttcgcct ctggctgagc caccccactt tgttgaacat
840
attagatcta ccttgatgtt tttaaaaaaa cacccatctc cagctcacac actgttttct
900
ggaaaataaag ccctactcta caaaaaaaat gaagatggct tgtgggaaaa gatctcttct
960
ccaggaagtt aaaaaacatg aattaccaaa gaaagcacct tcttggcctg acagaccatt
1020
ggtggggctg gcacgaatcc agatctggaa cctacatctg ttgggtctta ggtcttctcc
1080
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1200
aaaaaaaaaa a
1211

<210> 4568
<211> 120
<212> PRT
<213> Homo sapiens

<400> 4568
Met Pro Leu Leu Val Glu Gly Arg Arg Val Arg Leu Pro Gln Ser Ala
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Gly Asp Leu Val Arg Ala His Pro Pro Leu Glu Glu Arg Ala Arg Leu
            20   25   30
Leu Arg Gly Gln Ser Val Gln Gln Val Gly Pro Gln Gly Leu Leu Tyr
        35   40   45
Val Gln Gln Arg Glu Leu Ala Val Thr Ser Pro Lys Asp Gly Ser Ile
    50   55   60
Ser Ile Leu Gly Ser Asp Asp Ala Thr Thr Cys His Ile Val Val Leu
65   70   75   80
Arg His Thr Gly Asn Gly Ala Thr Cys Leu Thr His Cys Asp Gly Thr
                85   90   95
Asp Thr Lys Ala Glu Val Pro Leu Ile Met Asn Ser Ile Lys Ser Phe
            100   105   110
Ser Asp His Ala Gln Cys Gly Arg
        115   120

<210> 4569
<211> 1797
<212> DNA
<213> Homo sapiens

<400> 4569
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120
gacaatggcc tcgggaccct catgctgctg ggcccaggag agacagttct gaggcagaaa
180
ctcggcgtcc aaggggggcc gcgggtcagg cactgtggtg aagggaacgc cggggagtcc
240

ggccccacct tgcagctggg gacacggggg cgcaaacaga gggggcaggc tagtgtcccg
300
ctgccccagg aacagacctc agggccccag gagggtctgc aggcagctag gagcctgcca
360
agtgctggtg gaagtagagg ccgaaaaggc tggcgagcag ctggcaggca gccgtccacc
420
agatgaggta ggccaggacg ccacggagga agaggggagt aagcaggcca cccagggccc
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540
gctggctgag ganntgggtc gggggatagt agaggagctg ggcccaggcc ccaggaatag
600
cctcccagcg tcttgagcag aagtgtgcag ttgagggtga ggatgagcgc gtcaggtact
660
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720
cttcgatgcg gccagcctcc cttcgcagct gctccacccg ggccttggcc aggcacaggt
780
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960
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1080
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1140
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1797

<210> 4570

<211> 141
<212> PRT
<213> Homo sapiens

<400> 4570
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Met Leu Leu Tyr Leu Phe Arg Arg Ala Ala Ser Ile Thr Leu Ala Thr
20 25 30
Gln Thr Trp His Ile Arg Phe Gly Asp Asn Gly Leu Gly Thr Leu Met
35 40 45
Leu Leu Gly Pro Gly Glu Thr Val Leu Arg Gln Lys Leu Gly Val Gln
50 55 60
Gly Gly Pro Arg Val Arg His Cys Gly Glu Gly Asn Ala Gly Glu Ser
65 70 75 80
Gly Pro Thr Leu Gln Leu Gly Thr Arg Gly Arg Lys Gln Arg Gly Gln
85 90 95
Ala Ser Val Pro Leu Pro Gln Glu Gln Thr Ser Gly Pro Gln Glu Gly
100 105 110
Leu Gln Ala Ala Arg Ser Leu Pro Ser Ala Gly Gly Ser Arg Gly Arg
115 120 125
Lys Gly Trp Arg Ala Ala Gly Arg Gln Pro Ser Thr Arg
130 135 140

<210> 4571
<211> 1084
<212> DNA
<213> Homo sapiens

<400> 4571
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120
actcagttac acatcacgaa gtcaaatgcc aggggaaacc attagccgga atctacagga
180
aacgagaaga gaaaagaaat gctgggaacg cagtacggag cgccatgaag tccgaggaac
240
agaagatcaa agacgccagg aaaggtcccc tggtaccttt tccaaaccaa aaatctgaag
300
cagcagaacc tccaaaaact ccaccctcat cttgtgattc caccaatgca gccatcgcca
360
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480
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540
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600
aagcagttct cccggggtga ctttgtggtg gaataccacg gggacctcat cgagatcacc
660
gacgccaaga aacgggaggc tctgtacgca caggaccctt ccacgggctg ctacatgtac
720

tattttcagt atctgagcaa aacctactgg tgagtccact gttgcttaga gtggcttttc
780
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840
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960
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1080
gacc
1084

<210> 4572
<211> 126
<212> PRT
<213> Homo sapiens

<400> 4572
Lys Ser Pro Ser Arg Ala Asn Arg Pro Pro Glu Lys Lys Ala Gln Gly
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Lys Thr Gln Gln Asn Arg Lys Leu Thr Asp Phe Tyr Pro Val Arg Arg
20 25 30
Ser Ser Arg Lys Ser Lys Ala Glu Leu Gln Ser Glu Glu Arg Lys Arg
35 40 45
Ile Asp Glu Leu Ile Glu Ser Gly Lys Glu Glu Gly Met Lys Ile Asp
50 55 60
Leu Ile Asp Gly Lys Gly Arg Gly Val Ile Ala Thr Lys Gln Phe Ser
65 70 75 80
Arg Gly Asp Phe Val Val Glu Tyr His Gly Asp Leu Ile Glu Ile Thr
85 90 95
Asp Ala Lys Lys Arg Glu Ala Leu Tyr Ala Gln Asp Pro Ser Thr Gly
100 105 110
Cys Tyr Met Tyr Tyr Phe Gln Tyr Leu Ser Lys Thr Tyr Trp
115 120 125

<210> 4573
<211> 309
<212> DNA
<213> Homo sapiens

<400> 4573
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cccaagggag atgccggcag tcggggccca atggggatga gaggcccacc aggtccacag
120
ggcccccccag ggagccctgg ccgggctgga gctgtgggca cccctggaaa aaggggacct
180
tctggcccac aaggccttct tggcccccct gggcccccag cccctgttgg gccaccccat
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gcccggatct cccagcatgg agatccattg ctgtccaaca ccttcactga gaccaacccc
300

ttcacgcgt
309

<210> 4574
<211> 103
<212> PRT
<213> Homo sapiens

<400> 4574
Pro Gly Asp Gly Gly Leu Gln Asp Gln Val Gly Ala Trp Gly Leu Pro
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Gly Pro Thr Gly Pro Lys Gly Asp Ala Gly Ser Arg Gly Pro Met Gly
20 25 30
Met Arg Gly Pro Pro Gly Pro Gln Gly Pro Pro Gly Ser Pro Gly Arg
35 40 45
Ala Gly Ala Val Gly Thr Pro Gly Lys Arg Gly Pro Ser Gly Pro Gln
50 55 60
Gly Leu Leu Gly Pro Pro Gly Pro Pro Ala Pro Val Gly Pro Pro His
65 70 75 80
Ala Arg Ile Ser Gln His Gly Asp Pro Leu Leu Ser Asn Thr Phe Thr
85 90 95
Glu Thr Asn Pro Phe Thr Arg
100

<210> 4575
<211> 1068
<212> DNA
<213> Homo sapiens

<400> 4575
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120
ctccccgacc aggtggtcca gcaccgttcc acacagggcc agcttcaggc ctgtctccac
180
actttcaatc cgaggagcca gcacgccagg agtgtccaac aggaacatca ggggccgctc
240
agagacctga attttggaca tcacagctct ggtgatccca ggctcgccac ccaccctggt
300
ggctttccct ttcctgaggt gctgcctccg gagggagttg atgagggagg acttgcccac
360
gttggggacc ccaatgacca tgatacagta ctccaggttc tcttttcggt ggtagcggtg
420
gcttctccca atcagttcag tgaccatcgg gatgatctgc ttgacatttt catcctttac
480
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540
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600
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720

gcccgggaac cagcgcgcca cgtcgcgacc gcacaggggg aagttctccc gccaggcggc
780
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840
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900
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960
gctgggacta caggtgcccg ccaccacacc cacctaattt tcgtattttt agtagagacg
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1068

<210> 4576
<211> 107
<212> PRT
<213> Homo sapiens

<400> 4576
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Gln Ala Ala Leu His Leu Leu Gln Pro Leu Gly His Val Ala Arg Glu
20 25 30
Pro Ala Arg His Val Ala Thr Ala Gln Gly Glu Val Leu Pro Pro Gly
35 40 45
Gly Leu Gly Gly Ala Ala Gln Arg Ala Arg Gly Gln Ser His Gly Gly
50 55 60
Thr Val Pro Gly Asn Ala Pro Ala Ala Asp Leu Leu Ala Leu Ser Pro
65 70 75 80
Arg Leu Glu Arg Ser Gly Thr Ile Ser Thr His Cys Lys Leu Arg Leu
85 90 95
Pro Gly Ser Arg His Ser Pro Ala Ser Ala Ser
100 105

<210> 4577
<211> 3525
<212> DNA
<213> Homo sapiens

<400> 4577
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ctaacgaaga agagactggc tatggaggga cacgatttca gaggtgcttc tgagctgctc
120
gtgctgacct cagccctgtc cttcctgcag accctgctga aggtcgtgta cgtggagaat
180
gacatccagc acctgcagga catgtcacac ttcccagacc gggggagcga gaatgggaca
240
cccatggacg tgaaagccgg ggtgcgggtc atgcaggtca gtcctgacgg ccagcatttg
300
gcttcaggcg accgaagtgg aaatctgagg caagtgggcc ctggcagtgt ccagtgtaca
360
cctcccagct ccagctcagg ttctcagggc agtgggcaga agccctggcc ttggcacctc
420

ctgctgccca ttgggaatga ggggctgatc cacgagctgc acttcatgga cgagctggtc
480
aaggtggagg cccatgatgc tgaggtgctg tgcctggagt actccaagcc agagacgggg
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<211> 1007
<212> PRT

<213> Homo sapiens

<400> 4578

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Gly Gln Lys Pro Trp Pro Trp His Leu Leu Leu Pro Ile Gly Asn Glu
65                  70                  75                  80
Gly Leu Ile His Glu Leu His Phe Met Asp Glu Leu Val Lys Val Glu
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Ala His Asp Ala Glu Val Leu Cys Leu Glu Tyr Ser Lys Pro Glu Thr
            100                 105                 110
Gly Leu Thr Leu Leu Ala Ser Ala Ser Arg Asp Arg Leu Ile His Val
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Leu Asn Val Glu Lys Asn Tyr Asn Leu Glu Gln Thr Leu Asp Asp His
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Ser Ser Ser Ile Thr Ala Ile Lys Phe Ala Gly Asn Arg Asp Ile Gln
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Met Ile Ser Cys Gly Ala Asp Lys Ser Ile Tyr Phe Arg Ser Ala Gln
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Gln Gly Ser Asp Gly Leu His Phe Val Arg Thr His His Val Ala Glu
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Lys Thr Thr Leu Tyr Asp Met Asp Ile Asp Ile Thr Gln Lys Tyr Val
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Ala Val Ala Cys Gln Asp Arg Asn Val Arg Val Tyr Asn Thr Val Asn
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Gly Lys Gln Lys Lys Cys Tyr Lys Gly Ser Gln Gly Asp Glu Gly Ser
225                 230                 235                 240
Leu Leu Lys Val His Val Asp Pro Ser Gly Thr Phe Leu Ala Thr Ser
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Cys Ser Asp Lys Ser Ile Ser Val Ile Asp Phe Tyr Ser Gly Glu Cys
            260                 265                 270
Ile Ala Lys Met Phe Gly His Ser Gly Gly Cys Ala Ser Leu Leu Gly
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Met Pro Pro His Pro Pro Thr Pro Ser Asp Ser Glu Gly Lys Cys Ser
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Leu Ser Ala Leu Phe Ala Glu Ile Ile Thr Ser Met Lys Phe Thr Tyr
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Asp Cys His His Leu Ile Thr Val Ser Gly Asp Ser Cys Val Phe Ile
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Trp His Leu Gly Pro Glu Ile Thr Asn Cys Met Lys Gln His Leu Leu
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Glu Ile Asp His Arg Gln Gln Gln Gln His Thr Asn Asp Lys Lys Arg
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Ser Gly His Pro Arg Ser Trp Gln Pro Leu Pro Val His Gln Arg Asp
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Glu Ser Leu Pro Gly Pro His Gly Val Met Leu Gly Thr Gln Ser Ser
385                 390                 395                 400
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Gln Pro His Gly Arg Trp Ala Glu Arg Ala Gly Gln Glu Pro Leu Lys
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Thr Ile Leu Asp Ala Gln Asp Leu Asp Cys Tyr Phe Thr Pro Met Lys
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Pro Glu Ser Leu Glu Asn Ser Ile Leu Asp Ser Leu Glu Pro Gln Ser
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Leu Ile Leu Tyr Ser Leu Glu Ala Glu Val Thr Val Thr Gly Thr Asp
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Ser Gln Tyr Cys Arg Lys Glu Val Glu Ala Gly Pro Gly Asp Gln Gln
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Gly Asp Ser Tyr Leu Arg Val Ser Ser Asp Ser Pro Lys Asp Gln Ser
    530                 535                 540
Pro Pro Glu Gly Pro Thr Glu Asp Glu Leu Ser Leu Pro Glu Gly Pro
545                 550                 555                 560
Ser Val Pro Ser Ser Ser Leu Pro Gln Thr Pro Glu Gln Glu Lys Phe
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Leu Arg His His Phe Glu Thr Leu Thr Glu Ser Pro Cys Arg Ala Leu
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Gly Asp Val Glu Ala Ser Glu Ala Glu Asp His Phe Phe Asn Pro Arg
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Phe Thr His Thr Phe Pro Pro Arg Ala Thr Gln Cys Leu Val Lys Ser
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Pro Glu Val Lys Leu Met Asp Arg Gly Gly Ser Gln Pro Arg Ala Gly
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Thr Gly Tyr Ala Ser Pro Asp Arg Thr His Ser Val Pro Ser Ala Ser
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Val Thr Ala Pro Cys Leu Thr Ser Leu Ala Ser Cys Val Pro Ala Ser
        675                 680                 685
Ser Val Leu Pro Thr Asp Arg Asn Leu Pro Thr Pro Thr Ser Ala Pro
    690                 695                 700
Thr Pro Gly Leu Ala Gln Gly Val His Ala Pro Ser Thr Cys Ser Tyr
705                 710                 715                 720
Met Glu Ala Thr Ala Ser Ser Arg Ala Arg Ile Ser Arg Ser Ile Ser
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Leu Gly Asp Ser Glu Gly Pro Ile Val Ala Thr Leu Ala Gln Pro Leu
            740                 745                 750
Arg Arg Pro Ser Ser Val Gly Glu Leu Ala Ser Leu Gly Gln Glu Leu
        755                 760                 765
Gln Ala Ile Thr Thr Ala Thr Thr Pro Ser Leu Asp Ser Glu Gly Gln
    770                 775                 780
Glu Pro Ala Leu Arg Ser Trp Gly Asn His Glu Ala Arg Ala Asn Leu
785                 790                 795                 800
Arg Leu Thr Leu Ser Ser Ala Cys Asp Gly Leu Leu Gln Pro Pro Val
                805                 810                 815
Asp Thr Gln Pro Gly Val Thr Val Pro Ala Val Ser Phe Pro Ala Pro
            820                 825                 830
Ser Pro Val Glu Glu Ser Ala Leu Arg Leu His Gly Ser Ala Phe Arg
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        835                 840                 845
Pro Ser Leu Pro Ala Pro Glu Ser Pro Gly Leu Pro Ala His Pro Ser
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Asn Pro Gln Leu Pro Glu Ala Arg Pro Gly Ile Pro Gly Gly Thr Ala
865                 870                 875                 880
Ser Leu Leu Glu Pro Thr Ser Gly Trp Gly Thr Ser Cys Thr Gly Cys
                885                 890                 895
Arg Pro Pro Ser Lys Lys Pro Ser Thr Phe Thr Val Cys Trp Ser Pro
            900                 905                 910
Val Ala Arg Trp Thr Pro Gly Ser Ser Arg His Gly Leu Ser Trp Ser
        915                 920                 925
Pro Pro Ser Cys Gly Ser Thr Ala Ser Trp Arg Leu Asn Ala Trp Trp
    930                 935                 940
Gly Leu Val Trp Pro Gln Pro Arg Leu Cys Pro Ala Gln Asp Pro Arg
945                 950                 955                 960
Pro His Arg Arg Cys Thr Pro Trp Pro Ala Gln Thr Cys Arg Pro Cys
                965                 970                 975
Trp Asn Thr Thr Arg Ser Cys Trp Cys Arg Pro Cys Gly Gly Arg His
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Gly Gly Thr Glu Gly Ala Ala Pro Pro Pro Gln Pro Cys Cys Phe
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<211> 321
<212> DNA
<213> Homo sapiens

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<210> 4580
<211> 107
<212> PRT
<213> Homo sapiens

<400> 4580
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Xaa Lys Met Phe Gly His Ser Glu Ile Ile Thr Ser Met Lys Phe Thr
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Tyr Asp Cys His His Leu Ile Thr Val Ser Gly Asp Ser Cys Val Phe
            20                  25                  30
Ile Trp His Leu Gly Pro Glu Ile Thr Asn Cys Met Lys Gln His Leu
        35                  40                  45
Leu Glu Ile Asp His Arg Gln Gln Gln Gln His Thr Asn Asp Lys Lys
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    50                  55                  60
Arg Ser Gly Pro Pro Arg Gln Asp Thr Tyr Val Ser Thr Pro Ser Glu
65                  70                  75                  80
Ile His Ser Leu Ser Pro Gly Glu Gln Thr Glu Asp Asp Leu Glu Glu
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Glu Cys Glu Pro Glu Glu Met Leu Lys Thr Pro
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<211> 354
<212> PRT
<213> Homo sapiens

<400> 4582
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35 40 45
Leu Ala Lys Lys Glu Ala Lys Glu Arg Lys Lys Arg Glu Lys Met Gly
50 55 60
Trp Gly Glu Glu Tyr Met Gly Tyr Thr Asn Thr Asp Asn Pro Phe Gly
65 70 75 80
Asp Asn Asn Leu Leu Gly Thr Phe Ile Trp Asn Lys Ala Leu Glu Lys
85 90 95
Lys Gly Ile Ser His Leu Glu Glu Lys Glu Leu Lys Glu Arg Asn Lys
100 105 110
Arg Ile Gln Glu Asp Asn Arg Leu Glu Leu Gln Lys Val Lys Gln Leu
115 120 125
Arg Leu Glu Arg Glu Arg Glu Lys Ala Met Arg Glu Gln Glu Leu Glu
130 135 140
Met Leu Gln Arg Val Lys Gly Thr Glu His Phe Lys Thr Trp Glu Glu
145 150 155 160
Gln Glu Asp Asn Phe His Leu Gln Gln Ala Lys Leu Arg Ser Lys Ile
165 170 175
Arg Ile Arg Asp Gly Arg Ala Lys Pro Ile Asp Leu Leu Ala Lys Tyr
180 185 190
Ile Ser Ala Glu Asp Asp Asp Leu Ala Gly Glu Met His Glu Pro Tyr
195 200 205
Thr Phe Leu Asn Gly Leu Thr Val Ala Asp Met Glu Asp Leu Leu Glu
210 215 220
Asp Ile Gln Val Tyr Met Glu Leu Glu Gln Gly Lys Asn Ala Asp Phe
225 230 235 240
Trp Arg Asp Met Thr Thr Ile Thr Glu Asp Glu Ile Ser Lys Leu Arg
245 250 255
Lys Leu Glu Ala Ser Gly Lys Gly Pro Gly Glu Arg Arg Glu Gly Val
260 265 270
Asn Ala Ser Val Ser Ser Asp Val Gln Ser Val Phe Lys Gly Lys Thr
275 280 285
Tyr Asn Gln Leu Gln Val Ile Phe Gln Gly Ile Glu Gly Lys Ile Arg
290 295 300
Ala Gly Gly Pro Asn Leu Asp Met Gly Tyr Trp Glu Ser Leu Leu Gln

305 310 315 320
Gln Leu Arg Ala His Met Ala Arg Ala Arg Leu Arg Glu Arg His Gln
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Glu Ser

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<212> DNA
<213> Homo sapiens

<400> 4583
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<210> 4584
<211> 923
<212> PRT
<213> Homo sapiens

<400> 4584
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35 40 45
Gln Leu Leu Gln Ile Arg Gln Asp Val Glu Ser Cys Tyr Phe Ala Ala
50 55 60
Gln Thr Met Lys Met Lys Ile Gln Thr Ser Phe Tyr Glu Leu Pro Thr
65 70 75 80
Asp Ser His Ala Ser Leu Arg Asp Ser Leu Leu Thr His Ile Gln Asn
85 90 95
Leu Lys Asp Leu Ser Pro Val Ile Val Thr Gln Leu Ala Leu Ala Ile
100 105 110
Ala Asp Leu Ala Leu Gln Met Pro Ser Trp Lys Gly Cys Val Gln Thr
115 120 125
Leu Val Glu Lys Tyr Ser Asn Asp Val Thr Ser Leu Pro Phe Leu Leu
130 135 140
Glu Ile Leu Thr Val Leu Pro Glu Glu Val His Ser Arg Ser Leu Arg
145 150 155 160
Ile Gly Ala Asn Arg Arg Thr Glu Ile Ile Glu Asp Leu Ala Phe Tyr
165 170 175
Ser Ser Thr Val Val Ser Leu Leu Met Thr Cys Val Glu Lys Ala Gly
180 185 190
Thr Asp Glu Lys Met Leu Met Lys Val Phe Arg Cys Leu Gly Ser Trp
195 200 205
Phe Asn Leu Gly Val Leu Asp Ser Asn Phe Met Ala Asn Asn Lys Leu
210 215 220
Leu Ala Leu Leu Phe Glu Val Leu Gln Gln Asp Lys Thr Ser Ser Asn

```
225                 230                 235                 240
Leu His Glu Ala Ala Ser Asp Cys Val Cys Ser Ala Leu Tyr Ala Ile
                245                 250                 255
Glu Asn Val Glu Thr Asn Leu Pro Leu Ala Met Gln Leu Phe Gln Gly
            260                 265                 270
Val Leu Thr Leu Glu Thr Ala Tyr His Met Ala Val Ala Arg Glu Asp
        275                 280                 285
Leu Asp Lys Val Leu Asn Tyr Cys Arg Ile Phe Thr Glu Leu Cys Glu
    290                 295                 300
Thr Phe Leu Glu Lys Ile Val Cys Thr Pro Gly Gln Gly Leu Gly Asp
305                 310                 315                 320
Leu Arg Thr Leu Glu Leu Leu Leu Ile Cys Ala Gly His Pro Gln Tyr
                325                 330                 335
Glu Val Val Glu Ile Ser Phe Asn Phe Trp Tyr Arg Leu Gly Glu His
            340                 345                 350
Leu Tyr Lys Thr Asn Asp Glu Val Ile His Gly Ile Phe Lys Ala Tyr
        355                 360                 365
Ile Gln Arg Leu Leu His Ala Leu Ala Arg His Cys Gln Leu Glu Pro
    370                 375                 380
Asp His Glu Gly Val Pro Glu Glu Thr Asp Asp Phe Gly Glu Phe Arg
385                 390                 395                 400
Met Arg Val Ser Asp Leu Val Lys Asp Leu Ile Phe Leu Ile Gly Ser
                405                 410                 415
Met Glu Cys Phe Ala Gln Leu Tyr Ser Thr Leu Lys Glu Gly Asn Pro
            420                 425                 430
Pro Trp Glu Val Thr Glu Ala Val Leu Phe Ile Met Ala Ala Ile Ala
        435                 440                 445
Lys Ser Val Asp Pro Glu Asn Asn Pro Thr Leu Val Glu Val Leu Glu
    450                 455                 460
Gly Val Val Arg Leu Pro Glu Thr Val His Thr Ala Val Arg Tyr Thr
465                 470                 475                 480
Ser Ile Glu Leu Val Gly Glu Met Ser Glu Val Val Asp Arg Asn Pro
                485                 490                 495
Gln Phe Leu Asp Pro Val Leu Gly Tyr Leu Met Lys Gly Leu Cys Glu
            500                 505                 510
Lys Pro Leu Ala Ser Ala Ala Ala Lys Ala Ile His Asn Ile Cys Ser
        515                 520                 525
Val Cys Arg Asp His Met Ala Gln His Phe Asn Gly Leu Leu Glu Ile
    530                 535                 540
Ala Arg Ser Leu Asp Ser Phe Leu Leu Ser Pro Glu Ala Ala Val Gly
545                 550                 555                 560
Leu Leu Lys Gly Thr Ala Leu Val Leu Ala Arg Leu Pro Leu Asp Lys
                565                 570                 575
Ile Thr Glu Cys Leu Ser Glu Leu Cys Ser Val Gln Val Met Ala Leu
            580                 585                 590
Lys Lys Leu Leu Ser Gln Glu Pro Ser Asn Gly Ile Ser Ser Asp Pro
        595                 600                 605
Thr Val Phe Leu Asp Arg Leu Ala Val Ile Phe Arg His Thr Asn Pro
    610                 615                 620
Ile Val Glu Asn Gly Gln Thr His Pro Cys Gln Lys Val Ile Gln Glu
625                 630                 635                 640
Ile Trp Pro Val Leu Ser Glu Thr Leu Asn Lys His Arg Ala Asp Asn
                645                 650                 655
Arg Ile Val Glu Arg Cys Cys Arg Cys Leu Arg Phe Ala Val Arg Cys
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            660                 665                 670
Val Gly Lys Gly Ser Ala Ala Leu Leu Gln Pro Leu Val Thr Gln Met
        675                 680                 685
Val Asn Val Tyr His Val His Gln His Ser Cys Phe Leu Tyr Leu Gly
    690                 695                 700
Ser Ile Leu Val Asp Glu Tyr Gly Met Glu Glu Gly Cys Arg Gln Gly
705                 710                 715                 720
Leu Leu Asp Met Leu Gln Ala Leu Cys Ile Pro Thr Phe Gln Leu Leu
                725                 730                 735
Glu Gln Gln Asn Gly Leu Gln Asn His Pro Asp Thr Val Asp Asp Leu
            740                 745                 750
Phe Arg Leu Ala Thr Arg Phe Ile Gln Arg Ser Pro Val Thr Leu Leu
        755                 760                 765
Arg Ser Gln Val Val Ile Pro Ile Leu Gln Trp Ala Ile Ala Ser Thr
    770                 775                 780
Thr Leu Asp His Arg Asp Ala Asn Cys Ser Val Met Arg Phe Leu Arg
785                 790                 795                 800
Asp Leu Ile His Thr Gly Val Ala Asn Asp His Glu Glu Asp Phe Glu
                805                 810                 815
Leu Arg Lys Glu Leu Ile Gly Gln Val Met Asn Gln Leu Gly Gln Gln
            820                 825                 830
Leu Val Ser Gln Leu Leu His Thr Cys Cys Phe Cys Leu Pro Pro Tyr
        835                 840                 845
Thr Leu Pro Asp Val Ala Glu Val Leu Trp Glu Ile Met Gln Val Asp
    850                 855                 860
Arg Pro Thr Phe Cys Arg Trp Leu Glu Asn Ser Leu Lys Gly Leu Pro
865                 870                 875                 880
Lys Glu Thr Thr Val Gly Ala Val Thr Val Thr His Lys Gln Leu Thr
                885                 890                 895
Asp Phe His Lys Gln Val Thr Ser Ala Glu Glu Cys Lys Gln Val Cys
            900                 905                 910
Trp Ala Leu Arg Asp Phe Thr Arg Leu Phe Arg
        915                 920
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<210> 4585
<211> 1952
<212> DNA
<213> Homo sapiens

<400> 4585
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120
gaacggatgg agggaagcag ctcctacgaa gttccctctg tggctgctgc tgatctggag
180
gagggtgctg gtcagactag gagcttgcct gccacccccc ccaaagatgt tcacaagggt
240
gttggaggca tcatcttttc ctcctcaccg attttagact tgagtgaaag tggtctgtgc
300
cgtttggagg aggtctttag aatccccagc cttcaacaat tgcatctgca aaggaatgcc
360
ctgtgtgtga ttcctcaaga tttctttcag ttgcttccga acctgacttg gctggacctc
420

cggtacaata gaattaaagc gcttccttct gggattggag ctcaccagca tttgaaaact
480
ttgcttttag aaagaaatcc tatcaaaatg ttacctgtgg agctggggag cgtaaccacg
540
ctgaaagcac tgaacctaag acactgccct ctggaattcc ctcctcagct cgttgtgcag
600
aagggattgg tggctatcca gcgcttcctg cggatgtggg cagtagaaca ctctctcccc
660
agaaatccaa cttctcaaga ggctccaccg gttagagaga tgaccctccg tgacctcccg
720
agcccaggac tggagttgtc tggagaccac gcgtctaacc aaggagctgt gaacgctcag
780
gacccagagg gggctgtgat gaaagagaag gccagctttc tcccgcctgt ggaaaagcca
840
gacctgagtg aactcaggaa gtctgcggac tcctcagaga actggcccag cgaggaggag
900
atcaggcgct tttggaagct gaggcaggag attgttgagc acgtgaaggc agacgttctg
960
ggagatcagc tcttgacgag ggaattacct ccaaatctca aggcggcctt gaacattgag
1020
aaagaactac caaagccaag acacgttttc agaaggaaga cagcctcctc caggagcatc
1080
ttacccgacc tcttgtcacc gtaccaaatg gcgatccgag caaaaagact ggaagagagc
1140
cgagcggcgg cgctccgaga gctccaggag aagcaggctc tgatggagca gcagagacga
1200
gagaaaaggg cactgcagga gtggagagag cgagcccaga ggatgaggaa gaggaaggaa
1260
gagctcagca aactcctgcc tccgcggagg agcatggtgg catcaaagat tccctctgcc
1320
acagatctga tagataacag gaaagtacca ctgaatccgc ctggaaaaat gaaaccaagc
1380
aaagagaaat cgccacaagc aagtaaagaa atgagtgccc tgcaggagag aaatttagaa
1440
gagaagataa aacagcacgt cctccaaatg cgtgagcaaa gaagattcca tggccaggcc
1500
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1560
gaagtattga agctaaaatt gggattaacc ttgaacaaag atcgtcgacg ggcggccctc
1620
actggaaacc tttcgcttgg cctgccggca gcacagcctc aaaatacatt ttttaacaca
1680
aaatatggag aatcaggaaa tgttcgcaga taccagtgac accaggtggc tggactgatg
1740
gagacgtctt cagacaggag ccgctcagtc ttctttcccg gcgtcgcctc ctgtgtggtg
1800
ccggaagagc gccaggttca gtgttaccct gagggctgat ttcgcgcagc ctgttgtttt
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1920
aaggacactg tgaaaaaaaa aaaaaaaaaa aa
1952

<210> 4586

<211> 530
<212> PRT
<213> Homo sapiens

<400> 4586
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Leu Glu Glu Gly Ala Gly Gln Thr Arg Ser Leu Pro Ala Thr Pro Ser
20 25 30
Lys Asp Val His Lys Gly Val Gly Gly Ile Ile Phe Ser Ser Ser Pro
35 40 45
Ile Leu Asp Leu Ser Glu Ser Gly Leu Cys Arg Leu Glu Glu Val Phe
50 55 60
Arg Ile Pro Ser Leu Gln Gln Leu His Leu Gln Arg Asn Ala Leu Cys
65 70 75 80
Val Ile Pro Gln Asp Phe Phe Gln Leu Leu Pro Asn Leu Thr Trp Leu
85 90 95
Asp Leu Arg Tyr Asn Arg Ile Lys Ala Leu Pro Ser Gly Ile Gly Ala
100 105 110
His Gln His Leu Lys Thr Leu Leu Leu Glu Arg Asn Pro Ile Lys Met
115 120 125
Leu Pro Val Glu Leu Gly Ser Val Thr Thr Leu Lys Ala Leu Asn Leu
130 135 140
Arg His Cys Pro Leu Glu Phe Pro Pro Gln Leu Val Val Gln Lys Gly
145 150 155 160
Leu Val Ala Ile Gln Arg Phe Leu Arg Met Trp Ala Val Glu His Ser
165 170 175
Leu Pro Arg Asn Pro Thr Ser Gln Glu Ala Pro Pro Val Arg Glu Met
180 185 190
Thr Leu Arg Asp Leu Pro Ser Pro Gly Leu Glu Leu Ser Gly Asp His
195 200 205
Ala Ser Asn Gln Gly Ala Val Asn Ala Gln Asp Pro Glu Gly Ala Val
210 215 220
Met Lys Glu Lys Ala Ser Phe Leu Pro Pro Val Glu Lys Pro Asp Leu
225 230 235 240
Ser Glu Leu Arg Lys Ser Ala Asp Ser Ser Glu Asn Trp Pro Ser Glu
245 250 255
Glu Glu Ile Arg Arg Phe Trp Lys Leu Arg Gln Glu Ile Val Glu His
260 265 270
Val Lys Ala Asp Val Leu Gly Asp Gln Leu Leu Thr Arg Glu Leu Pro
275 280 285
Pro Asn Leu Lys Ala Ala Leu Asn Ile Glu Lys Glu Leu Pro Lys Pro
290 295 300
Arg His Val Phe Arg Arg Lys Thr Ala Ser Ser Arg Ser Ile Leu Pro
305 310 315 320
Asp Leu Leu Ser Pro Tyr Gln Met Ala Ile Arg Ala Lys Arg Leu Glu
325 330 335
Glu Ser Arg Ala Ala Ala Leu Arg Glu Leu Gln Glu Lys Gln Ala Leu
340 345 350
Met Glu Gln Gln Arg Arg Glu Lys Arg Ala Leu Gln Glu Trp Arg Glu
355 360 365
Arg Ala Gln Arg Met Arg Lys Arg Lys Glu Glu Leu Ser Lys Leu Leu
370 375 380
Pro Pro Arg Arg Ser Met Val Ala Ser Lys Ile Pro Ser Ala Thr Asp

385 390 395 400
Leu Ile Asp Asn Arg Lys Val Pro Leu Asn Pro Pro Gly Lys Met Lys
405 410 415
Pro Ser Lys Glu Lys Ser Pro Gln Ala Ser Lys Glu Met Ser Ala Leu
420 425 430
Gln Glu Arg Asn Leu Glu Glu Lys Ile Lys Gln His Val Leu Gln Met
435 440 445
Arg Glu Gln Arg Arg Phe His Gly Gln Ala Pro Leu Glu Glu Met Arg
450 455 460
Lys Ala Ala Glu Asp Leu Glu Ile Ala Thr Glu Leu Gln Asp Glu Val
465 470 475 480
Leu Lys Leu Lys Leu Gly Leu Thr Leu Asn Lys Asp Arg Arg Arg Ala
485 490 495
Ala Leu Thr Gly Asn Leu Ser Leu Gly Leu Pro Ala Ala Gln Pro Gln
500 505 510
Asn Thr Phe Phe Asn Thr Lys Tyr Gly Glu Ser Gly Asn Val Arg Arg
515 520 525
Tyr Gln
530

<210> 4587
<211> 1723
<212> DNA
<213> Homo sapiens

<400> 4587
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caacccccta gcaaggcgcc taagttgcac tctgaacctt caaagaaagg ggaaactcct
120
acggtcgatg gcacttggaa gaccccttcc ttcccaaaaa agaagacagc tgcttccagc
180
aatgggtcag gacagcccct ggacaagaaa gctgcagtgt cttggttgac ccctgccccc
240
tcaaaaaagg ctgattctgt tgctgctaaa gtagatttgc tgggggagtt ccagagtgcc
300
cttccaaaga tcaatagcca cccaacccgc tctcagaaga agagctccca gaagaaatcc
360
tctaaaaaga accatcctca gaagaatgcc ccacagaact ccacccaagc tcattcagag
420
aataaatgct ccggagcatc ccagaagttg ccacggaaga tggtggcaat tgactgtgag
480
atggtgggca caggaccaaa ggggcatgtt agttccttgg ctcgatgtag cattgtcaac
540
tacaacggag atgtgcttta tgacgagtac attcttcccc cctgccacat tgtggactac
600
cgaaccaggt ggagtggtat ccggaagcag cacatggtga atgccacacc cttcaagatt
660
gctcgaggcc agatcttgaa gatactcaca gggaagatag tggtggggca tgccatccac
720
aacgacttca aagcccttca gtactttcac cccaagtccc tcacccgtga cacctcccat
780
atccccccccc tcaaccggaa ggctgactgc ccggagaatg ccaccatgtc tctgaagcat
840

ctcaccaaga agctgctaaa ccgggatatc caggttggga agagcggaca ttcctctgtg
900
gaagatgccc aggccaccat ggagctatat aagttggttg aagtcgagtg ggaagagcac
960
ctagcccgga atccccctac agactagtgg cagtggggac gctggtgata tgaggaggca
1020
gaggcagcac ccaggagaaa cagggcagtg gaccaatgga cagctccacc agctccacat
1080
ctttggaagc tagatttggg gagagagaag ctctacccca gacttaatac ccattgaaat
1140
ttcacctcag gtgttgtgtc ctgtgtctgg ttaagtgtcc catggaaggg gaaagccttc
1200
acgtcagaac ccaaccctat acctttttact tcttaaatgg tgctaaccac aggtgtccca
1260
gggtgctctg tgccagttaa gatttttaac tttcaagggg cagggcatac tgggaaatgt
1320
agtttcccaa actgccttat cacttgggtg gacatatgtc tccttttatg ccttttggtc
1380
ttgagtaatt aacagcatcc tcttccacgc tcagaagtgt tctggttggg gccaggcatg
1440
gtcgtcacgc ctgtagtccc aacacttagg gagtccgagg cgggcggatc acctgagatc
1500
aggagttcaa gaccagcctg gccaacatgg cgaattcccg ttctctacta aaaatacaaa
1560
aaatgtgtgg ggtgtggtgg caggagcctg taatcctagc tactcaggag gctgaggcag
1620
gagaatcgct tgagcccagg aggcggagat tgcagtgagc cgagatcgtg tcactgcact
1680
ccagcctggg tgacaagagt gagactccgt ctccaaaaaa aaa
1723

<210> 4588
<211> 328
<212> PRT
<213> Homo sapiens

<400> 4588
Xaa Asn Phe Val Lys Lys Arg Arg Leu Leu Glu Arg Arg Gly Phe Leu
 1   5   10   15
Ser Lys Lys Asn Gln Pro Pro Ser Lys Ala Pro Lys Leu His Ser Glu
            20   25   30
Pro Ser Lys Lys Gly Glu Thr Pro Thr Val Asp Gly Thr Trp Lys Thr
        35   40   45
Pro Ser Phe Pro Lys Lys Lys Thr Ala Ala Ser Ser Asn Gly Ser Gly
    50   55   60
Gln Pro Leu Asp Lys Lys Ala Ala Val Ser Trp Leu Thr Pro Ala Pro
65   70   75   80
Ser Lys Lys Ala Asp Ser Val Ala Ala Lys Val Asp Leu Leu Gly Glu
                85   90   95
Phe Gln Ser Ala Leu Pro Lys Ile Asn Ser His Pro Thr Arg Ser Gln
            100   105   110
Lys Lys Ser Ser Gln Lys Lys Ser Ser Lys Lys Asn His Pro Gln Lys
        115   120   125
Asn Ala Pro Gln Asn Ser Thr Gln Ala His Ser Glu Asn Lys Cys Ser

```
    130                 135                 140
Gly Ala Ser Gln Lys Leu Pro Arg Lys Met Val Ala Ile Asp Cys Glu
145                 150                 155                 160
Met Val Gly Thr Gly Pro Lys Gly His Val Ser Ser Leu Ala Arg Cys
                165                 170                 175
Ser Ile Val Asn Tyr Asn Gly Asp Val Leu Tyr Asp Glu Tyr Ile Leu
            180                 185                 190
Pro Pro Cys His Ile Val Asp Tyr Arg Thr Arg Trp Ser Gly Ile Arg
        195                 200                 205
Lys Gln His Met Val Asn Ala Thr Pro Phe Lys Ile Ala Arg Gly Gln
    210                 215                 220
Ile Leu Lys Ile Leu Thr Gly Lys Ile Val Val Gly His Ala Ile His
225                 230                 235                 240
Asn Asp Phe Lys Ala Leu Gln Tyr Phe His Pro Lys Ser Leu Thr Arg
                245                 250                 255
Asp Thr Ser His Ile Pro Pro Leu Asn Arg Lys Ala Asp Cys Pro Glu
            260                 265                 270
Asn Ala Thr Met Ser Leu Lys His Leu Thr Lys Lys Leu Leu Asn Arg
        275                 280                 285
Asp Ile Gln Val Gly Lys Ser Gly His Ser Ser Val Glu Asp Ala Gln
    290                 295                 300
Ala Thr Met Glu Leu Tyr Lys Leu Val Glu Val Glu Trp Glu Glu His
305                 310                 315                 320
Leu Ala Arg Asn Pro Pro Thr Asp
                325
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<210> 4589
<211> 585
<212> DNA
<213> Homo sapiens

<400> 4589
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tgtgggttgg ggtggctgag ggagaaggga agcgagggtc gcggcgggac cagacgcccc
120
agtcccggcc cgcccgcgac tactgaaggc gctgccgcct gacctgaacg ggcacttgtg
180
ttccagctcc cctgggacct gtggccgccg cccacagacc atgctcctgg ggcgcctgac
240
ttcccagctg ttgagggccg ttccttgggc aggtaggaag ccccgcggcg ganctgggag
300
gatgcacacc tggttaggag tgcgggtctc agcagctccg ctggggcagg gcggtggcca
360
cacacacact ctttcccctc taagcttccg atgctcacag agggaacctc aggggttcag
420
gccaggaatg aggtgcgggg gatcctcgct gggacgaacc tgctgctccc caacccgacg
480
ggcctgtgtg gtctcgcgag cggtgaccgt ggcgtctggt tttctgcagg cggccgcccg
540
ccttggcccg tctctggagt gctgggcagc cgggtctgcg ggccc
585

<210> 4590

<211> 121
<212> PRT
<213> Homo sapiens

<400> 4590
Met Leu Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp
1 5 10 15
Ala Gly Arg Lys Pro Arg Gly Gly Xaa Gly Arg Met His Thr Trp Leu
20 25 30
Gly Val Arg Val Ser Ala Ala Pro Leu Gly Gln Gly Gly Gly His Thr
35 40 45
His Thr Leu Ser Pro Leu Ser Phe Arg Cys Ser Gln Arg Glu Pro Gln
50 55 60
Gly Phe Arg Pro Gly Met Arg Cys Gly Gly Ser Ser Leu Gly Arg Thr
65 70 75 80
Cys Cys Ser Pro Thr Arg Arg Ala Cys Val Val Ser Arg Ala Val Thr
85 90 95
Val Ala Ser Gly Phe Leu Gln Ala Ala Ala Arg Leu Gly Pro Ser Leu
100 105 110
Glu Cys Trp Ala Ala Gly Ser Ala Gly
115 120

<210> 4591
<211> 496
<212> DNA
<213> Homo sapiens

<400> 4591
aaatttggcc caccgcctac ttttgtagac gacgttttat gggaacacag acacccccgt
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ccgtgtactt ccatggcttc tttcacaggt cagctgcaga gctaagtaac tgtgacaggg
120
accacttggc taagaaagcc tccagtattt actcgactgc cctgtgcttt ggactcaaaa
180
gagctcctct ctggccctct ggccacgatc gtctccatga gacacggaag ctacgatgct
240
tggcagacag gcttgtgagc ccacaccctg cctccagccc aggctccagg tacctgcccc
300
agaattccct gcacaagtgg ccccaagctt gtgctggtct gtgggggttt cttccctggg
360
ctgttgtcct gggcatgtgc agtcctcagg ctgatgggca gctatgggaa ggctggtcat
420
gcaggctggg tatccacaca cctgcacacg tggcttctcc tagtgcagta tggagtcagg
480
gatgggccgg gaaggg
496

<210> 4592
<211> 152
<212> PRT
<213> Homo sapiens

<400> 4592
Met Gly Thr Gln Thr Pro Pro Ser Val Tyr Phe His Gly Phe Phe His

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            20                  25                  30
Lys Ala Ser Ser Ile Tyr Ser Thr Ala Leu Cys Phe Gly Leu Lys Arg
        35                  40                  45
Ala Pro Leu Trp Pro Ser Gly His Asp Arg Leu His Glu Thr Arg Lys
    50                  55                  60
Leu Arg Cys Leu Ala Asp Arg Leu Val Ser Pro His Pro Ala Ser Ser
65                  70                  75                  80
Pro Gly Ser Arg Tyr Leu Pro Gln Asn Ser Leu His Lys Trp Pro Gln
                85                  90                  95
Ala Cys Ala Gly Leu Trp Gly Phe Leu Pro Trp Ala Val Val Leu Gly
            100                 105                 110
Met Cys Ser Pro Gln Ala Asp Gly Gln Leu Trp Glu Gly Trp Ser Cys
        115                 120                 125
Arg Leu Gly Ile His Thr Pro Ala His Val Ala Ser Pro Ser Ala Val
    130                 135                 140
Trp Ser Gln Gly Trp Ala Gly Lys
145                 150
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<210> 4593
<211> 4783
<212> DNA
<213> Homo sapiens

<400> 4593

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120
tcaggtagct cctcttctgc taccactgtc acctccaagg tggcacccag ctggcccgag
180
tctcactcct ctgcagattc ggcatcttta gcaaagaaga aacccctctt cattacaact
240
gactcctcca agctagtatc tggtgttctg ggctcagctc ttaccagtgg gggcccaagc
300
ctctctgcca tggggaatgg ccgctccagc tcgcccacca gcagcctcac tcagcccatt
360
gagatgccaa ctctctcctc tagccccaca gaggagaggc caactgtggg gcctgggcag
420
caggacaatc ccctcctcaa aacctttagt aacgtctttg gcaggcactc aggcggcttt
480
ctgtcctccc cggcagattt ttcacaggag aacaaagctc cttttgaagc tgtgaaaagg
540
ttctcactgg atgaacgaag cttggcttgc agacaagact cggactccag caccaacagt
600
gacctgtcag atttgagtga ctctgaggag cagctgcagg ctaagacagg cctgaaggga
660
attccagagc acctgatggg gaagctgggc cccaatgggg agcgcagtgc tgagctgttg
720
ctgggcaaaa gcaaagggaa gcaggccccc aagggccggc ctcggactgc ccccctgaaa
780
gttggccagt cagtgctgaa agatgtaagc aaagtgaaga agctgaagca atctggagag
840
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ccctttcctgc aggatgggtc atgcatcaat gtggcacctc atctgcacaa gtgtcgtgaa
900
tgccgcctgg agcggtaccg gaagtttaag gaacaggagc aagatgattc tactgtagcc
960
tgccgtttct ttcacttccg gaggttgatc ttcactcgaa aaggggtgct ccgtgtggag
1020
gggtttttaa gccccccagca aagtgaccct gatgccatga acctgtggat tccctcttcc
1080
tccctagcag aagggataga tctagagacc tcaaaataca tcctggccaa tgttggggac
1140
cagttctgcc agctcgtaat gtctgagaag gaggccatga tgatggtgga gccacaccag
1200
aaagtggcat ggaagcgagc tgtgcgtggt gtacgggaga tgtgtgatgt gtgtgaaaca
1260
actctcttca acatccactg ggtttgtcgc aaatgtggat ttggggtctg ccttgactgt
1320
taccggctca ggaaaagccg gccacgcagt gagacagaag agatgggtga tgaagaagtt
1380
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1440
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aagtggggaa ttaaagcaaa ctgcccttgt atcagtcgac agaacaaatc tgtattgaga
1560
cctgccgtca ccaatgggat gtcacagctt cctagcataa accctagtgc ctcttctgga
1620
aacgaaacta ccttctctgg tggaggagga ccggcaccag taacaactcc agagccggac
1680
catgttccca aagccgacag cactgacatc agatctgaag agcctctgaa aacagacagt
1740
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1800
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<210> 4594
<211> 1145
<212> PRT
<213> Homo sapiens

<400> 4594
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35 40 45
Thr Val Thr Ser Lys Val Ala Pro Ser Trp Pro Glu Ser His Ser Ser
50 55 60
Ala Asp Ser Ala Ser Leu Ala Lys Lys Lys Pro Leu Phe Ile Thr Thr
65 70 75 80
Asp Ser Ser Lys Leu Val Ser Gly Val Leu Gly Ser Ala Leu Thr Ser
85 90 95
Gly Gly Pro Ser Leu Ser Ala Met Gly Asn Gly Arg Ser Ser Ser Pro
100 105 110
Thr Ser Ser Leu Thr Gln Pro Ile Glu Met Pro Thr Leu Ser Ser Ser
115 120 125
Pro Thr Glu Glu Arg Pro Thr Val Gly Pro Gly Gln Gln Asp Asn Pro
130 135 140
Leu Leu Lys Thr Phe Ser Asn Val Phe Gly Arg His Ser Gly Gly Phe
145 150 155 160
Leu Ser Ser Pro Ala Asp Phe Ser Gln Glu Asn Lys Ala Pro Phe Glu
165 170 175
Ala Val Lys Arg Phe Ser Leu Asp Glu Arg Ser Leu Ala Cys Arg Gln

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Asp Ser Asp Ser Ser Thr Asn Ser Asp Leu Ser Asp Leu Ser Asp Ser
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Glu Glu Gln Leu Gln Ala Lys Thr Gly Leu Lys Gly Ile Pro Glu His
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Leu Met Gly Lys Leu Gly Pro Asn Gly Glu Arg Ser Ala Glu Leu Leu
225                 230                 235                 240
Leu Gly Lys Ser Lys Gly Lys Gln Ala Pro Lys Gly Arg Pro Arg Thr
                245                 250                 255
Ala Pro Leu Lys Val Gly Gln Ser Val Leu Lys Asp Val Ser Lys Val
            260                 265                 270
Lys Lys Leu Lys Gln Ser Gly Glu Pro Phe Leu Gln Asp Gly Ser Cys
        275                 280                 285
Ile Asn Val Ala Pro His Leu His Lys Cys Arg Glu Cys Arg Leu Glu
    290                 295                 300
Arg Tyr Arg Lys Phe Lys Glu Gln Glu Gln Asp Asp Ser Thr Val Ala
305                 310                 315                 320
Cys Arg Phe Phe His Phe Arg Arg Leu Ile Phe Thr Arg Lys Gly Val
                325                 330                 335
Leu Arg Val Glu Gly Phe Leu Ser Pro Gln Gln Ser Asp Pro Asp Ala
            340                 345                 350
Met Asn Leu Trp Ile Pro Ser Ser Ser Leu Ala Glu Gly Ile Asp Leu
        355                 360                 365
Glu Thr Ser Lys Tyr Ile Leu Ala Asn Val Gly Asp Gln Phe Cys Gln
    370                 375                 380
Leu Val Met Ser Glu Lys Glu Ala Met Met Met Val Glu Pro His Gln
385                 390                 395                 400
Lys Val Ala Trp Lys Arg Ala Val Arg Gly Val Arg Glu Met Cys Asp
                405                 410                 415
Val Cys Glu Thr Thr Leu Phe Asn Ile His Trp Val Cys Arg Lys Cys
            420                 425                 430
Gly Phe Gly Val Cys Leu Asp Cys Tyr Arg Leu Arg Lys Ser Arg Pro
        435                 440                 445
Arg Ser Glu Thr Glu Glu Met Gly Asp Glu Glu Val Phe Ser Trp Leu
    450                 455                 460
Lys Cys Ala Lys Gly Gln Ser His Glu Pro Glu Asn Leu Met Pro Thr
465                 470                 475                 480
Gln Ile Ile Pro Gly Thr Ala Leu Tyr Asn Ile Gly Asp Met Val His
                485                 490                 495
Ala Ala Arg Gly Lys Trp Gly Ile Lys Ala Asn Cys Pro Cys Ile Ser
            500                 505                 510
Arg Gln Asn Lys Ser Val Leu Arg Pro Ala Val Thr Asn Gly Met Ser
        515                 520                 525
Gln Leu Pro Ser Ile Asn Pro Ser Ala Ser Ser Gly Asn Glu Thr Thr
    530                 535                 540
Phe Ser Gly Gly Gly Gly Pro Ala Pro Val Thr Thr Pro Glu Pro Asp
545                 550                 555                 560
His Val Pro Lys Ala Asp Ser Thr Asp Ile Arg Ser Glu Glu Pro Leu
                565                 570                 575
Lys Thr Asp Ser Ser Ala Ser Asn Ser Asn Ser Glu Leu Lys Ala Ile
            580                 585                 590
Arg Pro Pro Cys Pro Asp Thr Ala Pro Pro Ser Ser Ala Leu His Trp
        595                 600                 605
Leu Ala Asp Leu Ala Thr Gln Lys Ala Lys Glu Glu Thr Lys Glu Ala
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    610                 615                 620
Gly Ser Leu Arg Ser Val Leu Asn Lys Glu Ser His Ser Pro Phe Gly
625                 630                 635                 640
Leu Asp Ser Phe Asn Ser Thr Ala Lys Val Ser Pro Leu Thr Pro Lys
                645                 650                 655
Leu Phe Asn Ser Leu Leu Leu Gly Pro Thr Ala Ser Asn Asn Lys Thr
            660                 665                 670
Glu Gly Ser Ser Leu Arg Asp Leu Leu His Ser Gly Pro Gly Lys Leu
        675                 680                 685
Pro Gln Thr Pro Leu Asp Thr Gly Ile Pro Phe Pro Pro Val Phe Ser
    690                 695                 700
Thr Ser Ser Ala Gly Val Lys Ser Lys Ala Ser Leu Pro Asn Phe Leu
705                 710                 715                 720
Asp His Ile Ile Ala Ser Val Val Glu Asn Lys Lys Thr Ser Asp Ala
                725                 730                 735
Ser Lys Arg Ala Cys Asn Leu Thr Asp Thr Gln Lys Glu Val Lys Glu
            740                 745                 750
Met Val Met Gly Leu Asn Val Leu Asp Pro His Thr Ser His Ser Trp
        755                 760                 765
Leu Cys Asp Gly Arg Leu Leu Cys Leu His Asp Pro Ser Asn Lys Asn
    770                 775                 780
Asn Trp Lys Ile Phe Arg Glu Cys Trp Lys Gln Gly Gln Pro Val Leu
785                 790                 795                 800
Val Ser Gly Val His Lys Lys Leu Lys Ser Glu Leu Trp Lys Pro Glu
                805                 810                 815
Ala Phe Ser Gln Glu Phe Gly Asp Gln Asp Val Asp Leu Val Asn Cys
            820                 825                 830
Arg Asn Cys Ala Ile Ile Ser Asp Val Lys Val Arg Asp Phe Trp Asp
        835                 840                 845
Gly Phe Glu Ile Ile Cys Lys Arg Leu Arg Ser Glu Asp Gly Gln Pro
    850                 855                 860
Met Val Leu Lys Leu Lys Asp Trp Pro Pro Gly Glu Asp Phe Arg Asp
865                 870                 875                 880
Met Met Pro Thr Arg Phe Glu Asp Leu Met Glu Asn Leu Pro Leu Pro
                885                 890                 895
Glu Tyr Thr Lys Arg Asp Gly Arg Leu Asn Leu Ala Ser Arg Leu Pro
            900                 905                 910
Ser Tyr Phe Val Arg Pro Asp Leu Gly Pro Lys Met Tyr Asn Ala Tyr
        915                 920                 925
Gly Leu Ile Thr Ala Glu Asp Arg Arg Val Gly Thr Thr Asn Leu His
    930                 935                 940
Leu Asp Val Ser Asp Ala Val Asn Val Met Val Tyr Val Gly Ile Pro
945                 950                 955                 960
Ile Gly Glu Gly Ala His Asp Glu Glu Val Leu Lys Thr Ile Asp Glu
                965                 970                 975
Gly Asp Ala Asp Glu Val Thr Lys Gln Arg Ile His Asp Gly Lys Glu
            980                 985                 990
Lys Pro Gly Ala Leu Trp His Ile Tyr Ala Ala Lys Asp Ala Glu Lys
        995                 1000                1005
Ile Arg Glu Leu Leu Arg Lys Val Gly Glu Glu Gln Gly Gln Glu Asn
    1010                1015                1020
Pro Pro Asp His Asp Pro Ile His Asp Gln Ser Trp Tyr Leu Asp Gln
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Thr Leu Arg Lys Arg Leu Tyr Glu Glu Tyr Gly Val Gln Gly Trp Ala
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Ile Val Gln Phe Leu Gly Asp Ala Val Phe Ile Pro Ala Gly Ala Pro
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His Gln Val His Asn Leu Tyr Ser Cys Ile Lys Val Ala Glu Asp Phe
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Val Ser Pro Glu His Val Lys His Cys Phe Arg Leu Thr Gln Glu Phe
    1090                1095                1100
Arg His Leu Ser Asn Thr His Thr Asn His Glu Asp Lys Leu Gln Val
1105                1110                1115                1120
Lys Asn Ile Ile Tyr His Ala Val Lys Asp Ala Val Gly Thr Leu Lys
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Ala His Glu Ser Lys Leu Ala Arg Ser
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<211> 935
<212> DNA
<213> Homo sapiens

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120
actcatttgc cccgcaggta gatcttgggg gtctgccagc cttcgggggc ttcctttagc
180
cccgccttca gccagatgcg cctcaggtct ttctcgaact tgatctgctt gcgtctcagg
240
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300
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420
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720
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780
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<210> 4596

<211> 169
<212> PRT
<213> Homo sapiens

<400> 4596
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Arg Lys Gln Arg Ala Val Ser Gln Leu Ser Arg Gly Leu Thr Asp Ile
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Phe Leu Gly Thr Ser Ile Ser Ser Ser Ser Ser Trp Ala Pro Leu Arg
35 40 45
Gly Arg Glu Ala Ala Leu Pro Gly Pro Ala Gly Asp Xaa Ala Val Lys
50 55 60
Gly Pro Ala Asp Pro Ala Ala Gln His Ser Arg Asp Gly Gln Gly Gly
65 70 75 80
Trp Pro Pro Ala Gln Gly Thr Ala Ser Thr Ala Gly Lys Ser Gly Ala
85 90 95
Pro Gly Ala Trp Ser Val Gly Gly Ala Thr Gly Pro Arg Gly Ala Lys
100 105 110
Gly Pro Arg Thr Gly Arg Pro Ala Pro Ser Pro Gly Ser Pro Pro Arg
115 120 125
Glu Ser Arg Cys Leu Ala Pro Gly Pro Ser Arg Leu Asp Pro Gly Pro
130 135 140
Ala Xaa Ala Ala Ala Pro Gly Ala Leu Arg Pro Pro Ala Asp Pro Ser
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Gln Ala Arg Pro Arg Arg Gly Ser Asn
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<210> 4597
<211> 515
<212> DNA
<213> Homo sapiens

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120
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<210> 4598

<211> 135
<212> PRT
<213> Homo sapiens

<400> 4598
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Pro Gly Pro Trp Gly Val Gly Arg Gly Thr Cys Leu Thr Ala Gln Leu
35 40 45
Leu Leu Ser Ala Pro Phe Cys Leu Leu Pro Ala Leu Ser Gln Ala Val
50 55 60
Ser Pro Arg Asn Ser Leu Arg Asn Ile Leu Thr Leu Asn Ser Thr Ala
65 70 75 80
Glu Pro Ser Ser Trp Glu Ser Arg Glu Arg Pro Leu Gln Ser Arg Asn
85 90 95
Val Tyr Ser Ser Ala Ser Phe Ser Glu His Leu Asp Gly Gly Cys Ser
100 105 110
Pro Leu Val Leu Gln Ser Leu Ala Arg Arg Ile Ser Ser Thr Trp Leu
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Val Asp Gln Ser Leu Arg Glu
130 135

<210> 4599
<211> 2314
<212> DNA
<213> Homo sapiens

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240
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720

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780
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2314

<210> 4600
<211> 228
<212> PRT
<213> Homo sapiens

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Ile Met Asn Tyr Leu Val Thr Glu Gly Phe Lys Glu Ala Ala Glu Lys
35 40 45
Phe Arg Met Glu Ser Gly Ile Glu Pro Ser Val Asp Leu Glu Thr Leu
50 55 60
Asp Glu Arg Ile Lys Ile Arg Glu Met Ile Leu Lys Gly Gln Ile Gln
65 70 75 80
Glu Ala Ile Ala Leu Ile Asn Ser Leu His Pro Glu Leu Leu Asp Thr
85 90 95
Asn Arg Tyr Leu Tyr Phe His Leu Gln Gln Gln His Leu Ile Glu Leu
100 105 110
Ile Arg Gln Arg Glu Thr Glu Ala Ala Leu Glu Phe Ala Gln Thr Gln
115 120 125
Leu Ala Glu Gln Gly Glu Glu Ser Arg Glu Cys Leu Thr Glu Met Glu
130 135 140
Arg Thr Leu Ala Leu Leu Ala Phe Asp Ser Pro Glu Glu Ser Pro Phe
145 150 155 160
Gly Asp Leu Leu His Thr Met Gln Arg Gln Lys Val Trp Ser Glu Val
165 170 175
Asn Gln Ala Val Leu Asp Tyr Glu Asn Arg Glu Ser Thr Pro Lys Leu
180 185 190
Ala Lys Leu Leu Lys Leu Leu Leu Trp Ala Gln Asn Glu Leu Asp Gln
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Lys Lys Val Lys Tyr Pro Lys Met Thr Asp Leu Ser Lys Gly Val Ile
210 215 220
Glu Glu Pro Lys
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<210> 4601
<211> 916
<212> DNA
<213> Homo sapiens

<400> 4601
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180
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240
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300

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360
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600
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660
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720
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<210> 4602
<211> 305
<212> PRT
<213> Homo sapiens

<400> 4602
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Ala Val Arg Ser Tyr Tyr Glu Val Phe Leu Lys Ser Asp Arg Val Ala
35 40 45
Arg Met Val Gln Ser Gly Gly Cys Ser Ala Asn Asp Phe Arg Glu Val
50 55 60
Phe Lys Lys Asn Ile Glu Lys Arg Val Arg Ser Leu Pro Glu Ile Asp
65 70 75 80
Gly Leu Ser Lys Glu Thr Val Leu Ser Ser Trp Ile Ala Lys Tyr Asp
85 90 95
Ala Ile Tyr Arg Gly Glu Glu Asp Leu Cys Lys Gln Pro Asn Arg Met
100 105 110
Ala Leu Ser Ala Val Ser Glu Leu Ile Leu Ser Lys Glu Gln Leu Tyr
115 120 125
Glu Met Phe Gln Gln Ile Leu Gly Ile Lys Lys Leu Glu His Gln Leu
130 135 140
Leu Tyr Asn Ala Cys Gln Leu Asp Asn Ala Asp Glu Gln Ala Ala Gln
145 150 155 160
Ile Arg Arg Glu Leu Asp Gly Arg Leu Gln Leu Ala Asp Lys Met Ala
165 170 175
Lys Glu Arg Lys Phe Pro Lys Phe Ile Ala Lys Asp Met Glu Asn Met
180 185 190
Tyr Ile Glu Glu Leu Arg Ser Ser Val Asn Leu Leu Met Ala Asn Leu

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Glu Ser Leu Pro Val Ser Lys Gly Gly Pro Glu Phe Lys Leu Gln Lys
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Leu Lys Arg Ser Gln Asn Ser Ala Phe Leu Asp Ile Gly Asp Glu Asn
225                 230                 235                 240
Glu Ile Gln Leu Ser Lys Ser Asp Val Val Leu Ser Phe Thr Leu Glu
                245                 250                 255
Ile Val Ile Met Glu Val Gln Gly Leu Lys Ser Val Ala Pro Asn Arg
            260                 265                 270
Ile Val Tyr Cys Thr Met Glu Val Glu Gly Glu Lys Leu Gln Thr Asp
        275                 280                 285
Gln Ala Glu Ala Ser Arg Pro Gln Trp Gly Asp Ser Gly Glu Phe His
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Pro
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<210> 4603
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<212> DNA
<213> Homo sapiens

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960
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<210> 4604
<211> 666
<212> PRT
<213> Homo sapiens

<400> 4604
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35 40 45
Glu Ser Glu Ser Pro Gln Glu Ala Gly Arg Gly His Pro Ser Phe Leu
50 55 60
Pro Gln Gln Lys Glu Ser Ser Glu Ala Ser Glu Leu Ile Leu Tyr Ser

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65                  70                  75                  80
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Lys Glu Val Glu Ala Gly Pro Gly Asp Gln Gln Gly Asp Ser Tyr Leu
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Arg Val Ser Ser Asp Ser Pro Lys Asp Gln Ser Pro Pro Glu Asp Ser
        115                 120                 125
Gly Glu Ser Glu Ala Asp Leu Glu Cys Ser Phe Ala Ala Ile His Ser
    130                 135                 140
Pro Ala Pro Pro Pro Asp Pro Ala Pro Arg Phe Ala Thr Ser Leu Pro
145                 150                 155                 160
His Phe Pro Gly Cys Ala Gly Pro Thr Glu Asp Glu Leu Ser Leu Pro
                165                 170                 175
Glu Gly Pro Ser Val Pro Ser Ser Ser Leu Pro Gln Thr Pro Glu Gln
            180                 185                 190
Glu Lys Phe Leu Arg His His Phe Glu Thr Leu Thr Glu Ser Pro Cys
        195                 200                 205
Arg Ala Leu Gly Asp Val Glu Ala Ser Glu Ala Glu Asp His Phe Phe
    210                 215                 220
Asn Pro Arg Leu Ser Ile Ser Thr Gln Phe Leu Ser Ser Leu Gln Lys
225                 230                 235                 240
Ala Ser Arg Phe Thr His Thr Phe Pro Pro Arg Ala Thr Gln Cys Leu
                245                 250                 255
Val Lys Ser Pro Glu Val Lys Leu Met Asp Arg Gly Gly Ser Gln Pro
            260                 265                 270
Arg Ala Gly Thr Gly Tyr Ala Ser Pro Asp Arg Thr His Val Leu Ala
        275                 280                 285
Ala Gly Lys Ala Glu Glu Thr Leu Glu Ala Trp Arg Pro Pro Pro Pro
    290                 295                 300
Cys Leu Thr Ser Leu Ala Ser Cys Val Pro Ala Ser Ser Val Leu Pro
305                 310                 315                 320
Thr Asp Arg Asn Leu Pro Thr Pro Thr Ser Ala Pro Thr Pro Gly Leu
                325                 330                 335
Ala Gln Gly Val His Ala Pro Ser Thr Cys Ser Tyr Met Glu Ala Thr
            340                 345                 350
Ala Ser Ser Arg Ala Arg Ile Ser Arg Ser Ile Ser Leu Gly Asp Ser
        355                 360                 365
Glu Gly Pro Ile Val Ala Thr Leu Ala Gln Pro Leu Arg Arg Pro Ser
    370                 375                 380
Ser Val Gly Glu Leu Ala Ser Leu Gly Gln Glu Leu Gln Ala Ile Thr
385                 390                 395                 400
Thr Ala Thr Thr Pro Ser Leu Asp Ser Glu Gly Gln Glu Pro Ala Leu
                405                 410                 415
Arg Ser Trp Gly Asn His Glu Ala Arg Ala Asn Leu Arg Leu Thr Leu
            420                 425                 430
Ser Ser Ala Cys Asp Gly Leu Leu Leu Pro Pro Val Asp Thr Gln Pro
        435                 440                 445
Gly Val Thr Val Pro Ala Val Ser Phe Pro Ala Pro Ser Pro Val Glu
    450                 455                 460
Glu Ser Ala Leu Arg Leu His Gly Ser Ala Phe Arg Pro Ser Leu Pro
465                 470                 475                 480
Ala Pro Glu Ser Pro Gly Leu Pro Ala His Pro Ser Asn Pro Gln Leu
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Pro Glu Ala Arg Pro Gly Ile Pro Gly Gly Thr Ala Ser Leu Leu Glu
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Ser Glu Pro Trp Val Pro Val Glu Ala Leu Pro Pro Ser Pro Leu Glu
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Leu Ser Gly Trp Gly Thr Ser Cys Thr Gly Cys Arg Pro Pro Ser Lys
545                 550                 555                 560
Lys Pro Ser Thr Phe Thr Val Cys Trp Ser Pro Val Ala Arg Trp Thr
                565                 570                 575
Pro Gly Ser Ser Arg His Gly Leu Ser Trp Ser Pro Pro Ser Cys Gly
            580                 585                 590
Ser Thr Ala Ser Trp Arg Leu Asn Ala Trp Trp Gly Leu Val Trp Pro
        595                 600                 605
Gln Pro Arg Leu Cys Pro Ala Gln Asp Pro Arg Pro His Arg Arg Cys
    610                 615                 620
Thr Pro Trp Pro Ala Gln Thr Cys Arg Pro Cys Trp Asn Thr Thr Arg
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Ser Cys Trp Cys Arg Pro Cys Gly Gly Arg His Gly Gly Thr Glu Gly
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<211> 2998
<212> DNA
<213> Homo sapiens

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<211> 584
<212> PRT
<213> Homo sapiens

<400> 4606
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35 40 45
Asp Ser Gly Gly Arg Thr Lys Arg Tyr Val Val Phe Asn Asn Gly Thr
50 55 60
Leu Tyr Phe Asn Glu Val Gly Met Arg Glu Glu Gly Asp Tyr Thr Cys
65 70 75 80
Phe Ala Glu Asn Gln Val Gly Lys Asp Glu Met Arg Val Arg Val Lys
85 90 95
Val Val Thr Ala Pro Ala Thr Ile Arg Asn Lys Thr Cys Leu Ala Val
100 105 110
Gln Val Pro Tyr Gly Asp Val Val Thr Val Ala Cys Glu Ala Lys Gly
115 120 125
Glu Pro Met Pro Lys Val Thr Trp Leu Ser Pro Thr Asn Lys Val Ile
130 135 140
Pro Thr Ser Ser Glu Lys Tyr Gln Ile Tyr Gln Asp Gly Thr Leu Leu
145 150 155 160
Ile Gln Lys Ala Gln Arg Ser Asp Ser Gly Asn Tyr Thr Cys Leu Val
165 170 175
Arg Asn Ser Ala Gly Glu Asp Arg Lys Thr Val Trp Ile His Val Asn
180 185 190
Val Gln Pro Pro Lys Ile Asn Gly Asn Pro Asn Pro Ile Thr Thr Val
195 200 205
Arg Glu Ile Ala Ala Gly Gly Ser Arg Lys Leu Ile Asp Cys Lys Ala

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Glu Gly Ile Pro Thr Pro Arg Val Leu Trp Ala Phe Pro Glu Gly Val
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Val Leu Pro Ala Pro Tyr Tyr Gly Asn Arg Ile Thr Val His Gly Asn
                245                 250                 255
Gly Ser Leu Asp Ile Arg Ser Leu Arg Lys Ser Asp Ser Val Gln Leu
            260                 265                 270
Val Cys Met Ala Arg Asn Glu Gly Gly Glu Ala Arg Leu Ile Leu Gln
        275                 280                 285
Leu Thr Val Leu Glu Pro Met Glu Lys Pro Ile Phe His Asp Pro Ile
    290                 295                 300
Ser Glu Lys Ile Thr Ala Met Ala Gly His Thr Ile Ser Leu Asn Cys
305                 310                 315                 320
Ser Ala Ala Gly Thr Pro Thr Pro Ser Leu Val Trp Val Leu Pro Asn
                325                 330                 335
Gly Thr Asp Leu Gln Ser Gly Gln Gln Leu Gln Arg Phe Tyr His Lys
            340                 345                 350
Ala Asp Gly Met Leu His Ile Ser Gly Leu Ser Ser Val Asp Ala Gly
        355                 360                 365
Ala Tyr Arg Cys Val Ala Arg Asn Ala Ala Gly His Thr Glu Arg Leu
    370                 375                 380
Val Ser Leu Lys Val Gly Leu Lys Pro Glu Ala Asn Lys Gln Tyr His
385                 390                 395                 400
Asn Leu Val Ser Ile Ile Asn Gly Glu Thr Leu Lys Leu Pro Cys Thr
                405                 410                 415
Pro Pro Gly Ala Gly Gln Gly Arg Phe Ser Trp Thr Leu Pro Asn Gly
            420                 425                 430
Met His Leu Glu Gly Pro Gln Thr Leu Gly Arg Val Ser Leu Leu Asp
        435                 440                 445
Asn Gly Thr Leu Thr Val Arg Glu Ala Ser Val Phe Asp Arg Gly Thr
    450                 455                 460
Tyr Val Cys Arg Met Glu Thr Glu Tyr Gly Pro Ser Val Thr Ser Ile
465                 470                 475                 480
Pro Val Ile Val Ile Ala Tyr Pro Pro Arg Ile Thr Ser Glu Pro Thr
                485                 490                 495
Pro Val Ile Tyr Thr Arg Pro Gly Asn Thr Val Lys Leu Asn Cys Met
            500                 505                 510
Ala Met Gly Ile Pro Lys Ala Asp Ile Thr Trp Glu Leu Pro Asp Lys
        515                 520                 525
Ser His Leu Lys Ala Gly Val Gln Ala Arg Leu Tyr Gly Asn Arg Phe
    530                 535                 540
Leu His Pro Gln Gly Ser Leu Thr Ile Gln His Ala Thr Gln Arg Asp
545                 550                 555                 560
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                565                 570                 575
Lys Thr Thr Tyr Ile His Val Phe
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<211> 456
<212> DNA
<213> Homo sapiens

<400> 4607
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<211> 107
<212> PRT
<213> Homo sapiens

<400> 4608
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Phe Gln Met Thr Gln Glu Val Val Cys Asp Glu Cys Pro Asn Val Lys
35 40 45
Leu Val Asn Glu Glu Arg Thr Leu Glu Val Glu Ile Glu Pro Gly Val
50 55 60
Arg Asp Gly Met Glu Tyr Pro Phe Ile Gly Glu Gly Glu Pro His Val
65 70 75 80
Asp Gly Xaa Pro Gly Asp Leu Arg Phe Arg Ile Lys Val Val Lys His
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Pro Ile Phe Glu Arg Arg Gly Asp Asp Leu Tyr
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<211> 904
<212> DNA
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<211> 250
<212> PRT
<213> Homo sapiens

<400> 4610
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35 40 45
Gly Gly Thr Lys Val Pro Leu Glu Ala Arg Pro Val Arg Phe Leu Asp
50 55 60
Asn Phe Ser Ser Gly Arg Arg Gly Ala Thr Ser Ala Glu Ala Phe Leu
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Ala Ala Gly Tyr Gly Val Leu Phe Leu Tyr Arg Ala Arg Ser Ala Phe
85 90 95
Pro Tyr Ala His Arg Phe Pro Pro Gln Thr Trp Leu Ser Ala Leu Arg
100 105 110
Pro Ser Gly Pro Ala Leu Ser Gly Leu Leu Ser Leu Glu Ala Glu Glu
115 120 125
Asn Ala Leu Pro Gly Phe Ala Glu Ala Leu Arg Ser Tyr Gln Glu Ala
130 135 140
Ala Ala Ala Gly Thr Phe Leu Ala Val Glu Phe Thr Thr Leu Ala Asp
145 150 155 160
Tyr Leu His Leu Leu Gln Ala Ala Ala Gln Ala Leu Asn Pro Leu Gly
165 170 175
Pro Ser Ala Met Phe Tyr Leu Ala Ala Ala Val Ser Asp Phe Tyr Val
180 185 190
Pro Val Ser Glu Met Pro Glu His Lys Ile Gln Ser Ser Gly Gly Pro

195 200 205
Leu Gln Gly Lys Val Gln Leu Glu Asp Ile Leu His His Leu Glu Lys
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Leu Ile Pro Ala Ser Thr Val Lys Thr Gly
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<211> 1946
<212> DNA
<213> Homo sapiens

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1946

<210> 4612
<211> 532
<212> PRT
<213> Homo sapiens

<400> 4612
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Ala Ala Ala Ala Ile Ala Val Ala Ala Ala Glu Glu Glu Arg Arg Leu
35 40 45
Arg Gln Arg Asn Arg Leu Arg Leu Glu Glu Asp Lys Pro Ala Val Glu
50 55 60
Arg Cys Leu Glu Glu Leu Val Phe Gly Asp Val Glu Asn Asp Glu Asp
65 70 75 80
Ala Leu Leu Arg Arg Leu Arg Gly Pro Arg Val Gln Glu His Glu Asp
85 90 95
Ser Gly Asp Ser Glu Val Glu Asn Glu Ala Lys Gly Asn Phe Pro Pro
100 105 110
Gln Lys Lys Pro Val Trp Val Asp Glu Glu Asp Glu Asp Glu Glu Met
115 120 125
Val Asp Met Met Asn Asn Arg Phe Arg Lys Asp Met Met Lys Asn Ala
130 135 140
Ser Glu Ser Lys Leu Ser Lys Asp Asn Leu Lys Lys Arg Leu Lys Glu
145 150 155 160
Glu Phe Gln His Ala Met Gly Gly Val Pro Ala Trp Ala Glu Thr Thr

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Leu Leu Gln Arg Thr Gly Asn Phe Ile Ser Thr Ser Thr Ser Leu Pro
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Arg Gly Ile Leu Lys Met Lys Asn Cys Gln His Ala Asn Ala Glu Arg
    210                 215                 220
Pro Thr Val Ala Arg Ile Ser Ser Val Gln Phe His Pro Gly Ala Gln
225                 230                 235                 240
Ile Val Met Val Ala Gly Leu Asp Asn Ala Val Ser Leu Phe Gln Val
                245                 250                 255
Asp Gly Lys Thr Asn Pro Lys Ile Gln Ser Ile Tyr Leu Glu Arg Phe
            260                 265                 270
Pro Ile Phe Lys Ala Cys Phe Ser Ala Asn Gly Glu Glu Val Leu Ala
        275                 280                 285
Thr Ser Thr His Ser Lys Val Leu Tyr Val Tyr Asp Met Leu Ala Gly
    290                 295                 300
Lys Leu Ile Pro Val His Gln Val Arg Gly Leu Lys Glu Lys Ile Val
305                 310                 315                 320
Arg Ser Phe Glu Val Ser Pro Asp Gly Ser Phe Leu Leu Ile Asn Gly
                325                 330                 335
Ile Ala Gly Tyr Leu His Leu Leu Ala Met Lys Thr Lys Glu Leu Ile
            340                 345                 350
Gly Ser Met Lys Ile Asn Gly Arg Val Ala Ala Ser Thr Phe Ser Ser
        355                 360                 365
Asp Ser Lys Lys Val Tyr Ala Ser Ser Gly Asp Gly Glu Val Tyr Val
    370                 375                 380
Trp Asp Val Asn Ser Arg Lys Cys Leu Asn Arg Phe Val Asp Glu Gly
385                 390                 395                 400
Ser Leu Tyr Gly Leu Ser Ile Ala Thr Ser Arg Asn Gly Gln Tyr Val
                405                 410                 415
Ala Cys Gly Ser Asn Cys Gly Val Val Asn Ile Tyr Asn Gln Asp Ser
            420                 425                 430
Cys Leu Gln Glu Thr Asn Pro Lys Pro Ile Lys Ala Ile Met Asn Leu
        435                 440                 445
Val Thr Gly Val Thr Ser Leu Thr Phe Asn Pro Thr Thr Glu Ile Leu
    450                 455                 460
Ala Ile Ala Ser Glu Lys Met Lys Glu Ala Val Arg Leu Val His Leu
465                 470                 475                 480
Pro Ser Cys Thr Val Phe Ser Asn Phe Pro Val Ile Lys Asn Lys Asn
                485                 490                 495
Ile Ser His Val His Thr Met Asp Phe Ser Pro Arg Ser Gly Tyr Phe
            500                 505                 510
Ala Leu Gly Asn Glu Lys Gly Lys Ala Leu Met Tyr Arg Leu His His
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Tyr Ser Asp Phe
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<210> 4613
<211> 454
<212> DNA
<213> Homo sapiens

<400> 4613

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240
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454

<210> 4614
<211> 117
<212> PRT
<213> Homo sapiens

<400> 4614
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Glu Phe Thr Asn Gly Asn Leu Thr Met Ser Asn Glu Phe His Cys Lys
35 40 45
Asp Phe Leu Ile Phe Thr Thr Gln Ile Leu Thr Ile Leu Gln Leu Arg
50 55 60
Ser Leu Asn Ile Ile Tyr Asn Lys Gln Asn Leu Val Asn Leu Gln Lys
65 70 75 80
Ser Asn Ala Leu Lys Lys His Gln Ser Leu Cys Met Cys Arg Thr Asp
85 90 95
Pro Ala Pro Gln Gly Asn Thr Ala Gly Thr Val Pro Arg Thr Leu Thr
100 105 110
Ser Val Ser Leu Leu
115

<210> 4615
<211> 1350
<212> DNA
<213> Homo sapiens

<400> 4615
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240

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1350

<210> 4616
<211> 188
<212> PRT
<213> Homo sapiens

<400> 4616
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20 25 30
Arg Lys Asp Met Asp Glu Val Glu Glu Lys Ser Lys Asp Val Ile Asn
35 40 45
Phe Thr Ala Glu Lys Leu Ser Val Asp Glu Val Ser Gln Leu Val Ile
50 55 60
Ser Pro Leu Cys Gly Ala Ile Ser Leu Phe Val Gly Thr Thr Arg Asn

65 70 75 80
Asn Phe Glu Gly Lys Lys Val Ile Ser Leu Glu Tyr Glu Ala Tyr Leu
85 90 95
Pro Met Ala Glu Asn Glu Val Arg Lys Ile Cys Ser Asp Ile Arg Gln
100 105 110
Lys Trp Pro Val Lys His Ile Ala Val Phe His Leu Leu Gly Leu Val
115 120 125
Pro Val Ser Glu Ala Ser Thr Val Ile Ala Val Ser Ser Ala His Arg
130 135 140
Ala Ala Ser Leu Glu Ala Val Ser Tyr Ala Ile Asp Ser Leu Lys Ala
145 150 155 160
Lys Val Pro Ile Trp Lys Lys Glu Ile Tyr Glu Glu Ser Ser Thr Trp
165 170 175
Lys Gly Asn Lys Glu Cys Phe Trp Ala Ser Asn Ser
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<210> 4617
<211> 2266
<212> DNA
<213> Homo sapiens

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<210> 4618
<211> 197
<212> PRT
<213> Homo sapiens

<400> 4618
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Gln Pro Thr Ala Glu Pro Gly Leu Gly Ala Val Val Arg Ser Ile Lys
        35                  40                  45
Val Ser Gly Tyr Leu Asn Leu Leu Ala Asn Thr Ile Asp Asn Phe Thr
    50                  55                  60
His Gly Leu Ala Val Ala Ala Ser Phe Leu Val Ser Lys Lys Ile Gly
65                  70                  75                  80
Leu Leu Thr Thr Met Ala Ile Leu Leu His Glu Ile Pro His Glu Val
                85                  90                  95
Gly Asp Phe Ala Ile Leu Leu Arg Ala Gly Phe Asp Arg Trp Ser Ala
            100                 105                 110
Ala Lys Leu Gln Leu Ser Thr Ala Leu Gly Gly Leu Leu Gly Ala Gly
        115                 120                 125
Phe Ala Ile Cys Thr Gln Ser Pro Lys Gly Val Glu Glu Thr Ala Ala
    130                 135                 140
Trp Val Leu Pro Phe Thr Ser Gly Gly Phe Leu Tyr Ile Ala Leu Val
145                 150                 155                 160
Asn Val Leu Pro Asp Leu Leu Glu Glu Glu Asp Pro Trp Arg Ser Leu
                165                 170                 175
Gln Gln Leu Leu Leu Leu Cys Ala Gly Ile Val Val Met Val Leu Phe
            180                 185                 190
Ser Leu Phe Val Asp
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<210> 4619
<211> 539
<212> DNA
<213> Homo sapiens

<400> 4619
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<210> 4620
<211> 103
<212> PRT
<213> Homo sapiens

<400> 4620
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20 25 30
Leu Gln Ala Arg Pro Asn Pro Arg Phe Pro Gly Arg Cys Thr Pro Gly
35 40 45
Trp Glu Lys Leu Thr Asn Glu Ser Ser Trp Gln Pro Pro Gln Ala Pro
50 55 60
Pro Asp Trp Ala Ser Trp Leu Cys Cys Gln Asp Tyr Asp Pro Leu Pro
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Glu Ser Arg Arg Ser Pro Gln Ala Glu Arg Tyr Arg His Leu Cys Pro
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Tyr Leu Asn Gln Glu Val Pro
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<210> 4621
<211> 2588
<212> DNA
<213> Homo sapiens

<400> 4621
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2588

<210> 4622
<211> 403
<212> PRT
<213> Homo sapiens

<400> 4622
Met Ser Gly Ser Asp Gly Gly Leu Glu Glu Glu Pro Glu Leu Ser Ile
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Thr Leu Thr Leu Arg Met Leu Met His Gly Lys Glu Val Gly Ser Ile
20 25 30
Ile Gly Lys Lys Gly Glu Thr Val Lys Arg Ile Arg Glu Gln Ser Ser
35 40 45
Ala Arg Ile Thr Ile Ser Glu Gly Ser Cys Pro Glu Arg Ile Thr Thr
50 55 60
Ile Thr Gly Ser Thr Ala Ala Val Phe His Ala Val Ser Met Ile Ala
65 70 75 80
Phe Lys Leu Asp Glu Asp Leu Cys Ala Ala Pro Ala Asn Gly Gly Asn
85 90 95
Val Ser Arg Pro Pro Val Thr Leu Arg Leu Val Ile Pro Ala Ser Gln
100 105 110
Cys Gly Ser Leu Ile Gly Lys Ala Gly Thr Lys Ile Lys Glu Ile Arg
115 120 125
Glu Thr Thr Gly Ala Gln Val Gln Val Ala Gly Asp Leu Leu Pro Asn
130 135 140
Ser Thr Glu Arg Ala Val Thr Val Ser Gly Val Pro Asp Ala Ile Ile
145 150 155 160
Leu Cys Val Arg Gln Ile Cys Ala Val Ile Leu Glu Ser Pro Pro Lys
165 170 175
Gly Ala Thr Ile Pro Tyr His Pro Ser Leu Ser Leu Gly Thr Val Leu
180 185 190
Leu Ser Ala Asn Gln Gly Phe Ser Val Gln Gly Gln Tyr Gly Ala Val
195 200 205
Thr Pro Ala Glu Val Thr Lys Leu Gln Gln Leu Ser Ser His Ala Val
210 215 220
Pro Phe Ala Thr Pro Ser Val Val Pro Gly Leu Asp Pro Gly Thr Gln
225 230 235 240
Thr Ser Ser Gln Glu Phe Leu Val Pro Asn Asp Leu Ile Gly Cys Val
245 250 255
Ile Gly Arg Gln Gly Ser Lys Ile Ser Glu Ile Arg Gln Met Ser Gly
260 265 270
Ala His Ile Lys Ile Gly Asn Gln Ala Glu Gly Ala Gly Glu Arg His
275 280 285
Val Thr Ile Thr Gly Ser Pro Val Ser Ile Ala Leu Ala Gln Tyr Leu
290 295 300
Ile Thr Ala Cys Leu Glu Thr Ala Lys Ser Thr Ser Gly Gly Thr Pro
305 310 315 320
Gly Ser Ala Pro Ala Asp Leu Pro Thr Pro Phe Ser Pro Pro Leu Thr
325 330 335
Ala Leu Pro Thr Ala Pro Pro Gly Leu Leu Gly Thr Pro Tyr Ala Ile
340 345 350
Ser Leu Ser Asn Phe Ile Gly Leu Lys Pro Val Pro Phe Leu Ala Leu

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        355                 360                 365
Pro Pro Ala Ser Pro Gly Pro Pro Pro Gly Leu Ala Ala Tyr Thr Ala
    370                 375                 380
Lys Met Ala Ala Ala Asn Gly Ser Lys Lys Ala Glu Arg Gln Lys Phe
385                 390                 395                 400
Ser Pro Tyr
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<210> 4623
<211> 2220
<212> DNA
<213> Homo sapiens

<400> 4623
ntgatcacca agacacacaa agtagacctt gggctcccag agaagaaaaa gaagaagaaa
60
gtggtcaaag aaccagagac tcgatactca gttttaaaca atgatgatta ctttgctgat
120
gtttctcctt taagagctac atccccctct aagagtgtgg cccatgggca ggcacctgag
180
atgcctctag tgaagaaaaa gaagaagaaa aagaagggtg tcagcaccct ttgcgaggag
240
catgtagaac ctgagaccac gctgcctgct agacggacag agaagtcacc cagcctcagg
300
aagcaggtgt ttggccactt ggagttcctc agtggggaaa agaaaaataa gaagtcacct
360
ctagccatgt cccatgcctc tggggtgaaa acctccccag accctagaca gggtgaggag
420
gaaaccagag ttggcaagaa gctcaaaaaa cacaagaagg aaaaaaaggg ggcccaggac
480
cccacagcct tctcggtcca ggacccttgg ttctgtgagg ccagggaggc cagggatgtt
540
ggggacactt gctcagtggg gaagaaggat gaggaacagg cagccttggg gcagaaacgg
600
aagcggaaga gccccagaga acacaatggg aaggtgaaga agaaaaaaaa aatccaccag
660
gagggagatg ccctcccagg ccactccaag ccctccaggt ccatggagag cagccctagg
720
aaaggaagta aaaagaagcc agtcaaagtt gaggctccgg aatacatccc cataagtgat
780
gaccctaagg cctccgcaaa gaaaaagatg aagtccaaaa agaaggtaga gcagccagtc
840
atcgaggagc cagctctgaa aaggaagaaa aagaagaaga ggaaagagag tggggtagca
900
ggagaccctt ggaaggagga aacagacacg gacttagagg tggtgttgga aaaaaaaggc
960
aacatggatg aggcgcacat agaccaggtg aggcgaaagg ccttgcaaga agagatcgat
1020
cgcgagtcag gcaaaacgga agcttctgaa accaggaagt ggacgggaac ccagtttggc
1080
cagtgggata ctgctggttt tgagaacgag gaccaaaaac tgaaatttct cagacttatg
1140
ggtggcttca aaaacctgtc cccttcgttc agccgccccg ccagcacgat tgcaaggccc
1200

aacatggccc tcggcaagaa ggcggctgac agcctgcagc agaatctgca gcgggactac
1260
gaccgggcca tgagctggaa gtacagccgg ggagccggcc tcggcttctc caccgccccc
1320
aacaagatct tttacattga caggaacgct tccaagtcag tcaagctgga agattaaact
1380
ctagagtttt gtccccccaa aactgccaca attgctttga ttattccatt tatgctggag
1440
attacaaatt ttttttgtga aaaaatcaga tcttggtgag gacctcgagc agtaagatat
1500
aaataactcc cataagctta gcgttccagt aatggaacac taggcataaa tggtttattc
1560
agttgtgcaa atgaaagcca tctgacagtt ggctcacatt gaacacctgt ggagattaag
1620
gacgaggaca actatattga tgggcttgga tgaactgggg cagggcagct catatttcgg
1680
gagccaggag aacgagtgag tgctaaaacc tcctgttttc tgtgttaaac attccgtccc
1740
tgtttgagac atcagtatgt acagttaact tttgttgagt gtttagcagg tactagggac
1800
atactagtgt tttccttaat gtatttaatc ttcataatta tgaaatgggt gctattatta
1860
gccccatctt atagatgagg caactgaggt tcagggataa agtaataaaa ttgcctgggg
1920
tcacccagcc actaagtgca gggtgttgta cttttgtacc cgaagcccta agttcactat
1980
tcgccactct gaatgtcccc tttagggaat ttccaccaga atcctcgttg gggattgaaa
2040
tgtctttaga tggaggaaaa agttttatga caagtctgca tctctgataa aaagtggagt
2100
gaatgaggaa cggagaatcg caagctcctt ttccttcctt ttcctttccc ctgtcataga
2160
gcagctgtag gcagagaggt gtctgagttg ttaccaaaca catgtgactg agctgctgct
2220

<210> 4624
<211> 189
<212> PRT
<213> Homo sapiens

<400> 4624
Met Lys Ser Lys Lys Lys Val Glu Gln Pro Val Ile Glu Glu Pro Ala
 1   5   10   15
Leu Lys Arg Lys Lys Lys Lys Lys Arg Lys Glu Ser Gly Val Ala Gly
            20   25   30
Asp Pro Trp Lys Glu Glu Thr Asp Thr Asp Leu Glu Val Val Leu Glu
        35   40   45
Lys Lys Gly Asn Met Asp Glu Ala His Ile Asp Gln Val Arg Arg Lys
    50   55   60
Ala Leu Gln Glu Glu Ile Asp Arg Glu Ser Gly Lys Thr Glu Ala Ser
65   70   75   80
Glu Thr Arg Lys Trp Thr Gly Thr Gln Phe Gly Gln Trp Asp Thr Ala
                85   90   95
Gly Phe Glu Asn Glu Asp Gln Lys Leu Lys Phe Leu Arg Leu Met Gly

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            100                 105                 110
Gly Phe Lys Asn Leu Ser Pro Ser Phe Ser Arg Pro Ala Ser Thr Ile
        115                 120                 125
Ala Arg Pro Asn Met Ala Leu Gly Lys Lys Ala Ala Asp Ser Leu Gln
    130                 135                 140
Gln Asn Leu Gln Arg Asp Tyr Asp Arg Ala Met Ser Trp Lys Tyr Ser
145                 150                 155                 160
Arg Gly Ala Gly Leu Gly Phe Ser Thr Ala Pro Asn Lys Ile Phe Tyr
                165                 170                 175
Ile Asp Arg Asn Ala Ser Lys Ser Val Lys Leu Glu Asp
            180                 185
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<210> 4625
<211> 334
<212> DNA
<213> Homo sapiens

<400> 4625
cgggagcagc ggaagctgca ggagaaggag cagcagcggc ggctggagga catgcaggct
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ctgcggcggg aggaggagcg gcggcaggcg gagcgcgagc aggaatacaa gcggaaacag
120
ctggaggagc agcggcagtc agaacgtctc cagaggcagc tgcagcagga gcatgcctac
180
ctaaagtccc tgcagcagca gcaacagcag cagcagcttc agaaacagca gcagcagcag
240
ctcctgcctg gggacaggaa gcccctgtac cattatgggc ggggcatgaa tcccgctgac
300
aaaccagcct gggcccgaga gggagaagag agac
334

<210> 4626
<211> 111
<212> PRT
<213> Homo sapiens

<400> 4626
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Arg Glu Gln Arg Lys Leu Gln Glu Lys Glu Gln Gln Arg Arg Leu Glu
 1               5                  10                  15
Asp Met Gln Ala Leu Arg Arg Glu Glu Glu Arg Arg Gln Ala Glu Arg
            20                  25                  30
Glu Gln Glu Tyr Lys Arg Lys Gln Leu Glu Glu Gln Arg Gln Ser Glu
        35                  40                  45
Arg Leu Gln Arg Gln Leu Gln Gln Glu His Ala Tyr Leu Lys Ser Leu
    50                  55                  60
Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Lys Gln Gln Gln Gln Gln
65                  70                  75                  80
Leu Leu Pro Gly Asp Arg Lys Pro Leu Tyr His Tyr Gly Arg Gly Met
                85                  90                  95
Asn Pro Ala Asp Lys Pro Ala Trp Ala Arg Glu Gly Glu Glu Arg
            100                 105                 110
```

<210> 4627
<211> 1736

<212> DNA
<213> Homo sapiens

<400> 4627
nnagttgcct tgacctgcag ctccggcacc gcggacccgc cttctgccct cagcagcaga
60
cgctctgtcc cgcccgggca gctctgcgag gcagcggctg gagagggaac catggggact
120
gtgcacgccc ggagtttgga gcctcttcca tcaagtggac ctgattttgg aggattagga
180
gaagaagctg aatttgttga agttgagcct gaagctaaac aggaaattct tgaaaacaaa
240
gatgtggttg ttcaacatgt tcattttgat ggacttggaa ggactaaaga tgatatcatc
300
atttgtgaaa ttggagatgt tttcaaggcc aaaaacctaa ttgaggtaat gcggaaatct
360
catgaagccc gtgaaaaatt gctccgtctt ggaattttta gacaagtgga tgttttgatt
420
gacacatgtc aaggtgatgg cgcacttcca aatgggttag acgttacctt tgaagtaact
480
gaattgagga gattaacggg cagttataac accatggttg ggaacaatga aggcagtatg
540
gtacttggcc tcaagcttcc taatcttctt ggtcgtgcag aaaaggtgac ctttcagttt
600
tcctatggaa caaaagaaac ttcgtatggc ctgtccttct tcaaaccacg gcccggaaac
660
ttcgaaagaa atttctctgt aaacttatat aaagttactg gacagttccc ttggagctca
720
ctgcgggaga cggacagagg aatgtcagct gagtacagtt ttcccatatg gaagaccagc
780
cacactgtca agtgggaagg cgtatggcga gaactgggct gcctctcaag gacggcgtca
840
tttgctgttc gaaaagaaag cggacattca ctgaaatcat ctctttcgca cgccatggtc
900
atcgattctc ggaattcttc catcttacca aggagaggtg ctttgctgaa agttaaccag
960
gaactggcag gctacactgg cggggatgtg agcttcatca aagaagattt tgaacttcag
1020
ttgaacaagc aactcatatt tgattcagtt ttttcagcgt ctttctgggg cggaatgttg
1080
gtacccattg gtgataagcc gtcaagcatt gctgataggt tttaccttgg gggacccaca
1140
agcgtccgcg gattcagcat gcacagcatc gggccacaga gcgaaggaga ctacctaggt
1200
ggagaagcgt actgggccgg cggcctgcac ctctacaccc cattaccttt ccggccaggc
1260
cagggtggct ttggagaact tttccgaaca cacttctttc tcaacgcagg aaacctctgc
1320
aacctcaact atggggaggg ccccaaagct catattcgta agctggctga gtgcatccgc
1380
tggtcgtacg gggccgggat tgtcctcagg cttggcaaca tcgctcggtt ggaacttaat
1440
tactgcgtcc ccatgggagt acagacaggc gacaggatat gtgatggcgt ccagtttgga
1500

gctgggataa ggttcctgta gccgacaccc ctacaggaga agctctggga ctggggcagc
1560
agcaaggcgc ccatgccaca caccgtctct cgaggaaacg cggttcagcg attctttgac
1620
tgcggaccct gtgggaaacc ccgtcaataa atgttaaaga cacactcaaa aaaaaaaaaa
1680
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa
1736

<210> 4628
<211> 469
<212> PRT
<213> Homo sapiens

<400> 4628
Met Gly Thr Val His Ala Arg Ser Leu Glu Pro Leu Pro Ser Ser Gly
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Pro Asp Phe Gly Gly Leu Gly Glu Glu Ala Glu Phe Val Glu Val Glu
            20   25   30
Pro Glu Ala Lys Gln Glu Ile Leu Glu Asn Lys Asp Val Val Val Gln
        35   40   45
His Val His Phe Asp Gly Leu Gly Arg Thr Lys Asp Asp Ile Ile Ile
    50   55   60
Cys Glu Ile Gly Asp Val Phe Lys Ala Lys Asn Leu Ile Glu Val Met
65   70   75   80
Arg Lys Ser His Glu Ala Arg Glu Lys Leu Leu Arg Leu Gly Ile Phe
                85   90   95
Arg Gln Val Asp Val Leu Ile Asp Thr Cys Gln Gly Asp Gly Ala Leu
            100   105   110
Pro Asn Gly Leu Asp Val Thr Phe Glu Val Thr Glu Leu Arg Arg Leu
        115   120   125
Thr Gly Ser Tyr Asn Thr Met Val Gly Asn Asn Glu Gly Ser Met Val
    130   135   140
Leu Gly Leu Lys Leu Pro Asn Leu Leu Gly Arg Ala Glu Lys Val Thr
145   150   155   160
Phe Gln Phe Ser Tyr Gly Thr Lys Glu Thr Ser Tyr Gly Leu Ser Phe
                165   170   175
Phe Lys Pro Arg Pro Gly Asn Phe Glu Arg Asn Phe Ser Val Asn Leu
            180   185   190
Tyr Lys Val Thr Gly Gln Phe Pro Trp Ser Ser Leu Arg Glu Thr Asp
        195   200   205
Arg Gly Met Ser Ala Glu Tyr Ser Phe Pro Ile Trp Lys Thr Ser His
    210   215   220
Thr Val Lys Trp Glu Gly Val Trp Arg Glu Leu Gly Cys Leu Ser Arg
225   230   235   240
Thr Ala Ser Phe Ala Val Arg Lys Glu Ser Gly His Ser Leu Lys Ser
                245   250   255
Ser Leu Ser His Ala Met Val Ile Asp Ser Arg Asn Ser Ser Ile Leu
            260   265   270
Pro Arg Arg Gly Ala Leu Leu Lys Val Asn Gln Glu Leu Ala Gly Tyr
        275   280   285
Thr Gly Gly Asp Val Ser Phe Ile Lys Glu Asp Phe Glu Leu Gln Leu
    290   295   300
Asn Lys Gln Leu Ile Phe Asp Ser Val Phe Ser Ala Ser Phe Trp Gly

```
305                 310                 315                 320
Gly Met Leu Val Pro Ile Gly Asp Lys Pro Ser Ser Ile Ala Asp Arg
                325                 330                 335
Phe Tyr Leu Gly Gly Pro Thr Ser Val Arg Gly Phe Ser Met His Ser
            340                 345                 350
Ile Gly Pro Gln Ser Glu Gly Asp Tyr Leu Gly Gly Glu Ala Tyr Trp
        355                 360                 365
Ala Gly Gly Leu His Leu Tyr Thr Pro Leu Pro Phe Arg Pro Gly Gln
    370                 375                 380
Gly Gly Phe Gly Glu Leu Phe Arg Thr His Phe Phe Leu Asn Ala Gly
385                 390                 395                 400
Asn Leu Cys Asn Leu Asn Tyr Gly Glu Gly Pro Lys Ala His Ile Arg
                405                 410                 415
Lys Leu Ala Glu Cys Ile Arg Trp Ser Tyr Gly Ala Gly Ile Val Leu
            420                 425                 430
Arg Leu Gly Asn Ile Ala Arg Leu Glu Leu Asn Tyr Cys Val Pro Met
        435                 440                 445
Gly Val Gln Thr Gly Asp Arg Ile Cys Asp Gly Val Gln Phe Gly Ala
    450                 455                 460
Gly Ile Arg Phe Leu
465
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<210> 4629
<211> 706
<212> DNA
<213> Homo sapiens

<400> 4629
acgcgtgggc cggagaccca gcgtgggggg cgcagaggga gtccccctga gctgggcgcg
60
tcctcccgcg gcggtccgct ccttaagtcc cctgtgcgtc acctccttgc gtcggtcgcc
120
agcacccgca ttgcttcggc cctagtgcag gggcagcacg tgcgcactga accctggagt
180
cctgatctct agcctagctc aaagcctcca ccaggatcgg gtggcagctt ccatttgagg
240
ccatttctag gccagcggcc cagctgccag cttcacgtct cctgagttgg gggatctctg
300
gtcccctgtc ctgctttgtg gccaagggag cccaggatcc tggccagagg atgggcccgc
360
accccactcc tggttctggg tgcagttcgg cagatgggaa tccaggagct cagcttggac
420
accctcccca cctccggctc caagcccggt tccaagagga cccagggctg agcagaggct
480
tgtccccaat atcctccccc gcccctcatc tttcctattt gagggaagac tgacaccctc
540
aaagcccagc tggaggcatc tctgcccatt ctgcttagac ttagcgcacc ctggtctctg
600
ctcgaggaat ctgccctcag ctcccccccat tctgggggtc cacccaacac ccacacacac
660
ttccacggac caccctctct ctccctattg accatgccct cctctc
706

<210> 4630

<211> 140
<212> PRT
<213> Homo sapiens

<400> 4630
Met Val Asn Arg Glu Arg Glu Gly Gly Pro Trp Lys Cys Val Trp Val
1 5 10 15
Leu Gly Gly Pro Pro Glu Trp Gly Glu Leu Arg Ala Asp Ser Ser Ser
20 25 30
Arg Asp Gln Gly Ala Leu Ser Leu Ser Arg Met Gly Arg Asp Ala Ser
35 40 45
Ser Trp Ala Leu Arg Val Ser Val Phe Pro Gln Ile Gly Lys Met Arg
50 55 60
Gly Arg Gly Gly Tyr Trp Gly Gln Ala Ser Ala Gln Pro Trp Val Leu
65 70 75 80
Leu Glu Pro Gly Leu Glu Pro Glu Val Gly Arg Val Ser Lys Leu Ser
85 90 95
Ser Trp Ile Pro Ile Cys Arg Thr Ala Pro Arg Thr Arg Ser Gly Val
100 105 110
Arg Ala His Pro Leu Ala Arg Ile Leu Gly Ser Leu Gly His Lys Ala
115 120 125
Gly Gln Gly Thr Arg Asp Pro Pro Thr Gln Glu Thr
130 135 140

<210> 4631
<211> 2756
<212> DNA
<213> Homo sapiens

<400> 4631
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gcgctgaggg agttcgtggc ggtgacgggc gccgaggagg accgggcccg cttctttctc
120
gagtcggccg gctgggactt gcagatcgcg ctagcgagct tttatgagga cggaggggat
180
gaagacattg tgaccatttc gcaggcaacc cccagttcag tgtccagagg cacagccccc
240
agtgataata gagtgacatc cttcagagac ctcattcatg accaagatga agatgaggag
300
gaagaggaag gccagaggag caggttttat gctgggggct cagagagaag tggacagcag
360
attgttggcc ctcccaggaa gaaaagtccc aacgagctgg tggatgatct ctttaaaggt
420
gccaaagagc atggagctgt agctgtggag cgagtgacca agagccctgg agagaccagt
480
aaaccgagac catttgcagg aggtggctac cgccttgggg cagcaccaga ggaagagtct
540
gcctatgtgg caggagaaaa gaggcagcat tccagccaag atgttcatgt agtattgaaa
600
ctctggaaga gtggattcag cctggataat ggagaactca gaagctacca agacccatcc
660
aatgcccagt ttctggagtc tatccgcaga ggggaggtgc cagcagagct tcggaggcta
720

gctcacggtg gacaggtgaa cttggatatg gaggaccatc gggacgagga ctttgtgaag
780
cccaaaggag ccttcaaagc cttcactggc gagggtcaga aactgggcag cactgccccc
840
caggtgttga gtaccagctc tccagcccaa caggcagaaa atgaagccaa agccagctct
900
tccatcttaa tcgacgaatc agagcctacc acaaacatcc aaattcggct tgcagacggc
960
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1020
gtggatgccc ggccagccat ggctgccacc agctttatcc tcatgactac tttcccgaac
1080
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1140
gtgcagcggt taacataacc gcccagccag ctgcctggcc tccctcctgt gtttcccatg
1200
gccagtggcc atgccccatg gggatcgccc ctcctgcccc cttgtgcata cccagcagtc
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1320
ccttagttgc atttcctggg tttttgtgat gatcaatgga ctttaatgaa aaaaaaaata
1380
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1440
aagcaggctt taattgcttt aaaattatat ttatcttggg gcctgtggga ggaaacttcc
1500
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1560
ccgccagccc cacagatgac tggaggaagg aggggaaatg tgtagaaaga ggcttcgcca
1620
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1680
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1740
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1800
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1860
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1920
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1980
catcctaagt gagttcagaa tcagggtatc ttgccctata agataaacag tcaaaatgcc
2040
accgagctgt tcattagtga tgtgtggcaa atcaaatcaa ctgttgaaga aggggtgagt
2100
tttctgtgct acaagcacct gtcactgttg gtacttgcag gaggcttctg ctgggtatgt
2160
tttggaagtg agtgtcacta cttggctttg cttagcaggt tctgcttcac acttgttctt
2220
tgacctgctg acttgtgact tgcagaaaca taggcagtag tcctagcctg gtaaagaccc
2280
tccaccaccc ctataagttt gattgctatg caggtttggg agaggaggcc tattgggctc
2340

ttggatggaa ccctttcccg tattaaacaa accagagaca gaatcagtgc tgactcagga
2400
tctcctggtt tggaatcgta atgtgcctca atcctctttc caagcaggcc tcaccagtct
2460
ctttctcttt cctgcttcac ccctgcaatg agccaagaac caacactaca tccacctaga
2520
actgcagaag ggcttgtggt ttcaaccaag acccatcctg agcaagggac ttggcttggt
2580
gcttttgatc ccaaagttcc cacaccggca gtggcctgct ggggcaatgg catctgtcac
2640
ggtgttttct ccagcaggtg gagattatgg aacctacata tgggtctgga aaaactgtac
2700
actgttgtca ccttgaccat taaaaaccag aatgaggaca aaaaaaaaaa aaaaaa
2756

<210> 4632
<211> 372
<212> PRT
<213> Homo sapiens

<400> 4632
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Gly Ala Glu Glu Asp Arg Ala Arg Phe Phe Leu Glu Ser Ala Gly Trp
20 25 30
Asp Leu Gln Ile Ala Leu Ala Ser Phe Tyr Glu Asp Gly Gly Asp Glu
35 40 45
Asp Ile Val Thr Ile Ser Gln Ala Thr Pro Ser Ser Val Ser Arg Gly
50 55 60
Thr Ala Pro Ser Asp Asn Arg Val Thr Ser Phe Arg Asp Leu Ile His
65 70 75 80
Asp Gln Asp Glu Asp Glu Glu Glu Glu Glu Gly Gln Arg Ser Arg Phe
85 90 95
Tyr Ala Gly Gly Ser Glu Arg Ser Gly Gln Gln Ile Val Gly Pro Pro
100 105 110
Arg Lys Lys Ser Pro Asn Glu Leu Val Asp Asp Leu Phe Lys Gly Ala
115 120 125
Lys Glu His Gly Ala Val Ala Val Glu Arg Val Thr Lys Ser Pro Gly
130 135 140
Glu Thr Ser Lys Pro Arg Pro Phe Ala Gly Gly Gly Tyr Arg Leu Gly
145 150 155 160
Ala Ala Pro Glu Glu Glu Ser Ala Tyr Val Ala Gly Glu Lys Arg Gln
165 170 175
His Ser Ser Gln Asp Val His Val Val Leu Lys Leu Trp Lys Ser Gly
180 185 190
Phe Ser Leu Asp Asn Gly Glu Leu Arg Ser Tyr Gln Asp Pro Ser Asn
195 200 205
Ala Gln Phe Leu Glu Ser Ile Arg Arg Gly Glu Val Pro Ala Glu Leu
210 215 220
Arg Arg Leu Ala His Gly Gly Gln Val Asn Leu Asp Met Glu Asp His
225 230 235 240
Arg Asp Glu Asp Phe Val Lys Pro Lys Gly Ala Phe Lys Ala Phe Thr
245 250 255
Gly Glu Gly Gln Lys Leu Gly Ser Thr Ala Pro Gln Val Leu Ser Thr

```
            260                 265                 270
Ser Ser Pro Ala Gln Gln Ala Glu Asn Glu Ala Lys Ala Ser Ser Ser
        275                 280                 285
Ile Leu Ile Asp Glu Ser Glu Pro Thr Thr Asn Ile Gln Ile Arg Leu
    290                 295                 300
Ala Asp Gly Gly Arg Leu Val Gln Lys Phe Asn His Ser His Arg Ile
305                 310                 315                 320
Ser Asp Ile Arg Leu Phe Ile Val Asp Ala Arg Pro Ala Met Ala Ala
                325                 330                 335
Thr Ser Phe Ile Leu Met Thr Thr Phe Pro Asn Lys Glu Leu Ala Asp
            340                 345                 350
Glu Ser Gln Thr Leu Lys Glu Ala Asn Leu Leu Asn Ala Val Ile Val
        355                 360                 365
Gln Arg Leu Thr
    370
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<210> 4633
<211> 873
<212> DNA
<213> Homo sapiens

<400> 4633
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120
ctgcctccag acgctggcac tgaggggggtc caccgtcagg cactcagtca ggctgctcag
180
gagctctttc ttcatctcag ggggacagct aggggtggct ctggacagga aagaagggaa
240
gtaggtatgc agggtggaat ccggctttgc tccaaatgcc agcactttca gtcgggggta
300
gagctgacac agctgctcct gcaggctggg tgtcagggag ttgttcggca tataggcaaa
360
gtccagaagt gggaagaagt ccttggggcc aatcatgccg aagcccttgg taaggttggg
420
atgcatcagg agcagccgat ccaggtatgt gatggcaaag ggagacagag acttgatgcc
480
cagcacaggc agcatgatcc ccagccacac tttcagtccc tcggtgaggt tggcaaaacc
540
tgcttgaccc agggcccaca tgatggtgag acactttgct ggtcggctct ggtgggacct
600
cagcagttcc aggaacttgc ctaggtttgc cgtggcaatc ttgggcttgt cttgcaggat
660
ggcctggata cagatgcggt aaccatgtag tgactcccct ggtgtcttat ccagctcttg
720
caacatggtg aacagacagt gggccctggg tcaagcaggt tttgccaacc tcactgaggg
780
actgaaagtg tggctgggga tcatgctgcc tgtgctgggc atcaagtctc tgtctccctt
840
tgccatcacc cccttcacgc ggtcggagag agc
873

<210> 4634

<211> 242
<212> PRT
<213> Homo sapiens

<400> 4634
Met Leu Gln Glu Leu Asp Lys Thr Pro Gly Glu Ser Leu His Gly Tyr
1 5 10 15
Arg Ile Cys Ile Gln Ala Ile Leu Gln Asp Lys Pro Lys Ile Ala Thr
20 25 30
Ala Asn Leu Gly Lys Phe Leu Glu Leu Leu Arg Ser His Gln Ser Arg
35 40 45
Pro Ala Lys Cys Leu Thr Ile Met Trp Ala Leu Gly Gln Ala Gly Phe
50 55 60
Ala Asn Leu Thr Glu Gly Leu Lys Val Trp Leu Gly Ile Met Leu Pro
65 70 75 80
Val Leu Gly Ile Lys Ser Leu Ser Pro Phe Ala Ile Thr Tyr Leu Asp
85 90 95
Arg Leu Leu Leu Met His Pro Asn Leu Thr Lys Gly Phe Gly Met Ile
100 105 110
Gly Pro Lys Asp Phe Phe Pro Leu Leu Asp Phe Ala Tyr Met Pro Asn
115 120 125
Asn Ser Leu Thr Pro Ser Leu Gln Glu Gln Leu Cys Gln Leu Tyr Pro
130 135 140
Arg Leu Lys Val Leu Ala Phe Gly Ala Lys Pro Asp Ser Thr Leu His
145 150 155 160
Thr Tyr Phe Pro Ser Phe Leu Ser Arg Ala Thr Pro Ser Cys Pro Pro
165 170 175
Glu Met Lys Lys Glu Leu Leu Ser Ser Leu Thr Glu Cys Leu Thr Val
180 185 190
Asp Pro Leu Ser Ala Ser Val Trp Arg Gln Leu Tyr Pro Lys His Leu
195 200 205
Ser Gln Ser Ser Leu Leu Leu Glu His Leu Leu Ser Ser Trp Glu Gln
210 215 220
Ile Pro Lys Lys Val Gln Lys Ser Leu Gln Glu Thr Ile Gln Ser Leu
225 230 235 240
Lys Leu

<210> 4635
<211> 384
<212> DNA
<213> Homo sapiens

<400> 4635
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ttacaagagt cctgggtcag cccagaaagc ttttctccat tggttggggg aaggaggtga
120
agtggggccc gaggaggaag gccggtggtg tgtgggcaga gccagccagt ggtggccttc
180
ctcctcccga agatgagttt tgtagcccag gtgtttgcac actcacactt gctcactccc
240
tcacacacaa aaccctcact ctttgctttt tctggggaga gggaggccac tggcagaagc
300

gcctaccctg gccacagtca gttcccattc tcattttcta agaattttat cacaaaacag
360
tttgtcttga ggctgagatg gggg
384

<210> 4636
<211> 108
<212> PRT
<213> Homo sapiens

<400> 4636
Met Leu Gly Gly Pro Val Cys Ser Tyr Glu Leu Gly Gly Cys Pro Val
1 5 10 15
Thr Arg Val Leu Gly Gln Pro Arg Lys Leu Phe Ser Ile Gly Trp Gly
20 25 30
Lys Glu Val Lys Trp Gly Pro Arg Arg Lys Ala Gly Gly Val Trp Ala
35 40 45
Glu Pro Ala Ser Gly Gly Leu Pro Pro Pro Glu Asp Glu Phe Cys Ser
50 55 60
Pro Gly Val Cys Thr Leu Thr Leu Ala His Ser Leu Thr His Lys Thr
65 70 75 80
Leu Thr Leu Cys Phe Phe Trp Gly Glu Gly Gly His Trp Gln Lys Arg
85 90 95
Leu Pro Trp Pro Gln Ser Val Pro Ile Leu Ile Phe
100 105

<210> 4637
<211> 2162
<212> DNA
<213> Homo sapiens

<400> 4637
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gagcccccga tggaggccga ggccgcggac gctcccccgg gcggggttga gtcggcgctc
120
agctgcttct ctttcaacca ggactgcaca tccctagcaa ttggaactaa agccgggtat
180
aagctgtttt ctctgagttc tgtggagcag ctggatcaag tccacggaag caatgaaatc
240
ccggacgtct acatcgtgga gcgcctcttc tccagcagcc tggtggtggt agtcagtcac
300
acaaaaccac ggcagatgaa cgtgtatcac ttcaagaaag gcacagagat ctgtaattac
360
agctactcca gcaacatctt gtccataagg ctgaaccggc aaaggctgct ggtttgccta
420
gaagagtcca tttatattca caacattaaa gacatgaagc tgttgaagac cctcctggat
480
attcctgcaa acccaacagg tctatgtgct ctctctatca accattccaa ttcttacctg
540
gcctatcctg gaagcctgac ttcaggggag attgtgcttt atgatggaaa ctccctgaaa
600
acagtctgca ctattgctgc ccatgaggga acactagctg ccatcacctt caatgcctca
660

ggctccaaac tagcaagtgc gtctgaaaaa ggcacagtca tccgggtgtt ctctgtccct
720
gatgggcaaa agctctatga gttccggaga gggatgaaaa ggtatgtgac aatcagctct
780
ctagtgttca gtatggattc acaattcctc tgcgcctcca gtaacaccga gacggtacac
840
atcttcaagc tggaacaggt caccaacagt cgaccagaag agccttcgac ctggatggc
900
tacatgggaa agatgtttat ggctgctacc aactacctcc ctacccaggt gtcagacatg
960
atgcatcagg acagggcttt tgccactgca cgcttgaact tctccggaca gaggaacatc
1020
tgtaccctct caacgatcca gaagttgcca cggctgctag ttgcgtcatc cagtggacac
1080
ctttatatgt acaatttgga tcctcaggat ggaggagagt gtgtcttaat caaaacccac
1140
agcttgcttg gctcaggaac aacagaagag aataaagaaa atgacctcag accttcctta
1200
cctcagtctt atgcagcgac cgtagccaga ccaagtgcat cttcagcctc cacggtgcca
1260
ggttattctg aggacggcgg ggcgctgcga ggagaagtta ttcctgaaca tgagtttgcg
1320
acgggaccag tgtgtcttga tgatgagaat gagtttcctc ctataatctt gtgccgtgga
1380
aatcagaagg gcaaaacgaa gcagtcatga tgagaagcac acctcagaaa tcaggacatc
1440
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1500
gagcagaaag gggggcagga atcccgggtg ctccactgct taaaccacag gacctggtta
1560
actcctcacc aagcttccca cgaccctggt tgccaatggg cgcgggagac attgtataca
1620
catcatgcta tttaaaatac gttcaaacta tagtgtaaat gctaattaac catattggta
1680
tataaccgga attttatatt aaaaggggcc tccttttaa atatatgccg tgtaaaaaat
1740
gtacttatag gaacatctct ttgaattgta tttcttgtat attacatact tagagagaga
1800
ctcttttagc caggcaaagt ctttttggc tgtggctgga ataaatcatt tattacttgg
1860
gagtcccatt ttggacacta ataataaaat catggcaatg cattttgag gtttttatat
1920
attttttgt ttccttgtgg ttatagggga caggaggaac tctttaactt cttttaaatg
1980
cagtcatttc acccttaaaa ggagaggaag gggattgggc cacagactta tccatggact
2040
cgtctgctct gagatctgga aaacgaccta actttggtct aaatctgtgc tcctcaaggc
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2160
ga
2162

<210> 4638

<211> 446
<212> PRT
<213> Homo sapiens

<400> 4638
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Leu Ser Cys Phe Ser Phe Asn Gln Asp Cys Thr Ser Leu Ala Ile Gly
20 25 30
Thr Lys Ala Gly Tyr Lys Leu Phe Ser Leu Ser Ser Val Glu Gln Leu
35 40 45
Asp Gln Val His Gly Ser Asn Glu Ile Pro Asp Val Tyr Ile Val Glu
50 55 60
Arg Leu Phe Ser Ser Ser Leu Val Val Val Val Ser His Thr Lys Pro
65 70 75 80
Arg Gln Met Asn Val Tyr His Phe Lys Lys Gly Thr Glu Ile Cys Asn
85 90 95
Tyr Ser Tyr Ser Ser Asn Ile Leu Ser Ile Arg Leu Asn Arg Gln Arg
100 105 110
Leu Leu Val Cys Leu Glu Glu Ser Ile Tyr Ile His Asn Ile Lys Asp
115 120 125
Met Lys Leu Leu Lys Thr Leu Leu Asp Ile Pro Ala Asn Pro Thr Gly
130 135 140
Leu Cys Ala Leu Ser Ile Asn His Ser Asn Ser Tyr Leu Ala Tyr Pro
145 150 155 160
Gly Ser Leu Thr Ser Gly Glu Ile Val Leu Tyr Asp Gly Asn Ser Leu
165 170 175
Lys Thr Val Cys Thr Ile Ala Ala His Glu Gly Thr Leu Ala Ala Ile
180 185 190
Thr Phe Asn Ala Ser Gly Ser Lys Leu Ala Ser Ala Ser Glu Lys Gly
195 200 205
Thr Val Ile Arg Val Phe Ser Val Pro Asp Gly Gln Lys Leu Tyr Glu
210 215 220
Phe Arg Arg Gly Met Lys Arg Tyr Val Thr Ile Ser Ser Leu Val Phe
225 230 235 240
Ser Met Asp Ser Gln Phe Leu Cys Ala Ser Ser Asn Thr Glu Thr Val
245 250 255
His Ile Phe Lys Leu Glu Gln Val Thr Asn Ser Arg Pro Glu Glu Pro
260 265 270
Ser Thr Trp Ser Gly Tyr Met Gly Lys Met Phe Met Ala Ala Thr Asn
275 280 285
Tyr Leu Pro Thr Gln Val Ser Asp Met Met His Gln Asp Arg Ala Phe
290 295 300
Ala Thr Ala Arg Leu Asn Phe Ser Gly Gln Arg Asn Ile Cys Thr Leu
305 310 315 320
Ser Thr Ile Gln Lys Leu Pro Arg Leu Leu Val Ala Ser Ser Ser Gly
325 330 335
His Leu Tyr Met Tyr Asn Leu Asp Pro Gln Asp Gly Gly Glu Cys Val
340 345 350
Leu Ile Lys Thr His Ser Leu Leu Gly Ser Gly Thr Thr Glu Glu Asn
355 360 365
Lys Glu Asn Asp Leu Arg Pro Ser Leu Pro Gln Ser Tyr Ala Ala Thr
370 375 380
Val Ala Arg Pro Ser Ala Ser Ser Ala Ser Thr Val Pro Gly Tyr Ser

385 390 395 400
Glu Asp Gly Gly Ala Leu Arg Gly Glu Val Ile Pro Glu His Glu Phe
405 410 415
Ala Thr Gly Pro Val Cys Leu Asp Asp Glu Asn Glu Phe Pro Pro Ile
420 425 430
Ile Leu Cys Arg Gly Asn Gln Lys Gly Lys Thr Lys Gln Ser
435 440 445

<210> 4639
<211> 1007
<212> DNA
<213> Homo sapiens

<400> 4639
nnttttttttt aaaacaaaac attttattta atgcagaaat tctaaggtac aaaaacattt
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tgtaaatgtc agctgtgatc tactttcacc tagttacaga gttatgtaca aatcaagtca
120
ttaacatttt caatgtcaaa aatacagcac gctgttaaga gttctgtcag tgctcattat
180
cccactagat cccacaaagg gcaaactcaa agatgaaaca aaggcaacgc catcaataac
240
caccatattc cacaggcttt ctcccctagg acgtactaac agggagtttc cacagggaaa
300
aattctcttt taaaaaatta acagtaaaaa taggagttac ttactatcta gatgaacaca
360
attggttttc acaaaagctt ttgctgctgt ctggactcac catgcttttt tcttgagaga
420
aacataccaa acttttgtt gttgttgttg agacggagtt tcgctcttgt tgcccaggct
480
agagtgcaat ggcgtgatct cagctcactg caacctccgc ctcccaggct caagcgattc
540
tcccacctca gcctcccaag tagctaggac tacaggtgtg tgccaccaca cccagctaat
600
tttnnctgta gagacggtnn ttcaccatgt tgcccagact ggtctcaaat tcctgggctc
660
aagcaatcta acccccttgg cctcccaaag tgctgggata acaggtgtga gccaccatac
720
ccagctacaa agactctttt cccacataag gtcacattca cagggtccaa gtagacatct
780
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840
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900
atagacccat gccctctgca gaagggctga ggtttaggca aggccaattc cttcccctgt
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1007

<210> 4640
<211> 71
<212> PRT
<213> Homo sapiens

<400> 4640
Met Asn Thr Ile Gly Phe His Lys Ser Phe Cys Cys Cys Leu Asp Ser
1 5 10 15
Pro Cys Phe Phe Leu Glu Arg Asn Ile Pro Asn Phe Leu Leu Leu Leu
20 25 30
Leu Arg Arg Ser Phe Ala Leu Val Ala Gln Ala Arg Val Gln Trp Arg
35 40 45
Asp Leu Ser Ser Leu Gln Pro Pro Pro Pro Arg Leu Lys Arg Phe Ser
50 55 60
His Leu Ser Leu Pro Ser Ser
65 70

<210> 4641
<211> 1873
<212> DNA
<213> Homo sapiens

<400> 4641
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tcccgtcctg cgatgggttg cgacgggggа acaatcccca agaggcatga actggtgaag
120
gggccgaaga aggttgagaa ggtcgacaaa gatgctgaat tagtggccca atggaactat
180
tgtactctaa gtcaggaaat attaagacga ccaatagttg cctgtgaact tggcagactt
240
tataacaaag atgccgtcat tgaatttctc ttggacaaat ctgcagaaaa ggctcttggg
300
aaggcagcat ctcacattaa aagcattaag aatgtgacag agctgaagct ttctgataat
360
cctgcctggg aaggggataa aggaaacact aaaggtgaca agcacgatga cctccagcgg
420
gcgcgtttca tctgccccgt tgtgggcctg gagatgaacg gccgacacag gttctgcttc
480
cttcggtgct gcggctgtgt gttttctgag cgagccttga aagagataaa agcggaagtt
540
tgccacacgt gtggggctgc cttccaggag gatgatgtca tcatgctcaa tggcaccaag
600
gaggatgtgg acgtgctgaa gacaaggatg gaggagagaa ggctgagagc gaagctggaa
660
aagaaaacaa agaaacccaa ggcagcagag tctgtttcaa aaccagatgt cagtgaagaa
720
gccccagggc catcaaaagt taagacaggg aagcctgaag aagccagcct tgattctaga
780
gagaagaaaa ccaacttggc tcccaaaagc acagcaatga atgagagctc ttctggaaaa
840
gctgggaagc ctccgtgtgg agccacaaag aggtccatcg ctgacagtga agaatcggag
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gcctacaagt ccctctttac cactcacagc tccgccaagc gctccaagga ggagtctgcc
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cactgggtca cccacacgtc ctactgcttc tgaagcccgc actgccaccg ctcctgcccc
1020
agaaggttgt ttagtttcca cgtaggcagg tcgctttgtg cctctgagtg cgctgctgtg
1080

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1140
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1320
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1380
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1440
gcttcgaagg gcctcgtccc tctgctacag ccctgggagg agccaggatc cttgttggtc
1500
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1560
agttgggcac ccggtgattg ggttcaaaaa taaagctggt ctgcctcttc aaaaaaaaaa
1620
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa ttttttttt
1680
ggcccccccc aaaaaaaccc cccacccccc ccgcggcggg gtgttttttt ccccgcggcc
1740
gacccccctc ccccccggg ggggcgcggg ttgggggggcc ccccccggc ccccccgtgt
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1860
aaaaaagaga ggg
1873

<210> 4642
<211> 306
<212> PRT
<213> Homo sapiens

<400> 4642
Met Gly Cys Asp Gly Gly Thr Ile Pro Lys Arg His Glu Leu Val Lys
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Gly Pro Lys Lys Val Glu Lys Val Asp Lys Asp Ala Glu Leu Val Ala
            20   25   30
Gln Trp Asn Tyr Cys Thr Leu Ser Gln Glu Ile Leu Arg Arg Pro Ile
        35   40   45
Val Ala Cys Glu Leu Gly Arg Leu Tyr Asn Lys Asp Ala Val Ile Glu
    50   55   60
Phe Leu Leu Asp Lys Ser Ala Glu Lys Ala Leu Gly Lys Ala Ala Ser
65   70   75   80
His Ile Lys Ser Ile Lys Asn Val Thr Glu Leu Lys Leu Ser Asp Asn
                85   90   95
Pro Ala Trp Glu Gly Asp Lys Gly Asn Thr Lys Gly Asp Lys His Asp
            100   105   110
Asp Leu Gln Arg Ala Arg Phe Ile Cys Pro Val Val Gly Leu Glu Met
        115   120   125
Asn Gly Arg His Arg Phe Cys Phe Leu Arg Cys Cys Gly Cys Val Phe
    130   135   140
Ser Glu Arg Ala Leu Lys Glu Ile Lys Ala Glu Val Cys His Thr Cys

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145                 150                 155                 160
Gly Ala Ala Phe Gln Glu Asp Asp Val Ile Met Leu Asn Gly Thr Lys
                165                 170                 175
Glu Asp Val Asp Val Leu Lys Thr Arg Met Glu Glu Arg Arg Leu Arg
            180                 185                 190
Ala Lys Leu Glu Lys Lys Thr Lys Lys Pro Lys Ala Ala Glu Ser Val
        195                 200                 205
Ser Lys Pro Asp Val Ser Glu Glu Ala Pro Gly Pro Ser Lys Val Lys
    210                 215                 220
Thr Gly Lys Pro Glu Glu Ala Ser Leu Asp Ser Arg Glu Lys Lys Thr
225                 230                 235                 240
Asn Leu Ala Pro Lys Ser Thr Ala Met Asn Glu Ser Ser Ser Gly Lys
                245                 250                 255
Ala Gly Lys Pro Pro Cys Gly Ala Thr Lys Arg Ser Ile Ala Asp Ser
            260                 265                 270
Glu Glu Ser Glu Ala Tyr Lys Ser Leu Phe Thr Thr His Ser Ser Ala
        275                 280                 285
Lys Arg Ser Lys Glu Glu Ser Ala His Trp Val Thr His Thr Ser Tyr
    290                 295                 300
Cys Phe
305
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<210> 4643
<211> 1125
<212> DNA
<213> Homo sapiens

<400> 4643

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240
gagtctgggg gccgggccct ggagcaggag ctccctggag ctgtctttat cctctgtgat
300
gtgactcagg aagatgatat gaagaccctg gtttctgaga ccatccgccg atttggccgc
360
ctggattgtg ttgtcaacaa cgctggccac cacccacccc cacagaggcc tgaggagacc
420
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540
gtgggggcaa tcggccaggc ccaggcagtt ccctatgtgg ccaccaaggg ggcagtaaca
600
gccatgacca aagctttggc cctggatgaa agtccatatg gtgtccgagt caactgtatc
660
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780
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gaggtcgggg ctgcggcagt gttcctggcc tccgaagcca acttctgcac gggcattgaa
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ctgctcgtga cgggggggtgc agagctgggg tacgggtgca aggccagtcg gagcaccccc
900
gtggacgccc ccgatatccc ttcctgattt ctctcatttc tacttggggc ccccttccta
960
ggactctccc accccaaact ccaacctgta tcagatgcag cccccaagcc cttagactct
1020
aagcccagtt agcaaggtgc cgggtcaccc tgcaggttcc cataaaaacg atttgcagcc
1080
agaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa
1125

<210> 4644
<211> 270
<212> PRT
<213> Homo sapiens

<400> 4644
Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr Gly
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Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val Asp Ser
            20   25   30
Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly Gly Arg Ala
        35   40   45
Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu Cys Asp Val Thr
    50   55   60
Gln Glu Asp Asp Met Lys Thr Leu Val Ser Glu Thr Ile Arg Arg Phe
65   70   75   80
Gly Arg Leu Asp Cys Val Val Asn Asn Ala Gly His His Pro Pro Pro
                85   90   95
Gln Arg Pro Glu Glu Thr Ser Ala Gln Gly Phe Arg Gln Leu Leu Glu
            100   105   110
Leu Asn Leu Leu Gly Thr Tyr Thr Leu Thr Lys Leu Ala Leu Pro Tyr
        115   120   125
Leu Arg Lys Ser Gln Gly Asn Val Ile Asn Ile Ser Ser Leu Val Gly
    130   135   140
Ala Ile Gly Gln Ala Gln Ala Val Pro Tyr Val Ala Thr Lys Gly Ala
145   150   155   160
Val Thr Ala Met Thr Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly
                165   170   175
Val Arg Val Asn Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp
            180   185   190
Glu Glu Leu Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu
        195   200   205
Gly Met Leu Ala Gln Pro Leu Gly Arg Met Gly Gln Pro Ala Glu Val
    210   215   220
Gly Ala Ala Ala Val Phe Leu Ala Ser Glu Ala Asn Phe Cys Thr Gly
225   230   235   240
Ile Glu Leu Leu Val Thr Gly Gly Ala Glu Leu Gly Tyr Gly Cys Lys
                245   250   255
Ala Ser Arg Ser Thr Pro Val Asp Ala Pro Asp Ile Pro Ser
            260   265   270

<210> 4645
<211> 1725
<212> DNA
<213> Homo sapiens

<400> 4645
nggctctcgc ctaccggggg cttctctcac cgggactcgg gactcccggg aagtggaccg
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gcagaagagg gggctagcta gctgtctctg cggaccaggg agacccccgc gccccccggg
120
tgtgaggcgg cctcacaggg ccgggtgggc tggcgagccg acgcggcggc ggaggaggct
180
gtgaggagtg tgtggaacag gacccgggac agaggaacca tggctccgca gaacctgagc
240
acctttgcc tgttgctgct atacctcatc ggggcggtga ttgccggacg agatttctat
300
aagatcttgg gggtgcctcg aagtgcctct ataaaggata ttaaaaaggc ctataggaaa
360
ctagccctgc agcttcatcc cgaccggaac cctgatgatc cacaagccca ggagaaattc
420
caggatctgg gtgctgctta tgaggttctg tcagatagtg agaaacggaa acagtacgat
480
acttatggtg aagaaggatt aaaagatggt catcagagct cccatggaga catttttca
540
cacttctttg gggattttgg tttcatgttt ggaggaaccc ctcgtcagca agacagaaat
600
attccaagag gaagtgatat tattgtagat ctagaagtca ctttggaaga agtatatgca
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1200
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1320
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1380
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1440

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1725

<210> 4646
<211> 358
<212> PRT
<213> Homo sapiens

<400> 4646
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Pro Arg Ser Ala Ser Ile Lys Asp Ile Lys Lys Ala Tyr Arg Lys Leu
35 40 45
Ala Leu Gln Leu His Pro Asp Arg Asn Pro Asp Asp Pro Gln Ala Gln
50 55 60
Glu Lys Phe Gln Asp Leu Gly Ala Ala Tyr Glu Val Leu Ser Asp Ser
65 70 75 80
Glu Lys Arg Lys Gln Tyr Asp Thr Tyr Gly Glu Glu Gly Leu Lys Asp
85 90 95
Gly His Gln Ser Ser His Gly Asp Ile Phe Ser His Phe Phe Gly Asp
100 105 110
Phe Gly Phe Met Phe Gly Gly Thr Pro Arg Gln Gln Asp Arg Asn Ile
115 120 125
Pro Arg Gly Ser Asp Ile Ile Val Asp Leu Glu Val Thr Leu Glu Glu
130 135 140
Val Tyr Ala Gly Asn Phe Val Glu Val Val Arg Asn Lys Pro Val Ala
145 150 155 160
Arg Gln Ala Pro Gly Lys Arg Lys Cys Asn Cys Arg Gln Glu Met Arg
165 170 175
Thr Thr Gln Leu Gly Pro Gly Arg Phe Gln Met Thr Gln Glu Val Val
180 185 190
Cys Asp Glu Cys Pro Asn Val Lys Leu Val Asn Glu Glu Arg Thr Leu
195 200 205
Glu Val Glu Ile Glu Pro Gly Val Arg Asp Gly Met Glu Tyr Pro Phe
210 215 220
Ile Gly Glu Gly Glu Pro His Val Asp Gly Glu Pro Gly Asp Leu Arg
225 230 235 240
Phe Arg Ile Lys Val Val Lys His Pro Ile Phe Glu Arg Arg Gly Asp
245 250 255
Asp Leu Tyr Thr Asn Val Thr Ile Ser Leu Val Glu Ser Leu Val Gly
260 265 270
Phe Glu Met Asp Ile Thr His Leu Asp Gly His Lys Val His Ile Ser
275 280 285
Arg Asp Lys Ile Thr Arg Pro Gly Ala Lys Leu Trp Lys Lys Gly Glu

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    290                 295                 300
Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile
305                 310                 315                 320
Thr Phe Asp Val Asp Phe Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg
                325                 330                 335
Glu Gly Ile Lys Gln Leu Leu Lys Gln Gly Ser Val Gln Lys Val Tyr
            340                 345                 350
Asn Gly Leu Gln Gly Tyr
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<210> 4647
<211> 791
<212> DNA
<213> Homo sapiens

<400> 4647
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120
gatccccctg gaggaggcac cagcatcacc aagtaggtgc cacaggtata tatgggtgtc
180
ttccgcagca tttttagagg cagcccacag ctagtatttg ctgcttgatc ctctttcagt
240
gtgttggaga tggtggaacc agtcagggca gcaagcgttg ctgacgggga ggctctatac
300
cgagaaagtc tacttagaag catctcatta atgcttttgg cagattcgcc ctcttttctc
360
attagaattg tacgttcctg aagtgggttg gctacaaata caccattttc aaccacaagt
420
tcaaaaatgt ccatgaagac agaatgtccc ttcggtgttt tctcattcag gctggcagga
480
gaccagatcc aatagaagta agtgccatct gaagacaggt gcacagtgct catggtgctg
540
ccaatgggga ggtgattggc tggcattggc accacctggc acacctgaag ggtgttctgg
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tcaatgacct ggaaaaggga gtgaggttta ttatcgaaag agacaggccg gtggagaaga
660
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791

<210> 4648
<211> 188
<212> PRT
<213> Homo sapiens

<400> 4648
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Leu Ser Ser Asp Gly Thr Tyr Phe Tyr Trp Ile Trp Ser Pro Ala Ser
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            20                  25                  30
Leu Asn Glu Lys Thr Pro Lys Gly His Ser Val Phe Met Asp Ile Phe
        35                  40                  45
Glu Leu Val Val Glu Asn Gly Val Phe Val Ala Asn Pro Leu Gln Glu
    50                  55                  60
Arg Thr Ile Leu Met Arg Lys Glu Gly Glu Ser Ala Lys Ser Ile Asn
65                  70                  75                  80
Glu Met Leu Leu Ser Arg Leu Ser Arg Tyr Arg Ala Ser Pro Ser Ala
                85                  90                  95
Thr Leu Ala Ala Leu Thr Gly Ser Thr Ile Ser Asn Thr Leu Lys Glu
            100                 105                 110
Asp Gln Ala Ala Asn Thr Ser Cys Gly Leu Pro Leu Lys Met Leu Arg
        115                 120                 125
Lys Thr Pro Ile Tyr Thr Cys Gly Thr Tyr Leu Val Met Leu Val Pro
    130                 135                 140
Pro Pro Gly Gly Ser Gly Ser Ser Ala Thr Arg Ser Leu Phe Gly Gly
145                 150                 155                 160
Thr Ser Gly Leu Ser Ser Leu Lys Ile Leu Ala Ser Ser Leu Val Tyr
                165                 170                 175
Asn Ile Ser Asp Gly Gln Phe Thr Ser Arg Ala Asp
            180                 185
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<210> 4649
<211> 3276
<212> DNA
<213> Homo sapiens

<400> 4649

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180
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240
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300
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360
agggatttta agttatacat cacaacccgt ttgaggaatc cacattacct cccagaagtt
420
gccgtgaagg tctgtctcct caacttcatg atcacccccc tgggtctcca agatcaactc
480
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540
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660
tccaaagtgc tatctgaaga gatctcagag aaacagaaag ttgcttccat gacagaaacg
720
cagattgacg agactcggat gggctacaag ccagtggctg tgcattctgc caccatcttc
780
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ttttgtatct cggacctggc caacatcgag ccgatgtacc agtactccct gacttggttc
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900
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2220
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<210> 4650
<211> 965
<212> PRT
<213> Homo sapiens

<400> 4650
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20 25 30
Glu Val Ala Val Lys Val Cys Leu Leu Asn Phe Met Ile Thr Pro Leu
35 40 45
Gly Leu Gln Asp Gln Leu Leu Gly Ile Val Ala Ala Lys Glu Lys Pro
50 55 60
Glu Leu Glu Glu Lys Lys Asn Gln Leu Ile Val Glu Ser Ala Lys Asn
65 70 75 80
Lys Lys His Leu Lys Glu Ile Glu Asp Lys Ile Leu Glu Val Leu Ser
85 90 95
Met Ser Lys Gly Asn Ile Leu Glu Asp Glu Thr Ala Ile Lys Val Leu
100 105 110
Ser Ser Ser Lys Val Leu Ser Glu Glu Ile Ser Glu Lys Gln Lys Val
115 120 125
Ala Ser Met Thr Glu Thr Gln Ile Asp Glu Thr Arg Met Gly Tyr Lys

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    130                 135                 140
Pro Val Ala Val His Ser Ala Thr Ile Phe Phe Cys Ile Ser Asp Leu
145                 150                 155                 160
Ala Asn Ile Glu Pro Met Tyr Gln Tyr Ser Leu Thr Trp Phe Ile Asn
                165                 170                 175
Leu Tyr Met His Ser Leu Thr His Ser Thr Lys Ser Glu Glu Leu Asn
            180                 185                 190
Leu Arg Ile Lys Tyr Ile Ile Asp His Phe Thr Leu Ser Ile Tyr Asn
        195                 200                 205
Asn Val Cys Arg Ser Leu Phe Glu Lys Asp Lys Leu Leu Phe Ser Leu
    210                 215                 220
Leu Leu Thr Ile Gly Ile Met Lys Gln Lys Lys Glu Ile Thr Glu Glu
225                 230                 235                 240
Val Trp Tyr Phe Leu Leu Thr Gly Gly Ile Ala Leu Asp Asn Pro Tyr
                245                 250                 255
Pro Asn Pro Ala Pro Gln Trp Leu Ser Glu Lys Ala Trp Ala Glu Ile
            260                 265                 270
Val Arg Ala Ser Ala Leu Pro Lys Leu His Gly Leu Met Glu His Leu
        275                 280                 285
Glu Gln Asn Leu Gly Glu Trp Lys Leu Ile Tyr Asp Ser Ala Trp Pro
    290                 295                 300
His Glu Glu Gln Leu Pro Gly Ser Trp Lys Phe Ser Gln Gly Leu Glu
305                 310                 315                 320
Lys Met Val Ile Leu Arg Cys Leu Arg Pro Asp Lys Met Val Pro Ala
                325                 330                 335
Val Arg Glu Phe Ile Ala Glu His Met Gly Lys Leu Tyr Ile Glu Ala
            340                 345                 350
Pro Thr Phe Asp Leu Gln Gly Ser Tyr Asn Asp Ser Ser Cys Cys Ala
        355                 360                 365
Pro Leu Ile Phe Val Leu Ser Pro Ser Ala Asp Pro Met Ala Gly Leu
    370                 375                 380
Leu Lys Phe Ala Asp Asp Leu Gly Met Gly Gly Thr Arg Thr Gln Thr
385                 390                 395                 400
Ile Ser Leu Gly Gln Gly Gln Gly Pro Ile Ala Ala Lys Met Ile Asn
                405                 410                 415
Asn Ala Ile Lys Asp Gly Thr Trp Val Val Leu Gln Asn Cys His Leu
            420                 425                 430
Ala Ala Ser Trp Met Pro Thr Leu Glu Lys Ile Cys Glu Glu Val Ile
        435                 440                 445
Val Pro Glu Ser Thr Asn Ala Arg Phe Arg Leu Trp Leu Thr Ser Tyr
    450                 455                 460
Pro Ser Glu Lys Phe Pro Val Ser Ile Leu Gln Asn Gly Ile Lys Met
465                 470                 475                 480
Thr Asn Glu Pro Pro Lys Gly Leu Arg Ala Asn Leu Leu Arg Ser Tyr
                485                 490                 495
Leu Asn Asp Pro Ile Ser Asp Pro Val Phe Phe Gln Ser Cys Ala Lys
            500                 505                 510
Ala Val Met Trp Gln Lys Met Leu Phe Gly Leu Cys Phe Phe His Ala
        515                 520                 525
Val Val Gln Glu Arg Arg Asn Phe Gly Pro Leu Gly Trp Asn Ile Pro
    530                 535                 540
Tyr Glu Phe Asn Glu Ser Asp Leu Arg Ile Ser Met Trp Gln Ile Gln
545                 550                 555                 560
Met Phe Leu Asn Asp Tyr Lys Glu Val Pro Phe Asp Ala Leu Thr Tyr
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                565                 570                 575
Leu Thr Gly Glu Cys Asn Tyr Gly Gly Arg Val Thr Asp Asp Lys Asp
            580                 585                 590
Arg Arg Leu Leu Leu Ser Leu Leu Ser Met Phe Tyr Cys Lys Glu Ile
        595                 600                 605
Glu Glu Asp Tyr Tyr Ser Leu Ala Pro Gly Asp Thr Tyr Tyr Ile Pro
    610                 615                 620
Pro His Gly Ser Tyr Gln Ser Tyr Ile Asp Tyr Leu Arg Asn Leu Pro
625                 630                 635                 640
Ile Thr Ala His Pro Glu Val Phe Gly Leu His Glu Asn Ala Asp Ile
                645                 650                 655
Thr Lys Asp Asn Gln Glu Thr Asn Gln Leu Phe Glu Gly Val Leu Leu
            660                 665                 670
Thr Leu Pro Arg Gln Ser Gly Gly Ser Gly Lys Ser Pro Gln Glu Val
        675                 680                 685
Val Glu Glu Leu Ala Gln Asp Ile Leu Ser Lys Leu Pro Arg Asp Phe
    690                 695                 700
Asp Leu Glu Glu Val Met Lys Leu Tyr Pro Val Val Tyr Glu Glu Ser
705                 710                 715                 720
Met Asn Thr Val Leu Arg Gln Glu Leu Ile Arg Phe Asn Arg Leu Thr
                725                 730                 735
Lys Val Val Arg Arg Ser Leu Ile Asn Leu Gly Arg Ala Ile Lys Gly
            740                 745                 750
Gln Val Leu Met Ser Ser Glu Leu Glu Glu Val Phe Asn Ser Met Leu
        755                 760                 765
Val Gly Lys Val Pro Ala Met Trp Ala Ala Lys Ser Tyr Pro Ser Leu
    770                 775                 780
Lys Pro Leu Gly Gly Tyr Val Ala Asp Leu Leu Ala Arg Leu Thr Phe
785                 790                 795                 800
Phe Gln Glu Trp Ile Asp Lys Gly Pro Pro Val Val Phe Trp Ile Ser
                805                 810                 815
Gly Phe Tyr Phe Thr Gln Ser Phe Leu Thr Gly Val Ser Gln Asn Tyr
            820                 825                 830
Ala Arg Lys Tyr Thr Ile Pro Ile Asp His Ile Gly Phe Glu Phe Glu
        835                 840                 845
Val Thr Pro Gln Glu Thr Val Met Glu Asn Asn Pro Glu Asp Gly Ala
    850                 855                 860
Tyr Ile Lys Gly Leu Phe Leu Glu Gly Ala Arg Trp Asp Arg Lys Thr
865                 870                 875                 880
Met Gln Ile Gly Glu Ser Leu Pro Lys Ile Leu Tyr Asp Pro Leu Pro
                885                 890                 895
Ile Ile Trp Leu Lys Pro Gly Glu Ser Ala Met Phe Leu His Gln Asp
            900                 905                 910
Ile Tyr Val Cys Pro Val Tyr Lys Thr Ser Ala Arg Arg Gly Thr Leu
        915                 920                 925
Ser Thr Thr Gly His Ser Thr Asn Tyr Val Leu Ser Ile Glu Leu Pro
    930                 935                 940
Thr Asp Met Pro Gln Lys His Trp Ile Asn Arg Gly Val Ala Ser Leu
945                 950                 955                 960
Cys Gln Leu Asp Asn
                965
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<210> 4651
<211> 869

<212> DNA
<213> Homo sapiens

<400> 4651
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180
cagcagatgc ggcccatccc cacggtggcc cgcgcctacc cactggtggg ccacgcgctg
240
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360
gcagaaaatg tggaggtaat tttaactagt tcaaagcaaa ttgacaaatc ctctatgtac
420
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480
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540
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600
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720
agaatgagtg agatgatatt tccaagaata aagatgccct ggctttggct tgatctctgg
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869

<210> 4652
<211> 289
<212> PRT
<213> Homo sapiens

<400> 4652
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20 25 30
Gly Ala Ala Ser Ala Val Ser Leu Ala Gly Ala Ser Leu Val Leu Ser
35 40 45
Leu Leu Gln Arg Val Ala Ser Tyr Ala Arg Lys Trp Gln Gln Met Arg
50 55 60
Pro Ile Pro Thr Val Ala Arg Ala Tyr Pro Leu Val Gly His Ala Leu
65 70 75 80
Leu Met Lys Pro Asp Gly Arg Glu Phe Phe Gln Gln Ile Ile Glu Tyr
85 90 95
Thr Glu Glu Tyr Arg His Met Pro Leu Leu Lys Leu Trp Val Gly Pro

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            100                 105                 110
Val Pro Met Val Ala Leu Tyr Asn Ala Glu Asn Val Glu Val Ile Leu
        115                 120                 125
Thr Ser Ser Lys Gln Ile Asp Lys Ser Ser Met Tyr Lys Phe Leu Glu
    130                 135                 140
Pro Trp Leu Gly Leu Gly Leu Leu Thr Ser Thr Gly Asn Lys Trp Arg
145                 150                 155                 160
Ser Arg Arg Lys Met Leu Thr Pro Thr Phe His Phe Thr Ile Leu Glu
                165                 170                 175
Asp Phe Leu Asp Ile Met Asn Glu Gln Ala Asn Ile Leu Val Lys Lys
            180                 185                 190
Leu Glu Lys His Ile Asn Gln Glu Ala Phe Asn Cys Phe Phe Tyr Ile
        195                 200                 205
Thr Leu Cys Ala Leu Asp Ile Ile Cys Glu Thr Ala Met Gly Lys Asn
    210                 215                 220
Ile Gly Ala Gln Ser Asn Asp Asp Ser Glu Tyr Val Arg Ala Val Tyr
225                 230                 235                 240
Arg Met Ser Glu Met Ile Phe Pro Arg Ile Lys Met Pro Trp Leu Trp
                245                 250                 255
Leu Asp Leu Trp Tyr Leu Met Phe Lys Glu Gly Trp Glu His Lys Lys
            260                 265                 270
Ser Leu Lys Ile Leu His Thr Phe Thr His Ser Val Ile Pro Glu Arg
        275                 280                 285
Ala
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<210> 4653
<211> 1276
<212> DNA
<213> Homo sapiens

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120
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240
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aagaaggcct ccaaggagat ctaccagctg cgtgggcaga gccacaaaga gcccatccaa
1080
gtgcagacct ttagggagaa gatagcattc ttcacaaggc caaggatcaa catacctcct
1140
ctcccagccg acgacgtctg atggagtgca ttgtgcacat gaagtattta tccacctgtt
1200
ttattttcat gaagttctta gactagctga atttgtcttt aaaatatttg tgcaaagcta
1260
ttaatataca catttt
1276

<210> 4654
<211> 255
<212> PRT
<213> Homo sapiens

<400> 4654
Met Gly Ile Asp Ser Ile Leu Gly His Pro Phe Ala Ala Gln Ala Gly
1 5 10 15
Pro Tyr Ser Pro Glu Lys Phe Gln Pro Ser Pro Leu Lys Val Asp Lys
20 25 30
Glu Thr Asn Thr Glu Asp Leu Phe Leu Glu Glu Ala Ala Ser Leu Val
35 40 45
Lys Glu Arg Pro Ser Arg Arg Ala Arg Gly Ser Pro Phe Val Arg Ser
50 55 60
Gly Thr Ile Val Arg Ser Gln Thr Phe Ser Pro Gly Ala Arg Ser Gln
65 70 75 80
Tyr Val Cys Arg Leu Tyr Arg Ser Asp Ser Asp Ser Ser Thr Leu Pro
85 90 95
Arg Lys Ser Pro Phe Val Arg Asn Thr Leu Glu Arg Arg Thr Leu Arg
100 105 110
Tyr Lys Gln Ser Cys Arg Ser Ser Leu Ala Glu Leu Met Ala Arg Thr
115 120 125
Ser Leu Asp Leu Glu Leu Asp Leu Gln Ala Ser Arg Thr Arg Gln Arg
130 135 140
Gln Leu Asn Glu Glu Leu Cys Ala Leu Arg Glu Leu Arg Gln Arg Leu
145 150 155 160
Glu Asp Ala Gln Leu Arg Gly Gln Thr Asp Leu Pro Pro Trp Val Leu
165 170 175
Arg Asp Glu Arg Leu Arg Gly Leu Leu Arg Glu Ala Glu Arg Gln Thr
180 185 190
Arg Gln Thr Lys Leu Asp Tyr Arg His Glu Gln Ala Ala Glu Lys Met

```
        195                 200                 205
Leu Lys Lys Ala Ser Lys Glu Ile Tyr Gln Leu Arg Gly Gln Ser His
    210                 215                 220
Lys Glu Pro Ile Gln Val Gln Thr Phe Arg Glu Lys Ile Ala Phe Phe
225                 230                 235                 240
Thr Arg Pro Arg Ile Asn Ile Pro Pro Leu Pro Ala Asp Asp Val
                245                 250                 255
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<210> 4655
<211> 456
<212> DNA
<213> Homo sapiens

<400> 4655
gcggccgcgc aggtcctcgc gcttgcggaa ggtgcgcacg tactccatgc ggtccagcgc
60
cacgagcagc aggaacaggc cgggcacaca cacagacagc agcagcgtca gcgccttgcg
120
cgccacgggg tccgccgcgc cgcgccgcgc cgccttgtag ttctggaaga tgaagtagag
180
cttgatctcc agcacgaaga tgtaaaggaa ccacaggatc atggcgtagc cgcgcttggc
240
cgtgcgcacc tcggcgccca cccacacggc cacgtagcgc agcaccagca ggaagcacac
300
gtcgcccacc agcacgatga tgcacacgcc gatcttgcgc gggccctggt tctgctccac
360
caggtacgcg tccatgacgg ccatgctgcc catgatcacc agcgtggtca ggcacacgtg
420
gcgccggtcc gggggcggca gcaccatggt cggccg
456

<210> 4656
<211> 152
<212> PRT
<213> Homo sapiens

<400> 4656
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Ala Ala Ala Gln Val Leu Ala Leu Ala Glu Gly Ala His Val Leu His
 1               5                  10                  15
Ala Val Gln Arg His Glu Gln Gln Glu Gln Ala Gly His Thr His Arg
            20                  25                  30
Gln Gln Gln Arg Gln Arg Leu Ala Arg His Gly Val Arg Arg Ala Ala
        35                  40                  45
Pro Arg Arg Leu Val Val Leu Glu Asp Glu Val Glu Leu Asp Leu Gln
    50                  55                  60
His Glu Asp Val Lys Glu Pro Gln Asp His Gly Val Ala Ala Leu Gly
65                  70                  75                  80
Arg Ala His Leu Gly Ala His Pro His Gly His Val Ala Gln His Gln
                85                  90                  95
Gln Glu Ala His Val Ala His Gln His Asp Asp Ala His Ala Asp Leu
            100                 105                 110
Ala Arg Ala Leu Val Leu Leu His Gln Val Arg Val His Asp Gly His
        115                 120                 125
Ala Ala His Asp His Gln Arg Gly Gln Ala His Val Ala Pro Val Arg
```

```
    130                 135                 140
Gly Arg Gln His His Gly Arg Pro
145                 150

<210> 4657
<211> 723
<212> DNA
<213> Homo sapiens

<400> 4657
nnacgcgtga tggctggcgg agtcatggac aaggagtacg tgggttttgc tgccctcccc
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aaccagctgc accgcaagtc tgtcaagaag gggtttgact tcacgctaat ggtggcaggg
120
gagtcaggcc tagggaaatc caccctcatc aacagcctct tcctcaccaa cctctatgag
180
gatcgccagg tgccagaggc cagtgctcgc ttgacacaga ccctggccat tgagcgccgg
240
ggcgtagaga ttgaggaagg gggtgtgaaa gtgaagctga ccccttgtgga cacacctggc
300
tttggggact cagtggactg ctctgactgc tggcttccgg tggtgaaatt catcgaggag
360
caatttgagc agtaccttag ggatgagagt ggcctgaacc ggaagaacat ccaggactcc
420
cgagtccact gctgcctcta cttcatctca cccttcggcc gggctccggc ccctagatgt
480
ggcttcctcc gggcaataca cgagaaagtc aacatcatcc cagtcattgg caaagcggat
540
gccctgatgc cccaggaaac ccaggccctc aagcagaaga tccgggatca gttgaaggaa
600
gaggagatcc acatctacca gttccccgaa tgtgactctg atgaagatga agacttcaag
660
aggcaggatg cagagatgaa ggaaagcatc ccttttgcag tcgtgggatc atgcgaggtg
720
gta
723

<210> 4658
<211> 233
<212> PRT
<213> Homo sapiens

<400> 4658
Met Asp Lys Glu Tyr Val Gly Phe Ala Ala Leu Pro Asn Gln Leu His
 1               5                  10                  15
Arg Lys Ser Val Lys Lys Gly Phe Asp Phe Thr Leu Met Val Ala Gly
            20                  25                  30
Glu Ser Gly Leu Gly Lys Ser Thr Leu Ile Asn Ser Leu Phe Leu Thr
        35                  40                  45
Asn Leu Tyr Glu Asp Arg Gln Val Pro Glu Ala Ser Ala Arg Leu Thr
    50                  55                  60
Gln Thr Leu Ala Ile Glu Arg Arg Gly Val Glu Ile Glu Glu Gly Gly
65                  70                  75                  80
Val Lys Val Lys Leu Thr Leu Val Asp Thr Pro Gly Phe Gly Asp Ser
```

```
                85                  90                  95
Val Asp Cys Ser Asp Cys Trp Leu Pro Val Val Lys Phe Ile Glu Glu
            100                 105                 110
Gln Phe Glu Gln Tyr Leu Arg Asp Glu Ser Gly Leu Asn Arg Lys Asn
        115                 120                 125
Ile Gln Asp Ser Arg Val His Cys Cys Leu Tyr Phe Ile Ser Pro Phe
    130                 135                 140
Gly Arg Ala Pro Ala Pro Arg Cys Gly Phe Leu Arg Ala Ile His Glu
145                 150                 155                 160
Lys Val Asn Ile Ile Pro Val Ile Gly Lys Ala Asp Ala Leu Met Pro
                165                 170                 175
Gln Glu Thr Gln Ala Leu Lys Gln Lys Ile Arg Asp Gln Leu Lys Glu
            180                 185                 190
Glu Glu Ile His Ile Tyr Gln Phe Pro Glu Cys Asp Ser Asp Glu Asp
        195                 200                 205
Glu Asp Phe Lys Arg Gln Asp Ala Glu Met Lys Glu Ser Ile Pro Phe
    210                 215                 220
Ala Val Val Gly Ser Cys Glu Val Val
225                 230
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<210> 4659
<211> 864
<212> DNA
<213> Homo sapiens

<400> 4659
tttaaaagca gtggaaatta gtaaacaagg ttccgagcag gaaatgtctt gtggcctggg
60
agagaatctc accacaaatg aaaactacgt gaaaggccct gcactgaaaa tgcaagctca
120
ggcgccggtg gtcgttgtga cccaacctgg agtcggtccc ggtccggccc cccagaactc
180
caactggcag acaggcatgt gtgactgttt cagcgactgc ggagtctgtc tctgtggcac
240
attttgtttc ccgtgccttg ggtgtcaagt tgcagctgat atgaatgaat gctgtctgtg
300
tggaacaagc gtcgcaatga ggactctcta caggacccga tatggcatcc ctggatctat
360
ttgtgatgac tatatggcaa ctctttgctg tcctcattgt actctttgcc aaatcaagag
420
agatatcaac agaaggagag ccatgcgtac tttctaaaaa ctgatggtga aaagctctta
480
ccgaagcaac aaaattcagc agacacctct tcagcttgag ttcttcacca tcttttgcaa
540
ctgaaatatg atggatatgc ttaagtacaa ctgatggcat gaaaaaaatc aaatttttga
600
tttattataa atgaatgttg tccctgaact tagctaaatg gtgcaactta gtttctcctt
660
gctttcatat tatcgaattc gaatttcctg gcttataaac tttttaaatt acatttgaaa
720
tataaaccaa atgaaatatt ttactgataa gattcttcat gcttctttgc tctccttaaa
780
atgtcttttt cactagttag ttccaagggt cagtctcata attttgttct tatactttga
840

tttccttttt ctttttttt tttg
864

<210> 4660
<211> 192
<212> PRT
<213> Homo sapiens

<400> 4660
Met Pro Ser Val Val Leu Lys His Ile His His Ile Ser Val Ala Lys
1 5 10 15
Asp Gly Glu Glu Leu Lys Leu Lys Arg Cys Leu Leu Asn Phe Val Ala
20 25 30
Ser Val Arg Ala Phe His His Gln Phe Leu Glu Ser Thr His Gly Ser
35 40 45
Pro Ser Val Asp Ile Ser Leu Asp Leu Ala Lys Ser Thr Met Arg Thr
50 55 60
Ala Lys Ser Cys His Ile Val Ile Thr Asn Arg Ser Arg Asp Ala Ile
65 70 75 80
Ser Gly Pro Val Glu Ser Pro His Cys Asp Ala Cys Ser Thr Gln Thr
85 90 95
Ala Phe Ile His Ile Ser Cys Asn Leu Thr Pro Lys Ala Arg Glu Thr
100 105 110
Lys Cys Ala Thr Glu Thr Asp Ser Ala Val Ala Glu Thr Val Thr His
115 120 125
Ala Cys Leu Pro Val Gly Val Leu Gly Gly Arg Thr Gly Thr Asp Ser
130 135 140
Arg Leu Gly His Asn Asp His Arg Arg Leu Ser Leu His Phe Gln Cys
145 150 155 160
Arg Ala Phe His Val Val Phe Ile Cys Gly Glu Ile Leu Ser Gln Ala
165 170 175
Thr Arg His Phe Leu Leu Gly Thr Leu Phe Thr Asn Phe His Cys Phe
180 185 190

<210> 4661
<211> 153
<212> DNA
<213> Homo sapiens

<400> 4661
cggatctgca tgccgctcac cgtagacgag tacaaaattg gacagctgta catgatcagc
60
aaacacagcc atgaacagag tgaccgggga gaaggggtgg aggtcgtcca gaatgagccc
120
tttgaggacc ctcaccatgg ccatgggcag ttc
153

<210> 4662
<211> 51
<212> PRT
<213> Homo sapiens

<400> 4662
Arg Ile Cys Met Pro Leu Thr Val Asp Glu Tyr Lys Ile Gly Gln Leu

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 1               5                  10                  15
Tyr Met Ile Ser Lys His Ser His Glu Gln Ser Asp Arg Gly Glu Gly
            20                  25                  30
Val Glu Val Val Gln Asn Glu Pro Phe Glu Asp Pro His His Gly His
        35                  40                  45
Gly Gln Phe
    50
```

<210> 4663
<211> 1550
<212> DNA
<213> Homo sapiens

<400> 4663
atgttccggc acacggacag cctctttccc atcctactgc agacgttatc ggatgaatcg
60
gatgaggtga tcctgaagga cctggaggtg ctggcagaaa tcgcttcctc ccccgcaggc
120
cagacggatg acccaggccc cctcgatggc cctgacctcc aggccagcca ctcagagctc
180
caggtgccca cccctggcag agccggccta ctgaacacct ctggtaccaa aggcttagaa
240
tgttctcctt caactcccac catgaattct tacttttata agttcatgat caaccttctc
300
aagagattca gcagcgaacg gaagctcctg gaggtcagag gccctttcat catcaggcag
360
ctgtgcctcc tgctgaatgc ggagaacatc ttccactcaa tggcagacat cctgctgcgg
420
gaggaggacc tcaagttcgc ctcgaccatg gtccacgccc tcaacaccat cctgctgacc
480
tccacagagc tcttccagct aaggaaccag ctgaaggacc tgaagaccct ggagagccag
540
aacctgttct gctgcctgta ccgctcctgg tgccacaacc cagtcaccac ggtgtccctc
600
tgcttcctca cccagaacta ccggcacgcc tatgacctca tccagaagtt tggggacctg
660
gaggtcaccg tggacttcct cgcagaggtg gacaagctgg tgcagctgat tgagtgcccc
720
atcttcacat atctgcgcct gcagctgctg gacgtgaaga acaaccccta cctgatcaag
780
gccctctacg gcctgctcat gctcctgccg cagagcagcg ccttccagct gctctcgcac
840
cggctccagt gcgtgcccaa ccctgagctg ctgcagaccg aagacagtct aaaggcagcc
900
cccaagtccc agaaagctga ctcccctagc atcgactacg cagagctgct gcagcacttt
960
gagaaggtcc agaacaagca cctggaagtg cggcaccagc ggagcgggcg tggggaccac
1020
ctggaccgga gggttgtcct ctgacaggcc tggcacggag gagggcccac cgagtggtcc
1080
catgaaacac taagggtcgt cacgccctcc cgaggagctc aaggacctgc ctgtcaggac
1140
cagggctggg cctgccaacc cagggcagtg ttggggccgg aggctgctgt gtctgcccaa
1200

gctcctctca gagtccagtc cccaggcctc cagcgctgtc agctgcaccc tggcattctc
1260
acagagctgg ctgcccaccc agtgggggggc tatagcctca gagaccactc atcctctgga
1320
atcaacctct ttctaatacc ctcttggaaa aagagcttgc ccctcctcca gcacactaga
1380
gctctggcct tgtgtgtata tgtatacata cgtgaacaca tgcctgtgtg tgtgtgtgtg
1440
tgtgtacttg tatgcacgta ggcaccagca caaagatctg aatgatgcac cccacccca
1500
ccccaataaa gaaataacag aaaaccctca aaaaaaaaaa aaaaaaaaaa
1550

<210> 4664
<211> 347
<212> PRT
<213> Homo sapiens

<400> 4664
Met Phe Arg His Thr Asp Ser Leu Phe Pro Ile Leu Leu Gln Thr Leu
1 5 10 15
Ser Asp Glu Ser Asp Glu Val Ile Leu Lys Asp Leu Glu Val Leu Ala
20 25 30
Glu Ile Ala Ser Ser Pro Ala Gly Gln Thr Asp Asp Pro Gly Pro Leu
35 40 45
Asp Gly Pro Asp Leu Gln Ala Ser His Ser Glu Leu Gln Val Pro Thr
50 55 60
Pro Gly Arg Ala Gly Leu Leu Asn Thr Ser Gly Thr Lys Gly Leu Glu
65 70 75 80
Cys Ser Pro Ser Thr Pro Thr Met Asn Ser Tyr Phe Tyr Lys Phe Met
85 90 95
Ile Asn Leu Leu Lys Arg Phe Ser Ser Glu Arg Lys Leu Leu Glu Val
100 105 110
Arg Gly Pro Phe Ile Ile Arg Gln Leu Cys Leu Leu Leu Asn Ala Glu
115 120 125
Asn Ile Phe His Ser Met Ala Asp Ile Leu Leu Arg Glu Glu Asp Leu
130 135 140
Lys Phe Ala Ser Thr Met Val His Ala Leu Asn Thr Ile Leu Leu Thr
145 150 155 160
Ser Thr Glu Leu Phe Gln Leu Arg Asn Gln Leu Lys Asp Leu Lys Thr
165 170 175
Leu Glu Ser Gln Asn Leu Phe Cys Cys Leu Tyr Arg Ser Trp Cys His
180 185 190
Asn Pro Val Thr Thr Val Ser Leu Cys Phe Leu Thr Gln Asn Tyr Arg
195 200 205
His Ala Tyr Asp Leu Ile Gln Lys Phe Gly Asp Leu Glu Val Thr Val
210 215 220
Asp Phe Leu Ala Glu Val Asp Lys Leu Val Gln Leu Ile Glu Cys Pro
225 230 235 240
Ile Phe Thr Tyr Leu Arg Leu Gln Leu Leu Asp Val Lys Asn Asn Pro
245 250 255
Tyr Leu Ile Lys Ala Leu Tyr Gly Leu Leu Met Leu Leu Pro Gln Ser
260 265 270
Ser Ala Phe Gln Leu Leu Ser His Arg Leu Gln Cys Val Pro Asn Pro

```
        275                 280                 285
Glu Leu Leu Gln Thr Glu Asp Ser Leu Lys Ala Ala Pro Lys Ser Gln
    290                 295                 300
Lys Ala Asp Ser Pro Ser Ile Asp Tyr Ala Glu Leu Leu Gln His Phe
305                 310                 315                 320
Glu Lys Val Gln Asn Lys His Leu Glu Val Arg His Gln Arg Ser Gly
                325                 330                 335
Arg Gly Asp His Leu Asp Arg Arg Val Val Leu
            340                 345
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<210> 4665
<211> 1043
<212> DNA
<213> Homo sapiens

<400> 4665
nttcggcacg agggtggatc tcatcgaaag gcggcgcgat ctgtgtcggg cattaccaga
60
agagtcttca tgtggacagt ctcagggaca ccatgtagag aattttggtc tcgattcaga
120
aaagagaaag agccagtggt tgttgagaca gtagaagaga aaaaggaacc tatcctagtg
180
tgtccacctt tacgaagccg agcatacaca ccacctgaag atctccagag tcgtttggaa
240
tcttacgtta aagaagtttt tggttcatct cttcctagta attggcaaga catctccctg
300
gaagatagtc gtctaaagtt caatcttctg gctcatttag ctgatgactt gggtcatgta
360
gtccctaact ccagactcca ccagatgtgc agggttagag atgttcttga tttctataat
420
gtccctattc aagatagatc taaatttgat gaactcagtg ccagtaatct gccccccaat
480
ttgaaaatca cttggagtta ctaagcaatt cggaagagaa acacattgaa atcactgtct
540
ttccctgagc aaggggctg ctcattagat cttttgatac tttaccatgt gaaatactac
600
cagaactgtt ctctaaaccc actttttctg tagaggaatg tatcatcttt ttttttctca
660
tattacaaat ggacaaataa cggactttct attttcatat ttgctgaaac catttttaa
720
atgaaattag gtcattattt atgaaaagtt ttgagagggc actgtcaact tgggtttaag
780
acaggaggac attgcaagtt cacacctttc ataagcataa agtagttgca agaaagtatt
840
ttcatcctgt taggattcat atctaagata gagttatgca ttgcacatac acaaataaac
900
ttttattaga tagataccta taaaagaaac ataaaagtat gttgtgtatt actgacagtt
960
ctagattaat ttcttttaga attaaagtag atttgttaaa aaaaaaaaaa aaaaaaaaaa
1020
aaaaaaaaaa aaaaaaaaaa aaa
1043

<210> 4666

<211> 167
<212> PRT
<213> Homo sapiens

<400> 4666
Xaa Arg His Glu Gly Gly Ser His Arg Lys Ala Ala Arg Ser Val Ser
1 5 10 15
Gly Ile Thr Arg Arg Val Phe Met Trp Thr Val Ser Gly Thr Pro Cys
20 25 30
Arg Glu Phe Trp Ser Arg Phe Arg Lys Glu Lys Glu Pro Val Val Val
35 40 45
Glu Thr Val Glu Glu Lys Lys Glu Pro Ile Leu Val Cys Pro Pro Leu
50 55 60
Arg Ser Arg Ala Tyr Thr Pro Pro Glu Asp Leu Gln Ser Arg Leu Glu
65 70 75 80
Ser Tyr Val Lys Glu Val Phe Gly Ser Ser Leu Pro Ser Asn Trp Gln
85 90 95
Asp Ile Ser Leu Glu Asp Ser Arg Leu Lys Phe Asn Leu Leu Ala His
100 105 110
Leu Ala Asp Asp Leu Gly His Val Val Pro Asn Ser Arg Leu His Gln
115 120 125
Met Cys Arg Val Arg Asp Val Leu Asp Phe Tyr Asn Val Pro Ile Gln
130 135 140
Asp Arg Ser Lys Phe Asp Glu Leu Ser Ala Ser Asn Leu Pro Pro Asn
145 150 155 160
Leu Lys Ile Thr Trp Ser Tyr
165

<210> 4667
<211> 1031
<212> DNA
<213> Homo sapiens

<400> 4667
ntggccatgg gcacgtccct gtatgccccc gaggtatgta actgctctgc gcctgacacg
60
ggcaacatgg agctgctggt gaggtatggc accgaagcgc agaaggctcg ctggctgatt
120
cctctgctgg aggggaaagc ccgctcctgt tttgctatga ccgagcccca ggttgcctct
180
tcagatgcca ccaacattga ggcttccatc agagaggagg acagcttcta tgtcataaac
240
ggtcacaaat ggtggatcac aggcatcctg gatcctcgtt gccaactctg tgtgtttatg
300
ggaaaaacag acccacatgc accaagacac cggcagcagt ctgtgctctt ggttcccatg
360
gataccccag ggataaaaat catccggcct ctgacggtgt atggactgga agatgcacca
420
ggtggccatg gtgaagtccg atttgagcac gtgcgtgtgc ccaaagagaa catggtcctg
480
ggccctggcc gaggctttga gatcgcccag ggcagactgg gccccggcag gatccatcac
540
tgcatgaggc tgatcgggtt ctcagagagg gccctggcac tcatgaaggc ccgcgtgagt
600

gctttccccc gcacccagca ctgactcaga accaccacct tctgctttgc tgtcggactt
660
caattcctac ctgttttctg agtgcagtcc tagcaggtga agcaaggtga tgtccttgcc
720
aagaagttgc attcctgtct gctttgcatc tgctactttg ctgcagtttg gattcagagc
780
agaatggacc ccactctgtc gaggtgacct gaagggaaac gccaggctct gtagcagcag
840
agggcaaggt tccaaggtgt aaaggtcatg ctgctagcac attattaaaa atcagtctgg
900
gtgcaatggc tcacagctat aatcccagta ctttgggagg tctaggtagg agggttgctt
960
gaagccaagc atttgagacc agcctaggcg aaaaagagag actcagtctc tacaaaaaaa
1020
aaaaaaaaaa a
1031

<210> 4668
<211> 207
<212> PRT
<213> Homo sapiens

<400> 4668
Xaa Ala Met Gly Thr Ser Leu Tyr Ala Pro Glu Val Cys Asn Cys Ser
 1   5   10   15
Ala Pro Asp Thr Gly Asn Met Glu Leu Leu Val Arg Tyr Gly Thr Glu
            20   25   30
Ala Gln Lys Ala Arg Trp Leu Ile Pro Leu Leu Glu Gly Lys Ala Arg
        35   40   45
Ser Cys Phe Ala Met Thr Glu Pro Gln Val Ala Ser Ser Asp Ala Thr
    50   55   60
Asn Ile Glu Ala Ser Ile Arg Glu Glu Asp Ser Phe Tyr Val Ile Asn
65   70   75   80
Gly His Lys Trp Trp Ile Thr Gly Ile Leu Asp Pro Arg Cys Gln Leu
                85   90   95
Cys Val Phe Met Gly Lys Thr Asp Pro His Ala Pro Arg His Arg Gln
            100   105   110
Gln Ser Val Leu Leu Val Pro Met Asp Thr Pro Gly Ile Lys Ile Ile
        115   120   125
Arg Pro Leu Thr Val Tyr Gly Leu Glu Asp Ala Pro Gly Gly His Gly
    130   135   140
Glu Val Arg Phe Glu His Val Arg Val Pro Lys Glu Asn Met Val Leu
145   150   155   160
Gly Pro Gly Arg Gly Phe Glu Ile Ala Gln Gly Arg Leu Gly Pro Gly
                165   170   175
Arg Ile His His Cys Met Arg Leu Ile Gly Phe Ser Glu Arg Ala Leu
            180   185   190
Ala Leu Met Lys Ala Arg Val Ser Ala Phe Pro Arg Thr Gln His
        195   200   205

<210> 4669
<211> 683
<212> DNA
<213> Homo sapiens

<400> 4669
nnaagcttca gtgggctacg tggaatcata caagaaaaat atagagcaaa taaaaagaaa
60
cagaaagtat ttcaacacaa tgaacttaag aaagagactt gtgttcaggc aggttttcag
120
gacatgaaca taaaaaaaca gattcaggaa cagcaccagg ctgccattat tattcagaag
180
cattgtaaag cctttaaaat aaggaagcat tatctccaca ttagagcaac agtagtttct
240
attcaaagaa gatacagaaa actaactgca gtgcgtaccc aagcagttat ttgtatacag
300
tcttattaca gaggctttaa agtacgaaag gatattcaaa atatgcaccg ggctgccaca
360
ctaattcagt cattctatcg aatgcacagg gccaaagttg attattaaac aaagaaaact
420
gcaattgtgg ttatacagaa ttattatagg ttgtatgtta gagtaaaaac agaaagaaaa
480
aacttttag cagttcagaa atctgtccga actattcagg ctgcttttag aggcatgaaa
540
gttagacaaa aattgaaaaa atgtatcaga ggaaaagatg gcagccattg ttaaccaatc
600
tgcactctgc tgttacagaa gtaaaactca gtatgaagct gttcaaagtg aaggtgttat
660
gattcaagag tggtataaag ctt
683

<210> 4670
<211> 135
<212> PRT
<213> Homo sapiens

<400> 4670
Xaa Ser Phe Ser Gly Leu Arg Gly Ile Ile Gln Glu Lys Tyr Arg Ala
1 5 10 15
Asn Lys Lys Lys Gln Lys Val Phe Gln His Asn Glu Leu Lys Lys Glu
20 25 30
Thr Cys Val Gln Ala Gly Phe Gln Asp Met Asn Ile Lys Lys Gln Ile
35 40 45
Gln Glu Gln His Gln Ala Ala Ile Ile Ile Gln Lys His Cys Lys Ala
50 55 60
Phe Lys Ile Arg Lys His Tyr Leu His Ile Arg Ala Thr Val Val Ser
65 70 75 80
Ile Gln Arg Arg Tyr Arg Lys Leu Thr Ala Val Arg Thr Gln Ala Val
85 90 95
Ile Cys Ile Gln Ser Tyr Tyr Arg Gly Phe Lys Val Arg Lys Asp Ile
100 105 110
Gln Asn Met His Arg Ala Ala Thr Leu Ile Gln Ser Phe Tyr Arg Met
115 120 125
His Arg Ala Lys Val Asp Tyr
130 135

<210> 4671
<211> 657

<212> DNA
<213> Homo sapiens

<400> 4671
accggtccag ggcattcagg tgttcctcca ggcccaggag agtgctgcac acccgttcca
60
gcaccagcgc catccgcttc gaggttgagc ctcctgcagc agtggaatca ggggcctcct
120
ggggctcggc aggggctacc cggctccgct tccgcccagt aatggagact gcagccacgt
180
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<210> 4672
<211> 152
<212> PRT
<213> Homo sapiens

<400> 4672
Ala Arg Leu Leu Gln Trp Phe Gln His Leu Ser Ala Gly Ile His Gly
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Glu Ala Gly Val Arg Arg Ile Lys Met Ala Thr Ala Asp Glu Ile Val
            20   25   30
Lys Leu Met Leu Asp His Met Thr Asn Thr Thr Asn Ala Ser His Val
        35   40   45
Pro Val Gln Pro Gly Ser Ser Val Val Met Met Val Asn Asn Leu Gly
    50   55   60
Gly Leu Ser Phe Leu Glu Leu Gly Ile Ile Ala Asp Ala Thr Val Arg
65   70   75   80
Ser Leu Glu Gly Arg Gly Val Lys Ile Ala Arg Ala Leu Val Gly Thr
                85   90   95
Phe Met Ser Ala Leu Glu Met Pro Gly Ile Ser Leu Thr Leu Leu Leu
            100   105   110
Val Asp Glu Pro Leu Leu Lys Leu Ile Asp Ala Glu Thr Thr Ala Ala
        115   120   125
Ala Trp Pro Arg Ser Gly Trp Arg Trp Cys Trp Asn Gly Cys Ala Ala
    130   135   140
Leu Ser Trp Ala Trp Arg Asn Thr
145   150

<210> 4673
<211> 1335
<212> DNA
<213> Homo sapiens

<400> 4673
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240
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420
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480
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1140
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1335

<210> 4674

<211> 402
<212> PRT
<213> Homo sapiens

<400> 4674
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Ala Ser Cys Leu Val Asp Asp Thr Leu Ala Val Ala Gln Glu Lys Glu
20 25 30
Ala Asn Ser Leu Ala Ser Ser Gly Pro His Asn Leu Thr Tyr Pro Leu
35 40 45
Gly Pro Arg Asn Glu Asp Leu Ser Leu Asp Tyr Ala Ser Gln Pro Ala
50 55 60
Asn Leu Gln Phe Pro His Ile Met Pro Leu Ala Glu Asp Ile Lys Gly
65 70 75 80
Ser Cys Phe Gln Ser Gly Asn Lys Arg Asn His Glu Pro Phe Ile Ala
85 90 95
Pro Glu Arg Phe Gly Asn Ser Ser Val Gly Phe Gly Ser Asn Ser His
100 105 110
Ser Gln Ala Pro Glu Lys Val Thr Leu Leu Val Asp Gly Thr Arg Phe
115 120 125
Val Val Asn Pro Gln Ile Phe Thr Ala His Pro Asp Thr Met Leu Gly
130 135 140
Arg Met Phe Gly Pro Gly Arg Glu Tyr Asn Phe Thr Arg Pro Asn Glu
145 150 155 160
Lys Gly Glu Tyr Glu Ile Ala Glu Gly Ile Ser Ala Thr Val Phe Arg
165 170 175
Thr Val Leu Asp Tyr Tyr Lys Thr Gly Ile Ile Asn Cys Pro Asp Gly
180 185 190
Ile Ser Ile Pro Asp Leu Arg Asp Thr Cys Asp Tyr Leu Cys Ile Asn
195 200 205
Phe Asp Phe Asn Thr Ile Arg Cys Gln Asp Leu Ser Ala Leu Leu His
210 215 220
Glu Leu Ser Asn Asp Gly Ala His Lys Gln Phe Asp His Tyr Leu Glu
225 230 235 240
Glu Leu Ile Leu Pro Ile Met Val Gly Cys Ala Lys Lys Gly Glu Arg
245 250 255
Glu Cys His Ile Val Val Leu Thr Asp Glu Asp Ser Val Asp Trp Asp
260 265 270
Glu Asp His Pro Pro Pro Met Gly Glu Glu Tyr Ser Gln Ile Leu Tyr
275 280 285
Ser Ser Lys Leu Tyr Arg Phe Phe Lys Tyr Ile Glu Asn Arg Asp Val
290 295 300
Ala Lys Thr Val Leu Lys Glu Arg Gly Leu Lys Asn Ile Arg Ile Gly
305 310 315 320
Ile Glu Gly Tyr Pro Thr Cys Lys Glu Lys Ile Lys Arg Arg Pro Gly
325 330 335
Gly Arg Ser Glu Val Ile Tyr Asn Tyr Val Gln Arg Pro Phe Ile Gln
340 345 350
Met Ser Trp Glu Lys Glu Glu Gly Lys Ser Arg His Val Asp Phe Gln
355 360 365
Cys Val Arg Ser Lys Ser Leu Thr Asn Leu Val Ala Ala Gly Asp Asp
370 375 380
Val Leu Glu Asp Gln Glu Ile Leu Met His His Pro Pro Gln Val Asp

385 390 395 400
Glu Leu

<210> 4675
<211> 2868
<212> DNA
<213> Homo sapiens

<400> 4675
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120
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240
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360
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420
atgtcgactg cgggaagcaa gcggtcttct tcttcacgca atcgaggtcc tcatgggcgg
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540
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660
atgaggcgtt ctggaaggta catgtcttgc ggtgaaaatc atggtgtcag acccccaaac
720
ccagagcagt atttgactcc actgcagcag aaagaggtga cagtgagaca cctcaaaacc
780
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840
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900
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1080
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1320

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1980
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2160
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2340
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2400
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2460
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2520
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2640
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2700
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2760
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2868

<210> 4676

<211> 641
<212> PRT
<213> Homo sapiens

<400> 4676
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Lys Val Ser Pro Ala Ser Glu Ser Pro Phe Ser Glu Glu Glu Ser Arg
20 25 30
Glu Phe Asn Pro Ser Ser Ser Gly Arg Ser Ala Arg Thr Val Ser Ser
35 40 45
Asn Ser Phe Cys Ser Asp Asp Thr Gly Cys Pro Ser Ser Gln Ser Val
50 55 60
Ser Pro Val Lys Thr Pro Ser Asp Ala Gly Asn Ser Pro Ile Gly Phe
65 70 75 80
Cys Pro Gly Ser Asp Glu Gly Phe Thr Arg Lys Lys Cys Thr Ile Gly
85 90 95
Met Val Gly Glu Gly Ser Ile Gln Ser Ser Arg Tyr Lys Lys Glu Ser
100 105 110
Lys Ser Gly Leu Val Lys Pro Gly Ser Glu Ala Asp Phe Ser Ser Ser
115 120 125
Ser Ser Thr Gly Ser Ile Ser Ala Pro Glu Val His Met Ser Thr Ala
130 135 140
Gly Ser Lys Arg Ser Ser Ser Ser Arg Asn Arg Gly Pro His Gly Arg
145 150 155 160
Ser Asn Gly Ala Ser Ser His Lys Pro Gly Ser Ser Ser Ser Ser Pro
165 170 175
Arg Glu Lys Asp Leu Leu Ser Met Leu Cys Arg Asn Gln Leu Ser Pro
180 185 190
Val Asn Ile His Pro Ser Tyr Ala Pro Ser Ser Pro Ser Ser Ser Asn
195 200 205
Ser Gly Ser Tyr Lys Gly Ser Asp Cys Ser Pro Ile Met Arg Arg Ser
210 215 220
Gly Arg Tyr Met Ser Cys Gly Glu Asn His Gly Val Arg Pro Pro Asn
225 230 235 240
Pro Glu Gln Tyr Leu Thr Pro Leu Gln Gln Lys Glu Val Thr Val Arg
245 250 255
His Leu Lys Thr Lys Leu Lys Glu Ser Glu Arg Arg Leu His Glu Arg
260 265 270
Glu Ser Glu Ile Val Glu Leu Lys Ser Gln Leu Ala Arg Met Arg Glu
275 280 285
Asp Trp Ile Glu Glu Glu Cys His Arg Val Glu Ala Gln Leu Ala Leu
290 295 300
Lys Glu Ala Arg Lys Glu Ile Lys Gln Leu Lys Gln Val Ile Glu Thr
305 310 315 320
Met Arg Ser Ser Leu Ala Asp Lys Asp Lys Gly Ile Gln Lys Tyr Phe
325 330 335
Val Asp Ile Asn Ile Gln Asn Lys Lys Leu Glu Ser Leu Leu Gln Ser
340 345 350
Met Glu Met Ala His Ser Gly Ser Leu Arg Asp Glu Leu Cys Leu Asp
355 360 365
Phe Pro Cys Asp Ser Pro Glu Lys Ser Leu Thr Leu Asn Pro Pro Leu
370 375 380
Asp Thr Met Ala Asp Gly Leu Ser Leu Glu Glu Gln Val Thr Gly Glu

385 390 395 400
Gly Ala Asp Arg Glu Leu Leu Val Gly Asp Ser Ile Ala Asn Ser Thr
405 410 415
Asp Leu Phe Asp Glu Ile Val Thr Ala Thr Thr Thr Glu Ser Gly Asp
420 425 430
Leu Glu Leu Val His Ser Thr Pro Gly Ala Asn Val Leu Glu Leu Leu
435 440 445
Pro Ile Val Met Gly Gln Glu Glu Gly Ser Val Val Val Glu Arg Ala
450 455 460
Val Gln Thr Asp Val Val Pro Tyr Ser Pro Ala Ile Ser Glu Leu Ile
465 470 475 480
Gln Ser Val Leu Gln Lys Leu Gln Asp Pro Cys Pro Ser Ser Leu Ala
485 490 495
Ser Pro Asp Glu Ser Glu Pro Asp Ser Met Glu Ser Phe Pro Glu Ser
500 505 510
Leu Ser Ala Leu Val Val Asp Leu Thr Pro Arg Asn Pro Asn Ser Ala
515 520 525
Ile Leu Leu Ser Pro Val Glu Thr Pro Tyr Xaa Gln Cys Gly Cys Arg
530 535 540
Ser Ser Cys Lys Pro Pro His Glu Arg Ala Gly Xaa Phe Ala Ala Cys
545 550 555 560
Val Glu Glu Arg Leu Asp Gly Val Ile Pro Leu Ala Arg Gly Gly Val
565 570 575
Val Arg Gln Tyr Trp Ser Ser Ser Phe Leu Val Asp Leu Leu Ala Val
580 585 590
Ala Ala Pro Val Val Pro Thr Val Leu Trp Ala Phe Ser Thr Gln Arg
595 600 605
Gly Gly Thr Asp Pro Val Tyr Asn Ile Gly Ala Leu Leu Arg Gly Cys
610 615 620
Cys Val Val Ala Leu His Ser Leu Arg Arg Thr Ala Phe Arg Ile Lys
625 630 635 640
Thr

<210> 4677
<211> 940
<212> DNA
<213> Homo sapiens

<400> 4677
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120
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180
ataactgggc aagcatggct ttgttctcct tgatgttcat ggtccttttc agtaaagcat
240
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300
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420

cttggtgggg aactgaaagg ctactcgaag accaatacta cttcttctag acctgcttct
480
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720
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940

<210> 4678
<211> 133
<212> PRT
<213> Homo sapiens

<400> 4678
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Leu Phe Phe Ser His Ser Val Arg Cys Ala Arg Lys Gln Leu Leu Gly
20 25 30
Arg Thr Val Phe Ile Trp Phe Val Gly Gln Leu Leu Gly Gly Glu Leu
35 40 45
Lys Gly Tyr Ser Lys Thr Asn Thr Thr Ser Ser Arg Pro Ala Ser Ser
50 55 60
Arg Gly Ser Leu Ser Ser Ser Ser Ser Ser Ser Ser Ser Leu Thr Lys
65 70 75 80
Asp Ala Leu Pro Ser Ser Leu Lys Ser Asp Ser Thr Thr Ile Thr Ser
85 90 95
Gly Leu Val Phe Pro Phe Arg Ser Leu Cys Val Asn Pro Ala Lys Ser
100 105 110
Ser Val Ser Glu Ser Val Ser Ser Ile Lys Ile Leu Leu Ser Ser Ser
115 120 125
Val Lys Tyr Leu Glu
130

<210> 4679
<211> 2284
<212> DNA
<213> Homo sapiens

<400> 4679
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120

taattacagg aatagaatgt acaataaaaa gtacagaata atgagtgaca gggatcaaac
180
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240
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360
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1980
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2040
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2100
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2160
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2280
tgac
2284

<210> 4680
<211> 112
<212> PRT
<213> Homo sapiens

<400> 4680
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Thr Ser Phe His Arg Gly Thr Cys Leu Glu Phe Trp His Arg Gly Leu
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Thr Glu His Ser Ser Asp Ile Phe Leu Gln Leu Glu Met Leu Cys Trp
35 40 45
Ser Pro Cys Ser Leu Thr Phe Ser Arg Ala Ile Lys Ala Thr Ser Ser
50 55 60
Ile Ala Gly Pro Gln Thr Phe Gln Gly Lys His Cys Phe Thr Ser Cys
65 70 75 80
Arg Gln Leu Ile Ser Gln Lys Pro Leu Gln Lys Pro Val Leu Pro Gly
85 90 95
Thr Ala Gly Ala Gly Val Cys Lys Ile Lys Glu Gly Gln Leu Arg Thr
100 105 110

<210> 4681
<211> 906
<212> DNA
<213> Homo sapiens

<400> 4681
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120
acagaagtct aggtactgta cattcactaa ggctccttgt ttttgcaaat cgcgtttatg
180

acaaataacc ataaggcaaa cgaatctaaa ggaatggtta tgagtgtttc cagcgtacag
240
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360
aaaagaaaag ggaggaagaa aggaaaggtt tttttgtctg gtggtctgat ggaagaggaa
420
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480
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540
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660
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720
cgtgcttctg ttgctgtgtt aaaggtgacc tctcccacag gttttctgtg cctgcctgca
780
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acgcgt
906

<210> 4682
<211> 153
<212> PRT
<213> Homo sapiens

<400> 4682
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 1   5   10   15
Lys Glu Met Leu Gln Lys Phe Lys Phe Ser His Val Tyr Phe Lys Gln
            20   25   30
Phe Leu Phe His Gln Thr Thr Arg Gln Lys Asn Leu Ser Phe Leu Pro
        35   40   45
Pro Phe Ser Phe Phe Pro Ser Cys Thr His Leu Glu Asn Phe Thr Phe
    50   55   60
Leu Glu Ser Pro Gln Asn Asn Thr Lys Val Ile Val Gly Ala Thr Gly
65   70   75   80
Phe Met Leu Tyr Cys Gly Ala Arg Gly Lys Thr Cys Leu Tyr Ala Gly
                85   90   95
Asn Thr His Asn His Ser Phe Arg Phe Val Cys Leu Met Val Ile Cys
            100   105   110
His Lys Arg Asp Leu Gln Lys Gln Gly Ala Leu Val Asn Val Gln Tyr
        115   120   125
Leu Asp Phe Cys Val Leu Arg Thr Gln Lys Gly Ala Thr Leu Leu Phe
    130   135   140
Gly Pro Val Ser Gly His Leu Val Ile
145   150

<210> 4683
<211> 3246
<212> DNA
<213> Homo sapiens

<400> 4683
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gctgctgctg ccgccgccac ccctgtatac ccggcaccgc atgctcggtc cagagtccgt
120
cccgccccca aaacgatccc gcagcaaact catggcaccg cccgaatcgg gacgcacaat
180
ggcaccttcc actgcgacga ggcactggca tgcgcactgc ttcgcctcct gccggagtac
240
cgggatgcag agattgtgcg gacccgggat cccgaaaaac tcgcttcctg tgacatcgtg
300
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360
ttcacagaga ccatgagctc cctgtcccct gggaagccgt ggcagaccaa gctgagcagt
420
gcgggactca tctatctgca cttcgggcac aagctgctgg cccagttgct gggcactagt
480
gaagaggaca gcatggtggg caccctctat gacaagatgt atgagaactt tgtggaggag
540
gtggatgctg tggacaatgg gatctcccag tgggcagagg gggagcctcg atatgcactg
600
accactaccc tgagtgcacg agttgctcga cttaatccta cctggaacca ccccgaccaa
660
gacactgagg cagggttcaa gcgtgcaatg gatctggttc aagaggagtt tctgcagaga
720
ttagatttct accaacacag ctggctgcca gcccgggcct tggtggaaga ggcccttgcc
780
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840
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900
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960
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1020
gaccaggtca gtgggatccc tggctgcatc ttcgtccatg caagcggctt cattggcggt
1080
caccgcaccc gagagggtgc cttgagcatg gcccgtgcca ccttggccca gcgctcatac
1140
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1260
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1320
tgaaaccaca gtttctagga ttaaataacg tgaccaaatt cacaagtggc taaaaagtga
1380
cagaacaggg ccttaaccca aagtccatgc ttttttcccc tactgtaccc cactgcaact
1440

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1560
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1860
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1920
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1980
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2040
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2100
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2160
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2220
agtggtagcc aggattttgc tgccgtctgg ggaccagagc aggttggtca ccccacctcc
2280
tcgaaaccag ggaaggggga cacaggtctc tgttgagaca tcccataccc ggatagcagc
2340
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2400
aggtgtatgc ccagggtgag acagcacttg ggcacagcca gaagagggtc gggtagacaa
2460
ggaggtaggg tccagggtcc agataagaat gcagctctgg caggccacag ccaagacaga
2520
ggcactaagg ggcttccagg ccagagacgc cacatttcgc tgcagccggt gcttcaggga
2580
ggggactatg gtgctgctgg cattatacac acggactgag tcatctagca gggccactgc
2640
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2700
gacttgggca aattcagcga tcagatcttc gctcctgaga gacagatggg ggaacaggga
2760
cccatggagg gaagaggccc atcgacagag tgccagggcc cagccggatg ccgtcttcac
2820
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2880
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2940
tcttgtgcca tggtccagcc ttccaggggt ctttagggga tcctttgtca gttgtaggac
3000
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3060

caccagctcg ttattgtgct catatagggt gacttgaccc cgaggcggtg gaggagggaa
3120
caaccccaga gagcacatct tgccggttcg caggacgtct gcagtcggca aactcctggc
3180
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3240
ggtacc
3246

<210> 4684
<211> 385
<212> PRT
<213> Homo sapiens

<400> 4684
Xaa Pro Ala Ser Leu Gln Gly Ala Ala Tyr Gly Thr Pro Leu Pro Ala
 1   5   10   15
Arg Pro Leu Asn Ala Ala Ala Ala Ala Ala Thr Pro Val Tyr Pro Ala
            20   25   30
Pro His Ala Arg Ser Arg Val Arg Pro Ala Pro Lys Thr Ile Pro Gln
        35   40   45
Gln Thr His Gly Thr Ala Arg Ile Gly Thr His Asn Gly Thr Phe His
    50   55   60
Cys Asp Glu Ala Leu Ala Cys Ala Leu Leu Arg Leu Leu Pro Glu Tyr
65   70   75   80
Arg Asp Ala Glu Ile Val Arg Thr Arg Asp Pro Glu Lys Leu Ala Ser
                85   90   95
Cys Asp Ile Val Val Asp Val Gly Gly Glu Tyr Asp Pro Arg Arg His
            100   105   110
Arg Tyr Asp His His Gln Arg Ser Phe Thr Glu Thr Met Ser Ser Leu
        115   120   125
Ser Pro Gly Lys Pro Trp Gln Thr Lys Leu Ser Ser Ala Gly Leu Ile
    130   135   140
Tyr Leu His Phe Gly His Lys Leu Leu Ala Gln Leu Leu Gly Thr Ser
145   150   155   160
Glu Glu Asp Ser Met Val Gly Thr Leu Tyr Asp Lys Met Tyr Glu Asn
                165   170   175
Phe Val Glu Glu Val Asp Ala Val Asp Asn Gly Ile Ser Gln Trp Ala
            180   185   190
Glu Gly Glu Pro Arg Tyr Ala Leu Thr Thr Thr Leu Ser Ala Arg Val
        195   200   205
Ala Arg Leu Asn Pro Thr Trp Asn His Pro Asp Gln Asp Thr Glu Ala
    210   215   220
Gly Phe Lys Arg Ala Met Asp Leu Val Gln Glu Glu Phe Leu Gln Arg
225   230   235   240
Leu Asp Phe Tyr Gln His Ser Trp Leu Pro Ala Arg Ala Leu Val Glu
                245   250   255
Glu Ala Leu Ala Gln Arg Phe Gln Val Asp Pro Ser Gly Glu Ile Val
            260   265   270
Glu Leu Ala Lys Gly Ala Cys Pro Trp Lys Glu His Leu Tyr His Leu
        275   280   285
Glu Ser Gly Leu Ser Pro Pro Val Ala Ile Phe Phe Val Ile Tyr Thr
    290   295   300
Asp Gln Ala Gly Gln Trp Arg Ile Gln Cys Val Pro Lys Glu Pro His

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305                 310                 315                 320
Ser Phe Gln Ser Arg Leu Pro Leu Pro Glu Pro Trp Arg Gly Leu Arg
                325                 330                 335
Asp Glu Ala Leu Asp Gln Val Ser Gly Ile Pro Gly Cys Ile Phe Val
            340                 345                 350
His Ala Ser Gly Phe Ile Gly Gly His Arg Thr Arg Glu Gly Ala Leu
        355                 360                 365
Ser Met Ala Arg Ala Thr Leu Ala Gln Arg Ser Tyr Leu Pro Gln Ile
    370                 375                 380
Ser
385
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<210> 4685
<211> 618
<212> DNA
<213> Homo sapiens

<400> 4685
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120
gtccctgtgt ctctcatcct gtgctggtgg caggggtgag ccaccaactc ggaaggccca
180
gggtgaagtg tgggctgctg aggactgagc gatcacccac atgtccacac agccagccgg
240
gccgcagctg atgcccgagg acgcgctgga caccggtctg cagccgcttc caacctctcc
300
ggcctcagcc tccaggaggc acagcagatt ctcaacgtgt ccaagctgag ccctgaggag
360
gtccagaaga actatgaaca cttatttaag gtgaatgata aatccgtggg tggctccttc
420
tacctgcagt caaaggtggt ccgcgcaaag gagcgcctgg atgaggaact caaaatccag
480
gcccaggagg acagagaaaa agggcagatg ccccatacgt gactgctcgg ctcccccccgc
540
ccaccccgcc gcctctaatt tatagcttgg taataaattt cttttctgca aaaaaaagag
600
gctggagtgt gctcgcga
618

<210> 4686
<211> 106
<212> PRT
<213> Homo sapiens

<400> 4686
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Gly Leu Ser Asp His Pro His Val His Thr Ala Ser Arg Ala Ala Ala
 1               5                  10                  15
Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala Ala Ser Asn Leu
            20                  25                  30
Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu Asn Val Ser Lys
        35                  40                  45
Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His Leu Phe Lys Val
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```
    50                  55                  60
Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln Ser Lys Val Val
65                  70                  75                  80
Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile Gln Ala Gln Glu
                85                  90                  95
Asp Arg Glu Lys Gly Gln Met Pro His Thr
            100                 105
```

<210> 4687
<211> 309
<212> DNA
<213> Homo sapiens

<400> 4687
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gcaagatcgc ggcgctgtcg ctgagcgccc tcccggtgtc ctacgcgctc aaccacgtct
120
cggcgctctc gcacccccctg tgggtggcat tgatgagcgc cctaatcctg ggtctgcttt
180
tcgtggcggt ctacagcttg tcccatggcg aggtctccta tgacccactc tatgctggct
240
tcgctgtctt cgccttcacc tcgggtgggg acctcatcat cgctcttcag gaagacagct
300
atgggggggg
309

<210> 4688
<211> 90
<212> PRT
<213> Homo sapiens

<400> 4688
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Met Asp Ile Pro Pro Leu Ala Gly Lys Ile Ala Ala Leu Ser Leu Ser
 1               5                  10                  15
Ala Leu Pro Val Ser Tyr Ala Leu Asn His Val Ser Ala Leu Ser His
            20                  25                  30
Pro Leu Trp Val Ala Leu Met Ser Ala Leu Ile Leu Gly Leu Leu Phe
        35                  40                  45
Val Ala Val Tyr Ser Leu Ser His Gly Glu Val Ser Tyr Asp Pro Leu
    50                  55                  60
Tyr Ala Gly Phe Ala Val Phe Ala Phe Thr Ser Gly Gly Asp Leu Ile
65                  70                  75                  80
Ile Ala Leu Gln Glu Asp Ser Tyr Gly Gly
                85                  90
```

<210> 4689
<211> 898
<212> DNA
<213> Homo sapiens

<400> 4689
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60

cgctggcgct ggcggacgcc ggactgtcca ccagcatcag cccccgagga cctgatgttc
120
ctgctggaca gctcagccag cgtctctcac tacgagttct cccgggttcg ggagtttgtg
180
gggcagctgg tggctccact gccccctggca ccgnnggccc tgcgtgccag tctggtgcac
240
gtgggcagtc ggccatacac cgagttcccc ttcggccagc acagctcggg tgaggctgcc
300
caggatgcgg tgcgtgcttc tgcccagcgc atgggtgaca cccacactgg cctggcgctg
360
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420
gtgctggtgt gggtgacaga tggcggctcc agcgaccctg tgggcccccc catgcaggag
480
ctcaaggacc tgggcgtcac cgtgttcatt gtcagcaccg gccgaggcaa cttcctggag
540
ctgtcagccg ctgcctcagc ccctgccgag aagcacctgc actttgtgga cgtggatgac
600
ctgcacatca ttgtccaaga gctgaggggc tccattctcg acgcgatgcg gccacagcag
660
ctccatgcca cggagatcac gtccagcggc ttccgcctgg cctggccacc cctgctgacc
720
gcagactcgg gctactatgt gctggagctg gtgcccagcg cccagccggg ggctgcaaga
780
cgccagcagc tgccagggaa cgccacggac tggatctggg ccggcctcga cccggacacg
840
gactacgacg tggcgctagt gcctgagtcc aacgtgcgcc tcctgaggcc ccagatct
898

<210> 4690
<211> 299
<212> PRT
<213> Homo sapiens

<400> 4690
Xaa Pro Arg Pro Ser Arg Arg Ile Ala Pro Leu Asp Gly Ala Arg Leu
 1   5   10   15
Ala Leu Ser Leu Arg Trp Arg Trp Arg Thr Pro Asp Cys Pro Pro Ala
            20   25   30
Ser Ala Pro Glu Asp Leu Met Phe Leu Leu Asp Ser Ser Ala Ser Val
        35   40   45
Ser His Tyr Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val
    50   55   60
Ala Pro Leu Pro Leu Ala Pro Xaa Ala Leu Arg Ala Ser Leu Val His
65   70   75   80
Val Gly Ser Arg Pro Tyr Thr Glu Phe Pro Phe Gly Gln His Ser Ser
                85   90   95
Gly Glu Ala Ala Gln Asp Ala Val Arg Ala Ser Ala Gln Arg Met Gly
            100   105   110
Asp Thr His Thr Gly Leu Ala Leu Val Tyr Ala Lys Glu Gln Leu Phe
        115   120   125
Ala Glu Ala Ser Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp
    130   135   140
Val Thr Asp Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu

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145                 150                 155                 160
Leu Lys Asp Leu Gly Val Thr Val Phe Ile Val Ser Thr Gly Arg Gly
                165                 170                 175
Asn Phe Leu Glu Leu Ser Ala Ala Ala Ser Ala Pro Ala Glu Lys His
            180                 185                 190
Leu His Phe Val Asp Val Asp Asp Leu His Ile Ile Val Gln Glu Leu
        195                 200                 205
Arg Gly Ser Ile Leu Asp Ala Met Arg Pro Gln Gln Leu His Ala Thr
    210                 215                 220
Glu Ile Thr Ser Ser Gly Phe Arg Leu Ala Trp Pro Pro Leu Leu Thr
225                 230                 235                 240
Ala Asp Ser Gly Tyr Tyr Val Leu Glu Leu Val Pro Ser Ala Gln Pro
                245                 250                 255
Gly Ala Ala Arg Arg Gln Gln Leu Pro Gly Asn Ala Thr Asp Trp Ile
            260                 265                 270
Trp Ala Gly Leu Asp Pro Asp Thr Asp Tyr Asp Val Ala Leu Val Pro
        275                 280                 285
Glu Ser Asn Val Arg Leu Leu Arg Pro Gln Ile
    290                 295
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<210> 4691
<211> 2375
<212> DNA
<213> Homo sapiens

<400> 4691
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aataactata ctatcccaga agaagaaatt gggtctttct tatttcatgc tattaataag
120
ccaaatgctc ctatctggct catactcaat gaagctggac tatactggag agcagtagga
180
aatagcactt ttgctattgc ctgtcttcag agggctttga atttagctcc acttcaatac
240
caagatgttc ctcttgtcaa cttggccaac cttttgattc attacggcct tcatcttgat
300
gccactaagc tgctacttca agctttggcc atcaatagct ctgagcctct gacctttttg
360
agcctgggaa atgcttacct tgctctgaag aatatcagtg gggcacttga ggcctttaga
420
caggccttga aattaaccac caaatgtcca gagtgtgaaa acagcctgaa gttgatccgc
480
tgtatgcagt tttatccttt tctgtacaac atcacttctt ctgtttgcag tggtaattgt
540
catgagaaaa ccctggacaa cagccatgac aaacagaaat attttgacaa ctcacagtca
600
ctggatgctg ctgaagaaga gccctctgag agaggaacag aggaggaccc tgtattctct
660
gttgagaatt cagggaggga ctcagatgcc cttagacttg aaagtacggt ggttgaggag
720
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780
gctttggtgg atgaatttca acaggcatgg cctttggaag gctttggggg tgcactagag
840

atgaaagggc ggcgtctaga cttacaagga atacgggtgc tgaagaaagg tccccaggat
900
ggagtggcca gaagctcttg ctatggagac tgcagaagtg aagatgatga agcaacagaa
960
tggattacat tccaggtcaa acgtgtaaag aaacccaaag gagatcataa gaaaactcct
1020
gggaaaaaag tagaaacagg tcagatagaa aatggacatc gttaccaagc aaacctagag
1080
atcactggcc ccaaggtggc atctcctggg ccacaagggc tactagactg gaagaccagg
1140
aaagtgccat agacataatg taactggatt tcagcaaggc atttaacaga gcctcttatg
1200
atatccttgt gaaccagatg gagagatgtg ggcttgaagc cttcccattg cctacaggat
1260
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1320
tcaacaccat tctctgaacc aaccatgctc atgtttttac ctcagtgcct ttgcacatgc
1380
tattccctct gcctggaatg ccctgtgccc cctctgccct ctgccgtgct aaaatatcac
1440
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1500
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1560
gtaatgattt gtttatgttt accttcctta ctagactgtg agctcaagag caggccgtct
1620
taattattcc tttctgtacc cctagtgtct tttatggttc tcagcccctt ataacaggtg
1680
ctcaataaat atttttcaaa tgaaattatt aaatgtaaaa gaaaattaag atttttttgtg
1740
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1800
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1860
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1920
cctgcctatt ccattataac tccttcagaa aacccttccc agacaagaca gttctgctct
1980
tttcttgggg gatttgatgt aagtaaaggg cccacaccca aaaggtgggt acttacgaag
2040
gatattaata aacagagctt taaatttttt tgtagcttta aatagcttgt tgattgggaa
2100
catacacgtt agagtcaaac agactcctag tctgccagtt gctagccagg tgacctggac
2160
aagtcactta gtctctctga gtctctgttt tctcatctga gaaatgaggg ttaaaaccta
2220
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2280
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2340
acctgggcaa gaaagcaagg tgctgtctct aactt
2375

<210> 4692

<211> 383
<212> PRT
<213> Homo sapiens

<400> 4692
Xaa Asp Leu Lys Ala Lys Met Pro Asp Asp His Ala Arg Lys Ile Leu
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Leu Ser Arg Ile Asn Asn Tyr Thr Ile Pro Glu Glu Glu Ile Gly Ser
20 25 30
Phe Leu Phe His Ala Ile Asn Lys Pro Asn Ala Pro Ile Trp Leu Ile
35 40 45
Leu Asn Glu Ala Gly Leu Tyr Trp Arg Ala Val Gly Asn Ser Thr Phe
50 55 60
Ala Ile Ala Cys Leu Gln Arg Ala Leu Asn Leu Ala Pro Leu Gln Tyr
65 70 75 80
Gln Asp Val Pro Leu Val Asn Leu Ala Asn Leu Leu Ile His Tyr Gly
85 90 95
Leu His Leu Asp Ala Thr Lys Leu Leu Leu Gln Ala Leu Ala Ile Asn
100 105 110
Ser Ser Glu Pro Leu Thr Phe Leu Ser Leu Gly Asn Ala Tyr Leu Ala
115 120 125
Leu Lys Asn Ile Ser Gly Ala Leu Glu Ala Phe Arg Gln Ala Leu Lys
130 135 140
Leu Thr Thr Lys Cys Pro Glu Cys Glu Asn Ser Leu Lys Leu Ile Arg
145 150 155 160
Cys Met Gln Phe Tyr Pro Phe Leu Tyr Asn Ile Thr Ser Ser Val Cys
165 170 175
Ser Gly Asn Cys His Glu Lys Thr Leu Asp Asn Ser His Asp Lys Gln
180 185 190
Lys Tyr Phe Asp Asn Ser Gln Ser Leu Asp Ala Ala Glu Glu Glu Pro
195 200 205
Ser Glu Arg Gly Thr Glu Glu Asp Pro Val Phe Ser Val Glu Asn Ser
210 215 220
Gly Arg Asp Ser Asp Ala Leu Arg Leu Glu Ser Thr Val Val Glu Glu
225 230 235 240
Ser Asn Gly Ser Asp Glu Met Glu Asn Ser Asp Glu Thr Lys Met Ser
245 250 255
Glu Glu Ile Leu Ala Leu Val Asp Glu Phe Gln Gln Ala Trp Pro Leu
260 265 270
Glu Gly Phe Gly Gly Ala Leu Glu Met Lys Gly Arg Arg Leu Asp Leu
275 280 285
Gln Gly Ile Arg Val Leu Lys Lys Gly Pro Gln Asp Gly Val Ala Arg
290 295 300
Ser Ser Cys Tyr Gly Asp Cys Arg Ser Glu Asp Asp Glu Ala Thr Glu
305 310 315 320
Trp Ile Thr Phe Gln Val Lys Arg Val Lys Lys Pro Lys Gly Asp His
325 330 335
Lys Lys Thr Pro Gly Lys Lys Val Glu Thr Gly Gln Ile Glu Asn Gly
340 345 350
His Arg Tyr Gln Ala Asn Leu Glu Ile Thr Gly Pro Lys Val Ala Ser
355 360 365
Pro Gly Pro Gln Gly Leu Leu Asp Trp Lys Thr Arg Lys Val Pro
370 375 380

<210> 4693
<211> 794
<212> DNA
<213> Homo sapiens

<400> 4693
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gatgcgcctg cgcaacaagt tcggcgggga agatggcgga tgacaaggat tctctgccta
120
agcttaagga cctggcattt ctcaagaacc agctggaaag cctgcagcgg cgtgtagaag
180
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240
gattcctggc tggctatgtg gtggccaaac tgagggcatc agcagtattg ggctttgctg
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360
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420
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480
tcatccattt gctatctcca actttcctgc caccttcatc cttgcctccc ttcctgcaga
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600
gggactcgcc ccaagactgt ggcttcaagg accaccagcc ccttactctt caagccctga
660
ctgtggagtt ggtagatgcc tctgatcctc agtattctct ctggcaatgt tccacggctt
720
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780
gcccccttcac gcgt
794

<210> 4694
<211> 103
<212> PRT
<213> Homo sapiens

<400> 4694
Met Ala Asp Asp Lys Asp Ser Leu Pro Lys Leu Lys Asp Leu Ala Phe
 1   5   10   15
Leu Lys Asn Gln Leu Glu Ser Leu Gln Arg Arg Val Glu Asp Glu Val
            20   25   30
Asn Ser Gly Val Gly Gln Asp Gly Ser Leu Leu Ser Ser Pro Phe Leu
        35   40   45
Lys Gly Phe Leu Ala Gly Tyr Val Val Ala Lys Leu Arg Ala Ser Ala
    50   55   60
Val Leu Gly Phe Ala Val Gly Thr Cys Thr Gly Ile Tyr Ala Ala Gln
65   70   75   80
Ala Tyr Ala Val Pro Asn Val Glu Lys Thr Leu Arg Asp Tyr Leu Gln
                85   90   95
Leu Leu Arg Lys Gly Pro Asp

100

<210> 4695
<211> 2209
<212> DNA
<213> Homo sapiens

<400> 4695
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gaatacaccc ttctttcaac ggctattcaa agatcacctg gctgcaaagc tttctttcct
120
cgcctgtgct tcctccttaa ctatctctag ttaaagctat ctccaccacc aggccacaag
180
ctcccagaga acagagatcg tgtttttcat tattctgtcc atttccatcc cccactcccg
240
cccacttact gtgtgagtcc agcactgtgt gagtccttga taaaaacgat gagcaaatcc
300
ccaggccttg agtgggtcag cagtgaccac atctatccgc agggatccac ggggaagctg
360
gtgtgcgccg gataaaggta ggtggtccct ctggcacagg ccgccctaag gccaaggccc
420
cccagatgca gctcattcct ggctccctct gacagatggc aaccgccgat gagattgtga
480
aactcatgct cgaccacatg acaaacacca ccaacgcgtc ccatgtgcct gtgcagcccg
540
gtgggtagcc tctcgcccgc gtctcccaac ccctcctaca cctctgggga ggagacgccc
600
agagggtctc acctggggtg tcatgtctac ccgcaggctc ctcagttgtg atgatggtca
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acaacctggg tggcctgtca ttcctggaac tgggcatcat agccgacgct accgtccgct
720
ccctggggaa cgtggtcatt tgtggggtta ttgagggatg cctgccagga ggaaatcagg
780
acatctccct cccgacctca gagccccagc ttccaaggtc cttgcttttc tgttgttttc
840
tttccctgat gcccattttt ccctttgga ctgccacact ctggtattgc agagggccgc
900
ggggtgaaga ttgcccgtgc cctggtgggc accttcatgt cagcactgga gatgcctggc
960
atttctctca ccctcctgct ggtggatgag cctctcctga aactgataga tgctgaaacc
1020
actgcagcag cctggcctaa cgtggctgca gtctccatta ctgggcggaa gcggagccgg
1080
gtagcccctg ccgagcccca ggaggcccct gattccactg ctgcanngga ggctcagcct
1140
cgaagcngga tggcgctggt gctggaacgg gtgtgcagca ctctcctggg cctggaggaa
1200
cacctgaatg ccctggaccg ggctgctggt gacggcgact gtggcaccac ccacagccgt
1260
gcggccagag caatccagga gtggctgaag gagggcccac cccctgccag ccctgcccag
1320
ctgctctcca agttgtctgt tctgctcctg gagaagatgg gaggctcatc tggggcgctc
1380

tatggcctgt tcctgactgc ggctgcacag cccctgaagg ccaagaccag cctcccagcc
1440
tggtctgctg ccatggatgc cggcctggaa gccatgcaga agtatggcaa ggctgctcca
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ggggacagga ctatgctgga ttctctgtgg gcagcggagc aggagctcca agcctggaag
1560
agcccaggag ctgatctgtt acaagtcctg accaaagcag tcaagagtgc cgaagctgca
1620
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1740
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1800
gtgctgaggt ggcctttgtc acttccttct gccttccaac cctcaccttc ccccggcctg
1860
gccccattgg ccaacagaga atccagcata gtcctgtccc ctggagcagc cttgccatac
1920
ttctgcatgg cttccaggcc ggcatccatg gcagcagacc aggctggtgt ggggctggag
1980
gagatcgcaa agcaggtgaa cgtggtcacc aaggccatgg gtaccctggg ggtgagctta
2040
tcctcctgca gcgtccctgg ttccaaaccc accttcgagc tctcagccga cgaggtggag
2100
ctgggcctgg ggatccacgg ggaagctggt gtgcgccgga taaagatggc aaccgccgat
2160
gagattgtga aactcatgct cgaccacatg acaaacacca ccaacgcgt
2209

<210> 4696
<211> 302
<212> PRT
<213> Homo sapiens

<400> 4696
Cys Pro Phe Phe Pro Phe Gly Leu Pro His Ser Gly Ile Ala Glu Gly
1 5 10 15
Arg Gly Val Lys Ile Ala Arg Ala Leu Val Gly Thr Phe Met Ser Ala
20 25 30
Leu Glu Met Pro Gly Ile Ser Leu Thr Leu Leu Leu Val Asp Glu Pro
35 40 45
Leu Leu Lys Leu Ile Asp Ala Glu Thr Thr Ala Ala Ala Trp Pro Asn
50 55 60
Val Ala Ala Val Ser Ile Thr Gly Arg Lys Arg Ser Arg Val Ala Pro
65 70 75 80
Ala Glu Pro Gln Glu Ala Pro Asp Ser Thr Ala Ala Xaa Glu Ala Gln
85 90 95
Pro Arg Ser Xaa Met Ala Leu Val Leu Glu Arg Val Cys Ser Thr Leu
100 105 110
Leu Gly Leu Glu Glu His Leu Asn Ala Leu Asp Arg Ala Ala Gly Asp
115 120 125
Gly Asp Cys Gly Thr Thr His Ser Arg Ala Ala Arg Ala Ile Gln Glu
130 135 140
Trp Leu Lys Glu Gly Pro Pro Pro Ala Ser Pro Ala Gln Leu Leu Ser

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145                 150                 155                 160
Lys Leu Ser Val Leu Leu Leu Glu Lys Met Gly Gly Ser Ser Gly Ala
                165                 170                 175
Leu Tyr Gly Leu Phe Leu Thr Ala Ala Ala Gln Pro Leu Lys Ala Lys
            180                 185                 190
Thr Ser Leu Pro Ala Trp Ser Ala Ala Met Asp Ala Gly Leu Glu Ala
        195                 200                 205
Met Gln Lys Tyr Gly Lys Ala Ala Pro Gly Asp Arg Thr Met Leu Asp
    210                 215                 220
Ser Leu Trp Ala Ala Glu Gln Glu Leu Gln Ala Trp Lys Ser Pro Gly
225                 230                 235                 240
Ala Asp Leu Leu Gln Val Leu Thr Lys Ala Val Lys Ser Ala Glu Ala
                245                 250                 255
Ala Ala Glu Ala Thr Lys Asn Met Glu Ala Gly Ala Gly Arg Ala Ser
            260                 265                 270
Tyr Ile Ser Ser Ala Arg Leu Glu Gln Pro Asp Pro Gly Ala Val Ala
        275                 280                 285
Ala Ala Ala Ile Leu Arg Ala Ile Leu Glu Val Leu Gln Ser
    290                 295                 300
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<210> 4697
<211> 1047
<212> DNA
<213> Homo sapiens

<400> 4697
gctgaatatt gaaattgcct caggtacctc atttctgatt tgtccattat aattttgtat
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tggaaagtga ttggtgacaa atttttttata atgcatcatt gtgcgtccct gtatgcatac
120
taccttgtac tgaaaaatgg agtgctggca tacattggga attttcgcct gcttgcagag
180
catttccagc ccgtttgntg aatcagcgac caaaggctgt agtcactgga aacatggact
240
tgttttcatc tctaactctc cacctctcca cactcagcct gcagagcccg gccaacaatc
300
aagacagatg ggaccgtgtt cagaattcac acaaaagctg aaggatttat ggatgcggat
360
atacctctgg aattggtgtt ccatttgcca gtcaattatc cttcatgtct acctggtatc
420
tcgattaact ctgaacagtt gaccagggcc cagtgtgtga ctgtgaaaga gaagttactt
480
gagcaagcag agagcctttt gtcggagcct atggttcatg agctggttct ctggattcag
540
cagaatctca ggcatatcct cagccaacca gaaactggca gtggcagtga aaagtgtact
600
ttttcaacaa gcacgaccat ggatgatgga ttgtggataa ctcttttgca tttagatcac
660
atgagagcaa agactaaata tgtcaaaatt gtggagaagt gggcttcaga tttaaggctg
720
acaggaagac tgatgttcat gggtaaaata atactgattt tactacaggg agacagaaac
780
aacctcaagg tgccaaaaag ttaaatgttg agtatgaatc tggctatttt ctgctttaaa
840

tggtgtgtct ttaagtgtgt tttataacaa tgggatagat taattattaa gatgtttctg
900
ctttcattat tacaacctta atggatcttc cttttctttt taaagaatgt ctgactgcta
960
attacaagta caaacttgca aagcttgaag aataagattg cattttaaaa atcatgtcac
1020
ttaataaagt gacaggttat ttaaaaa
1047

<210> 4698
<211> 182
<212> PRT
<213> Homo sapiens

<400> 4698
Leu Ser Thr Ser Pro His Ser Ala Cys Arg Ala Arg Pro Thr Ile Lys
1 5 10 15
Thr Asp Gly Thr Val Phe Arg Ile His Thr Lys Ala Glu Gly Phe Met
20 25 30
Asp Ala Asp Ile Pro Leu Glu Leu Val Phe His Leu Pro Val Asn Tyr
35 40 45
Pro Ser Cys Leu Pro Gly Ile Ser Ile Asn Ser Glu Gln Leu Thr Arg
50 55 60
Ala Gln Cys Val Thr Val Lys Glu Lys Leu Leu Glu Gln Ala Glu Ser
65 70 75 80
Leu Leu Ser Glu Pro Met Val His Glu Leu Val Leu Trp Ile Gln Gln
85 90 95
Asn Leu Arg His Ile Leu Ser Gln Pro Glu Thr Gly Ser Gly Ser Glu
100 105 110
Lys Cys Thr Phe Ser Thr Ser Thr Thr Met Asp Asp Gly Leu Trp Ile
115 120 125
Thr Leu Leu His Leu Asp His Met Arg Ala Lys Thr Lys Tyr Val Lys
130 135 140
Ile Val Glu Lys Trp Ala Ser Asp Leu Arg Leu Thr Gly Arg Leu Met
145 150 155 160
Phe Met Gly Lys Ile Ile Leu Ile Leu Leu Gln Gly Asp Arg Asn Asn
165 170 175
Leu Lys Val Pro Lys Ser
180

<210> 4699
<211> 1441
<212> DNA
<213> Homo sapiens

<400> 4699
tctttttttt ttttttttt tacagtgatt tcaaacagtt taatgtaatt ccaagacaaa
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gtgtgattac atttctacac atatacaata tgcatatgtg agtttacaaa ttttaattaa
120
taagtcattt cacctcggag accgaaaaaa tgatcaaaaa gaaactatga gtaacaagct
180
ataacatagt tcaccacaat gggacccccc ccccctttt ctcaccctac agttagtaat
240

attacaatta aaataactat attcttctat atttttttctg ttaaaatcat ctcataaatt
300
tacaatgcta ttattagttt ccaagactaa tataaattca ctccattttt ctacaacgaa
360
aatgattaat ttagaagcac acgacgtcat gatgaaaaac acaagcattt tagtagcaag
420
gacttgatca gttaagaatt agttttcttg taaaacattc taaagccaag taaaatatcc
480
attcttataa catacctata atatgagact aaggaatagg ttacatatag gtctacaaca
540
cattggtttg tctttaaaaa aacaaaagta gacatttata aataaaaaag agggacaatt
600
cacataggaa aaagaggtac acgagaaaat actgttgcac gcaataattt tcacacagat
660
taacatggat taacactttt tattacagaa accgtacggt gaaggaacac aacagaccag
720
ggctttcata gggttattga gattgagctg agatgacctg ggagagaaag atctaggtga
780
gatgaccctg gggagggagc cacgttcctt ggacctggtg acttagtgtc gccgggtctc
840
ctcttccctg ttctcatttt ggggagtgag tctttctatc cagtgtcctg aattcatgag
900
cagttgaaag gtaaacattt ctgcagatcc attctctttc tatcctaatg gataccattt
960
ttggaaacgt gacagagtat cagaggctgc agctcagtac acgtggtcaa agcaaaacgg
1020
gatggaaact tccagtcact ctgatttgtt gcccccgtca cccactgatg cgcttgaagc
1080
tgggacccag tgagacagca gcagcaccct acagggcctg ctggctctgc cgtggtgagg
1140
tggatgacaa gggcacgcgc cacgcctcag ccccatgtgt gcggagtggc ctgggacaca
1200
gcccatgcac gtccaagaca ccagtcttga ctccgacctc taaagagctc cttctcctca
1260
tctgtaaagc tatacttctc ctatccaatt tggtttgata tatatacaca aacatatata
1320
tcaacatcta tctctataca gtgattctac taaattagaa attctgctgc cccaaagtat
1380
gactttcttg tctatttcat ttggttaaaa aaatgcacac acagaggatg aagagatgat
1440
t
1441

<210> 4700
<211> 116
<212> PRT
<213> Homo sapiens

<400> 4700
Met Asp Thr Ile Phe Gly Asn Val Thr Glu Tyr Gln Arg Leu Gln Leu
 1   5   10   15
Ser Thr Arg Gly Gln Ser Lys Thr Gly Trp Lys Leu Pro Val Thr Leu
            20   25   30
Ile Cys Cys Pro Arg His Pro Leu Met Arg Leu Lys Leu Gly Pro Ser

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        35                  40                  45
Glu Thr Ala Ala Ala Pro Tyr Arg Ala Cys Trp Leu Cys Arg Gly Glu
    50                  55                  60
Val Asp Asp Lys Gly Thr Arg His Ala Ser Ala Pro Cys Val Arg Ser
65                  70                  75                  80
Gly Leu Gly His Ser Pro Cys Thr Ser Lys Thr Pro Val Leu Thr Pro
                85                  90                  95
Thr Ser Lys Glu Leu Leu Leu Leu Ile Cys Lys Ala Ile Leu Leu Leu
            100                 105                 110
Ser Asn Leu Val
        115
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<210> 4701
<211> 812
<212> DNA
<213> Homo sapiens

<400> 4701
nctttttttt agtagagaca gggtttcact cttaccagga tgatctcgat ctccggacct
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cgtgatccgc ccacctccgc ctccgaaaat gctgggatta caggcctgag ccacntaccg
120
cctggccatt tttttcttga gacaaggtct tattctctcg ccaagaatgg agtgcagtgg
180
tgcaatgttg gctcactgca gcccaaacct cctgggctta agtgatcctc ctacctcagc
240
ctctcgagta gcnaggacca caggcgcnca ccatcacacc cagctaatgt tttattcttc
300
ngtagagatg gggtctcacc gtgtggccca ggctggcaac tgcatttttt tctcccagct
360
caaggaggga ggagcagccg agcccagcag gtacaacgtg ggtttgctct gtgctgggag
420
agctacaggg ctgtgcagag ccggcaggga caggacctgg ggctccagga ggcccccaca
480
tgctgcctct cagccacctg ccagccctgt tttatgaata tgtttaccgt ggctgtcact
540
ttgtcccggt ctgtcacaaa ggcacggaat ccttccccaa acaaggtgcc agccgtcctg
600
atggactcca agacggtctg acggtgctcg gacgccttca ggcggatctg ctcgcggatg
660
atgtctgcat tctcccgctc ggccttggcg cgcgcccggg cctcggtctc cactcgcagc
720
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780
tgcttctgca agaactcctc ctgcttccgt aa
812

<210> 4702
<211> 69
<212> PRT
<213> Homo sapiens

<400> 4702
Arg Gln Gly Phe Thr Leu Thr Arg Met Ile Ser Ile Ser Gly Pro Arg

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 1               5                  10                  15
Asp Pro Pro Thr Ser Ala Ser Glu Asn Ala Gly Ile Thr Gly Leu Ser
            20                  25                  30
His Xaa Pro Pro Gly His Phe Phe Leu Glu Thr Arg Ser Tyr Ser Leu
        35                  40                  45
Ala Lys Asn Gly Val Gln Trp Cys Asn Val Gly Ser Leu Gln Pro Lys
    50                  55                  60
Pro Pro Gly Leu Lys
65
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<210> 4703
<211> 513
<212> DNA
<213> Homo sapiens

<400> 4703
nnctgtttcc ttctttgatt gacaacttgt gttaaccctc gcacatctct gggccaattt
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ttgcttgtaa gtctttccgg agacccctgg aatttaaatc attagcaccg cgaccttccc
120
cgaagagtct tcgaagggtt gccgcttttc ggtggcgcag ttctcgcgag aaggaaaatg
180
gcagctcccg agcagccgct tgcgatatca aggggatgca cgagctcctc ctcgctttcc
240
ccgcctcggg ctgaccgaac ccttctggtc aggcacctgc cggctgagct tactgctgag
300
gagaaagagg acttgctgaa gtacttcggg gctcagtctg tgcgggtcct gtcagataag
360
gggcgactga aacatacagc ttttgccaca ttccctaatg aaaaagcagc tataaaggca
420
ttgacaagac tccatcaact gaaacttta ggtcatactt tagtcgttga atttgcaaaa
480
gagcaagatc gagttcactc cccatgtccc act
513

<210> 4704
<211> 112
<212> PRT
<213> Homo sapiens

<400> 4704
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Met Ala Ala Pro Glu Gln Pro Leu Ala Ile Ser Arg Gly Cys Thr Ser
 1               5                  10                  15
Ser Ser Ser Leu Ser Pro Pro Arg Ala Asp Arg Thr Leu Leu Val Arg
            20                  25                  30
His Leu Pro Ala Glu Leu Thr Ala Glu Glu Lys Glu Asp Leu Leu Lys
        35                  40                  45
Tyr Phe Gly Ala Gln Ser Val Arg Val Leu Ser Asp Lys Gly Arg Leu
    50                  55                  60
Lys His Thr Ala Phe Ala Thr Phe Pro Asn Glu Lys Ala Ala Ile Lys
65                  70                  75                  80
Ala Leu Thr Arg Leu His Gln Leu Lys Leu Leu Gly His Thr Leu Val
                85                  90                  95
Val Glu Phe Ala Lys Glu Gln Asp Arg Val His Ser Pro Cys Pro Thr
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100 105 110

<210> 4705
<211> 569
<212> DNA
<213> Homo sapiens

<400> 4705
ncagacccat actgtgtggg cacggtgctg gccagcagac cgcacacgct agatggccga
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aacattgacc cctagccatg cccaccccgg gggatgcagc cgtagagaac acggccgaag
120
gaaggatgga aaggacccag gagcgataac agtaaatcaa ataagatatt tgtcggtgga
180
attcctcaca attgtggtga gacagagctc agggaatact tcaagaagtt cggagtggtc
240
acggaggtag tcatgatcta tgacgccgag aagcagaggc cccgaggtaa gggcagatct
300
agtttgacct cggccttctc cctgctcctc cctcagatgg caaactatct cacccgccag
360
gcacacacag gtggcggctg tagcaaacag cctcaggaag ggacgatttg gagacaaatg
420
actaaaacgt gggctcctca tgtgcacccc attcagcctg tctgtgcttc ccgaggtcag
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540
ggcctggctt ctgtttttca ctgtccgga
569

<210> 4706
<211> 154
<212> PRT
<213> Homo sapiens

<400> 4706
Arg Thr Arg Pro Lys Glu Gly Trp Lys Gly Pro Arg Ser Asp Asn Ser
1 5 10 15
Lys Ser Asn Lys Ile Phe Val Gly Gly Ile Pro His Asn Cys Gly Glu
20 25 30
Thr Glu Leu Arg Glu Tyr Phe Lys Lys Phe Gly Val Val Thr Glu Val
35 40 45
Val Met Ile Tyr Asp Ala Glu Lys Gln Arg Pro Arg Gly Lys Gly Arg
50 55 60
Ser Ser Leu Thr Ser Ala Phe Ser Leu Leu Leu Pro Gln Met Ala Asn
65 70 75 80
Tyr Leu Thr Arg Gln Ala His Thr Gly Gly Gly Cys Ser Lys Gln Pro
85 90 95
Gln Glu Gly Thr Ile Trp Arg Gln Met Thr Lys Thr Trp Ala Pro His
100 105 110
Val His Pro Ile Gln Pro Val Cys Ala Ser Arg Gly Gln Thr Ser His
115 120 125
Ile Val Phe Trp Leu Val Leu Leu Lys Phe Leu Arg Leu Val Met Ser
130 135 140
Leu Gly Leu Ala Ser Val Phe His Cys Pro

145 150

<210> 4707
<211> 748
<212> DNA
<213> Homo sapiens

<400> 4707
ngtcctcttg tccttgagcg tcaaccttct ttccctgaag tggctggggt tcctgtttcc
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ttctttgatt gacaacttgt gttaaccctc gcacatctct gggccaattt ttgcttgtaa
120
gtctttccgg agacccctgg aatttaaatc attagcaccg cgcccttccc cgaagagtct
180
tcgaagggtt gccgcttttc ggtggcgcag ttctcgcgag aaggtgactt tctttctcgg
240
tatttcctgg tttccagaat ccttagcgcg aggcggaaaa aatatttctc ccagcttgtg
300
ttgatgccgc gattttgact gagacttctt cccacgattt ctgtttttgc ttctccaagg
360
aaaatggcag ctcccgagca gccgcttgcg atatcaaggg gatgcacgag ctcctcctcg
420
ctttccccgc ctcggggcga ccgaaccctt ctggtcaggc acctgccggc tgagcttact
480
gctgaggaga aagaggactt gctgaagtac ttcggggctc agtctgtgcg ggtcctgtca
540
gataaggggc gactgaaaca tacagctttt gccacattcc ctaatgaaaa agcagctata
600
aaggcattga caagactcca tcaactgaaa cttttaggtc atactttagt cgttgaattt
660
gcaaaagagc aagatcgagt tcactcccca tgtcccactt caggctctga aaaaaaaaaa
720
atgtctgatg accctgtcga agatgata
748

<210> 4708
<211> 128
<212> PRT
<213> Homo sapiens

<400> 4708
Met Ala Ala Pro Glu Gln Pro Leu Ala Ile Ser Arg Gly Cys Thr Ser
1 5 10 15
Ser Ser Ser Leu Ser Pro Pro Arg Gly Asp Arg Thr Leu Leu Val Arg
20 25 30
His Leu Pro Ala Glu Leu Thr Ala Glu Glu Lys Glu Asp Leu Leu Lys
35 40 45
Tyr Phe Gly Ala Gln Ser Val Arg Val Leu Ser Asp Lys Gly Arg Leu
50 55 60
Lys His Thr Ala Phe Ala Thr Phe Pro Asn Glu Lys Ala Ala Ile Lys
65 70 75 80
Ala Leu Thr Arg Leu His Gln Leu Lys Leu Leu Gly His Thr Leu Val
85 90 95
Val Glu Phe Ala Lys Glu Gln Asp Arg Val His Ser Pro Cys Pro Thr

100 105 110
Ser Gly Ser Glu Lys Lys Lys Met Ser Asp Asp Pro Val Glu Asp Asp
115 120 125

<210> 4709
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 4709
cgcagatccg ggccgcggct gtggggaggg cgacggagcg ggtgaccttc cggaggcggg
60
agcgagcgag gaggcccggg agcgccgagc gtcgccgccg ccgccgccat gaacaactcg
120
ggcgccgacg agatcgggaa gctcttcgtg ggcggtcttg actggagcac gacccaagag
180
actctgcgca gctacttttc ccaatatgga gaagtcgtag attgtgttat catgaaagat
240
aaaaccacca accagtctcg aggctttggg tttgtcaaat ttaaagaccc aaactgtgtg
300
gggacggtgc tggccagcag accgcacacg ctagatggcc gaaacatcga ccccaagcca
360
tgcacacccc gggggatgca gccggagaga acacggccga aggaaggatg gcagaaagga
420
cccaggagcg ataacagtaa atcaaataag atatttgtcg gtggaattcc tcacaattgt
480
ggtgagacag agctcaggga atacttcaag aagttcggag tggtcacgga ggtagtcatg
540
atctatgacg ccgagaagca gaggccccga ggttttggat ttattacttt cgaggacgaa
600
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<211> 304
<212> PRT
<213> Homo sapiens

<400> 4710
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Gln Ser Arg Gly Phe Gly Phe Val Lys Phe Lys Asp Pro Asn Cys Val
50 55 60
Gly Thr Val Leu Ala Ser Arg Pro His Thr Leu Asp Gly Arg Asn Ile
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Asp Pro Lys Pro Cys Thr Pro Arg Gly Met Gln Pro Glu Arg Thr Arg
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Pro Lys Glu Gly Trp Gln Lys Gly Pro Arg Ser Asp Asn Ser Lys Ser
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130 135 140
Ile Tyr Asp Ala Glu Lys Gln Arg Pro Arg Gly Phe Gly Phe Ile Thr
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Phe Glu Asp Glu Gln Ser Val Asp Gln Ala Val Asn Met His Phe His
165 170 175
Asp Ile Met Gly Lys Lys Val Glu Val Lys Arg Ala Glu Pro Arg Asp
180 185 190
Ser Lys Ser Gln Ala Pro Gly Gln Pro Gly Ala Ser Gln Trp Gly Ser
195 200 205
Arg Val Val Pro Asn Ala Ala Asn Gly Trp Ala Gly Gln Pro Pro Pro
210 215 220
Thr Trp Gln Gln Gly Tyr Gly Pro Gln Gly Met Trp Val Pro Ala Gly
225 230 235 240
Gln Ala Ile Gly Gly Tyr Gly Pro Pro Pro Ala Gly Arg Gly Ala Pro
245 250 255
Pro Pro Pro Pro Pro Phe Thr Ser Tyr Ile Val Ser Thr Pro Pro Gly
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Gln Phe Ser Phe Gly Tyr Gly Pro Pro Pro Pro Pro Pro Gly Ser Arg
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<210> 4711
<211> 2061
<212> DNA
<213> Homo sapiens

<400> 4711

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<212> PRT
<213> Homo sapiens

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35 40 45
Ala Gln Gln Leu Glu Glu Glu Gly Pro Met Glu Glu Glu Glu Ala Gln
50 55 60
Pro Met Ala Ala Pro Glu Gly Lys Arg Ser Leu Ala Asn Gly Pro Asn
65 70 75 80
Ala Gly Glu Gln Pro Gly Gln Val Ala Gly Ala Asp Phe Glu Ser Glu
85 90 95
Asp Glu Gly Glu Glu Phe Asp Asp Trp Glu Asp Asp Tyr Asp Tyr Pro
100 105 110
Glu Glu Glu Gln Leu Ser Gly Ala Gly Tyr Arg Val Ser Ala Ala Leu
115 120 125
Glu Glu Ala Asp Lys Met Phe Leu Arg Thr Arg Glu Pro Ala Leu Asp
130 135 140
Gly Gly Phe Gln Met His Tyr Glu Lys Thr Pro Phe Asp Gln Leu Ala
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Glu Leu Gly Cys Asp Glu Ile Ile Asp Arg Glu
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<210> 4713
<211> 1324
<212> DNA
<213> Homo sapiens

<400> 4713

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<210> 4714
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<212> PRT
<213> Homo sapiens

<400> 4714
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        35                  40                  45
Ala Ala Ser Arg Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg
    50                  55                  60
Ser Ala Ala Ala Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln
65                  70                  75                  80
Gln Ile Leu Asn Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn
                85                  90                  95
Tyr Glu His Leu Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe
            100                 105                 110
Tyr Leu Gln Ser Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu
        115                 120                 125
Leu Lys Ile Gln Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His
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Thr
145
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<210> 4715
<211> 2051
<212> DNA
<213> Homo sapiens

<400> 4715
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<210> 4716
<211> 239
<212> PRT
<213> Homo sapiens

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Pro Ala Lys Glu Phe Thr Asn His Trp Trp Asn Glu Leu Phe Asn Lys

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Thr Ala Ala Asn Leu Val Val Glu Thr Gly Gln Asp Gly Val Gln Ile
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Arg Ser Leu Ser Lys Glu Thr Thr Arg Tyr Asn His Pro Lys Pro Asn
65                  70                  75                  80
Leu Leu Tyr Gln Lys Phe Val Lys Met Ala Thr Leu Thr Ser Gly Gly
                85                  90                  95
Glu Lys Pro Asn Lys Asp Leu Glu Ser Cys Ser Asp Asp Asp Asn Gln
            100                 105                 110
Gly Ser Lys Ser Pro Lys Ile Leu Thr Asp Glu Met Leu Leu Gln Ala
        115                 120                 125
Cys Glu Gly Arg Thr Ala His Lys Ala Ala Arg Leu Gly Ile Thr Met
    130                 135                 140
Lys Ala Lys Leu Ala Arg Leu Glu Ala Gln Glu Gln Ala Phe Leu Ala
145                 150                 155                 160
Arg Leu Lys Gly Gln Asp Pro Gly Ala Pro Gln Leu Gln Ser Glu Ser
                165                 170                 175
Lys Pro Pro Lys Lys Lys Lys Lys Lys Arg Arg Gln Lys Glu Glu Glu
            180                 185                 190
Glu Ala Thr Ala Ser Glu Arg Asn Asp Ala Asp Glu Lys His Pro Glu
        195                 200                 205
His Ala Glu Gln Asn Ile Arg Lys Ser Lys Lys Lys Lys Arg Arg His
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<210> 4717
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<212> DNA
<213> Homo sapiens

<400> 4717

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<210> 4718
<211> 259
<212> PRT
<213> Homo sapiens

<400> 4718
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35 40 45
Arg Glu Glu Glu Glu Glu Asn Asp Asp Asp Asn Ser Leu Glu Gly Glu
50 55 60
Thr Phe Pro Leu Glu Arg Asp Glu Val Met Pro Pro Pro Leu Gln His
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Pro Gln Thr Asp Arg Leu Thr Cys Pro Lys Gly Leu Pro Trp Ala Pro
85 90 95
Lys Val Arg Glu Lys Asp Ile Glu Met Phe Leu Glu Ser Ser Arg Ser
100 105 110
Lys Phe Ile Gly Tyr Thr Leu Gly Ser Asp Thr Asn Thr Val Val Gly
115 120 125
Leu Pro Arg Pro Ile His Glu Ser Ile Lys Thr Leu Lys Gln His Lys
130 135 140
Tyr Thr Ser Ile Ala Glu Val Gln Ala Gln Met Lys Glu Glu Tyr Leu
145 150 155 160
Arg Ser Pro Leu Ser Gly Gly Glu Glu Glu Val Glu Gln Val Pro Ala
165 170 175
Glu Thr Leu Tyr Gln Gly Leu Leu Pro Ser Leu Pro Gln Tyr Met Ile
180 185 190
Ala Leu Leu Lys Ile Leu Leu Ala Ala Ala Pro Thr Ser Lys Ala Lys
195 200 205
Thr Asp Ser Ile Asn Ile Leu Ala Asp Val Leu Pro Glu Glu Met Pro
210 215 220
Thr Thr Val Leu Gln Ser Met Lys Leu Gly Val Asp Val Asn Arg His
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<210> 4719
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<212> DNA
<213> Homo sapiens

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420
acaagggcct gtgatggtgg ctatacttcc agttgcttca acctcagtgc catgttcctg
480
cagggtgccc caggctttcc caaggacatg gacctggcat gtaaatactc catgaaagcc
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589

<210> 4720
<211> 196
<212> PRT
<213> Homo sapiens

<400> 4720
Arg Thr Met Ala Gly Met Val Asp Phe Gln Asp Glu Glu Gln Val Lys
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Ser Phe Leu Glu Asn Met Glu Val Glu Cys Asn Tyr His Cys Tyr His
20 25 30
Glu Lys Asp Pro Asp Gly Cys Tyr Arg Leu Val Asp Tyr Leu Glu Gly
35 40 45
Ile Arg Lys Asn Phe Asp Glu Ala Ala Lys Val Leu Lys Phe Asn Cys
50 55 60
Glu Glu Asn Gln His Ser Asp Ser Cys Tyr Lys Leu Gly Ala Tyr Tyr
65 70 75 80
Val Thr Gly Lys Gly Gly Leu Thr Gln Asp Leu Lys Ala Ala Ala Arg
85 90 95
Cys Phe Leu Met Ala Cys Glu Lys Pro Gly Lys Lys Ser Ile Ala Ala
100 105 110
Cys His Asn Val Gly Leu Leu Ala His Asp Gly Gln Val Asn Glu Asp
115 120 125
Gly Gln Pro Asp Leu Gly Lys Ala Arg Asp Tyr Tyr Thr Arg Ala Cys

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    130                 135                 140
Asp Gly Gly Tyr Thr Ser Ser Cys Phe Asn Leu Ser Ala Met Phe Leu
145                 150                 155                 160
Gln Gly Ala Pro Gly Phe Pro Lys Asp Met Asp Leu Ala Cys Lys Tyr
                165                 170                 175
Ser Met Lys Ala Cys Asp Leu Gly His Ile Trp Ala Cys Ala Asn Ala
            180                 185                 190
Ser Arg Met Tyr
        195
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<210> 4721
<211> 1385
<212> DNA
<213> Homo sapiens

<400> 4721
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120
cggtgtaggc cgctgcaggc caccatgaac cggcttccgg atgactacga cccctacgcg
180
gttgaagagc ctagcgacga ggagccggct ttgagcagct ctgaggatga agtggatgtg
240
cttttacatg gaactcctga ccaaaaacga aaactcatca gagaatgtct taccggagaa
300
agtgaatcat ctagtgaaga tgaatttgaa aaggagatgg aagctgaatt aaattctacc
360
atgaaaacaa tggaggacaa gttatcctct ctgggaactg gatcttcctc aggaaatgga
420
aaagttgcaa cagctccgac aaggtactac gatgatatat attttgattc tgattccgag
480
gatgaagaca gagcagtaca ggtgaccaag aaaaaaaaga agaaacaaca caagattcca
540
acaaatgacg aattactgta tgatcctgaa aaagataaca gagatcaggc ctgggttgat
600
gcacagagaa ggggttacca tggtttggga ccacagagat cacgtcaaca acagcctgtt
660
ccaaatagtg atgctgtctt gaattgtcct gcctgcatga ccacactttg ccttgattgc
720
caaaggcatg aatcatacaa aactcaatat agagcaatgt ttgtaatgaa ttgttctatt
780
aacaaagagg aggttctaag atataaagcc tcagagaaca ggaagaaaag gcgggtccat
840
aagaagatga ggtctaaccg ggaagatgct gctgagaagg cagagacaga tgtggaagaa
900
atctatcacc cagtcatgtg cactgaatgt tccactgaag tggcagtcta cgacaaggat
960
gaagtctttc atttttcaa tgttttagca agccattcct aaacagccca actggcattt
1020
aattacccaa tactgtatat aaggcaaata tggacagtta ctttcctctt gcctgttcat
1080
atccttcagt gacattgagg aagcagtgtt tctcttttta aaggagaata gttgtcaacc
1140

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1200
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1260
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1320
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1380
agctt
1385

<210> 4722
<211> 285
<212> PRT
<213> Homo sapiens

<400> 4722
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Ser Asp Glu Glu Pro Ala Leu Ser Ser Ser Glu Asp Glu Val Asp Val
            20   25   30
Leu Leu His Gly Thr Pro Asp Gln Lys Arg Lys Leu Ile Arg Glu Cys
        35   40   45
Leu Thr Gly Glu Ser Glu Ser Ser Ser Glu Asp Glu Phe Glu Lys Glu
    50   55   60
Met Glu Ala Glu Leu Asn Ser Thr Met Lys Thr Met Glu Asp Lys Leu
65   70   75   80
Ser Ser Leu Gly Thr Gly Ser Ser Ser Gly Asn Gly Lys Val Ala Thr
                85   90   95
Ala Pro Thr Arg Tyr Tyr Asp Asp Ile Tyr Phe Asp Ser Asp Ser Glu
            100   105   110
Asp Glu Asp Arg Ala Val Gln Val Thr Lys Lys Lys Lys Lys Lys Gln
        115   120   125
His Lys Ile Pro Thr Asn Asp Glu Leu Leu Tyr Asp Pro Glu Lys Asp
    130   135   140
Asn Arg Asp Gln Ala Trp Val Asp Ala Gln Arg Arg Gly Tyr His Gly
145   150   155   160
Leu Gly Pro Gln Arg Ser Arg Gln Gln Gln Pro Val Pro Asn Ser Asp
                165   170   175
Ala Val Leu Asn Cys Pro Ala Cys Met Thr Thr Leu Cys Leu Asp Cys
            180   185   190
Gln Arg His Glu Ser Tyr Lys Thr Gln Tyr Arg Ala Met Phe Val Met
        195   200   205
Asn Cys Ser Ile Asn Lys Glu Glu Val Leu Arg Tyr Lys Ala Ser Glu
    210   215   220
Asn Arg Lys Lys Arg Arg Val His Lys Lys Met Arg Ser Asn Arg Glu
225   230   235   240
Asp Ala Ala Glu Lys Ala Glu Thr Asp Val Glu Glu Ile Tyr His Pro
                245   250   255
Val Met Cys Thr Glu Cys Ser Thr Glu Val Ala Val Tyr Asp Lys Asp
            260   265   270
Glu Val Phe His Phe Phe Asn Val Leu Ala Ser His Ser
        275   280   285

<210> 4723
<211> 1213
<212> DNA
<213> Homo sapiens

<400> 4723
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120
ggctggggac tgcacctccc tcctactcat ggtggacagc agtggggact agggaggggc
180
aggagaggtg gctgacgcca ggcagcagca gcagtgatgg ggccacgacg ccacagagca
240
agctccatcc tcccccagac cctggtggga gtccctgtgg gttggggtgg ggagtgggga
300
gaacccaccc caggccctcc ctctcccttc cccagacagt ctcctttcgg gctcaaccca
360
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420
aggggcaggn gtggcagcac aaatgaaggc agaggtgaga ggcgtgggca aggccactcc
480
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540
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600
aagccgtgcc cagtcgctgt gctctgagtc gtattccagc tcggcgccca cacacttgac
660
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720
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780
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960
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1020
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1080
ccggactctg ggcttgttgc ccttgttggc tgcagccatg gacgccctcc ctgccacgca
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1200
ggagccttgc tgt
1213

<210> 4724
<211> 54
<212> PRT
<213> Homo sapiens

<400> 4724
Met Gly Pro Arg Arg His Arg Ala Ser Ser Ile Leu Pro Gln Thr Leu
1 5 10 15
Val Gly Val Pro Val Gly Trp Gly Gly Glu Trp Gly Glu Pro Thr Pro
20 25 30
Gly Pro Pro Ser Pro Phe Pro Arg Gln Ser Pro Phe Gly Leu Asn Pro
35 40 45
Phe Leu Pro Ala Gly Asp
50

<210> 4725
<211> 366
<212> DNA
<213> Homo sapiens

<400> 4725
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atgcttgcaa tagacacggc ttcagacatc ctggcacatg tccacgtgta ctctcgcctg
120
tgcgcatgtg cacgtgtgta tatgcatatg tgcacaggtg cctgtgcctg tgtgaacaca
180
tgttctcacg tgtgtacctg cntctcttgc ccatgcntgt acgtgcacac gtgcctctgt
240
atgcatgcat gtatagctgt gtgcccatac cctcacgtga gaatacatat gcgcttgtgc
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cttcacctct gcatgcatgc tagtgtgctc ctgcgtgcat gggtgtgcat ctgtgcctgc
360
acgcgt
366

<210> 4726
<211> 122
<212> PRT
<213> Homo sapiens

<400> 4726
Xaa Phe Leu Glu Gly Glu Leu Gly Arg Ser Arg Arg Thr Pro Ala Gly
1 5 10 15
Gly Arg Gly Ala Met Leu Ala Ile Asp Thr Ala Ser Asp Ile Leu Ala
20 25 30
His Val His Val Tyr Ser Arg Leu Cys Ala Cys Ala Arg Val Tyr Met
35 40 45
His Met Cys Thr Gly Ala Cys Ala Cys Val Asn Thr Cys Ser His Val
50 55 60
Cys Thr Cys Xaa Ser Cys Pro Cys Xaa Tyr Val His Thr Cys Leu Cys
65 70 75 80
Met His Ala Cys Ile Ala Val Cys Pro Tyr Pro His Val Arg Ile His
85 90 95
Met Arg Leu Cys Leu His Leu Cys Met His Ala Ser Val Leu Leu Arg
100 105 110
Ala Trp Val Cys Ile Cys Ala Cys Thr Arg
115 120

<210> 4727
<211> 2031
<212> DNA
<213> Homo sapiens

<400> 4727
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cagctcactg caacctctgt ctcctgggtt cacatgattc tcctgcctca gcctcccaag
120
tagctgggat tacagggacc caccaccaca cccggctaat ttttttgta tttttactag
180
agacggggtt tcactatgtt ggccagactg gtctcgaact cctaacctca tgatccgctc
240
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300
acttacttct tcacttcctc gatggcctcc ggcaaccggc ggcaggtggt aagtagcagg
360
gagactgcga gttcggcggt ggtatctgtc aggacatctg gggtgtagcc aactcggatc
420
ccacgcttct tgatttcatc caaagccaag tggtcgatgc ccacagacat ggtgctgatg
480
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540
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660
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720
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780
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960
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1200
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1440

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1620
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1740
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1860
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1920
acccttctga atttccttac taataaaggc tatagggtct ccccttttaaa gaacagcttt
1980
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2031

<210> 4728
<211> 328
<212> PRT
<213> Homo sapiens

<400> 4728
Met Arg Pro Val Arg Leu Met Lys Val Phe Val Thr Arg Arg Ile Pro
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Ala Glu Gly Arg Val Ala Leu Ala Arg Ala Ala Asp Cys Glu Val Glu
20 25 30
Gln Trp Asp Ser Asp Glu Pro Ile Pro Ala Lys Glu Leu Glu Arg Gly
35 40 45
Val Ala Gly Ala His Gly Leu Leu Cys Leu Leu Ser Asp His Val Asp
50 55 60
Lys Arg Ile Leu Asp Ala Ala Gly Ala Asn Leu Lys Val Ile Ser Thr
65 70 75 80
Met Ser Val Gly Ile Asp His Leu Ala Leu Asp Glu Ile Lys Lys Arg
85 90 95
Gly Ile Arg Val Gly Tyr Thr Pro Asp Val Leu Thr Asp Thr Thr Ala
100 105 110
Glu Leu Ala Val Ser Leu Leu Leu Thr Thr Cys Arg Arg Leu Pro Glu
115 120 125
Ala Ile Glu Glu Val Lys Asn Gly Gly Trp Thr Ser Trp Lys Pro Leu
130 135 140
Trp Leu Cys Gly Tyr Gly Leu Thr Gln Ser Thr Val Gly Ile Ile Gly
145 150 155 160
Leu Gly Arg Ile Gly Gln Ala Ile Ala Arg Arg Leu Lys Pro Phe Gly
165 170 175
Val Gln Arg Phe Leu Tyr Thr Gly Arg Gln Pro Arg Pro Glu Glu Ala
180 185 190
Ala Glu Phe Gln Ala Glu Phe Val Ser Thr Pro Glu Leu Ala Ala Gln
195 200 205
Ser Asp Phe Ile Val Val Ala Cys Ser Leu Thr Pro Ala Thr Glu Gly

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    210                 215                 220
Leu Cys Asn Lys Asp Phe Phe Gln Lys Met Lys Glu Thr Ala Val Phe
225                 230                 235                 240
Ile Asn Ile Ser Arg Gly Asp Val Val Asn Gln Asp Asp Leu Tyr Gln
                245                 250                 255
Ala Leu Ala Ser Gly Lys Ile Ala Ala Ala Gly Leu Asp Val Thr Ser
            260                 265                 270
Pro Glu Pro Leu Pro Thr Asn His Pro Leu Leu Thr Leu Lys Asn Cys
        275                 280                 285
Val Ile Leu Pro His Ile Gly Ser Ala Thr His Arg Thr Arg Asn Thr
    290                 295                 300
Met Ser Leu Leu Ala Ala Asn Asn Leu Leu Ala Gly Leu Arg Gly Glu
305                 310                 315                 320
Pro Met Pro Ser Glu Leu Lys Leu
                325
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<210> 4729
<211> 753
<212> DNA
<213> Homo sapiens

<400> 4729
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120
cctgttgttg gatttgggga aatttttttgt ttgttttttta tgatttgtat ttgactgaga
180
gaaacccact gaagacgtct gcgtgagaat agagaccacc gaggccgact cgcgggccgc
240
tgcacccacc gccaaggaca aaaggagccc agcgctacta gctgcacccg attcctccca
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360
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420
aaaagccatt atgcagatgt agatcctgaa aaccagaact ttttacttga atcgaatttg
480
gggaagaaga agtatgaaac agaatttcat ccaggtacta cttcctttgg aatgtcagta
540
tttaatctga gcaatgcgat tgtgggcagt ggaatccttg ggctttctta tgccatggct
600
aatactggaa ttgctctttt tataattctc ttgacatttg tgtcaatatt ttccctgtat
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720
ggatataagg catctggatt agttggaaag ctt
753

<210> 4730
<211> 148
<212> PRT
<213> Homo sapiens

<400> 4730
Met Lys Lys Ala Glu Met Gly Arg Phe Ser Ile Ser Pro Asp Glu Asp
1 5 10 15
Ser Ser Ser Tyr Ser Ser Asn Ser Asp Phe Asn Tyr Ser Tyr Pro Thr
20 25 30
Lys Gln Ala Ala Leu Lys Ser His Tyr Ala Asp Val Asp Pro Glu Asn
35 40 45
Gln Asn Phe Leu Leu Glu Ser Asn Leu Gly Lys Lys Lys Tyr Glu Thr
50 55 60
Glu Phe His Pro Gly Thr Thr Ser Phe Gly Met Ser Val Phe Asn Leu
65 70 75 80
Ser Asn Ala Ile Val Gly Ser Gly Ile Leu Gly Leu Ser Tyr Ala Met
85 90 95
Ala Asn Thr Gly Ile Ala Leu Phe Ile Ile Leu Leu Thr Phe Val Ser
100 105 110
Ile Phe Ser Leu Tyr Ser Val His Leu Leu Leu Lys Thr Ala Asn Glu
115 120 125
Gly Gly Ser Leu Leu Tyr Glu Gln Leu Gly Tyr Lys Ala Ser Gly Leu
130 135 140
Val Gly Lys Leu
145

<210> 4731
<211> 2417
<212> DNA
<213> Homo sapiens

<400> 4731
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120
ttggaagaca gctgaggaaa aaggcgccaa taagacaaac tcacagatgg gatttatctc
180
cctcttgctt ttttttttttt tttttgcccc tggtaaaagt cagaacctgg gatgaccaga
240
aagtaacagg acagatttct cccagcaaat cagtctccac aaccaaatga atattgttct
300
ccaaggagtc aagctataga ctcacaatga caacgtggcc atggctcaaa acactctctg
360
aaattacaaa attgctttct gagccaattt aaaagtcaca tgattgaatc caagctattt
420
tactttaaat ggtccttttg ctttgcacct gagacctcgc ttggccacag acgtcattcg
480
ctggactccc tgggcactaa atgagtgtct agcatcctta aggctgctca acacacagcc
540
ccagactctg aatatgattc caagaaatat tctgaaaaaa gtcacatcgc tggaataaac
600
agtttcccaa gataactgct ttgaaaacca gtcccgttag tttctaaaag cccacctacg
660
gcaccttcct tccatcagag tctgctgccc gggtgggctg ggaaggaggg agatacaaag
720
aagaaagtag gcatgatcac tgggtcggtt cccaagccac cctcaccctc caagaaggca
780

tgaatggaac aaccccgaga acagagcacg tgtgaagaac caacacgaca ggcacgggat
840
ggcagcactg gtggaaggga ggcaaggagg ccgccagtgc caaggaggag agggggcaca
900
agcgcaggca gggaaggtgg caccaaaacc tagtaagaac aaagcaaaac caccgtggtt
960
tccacactgc tctctccctt tattcctctc tttcctgccc tgtataccaa cggcataaga
1020
agcctgcaca aagagaaaaa tccgtatatc cagttatatc tacacggtcc aaactggggg
1080
cgggggggaat tcaaacagct ttctaaagac gagacggcag tgaaaactct gagggagagg
1140
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1320
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1380
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1440
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1560
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1620
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1920
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1980
gaaacaccaa gggccaaaac gccagcagcc actaacccaa acccacgtct tcctcctgtc
2040
atttcctcat cctgacgctc acgggtgcaa ggactctcct tggccttcct catcctgctt
2100
tcaggcagca aacagaaatg gggaaatccc tggtggggcc aggagacaga aaggaacctc
2160
cagaacctcc ctgggtctct cccggccacc caaataaaag aaaactttaa tcagtaaagg
2220
cttctgaata catcgtaaaa gaaaacaaag catttctgag gcgtcctttc aataaccgga
2280
ggaaggcggc gtcaggaggg tgcttcctcg ggtcagagca gagagtttcc agacgctcaa
2340
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2400

cattccaaaa agtgaat
2417

<210> 4732
<211> 129
<212> PRT
<213> Homo sapiens

<400> 4732
Met Ser Ile Ser Arg Ala Val Leu Gly Glu Lys Glu Gly Gly Leu Gly
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Ser Val Ala Pro Cys Gln Pro Ala Leu Arg Glu Asp Arg Val Ser His
20 25 30
Ala Arg Met Ala Gly His Val Ser Val Leu Val Ser His Phe Pro Pro
35 40 45
Ser Val Thr Tyr Leu Gly Ile Pro Gln Gly Leu Leu Glu Cys Asp Cys
50 55 60
Pro Leu Pro Ser Cys Leu Gly Tyr Lys Ser Trp Pro Tyr Val Pro Ala
65 70 75 80
Val Arg Gly Ser Gly Asn Pro Thr Gln Pro Pro Val Leu Gly Trp Ser
85 90 95
Val Ser Ile His Pro Leu Val Val Ile Glu Ala Ala Leu Pro Val Leu
100 105 110
Gly Glu Asp Ile Trp Ala Thr Arg Ala Pro Leu Ala Pro Ser Arg Arg
115 120 125
Lys

<210> 4733
<211> 543
<212> DNA
<213> Homo sapiens

<400> 4733
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agcggccgcc gtgaccctct cggggatccc acgatgttct tctacctgag caagaaaatt
120
tccattccca ataacgtgaa gctgcagtgt gtatcctgga acaaggaaca agggttcata
180
gcatgcggtg gtgaagatgg attactgaaa gttttgaaat tagagacgca gacagatgat
240
gcaaaattga ggggccttgc agcccccagt aacctttcta tgaatcagac tcttgaaggt
300
catagtggtt ctgttcaagt tgtaacatgg aatgagcagt atcagaagtt gactaccagt
360
gatgaaaacg ggcttatcat tgtgtggatg ttatataaag gctcttggat tgaggagatg
420
atcaacaatc gaaataaatc agttgttcgc agtatgagct ggaatgctga cggacagaag
480
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540
tgg
543

<210> 4734
<211> 181
<212> PRT
<213> Homo sapiens

<400> 4734
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1 5 10 15
Val Glu Gly Leu Ser Gly Arg Arg Asp Pro Leu Gly Asp Pro Thr Met
20 25 30
Phe Phe Tyr Leu Ser Lys Lys Ile Ser Ile Pro Asn Asn Val Lys Leu
35 40 45
Gln Cys Val Ser Trp Asn Lys Glu Gln Gly Phe Ile Ala Cys Gly Gly
50 55 60
Glu Asp Gly Leu Leu Lys Val Leu Lys Leu Glu Thr Gln Thr Asp Asp
65 70 75 80
Ala Lys Leu Arg Gly Leu Ala Ala Pro Ser Asn Leu Ser Met Asn Gln
85 90 95
Thr Leu Glu Gly His Ser Gly Ser Val Gln Val Val Thr Trp Asn Glu
100 105 110
Gln Tyr Gln Lys Leu Thr Thr Ser Asp Glu Asn Gly Leu Ile Ile Val
115 120 125
Trp Met Leu Tyr Lys Gly Ser Trp Ile Glu Glu Met Ile Asn Asn Arg
130 135 140
Asn Lys Ser Val Val Arg Ser Met Ser Trp Asn Ala Asp Gly Gln Lys
145 150 155 160
Ile Cys Ile Val Tyr Glu Asp Gly Ala Val Ile Val Gly Ser Val Asp
165 170 175
Gly Asn Arg Ile Trp
180

<210> 4735
<211> 300
<212> DNA
<213> Homo sapiens

<400> 4735
ntggtcttct cagtacagca tggtggctgg ggcaggccga gagaatggca tggagacgcc
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gatgcacgag aacccggagt gggagaaggc ccgtcaggcc ctggccagca tcagcaagtc
120
aggagctgcc ggcggctctg ccaagtccag cagcaatggg cctgtggcca gtgcacagta
180
cgtgtcccag gcaaaagcct cagctttgca gcagcagcag tactaccagt ggtaccagca
240
ggacaactat gcctacccct acagctacta ctatcccatg cccccaggcc ccggcatgga
300

<210> 4736
<211> 93
<212> PRT
<213> Homo sapiens

<400> 4736
Met Val Ala Gly Ala Gly Arg Glu Asn Gly Met Glu Thr Pro Met His
1 5 10 15
Glu Asn Pro Glu Trp Glu Lys Ala Arg Gln Ala Leu Ala Ser Ile Ser
20 25 30
Lys Ser Gly Ala Ala Gly Gly Ser Ala Lys Ser Ser Ser Asn Gly Pro
35 40 45
Val Ala Ser Ala Gln Tyr Val Ser Gln Ala Lys Ala Ser Ala Leu Gln
50 55 60
Gln Gln Gln Tyr Tyr Gln Trp Tyr Gln Gln Asp Asn Tyr Ala Tyr Pro
65 70 75 80
Tyr Ser Tyr Tyr Tyr Pro Met Pro Pro Gly Pro Gly Met
85 90

<210> 4737
<211> 2602
<212> DNA
<213> Homo sapiens

<400> 4737
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120
caagctcggc ccctttcaac tctgccaaga atggctccca cctggctctc agacattccc
180
ctggtccaac ccccaggcca tcaagatgtc tcagagaggc ggctagacac ccagagacct
240
caagtgacca tgtgggaacg ggatgtttcc agtgacaggc aggagccagg gcggagaggc
300
aggtcctggg ggctggaggg gtcacaggcc ctgagccagc aggctgaggt gatcgttcgg
360
cagctgcaag agctgcggcg gctggaggag gaggtccggc tcctgcggga gacctcgctg
420
cagcagaaga tgaggctaga ggcccaggcc atggagctag aggctctggc acgggcggag
480
aaggccggcc gagctgaggc tgagggcctg cgtgctgctt tggctggggc tgaggttgtc
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cggaagaact tggaagaggg gaggcagcgg gagctggaag aggttcagag gctgcaccaa
600
gagcagctgt cctctttgac acaggctcac gaggaggctc tttccagttt gaccagcaag
660
gctgagggct tggagaagtc tctgagtagt ctggaaacca gaagagcagg ggaagccaag
720
gagctggccg aggctcagag ggaggccgag ctgcttcgga agcagctgag caagacccag
780
gaagacttgg aggctcaggt gaccctggtt gagaatctaa gaaaatatgt tggggaacaa
840
gtcccttctg aggtccacag ccagacatgg gaactggagc gacagaagct tctggaaacc
900
atgcagctct tgcaggagga ccgggacagc ctgcatgcca ccgcggagct gctgcaggtg
960
cgggtgcaga gcctcacaca catcctcgcc ctgcaggagg aggagctgac caggaaggtt
1020

caaccttcag attccctgga gcctgagttt accaggaagt gccagtccct gctgaaccgc
1080
tggcgggaga aggtgtttgc cctcatggtg cagctaaagg cccaggagct ggaacacagt
1140
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1260
gagcgtatgg gtgccaaggg cctgcagttg gagctgagcc gtgctcagga ggccaggcgt
1320
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1380
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1440
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1560
ccggtcacag atgtgagcct tgagttgcag cagttgcggg aagaacggaa ccgcctggat
1620
gcagaactgc agctgagtgc ccgcctcatc cagcaggagg tgggccgggc tcgggagcaa
1680
ggggaggcag agcggcagca gctgagcaag gtggcccagc agctggagca ggagctgcag
1740
cagacccagg agtccctggc tagcttgggg ctgcagctgg aggtagcacg ccagggccag
1800
caggagagca cagaggaggc tgccagtctg cggcaggagc tgacccagca gcaggaactc
1860
tacgggcaag ccctgcaaga aaaggtggct gaagtggaaa ctcggctgcg ggagcaactc
1920
tcagacacag agaggaggct gaacgaggct cggagggagc atgccaaggc cgtggtctcc
1980
ttgcgccaga ttcagcgcag agccgcccag gaaaaggagc ggagccagga actcaggcgt
2040
ctgcaggagg aggcccggaa ggaggagggg cagcgactgg cccggcgctt gcaggagcta
2100
gagagggata agaacctcat gctggccacc ttgcagcagg aaggtctcct ctcccgttac
2160
aagcagcagc gactgttgac agttcttcct tccctactgg ataagaagaa atctgtggtg
2220
tccagcccca ggcctccaga gtgttcagca tctgcacctg tagcagcagc agtgcccacc
2280
agggagtcca taaaagggtc cctctctgtc ctgctcgatg acctgcagga cctgagtgaa
2340
gccatttcca aagaggaagc tgtttgtcaa ggagacaacc ttgacagatg ctccagctcc
2400
aatccccaga tgagcagcta agcagctgac agttggaggg aaagccagcc tgggggctgg
2460
gaggatcctg gagaagtggg tggggacaga ccagcccttc cccatcctgg ggttgccctg
2520
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2580
aaaaaaaaaa aaaaaaaaaa aa
2602

<210> 4738
<211> 756
<212> PRT
<213> Homo sapiens

<400> 4738
Met Ala Pro Thr Trp Leu Ser Asp Ile Pro Leu Val Gln Pro Pro Gly
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His Gln Asp Val Ser Glu Arg Arg Leu Asp Thr Gln Arg Pro Gln Val
20 25 30
Thr Met Trp Glu Arg Asp Val Ser Ser Asp Arg Gln Glu Pro Gly Arg
35 40 45
Arg Gly Arg Ser Trp Gly Leu Glu Gly Ser Gln Ala Leu Ser Gln Gln
50 55 60
Ala Glu Val Ile Val Arg Gln Leu Gln Glu Leu Arg Arg Leu Glu Glu
65 70 75 80
Glu Val Arg Leu Leu Arg Glu Thr Ser Leu Gln Gln Lys Met Arg Leu
85 90 95
Glu Ala Gln Ala Met Glu Leu Glu Ala Leu Ala Arg Ala Glu Lys Ala
100 105 110
Gly Arg Ala Glu Ala Glu Gly Leu Arg Ala Ala Leu Ala Gly Ala Glu
115 120 125
Val Val Arg Lys Asn Leu Glu Glu Gly Arg Gln Arg Glu Leu Glu Glu
130 135 140
Val Gln Arg Leu His Gln Glu Gln Leu Ser Ser Leu Thr Gln Ala His
145 150 155 160
Glu Glu Ala Leu Ser Ser Leu Thr Ser Lys Ala Glu Gly Leu Glu Lys
165 170 175
Ser Leu Ser Ser Leu Glu Thr Arg Arg Ala Gly Glu Ala Lys Glu Leu
180 185 190
Ala Glu Ala Gln Arg Glu Ala Glu Leu Leu Arg Lys Gln Leu Ser Lys
195 200 205
Thr Gln Glu Asp Leu Glu Ala Gln Val Thr Leu Val Glu Asn Leu Arg
210 215 220
Lys Tyr Val Gly Glu Gln Val Pro Ser Glu Val His Ser Gln Thr Trp
225 230 235 240
Glu Leu Glu Arg Gln Lys Leu Leu Glu Thr Met Gln Leu Leu Gln Glu
245 250 255
Asp Arg Asp Ser Leu His Ala Thr Ala Glu Leu Leu Gln Val Arg Val
260 265 270
Gln Ser Leu Thr His Ile Leu Ala Leu Gln Glu Glu Glu Leu Thr Arg
275 280 285
Lys Val Gln Pro Ser Asp Ser Leu Glu Pro Glu Phe Thr Arg Lys Cys
290 295 300
Gln Ser Leu Leu Asn Arg Trp Arg Glu Lys Val Phe Ala Leu Met Val
305 310 315 320
Gln Leu Lys Ala Gln Glu Leu Glu His Ser Asp Ser Val Lys Gln Leu
325 330 335
Lys Gly Gln Val Ala Ser Leu Gln Glu Lys Val Thr Ser Gln Ser Gln
340 345 350
Glu Gln Ala Ile Leu Gln Arg Ser Leu Gln Asp Lys Ala Ala Glu Val
355 360 365
Glu Val Glu Arg Met Gly Ala Lys Gly Leu Gln Leu Glu Leu Ser Arg

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    370                 375                 380
Ala Gln Glu Ala Arg Arg Trp Trp Gln Gln Gln Thr Ala Ser Ala Glu
385                 390                 395                 400
Glu Gln Leu Arg Leu Val Val Asn Ala Val Ser Ser Ser Gln Ile Trp
                405                 410                 415
Leu Glu Thr Thr Met Ala Lys Val Glu Gly Ala Ala Ala Gln Leu Pro
            420                 425                 430
Ser Leu Asn Asn Arg Leu Ser Tyr Ala Val Arg Lys Val His Thr Ile
        435                 440                 445
Arg Gly Leu Ile Ala Arg Lys Leu Ala Leu Ala Gln Leu Arg Gln Glu
    450                 455                 460
Ser Cys Pro Leu Pro Pro Pro Val Thr Asp Val Ser Leu Glu Leu Gln
465                 470                 475                 480
Gln Leu Arg Glu Glu Arg Asn Arg Leu Asp Ala Glu Leu Gln Leu Ser
                485                 490                 495
Ala Arg Leu Ile Gln Gln Glu Val Gly Arg Ala Arg Glu Gln Gly Glu
            500                 505                 510
Ala Glu Arg Gln Gln Leu Ser Lys Val Ala Gln Gln Leu Glu Gln Glu
        515                 520                 525
Leu Gln Gln Thr Gln Glu Ser Leu Ala Ser Leu Gly Leu Gln Leu Glu
    530                 535                 540
Val Ala Arg Gln Gly Gln Gln Glu Ser Thr Glu Glu Ala Ala Ser Leu
545                 550                 555                 560
Arg Gln Glu Leu Thr Gln Gln Gln Glu Leu Tyr Gly Gln Ala Leu Gln
                565                 570                 575
Glu Lys Val Ala Glu Val Glu Thr Arg Leu Arg Glu Gln Leu Ser Asp
            580                 585                 590
Thr Glu Arg Arg Leu Asn Glu Ala Arg Arg Glu His Ala Lys Ala Val
        595                 600                 605
Val Ser Leu Arg Gln Ile Gln Arg Arg Ala Ala Gln Glu Lys Glu Arg
    610                 615                 620
Ser Gln Glu Leu Arg Arg Leu Gln Glu Glu Ala Arg Lys Glu Glu Gly
625                 630                 635                 640
Gln Arg Leu Ala Arg Arg Leu Gln Glu Leu Glu Arg Asp Lys Asn Leu
                645                 650                 655
Met Leu Ala Thr Leu Gln Gln Glu Gly Leu Leu Ser Arg Tyr Lys Gln
            660                 665                 670
Gln Arg Leu Leu Thr Val Leu Pro Ser Leu Leu Asp Lys Lys Lys Ser
        675                 680                 685
Val Val Ser Ser Pro Arg Pro Pro Glu Cys Ser Ala Ser Ala Pro Val
    690                 695                 700
Ala Ala Ala Val Pro Thr Arg Glu Ser Ile Lys Gly Ser Leu Ser Val
705                 710                 715                 720
Leu Leu Asp Asp Leu Gln Asp Leu Ser Glu Ala Ile Ser Lys Glu Glu
                725                 730                 735
Ala Val Cys Gln Gly Asp Asn Leu Asp Arg Cys Ser Ser Ser Asn Pro
            740                 745                 750
Gln Met Ser Ser
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<210> 4739
<211> 684
<212> DNA
<213> Homo sapiens

<400> 4739
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ggaagacttg accagtcttg gtgatgagaa ggccttcacc ctatgaacac aaccaagtct
120
tagccctctc tcctgctcct ttaaactctg aacttctagg atgggagaat gggaactttt
180
gcaggttgag attcatagtg aaatcgggtc aagaagtgat cagatgcaaa gcacagggca
240
gttcattact ataccatggc tgaggtcttc ctgggcacca ggccctgggc tcagcacttg
300
gctcagtctg caccttggac cctgccagag ccctccacag caggtgctct caggcaaggc
360
tgtgtgttgc tggccagacg ccttctgacc agcgtgcttt cttgaccaca gatcccttgg
420
ccaagcagga gggaaccatt agcagcctga ggagctggct ggctgggagc ctcggggacc
480
gcccagcctt gctcccagct cacccacaag atgtggacag ctcttgtgct catttggatt
540
ttctccttgt ccttatctga aagccatgcg gcatccaacg atccacgtaa gtgagaaagc
600
tgtgtgactg ctggatgggc ccacggtggc cacaaagcat gctgagccct tgaaagcagc
660
atctgcaaac ccaggccaac gcgt
684

<210> 4740
<211> 119
<212> PRT
<213> Homo sapiens

<400> 4740
Met Leu Leu Ser Arg Ala Gln His Ala Leu Trp Pro Pro Trp Ala His
 1   5   10   15
Pro Ala Val Thr Gln Leu Ser His Leu Arg Gly Ser Leu Asp Ala Ala
            20   25   30
Trp Leu Ser Asp Lys Asp Lys Glu Lys Ile Gln Met Ser Thr Arg Ala
        35   40   45
Val His Ile Leu Trp Val Ser Trp Glu Gln Gly Trp Ala Val Pro Glu
    50   55   60
Ala Pro Ser Gln Pro Ala Pro Gln Ala Ala Asn Gly Ser Leu Leu Leu
65   70   75   80
Gly Gln Gly Ile Cys Gly Gln Glu Ser Thr Leu Val Arg Arg Arg Leu
                85   90   95
Ala Ser Asn Thr Gln Pro Cys Leu Arg Ala Pro Ala Val Glu Gly Ser
            100   105   110
Gly Arg Val Gln Gly Ala Asp
        115

<210> 4741
<211> 411
<212> DNA
<213> Homo sapiens

<400> 4741
aaatttactt ctctcaggtc aacaggtgtt tttctttctt ttttttttt tttttccctt
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ttttttctta aaaaaaaaaa aggggttttt ctttgccccc cccgttcccc ccccttcccc
120
ttccgaaaaa aagaggggaa ttttttaaaa aacccgaaag gggggaaggg gggggtata
180
aaagataaaa tttggttttt tgggggggaa aatttggaca ccccaccctc gggttttttt
240
tccccacccc aaaaaatttt aaaaggggggc cctaaaaaaa atttttttctt taatttccaa
300
ataaaaaaaa aatggggttc caaaatcatt gaaaaatagg ggggactcca aaaccttgaa
360
ttttcccaag ggggaccact aaaatttacc ccttttttgg ggttttgggg g
411

<210> 4742
<211> 109
<212> PRT
<213> Homo sapiens

<400> 4742
Met Ile Leu Glu Pro His Phe Phe Phe Ile Trp Lys Leu Lys Lys Lys
1 5 10 15
Phe Phe Leu Gly Pro Pro Phe Lys Ile Phe Trp Gly Gly Glu Lys Lys
20 25 30
Pro Glu Gly Gly Val Ser Lys Phe Ser Pro Pro Lys Asn Gln Ile Leu
35 40 45
Ser Phe Ile Pro Pro Pro Phe Pro Pro Phe Gly Phe Phe Lys Lys Phe
50 55 60
Pro Ser Phe Phe Arg Lys Gly Lys Gly Gly Glu Arg Gly Gly Gln Arg
65 70 75 80
Lys Thr Pro Phe Phe Phe Leu Arg Lys Lys Arg Glu Lys Lys Lys Lys
85 90 95
Lys Glu Arg Lys Thr Pro Val Asp Leu Arg Glu Val Asn
100 105

<210> 4743
<211> 473
<212> DNA
<213> Homo sapiens

<400> 4743
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caaccggccc cacaaattct agcagtgcca agaagaagga taaaagagtt caaggtggaa
120
gagtgattga gtcccggtat ctgcagtatg aaaagaagac aacccaaaag gctcctgcag
180
gagatgggtc acagacccga gggaagatgt ctgaaggtgg aaggaaatcc agcctgctcc
240
agaaaagcaa agcagatagc agtggggtcg gaaagggtga cctgcagtcc acgttgctgg
300

aagggcatgg cacagctcca cctgacctgg atctctctgc tattaatgac aaaagcatcg
360
tcaaaaagac gccacagtta gcaaaaacaa tatcaaagaa acctgagtca acatcatttt
420
ctgcccctcg gaaaaagagc ccggatttat ctgaagcgaa tggaatgatg gag
473

<210> 4744
<211> 150
<212> PRT
<213> Homo sapiens

<400> 4744
Met Ala Asp Ser Ser Gly Arg Gly Ala Gly Lys Pro Ala Thr Gly Pro
1 5 10 15
Thr Asn Ser Ser Ser Ala Lys Lys Lys Asp Lys Arg Val Gln Gly Gly
20 25 30
Arg Val Ile Glu Ser Arg Tyr Leu Gln Tyr Glu Lys Lys Thr Thr Gln
35 40 45
Lys Ala Pro Ala Gly Asp Gly Ser Gln Thr Arg Gly Lys Met Ser Glu
50 55 60
Gly Gly Arg Lys Ser Ser Leu Leu Gln Lys Ser Lys Ala Asp Ser Ser
65 70 75 80
Gly Val Gly Lys Gly Asp Leu Gln Ser Thr Leu Leu Glu Gly His Gly
85 90 95
Thr Ala Pro Pro Asp Leu Asp Leu Ser Ala Ile Asn Asp Lys Ser Ile
100 105 110
Val Lys Lys Thr Pro Gln Leu Ala Lys Thr Ile Ser Lys Lys Pro Glu
115 120 125
Ser Thr Ser Phe Ser Ala Pro Arg Lys Lys Ser Pro Asp Leu Ser Glu
130 135 140
Ala Asn Gly Met Met Glu
145 150

<210> 4745
<211> 666
<212> DNA
<213> Homo sapiens

<400> 4745
gcatggagag aatatgataa gttagaatac gatgtaactg ttaccaggaa ccagatgcaa
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gagcagctgg atcaccttgg tgaagttcag acggaatcag caggaattca gcgtgcacag
120
attcagaaag aactttggcg aattcaggat gtcatggaag ggctgagtaa acataagcag
180
caaagaggta ctacagaaat aggtatgata ggatcaaagc ctttctcaac agttaagtac
240
aaaaatgagg gtccagatta tagactctac aagagtgaac cagagttaac aacagtggca
300
gaagttgatg aatctaatgg agaagaaaaa tcagaacctg tttcagagat agaaacttca
360
gttgttaaag gttcccactt tcctgttgga gtagtccctc caagagcaaa atcaccaaca
420

cccgaatctt cgacaatagc ttcctatgta accttgagga aaactaagaa gatgatggat
480
ctaagaacgg aaagaccaag aagtgcagtg gaacagctct gtttggctga aagtactcga
540
ccaaggatga ctgtggaaga gcaaatggaa agaataagaa gatatcaaca agcgtgcctg
600
agggagaaga aaaaagggtt aaatgttatc ggtgcttcag accagtcacc cttacaaagc
660
ccttaa
666

<210> 4746
<211> 221
<212> PRT
<213> Homo sapiens

<400> 4746
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Asn Gln Met Gln Glu Gln Leu Asp His Leu Gly Glu Val Gln Thr Glu
20 25 30
Ser Ala Gly Ile Gln Arg Ala Gln Ile Gln Lys Glu Leu Trp Arg Ile
35 40 45
Gln Asp Val Met Glu Gly Leu Ser Lys His Lys Gln Gln Arg Gly Thr
50 55 60
Thr Glu Ile Gly Met Ile Gly Ser Lys Pro Phe Ser Thr Val Lys Tyr
65 70 75 80
Lys Asn Glu Gly Pro Asp Tyr Arg Leu Tyr Lys Ser Glu Pro Glu Leu
85 90 95
Thr Thr Val Ala Glu Val Asp Glu Ser Asn Gly Glu Glu Lys Ser Glu
100 105 110
Pro Val Ser Glu Ile Glu Thr Ser Val Val Lys Gly Ser His Phe Pro
115 120 125
Val Gly Val Val Pro Pro Arg Ala Lys Ser Pro Thr Pro Glu Ser Ser
130 135 140
Thr Ile Ala Ser Tyr Val Thr Leu Arg Lys Thr Lys Lys Met Met Asp
145 150 155 160
Leu Arg Thr Glu Arg Pro Arg Ser Ala Val Glu Gln Leu Cys Leu Ala
165 170 175
Glu Ser Thr Arg Pro Arg Met Thr Val Glu Glu Gln Met Glu Arg Ile
180 185 190
Arg Arg Tyr Gln Gln Ala Cys Leu Arg Glu Lys Lys Lys Gly Leu Asn
195 200 205
Val Ile Gly Ala Ser Asp Gln Ser Pro Leu Gln Ser Pro
210 215 220

<210> 4747
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 4747
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acgcatactg acgccaaaat ccgtgctgaa aatggaacag ggtccagccc tcggggtcct
120
ggctgcagcc tccggcactt tgcctgcgaa cagaacctgc tgtcgcggcc agatggctct
180
gcttccttcc tgcaaggtga cacctctgtc ctggcgggtg tgtacgggcc ggccgaggtg
240
aaggtcagca aagagatttt caacaaggcc acactcgaag tgatcctgag gccgaagatt
300
gggctgcctg caggggtcag tggatggcag tcaggccttg ccttcttccc actggaatct
360
tccatcatcc ctgcaggtgt tgcagagaag agccgggagc ggctgatcag gaacacgtgc
420
gaggcggtgg tgctgggcac gttgcacccc cgcacctcca tcaccgtggt gctgcaggtt
480
gtcagcgatg ccggctctct cctggcctgt tgtctgaatg ccgcctgcat ggcattggtg
540
gatgcaggtg tgcccatgcg ggctctcttc tgtggggtcg cctgcgccct ggactctgat
600
gggaccctcg tgctggatcc tacatccaag caagaaaagg aggcccgggc agtcctgacc
660
tttgccctgg acagcgtgga acggaagctg ctgatgtcca gcaccaaggg gctctactca
720
gacactgagc tccagcagtg cctggctgcg gcccaggccg cttcgcaaca cgtcttccgt
780
ttctaccggg aatcgctgca gaggcgttac tccaagagct gaggcaagct ggggcaaggg
840
gccgctccca ttgcctccac ccactcaccc cctacagcct gaagcaaacc agcagcccag
900
ccttgcctct ctgacccatg ggctccttga gcctgcagct ctgtaaccac agggctcctg
960
tggggaggcc ttggcctgtg acagccccca ggcctggggg cacagatccc cccagcaagg
1020
ataacattca aaggagctca catttatgga atggatgaat caataaatta attcacttta
1080
aaaaaaaaaa a
1091

<210> 4748
<211> 273
<212> PRT
<213> Homo sapiens

<400> 4748
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Met Glu Glu Glu Thr His Thr Asp Ala Lys Ile Arg Ala Glu Asn Gly
            20   25   30
Thr Gly Ser Ser Pro Arg Gly Pro Gly Cys Ser Leu Arg His Phe Ala
        35   40   45
Cys Glu Gln Asn Leu Leu Ser Arg Pro Asp Gly Ser Ala Ser Phe Leu
    50   55   60
Gln Gly Asp Thr Ser Val Leu Ala Gly Val Tyr Gly Pro Ala Glu Val
65   70   75   80
Lys Val Ser Lys Glu Ile Phe Asn Lys Ala Thr Leu Glu Val Ile Leu

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                85                  90                  95
Arg Pro Lys Ile Gly Leu Pro Ala Gly Val Ser Gly Trp Gln Ser Gly
            100                 105                 110
Leu Ala Phe Phe Pro Leu Glu Ser Ser Ile Ile Pro Ala Gly Val Ala
        115                 120                 125
Glu Lys Ser Arg Glu Arg Leu Ile Arg Asn Thr Cys Glu Ala Val Val
    130                 135                 140
Leu Gly Thr Leu His Pro Arg Thr Ser Ile Thr Val Val Leu Gln Val
145                 150                 155                 160
Val Ser Asp Ala Gly Ser Leu Leu Ala Cys Cys Leu Asn Ala Ala Cys
                165                 170                 175
Met Ala Leu Val Asp Ala Gly Val Pro Met Arg Ala Leu Phe Cys Gly
            180                 185                 190
Val Ala Cys Ala Leu Asp Ser Asp Gly Thr Leu Val Leu Asp Pro Thr
        195                 200                 205
Ser Lys Gln Glu Lys Glu Ala Arg Ala Val Leu Thr Phe Ala Leu Asp
    210                 215                 220
Ser Val Glu Arg Lys Leu Leu Met Ser Ser Thr Lys Gly Leu Tyr Ser
225                 230                 235                 240
Asp Thr Glu Leu Gln Gln Cys Leu Ala Ala Ala Gln Ala Ala Ser Gln
                245                 250                 255
His Val Phe Arg Phe Tyr Arg Glu Ser Leu Gln Arg Arg Tyr Ser Lys
            260                 265                 270
Ser
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<210> 4749
<211> 2196
<212> DNA
<213> Homo sapiens

<400> 4749
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Gly Lys Thr Leu Leu Phe Val Arg Leu Leu Thr Gly Leu Tyr Arg Asp
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Thr Gln Thr Ser Ile Thr Asp Ser Cys Ala Val Tyr Arg Val Asn Asn
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Val Phe Val Val Asp Ser Ala Ala Phe Gln Arg Glu Val Lys Asp Val
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Thr Pro Ser Phe Leu Ile Ala Cys Asn Lys Gln Asp Ile Ala Met Ala
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Lys Ser Ala Lys Leu Ile Gln Gln Gln Leu Glu Lys Glu Leu Asn Thr
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225 230 235 240
Gln Leu Pro Leu Lys Val Glu Phe Leu Glu Cys Ser Ala Lys Gly Gly
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<212> PRT
<213> Homo sapiens

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35 40 45
Ser Leu Trp Pro Arg Ile Thr Phe Leu Leu Pro Pro Ala Pro Pro Pro
50 55 60
Met Leu Ala Ala Pro Gln Leu Ile Gln Arg Pro Val Met Leu Thr Lys
65 70 75 80
Phe Thr Pro Thr Thr Leu Pro Thr Ser Gln Asn Ser Ile His Pro Val
85 90 95
Arg Val Val Asn Gly Gln Thr Ala Thr Ile Ala Lys Thr Phe Pro Met

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Val Lys Ser His Thr Glu Thr Asp Glu Lys Gln Thr Glu Ser Arg Thr
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Ile Thr Pro Pro Ala Ala Pro Lys Pro Lys Arg Glu Glu Asn Pro Gln
                165                 170                 175
Lys Leu Ala Phe Met Val Ser Leu Gly Leu Val Thr His Asp His Leu
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Glu Glu Ile Gln Ser Lys Arg Gln Glu Arg Lys Arg Arg Thr Thr Ala
        195                 200                 205
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Ala Val Thr Tyr Leu Asn Ser Thr Met His Pro Gly Thr Arg Lys Arg
225                 230                 235                 240
Ala Asn Glu Glu His Trp Pro Lys Gly Asp Ile His Glu Asp Phe Cys
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Ser Val Cys Arg Lys Ser Gly Gln Leu Leu Met Cys Asp Thr Cys Ser
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Arg Val Tyr His Leu Asp Cys Leu Asp Pro Pro Leu Lys Thr Ile Pro
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Lys Gly Met Trp Ile Cys Pro Arg Cys Gln Asp Gln Met Leu Lys Lys
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35 40 45
Ser Asp Val Glu Gly Gly Glu Val Leu Tyr Leu Val His Tyr Cys Gly
50 55 60
Trp Asn Val Arg Tyr Asp Glu Trp Ile Lys Ala Asp Lys Ile Val Arg
65 70 75 80
Pro Ala Asp Lys Asn Val Pro Lys Ile Lys His Arg Lys Lys Ile Lys
85 90 95
Asn Lys Leu Asp Lys Glu Lys Asp Lys Asp Glu Lys Tyr Ser Pro Lys
100 105 110
Asn Cys Lys Leu Arg Arg Leu Ser Lys Pro Pro Phe Gln Thr Asn Pro
115 120 125
Ser Pro Glu Met Val Ser Lys Leu Asp Leu Thr Asp Ala Lys Asn Ser
130 135 140
Asp Thr Ala His Ile Lys Ser Ile Glu Ile Thr Ser Ile Leu Asn Gly
145 150 155 160
Leu Gln Ala Ser Glu Ser Ser Ala Glu Asp Ser Glu Gln Glu Asp Glu
165 170 175
Arg Gly Ala Gln Asp Met Asp Asn Asn Gly Lys Glu Glu Ser Lys Ile
180 185 190
Asp His Leu Thr Asn Asn Arg Asn Asp Leu Ile Ser Lys Glu Glu Gln
195 200 205
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225 230 235 240
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245 250 255
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Gln Ile Lys Arg Gly Lys Arg Arg Tyr Cys Asn Thr Glu Glu Cys Leu
275 280 285
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290 295 300
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305 310 315 320
Lys Asn Lys Ala Lys Met Thr Pro Thr Lys Lys Tyr Asn Gly Leu Glu
325 330 335
Glu Lys Arg Lys Ser Leu Arg Thr Thr Gly Phe Tyr Ser Gly Phe Ser
340 345 350
Glu Val Ala Glu Lys Arg Ile Lys Leu Leu Asn Asn Ser Asp Glu Arg
355 360 365
Leu Gln Asn Ser Arg Ala Lys Asp Arg Lys Asp Val Trp Ser Ser Ile
370 375 380
Gln Gly Gln Trp Pro Lys Lys Thr Leu Lys Glu Leu Phe Ser Asp Ser

385 390 395 400
Asp Thr Glu Ala Ala Ala Ser Pro Pro His Pro Ala Pro Glu Glu Gly
405 410 415
Val Ala Glu Glu Ser Leu Gln Thr Val Ala Glu Glu Glu Ser Cys Ser
420 425 430
Pro Ser Val Glu Leu Glu Lys Pro Pro Pro Val Asn Val Asp Ser Lys
435 440 445
Pro Ile Glu Glu Lys Thr Val Glu Val Asn Asp Arg Lys Ala Glu Phe
450 455 460
Pro Ser Ser Gly Ser Asn Ser Val Leu Asn Thr Pro Pro Thr Thr Pro
465 470 475 480
Glu Ser Pro Ser Ser Val Thr Val Thr Glu Gly Ser Arg Gln Gln Ser
485 490 495
Ser Val Thr Val Ser Glu Pro Leu Ala Pro Asn Gln Glu Glu Val Arg
500 505 510
Ser Ile Lys Ser Glu Thr Asp Ser Thr Ile Glu Val Asp Ser Val Ala
515 520 525
Gly Glu Leu Gln Asp Leu Gln Ser Glu Gly Asn Ser Ser Pro Ala Gly
530 535 540
Phe Asp Ala Ser Val Ser Ser Ser Ser Ser Asn Gln Pro Glu Pro Glu
545 550 555 560
His Pro Glu Lys Ala Cys Thr Gly Gln Lys Arg Val Lys Asp Ala Gln
565 570 575
Gly Gly Gly Ser Ser Ser Lys Lys Gln Lys Arg Ser His Lys Ala Thr
580 585 590
Val Val Asn Asn Thr Lys Lys Gly Lys Gly Thr Asn Ser Ser Asp Ser
595 600 605
Glu Glu Leu Ser Ala Gly Glu Ser Ile Thr Lys Ser Gln Pro Val Lys
610 615 620
Ser Val Ser Thr Gly Met Lys Ser His Ser Thr Lys Ser Pro Ala Arg
625 630 635 640
Thr Gln Ser Pro Gly Lys Cys Gly Lys Asn Gly Asp Lys Asp Pro Asp
645 650 655
Leu Lys Glu Pro Ser Asn Arg Leu Pro Lys Val Tyr Lys Trp Ser Phe
660 665 670
Gln Met Ser Asp Leu Glu Asn Met Thr Ser Ala Glu Arg Ile Thr Ile
675 680 685
Leu Gln Glu Lys Leu Gln Glu Asn Gln Lys His Tyr Leu Ser Leu Lys
690 695 700
Ser Glu Val Ala Ser Ile Asp Arg Arg Arg Lys Arg Leu Lys Lys Lys
705 710 715 720
Glu Arg Glu Ser Ala Ala Thr Ser Ser Ser Ser Ser Ser Pro Ser Ser
725 730 735
Ser Ser Ile Asn Ser Cys Cys Tyr Val Asn Phe Ser
740 745

<210> 4755
<211> 2093
<212> DNA
<213> Homo sapiens

<400> 4755
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120
cctatccgcc tgtctgagcc tcaggaaact agcctcatga cttcctccac acacttccct
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240
tcccacagca ccccacccct acccccgcag acttaactaa ggctggcagt ggccttcaac
300
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360
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420
acaccattat aaataagtta atgatttatt gtgtcgtctt caaattactg aagtggggag
480
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540
aaatatttcc tatttcagag gaatataaaa catcacactt agtgcttgct tcagcagcat
600
atatactaaa attggaacga tacagagaag attagcatga cccctgcgca aggatggcac
660
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720
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840
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1920
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1980
cctctgggtc ccaccaccca gccccccgtg tcagaacaat ctttgctctg tacaatcggc
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2093

<210> 4756
<211> 188
<212> PRT
<213> Homo sapiens

<400> 4756
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Leu Val Ala Thr Pro Gly Ile Asp Lys Leu Thr Glu Lys Ser Gln Val
20 25 30
Ser Glu Asp Gly Thr Leu Arg Ser Leu Glu Pro Glu Pro Gln Gln Ser
35 40 45
Leu Glu Asp Gly Ser Pro Ala Lys Gly Glu Pro Ser Gln Ala Trp Arg
50 55 60
Glu Gln Arg Arg Pro Ser Thr Ser Ser Ala Ser Gly Gln Trp Ser Pro
65 70 75 80
Thr Pro Glu Trp Val Leu Ser Trp Lys Ser Lys Leu Pro Leu Gln Thr
85 90 95
Ile Met Arg Leu Leu Gln Val Leu Val Pro Gln Val Glu Lys Ile Cys
100 105 110
Ile Asp Lys Gly Leu Thr Asp Glu Ser Glu Ile Leu Arg Phe Leu Gln
115 120 125
His Gly Thr Leu Val Gly Leu Leu Pro Val Pro His Pro Ile Leu Ile
130 135 140
Arg Lys Tyr Gln Ala Asn Ser Gly Thr Ala Met Trp Phe Arg Thr Tyr
145 150 155 160
Met Trp Gly Val Ile Tyr Leu Arg Asn Val Asp Pro Pro Val Trp Tyr
165 170 175
Asp Thr Asp Val Lys Leu Phe Glu Ile Gln Arg Val
180 185

<210> 4757
<211> 272
<212> DNA
<213> Homo sapiens

<400> 4757
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gctagtgggc tggcgttcca tccggcccgt gacctactgg ctgcagggga cgtggacggg
120
gacgtattcg tcttttccta ctcttgccaa gagggagaaa ccaaggagct ggtcatcagg
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tcacatctca aggcctgccg agctgtggcc ttctctgaag atgggcagaa gctcattact
240
gtctccaagg acaaagccat ccatgttcta ga
272

<210> 4758
<211> 90
<212> PRT
<213> Homo sapiens

<400> 4758
Xaa Met Glu Ala Pro Thr Arg Ile Arg Asp Thr Pro Glu Asp Ile Val
1 5 10 15
Leu Glu Ala Pro Ala Ser Gly Leu Ala Phe His Pro Ala Arg Asp Leu
20 25 30
Leu Ala Ala Gly Asp Val Asp Gly Asp Val Phe Val Phe Ser Tyr Ser
35 40 45
Cys Gln Glu Gly Glu Thr Lys Glu Leu Val Ile Arg Ser His Leu Lys
50 55 60
Ala Cys Arg Ala Val Ala Phe Ser Glu Asp Gly Gln Lys Leu Ile Thr
65 70 75 80
Val Ser Lys Asp Lys Ala Ile His Val Leu
85 90

<210> 4759
<211> 1087
<212> DNA
<213> Homo sapiens

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120
gaattcagct cttctcgagc gggatttctg cccctgtggg atgtggcggc cactgacttt
180
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240
tgtccggggt gggagggacc gtgagggagc cccagaatgg ggtgcatttg gtgctgaggc
300
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360
tcatcacggt cagtcattcc ttctcctttc cagggtgctg ggggctgggg ttccctggcc
420
caagggtcca gcctcctctc accccattcc aggtggcata ctgcagtctg gctctttctc
480
ccctccctcc ccacccaagc ctcacctccc cacccccttga acccccatgc aatgagcttc
540
taactcagag ctgatgaaca aaagcccccc cacccccaat gcctgcctcc tcactcctcc
600

gtcgctgccc ttcacacctt ttggtgctac ccctccccag agttaagcac tggatgtctc
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ctgatcccag gctgggaccc ctacccccac ccccttttgat cctttctact tccacggtga
720
aaggactgag gtcggactac agagggaaga gggacttccc ttgactgggt tgtgtttctt
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840
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960
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1080
aactgtg
1087

<210> 4760
<211> 78
<212> PRT
<213> Homo sapiens

<400> 4760
Xaa Ala Arg Phe Val Gly Thr Asn Gly Glu Glu Leu Ser Phe Asn Gln
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Thr Thr Ala Ala Thr Val Ser Val Pro Gln Asp Gly Cys Arg Leu Arg
20 25 30
Lys Gly Gln Thr Lys Thr Leu Phe Glu Phe Ser Ser Ser Arg Ala Gly
35 40 45
Phe Leu Pro Leu Trp Asp Val Ala Ala Thr Asp Phe Gly Gln Thr Asn
50 55 60
Gln Lys Phe Gly Phe Glu Leu Gly Pro Val Cys Phe Ser Ser
65 70 75

<210> 4761
<211> 3973
<212> DNA
<213> Homo sapiens

<400> 4761
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120
ttcgccgtgg agagcatccg gaagaagcgc gtgcggaagg gtaaagtcga gtatctggtg
180
aagtggaaag gatggccccc aaagtacagc acgtgggagc cagaagagca catcttggac
240
ccccgcctcg tcatggccta cgaggagaag gaggagagag accgagcatc ggggtatagg
300
aagagaggtc cgaaacccaa gcggcttctg ctgcagcggc tgtacagcat ggacctgcgg
360

agctcccaca aggccaaggg caaggagaag ctctgcttct ccctgacgtg cccactcggc
420
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480
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600
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720
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780
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1980

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3960
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3973

<210> 4762
<211> 251
<212> PRT
<213> Homo sapiens

<400> 4762
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Arg Lys Lys Arg Val Arg Lys Gly Lys Val Glu Tyr Leu Val Lys Trp
20 25 30
Lys Gly Trp Pro Pro Lys Tyr Ser Thr Trp Glu Pro Glu Glu His Ile
35 40 45
Leu Asp Pro Arg Leu Val Met Ala Tyr Glu Glu Lys Glu Glu Arg Asp
50 55 60
Arg Ala Ser Gly Tyr Arg Lys Arg Gly Pro Lys Pro Lys Arg Leu Leu
65 70 75 80
Leu Gln Arg Leu Tyr Ser Met Asp Leu Arg Ser Ser His Lys Ala Lys
85 90 95
Gly Lys Glu Lys Leu Cys Phe Ser Leu Thr Cys Pro Leu Gly Ser Gly
100 105 110
Ser Pro Glu Gly Val Val Lys Ala Gly Ala Pro Glu Leu Val Asp Lys
115 120 125
Gly Pro Leu Val Pro Thr Leu Pro Phe Pro Leu Arg Lys Pro Arg Lys
130 135 140
Ala His Lys Tyr Leu Arg Leu Ser Arg Lys Lys Phe Pro Pro Arg Gly
145 150 155 160
Pro Asn Leu Glu Ser His Ser His Arg Arg Glu Leu Phe Leu Gln Glu
165 170 175
Pro Pro Ala Pro Asp Val Leu Gln Ala Ala Gly Glu Trp Glu Pro Ala
180 185 190
Ala Gln Pro Pro Glu Glu Glu Ala Asp Ala Asp Leu Ala Glu Gly Pro
195 200 205
Pro Pro Trp Thr Pro Ala Leu Pro Ser Ser Glu Val Thr Val Thr Asp
210 215 220
Ile Thr Ala Asn Ser Ile Thr Val Thr Phe Arg Glu Ala Gln Ala Ala
225 230 235 240
Glu Gly Phe Phe Arg Asp Arg Ser Gly Lys Phe
245 250

<210> 4763
<211> 2158
<212> DNA
<213> Homo sapiens

<400> 4763
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120
agtgatgatt ttgacagtcc agtcaaggga cctttgtgta aatcagttac tccaacaaaa
180
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240
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360
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420
tctgtcataa caagtatgaa aacaggtgag cttgagaaag aaacagcccc tttgaggaaa
480
gatgcagata gttcaatatc agtcttagag atccatagtc aaaaagcaca aatagaggaa
540
cccgatcctc cagaaatgga aacttctctt gattcttctg agatggcaaa agatctctct
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660
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720
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780
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840
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900
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960
gattctgagt tcacaaaggt agaaatggat aatctggaca atgcccagac ctctggcata
1020
gaggagcctt ctgagacaaa gggttctatg caaaaaagca aattcaaata taagttggtt
1080
cctgaagaag aaaccactgc ctcagaaaat acagagataa cctctgaaag gcagaaagag
1140
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1260
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1320
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1380
acagctttgc aaaaaactga caaaaaggaa attttgaaaa aatcagagaa agatacaaat
1440

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1500
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1560
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1620
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1680
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1740
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1920
gaagatcaag aagaaaagaa aaaagattca aaaaaatcca aagcaaactt gcttgaaagg
1980
aggtcaacaa gaacaaggaa atgtataagc tacagatttg atgagtttga tgaagcaatt
2040
gatgaagcta ttgaagatga catcaaagaa gccgatggag gaggagttgg ccgaggaaaa
2100
gatatctcca ccatcacagg tcatcgtggg aaagacatct ctactatttt ggatgaaa
2158

<210> 4764
<211> 719
<212> PRT
<213> Homo sapiens

<400> 4764
Xaa Phe Gly Gly Asn Ile Lys Ser Ser His Glu Ile Thr Glu Lys Ser
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Thr Glu Glu Thr Glu Lys Leu Lys Asn Asp Gln Gln Ala Lys Ile Pro
            20   25   30
Leu Lys Lys Arg Glu Ile Lys Leu Ser Asp Asp Phe Asp Ser Pro Val
        35   40   45
Lys Gly Pro Leu Cys Lys Ser Val Thr Pro Thr Lys Glu Phe Leu Lys
    50   55   60
Asp Glu Ile Lys Gln Glu Glu Glu Thr Cys Lys Arg Ile Ser Thr Ile
65   70   75   80
Thr Ala Leu Gly His Glu Gly Lys Gln Leu Val Asn Gly Glu Val Ser
                85   90   95
Asp Glu Arg Val Ala Pro Asn Phe Lys Thr Glu Pro Ile Glu Thr Lys
            100   105   110
Phe Tyr Glu Thr Lys Glu Glu Ser Tyr Ser Pro Ser Lys Asp Arg Asn
        115   120   125
Ile Ile Thr Glu Gly Asn Gly Thr Glu Ser Leu Asn Ser Val Ile Thr
    130   135   140
Ser Met Lys Thr Gly Glu Leu Glu Lys Glu Thr Ala Pro Leu Arg Lys
145   150   155   160
Asp Ala Asp Ser Ser Ile Ser Val Leu Glu Ile His Ser Gln Lys Ala
                165   170   175
Gln Ile Glu Glu Pro Asp Pro Pro Glu Met Glu Thr Ser Leu Asp Ser

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            180                 185                 190
Ser Glu Met Ala Lys Asp Leu Ser Ser Lys Thr Ala Leu Ser Ser Thr
        195                 200                 205
Glu Ser Cys Thr Met Lys Gly Glu Glu Lys Ser Pro Lys Thr Lys Lys
    210                 215                 220
Asp Lys Arg Pro Pro Ile Leu Glu Cys Leu Glu Lys Leu Glu Lys Ser
225                 230                 235                 240
Lys Lys Thr Phe Leu Asp Lys Asp Ala Gln Arg Leu Ser Pro Ile Pro
                245                 250                 255
Glu Glu Val Pro Lys Ser Thr Leu Glu Ser Glu Lys Pro Gly Ser Pro
            260                 265                 270
Glu Ala Ala Glu Thr Ser Pro Pro Ser Asn Ile Ile Asp His Cys Glu
        275                 280                 285
Lys Leu Ala Ser Glu Lys Glu Val Val Glu Cys Gln Ser Thr Ser Thr
    290                 295                 300
Val Gly Gly Gln Ser Val Lys Lys Val Asp Leu Glu Thr Leu Lys Glu
305                 310                 315                 320
Asp Ser Glu Phe Thr Lys Val Glu Met Asp Asn Leu Asp Asn Ala Gln
                325                 330                 335
Thr Ser Gly Ile Glu Glu Pro Ser Glu Thr Lys Gly Ser Met Gln Lys
            340                 345                 350
Ser Lys Phe Lys Tyr Lys Leu Val Pro Glu Glu Glu Thr Thr Ala Ser
        355                 360                 365
Glu Asn Thr Glu Ile Thr Ser Glu Arg Gln Lys Glu Gly Ile Lys Leu
    370                 375                 380
Thr Ile Arg Ile Ser Ser Arg Lys Lys Lys Pro Asp Ser Pro Pro Lys
385                 390                 395                 400
Val Leu Glu Pro Glu Asn Lys Gln Glu Lys Thr Glu Lys Glu Glu Glu
                405                 410                 415
Lys Thr Asn Val Gly Arg Thr Leu Arg Arg Ser Pro Arg Ile Ser Arg
            420                 425                 430
Pro Thr Ala Lys Val Ala Glu Ile Arg Asp Gln Lys Ala Asp Lys Lys
        435                 440                 445
Arg Gly Glu Gly Glu Asp Glu Val Glu Glu Glu Ser Thr Ala Leu Gln
    450                 455                 460
Lys Thr Asp Lys Lys Glu Ile Leu Lys Lys Ser Glu Lys Asp Thr Asn
465                 470                 475                 480
Ser Lys Val Ser Lys Val Lys Pro Xaa Lys Ala Lys Phe Asp Gly Leu
                485                 490                 495
Val Leu Gly His Val Ala Asp Gly Asn Ile Pro Ala Met Met Lys Val
            500                 505                 510
Lys Gly Leu Ala Val Lys Asn His Leu Gln Leu Gln Lys Arg Arg Lys
        515                 520                 525
Lys Arg Lys Val Lys Lys Pro Ser Xaa Ala Asp Asp Asp Glu Pro Cys
    530                 535                 540
Lys Lys Cys Gly Leu Pro Asn His Pro Glu Leu Ile Leu Leu Cys Asp
545                 550                 555                 560
Ser Cys Asp Ser Gly Tyr His Thr Ala Cys Leu Arg Pro Pro Leu Met
                565                 570                 575
Ile Ile Pro Asp Gly Glu Trp Phe Cys Pro Pro Cys Gln His Lys Leu
            580                 585                 590
Leu Cys Glu Lys Leu Glu Glu Gln Leu Gln Asp Leu Asp Val Ala Leu
        595                 600                 605
Lys Lys Lys Glu Arg Ala Glu Arg Arg Lys Glu Arg Leu Val Tyr Val
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    610                 615                 620
Gly Ile Ser Ile Glu Asn Ile Ile Pro Pro Gln Glu Pro Asp Phe Ser
625                 630                 635                 640
Glu Asp Gln Glu Glu Lys Lys Lys Asp Ser Lys Lys Ser Lys Ala Asn
                645                 650                 655
Leu Leu Glu Arg Arg Ser Thr Arg Thr Arg Lys Cys Ile Ser Tyr Arg
            660                 665                 670
Phe Asp Glu Phe Asp Glu Ala Ile Asp Glu Ala Ile Glu Asp Asp Ile
        675                 680                 685
Lys Glu Ala Asp Gly Gly Gly Val Gly Arg Gly Lys Asp Ile Ser Thr
    690                 695                 700
Ile Thr Gly His Arg Gly Lys Asp Ile Ser Thr Ile Leu Asp Glu
705                 710                 715

<210> 4765
<211> 1707
<212> DNA
<213> Homo sapiens

<400> 4765
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agcctgcatt ctcaagcctc tgccacaact cggcatccag agccccggcg cacagagcac
120
agggctccct cttcaacgtg gcgaccagtg gccctgaccc tgctgacttt gtgcttggtg
180
ctgctgatag ggctggcagc cctggggctt ttgtttttc agtactacca gctctccaat
240
actggtcaag acaccatttc tcaaatggaa gaaagattag gaaatacgtc ccaagagttg
300
caatctcttc aagtccagaa tataaagctt gcaggaagtc tgcagcatgt ggctgaaaaa
360
ctctgtcgtg agctgtataa caaagctgga gcacacaggt gcagcccttg tacagaacaa
420
tggaaatggc atggagacaa ttgctaccag ttctataaag acagcaaaag ttgggaggac
480
tgtaaatatt tctgccttag tgaaaactct accatgctga agataaacaa acaagaagac
540
ctggaatttg ccgcgtctca gagctactct gagtttttct actcttattg gacagggctt
600
ttgcgccctg acagtggcaa ggcctggctg tggatggatg gaacccctttt cacttctgaa
660
ctgttccata ttataataga tgtcaccagc ccaagaagca gagactgtgt ggccatcctt
720
aatgggatga tcttctcaaa ggactgcaaa g attgaagc gttgtgtctg tgagagaagg
780
gcaggaatgg tgaagccaga gagcctccat gtcccccctg aaacattagg cgaaggtgac
840
tgattcgccc tctgcaacta caaatagcag agtgagccag gcggtgccaa agcaagggct
900
agttgagaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtacaaa
960
atgggttctc gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgcacg
1020
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tatttaacag tcacaagaag tcttatttac atgccaccaa ccaacctcag aaacccataa
1080
tgtcatctgc cttcttggct tagagataac ttttagctct ctttcttctc aatgtctaat
1140
atcacctccc tgttttcatg tcttccttac acttggtgga ataagaaact ttttgaagta
1200
gaggaaatac attgaggtaa catccttttc tctgacagtc aagtagtcca tcagaaattg
1260
gcagtcactt cccagattgt accagcaaat acacaaggaa ttctttttgt ttgtttcagt
1320
tcatactagt cccttcccaa tccatcagta aagaccccat ctgccttgtc catgccgttt
1380
cccaacaggg atgtcacttg atatgagaat ctcaaatctc aatgccttat aagcattcct
1440
tcctgtgtcc attaagactc tgataattgt ctcccctcca taggaatttc tcccaggaaa
1500
gaaatatatc cccatctccg tttcatatca gaactaccgt ccccgatatt cccttcagag
1560
agattaaaga ccagaaaaaa gtgagcctct tcatctgcac ctgtaatagt ttcagttcct
1620
attttcttcc attgacccat atttatacct ttcaggtact gaagatttaa taataataaa
1680
tgtaaatact gtgaaaaaaa aaaaaaa
1707

<210> 4766
<211> 280
<212> PRT
<213> Homo sapiens

<400> 4766
Leu Gln Ala Lys Tyr Asn Ser Thr Arg Asp Met Leu Asp Asp Asp Gly
1 5 10 15
Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
20 25 30
Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg
35 40 45
Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
50 55 60
Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn
65 70 75 80
Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr
85 90 95
Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
100 105 110
Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys
115 120 125
Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His
130 135 140
Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp
145 150 155 160
Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn
165 170 175
Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe

```
            180                 185                 190
Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala
        195                 200                 205
Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile
    210                 215                 220
Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu
225                 230                 235                 240
Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val
                245                 250                 255
Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro
            260                 265                 270
Pro Glu Thr Leu Gly Glu Gly Asp
        275                 280
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<210> 4767
<211> 1380
<212> DNA
<213> Homo sapiens

<400> 4767
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120
gacgtgagcg cctacagtgg gctcggggag gactctgcgg gcagtgccct ggaggaggac
180
gacgaagacg acgaggggga tggggagccc ccctacgagc ccgagtcggg gtgcgtggag
240
atcccggggc tgtcggagga ggaggaccca gccccgagcc ggaagatcca tttcagcacg
300
gcgcccatcc aagtgttcag cacttactcc aacgaggatt acgatcgtcg caacgaggat
360
gtggatccca tggcagcctc tgctgagtac gagctggaga agcgtgtgga gaggttggag
420
ctgttccctg tggagctgga gaaggactcc gagggcctgg gcatcagcat catcggcatg
480
ggcgccgggg cagacatggg cctggagaag ctgggtatct tcgtcaagac cgtgacggag
540
ggtggtgcgg cccatcggga tggcaggatc caggtgaatg atctcctggt ggaggtggat
600
ggaacaagtc tggtgggagt gacccagagc ttcgcggcgt ctgtgctccg gaacaccaag
660
ggccgagtgc ggtttatgat tggccgggag cggccgggag agcagagcga agtggcccag
720
ctaattcagc agactttgga acaggagcga tggcagcggg agatgatgga gcagagatac
780
gcccagtatg gggaggatga cgaggagacg ggagagtatg ccactgacga ggatgaggag
840
ctgagcccca cgttcccggg tggtgagatg gccatcgagg tgtttgagct agcggagaac
900
gaggatgcac tgtcccctgt ggacatggag cccgagaagc tggtgcacaa gttcaaggag
960
ctccagatca agcatgcggt cactgaggca gagatccagc agctgaaaag aaagctgcag
1020

agcctggagc aggagaaggg gcgctggcgg gtggagaagg cgcagttgga gcagagtgtg
1080
gaggagaaca aggagcgcat ggagaaactg gaaggctact ggggtgaggc ccagagcctg
1140
tgccaggctg tggacgagca cctgcgggag actcaggcgc agtaccaggc cctggagcgc
1200
aagtacagca aggccaagcg cctcatcaag gactaccagc agaaggagat cgagttcctg
1260
aaaaaggaga ctgcacagcg tcgggttctg gaggagtcgg agctggccag aaaggaggag
1320
atggacaagc tcctggacaa gatctcagaa ctggaaggaa acttgcaaac actgaggaat
1380

<210> 4768
<211> 460
<212> PRT
<213> Homo sapiens

<400> 4768
Xaa Arg Arg Gly Ala Val Ala Pro Pro Glu Arg Gly Val Gly Asn Gly
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Arg Ala Pro Glu Val Ala Pro Glu Glu Val Asp Glu Ser Lys Lys Glu
20 25 30
Asp Phe Ser Glu Ala Asp Leu Val Asp Val Ser Ala Tyr Ser Gly Leu
35 40 45
Gly Glu Asp Ser Ala Gly Ser Ala Leu Glu Glu Asp Asp Glu Asp Asp
50 55 60
Glu Gly Asp Gly Glu Pro Pro Tyr Glu Pro Glu Ser Gly Cys Val Glu
65 70 75 80
Ile Pro Gly Leu Ser Glu Glu Glu Asp Pro Ala Pro Ser Arg Lys Ile
85 90 95
His Phe Ser Thr Ala Pro Ile Gln Val Phe Ser Thr Tyr Ser Asn Glu
100 105 110
Asp Tyr Asp Arg Arg Asn Glu Asp Val Asp Pro Met Ala Ala Ser Ala
115 120 125
Glu Tyr Glu Leu Glu Lys Arg Val Glu Arg Leu Glu Leu Phe Pro Val
130 135 140
Glu Leu Glu Lys Asp Ser Glu Gly Leu Gly Ile Ser Ile Ile Gly Met
145 150 155 160
Gly Ala Gly Ala Asp Met Gly Leu Glu Lys Leu Gly Ile Phe Val Lys
165 170 175
Thr Val Thr Glu Gly Gly Ala Ala His Arg Asp Gly Arg Ile Gln Val
180 185 190
Asn Asp Leu Leu Val Glu Val Asp Gly Thr Ser Leu Val Gly Val Thr
195 200 205
Gln Ser Phe Ala Ala Ser Val Leu Arg Asn Thr Lys Gly Arg Val Arg
210 215 220
Phe Met Ile Gly Arg Glu Arg Pro Gly Glu Gln Ser Glu Val Ala Gln
225 230 235 240
Leu Ile Gln Gln Thr Leu Glu Gln Glu Arg Trp Gln Arg Glu Met Met
245 250 255
Glu Gln Arg Tyr Ala Gln Tyr Gly Glu Asp Asp Glu Glu Thr Gly Glu
260 265 270
Tyr Ala Thr Asp Glu Asp Glu Glu Leu Ser Pro Thr Phe Pro Gly Gly

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        275                 280                 285
Glu Met Ala Ile Glu Val Phe Glu Leu Ala Glu Asn Glu Asp Ala Leu
    290                 295                 300
Ser Pro Val Asp Met Glu Pro Glu Lys Leu Val His Lys Phe Lys Glu
305                 310                 315                 320
Leu Gln Ile Lys His Ala Val Thr Glu Ala Glu Ile Gln Gln Leu Lys
                325                 330                 335
Arg Lys Leu Gln Ser Leu Glu Gln Glu Lys Gly Arg Trp Arg Val Glu
            340                 345                 350
Lys Ala Gln Leu Glu Gln Ser Val Glu Glu Asn Lys Glu Arg Met Glu
        355                 360                 365
Lys Leu Glu Gly Tyr Trp Gly Glu Ala Gln Ser Leu Cys Gln Ala Val
    370                 375                 380
Asp Glu His Leu Arg Glu Thr Gln Ala Gln Tyr Gln Ala Leu Glu Arg
385                 390                 395                 400
Lys Tyr Ser Lys Ala Lys Arg Leu Ile Lys Asp Tyr Gln Gln Lys Glu
                405                 410                 415
Ile Glu Phe Leu Lys Lys Glu Thr Ala Gln Arg Arg Val Leu Glu Glu
            420                 425                 430
Ser Glu Leu Ala Arg Lys Glu Glu Met Asp Lys Leu Leu Asp Lys Ile
        435                 440                 445
Ser Glu Leu Glu Gly Asn Leu Gln Thr Leu Arg Asn
    450                 455                 460
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<210> 4769
<211> 1533
<212> DNA
<213> Homo sapiens

<400> 4769

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120
ggtcacacga ggggcatttt ccttgttgta agtgtagtct aaaccagtag gaaggaggtt
180
taattgccaa aaccagcgag aactcgggca ctgtggatac tacagtgggc agctgaacga
240
ggaccaagga gaatgtctaa gaggcctcca gccctgcgct cagtgaagac aggacaggaa
300
caacagagca tacatacctt ggaagggtgt gttctgatat actcgtatgg aaagttctga
360
caggtttttct ccctgggaag tgcagcacat accccaacac actggctctg ccagtgtgcc
420
aatcccagat ggtgcttgct ttgtgtgcac ccacacccaa acccctgccc tcccatatgc
480
tcttctgtgt gcccaggtag gccctgccct caggcagcag cttctgaaca cattcctctt
540
ggcgcagaca aaagaaagta cttcgtctgt ggaattcgag gctgagcctg agttctagca
600
caagaagacc gttgcagtcc agagatgaga aactggacca gaggcaaatc atgaacagaa
660
cgggagtcaa gagaaggggt ttctaagatg gagaagtggg ggcgggtgtg gatccagtgg
720
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gatgtggctt ccccaggttg caaccccaag gaagtctctg gaagcagcac cagtcctgat
780
gggggagcag aagagctgcc atcctcagtc agggtccgag tcagggtccg aggagagctg
840
ctgctccata gtctcgcaca tggcatcctg cagggacgta agatgacccc ggggactcat
900
ccccattggc tggatgactc tgttcctgtt ggggaaaggt gcagtggggc tggagagctt
960
gtcaaacatg gtcaccagct tcatggcctc gtgctccttc tgctcctctg tcatgccctc
1020
catagggtta ggcggcttct cctccaccct cccggtcaca gggtttatgc tggctttggc
1080
ttccttgtac tcatctgtgt ctgtgtcctc atcctctgag tactggccct cgggccggcc
1140
tcctgccatg aggcccctgg cagccagaag gccagcagca ttcccatagc ctgtgtactt
1200
gatgaatcgg ggcacactct cagagcacag gacaaacaag aactcggcag ccacctctt
1260
cacatctgtg tccaggtgtg tcatgaggcg gacaagcttg tttcggagca ggtcccccac
1320
ctcaggccga gtcctcacat cccgcagagg gggcaggacc tgggccttca ggaacttcct
1380
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1440
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1500
atccatatta actcccataa actctaagga tcc
1533

<210> 4770
<211> 237
<212> PRT
<213> Homo sapiens

<400> 4770
Met Gly Val Asn Met Asp Val Ile Asn Ala Leu Leu Ala Phe Leu Glu
1 5 10 15
Lys Arg Leu His Gln Thr His Arg Leu Lys Glu Cys Val Ala Pro Val
20 25 30
Leu Ser Val Leu Thr Glu Cys Ala Arg Met His Arg Pro Ala Arg Lys
35 40 45
Phe Leu Lys Ala Gln Val Leu Pro Pro Leu Arg Asp Val Arg Thr Arg
50 55 60
Pro Glu Val Gly Asp Leu Leu Arg Asn Lys Leu Val Arg Leu Met Thr
65 70 75 80
His Leu Asp Thr Asp Val Lys Arg Val Ala Ala Glu Phe Leu Phe Val
85 90 95
Leu Cys Ser Glu Ser Val Pro Arg Phe Ile Lys Tyr Thr Gly Tyr Gly
100 105 110
Asn Ala Ala Gly Leu Leu Ala Ala Arg Gly Leu Met Ala Gly Gly Arg
115 120 125
Pro Glu Gly Gln Tyr Ser Glu Asp Glu Asp Thr Asp Thr Asp Glu Tyr
130 135 140
Lys Glu Ala Lys Ala Ser Ile Asn Pro Val Thr Gly Arg Val Glu Glu

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145                 150                 155                 160
Lys Pro Pro Asn Pro Met Glu Gly Met Thr Glu Glu Gln Lys Glu His
                165                 170                 175
Glu Ala Met Lys Leu Val Thr Met Phe Asp Lys Leu Ser Ser Pro Thr
            180                 185                 190
Ala Pro Phe Pro Asn Arg Asn Arg Val Ile Gln Pro Met Gly Met Ser
        195                 200                 205
Pro Arg Gly His Leu Thr Ser Leu Gln Asp Ala Met Cys Glu Thr Met
    210                 215                 220
Glu Gln Gln Leu Ser Ser Asp Pro Asp Ser Asp Pro Asp
225                 230                 235
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<210> 4771
<211> 2653
<212> DNA
<213> Homo sapiens

<400> 4771
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120
tgggcaccac aggtaaggca ctgcctgggg gctggaggag gctggaggag gatgcccaag
180
ctccccacac tcctcacccc agaccgggga agctggatat cctccgtgtt gtcctctccc
240
catagctggt ctgaggctgt ggtttacacg caggcacagg taggcgattc tgagcatcaa
300
cgcagatgga ggggagggtg agccgtcgtg ggagaactgg cccaagacca gcacctggct
360
ggtgtcgcca gccccggctg cattggtggg tgaggcaggt ctggctggag tctgggtctg
420
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480
gaggcagcag gcacctagtg gtgccactgg gacacccggc tccaggactc cggatgtcac
540
acatgcgtga gtcttggcgt ctacaccccc ctcggggcca gtgggtgagc agtggcccgt
600
ggtccccgcc agagctcccc cagagtggac ttggctccgc cggacacagt gccctgctct
660
gagctgccgc tggctgctcc acgtctgaga ccacgcgacg ttgcctcatg aactgacgtg
720
gacagcagca ggggagacgc tgggtggttc tgtggccaag cacagcccgt gtcaggagca
780
caggccgtgc cctttcccag ggggcacact gggcatttct caatggcctt cacaggacgc
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aaaggggcac acagaggcag tggggaagct ggagttcttg ggctggcagg gaatggtggc
900
agccttcttg gccttcatga agggcctggc ttgctgggct aaggtcacag tgttctgagg
960
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1020
cccaggctag accctccata cacacccagg ctagaccctc catactcacc caggctagac
1080

cctccataca cacccaggct agaccctcca tactcaccca ggctagaccc tccatactca
1140
cccaggctag atcctccata cacacccagg ctagactctc cgtactcacc caggctagat
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1260
cccaggctag accctccgta cacacccaga ctagaggctt ggggctgaga aaagcagtca
1320
tgcctcctca ggaattacca gcagagaatg cccagccctc ttgatagtag caataattaa
1380
taggtttatc cccaaaggag cggaagctgt ggaatcctcc ccggcaatag gtcttagggt
1440
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1500
tctatcccac ccaccagccg gcccccaggc ctcccttcct cagtccttcc aggatatcgt
1560
cagggaggtt ctgggatccc caagtggtcc gaatccgggc tctaaggagt gtccgtggca
1620
tataaattag actctgctgt ggcaataaat aagaagctgg aaaaggaaaa agaaaagtta
1680
aagcaagaaa gactagagaa aataaaacag cgtgataaga ggctggagtg ggaaatgatg
1740
tgcagagtaa agccagatgt tgtccaagac aaagagacag agagaaatct tcagagaatt
1800
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1860
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1920
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1980
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2040
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2100
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2160
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2220
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2280
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2340
ataattttaa gcattgttcc tcagaacatt tgtaaaagga tatatttctg cttgaccagc
2400
gagatgtgca ttttgccagg atcatattgg tcatgtctat tggtgtatta tttcagtatc
2460
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2520
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2640
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2653

<210> 4772
<211> 182
<212> PRT
<213> Homo sapiens

<400> 4772
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20 25 30
Ile Lys Gln Arg Asp Lys Arg Leu Glu Trp Glu Met Met Cys Arg Val
35 40 45
Lys Pro Asp Val Val Gln Asp Lys Glu Thr Glu Arg Asn Leu Gln Arg
50 55 60
Ile Ala Thr Arg Gly Val Val Gln Leu Phe Asn Ala Val Gln Lys His
65 70 75 80
Gln Lys Asn Val Asp Glu Lys Val Lys Glu Ala Gly Ser Ser Met Arg
85 90 95
Lys Arg Ala Lys Leu Ile Ser Thr Val Ser Lys Lys Asp Phe Ile Ser
100 105 110
Val Leu Arg Gly Met Asp Gly Ser Thr Asn Glu Thr Ala Ser Ser Arg
115 120 125
Lys Lys Pro Lys Ala Lys Gln Thr Glu Val Lys Ser Glu Glu Gly Pro
130 135 140
Gly Trp Thr Ile Leu Arg Asp Asp Phe Met Met Gly Ala Ser Met Lys
145 150 155 160
Asp Trp Asp Lys Glu Ser Asp Gly Pro Asp Asp Ser Arg Pro Glu Ser
165 170 175
Ala Ser Asp Ser Asp Thr
180

<210> 4773
<211> 319
<212> DNA
<213> Homo sapiens

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<210> 4774
<211> 91
<212> PRT

<213> Homo sapiens

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Pro Asn Pro Ser Ser Leu Phe Pro Pro Ser Pro Gln Ala Arg Ala Ala
35 40 45
Met Gly Trp Arg Val Leu Ala Trp Thr Gln His Pro Ile Ser Ser Ala
50 55 60
Leu Ser Leu Asp Pro Ala Ser His Leu Leu Ser Ser Gln Gly Gly Gly
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Ser Trp Glu Pro His Pro Gln Pro Leu His Ala
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<210> 4775
<211> 433
<212> DNA
<213> Homo sapiens

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180
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300
cccttgcact tgctctctct gcttctccta actatacatg cggctcatcc tgtaacttcc
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<210> 4776
<211> 97
<212> PRT
<213> Homo sapiens

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35 40 45
Thr Ala Thr Ser Leu Pro Leu His Leu Leu Ser Leu Leu Leu Leu Thr
50 55 60
Ile His Ala Ala His Pro Val Thr Ser Phe Gln Phe Leu Leu Thr Phe

65 70 75 80
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Asn

<210> 4777
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<212> DNA
<213> Homo sapiens

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420
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540
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600
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660
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2100
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<210> 4778
<211> 144
<212> PRT
<213> Homo sapiens

<400> 4778
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20 25 30
Arg Ala Glu Asn Arg Glu Leu Gly Lys Arg Val Gln Ala Leu Gln Glu
35 40 45
Glu Ser Arg Tyr Leu Arg Ala Val Leu Ala Asn Glu Thr Gly Leu Ala
50 55 60
Arg Leu Leu Ser Arg Leu Ser Gly Val Gly Leu Arg Leu Thr Thr Ser
65 70 75 80
Leu Phe Arg Asp Ser Pro Ala Gly Asp His Asp Tyr Ala Leu Pro Val
85 90 95
Gly Lys Gln Lys Gln Asp Leu Leu Glu Glu Asp Asp Ser Ala Gly Gly
100 105 110
Val Cys Leu His Val Asp Lys Asp Lys Val Ser Val Glu Phe Cys Ser

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<210> 4779
<211> 4467
<212> DNA
<213> Homo sapiens

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420
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<210> 4780

<211> 1241
<212> PRT
<213> Homo sapiens

<400> 4780
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Ser Asp Pro Ser Asp Gly Gln Arg Arg Arg Gln Gln Gln Gln Gln Gln
35 40 45
Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Gln Gln Pro Gln Val Leu
50 55 60
Ser Ser Glu Gly Gly Gln Leu Arg His Asn Pro Leu Asp Ile Gln Met
65 70 75 80
Leu Ser Arg Gly Leu His Glu Gln Ile Phe Gly Gln Gly Gly Glu Met
85 90 95
Pro Gly Glu Ala Ala Val Arg Arg Ser Val Glu His Leu Gln Lys His
100 105 110
Gly Leu Trp Gly Gln Pro Ala Val Pro Leu Pro Asp Val Glu Leu Arg
115 120 125
Leu Pro Pro Leu Tyr Gly Asp Asn Leu Asp Gln His Phe Arg Leu Leu
130 135 140
Ala Gln Lys Gln Ser Leu Pro Tyr Leu Glu Ala Ala Asn Leu Leu Leu
145 150 155 160
Gln Ala Gln Leu Pro Pro Lys Pro Pro Ala Trp Ala Trp Ala Glu Gly
165 170 175
Trp Thr Arg Tyr Gly Pro Glu Gly Glu Ala Val Pro Val Ala Ile Pro
180 185 190
Glu Glu Arg Ala Leu Val Phe Asp Val Glu Val Cys Leu Ala Glu Gly
195 200 205
Thr Cys Pro Thr Leu Ala Val Ala Ile Ser Pro Ser Ala Trp Tyr Ser
210 215 220
Trp Cys Ser Gln Arg Leu Val Glu Glu Arg Tyr Ser Trp Thr Ser Gln
225 230 235 240
Leu Ser Pro Ala Asp Leu Ile Pro Leu Glu Val Pro Thr Gly Ala Ser
245 250 255
Ser Pro Thr Gln Arg Asp Trp Gln Glu Gln Leu Val Val Gly His Asn
260 265 270
Val Ser Phe Asp Arg Ala His Ile Arg Glu Gln Tyr Leu Ile Gln Gly
275 280 285
Ser Arg Met Arg Phe Leu Asp Thr Met Ser Met His Met Ala Ile Ser
290 295 300
Gly Leu Ser Ser Phe Gln Arg Ser Leu Trp Ile Ala Ala Lys Gln Gly
305 310 315 320
Lys His Lys Val Gln Pro Pro Thr Lys Gln Gly Gln Lys Ser Gln Arg
325 330 335
Lys Ala Arg Arg Gly Pro Ala Ile Ser Ser Trp Asp Trp Leu Asp Ile
340 345 350
Ser Ser Val Asn Ser Leu Ala Glu Val His Arg Leu Tyr Val Gly Gly
355 360 365
Pro Pro Leu Glu Lys Glu Pro Arg Glu Leu Phe Val Lys Gly Thr Met
370 375 380
Lys Asp Ile Arg Glu Asn Phe Gln Asp Leu Met Gln Tyr Cys Ala Gln

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Asp Val Trp Ala Thr His Glu Val Phe Gln Gln Gln Leu Pro Leu Phe
                405                 410                 415
Leu Glu Arg Cys Pro His Pro Val Thr Leu Ala Gly Met Leu Glu Met
            420                 425                 430
Gly Val Ser Tyr Leu Pro Val Asn Gln Asn Trp Glu Arg Tyr Leu Ala
        435                 440                 445
Glu Ala Gln Gly Thr Tyr Glu Glu Leu Gln Arg Glu Met Lys Lys Ser
    450                 455                 460
Leu Met Asp Leu Ala Asn Asp Ala Cys Gln Leu Leu Ser Gly Glu Arg
465                 470                 475                 480
Tyr Lys Glu Asp Pro Trp Leu Trp Asp Leu Glu Trp Asp Leu Gln Glu
                485                 490                 495
Phe Lys Gln Lys Lys Ala Lys Lys Val Lys Lys Glu Pro Ala Thr Ala
            500                 505                 510
Ser Lys Leu Pro Ile Glu Gly Ala Gly Ala Pro Gly Asp Pro Met Asp
        515                 520                 525
Gln Glu Asp Leu Gly Pro Cys Ser Glu Glu Glu Glu Phe Gln Gln Asp
    530                 535                 540
Val Met Ala Arg Ala Cys Leu Gln Lys Leu Lys Gly Thr Thr Glu Leu
545                 550                 555                 560
Leu Pro Lys Arg Pro Gln His Leu Pro Gly His Pro Gly Trp Tyr Arg
                565                 570                 575
Lys Leu Cys Pro Arg Leu Asp Asp Pro Ala Trp Thr Pro Gly Pro Ser
            580                 585                 590
Leu Leu Ser Leu Gln Met Arg Val Thr Pro Lys Leu Met Ala Leu Thr
        595                 600                 605
Trp Asp Gly Phe Pro Leu His Tyr Ser Glu Arg His Gly Trp Gly Tyr
    610                 615                 620
Leu Val Pro Gly Arg Arg Asp Asn Leu Ala Lys Leu Pro Thr Gly Thr
625                 630                 635                 640
Thr Leu Glu Ser Ala Gly Val Val Cys Pro Tyr Arg Ala Ile Glu Ser
                645                 650                 655
Leu Tyr Arg Lys His Cys Leu Glu Gln Gly Lys Gln Gln Leu Met Pro
            660                 665                 670
Gln Glu Ala Gly Leu Ala Glu Glu Phe Leu Leu Thr Asp Asn Ser Ala
        675                 680                 685
Ile Trp Gln Thr Val Glu Glu Leu Asp Tyr Leu Glu Val Glu Ala Glu
    690                 695                 700
Ala Lys Met Glu Asn Leu Arg Ala Ala Val Pro Gly Gln Pro Leu Ala
705                 710                 715                 720
Leu Thr Ala Arg Gly Gly Pro Lys Asp Thr Gln Pro Ser Tyr His His
                725                 730                 735
Gly Asn Gly Pro Tyr Asn Asp Val Asp Ile Pro Gly Cys Trp Phe Phe
            740                 745                 750
Lys Leu Pro His Lys Asp Gly Asn Ser Cys Asn Val Gly Ser Pro Phe
        755                 760                 765
Ala Lys Asp Phe Leu Pro Lys Met Glu Asp Gly Thr Leu Gln Ala Gly
    770                 775                 780
Pro Gly Gly Ala Ser Gly Pro Arg Ala Leu Glu Ile Asn Lys Met Ile
785                 790                 795                 800
Ser Phe Trp Arg Asn Ala His Lys Arg Ile Ser Ser Gln Met Val Val
                805                 810                 815
Trp Leu Pro Arg Ser Ala Leu Pro Arg Ala Val Ile Arg His Pro Asp
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Tyr Asp Glu Glu Gly Leu Tyr Gly Ala Ile Leu Pro Gln Val Val Thr
        835                 840                 845
Ala Gly Thr Ile Thr Arg Arg Ala Val Glu Pro Thr Trp Leu Thr Ala
    850                 855                 860
Ser Asn Ala Arg Pro Asp Arg Val Gly Ser Glu Leu Lys Ala Met Val
865                 870                 875                 880
Gln Ala Pro Pro Gly Tyr Thr Leu Val Gly Ala Asp Val Asp Ser Gln
                885                 890                 895
Glu Leu Trp Ile Ala Ala Val Leu Gly Asp Ala His Phe Ala Gly Met
            900                 905                 910
His Gly Cys Thr Ala Phe Gly Trp Met Thr Leu Gln Gly Arg Lys Ser
        915                 920                 925
Arg Gly Thr Asp Leu His Ser Lys Thr Ala Thr Thr Val Gly Ile Ser
    930                 935                 940
Arg Glu His Ala Lys Ile Phe Asn Tyr Gly Arg Ile Tyr Gly Ala Gly
945                 950                 955                 960
Gln Pro Phe Ala Glu Arg Leu Leu Met Gln Phe Asn His Arg Leu Thr
                965                 970                 975
Gln Gln Glu Ala Ala Glu Lys Ala Gln Gln Met Tyr Ala Ala Thr Lys
            980                 985                 990
Gly Leu Arg Trp Tyr Arg Leu Ser Asp Glu Gly Glu Trp Leu Val Arg
        995                 1000                1005
Glu Leu Asn Leu Pro Val Asp Arg Thr Glu Gly Gly Trp Ile Ser Leu
    1010                1015                1020
Gln Asp Leu Arg Lys Val Gln Arg Glu Thr Ala Arg Lys Ser Gln Trp
1025                1030                1035                1040
Lys Lys Trp Glu Val Val Ala Glu Arg Ala Trp Lys Gly Gly Thr Glu
                1045                1050                1055
Ser Glu Met Phe Asn Lys Leu Glu Ser Ile Ala Thr Ser Asp Ile Pro
            1060                1065                1070
Arg Thr Pro Val Leu Gly Cys Cys Ile Ser Arg Ala Leu Glu Pro Ser
        1075                1080                1085
Ala Val Gln Glu Glu Phe Met Thr Ser Arg Val Asn Trp Val Val Gln
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Ser Ser Ala Val Asp Tyr Leu His Leu Met Leu Val Ala Met Lys Trp
1105                1110                1115                1120
Leu Phe Glu Glu Phe Ala Ile Asp Gly Arg Phe Cys Ile Ser Ile His
                1125                1130                1135
Asp Glu Val Arg Tyr Leu Val Arg Glu Glu Asp Arg Tyr Arg Ala Ala
            1140                1145                1150
Leu Ala Leu Gln Ile Thr Asn Leu Leu Thr Arg Cys Met Phe Ala Tyr
        1155                1160                1165
Lys Leu Gly Leu Asn Asp Leu Pro Gln Ser Val Ala Phe Phe Ser Ala
    1170                1175                1180
Val Asp Ile Tyr Arg Cys Leu Arg Lys Glu Val Thr Met Asp Cys Lys
1185                1190                1195                1200
Thr Pro Ser Asn Pro Thr Gly Met Glu Arg Arg Tyr Gly Ile Pro Gln
                1205                1210                1215
Gly Glu Ala Leu Asp Ile Tyr Gln Ile Ile Glu Leu Thr Lys Gly Ser
            1220                1225                1230
Leu Glu Lys Arg Ser Gln Pro Gly Pro
        1235                1240
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<210> 4781
<211> 344
<212> DNA
<213> Homo sapiens

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120
gggggccaga ccaggaagct gacggcctcc aggacggtgt cagagaagca ccagggcaaa
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240
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344

<210> 4782
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<212> PRT
<213> Homo sapiens

<400> 4782
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Gln Gly Asn Gly Gly Gln Thr Arg Lys Leu Thr Ala Ser Arg Thr Val
        35   40   45
Ser Glu Lys His Gln Gly Lys Ala Ala Thr Thr Ala Lys Thr Leu Ile
    50   55   60
Pro Lys Ser Gln His Arg Met Leu Ala Pro Thr Gly Ala Val Ser Thr
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Arg Thr Arg Gln Lys Gly Val Thr Thr Ala Val Ile Pro Pro Lys Glu
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Lys Lys Pro Gln Ala Thr Pro Pro Pro Ala Pro Phe Gln
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<210> 4783
<211> 1143
<212> DNA
<213> Homo sapiens

<400> 4783
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1143

<210> 4784
<211> 212
<212> PRT
<213> Homo sapiens

<400> 4784
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Ala Leu Asn Leu Ser Leu Cys Lys Gln Ile Thr Asp Ser Ser Leu Gly
35 40 45
Arg Ile Ala Gln Tyr Leu Lys Gly Leu Glu Val Leu Glu Leu Gly Gly
50 55 60
Cys Ser Asn Ile Thr Asn Thr Gly Leu Leu Leu Ile Ala Trp Gly Leu
65 70 75 80
Gln Arg Leu Lys Ser Leu Asn Leu Arg Ser Cys Arg His Leu Ser Asp
85 90 95
Val Gly Ile Gly His Leu Ala Gly Met Thr Arg Ser Ala Ala Glu Gly
100 105 110
Cys Leu Gly Leu Glu Gln Leu Thr Leu Gln Asp Cys Gln Lys Leu Thr

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Asp Leu Ser Leu Lys His Ile Ser Arg Gly Leu Thr Gly Leu Arg Leu
    130                 135                 140
Leu Asn Leu Ser Phe Cys Gly Gly Ile Ser Asp Ala Gly Leu Leu His
145                 150                 155                 160
Leu Ser His Met Gly Ser Leu Arg Ser Leu Asn Leu Arg Ser Cys Asp
                165                 170                 175
Asn Ile Ser Asp Thr Gly Ile Met His Leu Ala Met Gly Ser Leu Arg
            180                 185                 190
Leu Ser Gly Leu Asp Val Ser Phe Cys Asp Lys Val Gly Asp Gln Ser
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<210> 4785
<211> 3289
<212> DNA
<213> Homo sapiens

<400> 4785

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<210> 4786
<211> 322
<212> PRT
<213> Homo sapiens

<400> 4786
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Val Gly Ala Asp Asn Val Gly Ser Lys Gln Met Gln Gln Ile Arg Met
35 40 45
Ser Leu Arg Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met
50 55 60
Arg Lys Ala Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Lys
65 70 75 80
Leu Leu Pro His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu
85 90 95
Asp Leu Thr Glu Ile Arg Asp Met Leu Leu Ala Asn Lys Val Pro Ala
100 105 110
Ala Ala Arg Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala
115 120 125
Gln Asn Thr Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu
130 135 140
Gly Ile Thr Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp
145 150 155 160
Val Gln Leu Ile Lys Thr Gly Asp Lys Val Gly Ala Ser Glu Ala Thr
165 170 175
Leu Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Phe Gly Leu Val Ile
180 185 190
Gln Gln Val Phe Asp Asn Gly Ser Ile Tyr Asn Pro Glu Val Leu Asp

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        195                 200                 205
Ile Thr Glu Glu Thr Leu His Ser Arg Phe Leu Glu Gly Val Arg Asn
    210                 215                 220
Val Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr Val Ala Ser Val
225                 230                 235                 240
Pro His Ser Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Leu Ser Val
                245                 250                 255
Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val Lys Ala Phe Leu
            260                 265                 270
Ala Asp Pro Ser Ala Phe Val Ala Ala Ala Pro Val Ala Ala Ala Thr
        275                 280                 285
Thr Ala Ala Pro Ala Ala Ala Ala Ala Ala Ala Pro Ala Lys Val Glu
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Ala Lys Glu Glu Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu
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<210> 4787
<211> 1258
<212> DNA
<213> Homo sapiens

<400> 4787
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<210> 4788
<211> 197
<212> PRT
<213> Homo sapiens

<400> 4788
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Pro Gly Pro Ser Ser Ser Ile Gly Ser Pro Gln Ala Ser Ser Pro Pro
35 40 45
Arg Pro Asn His Tyr Leu Leu Ile Asp Thr Gln Gly Val Pro Tyr Thr
50 55 60
Val Leu Val Asp Glu Glu Ser Gln Arg Glu Pro Gly Ala Ser Gly Ala
65 70 75 80
Pro Gly Gln Lys Lys Cys Tyr Ser Cys Pro Val Cys Ser Arg Val Phe
85 90 95
Glu Tyr Met Ser Tyr Leu Gln Arg His Ser Ile Thr His Ser Glu Val
100 105 110
Lys Pro Phe Glu Cys Asp Ile Cys Gly Lys Ala Phe Lys Arg Ala Ser
115 120 125
His Leu Ala Arg His His Ser Ile His Leu Ala Gly Gly Gly Arg Pro
130 135 140
His Gly Cys Pro Leu Cys Pro Arg Arg Phe Arg Asp Ala Gly Glu Leu
145 150 155 160
Ala Gln His Ser Arg Val His Ser Gly Glu Arg Pro Phe Gln Cys Pro
165 170 175
His Cys Pro Arg Arg Phe Met Glu Gln Asn Thr Leu Gln Lys His Thr
180 185 190
Arg Trp Lys His Pro
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<210> 4789
<211> 1515
<212> DNA
<213> Homo sapiens

<400> 4789
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<210> 4790
<211> 241
<212> PRT

<213> Homo sapiens

<400> 4790

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            20                  25                  30
Pro Glu Glu Leu Gly His Phe Tyr Asp Tyr Pro Met Ala Leu Phe Ser
        35                  40                  45
Thr Phe Glu Leu Phe Leu Thr Ile Ile Asp Gly Pro Ala Asn Tyr Asn
    50                  55                  60
Val Asp Leu Pro Phe Met Tyr Ser Ile Thr Tyr Ala Ala Phe Ala Ile
65                  70                  75                  80
Ile Ala Thr Leu Leu Met Leu Asn Leu Leu Ile Ala Met Met Gly Asp
                85                  90                  95
Thr His Trp Arg Val Ala His Glu Arg Asp Glu Leu Trp Arg Ala Gln
            100                 105                 110
Ile Val Ala Thr Thr Val Met Leu Glu Arg Lys Leu Pro Arg Cys Leu
        115                 120                 125
Trp Pro Arg Ser Gly Ile Cys Gly Arg Glu Tyr Gly Leu Gly Asp Arg
    130                 135                 140
Trp Phe Leu Arg Val Glu Asp Arg Gln Asp Leu Asn Arg Gln Arg Ile
145                 150                 155                 160
Gln Arg Tyr Ala Gln Ala Phe His Thr Arg Gly Ser Glu Asp Leu Asp
                165                 170                 175
Lys Asp Ser Val Glu Lys Leu Glu Leu Gly Cys Pro Phe Ser Pro His
            180                 185                 190
Leu Ser Leu Pro Met Pro Ser Val Ser Arg Ser Thr Ser Arg Ser Ser
        195                 200                 205
Ala Asn Trp Glu Arg Leu Arg Gln Gly Thr Leu Arg Arg Asp Leu Arg
    210                 215                 220
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<210> 4791
<211> 4481
<212> DNA
<213> Homo sapiens

<400> 4791

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360
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Pro Ser Arg Tyr Thr Lys Ile Asn Ser Arg Trp Ile Lys Asp Leu Asn
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Ala Ile Thr Thr Lys Thr Lys Ile Asp Lys Trp Asp Leu Ile Lys Leu
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Asn Asn Phe Cys Thr Ala Lys Glu Thr Ile Asn Arg Val Asp Arg Gln

130 135 140
Pro Thr Glu Trp Glu Lys Val Leu Ala Trp Glu Lys Ile Phe Ser Asn
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Gln Ile Tyr

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Thr Ser Ser Val Ala Gly Arg Gln Pro Gly Ala Phe Ser Glu Glu Lys
50 55 60
Gly Pro Val Ile Ile Pro Gln Met Leu Leu Glu Leu Trp Ala Gln Gly
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<210> 4795
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<212> PRT

<213> Homo sapiens

<400> 4796

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Lys Leu Thr Gln Asn Gly Thr Arg Ser Gln Trp Gly Leu Ser Leu Pro
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<212> DNA
<213> Homo sapiens

<400> 4797

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Gly Gly Cys Val Met Thr Ile Gly Glu Met Leu Arg Ser Phe Leu Thr
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Lys Leu Glu Trp Phe Ser Thr Leu Phe Pro Arg Ile Pro Val Pro Val
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Gln Lys Asn Ile Asp Gln Gln Ile Lys Thr Arg Pro Arg Lys Ile Lys
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Arg Glu Ala Lys Glu Arg Glu Lys Glu Arg Arg Arg Ser Arg Ser Ile
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Asp Arg Gly Leu Glu Arg Arg Arg Ser Arg Ser Arg Glu Arg His Arg
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Tyr Asp Lys Glu Arg Gly Asn Glu Arg Glu Lys Glu Arg Glu Arg Ser
225 230 235 240
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Asp Ser Lys Lys Glu Lys Lys His Ser Arg Ser Arg Ser Arg Glu Arg

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Asp Ser Lys Asp Gln Ser Asp Lys His Asp Arg Arg Arg Ser Gln Ser
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cagttccccc cttcttgtga gactggtcca ggcagccctt ctggacactg catgatca
358

<210> 4800
<211> 119
<212> PRT
<213> Homo sapiens

<400> 4800
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Ala Ser Leu Ala Gly Glu Arg Val Ala Leu Asp His Leu Ser Gly Arg
 1               5                  10                  15
Ser Gln Asp Pro Leu Ser Val Leu Leu Pro Arg Gly Leu Leu Arg Leu
            20                  25                  30
Pro Pro Cys Gly His Arg Gly Ala Leu Asp Gln Pro His His Arg Val
        35                  40                  45
Ala Gln Pro His Leu Gln Val Val Arg Gln Arg Ser Pro Pro Ala Ser
    50                  55                  60
Trp Ser Pro Pro Pro Arg Ala Leu Ser His Val Phe Leu Phe Gly Asp
65                  70                  75                  80
Arg Pro Phe Trp Trp Val His Glu Ser Gly Tyr Tyr Ser Gln Ala Pro
```

```
                85                  90                  95
Ala Gln Val His Gln Phe Pro Ser Ser Cys Glu Thr Gly Pro Gly Ser
            100                 105                 110
Pro Ser Gly His Cys Met Ile
        115
```

<210> 4801
<211> 1447
<212> DNA
<213> Homo sapiens

<400> 4801
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agccggggcc tggtcggcag ctgggccgcc atggagtcca cgctgggcgc gggcatcgtg
120
atagccgagg cgctacagaa ccagctagcc tggctggaga acgtgtggct ctggatcacc
180
tttctgggcg atcccaagat cctctttctg ttctacttcc ccgcggccta ctacgcctcc
240
cgccgtgtgg gcatcgcggt gctctggatc agcctcatca ccgagtggct caacctcatc
300
ttcaagtggt ttctttttgg agacaggccc ttttggtggg tccatgagtc tggttactac
360
agccaggctc cagcccaggt tcaccagttc ccctcttctt gtgagactgg tccaggcagc
420
ccttctggac actgcatgat cacaggagca gccctctggc ccataatgac agccctgtct
480
tcgcaggtgg ccactcgggc ccgcagccgc tgggtaaggg tgatgcctag cctggcttat
540
tgcaccttcc ttttggcggt tggcttgtcg cgaatcttca tcttagcaca tttccctcac
600
caggtgctgg ctggcctaat aactggcgct gtcctgggct ggctgatgac tnnccccgag
660
tgcctatgga gcgggagcnt aagcttctat gggttgactg cactggccct catgctaggc
720
accagcctca tctattggac cctctttaca ctgggcctgg atctttcttg gtccatcagc
780
ctagccttca agtggtgtga gcggcctgag tggatacacg tggatagccg gccctttgcc
840
tccctgagcc gtgactcagg ggctgccctg ggcctgggca ttgccttgca ctctccctgc
900
tatgcccagg tgcgtcgggc acagctggga aatggccaga agatagcctg ccttgtgctg
960
gccatggggc tgctgggccc cctggactgg ctgggccacc cccctcagat cagcctcttc
1020
tacattttca atttcctcaa gtacaccctc tggccatgcc tagtcctggc cctcgtgccc
1080
tgggcagtgc acatgttcag tgcccaggaa gcaccgccca tccactcttc ctgacttctt
1140
gtgtgcctcc ctttcctttc cctcccacaa agccaacact ctgtgaccac cacactccag
1200
gaggcagccc catccccttc cagcccctaa gtaggccctc ccctccctaa atctgcttcc
1260

gcaccacctg gtcttagccc caaagatggg ccttctctct cccagataag ttggtcctcc
1320
ctctgccttt cctctcaagc ccccaaagag caaaggcaac agcaagacca gcgggttctt
1380
gcaacactgt gaggggcagc cagggcggcc ccaataaagc ccttgaatac tttgaaaaaa
1440
aaaaaaa
1447

<210> 4802
<211> 377
<212> PRT
<213> Homo sapiens

<400> 4802
Leu Glu Ile Arg Gly Ser Thr Leu Leu Arg Cys Leu Asp Ser Gly Phe
1 5 10 15
Arg Pro Gly Ala Ser Arg Gly Leu Val Gly Ser Trp Ala Ala Met Glu
20 25 30
Ser Thr Leu Gly Ala Gly Ile Val Ile Ala Glu Ala Leu Gln Asn Gln
35 40 45
Leu Ala Trp Leu Glu Asn Val Trp Leu Trp Ile Thr Phe Leu Gly Asp
50 55 60
Pro Lys Ile Leu Phe Leu Phe Tyr Phe Pro Ala Ala Tyr Tyr Ala Ser
65 70 75 80
Arg Arg Val Gly Ile Ala Val Leu Trp Ile Ser Leu Ile Thr Glu Trp
85 90 95
Leu Asn Leu Ile Phe Lys Trp Phe Leu Phe Gly Asp Arg Pro Phe Trp
100 105 110
Trp Val His Glu Ser Gly Tyr Tyr Ser Gln Ala Pro Ala Gln Val His
115 120 125
Gln Phe Pro Ser Ser Cys Glu Thr Gly Pro Gly Ser Pro Ser Gly His
130 135 140
Cys Met Ile Thr Gly Ala Ala Leu Trp Pro Ile Met Thr Ala Leu Ser
145 150 155 160
Ser Gln Val Ala Thr Arg Ala Arg Ser Arg Trp Val Arg Val Met Pro
165 170 175
Ser Leu Ala Tyr Cys Thr Phe Leu Leu Ala Val Gly Leu Ser Arg Ile
180 185 190
Phe Ile Leu Ala His Phe Pro His Gln Val Leu Ala Gly Leu Ile Thr
195 200 205
Gly Ala Val Leu Gly Trp Leu Met Thr Xaa Pro Glu Cys Leu Trp Ser
210 215 220
Gly Ser Xaa Ser Phe Tyr Gly Leu Thr Ala Leu Ala Leu Met Leu Gly
225 230 235 240
Thr Ser Leu Ile Tyr Trp Thr Leu Phe Thr Leu Gly Leu Asp Leu Ser
245 250 255
Trp Ser Ile Ser Leu Ala Phe Lys Trp Cys Glu Arg Pro Glu Trp Ile
260 265 270
His Val Asp Ser Arg Pro Phe Ala Ser Leu Ser Arg Asp Ser Gly Ala
275 280 285
Ala Leu Gly Leu Gly Ile Ala Leu His Ser Pro Cys Tyr Ala Gln Val
290 295 300
Arg Arg Ala Gln Leu Gly Asn Gly Gln Lys Ile Ala Cys Leu Val Leu

```
305                 310                 315                 320
Ala Met Gly Leu Leu Gly Pro Leu Asp Trp Leu Gly His Pro Pro Gln
                325                 330                 335
Ile Ser Leu Phe Tyr Ile Phe Asn Phe Leu Lys Tyr Thr Leu Trp Pro
            340                 345                 350
Cys Leu Val Leu Ala Leu Val Pro Trp Ala Val His Met Phe Ser Ala
        355                 360                 365
Gln Glu Ala Pro Pro Ile His Ser Ser
    370                 375
```

<210> 4803
<211> 564
<212> DNA
<213> Homo sapiens

<400> 4803
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ataaaaaaag agagagagtg cctgtgtgca catgctgccc tgtacctagc cacatgactt
120
ccaaaacctg ctaatgcctg atttccatta cgtgctactc ctcaaatggc agcggcttct
180
gaatattaca gagatggtgt gctgtttgct tttctctttt gttgtagcat aaaactgttc
240
attttagctt agtgacattt gtcaagaata gcaacctttt tgcttccaag ggacttgaag
300
gaagttaaat ttagatgctt tcctctcttc ttattttgtg gaggtatttc ctgttcagta
360
gcaaatcagt tatagaatat attagcattg ttatatttta aactaatgac taatcatttc
420
agctttattc atactgttgc attttatatt tcacagggag caatagaaaa agtgaaagaa
480
agtgacaaac tagttgcaac aagtaaaatc accctacaag acaaacagaa catggtgaag
540
agagtcagca tcatgtctta cgcg
564

<210> 4804
<211> 53
<212> PRT
<213> Homo sapiens

<400> 4804
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Met Thr Asn His Phe Ser Phe Ile His Thr Val Ala Phe Tyr Ile Ser
 1               5                  10                  15
Gln Gly Ala Ile Glu Lys Val Lys Glu Ser Asp Lys Leu Val Ala Thr
            20                  25                  30
Ser Lys Ile Thr Leu Gln Asp Lys Gln Asn Met Val Lys Arg Val Ser
        35                  40                  45
Ile Met Ser Tyr Ala
    50
```

<210> 4805
<211> 1619

<212> DNA
<213> Homo sapiens

<400> 4805
ggccttggat acctggcccg ggatgctggg cggcgtcagg taaccatgga gaaagagctg
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cggagtacca ttcttttcaa tgcctacaaa aaggagatat ttaccaccaa caatggctac
120
aaatccatgc agaaaaaact tcggagtaat tggaagattc agagcttaaa agatgaaatc
180
acatctgaga agttaaatgg agtaaaactg tggattacag ctgggccaag ggaaaaattt
240
actgcagctg agtttgaaat cctgaagaaa tatcttgaca ctggtgggga tgtccttgtg
300
atgctagggg aaggtggaga atccagattt gacaccaata ttaacttttt actagaagaa
360
tatggaatca tggttaataa tgatgctgtg gttagaaatg tatatcacaa atatttccat
420
cctaaagaag ctctagtttc cagtggagtc ttgaacaggg aaattagccg agctgcagga
480
aaggctgtgc tggcgatcat tgatgaggaa agcagtggaa acaatgccca ggctctcacc
540
tttgtgtatc cttttggtgc cacattgagt gtcatgaaac cagcagtggc ggttctgtct
600
acaggttctg tctgcttccc acttaacaga cccattttgg ctttctatca ctcaaagaac
660
caaggtggga agctggcagt gcttggttca tgtcacatgt tcagtgatca atatttggac
720
aaagaagaaa acagcaaaat catggatgtt gttgttttcc agtggctcac gacaggagac
780
atccacctaa accagattga tgctgaggac ccagagattt ctgactacat gatgctgccc
840
tacacagcca ccctatcaaa gcggaatcga gagtgtctcc aggagagtga tgagatccca
900
agggacttta ccaccctctt cgacctgtcc atcttccagc tggataccac ctccttccac
960
agcgtcatcg aggctcacga gcagctaaat gtgaaacatg aaccactcca gctcatccag
1020
cctcagtttg agacgccgct gccaaccctt cagcctgcgg tttttcctcc cagtttccgg
1080
gagttaccac ctcctcctct ggagctattt gatttagatg aaacgttctc ctctgagaag
1140
gcacggctgg ctcagattac caataagtgt actgaagaag acctggaatt ttatgtcagg
1200
aagtgtggtg atattcttgg agtaaccagt aaactaccaa aggaccaaca ggatgccaaa
1260
catatccttg agcacgtctt cttccaagtg gtggagttca agaaattgaa ccaggaacat
1320
gacatcgata caagtgaaac agcattccag aacaatttct gaagaccatg cctcttgaag
1380
ctttttctgc ctcctgattc tctctttgta aactattttc aaattgtttt tcaactcctt
1440
atcaaaattg tttatacact ctttcctcca tgagctctgg aaggtatatg catcttctgt
1500

aatactcaga taggtataag atttttcaca aaatccttat gtaagataca ttccattttt
1560
aaaaattaaa tgtatggttg catctgtctt tttataccct aaaaaaaaaa aaaaaaaaa
1619

<210> 4806
<211> 438
<212> PRT
<213> Homo sapiens

<400> 4806
Met Glu Lys Glu Leu Arg Ser Thr Ile Leu Phe Asn Ala Tyr Lys Lys
1 5 10 15
Glu Ile Phe Thr Thr Asn Asn Gly Tyr Lys Ser Met Gln Lys Lys Leu
20 25 30
Arg Ser Asn Trp Lys Ile Gln Ser Leu Lys Asp Glu Ile Thr Ser Glu
35 40 45
Lys Leu Asn Gly Val Lys Leu Trp Ile Thr Ala Gly Pro Arg Glu Lys
50 55 60
Phe Thr Ala Ala Glu Phe Glu Ile Leu Lys Lys Tyr Leu Asp Thr Gly
65 70 75 80
Gly Asp Val Leu Val Met Leu Gly Glu Gly Gly Glu Ser Arg Phe Asp
85 90 95
Thr Asn Ile Asn Phe Leu Leu Glu Glu Tyr Gly Ile Met Val Asn Asn
100 105 110
Asp Ala Val Val Arg Asn Val Tyr His Lys Tyr Phe His Pro Lys Glu
115 120 125
Ala Leu Val Ser Ser Gly Val Leu Asn Arg Glu Ile Ser Arg Ala Ala
130 135 140
Gly Lys Ala Val Leu Ala Ile Ile Asp Glu Glu Ser Ser Gly Asn Asn
145 150 155 160
Ala Gln Ala Leu Thr Phe Val Tyr Pro Phe Gly Ala Thr Leu Ser Val
165 170 175
Met Lys Pro Ala Val Ala Val Leu Ser Thr Gly Ser Val Cys Phe Pro
180 185 190
Leu Asn Arg Pro Ile Leu Ala Phe Tyr His Ser Lys Asn Gln Gly Gly
195 200 205
Lys Leu Ala Val Leu Gly Ser Cys His Met Phe Ser Asp Gln Tyr Leu
210 215 220
Asp Lys Glu Glu Asn Ser Lys Ile Met Asp Val Val Val Phe Gln Trp
225 230 235 240
Leu Thr Thr Gly Asp Ile His Leu Asn Gln Ile Asp Ala Glu Asp Pro
245 250 255
Glu Ile Ser Asp Tyr Met Met Leu Pro Tyr Thr Ala Thr Leu Ser Lys
260 265 270
Arg Asn Arg Glu Cys Leu Gln Glu Ser Asp Glu Ile Pro Arg Asp Phe
275 280 285
Thr Thr Leu Phe Asp Leu Ser Ile Phe Gln Leu Asp Thr Thr Ser Phe
290 295 300
His Ser Val Ile Glu Ala His Glu Gln Leu Asn Val Lys His Glu Pro
305 310 315 320
Leu Gln Leu Ile Gln Pro Gln Phe Glu Thr Pro Leu Pro Thr Leu Gln
325 330 335
Pro Ala Val Phe Pro Pro Ser Phe Arg Glu Leu Pro Pro Pro Pro Leu

```
            340                 345                 350
Glu Leu Phe Asp Leu Asp Glu Thr Phe Ser Ser Glu Lys Ala Arg Leu
        355                 360                 365
Ala Gln Ile Thr Asn Lys Cys Thr Glu Glu Asp Leu Glu Phe Tyr Val
    370                 375                 380
Arg Lys Cys Gly Asp Ile Leu Gly Val Thr Ser Lys Leu Pro Lys Asp
385                 390                 395                 400
Gln Gln Asp Ala Lys His Ile Leu Glu His Val Phe Phe Gln Val Val
                405                 410                 415
Glu Phe Lys Lys Leu Asn Gln Glu His Asp Ile Asp Thr Ser Glu Thr
            420                 425                 430
Ala Phe Gln Asn Asn Phe
        435
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<210> 4807
<211> 1177
<212> DNA
<213> Homo sapiens

<400> 4807
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ccttgaacac tgcctccacg tcgccggctc aatctgggcg agaacccaga cttccaccgc
120
agccccgcaa tctgcagacc tcagcggcag cgcaggtggc agacctgcct cctttgcctg
180
tgagtcatgg cagctcccat gaatggccaa gtgtgtgtgg tgactggtgc ctccaggggt
240
attggccgtg gcattgcctt gcagctctgc aaagcaggcg ccacagttta catcactggc
300
cgccatctgg acacccttcg cgttgttgct caggaggcac aatccctcgg gggccaatgt
360
gtgcctgtgg tgtgcgattc aagccaggag agtgaagtgc gaagcctgtt tgagcaagtg
420
gatcgggaac agcaagggcg tctagatgtg ctggtcaaca atgcttatgc aggggtccag
480
acgatcctga acaccaggaa taaggcattc tgggaaaccc ctgcctccat gtgggatgat
540
atcaacaacg tcggactcag aggccactac ttttgctcag tgtatggggc acggctgatg
600
gtaccagctg gccaggggct catcgtggtc atctcctccc caggaagcct gcagtatatg
660
ttcaatgtcc cctatggtgt gggcaaagct gcgtgtgaca agctggctgc tgactgtgcc
720
cacgagctgc ggcgccatgg ggtcagctgt gtgtctctgt ggccggggat tgtgcagaca
780
gaactgctga aggagcatat ggcaaaggag gaggtcctgc aggatcctgt gttgaagcag
840
ttcaaatcag ccttctcatc tgcggaaacc acagaattga gtggcaaatg tgtggtggct
900
ttggcaacag atcccaatat cctgagcctg agtggtaagg tgctgccatc ctgtgacctt
960
gctcgacgct atggccttcg ggatgtggac ggccgccccg tccaagacta tttgtctttg
1020

agctctgttc tctcacacgt gtccggcctg ggctggctgg cctcctacct gccctccttc
1080
ctccgtgtgc ccaagtggat tattgccctc tacactagca agttctaacc ctcctggtct
1140
gacactacgt ctctgcttgt ctgagaagac aacgcgt
1177

<210> 4808
<211> 313
<212> PRT
<213> Homo sapiens

<400> 4808
Met Ala Ala Pro Met Asn Gly Gln Val Cys Val Val Thr Gly Ala Ser
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Arg Gly Ile Gly Arg Gly Ile Ala Leu Gln Leu Cys Lys Ala Gly Ala
20 25 30
Thr Val Tyr Ile Thr Gly Arg His Leu Asp Thr Leu Arg Val Val Ala
35 40 45
Gln Glu Ala Gln Ser Leu Gly Gly Gln Cys Val Pro Val Val Cys Asp
50 55 60
Ser Ser Gln Glu Ser Glu Val Arg Ser Leu Phe Glu Gln Val Asp Arg
65 70 75 80
Glu Gln Gln Gly Arg Leu Asp Val Leu Val Asn Asn Ala Tyr Ala Gly
85 90 95
Val Gln Thr Ile Leu Asn Thr Arg Asn Lys Ala Phe Trp Glu Thr Pro
100 105 110
Ala Ser Met Trp Asp Asp Ile Asn Asn Val Gly Leu Arg Gly His Tyr
115 120 125
Phe Cys Ser Val Tyr Gly Ala Arg Leu Met Val Pro Ala Gly Gln Gly
130 135 140
Leu Ile Val Val Ile Ser Ser Pro Gly Ser Leu Gln Tyr Met Phe Asn
145 150 155 160
Val Pro Tyr Gly Val Gly Lys Ala Ala Cys Asp Lys Leu Ala Ala Asp
165 170 175
Cys Ala His Glu Leu Arg Arg His Gly Val Ser Cys Val Ser Leu Trp
180 185 190
Pro Gly Ile Val Gln Thr Glu Leu Leu Lys Glu His Met Ala Lys Glu
195 200 205
Glu Val Leu Gln Asp Pro Val Leu Lys Gln Phe Lys Ser Ala Phe Ser
210 215 220
Ser Ala Glu Thr Thr Glu Leu Ser Gly Lys Cys Val Val Ala Leu Ala
225 230 235 240
Thr Asp Pro Asn Ile Leu Ser Leu Ser Gly Lys Val Leu Pro Ser Cys
245 250 255
Asp Leu Ala Arg Arg Tyr Gly Leu Arg Asp Val Asp Gly Arg Pro Val
260 265 270
Gln Asp Tyr Leu Ser Leu Ser Ser Val Leu Ser His Val Ser Gly Leu
275 280 285
Gly Trp Leu Ala Ser Tyr Leu Pro Ser Phe Leu Arg Val Pro Lys Trp
290 295 300
Ile Ile Ala Leu Tyr Thr Ser Lys Phe
305 310

<210> 4809
<211> 999
<212> DNA
<213> Homo sapiens

<400> 4809
tccggagagg gccttgtcac attctcctac tccccaagtg aggcctccgt ccttctgttc
60
cccatgtgag gcctccatgg aatgaggagg ggtctgtccc agcagtgcct accctgcttc
120
tcctgtaaga gactgttccc tcctcccaca cttccttgag aagcacttgc ccctccagga
180
taacagcatc actgagcctg gggaacagac agtccctagt ccaagccctg gaggtaagaa
240
aggaggggcc ggccaggatg ctcagtgtgg tcagcatagg ccaggcccct gctaccttga
300
ccctgagggc cagagcacag gcggaactcg gacatagggc cacaggtgac tgcttaatga
360
caaccatgct agctcctggc aatgaggggt caggagcgtg tgtgaataat ggggcacctg
420
acccagggct ggggtacaga gggtgggggt tacaaatggt tcatctgtcg caggacacct
480
ggaggatgag gaaagagccc ccaggcaaac ccattctgtg agcaattccc atctgctgtc
540
tccaaatcct gtctagactc tgaccctgct ggcccccttcc agggctccca gcctggttgc
600
cacagcggcc tcctaaccaa cacccctgcg gctctggtac cagcccacgc cagacagaga
660
agccagccat cattgctcct gtcttcctcc ccgagaaagt cgaggtcctg gcagggctca
720
gggcctatgt ggccaggccc tggatacttc cctgacctca cctcccctac agcacagccc
780
cttcagctcc tgggggcttt gcacggctgc tcctttcctc cccctctgcc ctcaggccag
840
ccttgtccct gatcactacc ttcttcattt ctgtacctgg ctgacatctg tccttccccg
900
ccaactacaa ggtagacccc gggagggcag ggatggtgca ctgtgttcag ggtgcatttg
960
ccgccagtgg agggaggcac ccaggccact cccgccggc
999

<210> 4810
<211> 120
<212> PRT
<213> Homo sapiens

<400> 4810
Gly Lys Ser Pro Gln Ala Asn Pro Phe Cys Glu Gln Phe Pro Ser Ala
1 5 10 15
Val Ser Lys Ser Cys Leu Asp Ser Asp Pro Ala Gly Pro Phe Gln Gly
20 25 30
Ser Gln Pro Gly Cys His Ser Gly Leu Leu Thr Asn Thr Pro Ala Ala
35 40 45
Leu Val Pro Ala His Ala Arg Gln Arg Ser Gln Pro Ser Leu Leu Leu

```
    50                  55                  60
Ser Ser Ser Pro Arg Lys Ser Arg Ser Trp Gln Gly Ser Gly Pro Met
65                  70                  75                  80
Trp Pro Gly Pro Gly Tyr Phe Pro Asp Leu Thr Ser Pro Thr Ala Gln
                85                  90                  95
Pro Leu Gln Leu Leu Gly Ala Leu His Gly Cys Ser Phe Pro Pro Pro
            100                 105                 110
Leu Pro Ser Gly Gln Pro Cys Pro
        115                 120
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<210> 4811
<211> 3207
<212> DNA
<213> Homo sapiens

<400> 4811
nttagtctgc ccccacctct gcacccgccc ccggagggca cccgaggacc atgactatga
60
cagatcctgc ctcgatggcc ccgccacccc gagaagagga ggaagaagag gaggaggagg
120
atgaacccgt cccagaagcc cccagcccca cccaggagcg ccggcagaag cctgttgtgc
180
acccctcggc acctgccccc ctccctaagg actacgcttt taccttcttc gaccccaatg
240
acccggcgtg ccaggagatc ctgtttgacc ctcagaccac catccccgag ctgtttgcca
300
ttgtgcgcca gtgggtgccc caagtccagc acaagataga cgtcatcggc aatgagattc
360
tgcgccgagg ctgccatgtg aacgatcgtg acgggctgac cgacatgaca ctgctccact
420
atgcgtgcaa agctggggcc cacggagtcg gggacccgcg gcagcgtgcg cctctcgcag
480
cagctgctgg cgctgggcga gatgtgacgc tgcgtagcgc tggaccaaca tgaacgcgct
540
tcactacgcg gcctattttg atgtgcccga cctcgtgcgt gtgctgctga agggtgcgag
600
gccgcgagtg gtgaactcca cgtgcagtga cttcaaccac ggctcagccc tgcacatcgc
660
tgcttccagc ctgtgcctgg gcgccgcaaa tgtttgctgg agcacggcgc caaccctgcg
720
ctgaggaatc gaaaaggaca ggtgccggcg gaggtggtcc cagatcctat ggacatgtcc
780
ctggacaagg cagaggcggc actggtggcc aaggagctgc ggacgcttct ggaagaggca
840
gtgccactat cttgcgccct ccccaaggtc acgctaccca actatgacaa cgtcccaggc
900
aatctcatgc ttagcgcact gggcttgcgc ctgggagacc gcgtgctgct ggatggccag
960
aagacgggca cactgcggtt ctgtgggacc acggagtttg ccagcggcag ttgggtgggc
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1080
atctgccctc ccaagcaggg tctctttgcc tccgtgtcca agatctccaa ggcagtggac
1140

gcacccccct cctctgtcac ctccacaccc ggacccccc ggatggactt ctcccgtgtc
1200
accggcaaag gccgcaggga acacaaaggc aagaagaaga ccccatcatc cccatctctg
1260
ggcagcttgc agcagcgtga cggggccaag gctgaggttg gagaccaggt ccttgtcgcg
1320
ggccagaagc aggggatcgt gcgcttctac gggaagacag actttgcccc aggttactgg
1380
tatggcattg agctggacca gcccacaggc aagcatgatg gctctgtctt cggtgtccgg
1440
tacttcactt gccccccgag gcatggggtc ttcgcaccag catcccgtat tcagaggatt
1500
ggcggatcca ctgattcccc cggggacagc gttggagcca aaaaagtgca tcaagtgaca
1560
atgacgcagc ccaaacgcac cttcaccaca gtccggaccc caaaggacat tgcatcagag
1620
aactccattt ccaggttgct gttctgctgc tggttccct ggatgctgag ggcggagatg
1680
cagtcttaga ggccctggac acctgacaaa gagacagagt ccccactagc atctcctgac
1740
acccgaggag ccctgagtca ccctgagata gagattccca gtaacacatc cagagtagag
1800
acccctgtta gccagccctc gatcattgag gccccattat taacagatac tcccataata
1860
acccccaaat acagacccca tgtcacccag aaagagattc cctgagtagc accttcaggc
1920
tagtccctat ccccaacccc tcagagcaga ttcccagatt aacagatttc catatcaccc
1980
caaatgatgg tgaccctctc cacataatgc attacaacag aacattcttg aatcacccaa
2040
ccctggatca gaaacctccc cattaacaaa cactgccct taagtcctct tgaaataaac
2100
ataggtcaca cccccaaagc aaaagagtaa cagacattca tgtcattgtt ccccatttaa
2160
catcagtcct ctcaagatgt cgtgacccca tggtcaccct gaagccctta gattccaacc
2220
cctcaatcag agacttcctt cattaacaaa gacccttgtt cttatccctc aagaagaaac
2280
ccaccataac cagcccactg tcacccctaa tttacagaca ccaaaacagt cctggaagtg
2340
ctaattacag gacccccaa gtcttcctac cctctgcacc ctcaagaaac ccccagtgcc
2400
ttgtatgaag cccaccccac atggcccaca gctcctgtgc tggccagact cccagaaaat
2460
tctctatttt ttaagtaacg acttcccct ttgggggacc ccaaaatttg gaggccccat
2520
tctaggactc tggggatccc aaaccctaga gtacacacgt cccaaactcc cctgtgccct
2580
caagtcctac agcccctaga agaccccaat gccgtaactc ctaggacccc caaatcatgg
2640
aatcccaaat ccccagggaa tcccaaattt gaaaatccaa tcccaagtcc ccaggaaacc
2700
caatcatgag gtccttgtgc ctggtatgga ggagactgca gtcaggatat gcattccagg
2760

ctcccagaca cctcaagccc tattcacagg caccaggaaa ccccacacag gaattcccat
2820
ccctggaaac tggagaattt caatgccccg agtccatggg tttcaagaca ccaaattcca
2880
agagccccag ccctaaggga accccaaatc ctaaagcctc catctctaat aaatggaagg
2940
ccccaaggcc ctgaggggat ctcaaatcct ggaaccccga tttcaatcta cgttctagtc
3000
actggcctca aaggacccca cagcacctgg gccagaccaa cagctcgagg gagaacctga
3060
aggcccaggg ggtccagggc ggacctgggg ccccgaccac caaggacagc tcacgactgc
3120
cccttcactg catgtcccca aactcagcat gactcctgtc ctcttcaata aagacgtttc
3180
tatggccaaa aaaaaaaaaa aaaaaaa
3207

<210> 4812
<211> 306
<212> PRT
<213> Homo sapiens

<400> 4812
Met Asp Met Ser Leu Asp Lys Ala Glu Ala Ala Leu Val Ala Lys Glu
1 5 10 15
Leu Arg Thr Leu Leu Glu Glu Ala Val Pro Leu Ser Cys Ala Leu Pro
20 25 30
Lys Val Thr Leu Pro Asn Tyr Asp Asn Val Pro Gly Asn Leu Met Leu
35 40 45
Ser Ala Leu Gly Leu Arg Leu Gly Asp Arg Val Leu Leu Asp Gly Gln
50 55 60
Lys Thr Gly Thr Leu Arg Phe Cys Gly Thr Thr Glu Phe Ala Ser Gly
65 70 75 80
Ser Trp Val Gly Val Glu Leu Asp Glu Pro Glu Gly Lys Asn Asp Gly
85 90 95
Ser Val Gly Gly Val Arg Tyr Phe Ile Cys Pro Pro Lys Gln Gly Leu
100 105 110
Phe Ala Ser Val Ser Lys Ile Ser Lys Ala Val Asp Ala Pro Pro Ser
115 120 125
Ser Val Thr Ser Thr Pro Gly Pro Pro Arg Met Asp Phe Ser Arg Val
130 135 140
Thr Gly Lys Gly Arg Arg Glu His Lys Gly Lys Lys Lys Thr Pro Ser
145 150 155 160
Ser Pro Ser Leu Gly Ser Leu Gln Gln Arg Asp Gly Ala Lys Ala Glu
165 170 175
Val Gly Asp Gln Val Leu Val Ala Gly Gln Lys Gln Gly Ile Val Arg
180 185 190
Phe Tyr Gly Lys Thr Asp Phe Ala Pro Gly Tyr Trp Tyr Gly Ile Glu
195 200 205
Leu Asp Gln Pro Thr Gly Lys His Asp Gly Ser Val Phe Gly Val Arg
210 215 220
Tyr Phe Thr Cys Pro Pro Arg His Gly Val Phe Ala Pro Ala Ser Arg
225 230 235 240
Ile Gln Arg Ile Gly Gly Ser Thr Asp Ser Pro Gly Asp Ser Val Gly

245 250 255
Ala Lys Lys Val His Gln Val Thr Met Thr Gln Pro Lys Arg Thr Phe
260 265 270
Thr Thr Val Arg Thr Pro Lys Asp Ile Ala Ser Glu Asn Ser Ile Ser
275 280 285
Arg Leu Leu Phe Cys Cys Trp Phe Pro Trp Met Leu Arg Ala Glu Met
290 295 300
Gln Ser
305

<210> 4813
<211> 400
<212> DNA
<213> Homo sapiens

<400> 4813
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gtgggtgtcc tgcacatgct gctgtctcct tggggctctg cacctgccct cctgtctgcc
120
agtgactgtg ggtgggaaag gaggccgtgg tggctgcagc tttcctctgc aaacctccac
180
ctcgcccaca gggcttggct tttcctccag ctgtccagga aaccaccatc atgattgtta
240
aacacagatt tgaacattca cgaagaaact tccagggtga gccaaaccct cttcctcccc
300
actgcacctc caagcagcct tcctgaaagg gaaaagagta cagacctgcc ctctggggac
360
ccctgtgccc tgccatgacc agcctttccc cttcacgcgt
400

<210> 4814
<211> 125
<212> PRT
<213> Homo sapiens

<400> 4814
Met Ala Gly His Arg Gly Pro Gln Arg Ala Gly Leu Tyr Ser Phe Pro
1 5 10 15
Phe Gln Glu Gly Cys Leu Glu Val Gln Trp Gly Gly Arg Gly Phe Gly
20 25 30
Ser Pro Trp Lys Phe Leu Arg Glu Cys Ser Asn Leu Cys Leu Thr Ile
35 40 45
Met Met Val Val Ser Trp Thr Ala Gly Gly Lys Ala Lys Pro Cys Gly
50 55 60
Arg Gly Gly Gly Leu Gln Arg Lys Ala Ala Ala Thr Thr Ala Ser Phe
65 70 75 80
Pro Thr His Ser His Trp Gln Thr Gly Gly Gln Val Gln Ser Pro Lys
85 90 95
Glu Thr Ala Ala Cys Ala Gly His Pro Pro Gly Thr Ala Phe Ser Leu
100 105 110
Ile Leu Pro Val Pro Pro Thr Cys Trp Val Ser Val Ala
115 120 125

<210> 4815
<211> 528
<212> DNA
<213> Homo sapiens

<400> 4815
nngcgcgcca ggagctctgc attgaaggca ctggggtaaa gtgaatgccg aagacagaag
60
atttggatga tacaccactg actttctttg tttggaatac acgttatgaa ccctttctgg
120
agcatgtcta caagctctgt acgcaaacga tctgaaggtg aagagaagac attaacaggg
180
gacgtgaaaa ccagtcctcc acgaactgca ccaaagaaac agctaccttc tattcccaaa
240
aatgctttgc ccataactaa gcctacatca cctgccccag cagcacagtc aacaaatggc
300
acccatgcct cttacggacc cttctacctg gaatattcac tccttgcaga atttaccttg
360
gttgtgaagc agaagctacc aggcgtctat gtgcagccat cttatcgctc tgcattaatg
420
tagtttggag taatattcat acggcatgga ctttaccaag atggcgtatt taagtttaca
480
gtttacatcc ctgataacta tccagatggt gactgtccac gcttggtg
528

<210> 4816
<211> 105
<212> PRT
<213> Homo sapiens

<400> 4816
Met Asn Pro Phe Trp Ser Met Ser Thr Ser Ser Val Arg Lys Arg Ser
 1   5   10   15
Glu Gly Glu Glu Lys Thr Leu Thr Gly Asp Val Lys Thr Ser Pro Pro
            20   25   30
Arg Thr Ala Pro Lys Lys Gln Leu Pro Ser Ile Pro Lys Asn Ala Leu
        35   40   45
Pro Ile Thr Lys Pro Thr Ser Pro Ala Pro Ala Ala Gln Ser Thr Asn
    50   55   60
Gly Thr His Ala Ser Tyr Gly Pro Phe Tyr Leu Glu Tyr Ser Leu Leu
65   70   75   80
Ala Glu Phe Thr Leu Val Val Lys Gln Lys Leu Pro Gly Val Tyr Val
                85   90   95
Gln Pro Ser Tyr Arg Ser Ala Leu Met
            100   105

<210> 4817
<211> 1106
<212> DNA
<213> Homo sapiens

<400> 4817
nntgatcagg aagcgggagc gtagggccac gcctgcggcg ctgctggttg aggctgtgtg
60

ggtgggggac gggccgaggc gatggcggag aagtttgacc acctagagga gcacctggag
120
aagttcgtgg agaacattcg gcagctcggc atcatcgtca gtgacttcca gcccagcagc
180
caggccgggc tcaaccaaaa gctgaatttt attgttactg gcttacagga tattgacaag
240
tgcagacagc agcttcatga tattactgta ccgttagaag tttttgaata tatagatcaa
300
ggtcgaaatc cccagctcta caccaaagag tgcctggaga gggctctagc taaaaatgag
360
caagttaaag gcaagatcga caccatgaag aaatttaaaa gcctgttgat tcaagaactt
420
tctaaagtat ttccggaaga catggctaag tatcgaagca tccgggggga ggatcacccg
480
ccttcttaac cagctcaccc tccctgtgtg aagatccccc gggactgcga tgcggcgtga
540
ggctgggact gcgagtgctg acgccacctt cctgctgagg tgggactggg ccctggacac
600
acccctcagc ccctctgtcc tcattgtttg gcctcatggg accgaggggc tggaggagag
660
gcggagctgt gccccagctg ttccagcagc ttgtctggcg tcaactggct ttcagagtgc
720
tgacccctca tcactgtggg gatcattctc tctgagggca gatgaggcgc aggaaaatag
780
tcttggaaat gttaaatatg atgggtaaat taaaagtttt acaacattct acctaatatt
840
tttcttttaa catacttttt ctgttctatt gtattatggt gtccgaaagc taaataacga
900
ctaggaaaaa tttttttaaa aaaagaaaaa tcagtttaat gtgggaagta cttaagtggt
960
attatatttt acattttcaa gtatagtgca taaagaatgt tttaaatgta actgttttca
1020
tggatttcaa ttagacatgc ctataataaa ctaagtatgt ggcttaaaaa aaaaaaaaaa
1080
aaaaaaaaaa aaaaaaaaaa aaaaaa
1106

<210> 4818
<211> 135
<212> PRT
<213> Homo sapiens

<400> 4818
Met Ala Glu Lys Phe Asp His Leu Glu Glu His Leu Glu Lys Phe Val
1 5 10 15
Glu Asn Ile Arg Gln Leu Gly Ile Ile Val Ser Asp Phe Gln Pro Ser
20 25 30
Ser Gln Ala Gly Leu Asn Gln Lys Leu Asn Phe Ile Val Thr Gly Leu
35 40 45
Gln Asp Ile Asp Lys Cys Arg Gln Gln Leu His Asp Ile Thr Val Pro
50 55 60
Leu Glu Val Phe Glu Tyr Ile Asp Gln Gly Arg Asn Pro Gln Leu Tyr
65 70 75 80
Thr Lys Glu Cys Leu Glu Arg Ala Leu Ala Lys Asn Glu Gln Val Lys

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                85                  90                  95
Gly Lys Ile Asp Thr Met Lys Lys Phe Lys Ser Leu Leu Ile Gln Glu
            100                 105                 110
Leu Ser Lys Val Phe Pro Glu Asp Met Ala Lys Tyr Arg Ser Ile Arg
        115                 120                 125
Gly Glu Asp His Pro Pro Ser
    130                 135

<210> 4819
<211> 1655
<212> DNA
<213> Homo sapiens

<400> 4819
cggccgcggc ccggactccg cggtgggcga gcgccctgtg aggtgaccat ggaggctggt
60
ggcctcccct tggagctgtg gcgcatgatc ttagcctact tgcaccttcc cgacctgggc
120
cgctgcagcc tggtatgcag ggcctggtat gaactgatcc tcagtctcga cagcacccgc
180
tggcggcagc tgtgtctggg ttgcaccgag tgccgccatc ccaattggcc caaccagcca
240
gatgtggagc ctgagtcttg gagagaagcc ttcaagcagc attaccttgc atccaagaca
300
tggaccaaga atgccttgga cttggagtct tccatctgct tttctctatt ccgccggagg
360
agggaacgac gtaccctgag tgttgggcca ggccgtgagt ttgacagcct gggcagtgcc
420
ttggccatgg ccagcctgta tgaccgaatt gtgctcttcc caggtgtgta cgaagagcaa
480
ggtgaaatca tcttgaaggt gcctgtggag attgtagggc aggggaagtt gggtgaagtg
540
gccctgctgg ccagcattga tcagcactgc tcaaccacac gcctgtgcaa cctcgtcttc
600
acgccagcct ggttctcacc catcatgtat aagacaacat caggtcacgt ccagtttgac
660
aactgcaact ttgagaacgg gcacatccag gtccatggcc cgggtacttg ccaagtgaag
720
ttctgtacct tcaaaaacac ccatatcttc ctgcacaacg tgcccctgtg tgtcctggaa
780
aactgtgaat ttgtgggcag tgaaaacaac tctgtgactg ttgagggtca cccatctgcg
840
gataagaact gggcctacaa gtatctacta gggcttatca agtcctcacc cacttttctc
900
cccacagagg actctgactt tttaatgtcc ctggacctag agagccggga ccaggcctgg
960
agcccaaaga cctgtgacat tgttatcgag ggcagccaga gccctaccag cccagcttct
1020
agctccccaa agccaggctc caaggctggc tcacaggagg cagaggtggg tagtgatggt
1080
gaaagggtgg cccagacccc ggacagcagc gatggaggcc tgagtcccag cggtgaggat
1140
gaagatgagg accagctgat gtacagacta tcctaccaag tgcagggccc acgccctgta
1200
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ttgggggget catttctggg cccacctcta ccaggagcat ccattcagct gcccagctgc
1260
ctagtgctga actcactgca gcaggagctg cagaaggata aggaggccat ggcactggcc
1320
aactccgtgc agggctgcct catccgcaag tgcctcttcc gggacgggaa gggaggcgtc
1380
ttcgtctgct cccacggcag agccaagatg gaaggaaaca tcttccggaa cctgacttac
1440
gcagtgcggt gtatacataa tagcaagatc atcatgctca ggaacgacat ttaccgctgc
1500
cgagcgtcag gcatctttct tcgcttggag ggcggtggct tgattgccgg caacaacatt
1560
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1620
aaccctcgtg ccgaattctt ggcctcgagg gccaa
1655

<210> 4820
<211> 551
<212> PRT
<213> Homo sapiens

<400> 4820
Arg Pro Arg Pro Gly Leu Arg Gly Gly Arg Ala Pro Cys Glu Val Thr
1 5 10 15
Met Glu Ala Gly Gly Leu Pro Leu Glu Leu Trp Arg Met Ile Leu Ala
20 25 30
Tyr Leu His Leu Pro Asp Leu Gly Arg Cys Ser Leu Val Cys Arg Ala
35 40 45
Trp Tyr Glu Leu Ile Leu Ser Leu Asp Ser Thr Arg Trp Arg Gln Leu
50 55 60
Cys Leu Gly Cys Thr Glu Cys Arg His Pro Asn Trp Pro Asn Gln Pro
65 70 75 80
Asp Val Glu Pro Glu Ser Trp Arg Glu Ala Phe Lys Gln His Tyr Leu
85 90 95
Ala Ser Lys Thr Trp Thr Lys Asn Ala Leu Asp Leu Glu Ser Ser Ile
100 105 110
Cys Phe Ser Leu Phe Arg Arg Arg Arg Glu Arg Arg Thr Leu Ser Val
115 120 125
Gly Pro Gly Arg Glu Phe Asp Ser Leu Gly Ser Ala Leu Ala Met Ala
130 135 140
Ser Leu Tyr Asp Arg Ile Val Leu Phe Pro Gly Val Tyr Glu Glu Gln
145 150 155 160
Gly Glu Ile Ile Leu Lys Val Pro Val Glu Ile Val Gly Gln Gly Lys
165 170 175
Leu Gly Glu Val Ala Leu Leu Ala Ser Ile Asp Gln His Cys Ser Thr
180 185 190
Thr Arg Leu Cys Asn Leu Val Phe Thr Pro Ala Trp Phe Ser Pro Ile
195 200 205
Met Tyr Lys Thr Thr Ser Gly His Val Gln Phe Asp Asn Cys Asn Phe
210 215 220
Glu Asn Gly His Ile Gln Val His Gly Pro Gly Thr Cys Gln Val Lys
225 230 235 240
Phe Cys Thr Phe Lys Asn Thr His Ile Phe Leu His Asn Val Pro Leu

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                245                 250                 255
Cys Val Leu Glu Asn Cys Glu Phe Val Gly Ser Glu Asn Asn Ser Val
            260                 265                 270
Thr Val Glu Gly His Pro Ser Ala Asp Lys Asn Trp Ala Tyr Lys Tyr
        275                 280                 285
Leu Leu Gly Leu Ile Lys Ser Ser Pro Thr Phe Leu Pro Thr Glu Asp
    290                 295                 300
Ser Asp Phe Leu Met Ser Leu Asp Leu Glu Ser Arg Asp Gln Ala Trp
305                 310                 315                 320
Ser Pro Lys Thr Cys Asp Ile Val Ile Glu Gly Ser Gln Ser Pro Thr
                325                 330                 335
Ser Pro Ala Ser Ser Ser Pro Lys Pro Gly Ser Lys Ala Gly Ser Gln
            340                 345                 350
Glu Ala Glu Val Gly Ser Asp Gly Glu Arg Val Ala Gln Thr Pro Asp
        355                 360                 365
Ser Ser Asp Gly Gly Leu Ser Pro Ser Gly Glu Asp Glu Asp Glu Asp
    370                 375                 380
Gln Leu Met Tyr Arg Leu Ser Tyr Gln Val Gln Gly Pro Arg Pro Val
385                 390                 395                 400
Leu Gly Gly Ser Phe Leu Gly Pro Pro Leu Pro Gly Ala Ser Ile Gln
                405                 410                 415
Leu Pro Ser Cys Leu Val Leu Asn Ser Leu Gln Gln Glu Leu Gln Lys
            420                 425                 430
Asp Lys Glu Ala Met Ala Leu Ala Asn Ser Val Gln Gly Cys Leu Ile
        435                 440                 445
Arg Lys Cys Leu Phe Arg Asp Gly Lys Gly Gly Val Phe Val Cys Ser
    450                 455                 460
His Gly Arg Ala Lys Met Glu Gly Asn Ile Phe Arg Asn Leu Thr Tyr
465                 470                 475                 480
Ala Val Arg Cys Ile His Asn Ser Lys Ile Ile Met Leu Arg Asn Asp
                485                 490                 495
Ile Tyr Arg Cys Arg Ala Ser Gly Ile Phe Leu Arg Leu Glu Gly Gly
            500                 505                 510
Gly Leu Ile Ala Gly Asn Asn Ile Tyr His Asn Ala Glu Ala Gly Val
        515                 520                 525
Asp Ile Arg Lys Lys Ser Asn Pro Leu Gln Ile Gly Asn Pro Arg Ala
    530                 535                 540
Glu Phe Leu Ala Ser Arg Ala
545                 550
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<210> 4821
<211> 585
<212> DNA
<213> Homo sapiens

<400> 4821
ggccgcgtgg aggtgctgac cgatgccgga ggttgggtgc tgattgaccg gagcggccgt
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cactttggta caatcctcaa ttacctgcgg gatgggtctg tgccactgcc ggagagtacg
120
agagaactgg gggagctgct gggcgaagca cgctactacc tggtgcaggg cctgattgag
180
gactgccagc tggcgctgca gcaaaaaagg gagacgctgt ccccgctgtg cctcatcccc
240

atggtgacat ctccccggga ggagcagcag ctcctggcca gcacctccaa gcccgtggtg
300
aagctcctgc acaaccgcag taacaacaag tactcctaca ccagcacttc agatgacaac
360
ctacttaaga acatcgagct gttcgacaag ctggccctgc gcttccacgg gcggctactc
420
ttcctcaagg atgtcctggg ggacgagatc tgctgctggt ctttctacgg gcagggccgc
480
aaaatcgccg aggtgtgctg cacctccatt gtctatgcta cggagaagaa gcagaccaag
540
gtcagagggg ctccagagcc tatgttgggg gctgggggtg gccac
585

<210> 4822
<211> 195
<212> PRT
<213> Homo sapiens

<400> 4822
Gly Arg Val Glu Val Leu Thr Asp Ala Gly Gly Trp Val Leu Ile Asp
1 5 10 15
Arg Ser Gly Arg His Phe Gly Thr Ile Leu Asn Tyr Leu Arg Asp Gly
20 25 30
Ser Val Pro Leu Pro Glu Ser Thr Arg Glu Leu Gly Glu Leu Leu Gly
35 40 45
Glu Ala Arg Tyr Tyr Leu Val Gln Gly Leu Ile Glu Asp Cys Gln Leu
50 55 60
Ala Leu Gln Gln Lys Arg Glu Thr Leu Ser Pro Leu Cys Leu Ile Pro
65 70 75 80
Met Val Thr Ser Pro Arg Glu Glu Gln Gln Leu Leu Ala Ser Thr Ser
85 90 95
Lys Pro Val Val Lys Leu Leu His Asn Arg Ser Asn Asn Lys Tyr Ser
100 105 110
Tyr Thr Ser Thr Ser Asp Asp Asn Leu Leu Lys Asn Ile Glu Leu Phe
115 120 125
Asp Lys Leu Ala Leu Arg Phe His Gly Arg Leu Leu Phe Leu Lys Asp
130 135 140
Val Leu Gly Asp Glu Ile Cys Cys Trp Ser Phe Tyr Gly Gln Gly Arg
145 150 155 160
Lys Ile Ala Glu Val Cys Cys Thr Ser Ile Val Tyr Ala Thr Glu Lys
165 170 175
Lys Gln Thr Lys Val Arg Gly Ala Pro Glu Pro Met Leu Gly Ala Gly
180 185 190
Gly Gly His
195

<210> 4823
<211> 1984
<212> DNA
<213> Homo sapiens

<400> 4823
nggtttttgt tttttgagcc gcaccccgcg gaggcgagga agcagcagcc gcagcacagc
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agcagctcca atggcgttaa aatggagaat gatgaatcag caaaagaaga gaaatctgac
120
ttaaaggaaa aatctacagg aagtaagaag gccaatagat ttcatcctta ttcaaaagac
180
aagaattcgg gcactggaga aaagaagggt ccaaatcgta acagagtttt cattagcaac
240
atcccatatg acatgaaatg gcaagctatt aaagatctaa tgagagagaa agttggtgag
300
gttacatacg tggagctctt taaggatgcg gaaggaaaat caaggggttg tggtgtggtt
360
gaattcaaag atgaagaatt cgtaaagaaa gccctagaaa ctatgaacaa atatgatctt
420
agtggaagac cccttaatat taaagaggat cctgatggag aaaatgctcg tagggcattg
480
cagcgaacag gaggatcatt tccaggagga cacgtccctg atatgggatc agggttgatg
540
aatttaccac cttccatact caataatcca aacattcctc ctgaagtcat cagtaatttg
600
caggccggta gacttggttc cacaattttt gttgccaatc ttgacttcaa agttggttgg
660
aagaagctaa aggaagtgtt cagcatagct ggaactgtga agcgggcaga tattaaagaa
720
gacaaagatg gcaagagcag aggaatgggc actgtcactt ttgagcaagc aattgaagca
780
gttcaagcaa tttctatgtt caatgggcag tttttatttg atagacctat gcatgtgaaa
840
atggatgaca agtctgttcc tcatgaagag taccgttcac ctgatggtaa aacaccacaa
900
ttaccacgtg gtcttggagg cattgggatg ggacttggtc cgggtggaca gcctattagt
960
gccagccagt tgaacatagg tggagtaatg ggaaatttag gtccaggtgg tatgggaatg
1020
gatggtccag gttttggagg aatgaataga attggaggag gaatagggtt tggtggtctg
1080
gaagcaatga atagcatggg aggatttgga ggagttggcc gaatgggaga gctgtaccgt
1140
ggtgcgatga ctagtagcat ggagcgagat ttcggacgtg gtgatattgg aataaatcga
1200
gcctttggcg attcctttgg tagacttggc agtgcaatga ttggagggat tacaggaaga
1260
ataggatctt ctaacatggg tccagtagga tctggaataa gtggtggaat gggtagcatg
1320
aacagtgtga ctggaggaat ggggatggga ctggaccgga tgagttccag ctttgataga
1380
atgggaccag gtataggagc tatactggaa aggagcatcg atatggatcg aggattttta
1440
tcgggtccaa tgggaagcgg aatgagagag agaataggct ccaaaggcaa ccagatattt
1500
gtcagaaatc taccttttga cttgacttgg cagaaactaa aagagaaatt cagtcagtgt
1560
ggtcatgtaa tgtttgcaga aataaaaatg gagaatggaa agtcaaaagg ctgtggaaca
1620
gtcagatttg actccccaga atcagctgaa aaagcctgca gaataatgaa tggcataaaa
1680

atcagtggca gagaaattga tgttcgcttg gatcgtaatg cataatttca agccatggtt
1740
ggaacattcc tacatctgtt ttgctgaatc tcctagtaaa agtcattttt ttaaagtaat
1800
attgtatgct tacaaaagct gtaaaaatga acttttaaaa ctcccaccag cttttaacag
1860
gtataatggt aaaaatatac tgtaaatttt tggtaatctc aagtttgggt ttttaaagac
1920
agcaagtctg gtcattcagt ttaaatgaat gggtatactg gtttttaatg aaataagcca
1980
tttt
1984

<210> 4824
<211> 547
<212> PRT
<213> Homo sapiens

<400> 4824
Met Glu Asn Asp Glu Ser Ala Lys Glu Glu Lys Ser Asp Leu Lys Glu
1 5 10 15
Lys Ser Thr Gly Ser Lys Lys Ala Asn Arg Phe His Pro Tyr Ser Lys
20 25 30
Asp Lys Asn Ser Gly Thr Gly Glu Lys Lys Gly Pro Asn Arg Asn Arg
35 40 45
Val Phe Ile Ser Asn Ile Pro Tyr Asp Met Lys Trp Gln Ala Ile Lys
50 55 60
Asp Leu Met Arg Glu Lys Val Gly Glu Val Thr Tyr Val Glu Leu Phe
65 70 75 80
Lys Asp Ala Glu Gly Lys Ser Arg Gly Cys Gly Val Val Glu Phe Lys
85 90 95
Asp Glu Glu Phe Val Lys Lys Ala Leu Glu Thr Met Asn Lys Tyr Asp
100 105 110
Leu Ser Gly Arg Pro Leu Asn Ile Lys Glu Asp Pro Asp Gly Glu Asn
115 120 125
Ala Arg Arg Ala Leu Gln Arg Thr Gly Gly Ser Phe Pro Gly Gly His
130 135 140
Val Pro Asp Met Gly Ser Gly Leu Met Asn Leu Pro Pro Ser Ile Leu
145 150 155 160
Asn Asn Pro Asn Ile Pro Pro Glu Val Ile Ser Asn Leu Gln Ala Gly
165 170 175
Arg Leu Gly Ser Thr Ile Phe Val Ala Asn Leu Asp Phe Lys Val Gly
180 185 190
Trp Lys Lys Leu Lys Glu Val Phe Ser Ile Ala Gly Thr Val Lys Arg
195 200 205
Ala Asp Ile Lys Glu Asp Lys Asp Gly Lys Ser Arg Gly Met Gly Thr
210 215 220
Val Thr Phe Glu Gln Ala Ile Glu Ala Val Gln Ala Ile Ser Met Phe
225 230 235 240
Asn Gly Gln Phe Leu Phe Asp Arg Pro Met His Val Lys Met Asp Asp
245 250 255
Lys Ser Val Pro His Glu Glu Tyr Arg Ser Pro Asp Gly Lys Thr Pro
260 265 270
Gln Leu Pro Arg Gly Leu Gly Gly Ile Gly Met Gly Leu Gly Pro Gly

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        275                 280                 285
Gly Gln Pro Ile Ser Ala Ser Gln Leu Asn Ile Gly Gly Val Met Gly
    290                 295                 300
Asn Leu Gly Pro Gly Gly Met Gly Met Asp Gly Pro Gly Phe Gly Gly
305                 310                 315                 320
Met Asn Arg Ile Gly Gly Gly Ile Gly Phe Gly Gly Leu Glu Ala Met
                325                 330                 335
Asn Ser Met Gly Gly Phe Gly Gly Val Gly Arg Met Gly Glu Leu Tyr
            340                 345                 350
Arg Gly Ala Met Thr Ser Ser Met Glu Arg Asp Phe Gly Arg Gly Asp
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<400> 4825

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<212> PRT
<213> Homo sapiens

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Ser Met Lys Arg Gly Leu Asp Val Gln Met Glu Thr Cys Arg Arg Leu
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Ile Thr Gln Ser Gly Asp Arg Lys Ser Pro Ala Phe Thr Ala Val Pro
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Met Glu Asp Cys Leu Leu Gly Gly Thr Arg Val Ser Leu Pro Glu Asp
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Leu Leu Glu Asp Pro Glu Ile Phe Phe Asp Val Val Ser Leu Ser Thr
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Trp Gln Glu Val Leu Ser Asp Ser Gln Arg Glu His Leu Gln Gln Phe

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Ile Ala Gln Lys Leu Phe Arg Asp Gly His Phe Asn Pro Glu Val Val
    130                 135                 140
Lys Tyr Arg Gln Leu Cys Phe Lys Ser Gln Tyr Lys Arg Tyr Leu Asn
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Glu Cys Gly Asp Thr Ala Leu Ser Ser Asp Glu Glu Asp Leu Ser Ser
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1060 1065 1070
Pro Thr Glu Ala Ser Ser Ser Ala Phe Arg Leu Met Pro Ala Leu Gly
1075 1080 1085
Val Ser Val Ala Asp Gln Lys Gly Lys Ser Thr Val Ala Ser Ser Glu
1090 1095 1100
Ala Lys Pro Ala Ala Thr Ile Arg Ile Val Gln Gly Leu Gly Val Met
1105 1110 1115 1120
Pro Pro Lys Ala Gly Gln Thr Ile Thr Val Ala Thr His Ala Lys Gln
1125 1130 1135
Gly Ala Ser Val Ala Ser Gly Ser Gly Thr Val His Thr Ser Ala Val
1140 1145 1150
Ser Leu Pro Ser Met Asn Ala Ala Val Ser Lys Thr Val Ala Val Ala
1155 1160 1165
Ser Gly Ala Ala Ser Thr Pro Ile Ser Ile Ser Thr Gly Ala Pro Thr
1170 1175 1180
Val Arg Gln Val Pro Val Ser Thr Thr Val Val Ser Thr Ser Gln Ala
1185 1190 1195 1200
Gly Lys Leu Pro Thr Arg Ile Thr Val Pro Leu Ser Val Ile Ser Gln
1205 1210 1215
Pro Met Lys Gly Lys Ser Val Val Thr Ala Pro Ile Ile Lys Gly Asn
1220 1225 1230
Leu Gly Ala Asn Leu Ser Gly Leu Gly Arg Asn Ile Ile Leu Thr Thr
1235 1240 1245
Met Pro Ala Gly Thr Lys Leu Ile Ala Gly Asn Lys Pro Val Ser Phe
1250 1255 1260
Leu Thr Ala Gln Gln Leu Gln Gln Leu Gln Gln Gln Gly Gln Ala Thr
1265 1270 1275 1280
Gln Val Arg Ile Gln Thr Val Pro Ala Ser Xaa Leu Gln Gln Gly Thr
1285 1290 1295
Ala Ser Gly Ser Ser Lys Ala Val Ser Thr Val Val Val Thr Thr Ala
1300 1305 1310
Pro Ser Pro Lys Gln Ala Pro Glu Gln Gln
1315 1320

<210> 4829
<211> 1605
<212> DNA
<213> Homo sapiens

<400> 4829

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120
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180
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240
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300
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360
caagataagg accaatgtat tctcattact ggggaaagtg gagcaggaaa aacagaggcc
420
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480
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540
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600
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660
cagccaagag gtgaaagaaa cttccatgtg ttctatcagc tgctctctgg tgcctctgaa
720
gagctcctca ataaacttaa gcttgagagg gatttcagca ggtataacta cctgagtctg
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840
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900
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960
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1020
tcagttctag aacgagcatt cagtttccga acagttgagg ccaaacagga gaaagtttca
1080
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1140
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1200
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1260
agctttgagc agttcattat taattattgt aacgaaaagc tgcaacaaat cttcattgaa
1320
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1380
gactacttca ataatgctat catttgtgac ctaatagaaa ataacacaaa tggaatcctg
1440
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1605

<210> 4830
<211> 512
<212> PRT
<213> Homo sapiens

<400> 4830
Met Ala Lys Met Glu Val Lys Thr Ser Leu Leu Asp Asn Met Ile Gly
1 5 10 15
Val Gly Asp Met Val Leu Leu Glu Pro Leu Asn Glu Glu Thr Phe Ile
20 25 30
Asn Asn Leu Lys Lys Arg Phe Asp His Ser Glu Ile Tyr Thr Tyr Ile
35 40 45
Gly Ser Val Val Ile Ser Val Asn Pro Tyr Arg Ser Leu Pro Ile Tyr
50 55 60
Ser Pro Glu Lys Val Glu Glu Tyr Arg Asn Arg Asn Phe Tyr Glu Leu
65 70 75 80
Ser Pro His Ile Phe Ala Leu Ser Asp Glu Ala Tyr Arg Ser Leu Arg
85 90 95
Asp Gln Asp Lys Asp Gln Cys Ile Leu Ile Thr Gly Glu Ser Gly Ala
100 105 110
Gly Lys Thr Glu Ala Ser Lys Leu Val Met Ser Tyr Val Ala Ala Val
115 120 125
Cys Gly Lys Gly Ala Glu Val Asn Gln Val Lys Glu Gln Leu Leu Gln
130 135 140
Ser Asn Pro Val Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg Asn
145 150 155 160
Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met Asp Ile Glu Phe Asp Phe
165 170 175
Lys Gly Asp Pro Leu Gly Gly Val Ile Ser Asn Tyr Leu Leu Glu Lys
180 185 190
Ser Arg Val Val Lys Gln Pro Arg Gly Glu Arg Asn Phe His Val Phe
195 200 205
Tyr Gln Leu Leu Ser Gly Ala Ser Glu Glu Leu Leu Asn Lys Leu Lys
210 215 220
Leu Glu Arg Asp Phe Ser Arg Tyr Asn Tyr Leu Ser Leu Asp Ser Ala
225 230 235 240
Lys Val Asn Gly Val Asp Asp Ala Ala Asn Phe Arg Thr Val Arg Asn
245 250 255
Ala Met Gln Ile Val Gly Phe Met Asp His Glu Ala Glu Ser Val Leu
260 265 270
Ala Val Val Ala Ala Val Leu Lys Leu Gly Asn Ile Glu Phe Lys Pro
275 280 285
Glu Ser Arg Val Asn Gly Leu Asp Glu Ser Lys Ile Lys Asp Lys Asn
290 295 300
Glu Leu Lys Glu Ile Cys Glu Leu Thr Gly Ile Asp Gln Ser Val Leu
305 310 315 320
Glu Arg Ala Phe Ser Phe Arg Thr Val Glu Ala Lys Gln Glu Lys Val
325 330 335
Ser Thr Thr Leu Asn Val Ala Gln Ala Tyr Tyr Ala Arg Asp Ala Leu
340 345 350
Ala Lys Asn Leu Tyr Ser Arg Leu Phe Ser Trp Leu Val Asn Arg Ile
355 360 365
Asn Glu Ser Ile Lys Ala Gln Thr Lys Val Arg Lys Lys Val Met Gly

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    370                 375                 380
Val Leu Asp Ile Tyr Gly Phe Glu Ile Phe Glu Asp Asn Ser Phe Glu
385                 390                 395                 400
Gln Phe Ile Ile Asn Tyr Cys Asn Glu Lys Leu Gln Gln Ile Phe Ile
                405                 410                 415
Glu Leu Thr Leu Lys Glu Glu Gln Glu Glu Tyr Ile Arg Glu Asp Ile
            420                 425                 430
Glu Trp Thr His Ile Asp Tyr Phe Asn Asn Ala Ile Ile Cys Asp Leu
        435                 440                 445
Ile Glu Asn Asn Thr Asn Gly Ile Leu Ala Met Leu Asp Glu Glu Cys
    450                 455                 460
Leu Arg Pro Gly Thr Val Thr Asp Glu Thr Phe Leu Glu Lys Leu Asn
465                 470                 475                 480
Gln Val Cys Ala Thr His Gln His Phe Glu Ser Arg Met Ser Lys Cys
                485                 490                 495
Ser Arg Phe Leu Asn Asp Thr Ser Leu Pro His Ser Cys Phe Arg Ile
            500                 505                 510
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<210> 4831
<211> 578
<212> DNA
<213> Homo sapiens

<400> 4831
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atgctgagct cagacttcag gcccagcctg ccgctgcccc acttcaacaa gcacctgctg
120
ggcgccgagc acggggacga gccgcgccac gggggcctca ctctgcgcct gggcctccac
180
cagcagagcg tgctcggcgg ccaggaccag ctgcgcgtcc gtgtgacgga gctggaggac
240
gaggtgcgca acctgcgcaa gatcaatcgg gacctgttcg acttctccac gcgcttcatc
300
acgcggccgg ccaagtgagg cccggagacc ccggcccgag gcgcccaggc ctgagcccca
360
tgcctcccag caaccagggc ccgcgggtgt ggcccccacc agcccaggcc tggactctcc
420
tcagttctgt gtcgtgttcg ggtttttcct ctgtgactgg gccgtcttgg tgtctcgtgg
480
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540
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa
578

<210> 4832
<211> 105
<212> PRT
<213> Homo sapiens

<400> 4832
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Arg Thr Val Ala Leu Lys Gly Pro Val Thr Asn Ala Ala Ile Leu Leu
 1               5                  10                  15
Ala Pro Val Ser Met Leu Ser Ser Asp Phe Arg Pro Ser Leu Pro Leu
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            20                  25                  30
Pro His Phe Asn Lys His Leu Leu Gly Ala Glu His Gly Asp Glu Pro
        35                  40                  45
Arg His Gly Gly Leu Thr Leu Arg Leu Gly Leu His Gln Gln Ser Val
    50                  55                  60
Leu Gly Gly Gln Asp Gln Leu Arg Val Arg Val Thr Glu Leu Glu Asp
65                  70                  75                  80
Glu Val Arg Asn Leu Arg Lys Ile Asn Arg Asp Leu Phe Asp Phe Ser
                85                  90                  95
Thr Arg Phe Ile Thr Arg Pro Ala Lys
            100                 105
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<210> 4833
<211> 872
<212> DNA
<213> Homo sapiens

<400> 4833
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ctttgagaag gaactgagta ggcagtgaga agagtcgagt gaagcctggc ccgtgagtgc
120
ctcaacaact gagatgaacg tcgactcgct tgcaggcaag ttgtcactca gcagcgatct
180
gaactatatc ctgggttcca gaaaaggcag aggttcttac cgaaagcagg ggaggaagcc
240
gcagcccaag gaggtcgtca cttgccggga aggtggctcg ggccaggctg cactcaaaac
300
ccgtgctctg tccacactgc tacggggcca gagccaagga agcttccact tcttccccca
360
gacagcccca acagcggcta ccccaaggag ccagcagcct tgtgtcctgg gatccccagc
420
ccctgcagaa tgacccacca ggatctgagc atcacagcca aactcatcaa tggaggtgta
480
gcagggctcg tgggggtgac ctgcgtgttc cccatcgact tggccaagac tcgcctgcag
540
aaccagcatg ggaaagccat gtacaaagga atgatcgact gcctgatgaa gacggctcgg
600
gcggagggct tcttcggcat gtaccgaggg gctgcagtga acctcactct ggtcactcca
660
gagaaggcca tcaagctggc ggccaacgac tttttccggc ggctgctcat ggaagatggg
720
atgcagcgga acctgaagat ggagatgctt gccgggtgtg gggctgggat gtgccaggtc
780
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840
cgtccatcat cagggctcgg cctcagcacc ct
872

<210> 4834
<211> 147
<212> PRT
<213> Homo sapiens

<400> 4834
Met Thr His Gln Asp Leu Ser Ile Thr Ala Lys Leu Ile Asn Gly Gly
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Val Ala Gly Leu Val Gly Val Thr Cys Val Phe Pro Ile Asp Leu Ala
20 25 30
Lys Thr Arg Leu Gln Asn Gln His Gly Lys Ala Met Tyr Lys Gly Met
35 40 45
Ile Asp Cys Leu Met Lys Thr Ala Arg Ala Glu Gly Phe Phe Gly Met
50 55 60
Tyr Arg Gly Ala Ala Val Asn Leu Thr Leu Val Thr Pro Glu Lys Ala
65 70 75 80
Ile Lys Leu Ala Ala Asn Asp Phe Phe Arg Arg Leu Leu Met Glu Asp
85 90 95
Gly Met Gln Arg Asn Leu Lys Met Glu Met Leu Ala Gly Cys Gly Ala
100 105 110
Gly Met Cys Gln Val Val Val Thr Cys Pro Met Glu Met Leu Lys Ile
115 120 125
Gln Leu Gln Ala Cys Trp Thr Pro Gly Arg Pro Ser Ser Gly Leu Gly
130 135 140
Leu Ser Thr
145

<210> 4835
<211> 1846
<212> DNA
<213> Homo sapiens

<400> 4835
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120
cagtgggaga tccagaatac cagccatctg gccgttgatg gggaccgggc agctgcttgg
180
cccgtgggta ttccagcacc atcccgcccg gcctcccgct ttgaggtgct gcgctgggac
240
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300
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660
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720
cgcgtggccc atgcagatgt cttcgcacct gtcaaggccc acgtggcaga gctggagcgg
780

cgtttccccg gtgcccgggt gccatggctc agtgtgcaga cagccgcacc ctcaccactg
840
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900
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960
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1020
gggcctgggc ccccagagct ggggccgtga cactggccgc tttgatcgcc aggcagccag
1080
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1140
gaacaagaag aggagctgct ggagagcctg gatgtgtacg agctgttcct ccacttctcc
1200
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1260
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1320
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1380
tgaccccacc ctgtccccgt gggcccgtgg cattggccac accccacccc acttctcccc
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1500
tggcccactg gtcccctctc tggctctgtg ggtccctggg ctctggacaa gcactggggg
1560
acgtgccccc agagccaccc acttctcatc ccaaacccag tttccctgcc ccctgacgct
1620
gctgattcgg gctgtggcct ccacgtattt atgcagtaca gtctgcctga cgccagccct
1680
gcctctgggc cctgggggct gggctgtaga agagttgttg gggaaggagg gagctgagga
1740
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1800
tggccaagtg tggaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa
1846

<210> 4836
<211> 349
<212> PRT
<213> Homo sapiens

<400> 4836
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His Met Tyr Gln Leu His Lys Ala Phe Ala Arg Ala Glu Leu Glu Arg
20 25 30
Thr Tyr Gln Glu Ile Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser
35 40 45
His Leu Ala Val Asp Gly Asp Arg Ala Ala Ala Trp Pro Val Gly Ile
50 55 60
Pro Ala Pro Ser Arg Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp
65 70 75 80
Tyr Phe Thr Glu Gln His Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg

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                85                  90                  95
Cys Pro Leu Arg Gly Ala Asp Arg Ala Asp Val Ala Asp Val Leu Gly
            100                 105                 110
Thr Ala Leu Glu Glu Leu Asn Arg Arg Tyr His Pro Ala Leu Arg Leu
        115                 120                 125
Gln Lys Gln Gln Leu Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg
    130                 135                 140
Gly Met Glu Tyr Thr Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln
145                 150                 155                 160
Gly Gly Arg Arg Pro Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu
                165                 170                 175
Ser Arg Val Glu Ile Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg
            180                 185                 190
Leu Thr Val Leu Leu Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Pro
        195                 200                 205
Gly Phe Leu Glu Ala Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala
    210                 215                 220
Ala Ala Ala Leu Thr Leu Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln
225                 230                 235                 240
Arg Val Ala His Ala Asp Val Phe Ala Pro Val Lys Ala His Val Ala
                245                 250                 255
Glu Leu Glu Arg Arg Phe Pro Gly Ala Arg Val Pro Trp Leu Ser Val
            260                 265                 270
Gln Thr Ala Ala Pro Ser Pro Leu Arg Leu Met Asp Leu Leu Ser Lys
        275                 280                 285
Lys His Pro Leu Asp Thr Leu Phe Leu Leu Ala Gly Pro Asp Thr Val
    290                 295                 300
Leu Thr Pro Asp Phe Leu Asn Arg Cys Arg Met His Ala Ile Ser Gly
305                 310                 315                 320
Trp Gln Ala Phe Phe Pro Met His Phe Gln Ala Phe His Pro Ala Val
                325                 330                 335
Ala Pro Pro Gln Gly Pro Gly Pro Pro Glu Leu Gly Pro
            340                 345
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<210> 4837
<211> 906
<212> DNA
<213> Homo sapiens

<400> 4837
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gaggaagaag acagtgacga aggggaaaga acaattgaaa ctgcaaaagg gattaatgga
120
actgtaaatt atgatagtgt caattctgac aactctaagc caaagatatt taaaagtcaa
180
atagagaaca taaatttgac caatggcagc aatgggagga acacagagtc cccagctgcc
240
attcaccctt gtggaaatcc tacagtgatt gaggacgctt tggacaagat taaaagcaat
300
gaccctgaca ccacagaagt caatttgaac aacattgaga acatcacaac acagaccctt
360
acccgctttg ctgaagccct caaggacaac actgtggtga agacgttcag tctggccaac
420

acgcatgccg acgacagtgc agccatggcc attgcagaga tgctcaaagt caatgagcac
480
atcaccaacg taaacgtcga gtccaacttc ataacgggaa aggggatcct ggccatcatg
540
agagctctcc agcacaacac ggtgctcacg gagctgcgtt tccataacca gaggcacatc
600
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660
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720
agaaatatgg ataaacagag gcaaaaacgt ttgcaggagc aaaaacagca ggagggatac
780
gatggaggac ccaatcttag gaccaaagtc tggcaaagag gaacacctag cccttcccct
840
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900
acgcgt
906

<210> 4838
<211> 302
<212> PRT
<213> Homo sapiens

<400> 4838
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Gln Glu Glu Glu Glu Glu Glu Asp Ser Asp Glu Gly Glu Arg Thr Ile
            20   25   30
Glu Thr Ala Lys Gly Ile Asn Gly Thr Val Asn Tyr Asp Ser Val Asn
        35   40   45
Ser Asp Asn Ser Lys Pro Lys Ile Phe Lys Ser Gln Ile Glu Asn Ile
    50   55   60
Asn Leu Thr Asn Gly Ser Asn Gly Arg Asn Thr Glu Ser Pro Ala Ala
65   70   75   80
Ile His Pro Cys Gly Asn Pro Thr Val Ile Glu Asp Ala Leu Asp Lys
                85   90   95
Ile Lys Ser Asn Asp Pro Asp Thr Thr Glu Val Asn Leu Asn Asn Ile
            100   105   110
Glu Asn Ile Thr Thr Gln Thr Leu Thr Arg Phe Ala Glu Ala Leu Lys
        115   120   125
Asp Asn Thr Val Val Lys Thr Phe Ser Leu Ala Asn Thr His Ala Asp
    130   135   140
Asp Ser Ala Ala Met Ala Ile Ala Glu Met Leu Lys Val Asn Glu His
145   150   155   160
Ile Thr Asn Val Asn Val Glu Ser Asn Phe Ile Thr Gly Lys Gly Ile
                165   170   175
Leu Ala Ile Met Arg Ala Leu Gln His Asn Thr Val Leu Thr Glu Leu
            180   185   190
Arg Phe His Asn Gln Arg His Ile Met Gly Ser Gln Val Glu Met Glu
        195   200   205
Ile Val Lys Leu Leu Lys Glu Asn Thr Thr Leu Leu Arg Leu Gly Tyr
    210   215   220
His Phe Glu Leu Pro Gly Pro Arg Met Ser Met Thr Ser Ile Leu Thr

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225                 230                 235                 240
Arg Asn Met Asp Lys Gln Arg Gln Lys Arg Leu Gln Glu Gln Lys Gln
                245                 250                 255
Gln Glu Gly Tyr Asp Gly Gly Pro Asn Leu Arg Thr Lys Val Trp Gln
            260                 265                 270
Arg Gly Thr Pro Ser Pro Ser Pro Tyr Val Ser Pro Arg His Ser Pro
        275                 280                 285
Trp Ser Ser Pro Lys Leu Pro Tyr Gly Glu Thr Thr Thr Arg
    290                 295                 300
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<210> 4839
<211> 1313
<212> DNA
<213> Homo sapiens

<400> 4839
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cggcagaaac tggagaaagc gagagacgtc gccagggacc cagggacctc tccctccagt
120
tccccgggcc cgcccggccc tgatggccac tcacgctata gcgcccactc tgtcctgggc
180
catcccgcgc cagcagtgta gcccccagcc cgggcgcctg aatgctctcc ctccggatcg
240
ctgctcgggt ccccactttg gcgaccgntg cccccgagtc ctgcttcccc ggggcctgct
300
ctgtatcagg cgcctgcgcc ttcaagggta cccggcccgc ctgccctccc caagagccga
360
gtttgcgctc ctcccggaat cgtttgagag aaggacaaac ttttggcagg atggaaatct
420
agatgagcct gtccggagca gaacacccct gattagccag gcccaccgcc atccacatct
480
gctcggcaaa gaaggaaggc agcttgttcc agaccttggt gagcagctgc agactgcctg
540
cctagaacag cctccttact ccagcctggc agggaaggaa ggaacctgac ttgcttcgca
600
ggatctggaa gctcagccgg cagagctgag agccgcagtt gcatcctgga gcctgatgct
660
agaagcagct tccgtctttg ggttcttgct gcctcggcct ctgctctgtt cagtttgctg
720
ttgtgttttt ctcccccatg ttggggtggt ggggtacagg gaaataaaat gctttctccc
780
aggcccctaa tccttcccca tgcctccatc agcctcaaag ctgctgacag tcatgaactg
840
caccttccag ccctgcccat aagctactca aagcaaattc aaattctctt ctggccaggg
900
ggaagggcag atgctccctc cttcctcaag cctccctggc tcattgatcc attttgaggg
960
catttggggg tcaaagttga gaccagattg cttcagtttg tataaaatta gcatttctta
1020
tcacaccaag gccacacctg ttctctggcc tcacaaacca gtgaggatgt aaaggtttgt
1080
tgaggtggag gaacagaagt gaaatgagca atctgctcca tttagaagtc agtcgcttcg
1140

gctgttcatt ccactaatat ttatctagta cctattctgt gccaagcatt gtctctacct
1200
cagtttgcca caaatatgaa aaaaaaaaaa ttcttggaac tgtgaggctt caatgtgttg
1260
tggaccaata tacaaataaa ccaatggaaa agaaaaaaaa aaaaaaaaaa aaa
1313

<210> 4840
<211> 66
<212> PRT
<213> Homo sapiens

<400> 4840
Xaa Ala Leu Arg Ala Pro Thr Arg Gly Arg Gly Asn Val Val Gly Trp
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Gly Thr Pro Ala Arg Gln Lys Leu Glu Lys Ala Arg Asp Val Ala Arg
20 25 30
Asp Pro Gly Thr Ser Pro Ser Ser Ser Pro Gly Pro Pro Gly Pro Asp
35 40 45
Gly His Ser Arg Tyr Ser Ala His Ser Val Leu Gly His Pro Ala Pro
50 55 60
Ala Val
65

<210> 4841
<211> 558
<212> DNA
<213> Homo sapiens

<400> 4841
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<213> Homo sapiens

<400> 4842

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Asp Leu Asn Thr Ile Tyr Ser Tyr Leu His Gly Met Glu Ile Leu Ser
100 105 110
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Glu Arg Tyr Ser Gly Asn Gln Val Leu Phe Cys Ser Glu Thr Ile Ala
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Arg Cys Trp Tyr Ile Leu Leu Ser Gly Ser Val Leu Val Lys Gly Ser
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Gln Thr Ile Thr Asp Asp Val Glu Val Asn Ser Tyr Leu Ser Leu Pro
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Ala Asp Leu Thr Lys Met His Leu Thr Glu Asn Pro His Pro Gln Val
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Thr His Val Ser Ser Ser Gln Ser Gly Cys Ser Ile Ala Ser Asp Ser
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        275                 280                 285
Gly Asp Val Asp Leu Thr Arg Leu Pro Glu Gly Pro Val Asp Ser Glu
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Asp Asp Glu Glu Glu Asp Glu Glu Ile Asp Arg Thr Asp Pro Leu Gln
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Gly Arg Asp Leu Val Arg Glu Cys Leu Glu Lys Glu Pro Ala Asp Lys
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Gly Gln Glu Leu Asp Ser Trp Tyr Val Ile Leu Asn Gly Thr Val Glu
385                 390                 395                 400
Ile Ser His Pro Asp Gly Lys Val Glu Asn Leu Phe Met Gly Asn Ser
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Phe Gly Ile Thr Pro Thr Leu Asp Lys Gln Tyr Met His Gly Ile Val
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Arg Thr Lys Val Asp Asp Cys Gln Phe Val Cys Ile Ala Gln Gln Asp
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Tyr Trp Arg Ile Leu Asn His Val Glu Lys Asn Thr His Lys Val Glu
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Glu Glu Gly Glu Ile Val Met Val His Glu His Arg Glu Leu Asp Arg
465                 470                 475                 480
Ser Gly Thr Arg Lys Gly His Ile Val Ile Lys Ala Thr Pro Glu Arg
                485                 490                 495
Leu Ile Met His Leu Ile Glu Glu His Ser Ile Val Asp Pro Thr Tyr
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Ile Glu Asp Phe Leu Leu Thr Tyr Arg Thr Phe Leu Glu Ser Pro Leu
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Asp Lys Val Thr Arg Ile Val Leu Leu Trp Val Asn Asn His Phe Asn
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Asp Phe Glu Gly Asp Pro Ala Met Thr Arg Phe Leu Glu Glu Phe Glu
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Lys Asn Leu Glu Asp Thr Lys Met Asn Gly His Leu Arg Leu Leu Asn
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Ile Ala Cys Ala Ala Lys Ala Lys Trp Arg Gln Val Val Leu Gln Lys
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Gln Asn Phe Glu Asn Ile Thr Phe Met Lys Ala Val Glu Ile Leu Arg
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Asn Asn Thr His Leu Ala Leu Thr Val Lys Thr Asn Ile Phe Val Phe
        675                 680                 685
Lys Glu Leu Leu Phe Arg Thr Glu Gln Glu Lys Ser Gly Val Pro His
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Ile Pro Lys Ile Ala Glu Lys Lys Ser Asn Arg His Ser Ile Gln His
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Val Pro Gly Asp Ile Glu Gln Thr Ser Gln Glu Lys Gly Ser Lys Lys
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Val Lys Ala Asn Thr Val Ser Gly Gly Arg Asn Lys Ile Arg Lys Ile
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Leu Asp Lys Thr Arg Phe Ser Ile Leu Pro Pro Lys Leu Phe Ser Asp
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Gly Gly Leu Ser Gln Ser Gln Asp Asp Ser Ile Val Gly Thr Arg His
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Cys Arg His Ser Leu Ala Ile Met Pro Ile Pro Gly Thr Leu Ser Ser
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Asn Pro Ser Asp Ile Pro Asp Gln Val Ile Arg Val Phe Lys Val Asp
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Val Val Phe His Ala Val His Glu Phe Gly Leu Thr Gly Ala Ser Asp
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Thr Tyr Ser Leu Cys Glu Val Ser Val Thr Pro Glu Gly Val Ile Lys
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Gln Arg Arg Leu Pro Asp Gln Phe Ser Lys Leu Ala Asp Arg Ile Gln
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Cys Ser Asp Glu Asp Ala Gln Glu Leu Val Lys Glu Ser Gln Leu Ser
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Leu Phe Lys Leu Asn Ser Lys Thr Gly Asn Thr His Leu Lys Arg Phe
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Glu Asp Ile Val Asn Gln Glu Thr Phe Trp Val Ala Ser Glu Ile Leu
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Thr Trp Glu Lys Leu Pro Ser Lys Tyr Glu Lys His Leu Gln Asp Leu
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Val Lys Lys Asp Met Thr Phe Leu His Glu Gly Asn Asp Ser Lys Val
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Leu Asn Ala Lys Lys Leu Tyr Glu Asp Ala Gln Met Ala Arg Lys Val
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Lys Gln Tyr Leu Ser Ser Leu Asp Val Glu Thr Asp Glu Glu Lys Phe
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Gln Met Met Ser Leu Gln Trp Glu Pro Ala Tyr Gly Thr Leu Thr Lys
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3286

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<211> 626
<212> PRT
<213> Homo sapiens

<400> 4846
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35 40 45
Phe Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val
50 55 60
Lys Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro
65 70 75 80
Leu Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn
85 90 95
Gln Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser

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                100                 105                 110
Met Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn
        115                 120                 125
Ser Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys Ala
    130                 135                 140
Ser Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro
145                 150                 155                 160
Arg Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser
                165                 170                 175
Pro Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln
            180                 185                 190
Gly Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr
        195                 200                 205
Ser Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu
    210                 215                 220
Ser Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe
225                 230                 235                 240
Arg Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln
                245                 250                 255
Glu Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly
            260                 265                 270
Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr
        275                 280                 285
Ser Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly Asn
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Leu Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly Glu
305                 310                 315                 320
Asn Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg
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Ser Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro
            340                 345                 350
Thr Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu Leu
        355                 360                 365
Gly Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr
    370                 375                 380
Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser Pro
385                 390                 395                 400
Glu Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu Leu
                405                 410                 415
Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg
            420                 425                 430
Asp Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro Gly
        435                 440                 445
Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu Ser
    450                 455                 460
Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr Leu
465                 470                 475                 480
His Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile Leu
                485                 490                 495
Arg Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser Lys
            500                 505                 510
Arg Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val Thr
        515                 520                 525
Gly Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly Tyr
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    530                 535                 540
Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu Met
545                 550                 555                 560
Leu Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala Ile
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Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His Ile
            580                 585                 590
Ser Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala Arg
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Gln Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala Gln Leu
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Met Tyr
625
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<210> 4847
<211> 2804
<212> DNA
<213> Homo sapiens

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240
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300
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420
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<210> 4848
<211> 242
<212> PRT
<213> Homo sapiens

<400> 4848
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Ile Leu Gln Asp Met Tyr Lys Thr Lys Lys Lys Lys Thr Arg Val Ile
35 40 45
Leu Arg Met Leu Pro Ile Ser Gly Thr Cys Lys Ala Phe Leu Glu Asp
50 55 60
Met Lys Lys Tyr Ala Glu Thr Phe Leu Glu Pro Trp Phe Lys Ala Pro
65 70 75 80
Asn Lys Gly Thr Phe Gln Ile Val Tyr Lys Ser Arg Asn Asn Ser His
85 90 95
Val Asn Arg Glu Glu Val Ile Arg Glu Leu Ala Gly Ile Val Cys Thr
100 105 110
Leu Asn Ser Glu Asn Lys Val Asp Leu Thr Asn Pro Gln Tyr Thr Val
115 120 125
Val Val Glu Ile Ile Lys Ala Val Cys Cys Leu Ser Val Val Lys Asp
130 135 140
Tyr Met Leu Phe Arg Lys Tyr Asn Leu Gln Glu Val Val Lys Ser Pro
145 150 155 160
Lys Asp Pro Ser Gln Leu Asn Ser Lys Gln Gly Asn Gly Lys Glu Ala
165 170 175
Lys Leu Glu Ser Ala Asp Lys Ser Asp Gln Asn Asn Thr Ala Glu Gly
180 185 190
Lys Asn Asn Gln Gln Val Pro Glu Asn Thr Glu Glu Leu Gly Gln Thr
195 200 205
Lys Pro Thr Ser Asn Pro Gln Val Val Asn Glu Gly Gly Ala Lys Pro
210 215 220
Glu Leu Ala Ser Gln Ala Thr Glu Gly Ser Lys Ser Asn Glu Asn Asp
225 230 235 240
Phe Ser

<210> 4849
<211> 321
<212> DNA
<213> Homo sapiens

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321

<210> 4850
<211> 90
<212> PRT
<213> Homo sapiens

<400> 4850
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Gln Glu Arg Gly Ser Ala His Leu Val Ala Leu Lys Cys Ile Pro Lys
        35   40   45
Lys Ala Leu Arg Gly Lys Glu Ala Leu Val Glu Asn Glu Ile Ala Val
    50   55   60
Leu Arg Arg Ile Ser His Pro Asn Ile Val Ala Leu Glu Asp Val His
65   70   75   80
Glu Ser Pro Ser His Leu Tyr Leu Ala Met
                85   90

<210> 4851
<211> 820
<212> DNA
<213> Homo sapiens

<400> 4851
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240
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720
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780
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820

<210> 4852
<211> 207
<212> PRT
<213> Homo sapiens

<400> 4852
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20 25 30
Ser Ala Ala Leu His Arg Arg Val Ala Ala Met Arg Glu Ala Gly Thr
35 40 45
Ala Leu Pro Asp Gln Tyr Gln Glu Asp Ala Ser Asp Met Lys Asp Met
50 55 60
Ser Lys Tyr Lys Pro His Ile Leu Leu Ser Gln Glu Asn Thr Gln Ile
65 70 75 80
Arg Asp Leu Gln Gln Glu Asn Arg Glu Leu Trp Ile Ser Leu Glu Glu
85 90 95
His Gln Asp Ala Leu Glu Leu Ile Met Ser Lys Tyr Arg Lys Gln Met
100 105 110
Leu Gln Leu Met Val Ala Lys Lys Ala Val Asp Ala Glu Pro Val Leu
115 120 125
Lys Ala His Gln Ser His Ser Ala Glu Ile Glu Ser Gln Ile Asp Arg
130 135 140
Ile Cys Glu Met Gly Glu Val Met Arg Lys Ala Val Gln Val Asp Asp
145 150 155 160
Asp Gln Phe Cys Lys Ile Gln Glu Lys Leu Ala Gln Leu Glu Leu Glu
165 170 175
Asn Lys Glu Leu Arg Glu Leu Leu Ser Ile Ser Ser Glu Ser Leu Gln
180 185 190
Ala Arg Lys Glu Asn Ser Met Asp Thr Ala Ser Gln Ala Ile Lys
195 200 205

<210> 4853
<211> 1467
<212> DNA
<213> Homo sapiens

<400> 4853
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120

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1467

<210> 4854
<211> 311
<212> PRT
<213> Homo sapiens

<400> 4854
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Glu Asn Pro Glu Gln Val Ala Ser Glu Gly Leu Pro Glu Pro Val Leu
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Arg Lys Val Glu Leu Pro Val Pro Thr His Arg Arg Pro Val Gln Ala
    50                  55                  60
Trp Val Glu Ser Leu Arg Gly Phe Glu Gln Glu Arg Val Gly Leu Ala
65                  70                  75                  80
Asp Leu His Pro Asp Val Phe Ala Thr Ala Pro Arg Leu Asp Ile Leu
                85                  90                  95
His Gln Val Ala Met Trp Gln Lys Asn Phe Lys Arg Ile Ser Tyr Ala
            100                 105                 110
Lys Thr Lys Thr Arg Ala Glu Val Arg Gly Gly Gly Arg Lys Pro Xaa
        115                 120                 125
Ala Ala Glu Arg His Trp Ala Gly Pro Ala Trp Gln His Pro Leu Ser
    130                 135                 140
Ala Leu Ala Arg Arg Arg Cys Cys Pro Trp Pro Pro Gly Pro Thr Ser
145                 150                 155                 160
Tyr Tyr Tyr Met Leu Pro Met Lys Val Arg Ala Leu Gly Leu Lys Val
                165                 170                 175
Ala Leu Thr Val Lys Leu Ala Gln Asp Asp Leu His Ile Met Asp Ser
            180                 185                 190
Leu Glu Leu Pro Thr Gly Asp Pro Gln Tyr Leu Thr Glu Leu Ala His
        195                 200                 205
Tyr Arg Arg Trp Gly Asp Ser Val Leu Leu Val Asp Leu Thr His Glu
    210                 215                 220
Glu Met Pro Gln Ser Ile Val Glu Ala Thr Ser Arg Leu Lys Thr Phe
225                 230                 235                 240
Asn Leu Ile Pro Ala Val Gly Leu Asn Val His Ser Met Leu Lys His
                245                 250                 255
Gln Thr Leu Val Leu Thr Leu Pro Thr Val Ala Phe Leu Glu Asp Lys
            260                 265                 270
Leu Leu Trp Gln Asp Ser Arg Tyr Arg Pro Leu Tyr Pro Phe Ser Leu
        275                 280                 285
Pro Tyr Ser Asp Phe Pro Arg Pro Leu Pro His Ala Thr Gln Gly Pro
    290                 295                 300
Ala Ala Thr Pro Tyr His Cys
305                 310
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<210> 4855
<211> 750
<212> DNA
<213> Homo sapiens

<400> 4855
nncgcaggag taacctactt ggtctcctgc tttcgcgaca tggccttcaa ttttggggct
60
ccctcgggca cctccggtac cgctgcagcc accgcggccc ccgcgggtgg gtttggagga
120
tttgggacaa catctacaac tgcaggttct gcattcagct tttctgcccc aactaacaca
180
ggcactactg gactctttgg tggtactcag aacaaaggtt ttggatttgg tactggtttt
240

ggcacaacaa cgggaactag tactggttta ggtactggtt tgggaactgg actgggattt
300
ggaggattta atacacagca gcagcagcag caaactacat taggtggtct cttcagtcag
360
cctacacaag ctcctaccca gtccaaccag ctgataaata ctgcgagtgc tctttctgct
420
ccaacgctgt tgggagatga gagagatgct attttggcaa aatggaatca actgcaggcc
480
ttttggggaa caggaaaagg gtatttcaac aataatattc cgccagtgga attcacacaa
540
gaaaatccct tttgccgatt taaggcagta ggttatagtt gcatgcccag taataaagat
600
gaagacgggc tagtggtttt agttttcaac aaaaaagaaa cagagattcg aagccaacaa
660
caacagttgg tagaatcatt gcataaagtt ttgggaggaa accagaccct tactgtaaat
720
gtagagggca ctaaaacatt gccagatgat
750

<210> 4856
<211> 237
<212> PRT
<213> Homo sapiens

<400> 4856
Met Ala Phe Asn Phe Gly Ala Pro Ser Gly Thr Ser Gly Thr Ala Ala
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Ala Thr Ala Ala Pro Ala Gly Gly Phe Gly Gly Phe Gly Thr Thr Ser
20 25 30
Thr Thr Ala Gly Ser Ala Phe Ser Phe Ser Ala Pro Thr Asn Thr Gly
35 40 45
Thr Thr Gly Leu Phe Gly Gly Thr Gln Asn Lys Gly Phe Gly Phe Gly
50 55 60
Thr Gly Phe Gly Thr Thr Thr Gly Thr Ser Thr Gly Leu Gly Thr Gly
65 70 75 80
Leu Gly Thr Gly Leu Gly Phe Gly Gly Phe Asn Thr Gln Gln Gln Gln
85 90 95
Gln Gln Thr Thr Leu Gly Gly Leu Phe Ser Gln Pro Thr Gln Ala Pro
100 105 110
Thr Gln Ser Asn Gln Leu Ile Asn Thr Ala Ser Ala Leu Ser Ala Pro
115 120 125
Thr Leu Leu Gly Asp Glu Arg Asp Ala Ile Leu Ala Lys Trp Asn Gln
130 135 140
Leu Gln Ala Phe Trp Gly Thr Gly Lys Gly Tyr Phe Asn Asn Asn Ile
145 150 155 160
Pro Pro Val Glu Phe Thr Gln Glu Asn Pro Phe Cys Arg Phe Lys Ala
165 170 175
Val Gly Tyr Ser Cys Met Pro Ser Asn Lys Asp Glu Asp Gly Leu Val
180 185 190
Val Leu Val Phe Asn Lys Lys Glu Thr Glu Ile Arg Ser Gln Gln Gln
195 200 205
Gln Leu Val Glu Ser Leu His Lys Val Leu Gly Gly Asn Gln Thr Leu
210 215 220
Thr Val Asn Val Glu Gly Thr Lys Thr Leu Pro Asp Asp

225 230 235

<210> 4857
<211> 2887
<212> DNA
<213> Homo sapiens

<400> 4857
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ctcgggagct ccagtcaggc cgcctgcctc aaacagatcc ttctgctgca attggacctc
120
atcgaacagc agcagcagca gctgcaggcc aaggaaaagg agatcgagga gctgaagtca
180
gagagagaca cgctccttgc tcggattgaa cgtatggaaa ggcggatgca gctggtaaag
240
aaggataacg agaaagaaag gcacaagctg tttcagggct atgaaactga agagagagag
300
gaaacagagc tatctgagaa aattaaactg gagtgccagc cggagctttc cgagacatcc
360
cagactctgc ctcccaagcc cttctcatgt gggcggagtg gaaagggaca taaaaggaaa
420
tccccatttg gaagtacaga aagaaagact cctgttaaaa agctggctcc tgaattttca
480
aaagtcaaaa caaaaactcc taagcactct cctattaaag aggaaccctg tggttcctta
540
tctgaaactg tttgtaaacg tgaattgagg agccaagaaa ccccagaaaa gccccggtct
600
tcagtggaca ccccaccaag actctccact ccccaaaagg gacccagcac ccatcccaag
660
gagaaagcct tctcaagtga gatagaagat ttgccgtacc tttccaccac agaaatgtat
720
ttgtgtcgtt ggcaccagcc tcccccatca ccgttaccat tacgggaatc ctctccaaag
780
aaggaggaga ctgtagcaag taaggcatag agaacacttg ctcttatacc ctagtggtgg
840
cggtcaagct aacaagtgtg aaaatgcctt tggcattttt aaaaaagtgc aatcaataaa
900
gcagagttct gtcaagaatg agtaagttaa cagccagaga cagacactgt gcaggcattg
960
caaatagatg gaattacagc aaaatgtgct caatgtattt gcctgcttac aacactggga
1020
gatgtgtttg ccagtaagtt gctcatcaca agagcaccag acttgggggt gtaatctccg
1080
gcaacttgca tgccctctga aagaagggtt ttctgtgctg tgaaatgcat agaactatac
1140
tttgccatgc acgactgttc ctgcaattga tattgtgtga aatctgggag ggtggtcttt
1200
gggtgttctc aggggccaat ggtaattttt gggttgggga gccagcttgg ggtggggaat
1260
tttcacctgg gcctccgctc tttaactata taaacattta tctgtatatc tatgtccctg
1320
tctgggggggc aggaggaatc tgccaaagac caacagtctt actttatctt actatacttc
1380

acaaaggttc taaaatgtga agagtttgtt tgaaaaatag tttgtagacc attttattta
1440
aatatatgaa caaccaatgg gctactgcaa tccaagtaaa ctcttcacat tttagaacct
1500
ttgtgaagta tagtaagata aagtaagact gttggtcttt ggcagattcc tcctgccccc
1560
cagacaggga catagatata cagataaatg tttatatagt taaagagcgg aggcccaggt
1620
gaaaattccc caccccaagc tggctcccca acccaaaaat taccattggc ccctgagaac
1680
acccaaagac caccctccca gatttcacac aatatcaatt gcaggaacag tcgtgcatgg
1740
caaagtatag ttctatgcat ttcacagcac agaaaaccct tctttcagag ggcatgcaag
1800
ttgccggaga ttacaccccc aagtctggtg ctcttgtgat gagcaactta ctggcaaaca
1860
catctcccag tgttgtaagc aggcaaatac attgagcaca ttttgctgta attccatcta
1920
tttgcaatgc ctgcacagtg tctgtctctg gctgttaact tactcattct tgacagaact
1980
ctgctttatt gattgcactt ttttaaaaat gccaaaggca ttttcacact tgttagcttg
2040
accgccacca ctagggtata agagcaagtg ttctctatgc cttacttgct acagtctcct
2100
ccttctttgg agaggattcc cgtaatggta acggtgatgg gggaggctgg tgccaacgac
2160
acaaatacat ttctgtggtg gaaaggtacg gcaaatcttc tatctcactt gagaaggctt
2220
tctccttggg atgggtgctg ggtccctttt ggggagtgga gagtcttggt ggggtgtcca
2280
ctgaagaccg gggcttttct ggggtttctt ggctcctcaa ttcacgttta caaacagttt
2340
cagataagga accacagggt tcctctttaa taggagagtg cttaggagtt tttgttttga
2400
cttttgaaaa ttcaggagcc agctttttaa caggagtctt tctttctgta cttccaaatg
2460
ggggtagaag tctaacccct ccacccccctc tcctccccag cagtcccacg cgggtatggg
2520
agagaatgaa gttctttgtc tctaagggat tcaaaccaga aacggaggga cctctggttc
2580
ccagagggag gaaaatccat gatgtctgct gcccagggag ctattgccac cgcctccttg
2640
ggatgaagta ttgccagcta ccaacagttc cttcccaacg gccatcttcc agccttctta
2700
aacgactcct agcatcttcg ggaggctcct gaaggactga agcaaaggaa atctctgaag
2760
ggatttagtc cttgaaaggg agtagggata cttagggtgt tctgtgttga gcgcttcttc
2820
ctatctctcc agcttcatgt atgtgtgtct ttatgtccaa gcaattgagc caacaagtcc
2880
tcagaat
2887

<210> 4858

<211> 269
<212> PRT
<213> Homo sapiens

<400> 4858
Xaa Gly Arg Arg Gly Gln Met Glu Glu Tyr Glu Glu Glu Pro Ser Arg
1 5 10 15
Gly Trp Trp Arg Leu Gly Ser Ser Ser Gln Ala Ala Cys Leu Lys Gln
20 25 30
Ile Leu Leu Leu Gln Leu Asp Leu Ile Glu Gln Gln Gln Gln Gln Leu
35 40 45
Gln Ala Lys Glu Lys Glu Ile Glu Glu Leu Lys Ser Glu Arg Asp Thr
50 55 60
Leu Leu Ala Arg Ile Glu Arg Met Glu Arg Arg Met Gln Leu Val Lys
65 70 75 80
Lys Asp Asn Glu Lys Glu Arg His Lys Leu Phe Gln Gly Tyr Glu Thr
85 90 95
Glu Glu Arg Glu Glu Thr Glu Leu Ser Glu Lys Ile Lys Leu Glu Cys
100 105 110
Gln Pro Glu Leu Ser Glu Thr Ser Gln Thr Leu Pro Pro Lys Pro Phe
115 120 125
Ser Cys Gly Arg Ser Gly Lys Gly His Lys Arg Lys Ser Pro Phe Gly
130 135 140
Ser Thr Glu Arg Lys Thr Pro Val Lys Lys Leu Ala Pro Glu Phe Ser
145 150 155 160
Lys Val Lys Thr Lys Thr Pro Lys His Ser Pro Ile Lys Glu Glu Pro
165 170 175
Cys Gly Ser Leu Ser Glu Thr Val Cys Lys Arg Glu Leu Arg Ser Gln
180 185 190
Glu Thr Pro Glu Lys Pro Arg Ser Ser Val Asp Thr Pro Pro Arg Leu
195 200 205
Ser Thr Pro Gln Lys Gly Pro Ser Thr His Pro Lys Glu Lys Ala Phe
210 215 220
Ser Ser Glu Ile Glu Asp Leu Pro Tyr Leu Ser Thr Thr Glu Met Tyr
225 230 235 240
Leu Cys Arg Trp His Gln Pro Pro Pro Ser Pro Leu Pro Leu Arg Glu
245 250 255
Ser Ser Pro Lys Lys Glu Glu Thr Val Ala Ser Lys Ala
260 265

<210> 4859
<211> 689
<212> DNA
<213> Homo sapiens

<400> 4859
cctgctgagg acatgaggac ccgtcttttt gcagtgccag gcagggtggc caaagaggac
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tggactctgg acctggagcc ccgtggtcca gttcacattc accccacaag agtttcagga
120
ggcctcccac ggtgcctgtg ctgggtggcg gtggtggtgc caagaggaat ggaatgtcct
180
gggctccttc aggagctctc tacccagggg caaggagagc ccagagagaa gcgccctggt
240

ctcttgagct tcctgatctg ctcctgtccc ccgctctcct ccactccctt gcctttccct
300
aggttgtccc ctccctgggc ttttgtgtgt tttgggagat gtcacctaac caggacattg
360
atattcaatc ccatcccccc tcctcccacc ctgccccact ttgatttaat cctttggctg
420
tgggctgagg cctcccaggg aagttgggtg gggtgggtgt tgagaccccc tcagaccagc
480
acagagacct gtccttgtgc agtctgcacc ctgcactccc tcccttgcct gtagatgttc
540
tggatgacag tagaggaaat ggacaaggtc agtttgaata tcccagaaca cagtgctctg
600
tctcctccca ccagtccagt tagcttccct tctggaccaa tagacgaggg gagaccccat
660
ggatcctctg gctgggaagc acctgacca
689

<210> 4860
<211> 173
<212> PRT
<213> Homo sapiens

<400> 4860
Met Arg Thr Arg Leu Phe Ala Val Pro Gly Arg Val Ala Lys Glu Asp
1 5 10 15
Trp Thr Leu Asp Leu Glu Pro Arg Gly Pro Val His Ile His Pro Thr
20 25 30
Arg Val Ser Gly Gly Leu Pro Arg Cys Leu Cys Trp Val Ala Val Val
35 40 45
Val Pro Arg Gly Met Glu Cys Pro Gly Leu Leu Gln Glu Leu Ser Thr
50 55 60
Gln Gly Gln Gly Glu Pro Arg Glu Lys Arg Pro Gly Leu Leu Ser Phe
65 70 75 80
Leu Ile Cys Ser Cys Pro Pro Leu Ser Ser Thr Pro Leu Pro Phe Pro
85 90 95
Arg Leu Ser Pro Pro Trp Ala Phe Val Cys Phe Gly Arg Cys His Leu
100 105 110
Thr Arg Thr Leu Ile Phe Asn Pro Ile Pro Leu Pro Pro Thr Leu Pro
115 120 125
His Phe Asp Leu Ile Leu Trp Leu Trp Ala Glu Ala Ser Gln Gly Ser
130 135 140
Trp Val Gly Trp Val Leu Arg Pro Pro Gln Thr Ser Thr Glu Thr Cys
145 150 155 160
Pro Cys Ala Val Cys Thr Leu His Ser Leu Pro Cys Leu
165 170

<210> 4861
<211> 1622
<212> DNA
<213> Homo sapiens

<400> 4861
ctgcagactt ccggcggcgc gctgcaggcg cggggaacac caatggcggg gtacttgaag
60

ctggtgtgtg tttcctttca gcgtcaaggg ttccacactg ttgggagtcg ctgcaagaat
120
cggacaggcg ctgagcacct gtggctgacc cgacatctca gggacccatt tgtgaaggct
180
gcgaaggtgg agagttaccg gtgtcgaagc gccttcaagc tcctggaggt gaacgagagg
240
caccagattc tgcggcccgg ccttcgggtg ttagactgtg gggcagctcc tggggcctgg
300
agtcaggtgg cggtgcagaa ggtcaacgcc gcaggcacag atcccagctc tcctgttggc
360
ttcgtgcttg gggtagatct tcttcacata ttccccctgg aaggagcaac ttttctgtgc
420
cctgctgacg tgactgaccc gagaacctca cagagaatcc tcgaggtgct tcctggcagg
480
agagcagatg tgattctgag cgacatggcg cccaatgcca cagggttccg ggacctcgat
540
catgacaggc tcatcagcct gtgcctgacc cttctcagcg tgaccccaga catcctgcaa
600
cctgggggga cattcctttg taaaacctgg gctggaagtc aaagccgtcg gttacagagg
660
agactgacag aggaattcca gaatgtaagg atcatcaaac ctgaagccag caggaaagag
720
tcatcagaag tgtacttctt ggccacacag taccacggaa ggaagggcac tgtgaagcag
780
tgaggatttc ttgtgccatt ttcataatgg tcattagctc cttttaagct agaaacgtag
840
cctgagctcc tgaagagttc ctgggagatt tgagctgatt ttggagatgg agcaggacaa
900
gtggggagtc tctctctctc tttctctctc tctcttttta accaaaaaga gatgacaaaa
960
ctaagttcag gggccatgga aaatgaaaaa gtccgctata ttgtgatttg ggaagagaaa
1020
gttatcaaga gaaagaggtg aggatggaag gatggagaaa aacagactgt gggaaggatc
1080
agaaggaatc cgccgaggca gggatgggtg tgcccatgtg tgccttgacg ggacttcatc
1140
ttatagactg ttaaactgtc acacacaaac aggctttcca cccctgctct gagagcacca
1200
cgcacagatt tccagttctt agtgtggctg tttaaagtag aaaatctggg ggctgggtga
1260
ggccactcat gcctgtaaac ccagggcttt agaaggctga ggctggggga ttgcttgaag
1320
tcaggagttc aagaccaacc tgggcaacat agcaacaccc cccatgtcta caaaaatgaa
1380
aaaccaaaaa gcaaaccaaa agaaaaatct gaaatttcca tctggggatt aacttctgtc
1440
tttctggtga acaatatagc aattcacgca ttcttcaagc agcaaaagtt cccggaacaa
1500
ttagggaaga cgtatggtct gaatttatcc aggcagtggg tctgctttgg tttttgctgg
1560
aaatttatat cagtgtctgg gctcccaaga acataaatgt aattgccaaa gcaaaaaaaa
1620
aa
1622

<210> 4862
<211> 260
<212> PRT
<213> Homo sapiens

<400> 4862
Leu Gln Thr Ser Gly Gly Ala Leu Gln Ala Arg Gly Thr Pro Met Ala
1 5 10 15
Gly Tyr Leu Lys Leu Val Cys Val Ser Phe Gln Arg Gln Gly Phe His
20 25 30
Thr Val Gly Ser Arg Cys Lys Asn Arg Thr Gly Ala Glu His Leu Trp
35 40 45
Leu Thr Arg His Leu Arg Asp Pro Phe Val Lys Ala Ala Lys Val Glu
50 55 60
Ser Tyr Arg Cys Arg Ser Ala Phe Lys Leu Leu Glu Val Asn Glu Arg
65 70 75 80
His Gln Ile Leu Arg Pro Gly Leu Arg Val Leu Asp Cys Gly Ala Ala
85 90 95
Pro Gly Ala Trp Ser Gln Val Ala Val Gln Lys Val Asn Ala Ala Gly
100 105 110
Thr Asp Pro Ser Ser Pro Val Gly Phe Val Leu Gly Val Asp Leu Leu
115 120 125
His Ile Phe Pro Leu Glu Gly Ala Thr Phe Leu Cys Pro Ala Asp Val
130 135 140
Thr Asp Pro Arg Thr Ser Gln Arg Ile Leu Glu Val Leu Pro Gly Arg
145 150 155 160
Arg Ala Asp Val Ile Leu Ser Asp Met Ala Pro Asn Ala Thr Gly Phe
165 170 175
Arg Asp Leu Asp His Asp Arg Leu Ile Ser Leu Cys Leu Thr Leu Leu
180 185 190
Ser Val Thr Pro Asp Ile Leu Gln Pro Gly Gly Thr Phe Leu Cys Lys
195 200 205
Thr Trp Ala Gly Ser Gln Ser Arg Arg Leu Gln Arg Arg Leu Thr Glu
210 215 220
Glu Phe Gln Asn Val Arg Ile Ile Lys Pro Glu Ala Ser Arg Lys Glu
225 230 235 240
Ser Ser Glu Val Tyr Phe Leu Ala Thr Gln Tyr His Gly Arg Lys Gly
245 250 255
Thr Val Lys Gln
260

<210> 4863
<211> 355
<212> DNA
<213> Homo sapiens

<400> 4863
ctgggggctc actttcgggt gcacctggtg aagatggtca ttctgacaga gcctgagggt
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gccccaaata tcacagccaa cctcacctcg tccctgctga gcgtctgtgg gtggagccag
120
accatcaacc ctgaggacga cacggatcct ggccatgctg acctggtcct ctatatcact
180

aggtttgacc tggagttgcc tgatggtaac ncggcagtgc ggggcgtcac ccagctgggc
240
ggggcctgct ccccaacctg gagctgcctc attaccgagg acactggctt cgacctggga
300
gtcaccattg cccatgagat tgggcacagc ttcggcctgg agcacgacgg cgcgc
355

<210> 4864
<211> 118
<212> PRT
<213> Homo sapiens

<400> 4864
Leu Gly Ala His Phe Arg Val His Leu Val Lys Met Val Ile Leu Thr
1 5 10 15
Glu Pro Glu Gly Ala Pro Asn Ile Thr Ala Asn Leu Thr Ser Ser Leu
20 25 30
Leu Ser Val Cys Gly Trp Ser Gln Thr Ile Asn Pro Glu Asp Asp Thr
35 40 45
Asp Pro Gly His Ala Asp Leu Val Leu Tyr Ile Thr Arg Phe Asp Leu
50 55 60
Glu Leu Pro Asp Gly Asn Xaa Ala Val Arg Gly Val Thr Gln Leu Gly
65 70 75 80
Gly Ala Cys Ser Pro Thr Trp Ser Cys Leu Ile Thr Glu Asp Thr Gly
85 90 95
Phe Asp Leu Gly Val Thr Ile Ala His Glu Ile Gly His Ser Phe Gly
100 105 110
Leu Glu His Asp Gly Ala
115

<210> 4865
<211> 444
<212> DNA
<213> Homo sapiens

<400> 4865
accggtgaga agccctacaa atgtgaggtc tgcagcaagg ccttctccca gagctctgac
60
ctcatcaaac accagcgcac ccacactggc gagcggccct acaaatgtcc ccgttgcggc
120
aaggccttcg ccgacagctc ttacctgctt cgccaccagc gcactcactc tggccagaag
180
ccctacaagt gcccacattg tggcaaggcc ttcggcgaca gctcctacct cctgcgacac
240
cagcgcaccc acagccacga gcggccctac agctgcaccg agtgcggcaa gtgctatagc
300
cagaactcgt ccctgcgcag ccatcagagg gtgcacaccg gtcagaggcc cttcagctgt
360
ggcatctgcg gcaagagctt ctcccagcgg tcggcccttа tcccccatgc ccgcagccac
420
gcccgggaga agcccttcac gcgt
444

<210> 4866

<211> 148
<212> PRT
<213> Homo sapiens

<400> 4866
Thr Gly Glu Lys Pro Tyr Lys Cys Glu Val Cys Ser Lys Ala Phe Ser
1 5 10 15
Gln Ser Ser Asp Leu Ile Lys His Gln Arg Thr His Thr Gly Glu Arg
20 25 30
Pro Tyr Lys Cys Pro Arg Cys Gly Lys Ala Phe Ala Asp Ser Ser Tyr
35 40 45
Leu Leu Arg His Gln Arg Thr His Ser Gly Gln Lys Pro Tyr Lys Cys
50 55 60
Pro His Cys Gly Lys Ala Phe Gly Asp Ser Ser Tyr Leu Leu Arg His
65 70 75 80
Gln Arg Thr His Ser His Glu Arg Pro Tyr Ser Cys Thr Glu Cys Gly
85 90 95
Lys Cys Tyr Ser Gln Asn Ser Ser Leu Arg Ser His Gln Arg Val His
100 105 110
Thr Gly Gln Arg Pro Phe Ser Cys Gly Ile Cys Gly Lys Ser Phe Ser
115 120 125
Gln Arg Ser Ala Leu Ile Pro His Ala Arg Ser His Ala Arg Glu Lys
130 135 140
Pro Phe Thr Arg
145

<210> 4867
<211> 391
<212> DNA
<213> Homo sapiens

<400> 4867
ggatcccaga gggagttcta tctggacttg ccccaagcag gttgctaggc agtagcctca
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tatccttggt gggaggatga gaaggacaaa aagaggcaac cagcctaggg acatcggcct
120
ccttctccac atccccattc tggtaggaaa agtcacccat gccaggatat ccccagccca
180
gagacagccc caggggggtgc tgcctggaga cagccgggat agcttcagtc tcctgaccct
240
gacacgggct gcaccaccag acaatgggca ttttcaggcc agactctggc acaaagagaa
300
ggggcagggc caaggctatg gcccacaagc tcctcagcag ctgagatggg tgcaggaggt
360
agcgctctac tcccatagct ccccactgta t
391

<210> 4868
<211> 125
<212> PRT
<213> Homo sapiens

<400> 4868
Met Gly Val Glu Arg Tyr Leu Leu His Pro Ser Gln Leu Leu Arg Ser

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 1               5                  10                  15
Leu Trp Ala Ile Ala Leu Ala Leu Pro Leu Leu Phe Val Pro Glu Ser
            20                  25                  30
Gly Leu Lys Met Pro Ile Val Trp Trp Cys Ser Pro Cys Gln Gly Gln
        35                  40                  45
Glu Thr Glu Ala Ile Pro Ala Val Ser Arg Gln His Pro Leu Gly Leu
    50                  55                  60
Ser Leu Gly Trp Gly Tyr Pro Gly Met Gly Asp Phe Ser Tyr Gln Asn
65                  70                  75                  80
Gly Asp Val Glu Lys Glu Ala Asp Val Pro Arg Leu Val Ala Ser Phe
                85                  90                  95
Cys Pro Ser His Pro Pro Thr Lys Asp Met Arg Leu Leu Pro Ser Asn
            100                 105                 110
Leu Leu Gly Ala Ser Pro Asp Arg Thr Pro Ser Gly Ile
        115                 120                 125
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<210> 4869
<211> 418
<212> DNA
<213> Homo sapiens

<400> 4869
cccgggaaga gggtcgcccg ccataaatgc ggaaacagtt aaatggcgat gggaatagga
60
tgggaactca atggtgttgc tacctttgga tggactcgga ggcagcccag cttcctggga
120
caggactgca cggactgcct ggggaggggt ctttggcccc ccggttcctg caggggggct
180
cggggaggcc ctgtgagcag ttggtcacag gtgggtccca ttcgatgcga tcctgttcct
240
ccccaacagc cctggagaag ggggacgttg cctgctgtgg ctgcggctgt tttcctggcc
300
tgtgagaggc ggggccagag tggccgttgg gaatctgggt gttgcaaggt gaccacaaac
360
agctctctgg gggaggagga ggaaaatgca attgattttc aggagccttc tgaggtcg
418

<210> 4870
<211> 125
<212> PRT
<213> Homo sapiens

<400> 4870
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Met Ala Met Gly Ile Gly Trp Glu Leu Asn Gly Val Ala Thr Phe Gly
 1               5                  10                  15
Trp Thr Arg Arg Gln Pro Ser Phe Leu Gly Gln Asp Cys Thr Asp Cys
            20                  25                  30
Leu Gly Arg Gly Leu Trp Pro Pro Gly Ser Cys Arg Gly Ala Arg Gly
        35                  40                  45
Gly Pro Val Ser Ser Trp Ser Gln Val Gly Pro Ile Arg Cys Asp Pro
    50                  55                  60
Val Pro Pro Gln Gln Pro Trp Arg Arg Gly Thr Leu Pro Ala Val Ala
65                  70                  75                  80
Ala Ala Val Phe Leu Ala Cys Glu Arg Arg Gly Gln Ser Gly Arg Trp
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85 90 95
Glu Ser Gly Cys Cys Lys Val Thr Thr Asn Ser Ser Leu Gly Glu Glu
100 105 110
Glu Glu Asn Ala Ile Asp Phe Gln Glu Pro Ser Glu Val
115 120 125

<210> 4871
<211> 1354
<212> DNA
<213> Homo sapiens

<400> 4871
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480
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1260

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1354

<210> 4872
<211> 90
<212> PRT
<213> Homo sapiens

<400> 4872
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            20   25   30
His Ala Pro Ser Glu Ser Gly Gly His Leu Pro Val Pro Ala Ser Pro
        35   40   45
Val Pro Ala Pro Ala Ala Ala Trp Ser Val Ser Thr Ala Ala Ala Ala
    50   55   60
Pro Ala Ala Cys Arg Pro Ala Ala Gly Ala Gly Pro Cys Gln Gly His
65   70   75   80
Gln Gly Leu Pro Gly Ser Pro Leu Pro Glu
                85   90

<210> 4873
<211> 948
<212> DNA
<213> Homo sapiens

<400> 4873
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120
ccactgtgag ttgaactctt tcgtgttgac cggccactct ccgtgctctg gatgatgtcg
180
gaacacgacc tggccgatgt ggttcaaatt gcagtggaag acctgagccc tgaccaccca
240
ggtacagagc tgtgggacag tgttgttttg gagaatcatg tagtgacaga tgaagacgaa
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360
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420
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480
cacagcccca tccaggttcc catggtggcc ggctcccctc tcaggacaac ccagatgtgc
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660
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720

cgaacacatg gcatcctgcc aggatgacct gaagtcatcc tcacctttcc tttccacata
780
aagccggccc atacaccttt tctttggaac taacccacca gatcttagaa gatgtacacg
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<210> 4874
<211> 128
<212> PRT
<213> Homo sapiens

<400> 4874
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20 25 30
Leu Glu Asn His Val Val Thr Asp Glu Asp Glu Pro Ala Leu Lys Arg
35 40 45
Gln Arg Leu Glu Ile Asn Cys Gln Asp Pro Ser Ile Lys Ser Phe Leu
50 55 60
Tyr Ser Ile Asn Gln Thr Ile Cys Leu Arg Leu Asp Ser Ile Glu Ala
65 70 75 80
Lys Leu Gln Ala Leu Glu Ala Thr Cys Lys Ser Leu Glu Glu Lys Leu
85 90 95
Asp Leu Val Thr Asn Lys Gln His Ser Pro Ile Gln Val Pro Met Val
100 105 110
Ala Gly Ser Pro Leu Arg Thr Thr Gln Met Cys Asn Lys Val Arg Trp
115 120 125

<210> 4875
<211> 1255
<212> DNA
<213> Homo sapiens

<400> 4875
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180
aaaatacttt gcagctggtg agaaatatca tacctcctct gtcttccaca aagcacaaag
240
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420
gccccaatgc tgttcatgag gtggagaagt ggctgccccg gctgcatgct cttgtcgtag
480

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1020
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1255

<210> 4876
<211> 230
<212> PRT
<213> Homo sapiens

<400> 4876
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20 25 30
Val Gly Thr Gly Leu Gly Arg Asp Asp Ala Leu Leu Arg Asn Val Gln
35 40 45
Gly Ile Leu Glu Val Ser Lys Ala Arg Asp Ile Pro Val Val Ile Asp
50 55 60
Ala Asp Gly Leu Trp Leu Val Ala Gln Gln Pro Ala Leu Ile His Gly
65 70 75 80
Tyr Arg Lys Ala Val Leu Thr Pro Asn His Val Glu Phe Ser Arg Leu
85 90 95
Tyr Asp Ala Val Leu Arg Gly Pro Met Asp Ser Asp Asp Ser His Gly
100 105 110
Ser Val Leu Arg Leu Ser Gln Ala Leu Gly Asn Val Thr Val Val Gln
115 120 125
Lys Gly Glu Arg Asp Ile Leu Ser Asn Gly Gln Gln Val Leu Val Cys
130 135 140
Ser Gln Glu Gly Ser Ser Arg Arg Cys Gly Gly Gln Gly Asp Leu Leu
145 150 155 160
Ser Gly Ser Leu Gly Val Leu Val His Trp Ala Leu Leu Ala Gly Pro

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                165                 170                 175
Gln Lys Thr Asn Gly Ser Ser Pro Leu Leu Val Ala Ala Phe Gly Ala
            180                 185                 190
Cys Ser Leu Thr Arg Gln Cys Asn His Gln Ala Phe Gln Lys His Gly
        195                 200                 205
Arg Ser Thr Thr Thr Ser Asp Met Ile Ala Glu Val Gly Ala Ala Phe
    210                 215                 220
Ser Lys Leu Phe Glu Thr
225                 230
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<210> 4877
<211> 1182
<212> DNA
<213> Homo sapiens

<400> 4877
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<210> 4878
<211> 122
<212> PRT
<213> Homo sapiens

<400> 4878
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Leu Ile Ile Leu Leu Gln Gly Leu Gln Gly Arg Val Thr Thr Val Asp
            20   25   30
Leu Arg Asp Glu Ser Val Ala His Gly Arg Ile Asp Asn Val Asp Ala
        35   40   45
Phe Met Asn Ile Arg Leu Ala Lys Val Thr Tyr Thr Asp Arg Trp Gly
    50   55   60
His Gln Val Lys Leu Asp Asp Leu Phe Val Thr Gly Arg Asn Val Arg
65   70   75   80
Tyr Val His Ile Pro Asp Asp Val Asn Ile Thr Ser Thr Ile Glu Gln
                85   90   95
Gln Leu Gln Ile Ile His Arg Val Arg Asn Phe Gly Gly Lys Gly Gln
            100   105   110
Gly Arg Trp Glu Phe Pro Pro Lys Lys Leu
        115   120

<210> 4879
<211> 1941
<212> DNA
<213> Homo sapiens

<400> 4879
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1920
tttagatgtt gaaaaaaaaa a
1941

<210> 4880
<211> 202
<212> PRT
<213> Homo sapiens

<400> 4880
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His Lys Pro Gly Leu Gly Lys Cys Pro Asp Leu Pro Gly Gly His Thr

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        35                  40                  45
Ala Thr Ala Ser Gly Pro His Val Lys Ser His Leu Thr Arg Val Val
    50                  55                  60
Thr Thr Val Leu Phe Trp Gly Phe Ser Lys Ala Ser Pro Val Val Leu
65                  70                  75                  80
Arg Gly His Ser Glu Gln Ala Asn Thr Ala Arg Val Thr His Tyr Thr
                85                  90                  95
Gln Arg Lys Asp Asn Glu Gln Met Ala Ile Val Glu Asn Ser Val Val
            100                 105                 110
Cys Phe Ser Asn Ala Thr Tyr Phe Ser Arg Gln Val Ile Leu Pro Met
        115                 120                 125
Met Thr Ser Ala Thr Lys Leu Arg Ala Arg Gly Leu Pro Met Arg Leu
    130                 135                 140
Val Glu Ser Asn His Val Cys Ser Glu Ala Ser Gly Pro Ser Arg Pro
145                 150                 155                 160
Cys His Arg Pro Glu His Arg Thr Val Ile Met Gln Arg Ala Val Thr
                165                 170                 175
Glu Ala Gly Val Ser Val Gly Gly Gly Glu Glu Gly Thr Ser Ala Phe
            180                 185                 190
Tyr Ile Arg Ser Glu Ala Thr Val Arg Lys
        195                 200
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<210> 4881
<211> 1333
<212> DNA
<213> Homo sapiens

<400> 4881

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720
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1333

<210> 4882
<211> 100
<212> PRT
<213> Homo sapiens

<400> 4882
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Arg Glu Ala Thr Gly Val Glu Asn Arg Val Thr Ser Pro Leu Pro Pro
20 25 30
Leu Pro Phe Leu Pro Ser Gln Pro Leu Gly Phe Gly Tyr Met Thr Gln
35 40 45
Gln Leu Met Asn Leu Ala Gly Gly Ala Val Val Leu Ala Leu Glu Gly
50 55 60
Gly His Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ala
65 70 75 80
Ala Leu Leu Gly Asn Arg Val Ser Arg Leu Pro Pro Pro Ser Met Leu
85 90 95
Leu Ser Gly Arg
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<210> 4883
<211> 1371
<212> DNA
<213> Homo sapiens

<400> 4883
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cgcttcctga aaaaaacaaa acaaaagctg accgtatgtc ctatcatcaa tggggaagac
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<210> 4884<211> 410
<212> PRT
<213> Homo sapiens

<400> 4884
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Leu Arg Leu Leu Asn Phe Gln His Asn Phe Ile Thr Arg Ile Gln Asn
35 40 45

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Ile Ser Asn Leu Gln Lys Leu Ile Ser Leu Asp Leu Tyr Asp Asn Gln
    50                  55                  60
Ile Glu Glu Ile Ser Gly Leu Ser Thr Leu Arg Cys Leu Arg Val Leu
65                  70                  75                  80
Leu Leu Gly Lys Asn Arg Ile Lys Lys Ile Ser Asn Leu Glu Asn Leu
                85                  90                  95
Lys Ser Leu Asp Val Leu Asp Leu His Gly Asn Gln Ile Thr Lys Ile
            100                 105                 110
Glu Asn Ile Asn His Leu Cys Glu Leu Arg Val Leu Asn Leu Ala Arg
        115                 120                 125
Asn Phe Leu Ser His Val Asp Asn Leu Asn Gly Leu Asp Ser Leu Thr
    130                 135                 140
Glu Leu Asn Leu Arg His Asn Gln Ile Thr Phe Val Arg Asp Val Asp
145                 150                 155                 160
Asn Leu Pro Cys Leu Gln His Leu Phe Leu Ser Phe Asn Asn Ile Ser
                165                 170                 175
Ser Phe Asp Ser Val Ser Cys Leu Ala Asp Ser Ser Ser Leu Ser Asp
            180                 185                 190
Ile Thr Phe Asp Gly Asn Pro Ile Ala Gln Glu Ser Trp Tyr Lys His
        195                 200                 205
Thr Val Leu Gln Asn Met Met Gln Leu Arg Gln Leu Asp Met Lys Arg
    210                 215                 220
Ile Thr Glu Glu Glu Arg Arg Met Ala Ser Val Leu Ala Lys Lys Glu
225                 230                 235                 240
Glu Glu Lys Lys Arg Glu Ser His Lys Gln Ser Leu Leu Lys Glu Lys
                245                 250                 255
Lys Arg Leu Thr Ile Asn Asn Val Ala Arg Gln Trp Asp Leu Gln Gln
            260                 265                 270
Arg Val Ala Asn Ile Ala Thr Asn Glu Asp Arg Lys Asp Ser Asp Ser
        275                 280                 285
Pro Gln Asp Pro Cys Gln Ile Asp Gly Ser Thr Leu Ser Ala Phe Pro
    290                 295                 300
Glu Glu Thr Gly Pro Leu Asp Ser Gly Leu Asn Asn Ala Leu Gln Gly
305                 310                 315                 320
Leu Ser Val Ile Asp Thr Tyr Leu Val Glu Val Asp Gly Asp Thr Leu
                325                 330                 335
Ser Leu Tyr Gly Ser Gly Ala Leu Glu Ser Leu Asp Arg Asn Trp Ser
            340                 345                 350
Val Gln Thr Ala Gly Met Ile Thr Thr Val Ser Phe Thr Phe Ile Glu
        355                 360                 365
Phe Asp Glu Ile Val Gln Val Leu Pro Lys Leu Lys Ile Lys Phe Pro
    370                 375                 380
Asn Ser Leu His Leu Lys Phe Lys Glu Thr Asn Leu Val Met Gln Gln
385                 390                 395                 400
Phe Asn Ala Leu Ala Gln Leu Arg Arg Tyr
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<210> 4885
<211> 489
<212> DNA
<213> Homo sapiens

<400> 4885

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120
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180
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240
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300
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489

<210> 4886
<211> 77
<212> PRT
<213> Homo sapiens

<400> 4886
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Asn Pro Met Gln Val Phe Gln Gly Phe Met Ser Phe Lys Asp Val Ala
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Val Asn Phe Thr Arg Xaa Glu Trp Arg Glu Leu Asp Leu Ala Gln Arg
35 40 45
Val Leu Tyr Arg Asp Val Met Leu Glu Asn Tyr Arg Asn Leu Val Ser
50 55 60
Leu Val Gly Phe Pro Phe Ser Lys Pro Gly Ile Ile Ser
65 70 75

<210> 4887
<211> 2271
<212> DNA
<213> Homo sapiens

<400> 4887
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120
acttcactgt agtttattat ccctgaccct ccacaatgtg attaccaacc gctaggatga
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gttgcatctt attataaagt agcaaattac aagattgtaa cattagactt tttaagaaaa
240
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300
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360

cagcatctat ctctattaaa tgtagaggaa ttgacaaaag aggggaaaga aagttgttag
420
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480
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1380
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1980

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2040
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2160
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2271

<210> 4888
<211> 429
<212> PRT
<213> Homo sapiens

<400> 4888
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20 25 30
Ser Ala His Tyr His Val Asn Phe Ser Gln Ala Ile Ser Gln Asp Val
35 40 45
Asn Leu His Glu Ala Ile Leu Leu Cys Pro Asn Asn Thr Phe Arg Arg
50 55 60
Asp Pro Thr Ala Arg Thr Ser Gln Ser Gln Glu Pro Phe Leu Gln Leu
65 70 75 80
Asn Ser His Thr Thr Asn Pro Glu Gln Thr Leu Pro Gly Thr Asn Leu
85 90 95
Thr Gly Phe Leu Ser Pro Val Asp Asn His Met Arg Asn Leu Thr Ser
100 105 110
Gln Asp Leu Leu Tyr Asp Leu Asp Ile Asn Ile Phe Asp Glu Ile Asn
115 120 125
Leu Met Ser Leu Ala Thr Glu Asp Asn Phe Asp Pro Ile Asp Val Ser
130 135 140
Gln Leu Phe Asp Glu Pro Asp Ser Asp Ser Gly Leu Ser Leu Asp Ser
145 150 155 160
Ser His Asn Asn Thr Ser Val Ile Lys Ser Asn Ser Ser His Ser Val
165 170 175
Cys Asp Glu Gly Ala Ile Gly Tyr Cys Thr Asp His Glu Ser Ser Ser
180 185 190
His His Asp Leu Glu Gly Ala Val Gly Gly Tyr Tyr Pro Glu Pro Ser
195 200 205
Lys Leu Cys His Leu Asp Gln Ser Asp Ser Asp Phe His Gly Asp Leu
210 215 220
Thr Phe Gln His Val Phe His Asn His Thr Tyr His Leu Gln Pro Thr
225 230 235 240
Ala Pro Glu Ser Thr Ser Asp Xaa Phe Pro Xaa Ala Gly Lys Ser Gln
245 250 255
Lys Ile Arg Ser Arg Tyr Leu Glu Asp Pro Asp Arg Thr Leu Ser Arg
260 265 270
Asp Asp Gln Arg Ala Lys Ala Leu His Ile Pro Phe Ser Val Asp Glu
275 280 285
Ile Val Gly Met Pro Val Asp Ser Phe Asn Ser Met Leu Ser Arg Tyr

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    290                 295                 300
Tyr Leu Thr Asp Leu Gln Val Ser Leu Ile Arg Asp Ile Arg Arg Arg
305                 310                 315                 320
Gly Lys Asn Lys Val Ala Ala Gln Asn Cys Arg Lys Arg Lys Leu Asp
                325                 330                 335
Ile Ile Leu Asn Leu Glu Asp Asp Val Cys Asn Leu Gln Ala Lys Lys
            340                 345                 350
Glu Thr Leu Lys Arg Glu Gln Ala Gln Cys Asn Lys Ala Ile Asn Ile
        355                 360                 365
Met Lys Gln Lys Leu His Asp Leu Tyr His Asp Ile Phe Ser Arg Leu
    370                 375                 380
Arg Asp Asp Gln Gly Arg Pro Val Asn Pro Asn His Tyr Ala Leu Gln
385                 390                 395                 400
Cys Thr His Asp Gly Ser Ile Leu Ile Val Pro Lys Glu Leu Val Ala
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Ser Gly His Lys Lys Glu Thr Gln Lys Gly Lys Arg Lys
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<210> 4889
<211> 619
<212> DNA
<213> Homo sapiens

<400> 4889
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120
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180
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240
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420
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480
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619

<210> 4890
<211> 90
<212> PRT
<213> Homo sapiens

<400> 4890
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Arg Thr Gly Gln Pro Gln Pro Ala Pro Thr Arg Val Asn Ile Ser Arg
35 40 45
Pro Ser Pro Thr Leu Phe Pro Asp Ser Gln Gln Thr Asp Val Gly Ser
50 55 60
Arg Thr Asp Pro Phe Thr His Thr His Thr His Ser His Ser Phe Ala
65 70 75 80
His Ile His Ser Cys Thr His Ala Met Tyr
85 90

<210> 4891
<211> 1998
<212> DNA
<213> Homo sapiens

<400> 4891
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120
aatcaccgcc ccgccctccc tcaatgtctc cgaggcaggt gcggccacag ccggtgctgc
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1080

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1980
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1998

<210> 4892
<211> 216
<212> PRT
<213> Homo sapiens

<400> 4892
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20 25 30
Ile Lys Arg Gly Arg Gln Ala Glu Glu Glu Cys Ala His Arg Gly Ser
35 40 45
Pro Leu Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly His Ile Leu Ser
50 55 60
Ser Asp Arg Ala Ala Ala Gly Met Val Trp Lys Pro Lys Ser Cys Glu
65 70 75 80
Pro Ile Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala Arg Leu Asn Glu
85 90 95
Ser Thr Thr Phe Val Leu Gly Ser Arg Ala Asn Lys Ala Leu Gly Met
100 105 110
Gly Gly Thr Arg Gly Arg Ile Tyr Ile Lys His Pro His Leu Phe Lys

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        115                 120                 125
Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala Glu Gln His His
    130                 135                 140
Met Arg Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu Ile Glu Glu Asp
145                 150                 155                 160
Ile Arg Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly Cys Leu Asp Leu
                165                 170                 175
Lys Leu Glu Glu Leu Lys Ser Phe Val Leu Pro Ser Trp Met Val Glu
            180                 185                 190
Lys Met Arg Lys Tyr Met Glu Thr Leu Arg Thr Glu Asn Glu His Arg
        195                 200                 205
Ala Val Glu Ala Pro Pro Gln Thr
    210                 215
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<210> 4893
<211> 5212
<212> DNA
<213> Homo sapiens

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3780
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4260

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4620
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4680
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4740
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4800
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4860
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4920
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4980
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5040
ggaatatatg tatctagcaa gctcctcaga ctagtcaact ttcttaatag tctgcatatt
5100
tgtatattgc ccagaaaggg acacttttttg gaatatactt tctttttttt aacttatttc
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5212

<210> 4894
<211> 399
<212> PRT
<213> Homo sapiens

<400> 4894
Met Asp Met Phe Ser Leu Asp Met Ile Ile Ser Asp Pro Ala Ala Glu
1 5 10 15
Ala Ser Arg Ala Gly Lys Lys Gln Leu Arg Gly Val Gln Asn Pro Cys
20 25 30
Pro Ser Ala Arg Ala Arg Pro Arg His Lys Ser Leu Asn Ile Lys Asp
35 40 45
Lys Ile Ser Glu Trp Glu Gly Lys Lys Glu Val Pro Thr Pro Ala Pro
50 55 60
Ser Arg Arg Ala Asp Gly Gln Glu Asp Tyr Leu Pro Ser Ser Thr Val
65 70 75 80
Glu Arg Arg Ser Ser Asp Gly Val Arg Thr Gln Val Thr Glu Ala Lys
85 90 95
Asn Gly Met Arg Pro Gly Thr Glu Ser Thr Glu Lys Glu Arg Asn Lys
100 105 110
Gly Ala Val Asn Val Gly Gly Gln Asp Pro Glu Pro Gly Gln Asp Leu

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        115                 120                 125
Ser Gln Pro Glu Arg Glu Val Asp Pro Ser Trp Gly Arg Gly Arg Glu
    130                 135                 140
Pro Arg Leu Gly Lys Leu Arg Phe Gln Asn Asp His Leu Ser Val Leu
145                 150                 155                 160
Lys Gln Val Lys Lys Leu Glu Gln Ala Leu Lys Asp Gly Ser Ala Gly
                165                 170                 175
Leu Asp Pro Gln Leu Pro Gly Thr Cys Tyr Ser Pro His Cys Pro Pro
            180                 185                 190
Asp Lys Ala Glu Ala Gly Ser Thr Leu Pro Glu Asn Leu Gly Gly Gly
        195                 200                 205
Ser Gly Ser Glu Val Ser Gln Arg Val His Pro Ser Asp Leu Glu Gly
    210                 215                 220
Arg Glu Pro Thr Pro Glu Leu Val Glu Asp Arg Lys Gly Ser Cys Arg
225                 230                 235                 240
Arg Pro Trp Asp Arg Ser Leu Glu Asn Val Tyr Arg Gly Ser Glu Gly
                245                 250                 255
Ser Pro Thr Lys Pro Phe Ile Asn Pro Leu Pro Lys Pro Arg Arg Thr
            260                 265                 270
Phe Lys His Ala Gly Glu Gly Asp Lys Asp Gly Lys Pro Gly Ile Gly
        275                 280                 285
Phe Arg Lys Glu Lys Arg Asn Leu Pro Pro Leu Pro Ser Leu Pro Pro
    290                 295                 300
Pro Pro Leu Pro Ser Ser Pro Pro Pro Ser Ser Val Asn Arg Arg Leu
305                 310                 315                 320
Trp Thr Gly Arg Gln Lys Ser Ser Ala Asp His Arg Lys Ser Tyr Glu
                325                 330                 335
Phe Glu Asp Leu Leu Gln Ser Ser Ser Glu Ser Ser Arg Val Asp Trp
            340                 345                 350
Tyr Ala Gln Thr Lys Leu Gly Leu Thr Arg Thr Leu Ser Glu Glu Asn
        355                 360                 365
Val Tyr Glu Asp Ile Leu Asp Pro Pro Met Lys Glu Asn Pro Tyr Glu
    370                 375                 380
Asp Ile Glu Leu His Gly Arg Cys Leu Gly Lys Lys Xaa Val Ser
385                 390                 395
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<210> 4895
<211> 1087
<212> DNA
<213> Homo sapiens

<400> 4895

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120
catcctgatt cagcaagtga gaaaaatcca gttacactct taaaggaatt gtcagtgata
180
aagtctcgat atcaaacttt gtatgcccgc tttaaaccag ttgctgttga gcagaaagag
240
agtaagagcc gcatttgtgc tactgtgaaa aagactatga atatgataca aaaactacag
300
aagcaaacag acctggaggt aatgctttca gttgacagct gtcaccactg actaaagaag
360
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agaaaactgc ggcagagcaa ttcaaatttc acatgccaga tttatgaaga aatggacttg
420
gaaaggaaat tctaacagag aagagcttaa ttccggagaa atttaggaag atgtcttgtt
480
aacccttgat gtctagagat tgggggctgg tgaagggggt ttggcttcaa tgactggata
540
atgatatctt tcatgagaga gattataaga agaagggcag ataatatatg aataaagttc
600
agccaaaagg atcaaatgag aataaaacga tttaaatata tgtacacacg catgcacaca
660
cacacttagt cttgtaattt caggccagaa attctcaaca ctattttgca tctgttttct
720
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780
ttcagtcatt cggtatgtgg ctttgtaaat taaagtatag gcaaaacatt tgtgttatac
840
atgatatata atttcatttt gtaaatgttg attgcacatg tggtcacatt attgttgaga
900
ctgcttttat gtgacctgta gtctcccaca gaacctaaag taataagctg gcttttctgt
960
gatagccacg tttgcgtatt tctttcccta tttcccttgc ctgctaatgt tgaacagcat
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1080
ttccttc
1087

<210> 4896
<211> 109
<212> PRT
<213> Homo sapiens

<400> 4896
Met Glu Ala Glu Val Asp Lys Leu Glu Leu Met Phe Gln Lys Ala Glu
 1   5   10   15
Ser Asp Leu Asp Tyr Ile Gln Tyr Arg Leu Glu Tyr Glu Ile Lys Thr
            20   25   30
Asn His Pro Asp Ser Ala Ser Glu Lys Asn Pro Val Thr Leu Leu Lys
        35   40   45
Glu Leu Ser Val Ile Lys Ser Arg Tyr Gln Thr Leu Tyr Ala Arg Phe
    50   55   60
Lys Pro Val Ala Val Glu Gln Lys Glu Ser Lys Ser Arg Ile Cys Ala
65   70   75   80
Thr Val Lys Lys Thr Met Asn Met Ile Gln Lys Leu Gln Lys Gln Thr
                85   90   95
Asp Leu Glu Val Met Leu Ser Val Asp Ser Cys His His
            100   105

<210> 4897
<211> 1733
<212> DNA
<213> Homo sapiens

<400> 4897

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120
ccacgatgcc cagctaattt ttgtattttt agtaaagaca gggtttcacc atgttggcta
180
ggctggtctc aaactcctga tnccacccgc ctcggcctcc caaagtgctg ggattacagg
240
cgtgaaccac cgcgcccggg tgacctttgg aacttctgac cgactggctt caagttgagg
300
ttcccacaat tccctctgta ggttcaattt gctggagtgg ctcacaaaac taagggaaat
360
acatttactg gtttattata aaggatatta taaaagatac agataaagag atgcataggg
420
tgaggtatga aggaagggca tggagcttcc tgtgccctcc ctgggcgcac cacccttcta
480
gaacctctgt atgttcagtt atctggaagc tctctgaatc cagtcccctt ggtttttatg
540
gaagcttcat gacagcagca ttccttctag caggatatgg ggtgggaccg tctctggaat
600
gagttttatg acccaccatc agaaaggtag ggaagattag agtcctgtct tgggcaggta
660
aaaggaaggg caggaggtta gagtgattgt ctcctgaggc ctgacacacc caatgttgta
720
acaaaagagt gtaacaaggg ctgtgggagt tatgagccag gaactgtgga cgaaaatgaa
780
tgcgtgtgtt tgtatatatg tgtgtctgtg tatttatata tatatgtgtg tatatacaaa
840
tacacacaca cacacgccac cacaaagcca aaaaagaaga agtgatcatt tttctaagtg
900
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960
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1020
tgtgaatgga tatggagata agagaggtga ttacattaag atgaggccgt caggggccc
1080
ctcatccaat ctcaccagtg tccttataag agaaaatctg gacacacaaa gagacaccag
1140
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1200
aagaaaccaa ccctgcgaac accttggtct tggacttcca gcctccagga ctgtgagaaa
1260
ataaatgtct tttgtttaag ccactcagtc tctggtattt tcttatgaga gccagagcag
1320
accaacacag agggtcaggg gaagcgtcta tggggaggtg actcatgtac tgagtcttga
1380
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1440
cagtgtgctc cgggaaccag gagaagatga gggaggccag ggcctaagga gggcagggta
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1560
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1620

agctcctatt ttaggaggtg gcctctggct gtgtctaatg gagttgacaa gaataaaagt
1680
agaaggagaa gaccaaggag gaggacgcca ggtgagagca ggtggtggtc agg
1733

<210> 4898
<211> 92
<212> PRT
<213> Homo sapiens

<400> 4898
Xaa Phe Val Ala Arg Ala Gly Val Gln Trp Arg Asp Leu Ser Ser Leu
1 5 10 15
Gln Pro Leu Pro Leu Arg Phe Lys Gln Phe Ser Cys Phe Ser Leu Pro
20 25 30
Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Cys Pro Ala Asn Phe Cys
35 40 45
Ile Phe Ser Lys Asp Arg Val Ser Pro Cys Trp Leu Gly Trp Ser Gln
50 55 60
Thr Pro Asp Xaa Thr Arg Leu Gly Leu Pro Lys Cys Trp Asp Tyr Arg
65 70 75 80
Arg Glu Pro Pro Arg Pro Gly Asp Leu Trp Asn Phe
85 90

<210> 4899
<211> 444
<212> DNA
<213> Homo sapiens

<400> 4899
ccggcccatc aaagactggc taaagcatca gccataaatg gggacaaacg tggggccagc
60
agcttctgtt cggggtctcg gcatcagcaa accgcagcag ctttggagaa gggtccgtga
120
gtggcggctc tggaggcagc aacggggtcc tttggggtgg gtgggagttc tgctggattc
180
aggtggaggt gaacatctgc cgttcccaca gccctgcgtg caccccaaa tgctgctggc
240
ccacagaatc agccagtgcc acggccccac cacagccagg cttggccctg tcagcggcca
300
gcatcccgag ggccagggtc cgagtgtcct caccaaggag gctcttggcg tcgctgtgcc
360
ggctcccatg ggccttctgc tgggtcgagg gtaggtctcc tcctcccccc ttgccctggc
420
attaaactga tggtcaggct ggga
444

<210> 4900
<211> 118
<212> PRT
<213> Homo sapiens

<400> 4900
Met Gly Thr Asn Val Gly Pro Ala Ala Ser Val Arg Gly Leu Gly Ile

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 1               5                  10                  15
Ser Lys Pro Gln Gln Leu Trp Arg Arg Val Arg Glu Trp Arg Leu Trp
            20                  25                  30
Arg Gln Gln Arg Gly Pro Leu Gly Trp Val Gly Val Leu Leu Asp Ser
        35                  40                  45
Gly Gly Gly Glu His Leu Pro Phe Pro Gln Pro Cys Val His Pro Gln
    50                  55                  60
Met Leu Leu Ala His Arg Ile Ser Gln Cys His Gly Pro Thr Thr Ala
65                  70                  75                  80
Arg Leu Gly Pro Val Ser Gly Gln His Pro Glu Gly Gln Gly Pro Ser
                85                  90                  95
Val Leu Thr Lys Glu Ala Leu Gly Val Ala Val Pro Ala Pro Met Gly
            100                 105                 110
Leu Leu Leu Gly Arg Gly
        115
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<210> 4901
<211> 1520
<212> DNA
<213> Homo sapiens

<400> 4901
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attcccagcc agaacggagc ttaagccggg caggcgatgc gaatgacgga gtagcgagct
120
gcacggcggc gtgctgcgct gttgaggacg ctgtcccgcg cgctcccagg ccgccccgag
180
gcttggggtc ttcgaaggat aatcggcgcc cggggccgaa cagcgggggc acacggggcg
240
ctgccgaagt gcaaggccac ggccagagct cgagcccgac gcgctgtctg gagtcgtagg
300
ttggcgccgt ttggggtcgg ggtctgaggc ttgggcgctg cctgggccga gcggagatcg
360
gggtttgcct cccgtccccg ctcaggaccc tgacgtggct gaagcggccc cgggagcatg
420
agcgggcagc gcgtggacgt caaggtggtg atgctgggca aggagtacgt gggcaagact
480
agcctggtgg agcgctacgt gcacgaccgc tttctggtgg ggccttatca gaacaccatc
540
ggggccgcct tcgtggccaa ggtgatgtcg gtcggagacc ggactgtgac attaggtatt
600
tgggacacag caggctctga gcgctatgag gccatgagta gaatctacta tcggggtgcc
660
aaggctgcca tcgtctgcta tgacctcaca gacagcagca gctttgagcg agcaaagttc
720
tgggtgaagg aactgcgcag cctagaggag ggctgccaaa tctacttatg tggcaccaag
780
agtgacctgc tggaagaaga ccggaggcgt cgacgtgtgg acttccacga cgtccaggac
840
tatgcagaca gtagctgctc ctcagccctt tgggggggtgg gggtgtgtgg ctgtctgggt
900
ggatcaaaga aaatagggac tgccttggct gccagggcaa ggtgctctag gaggtcttcc
960

tggcctcctt gaactgtggg gtccaggaga ctccctgaac tgctagccct ccctttgtc
1020
tgtttatcta attctcaggt atgaggcttt agtcacttct ctttacagat atcaaagctc
1080
agctctttga aacatccagc aagacaggcc agagtgtggg tgagtgctgt gctggagcct
1140
cacagcagga acatgcaggg gcaccagagg aagctgaata gggcacagag ggctgggtca
1200
ctgggagatc ccagggctac tggcattggg ccctcgctga tcatcatttt tcctgccaga
1260
cgagctcttc cagaaagtgg cagaggatta cgtcagtgtg gctgccttcc aggtgatgac
1320
agaggacaag ggcgtggatc tgggccagaa gccaaacccc tacttctaca gctgttgtca
1380
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1440
ccagctcctt tctgggcttg ggtagtcaaa tgtctgagct acgccaggtc ctcatgtcag
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cagagtggcg cctgcctgtc
1520

<210> 4902
<211> 184
<212> PRT
<213> Homo sapiens

<400> 4902
Met Ser Gly Gln Arg Val Asp Val Lys Val Val Met Leu Gly Lys Glu
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Tyr Val Gly Lys Thr Ser Leu Val Glu Arg Tyr Val His Asp Arg Phe
20 25 30
Leu Val Gly Pro Tyr Gln Asn Thr Ile Gly Ala Ala Phe Val Ala Lys
35 40 45
Val Met Ser Val Gly Asp Arg Thr Val Thr Leu Gly Ile Trp Asp Thr
50 55 60
Ala Gly Ser Glu Arg Tyr Glu Ala Met Ser Arg Ile Tyr Tyr Arg Gly
65 70 75 80
Ala Lys Ala Ala Ile Val Cys Tyr Asp Leu Thr Asp Ser Ser Ser Phe
85 90 95
Glu Arg Ala Lys Phe Trp Val Lys Glu Leu Arg Ser Leu Glu Glu Gly
100 105 110
Cys Gln Ile Tyr Leu Cys Gly Thr Lys Ser Asp Leu Leu Glu Glu Asp
115 120 125
Arg Arg Arg Arg Arg Val Asp Phe His Asp Val Gln Asp Tyr Ala Asp
130 135 140
Ser Ser Cys Ser Ser Ala Leu Trp Gly Val Gly Val Cys Gly Cys Leu
145 150 155 160
Gly Gly Ser Lys Lys Ile Gly Thr Ala Leu Ala Ala Arg Ala Arg Cys
165 170 175
Ser Arg Arg Ser Ser Trp Pro Pro
180

<210> 4903
<211> 1064

<212> DNA
<213> Homo sapiens

<400> 4903
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cttcggaaag tctcatccac ccccacatcg cctctttagg aagtcactta atgttgggct
120
tcattattcc cacatccctt tccttactac ttgcctgcac ttcttgagaa aaagactgca
180
gaaaggagag gtggggcttt cagtagaaac aagcaaaccg cagtccctgt gggggggactc
240
tccaggaaga aggttccgca agaaccgtgg gcgacagtta tggagaagcg tctgcaggag
300
gctcagctgt acaaggagga agggaaccag cgctaccggg aagggaagta ccgagatgct
360
gtgagtaggt accatcgagc tctgcttcag ctgcggggtc tggatccgna gtctgccctc
420
tccgttacct aatctcggac ctcagggccc nggccctcac gcctgnaaca agaaaacata
480
ttgcatacca cccagacaga ctgctataac aatctagctg cttgtctcct tcagatggag
540
cccgtgaact acgaacgagt gagagaatat agtcagaaag tcctggaacg acagcctgat
600
aatgccaagg ccttgtatcg ggccggagtg gccttttcc atctgcagga ctatgaccag
660
gcccgccact acctcctggc tgccgtgaat aggcagccta aagatgccaa cgtccggcgg
720
tacctccagc tgacacagtc agaactcagc agctaccata gaaaagagaa gcagctctac
780
ctgggcatgt ttggttaaca aagaagaaag atgctcctcc agttgaactt aggtggacca
840
ttaaacatgc atgaaggaga aatctgagcc tcagcaagag aaattaaccc tatacctctg
900
acccaggtgg atttttgttt ctagttctgc acaaacttca ctacttagac agtctgagtc
960
tttttctgtc tatccatctg tttatttcta tacctttcaa tacatgttat tgttgcagat
1020
atttggcttg agaaatataa tcagaaaaca taaaaaaaaa aaaa
1064

<210> 4904
<211> 106
<212> PRT
<213> Homo sapiens

<400> 4904
Cys Trp Ala Ser Leu Phe Pro His Pro Phe Pro Tyr Tyr Leu Pro Ala
 1   5   10   15
Leu Leu Glu Lys Lys Thr Ala Glu Arg Arg Gly Gly Ala Phe Ser Arg
            20   25   30
Asn Lys Gln Thr Ala Val Pro Val Gly Gly Leu Ser Arg Lys Lys Val
        35   40   45
Pro Gln Glu Pro Trp Ala Thr Val Met Glu Lys Arg Leu Gln Glu Ala

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    50                  55                  60
Gln Leu Tyr Lys Glu Glu Gly Asn Gln Arg Tyr Arg Glu Gly Lys Tyr
65                  70                  75                  80
Arg Asp Ala Val Ser Arg Tyr His Arg Ala Leu Leu Gln Leu Arg Gly
                85                  90                  95
Leu Asp Pro Xaa Ser Ala Leu Ser Val Thr
            100                 105
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<210> 4905
<211> 615
<212> DNA
<213> Homo sapiens

<400> 4905
cccggcagcc acgtggcgga tggtgttccg cgacaggctc agatgcagca ggcctgtcat
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gttggccagg tcgcggcggc gcacggaggc gatgaagttg tctgccagcc gcagctcggc
120
tgcccggcgg tccagcgagg gtggcacgaa caggaggcct gcccctgggc acagcacgct
180
taggggcagc gactgtgtct ggcagcggca gcggcgggga catgggctgg gtgtgccgag
240
acactggagg acctcgacct ctcctacaac aacctcgagc agctgccctg ggaggccctg
300
ggccgcctgg gcaacgtcaa cacgttgggc ctcgaccaca acctgctggc ttctgtgccc
360
gccggcgctt tttcccgcct gcacaagctg gcccggctgg acatgacctc caaccgcctg
420
accacaatcc cacccgaccc actcttctcc cgcctgcccc tgctcgccag gccccggggc
480
tcgcccgcct ctgccctggt gctggccttt ggcgggaacc ccctgcactg caactgcgag
540
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600
gctctgggcg gccgc
615

<210> 4906
<211> 144
<212> PRT
<213> Homo sapiens

<400> 4906
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Gly Gln Arg Leu Cys Leu Ala Ala Ala Ala Ala Gly Thr Trp Ala Gly
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Cys Ala Glu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu Glu
            20                  25                  30
Gln Leu Pro Trp Glu Ala Leu Gly Arg Leu Gly Asn Val Asn Thr Leu
        35                  40                  45
Gly Leu Asp His Asn Leu Leu Ala Ser Val Pro Ala Gly Ala Phe Ser
    50                  55                  60
Arg Leu His Lys Leu Ala Arg Leu Asp Met Thr Ser Asn Arg Leu Thr
65                  70                  75                  80
Thr Ile Pro Pro Asp Pro Leu Phe Ser Arg Leu Pro Leu Leu Ala Arg
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                85                  90                  95
Pro Arg Gly Ser Pro Ala Ser Ala Leu Val Leu Ala Phe Gly Gly Asn
            100                 105                 110
Pro Leu His Cys Asn Cys Glu Leu Val Trp Leu Arg Arg Leu Ala Arg
        115                 120                 125
Glu Asp Asp Leu Glu Ala Cys Ala Ser Pro Pro Ala Leu Gly Gly Arg
    130                 135                 140
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<210> 4907
<211> 1748
<212> DNA
<213> Homo sapiens

<400> 4907
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ccctgatatt acctcttttt cctcattttt tatactacct tttaaaataa agcaggaaat
120
gtggccagca gctggtcccg tctcttctgc cccaacagct gtatccacag gttgtgaggc
180
gggaacgact gttctgtaac ccctacaacg gagcctggca ggaaggaaat cacctaaaaa
240
agaaactgtc agagagattt aatagtcaca tgttatcatt aggagttggt tactgtgtca
300
cattcatgct tttagctaaa cactttaaga ttcaatatta ctttttttct ctcctctgaa
360
atgtgtccgg tgaagatgtc ccactaaggt aagtttgaca tggtgtaagg gagttgaaag
420
gggtaaacgc ggataaagag cagattactt gaccctacat tttaagagaa gacgacgcct
480
tccgggcgca cgccgagcag aactccaccg acaccttatc cttgtccaca tggagacaga
540
ctcctcccgc cgagtcgtcc tcttccagca ggtcctgctt ctgctttccc accggcagag
600
cgtagtcgtg gtcaccggcg ggcgagtctc tgaagagcga ggtggtcagc cgcagtccca
660
cgccgctcag ccggctcagc aagcgagcca gtccagtctc gttggctaag actgcccgta
720
ggtagcgact ctcctcctgc agtgcctgta cgcgtttgcc cagctcccga ttctcggccc
780
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840
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1320
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1440
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1620
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1748

<210> 4908
<211> 55
<212> PRT
<213> Homo sapiens

<400> 4908
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Pro Tyr Pro Cys Pro His Gly Asp Arg Leu Leu Pro Pro Ser Arg Pro
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Leu Pro Ala Gly Pro Ala Ser Ala Phe Pro Pro Ala Glu Arg Ser Arg
35 40 45
Gly His Arg Arg Ala Ser Leu
50 55

<210> 4909
<211> 1960
<212> DNA
<213> Homo sapiens

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240
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300
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480
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600
ctcatggact tcggcttccc ccagaccacc gacagcaaga tcctgcagga gtacatcact
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1020
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1960

<210> 4910
<211> 423
<212> PRT
<213> Homo sapiens

<400> 4910
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Phe Met Pro Ile Leu Met Glu Lys Glu Glu Glu Gly Met Leu Ser Pro
35 40 45
Ile Leu Ala His Gly Gly Val Arg Phe Met Trp Ile Lys His Asn Asn
50 55 60
Leu Tyr Leu Val Ala Thr Ser Lys Lys Asn Ala Cys Val Ser Leu Val
65 70 75 80
Phe Ser Phe Leu Tyr Lys Val Val Gln Val Phe Ser Glu Tyr Phe Lys
85 90 95
Glu Leu Glu Glu Glu Ser Ile Arg Asp Asn Phe Val Ile Ile Tyr Glu
100 105 110
Leu Leu Asp Glu Leu Met Asp Phe Gly Phe Pro Gln Thr Thr Asp Ser
115 120 125
Lys Ile Leu Gln Glu Tyr Ile Thr Gln Gln Ser Asn Lys Leu Glu Thr
130 135 140
Gly Lys Ser Arg Val Pro Pro Thr Val Thr Asn Ala Val Ser Trp Arg
145 150 155 160
Ser Glu Gly Ile Lys Tyr Lys Lys Asn Glu Val Phe Ile Asp Val Ile
165 170 175
Glu Ser Val Asn Leu Leu Val Asn Ala Asn Gly Ser Val Leu Leu Ser
180 185 190
Glu Ile Val Gly Thr Ile Lys Met Arg Val Phe Leu Ser Gly Met Pro
195 200 205
Glu Leu Arg Leu Gly Leu Asn Asp Lys Val Leu Phe Asp Asn Thr Gly
210 215 220
Arg Gly Lys Ser Lys Ser Val Glu Leu Glu Asp Val Lys Phe His Gln
225 230 235 240
Cys Val Arg Leu Ser Arg Phe Glu Asn Asp Arg Thr Ile Ser Phe Ile
245 250 255
Pro Pro Asp Gly Glu Phe Glu Leu Met Ser Tyr Arg Leu Asn Thr His
260 265 270
Val Lys Pro Leu Ile Trp Ile Glu Ser Val Ile Glu Lys Phe Ser His
275 280 285
Ser Arg Ile Glu Tyr Met Val Lys Ala Lys Gly Gln Phe Lys Lys Gln
290 295 300
Ser Val Ala Asn Gly Val Glu Ile Ser Val Pro Val Pro Ser Asp Ala
305 310 315 320
Asp Ser Pro Arg Phe Lys Thr Ser Val Gly Ser Ala Lys Tyr Val Pro
325 330 335
Glu Arg Asn Val Val Ile Trp Ser Ile Lys Ser Phe Pro Gly Gly Lys
340 345 350
Glu Tyr Leu Met Arg Ala His Phe Gly Leu Pro Ser Val Glu Lys Glu
355 360 365
Glu Val Glu Gly Arg Pro Pro Ile Gly Val Lys Phe Glu Ile Pro Tyr

370 375 380
Phe Thr Val Ser Gly Ile Gln Val Arg Tyr Met Lys Ile Ile Glu Lys
385 390 395 400
Ser Gly Tyr Gln Ala Leu Pro Trp Val Arg Tyr Ile Thr Gln Ser Gly
405 410 415
Asp Tyr Gln Leu Arg Thr Ser
420

<210> 4911
<211> 1862
<212> DNA
<213> Homo sapiens

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120
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180
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240
tgtttgctcg gtgctgttct ctcgataaat cacaacaaag cttccagagg gagaggaagg
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360
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420
caaatagatg tggacactgt ttttgaagtc gaagatgaga atatggtttt ggcatcttat
480
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600
atcaactgta gacccaatgg gaaaacccct cttcacgtgg cttgtgaaat ggccaatgtg
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720
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780
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840
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1020
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1560
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1620
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tt
1862

<210> 4912
<211> 453
<212> PRT
<213> Homo sapiens

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            20   25   30
Leu Lys Ala Ile Leu Ile Gln Arg Gln Ile Asp Val Asp Thr Val Phe
        35   40   45
Glu Val Glu Asp Glu Asn Met Val Leu Ala Ser Tyr Lys Gln Gly Tyr
    50   55   60
Trp Leu Pro Ser Tyr Lys Leu Lys Ser Ser Trp Ala Thr Gly Leu His
65   70   75   80
Leu Ser Val Leu Phe Gly His Val Glu Cys Leu Leu Val Leu Leu Asp
                85   90   95
His Asn Ala Thr Ile Asn Cys Arg Pro Asn Gly Lys Thr Pro Leu His
            100   105   110
Val Ala Cys Glu Met Ala Asn Val Asp Cys Val Lys Ile Leu Cys Asp
        115   120   125
Arg Gly Ala Lys Leu Asn Cys Tyr Ser Leu Ser Gly His Thr Ala Leu
    130   135   140
His Phe Cys Thr Thr Pro Ser Ser Ile Leu Cys Ala Lys Gln Leu Val
145   150   155   160
Trp Arg Val Thr Gln Val Asn His Met Leu Gly Asn Ser Leu Val Asn
                165   170   175
Glu Val Glu His Val Thr Gln Val Asn His Met Leu Gly Asn Ser Leu

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            180                 185                 190
Val Asn Glu Val Glu His Gly Ala Asn Val Asn Met Lys Thr Asn Asn
        195                 200                 205
Gln Asp Glu Glu Thr Pro Leu His Thr Ala Ala His Phe Gly Leu Ser
    210                 215                 220
Glu Leu Val Ala Phe Tyr Val Glu His Gly Ala Ile Val Asp Ser Val
225                 230                 235                 240
Asn Ala His Met Glu Thr Pro Leu Ala Ile Ala Ala Tyr Trp Ala Leu
                245                 250                 255
Arg Phe Lys Glu Gln Glu Tyr Ser Thr Glu His His Leu Val Cys Arg
            260                 265                 270
Met Leu Leu Asp Tyr Lys Ala Glu Val Asn Ala Arg Asp Asp Asp Phe
        275                 280                 285
Lys Ser Pro Leu His Lys Ala Ala Trp Asn Cys Asp His Val Leu Met
    290                 295                 300
His Met Met Leu Glu Ala Gly Ala Glu Ala Asn Leu Met Asp Ile Asn
305                 310                 315                 320
Gly Cys Ala Ala Ile Gln Tyr Val Leu Lys Val Thr Ser Val Arg Pro
                325                 330                 335
Ala Ala Gln Pro Glu Ile Cys Tyr Gln Leu Leu Leu Asn His Gly Ala
            340                 345                 350
Ala Arg Ile Tyr Pro Pro Gln Phe His Lys Val Ile Gln Ala Cys His
        355                 360                 365
Ser Cys Pro Lys Ala Ile Glu Val Val Val Asn Ala Tyr Glu His Ile
    370                 375                 380
Arg Trp Asn Thr Lys Trp Arg Arg Ala Ile Pro Asp Asp Asp Leu Glu
385                 390                 395                 400
Val Asn Asn Arg Phe Pro Ser Asn Ser Phe His Tyr Gln Val Leu Pro
                405                 410                 415
Asp Cys Ser Arg Ser Thr Glu Asn Cys Asn Lys Lys Val Gly Phe Glu
            420                 425                 430
Asn Ala Phe Lys Ala Tyr Ser Asn Ala Met Arg Gln Arg Val Ile Lys
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Cys Arg Phe Glu Ser
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<210> 4913
<211> 2090
<212> DNA
<213> Homo sapiens

<400> 4913
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1920
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1980

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2090

<210> 4914
<211> 529
<212> PRT
<213> Homo sapiens

<400> 4914
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Asn Pro Asn Pro Leu Ile Asn Val Arg Asp Arg Leu Phe His Ala Leu
35 40 45
Phe Phe Lys Met Ala Val Thr Tyr Ser Arg Leu Phe Pro Pro Ala Phe
50 55 60
Arg Arg Leu Phe Glu Phe Phe Val Leu Leu Lys Ala Leu Phe Val Leu
65 70 75 80
Phe Val Leu Ala Tyr Ile His Ile Val Phe Ser Arg Ser Pro Ile Asn
85 90 95
Cys Leu Glu His Val Arg Asp Lys Trp Pro Arg Glu Gly Ile Leu Arg
100 105 110
Val Glu Val Arg His Asn Ser Ser Arg Ala Pro Val Phe Leu Gln Phe
115 120 125
Cys Asp Ser Gly Gly Arg Gly Ser Phe Pro Gly Leu Ala Val Glu Pro
130 135 140
Gly Ser Asn Leu Asp Met Glu Asp Glu Glu Glu Glu Glu Leu Thr Met
145 150 155 160
Glu Met Phe Gly Asn Ser Ser Ile Lys Phe Glu Leu Asp Ile Glu Pro
165 170 175
Lys Val Phe Lys Pro Pro Ser Ser Thr Glu Ala Leu Asn Asp Ser Gln
180 185 190
Glu Phe Pro Phe Pro Glu Thr Pro Thr Lys Val Trp Pro Gln Asp Glu
195 200 205
Tyr Ile Val Glu Tyr Ser Leu Glu Tyr Gly Phe Leu Arg Leu Ser Gln
210 215 220
Ala Thr Arg Gln Arg Leu Ser Ile Pro Val Met Val Val Thr Leu Asp
225 230 235 240
Pro Thr Arg Asp Gln Cys Phe Gly Asp Arg Phe Ser Arg Leu Leu Leu
245 250 255
Asp Glu Phe Leu Gly Tyr Asp Asp Ile Leu Met Ser Ser Val Lys Gly
260 265 270
Leu Ala Glu Asn Glu Glu Asn Lys Gly Phe Leu Arg Asn Val Val Ser
275 280 285
Gly Glu His Tyr Arg Phe Val Ser Met Trp Met Ala Arg Thr Ser Tyr
290 295 300
Leu Ala Ala Phe Ala Ile Met Val Ile Phe Thr Leu Ser Val Ser Met
305 310 315 320
Leu Leu Arg Tyr Ser His His Gln Ile Phe Val Phe Ile Val Asp Leu
325 330 335
Leu Gln Met Leu Glu Met Asn Met Ala Ile Ala Phe Pro Ala Ala Pro

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            340                 345                 350
Leu Leu Thr Val Ile Leu Ala Leu Val Gly Met Glu Ala Ile Met Ser
        355                 360                 365
Glu Phe Phe Asn Asp Thr Thr Thr Ala Phe Tyr Ile Ile Leu Ile Val
    370                 375                 380
Trp Leu Ala Asp Gln Tyr Asp Ala Ile Cys Cys His Thr Ser Thr Ser
385                 390                 395                 400
Lys Arg His Trp Leu Arg Phe Phe Tyr Leu Tyr His Phe Ala Phe Tyr
                405                 410                 415
Ala Tyr His Tyr Arg Phe Asn Gly Gln Tyr Ser Ser Leu Ala Leu Val
            420                 425                 430
Thr Ser Trp Leu Phe Ile Gln His Ser Met Ile Tyr Phe Phe His His
        435                 440                 445
Tyr Glu Leu Pro Ala Ile Leu Gln Gln Val Arg Ile Gln Glu Met Leu
    450                 455                 460
Leu Gln Ala Pro Pro Leu Gly Pro Gly Thr Pro Thr Ala Leu Pro Asp
465                 470                 475                 480
Asp Met Asn Asn Asn Ser Gly Ala Pro Ala Thr Ala Pro Asp Ser Ala
                485                 490                 495
Gly Gln Pro Pro Ala Leu Gly Pro Val Phe Glu Leu Val Ser Lys Glu
            500                 505                 510
Arg Gly Trp Gly Ser Ala Glu Gly Ser Gly Gly Val Leu Val Gly Leu
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<210> 4915
<211> 1157
<212> DNA
<213> Homo sapiens

<400> 4915

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660
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<210> 4916
<211> 59
<212> PRT
<213> Homo sapiens

<400> 4916
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Ala Gly Ala Ser Arg Lys Arg Lys Glu Val Pro Ser Arg Leu Arg Thr
            20   25   30
Trp Gly Pro Gly Gly Asp Ala Pro Arg Gly Ser Gly Leu Lys Arg Pro
        35   40   45
Arg Gly Pro Arg Gly Pro Ser Ala Ala Pro Arg
    50   55

<210> 4917
<211> 1544
<212> DNA
<213> Homo sapiens

<400> 4917
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ccagctcccc cagccgcggg cacctgagct ctccgcggcc accaggggggc gcccgcggcc
120
cagtctgggc gcgagagccg ccaagcgccc actccgttcc tcctggtgcc ccgccccgtc
180
cggccgcggc cccgcccctc ccggcgcccc gccccgtccg gcagcggcct cgctccctcc
240
gatcccccgc gcgcccggga cccctggccc cactgttggg ccagctcgcc gggtccggcc
300
atgggccccg ccgctcgccc cgcgctgaga tcgccgccgc cgcctccgcc gccgcctccg
360
tctccgctgc tgctgctgct gcccctgctg ccgctgtggc tgggcctggc ggggcccggg
420

gccgcggcgg acggcagcga gccggcggcc ggggcggggc ggggcggagc ccgcgccgtg
480
cgggtggacg tgagactgcc gcgccaggac gctctggtcc tggagggcgt caggatcggc
540
tccgaagccg acccggcgcc cctgctgggc ggtcgtctgc tgctgatgga tgtcgtggat
600
gctgagcagg aggcacccgc agatggctgg attgcagtgg catatgtggg caaggagcag
660
gcggcccagt tccaccagga gaataagggc agtggcccgc aggcctatcc caaggccctg
720
gtccagcaga tgcggcgggc cctcttcctg ggtgcctctg ccctgcttct tctcatcctg
780
aaccacaacg tggtccgaga gctggacata tcccagcttc tgctcaggcc agtgatcgtc
840
ctccattatt cctccaatgt caccaagctg ttggatgcat tgctgcagag gacccaggcc
900
acggctgaga tcaccagcgg agagtccctg tctgccaata tcgagtggaa gttgaccttg
960
tggaccacct gtggcctctc caaggatggc tatggaggat ggcaggactt ggtctgcctt
1020
ggaggcagtc gtgcccagga gcagaaaccc ctgcagcagc tgtggaacgc catcctgctg
1080
gtggccatgc tcctgtgcac aggcctcgtg gtccaggccc agcggcaggc gtcgcggcag
1140
agccagcggg agctcggagg ccaggtggac ctgtttaagc gccgcgtggt gcggagactg
1200
gcatccctca agacacggcg ctgccggctg agcagggcag cgcagggcct cccagatccg
1260
ggtgctgaga cctgtgcggt gtgcctggac tacttctgca acaaacaggc tagtgccccg
1320
gtggctccgg gtgctgccct gtaagcacga gtttcaccga gactgtgtgg acccctggct
1380
gatgctccag cagacctgcc cactgtgcaa attcaacgtc ctgggtgagc accaggggtg
1440
gggtccctcg gcctactctg cctgctcctc acctgatgcc tctctccctg ttcttcttcc
1500
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1544

<210> 4918
<211> 347
<212> PRT
<213> Homo sapiens

<400> 4918
Met Gly Pro Ala Ala Arg Pro Ala Leu Arg Ser Pro Pro Pro Pro Pro
 1   5   10   15
Pro Pro Pro Pro Ser Pro Leu Leu Leu Leu Leu Pro Leu Leu Pro Leu
            20   25   30
Trp Leu Gly Leu Ala Gly Pro Gly Ala Ala Ala Asp Gly Ser Glu Pro
        35   40   45
Ala Ala Gly Ala Gly Arg Gly Gly Ala Arg Ala Val Arg Val Asp Val
    50   55   60
Arg Leu Pro Arg Gln Asp Ala Leu Val Leu Glu Gly Val Arg Ile Gly

65 70 75 80
Ser Glu Ala Asp Pro Ala Pro Leu Leu Gly Gly Arg Leu Leu Leu Met
85 90 95
Asp Val Val Asp Ala Glu Gln Glu Ala Pro Ala Asp Gly Trp Ile Ala
100 105 110
Val Ala Tyr Val Gly Lys Glu Gln Ala Ala Gln Phe His Gln Glu Asn
115 120 125
Lys Gly Ser Gly Pro Gln Ala Tyr Pro Lys Ala Leu Val Gln Gln Met
130 135 140
Arg Arg Ala Leu Phe Leu Gly Ala Ser Ala Leu Leu Leu Leu Ile Leu
145 150 155 160
Asn His Asn Val Val Arg Glu Leu Asp Ile Ser Gln Leu Leu Leu Arg
165 170 175
Pro Val Ile Val Leu His Tyr Ser Ser Asn Val Thr Lys Leu Leu Asp
180 185 190
Ala Leu Leu Gln Arg Thr Gln Ala Thr Ala Glu Ile Thr Ser Gly Glu
195 200 205
Ser Leu Ser Ala Asn Ile Glu Trp Lys Leu Thr Leu Trp Thr Thr Cys
210 215 220
Gly Leu Ser Lys Asp Gly Tyr Gly Gly Trp Gln Asp Leu Val Cys Leu
225 230 235 240
Gly Gly Ser Arg Ala Gln Glu Gln Lys Pro Leu Gln Gln Leu Trp Asn
245 250 255
Ala Ile Leu Leu Val Ala Met Leu Leu Cys Thr Gly Leu Val Val Gln
260 265 270
Ala Gln Arg Gln Ala Ser Arg Gln Ser Gln Arg Glu Leu Gly Gly Gln
275 280 285
Val Asp Leu Phe Lys Arg Arg Val Val Arg Arg Leu Ala Ser Leu Lys
290 295 300
Thr Arg Arg Cys Arg Leu Ser Arg Ala Ala Gln Gly Leu Pro Asp Pro
305 310 315 320
Gly Ala Glu Thr Cys Ala Val Cys Leu Asp Tyr Phe Cys Asn Lys Gln
325 330 335
Ala Ser Ala Pro Val Ala Pro Gly Ala Ala Leu
340 345

<210> 4919
<211> 1362
<212> DNA
<213> Homo sapiens

<400> 4919
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ctgggagggg tttgtgggtg aactcggggt ccaccgcccg ctgaggagat ggatgaggac
120
gggcttcctc tcatggggtc aggcatagac ctgaccaagg tgccagctat tcaacagaaa
180
agaacggtgg cttttctaaa ccaatttgtg gtgcacactg tacagttcct caaccgcttt
240
tctacagttt gtgaggagaa actggcagac ctttcacttc gtatccaaca aattgaaaca
300
actctcaata ttttagatgc aaagttgtca tctatcccag gcctagatga tgtcacagtt
360

gaagtatctc ctttaaatgt caccagtgtc acaaatggag cacatcctga agccacttca
420
gagcaaccac agcagaacag tacacaagac tctggactac aggaaagtga agtatcagca
480
gaaaatatct taactgtagc caaggatcca agatatgcca gatatctcaa aatggttcaa
540
gtgggtgtac cagtgatggc aataagaaac aaaatgatat cagaaggact agacccagat
600
cttcttgaga ggccagatgc tccagtgcct gatggcgaaa gtgagaaaac tgtagaagaa
660
agttcagata gcgaatcttc ttttagtgat taagcttaat tttgataaga attacatatg
720
catgcatagg ggtacattta cattctgtaa gagattgagc ctgaactctc ttagtcataa
780
aaacatcaaa tggccacatg tccactacca agcttcttct atgttaaaaa aataataata
840
aagcagtttt aacctgccca gtatgtcttg ttgctaaaat aanggccctc aaattgaaaa
900
ttnggatacc ctaaataaag taccaattag tgctccaaat actaagatag aatattttag
960
agatgcaatg agcaattaca gtcaggcacg ggttgtcacg cctgtaatcc cagcactttg
1020
ggaggccgag gcgagtggat aacctgaggt caggagttca agaccagcct ggccaacatg
1080
gtgaaacctc catctctact aaaaatacaa aaagtagctg ggcgtggtga caaaaattag
1140
ctgggcgtag tggcaggtgc ctgtaatccc agctactcgg gaagctgagg caggagaatc
1200
acttgaaccc agaaggtaaa ggtttcagtg agctgagatt gcgtcattgc actccagcca
1260
tggcgacaag agtgaaactc tgtcttaaaa ataaaaagag atgcaatgag caattttaaa
1320
tgaagtcagt gtgagtttag tgatcaatag tagacccaat gc
1362

<210> 4920
<211> 194
<212> PRT
<213> Homo sapiens

<400> 4920
Met Asp Glu Asp Gly Leu Pro Leu Met Gly Ser Gly Ile Asp Leu Thr
1 5 10 15
Lys Val Pro Ala Ile Gln Gln Lys Arg Thr Val Ala Phe Leu Asn Gln
20 25 30
Phe Val Val His Thr Val Gln Phe Leu Asn Arg Phe Ser Thr Val Cys
35 40 45
Glu Glu Lys Leu Ala Asp Leu Ser Leu Arg Ile Gln Gln Ile Glu Thr
50 55 60
Thr Leu Asn Ile Leu Asp Ala Lys Leu Ser Ser Ile Pro Gly Leu Asp
65 70 75 80
Asp Val Thr Val Glu Val Ser Pro Leu Asn Val Thr Ser Val Thr Asn
85 90 95
Gly Ala His Pro Glu Ala Thr Ser Glu Gln Pro Gln Gln Asn Ser Thr

100 105 110
Gln Asp Ser Gly Leu Gln Glu Ser Glu Val Ser Ala Glu Asn Ile Leu
115 120 125
Thr Val Ala Lys Asp Pro Arg Tyr Ala Arg Tyr Leu Lys Met Val Gln
130 135 140
Val Gly Val Pro Val Met Ala Ile Arg Asn Lys Met Ile Ser Glu Gly
145 150 155 160
Leu Asp Pro Asp Leu Leu Glu Arg Pro Asp Ala Pro Val Pro Asp Gly
165 170 175
Glu Ser Glu Lys Thr Val Glu Glu Ser Ser Asp Ser Glu Ser Ser Phe
180 185 190
Ser Asp

<210> 4921
<211> 1272
<212> DNA
<213> Homo sapiens

<400> 4921
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tctcggctcc ttgtggccca aaggccctaa ccggggtccg gcggtctgtg ccctagggta
120
tcttccccgt tgccccttg gggcgggatg gctgcggaag aagaagacga ggtggagtgg
180
gtagtggaga gcatcgcggg gctcctgcga ggcccagact ggtccatccc catcttggac
240
tttgtggaac agaaatgtga agtttttgat gatgaagaag aaagcaaatt gacctataca
300
gagattcatc aggaatacaa agaactagtt gaaaagctgt tagaaggtta cctcaaagaa
360
attggaatta atgaagatca atttcaagaa gcatgcactt ctcctcttgc aaagacccat
420
acatcacagg ccattttgca acctgtgttg gcagcagaag attttactat ctttaaagca
480
atgatggtcc agaaaaacat tgaaatgcag ctgcaagcca ttcgaataat tcaagagaga
540
aatggtgtat tacctgactg cttaaccgat ggctctgatg tggtcagtga ccttgaacac
600
gaagagatga aaatcctgag ggaagttctt agaaaatcaa aagaggaata tgaccaggaa
660
gaagaaagga agaggaaaaa acagttatca gaggctaaaa cagaagagcc cacagtgcat
720
tccagtgaag ctgcaataat gaataattcc caaggggatg gtgaacattt tgcacaccca
780
ccctcagaag ttaaaatgca ttttgctaat cagtcaatag aacctttggg aagaaaagtg
840
gaaaggtctg aaacttcctc cctcccacaa aaaggcctga agattcctgg cttagagcat
900
gcgagcattg aaggaccaat agcaaactta tcagtacttg gaacagaaga acttcggcaa
960
cgagaacact atctcaagca gaagagagat aagttgatgt ccatgagaaa ggatatgagg
1020

actaaacaga tacaaaatat ggagcagaaa ggaaaaccca ctggggaggt agaggaaatg
1080
acagagaaac cagaaatgac agcagaggag aagcaaacat tactaaagag gagattgctt
1140
gcagagaaac tcaaagaaga agttattaat aagtaataat taagaacaat ttaacaaaat
1200
ggaagttcaa attgtcttaa aaataaatta tttagtcctt acactgaaaa aaaaaaaaaa
1260
aaaaaataaa aa
1272

<210> 4922
<211> 342
<212> PRT
<213> Homo sapiens

<400> 4922
Met Ala Ala Glu Glu Glu Asp Glu Val Glu Trp Val Val Glu Ser Ile
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Ala Gly Leu Leu Arg Gly Pro Asp Trp Ser Ile Pro Ile Leu Asp Phe
20 25 30
Val Glu Gln Lys Cys Glu Val Phe Asp Asp Glu Glu Glu Ser Lys Leu
35 40 45
Thr Tyr Thr Glu Ile His Gln Glu Tyr Lys Glu Leu Val Glu Lys Leu
50 55 60
Leu Glu Gly Tyr Leu Lys Glu Ile Gly Ile Asn Glu Asp Gln Phe Gln
65 70 75 80
Glu Ala Cys Thr Ser Pro Leu Ala Lys Thr His Thr Ser Gln Ala Ile
85 90 95
Leu Gln Pro Val Leu Ala Ala Glu Asp Phe Thr Ile Phe Lys Ala Met
100 105 110
Met Val Gln Lys Asn Ile Glu Met Gln Leu Gln Ala Ile Arg Ile Ile
115 120 125
Gln Glu Arg Asn Gly Val Leu Pro Asp Cys Leu Thr Asp Gly Ser Asp
130 135 140
Val Val Ser Asp Leu Glu His Glu Glu Met Lys Ile Leu Arg Glu Val
145 150 155 160
Leu Arg Lys Ser Lys Glu Glu Tyr Asp Gln Glu Glu Glu Arg Lys Arg
165 170 175
Lys Lys Gln Leu Ser Glu Ala Lys Thr Glu Glu Pro Thr Val His Ser
180 185 190
Ser Glu Ala Ala Ile Met Asn Asn Ser Gln Gly Asp Gly Glu His Phe
195 200 205
Ala His Pro Pro Ser Glu Val Lys Met His Phe Ala Asn Gln Ser Ile
210 215 220
Glu Pro Leu Gly Arg Lys Val Glu Arg Ser Glu Thr Ser Ser Leu Pro
225 230 235 240
Gln Lys Gly Leu Lys Ile Pro Gly Leu Glu His Ala Ser Ile Glu Gly
245 250 255
Pro Ile Ala Asn Leu Ser Val Leu Gly Thr Glu Glu Leu Arg Gln Arg
260 265 270
Glu His Tyr Leu Lys Gln Lys Arg Asp Lys Leu Met Ser Met Arg Lys
275 280 285
Asp Met Arg Thr Lys Gln Ile Gln Asn Met Glu Gln Lys Gly Lys Pro

290 295 300
Thr Gly Glu Val Glu Glu Met Thr Glu Lys Pro Glu Met Thr Ala Glu
305 310 315 320
Glu Lys Gln Thr Leu Leu Lys Arg Arg Leu Leu Ala Glu Lys Leu Lys
325 330 335
Glu Glu Val Ile Asn Lys
340

<210> 4923
<211> 765
<212> DNA
<213> Homo sapiens

<400> 4923
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aagccttctg ctcctnctcc aaggacctca tttagctccg ccagcaggtc atcatcagcc
120
tccaagtcgt cctcatccgt cccctcctcc tcatcctcat ccgggtctct catgcacagg
180
ctggccatct tctcaatggc ctccatcggc aagggacctt tgcctttgag cttctccagg
240
gctgggggct ggcccccgac caaagccaag aactcagcct ccagttcttc atcgttagcc
300
ccgtcctcag ggatcatcag gccatctggg gagaggtcaa ccagcaggcc cagctggcgg
360
gcggccgcgg cgcctctgcc cgggggtccc gggggtcctt cctcttgtgc atcttcaagg
420
ctggatgccc ggaccacctg cccccaagcc cggccttgcc ctgccccttc cccgggctct
480
gtcgccgcgc actcgccctt cctgagtcct gcactcctcg tcggcgccct gcggccggtc
540
gatcccgagc cctcgcttcc ctgcttggcc gtcccacttc cgcctcgggc ctcgggcgcc
600
gccgcacctn ggagcgcggc cagctgggct cgccgaggtc tgccgagccg aaactacaac
660
tcccggcaga tttctcaagg ggaagataaa atgactaaga ggaagaagct gcggacctca
720
gctcccctga tgaggaaaca ggatctccct gccggctcct ccgtc
765

<210> 4924
<211> 255
<212> PRT
<213> Homo sapiens

<400> 4924
Ser Pro Ala Pro Asp Glu Gly Pro Gln Ala Ser Ala Gly Pro Gln Glu
1 5 10 15
Val Gly Ser Leu Lys Pro Ser Ala Pro Xaa Pro Arg Thr Ser Phe Ser
20 25 30
Ser Ala Ser Arg Ser Ser Ser Ala Ser Lys Ser Ser Ser Ser Val Pro
35 40 45
Ser Ser Ser Ser Ser Ser Gly Ser Leu Met His Arg Leu Ala Ile Phe

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    50                  55                  60
Ser Met Ala Ser Ile Gly Lys Gly Pro Leu Pro Leu Ser Phe Ser Arg
65                  70                  75                  80
Ala Gly Gly Trp Pro Pro Thr Lys Ala Lys Asn Ser Ala Ser Ser Ser
                85                  90                  95
Ser Ser Leu Ala Pro Ser Ser Gly Ile Ile Arg Pro Ser Gly Glu Arg
            100                 105                 110
Ser Thr Ser Arg Pro Ser Trp Arg Ala Ala Ala Ala Pro Leu Pro Gly
        115                 120                 125
Gly Pro Gly Gly Pro Ser Ser Cys Ala Ser Ser Arg Leu Asp Ala Arg
    130                 135                 140
Thr Thr Cys Pro Gln Ala Arg Pro Cys Pro Ala Pro Ser Pro Gly Ser
145                 150                 155                 160
Val Ala Ala His Ser Pro Phe Leu Ser Pro Ala Leu Leu Val Gly Ala
                165                 170                 175
Leu Arg Pro Val Asp Pro Glu Pro Ser Leu Pro Cys Leu Ala Val Pro
            180                 185                 190
Leu Pro Pro Arg Ala Ser Gly Ala Ala Ala Pro Xaa Ser Ala Ala Ser
        195                 200                 205
Trp Ala Arg Arg Gly Leu Pro Ser Arg Asn Tyr Asn Ser Arg Gln Ile
    210                 215                 220
Ser Gln Gly Glu Asp Lys Met Thr Lys Arg Lys Lys Leu Arg Thr Ser
225                 230                 235                 240
Ala Pro Leu Met Arg Lys Gln Asp Leu Pro Ala Gly Ser Ser Val
                245                 250                 255
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<210> 4925
<211> 374
<212> DNA
<213> Homo sapiens

<400> 4925
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ggatcggatg aaaatgaaat ggaagaacat gaactcaaag atgaggagga tggtaaagac
120
agtgatgagg ccgaggacgc tgagctctat gatgaccttt actgcccagc atgtgacaaa
180
tcgttcaaga cagaaaaggc catgaagaat cacgagaagt caaagaagca tcgggaaatg
240
gtggccttgc taaaacaaca gctggaggag gaagaagaaa atttttcaag acctcaaatt
300
gatgaaaatc cattagatga caattctgag gaagaaatgg aagatgcacc aaaacaaaag
360
ctttctaaaa aaaa
374

<210> 4926
<211> 124
<212> PRT
<213> Homo sapiens

<400> 4926
Ala Asn Leu Glu Lys Glu Leu Gln Glu Met Glu Ala Arg Tyr Glu Lys

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 1               5                  10                  15
Glu Phe Gly Asp Gly Ser Asp Glu Asn Glu Met Glu Glu His Glu Leu
            20                  25                  30
Lys Asp Glu Glu Asp Gly Lys Asp Ser Asp Glu Ala Glu Asp Ala Glu
        35                  40                  45
Leu Tyr Asp Asp Leu Tyr Cys Pro Ala Cys Asp Lys Ser Phe Lys Thr
    50                  55                  60
Glu Lys Ala Met Lys Asn His Glu Lys Ser Lys Lys His Arg Glu Met
65                  70                  75                  80
Val Ala Leu Leu Lys Gln Gln Leu Glu Glu Glu Glu Glu Asn Phe Ser
                85                  90                  95
Arg Pro Gln Ile Asp Glu Asn Pro Leu Asp Asp Asn Ser Glu Glu Glu
            100                 105                 110
Met Glu Asp Ala Pro Lys Gln Lys Leu Ser Lys Lys
        115                 120
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<210> 4927
<211> 1649
<212> DNA
<213> Homo sapiens

<400> 4927

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120
attcagttat ctggagcaga acaactagaa gctttgaaag cttttgtgga agcaatggta
180
aatgagaatg tcagtctcgt gatctcgcgg cagttgctga ctgatttttg cacacatctt
240
cctaacttgc ctgatagcac agccaaagaa atctatcact tcaccttgga aaagatccag
300
cctagagtca tttcatttga ggagcaggtt gcttccataa gacagcatct tgcatctata
360
tatgagaaag aagaagattg gagaaatgca gcccaagtgt tggtgggaat tcctttggaa
420
acaggacaaa aacagtacaa tgtagattat aaactggaga cttacttgaa gattgctagg
480
ctatatctgg aggatgatga tccagtccag gcagaggctt acataaatcg agcatcgttg
540
cttcagaatg aatcaaccaa tgaacaatta cagatacatt ataaggtatg ctatgcacgt
600
gttcttgatt atagaagaaa attcattgaa gctgcacaaa ggtacaatga gctctcttac
660
aagacaatag tccacgaaag tgaaagacta gaggccttaa aacatgcttt gcactgtacg
720
atcttagcat cagcaggaca gcagcgttct cggatgctgg ctacccttt taaggatgaa
780
aggtgccagc aacttgctgc ttatgggatc ctagagaaaa tgtatctaga caggatcatc
840
agagggaacc agcttcaaga atttgctgcc atgctgatgc ctcaccaaaa agcaactaca
900
gctgatggtt ccagcatctt ggacagagct gttattgaac acaatttgtt gtctgcaagc
960
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aaattatata ataatattac cttcgaagaa cttggagctc ttttagagat ccctgcagct
1020
aaggcggaaa agatagcatc tcaaatgata accgaaggac gtatgaatgg atttattgac
1080
cagattgatg gaatagttca ttttgaaaca cgagaagccc tgccaacgtg ggataagcag
1140
atccaatcac tttgtttcca agtgaataac cttttggaga aaattagtca aacagcacca
1200
gaatggacag cacaagccat ggaagcccag atggctcagt gaatccttgc agaacttctg
1260
tgcacatgac atctttttcc atgttgtgca gatcagtttc actatctcca aagcatttgc
1320
atcatgacct tatacatttc aatccctttt atgctggatt ccgtttaaag aagacattat
1380
tagagcagga agtacaagca tttaaaatat gtagttccca tatatttcag ggtctctgtg
1440
tattaagcta actcagatgt tttgaaagct ttttctttaa acagaggtga aatatctgtg
1500
gctaaaaagt ttgagatttg tgataacttt gtagtcatgt aaaacttaag tgcttcatgc
1560
ctctccaaat gtggttattc taataaatgg agaaatgagc caaaaaaaag tagtactttg
1620
tttttaaaaa aaaaaaaaaa aaaaaaaaa
1649

<210> 4928
<211> 405
<212> PRT
<213> Homo sapiens

<400> 4928
Met Ala Ala Val Arg Gln Asp Leu Ala Gln Leu Met Asn Ser Ser Gly
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Ser His Lys Asp Leu Ala Gly Lys Tyr Arg Gln Ile Leu Glu Lys Ala
            20   25   30
Ile Gln Leu Ser Gly Ala Glu Gln Leu Glu Ala Leu Lys Ala Phe Val
        35   40   45
Glu Ala Met Val Asn Glu Asn Val Ser Leu Val Ile Ser Arg Gln Leu
    50   55   60
Leu Thr Asp Phe Cys Thr His Leu Pro Asn Leu Pro Asp Ser Thr Ala
65   70   75   80
Lys Glu Ile Tyr His Phe Thr Leu Glu Lys Ile Gln Pro Arg Val Ile
                85   90   95
Ser Phe Glu Glu Gln Val Ala Ser Ile Arg Gln His Leu Ala Ser Ile
            100   105   110
Tyr Glu Lys Glu Glu Asp Trp Arg Asn Ala Ala Gln Val Leu Val Gly
        115   120   125
Ile Pro Leu Glu Thr Gly Gln Lys Gln Tyr Asn Val Asp Tyr Lys Leu
    130   135   140
Glu Thr Tyr Leu Lys Ile Ala Arg Leu Tyr Leu Glu Asp Asp Asp Pro
145   150   155   160
Val Gln Ala Glu Ala Tyr Ile Asn Arg Ala Ser Leu Leu Gln Asn Glu
                165   170   175
Ser Thr Asn Glu Gln Leu Gln Ile His Tyr Lys Val Cys Tyr Ala Arg

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            180                 185                 190
Val Leu Asp Tyr Arg Arg Lys Phe Ile Glu Ala Ala Gln Arg Tyr Asn
        195                 200                 205
Glu Leu Ser Tyr Lys Thr Ile Val His Glu Ser Glu Arg Leu Glu Ala
    210                 215                 220
Leu Lys His Ala Leu His Cys Thr Ile Leu Ala Ser Ala Gly Gln Gln
225                 230                 235                 240
Arg Ser Arg Met Leu Ala Thr Leu Phe Lys Asp Glu Arg Cys Gln Gln
                245                 250                 255
Leu Ala Ala Tyr Gly Ile Leu Glu Lys Met Tyr Leu Asp Arg Ile Ile
            260                 265                 270
Arg Gly Asn Gln Leu Gln Glu Phe Ala Ala Met Leu Met Pro His Gln
        275                 280                 285
Lys Ala Thr Thr Ala Asp Gly Ser Ser Ile Leu Asp Arg Ala Val Ile
    290                 295                 300
Glu His Asn Leu Leu Ser Ala Ser Lys Leu Tyr Asn Asn Ile Thr Phe
305                 310                 315                 320
Glu Glu Leu Gly Ala Leu Leu Glu Ile Pro Ala Ala Lys Ala Glu Lys
                325                 330                 335
Ile Ala Ser Gln Met Ile Thr Glu Gly Arg Met Asn Gly Phe Ile Asp
            340                 345                 350
Gln Ile Asp Gly Ile Val His Phe Glu Thr Arg Glu Ala Leu Pro Thr
        355                 360                 365
Trp Asp Lys Gln Ile Gln Ser Leu Cys Phe Gln Val Asn Asn Leu Leu
    370                 375                 380
Glu Lys Ile Ser Gln Thr Ala Pro Glu Trp Thr Ala Gln Ala Met Glu
385                 390                 395                 400
Ala Gln Met Ala Gln
                405
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<210> 4929
<211> 5907
<212> DNA
<213> Homo sapiens

<400> 4929
ntaatcgcgg gcgctttggc gccatcttta gatggcggga gtaagaggaa aacgattgtg
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aggcgggaac ggctttctgc tgcctttctt gggccccgaa aagggtcagc tggccgggct
120
ttggggcgcg tgccctgagg cgcggagcgc gtttgctacg atgcgggggc tgctcggggc
180
tccgtccccc gggctgggga cgcgccgaat gtgaccgcct cccgctcccc cacccgccgc
240
ggggaggagg agcgggcgag aagctgccgc cgaacgacag gacgttgggg cggcctggct
300
ccctcaggta taagtattgt ttaagctgca tcaatggagc acatacaggg agcttggaag
360
acgatcagca atggttttgg attcaaagat gccgtgtttg atggctccag ctgcatctct
420
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<212> PRT
<213> Homo sapiens

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35 40 45
Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn
50 55 60
Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp
65 70 75 80
Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys
85 90 95
Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu
100 105 110
Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val
115 120 125
Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala Arg Lys
130 135 140
Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe Leu Leu
145 150 155 160
Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu His Cys
165 170 175
Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile Arg Gln
180 185 190
Leu Leu Leu Phe Pro Asn Ser Thr Ile Gly Asp Ser Gly Val Pro Ala
195 200 205
Leu Pro Ser Leu Thr Met Arg Arg Met Arg Glu Ser Val Ser Arg Met
210 215 220
Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe Thr Phe

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Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu Ser Ala
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Ser Pro Ser Ala Leu Ser Ser Ser Pro Asn Asn Leu Ser Pro Thr Gly
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Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro
305                 310                 315                 320
Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg
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Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met Leu Ser
            340                 345                 350
Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp
        355                 360                 365
His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro
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Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr
385                 390                 395                 400
Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys Asp Asn
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Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr Lys His
            420                 425                 430
Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile Asp Ile
        435                 440                 445
Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile
    450                 455                 460
Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu Gly Leu
465                 470                 475                 480
Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser Arg Trp
                485                 490                 495
Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu Trp Met
            500                 505                 510
Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser Phe Gln
        515                 520                 525
Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly
    530                 535                 540
Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met
545                 550                 555                 560
Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr Lys Asn
                565                 570                 575
Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
            580                 585                 590
Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu
        595                 600                 605
Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu Pro Ser
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Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr Leu Thr
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<212> DNA
<213> Homo sapiens

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<210> 4932
<211> 87
<212> PRT
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Thr Gln Gly Thr Arg Lys Ile Leu Tyr Pro Tyr Ala His Leu Ser Ala
35 40 45
Glu Asp Phe Asn Ile Tyr Gly His Gly Gly Arg Gln Phe Trp Leu Val
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Ser Ser Cys Phe Phe Phe Leu Leu Gly Gly Ala Ser Thr Cys Met Arg
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Ala Ser Trp His Arg Ser Thr
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<211> 181
<212> PRT
<213> Homo sapiens

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20 25 30
Ala Tyr Ile Glu Ser Gln Gly Ala His Arg Ala Gly Leu Ala Lys Ile
35 40 45
Ile Pro Pro Lys Glu Trp Lys Pro Arg Gln Thr Tyr Asp Asp Ile Asp
50 55 60
Asp Val Val Ile Pro Ala Pro Ile Gln Gln Val Val Thr Gly Gln Ser
65 70 75 80
Gly Leu Phe Thr Gln Tyr Asn Ile Gln Lys Lys Ala Met Thr Val Gly
85 90 95
Glu Tyr Arg Arg Leu Ala Asn Ser Glu Lys Tyr Cys Thr Pro Arg His
100 105 110
Gln Asp Phe Asp Asp Leu Glu Arg Lys Tyr Trp Lys Asn Leu Thr Phe
115 120 125
Val Ser Pro Ile Tyr Gly Ala Asp Ile Ser Gly Ser Leu Tyr Asp Asp
130 135 140
Val Ser Met Arg Leu Arg Gly Arg Thr Gly Thr Ser Phe Leu Val Gly
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Gly Gly Gly Arg Ala Leu Asn Gly Thr Leu Pro Trp Gln Met Lys Leu
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Pro Gly Arg Gln Gly
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<210> 4935
<211> 1668
<212> DNA
<213> Homo sapiens

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<211> 337
<212> PRT
<213> Homo sapiens

<400> 4936
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35 40 45
Gly Gly Glu Asp Asp Leu Val Thr Val Trp Ser Phe Val Asp Cys Arg
50 55 60
Val Ile Ala Arg Gly His Gly His Lys Ser Trp Val Ser Val Val Ala
65 70 75 80
Phe Asp Pro Tyr Thr Thr Ser Val Glu Glu Gly Asp Pro Met Glu Phe
85 90 95
Ser Gly Ser Asp Glu Asp Phe Gln Asp Leu Leu His Phe Gly Glu Ile
100 105 110
Glu Gln Ile Val His Ser Pro Gly Ser Pro Asn Gly Thr Leu Gln Thr
115 120 125
Ala Ala Pro Ser Val Thr Tyr Arg Phe Gly Ser Val Gly Gln Asp Thr
130 135 140
Gln Leu Cys Leu Trp Asp Leu Thr Glu Asp Ile Leu Phe Pro His Gln
145 150 155 160
Pro Leu Ser Arg Ala Arg Thr His Thr Asn Val Met Asn Ala Thr Ser
165 170 175
Pro Pro Ala Gly Ser Asn Gly Asn Ser Val Thr Thr Pro Gly Asn Ser
180 185 190
Val Pro Pro Pro Leu Pro Arg Ser Asn Ser Leu Pro His Ser Ala Val
195 200 205
Ser Asn Ala Gly Ser Lys Ser Ser Val Met Asp Gly Ala Ile Ala Ser
210 215 220
Gly Val Ser Lys Phe Ala Thr Leu Ser Leu His Asp Arg Lys Glu Arg
225 230 235 240
His His Glu Lys Asp His Lys Arg Asn His Ser Met Gly His Ile Ser
245 250 255
Ser Lys Ser Ser Asp Lys Leu Asn Leu Val Thr Lys Thr Lys Thr Asp
260 265 270
Pro Ala Lys Thr Leu Gly Thr Pro Leu Cys Pro Arg Met Glu Asp Val
275 280 285
Pro Leu Leu Glu Pro Leu Ile Cys Lys Lys Ile Ala His Glu Arg Leu
290 295 300
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Pro

<210> 4937
<211> 715
<212> DNA
<213> Homo sapiens

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600
gctcccactg aggtcttgag aaggtaatgg ggagagccac ttgcccctgc ctctgtcccc
660
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715

<210> 4938
<211> 109
<212> PRT
<213> Homo sapiens

<400> 4938
Met Lys Arg Gly Val Pro His Ser Leu Gly Pro Gly Thr Lys Leu Ser
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Ser Val Val Leu Ile Cys Arg Ala Ser Ala Leu Ser Arg Tyr Leu Val
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Val Ala Glu Pro Trp Pro Thr Arg Ser Gln Gly Gly Arg Gln Pro Gly
35 40 45
Cys Thr Leu Thr Leu Gly Val Cys Ala Asp Gly Arg Trp Glu Glu Thr
50 55 60
Asp Gln Gln Glu Val Phe Ser Ser Gly Val Ala Ser Pro Thr Leu Asn
65 70 75 80
Leu Arg Ala Ser Ser Ser Pro Ala Lys Ala Arg Ala Leu Ser Arg Pro

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                85                  90                  95
Trp Ala Leu Tyr Lys Gln Arg Glu Ala Pro Glu Leu Val
            100                 105
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<210> 4939
<211> 730
<212> DNA
<213> Homo sapiens

<400> 4939
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120
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300
ccttccaaag cttcaccagc gccagcagcg ctgatgtgtg ggaccacatc acccccccata
360
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480
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540
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600
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ccatcggccg
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<210> 4940
<211> 158
<212> PRT
<213> Homo sapiens

<400> 4940
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 1               5                  10                  15
Ala Val Trp Glu Pro Ala Gly Ser Ser Pro Gln Leu Ser Ser Ala Pro
            20                  25                  30
Ala Asp Ser Ser Ala Ser Thr Arg Pro Pro Gln Gly Pro Pro Ser Leu
        35                  40                  45
Asp Ser Lys Ala Ser Thr Trp Leu Pro Leu Pro Val Thr Ser Ser Ser
    50                  55                  60
Ala Glu Pro Ser Arg Pro Asn Ser Cys Pro Pro Ala Cys Ser Pro Ala
65                  70                  75                  80
Ala Ala Ser Ser Phe Ser Phe Glu Ser Gln Pro Cys Pro Ser Ala Pro
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                85                  90                  95
Ser Lys Ala Ser Pro Ala Pro Ala Ala Leu Met Cys Gly Thr Thr Ser
            100                 105                 110
Pro Pro Ile Ile Pro Ala Ala Thr Glu Pro Val Cys Ala Ser Ser Arg
        115                 120                 125
Ser Gly Arg Pro Thr Ala Thr Ala Cys Ser Leu Gln Pro Leu Leu Asp
    130                 135                 140
Val Leu Ser Ala Ser Ala Ser Ser Ser Ser Val Ser Leu Ala
145                 150                 155

<210> 4941
<211> 1718
<212> DNA
<213> Homo sapiens

<400> 4941
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120
gatctgctcc tgggcagcct gaaggagaag cccgtcacca aggagggccg ggcttccatc
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gtgcccctgg cggcagccag cggcctgtgc gagctcctgt ccgtcaacag ctgcatgggc
240
cgtgtgaggc gcatctaccc tcagctgctc ctggccctgc tcattcaggt ccattaccac
300
atcggcctca acctgcctgg ctgcgtggct cctcccaagg acaccaagaa gggtgcacag
360
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420
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480
caggtggaga gccaccaccg cggagtggcc ttgctggcaa gggccatggt gcagtactcc
540
tgccaggagc tgtgccgcat cctctacctg ctcatcccgc tcctggagcg aggcgacgag
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aagcacagga tcacggccac cgccttcttc gtggagctcc tccagatgga gcaggtgcgc
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cggatccccg aggaatactc tctggggcgg atggcagaag gcctgagcca ccacgacccc
720
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780
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960
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gcaccacgca ctcaggccat ggaggagcag ctggtcagca ccttggtgcc cctactgctg
1080
accatgcagg agggcaactc caaggtaagc cagaagtgtg tgaagaccct gttacgctgt
1140
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caacagcaga cagtggccaa aatttgcaag tgccttgtga acacccaccg agacagcgcc
1260
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1320
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1380
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1440
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1500
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1560
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1620
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1680
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1718

<210> 4942
<211> 469
<212> PRT
<213> Homo sapiens

<400> 4942
Met Gly Arg Val Arg Arg Ile Tyr Pro Gln Leu Leu Leu Ala Leu Leu
1 5 10 15
Ile Gln Val His Tyr His Ile Gly Leu Asn Leu Pro Gly Cys Val Ala
20 25 30
Pro Pro Lys Asp Thr Lys Lys Gly Ala Gln Pro Ser Pro Phe Val Pro
35 40 45
Val Arg Trp Val Val Lys Val Val Lys Thr Leu Leu Leu Arg Met Gly
50 55 60
Cys Ser Tyr Glu Thr Thr Phe Leu Glu Asp Gln Gly Gly Trp Glu Leu
65 70 75 80
Met Glu Gln Val Glu Ser His His Arg Gly Val Ala Leu Leu Ala Arg
85 90 95
Ala Met Val Gln Tyr Ser Cys Gln Glu Leu Cys Arg Ile Leu Tyr Leu
100 105 110
Leu Ile Pro Leu Leu Glu Arg Gly Asp Glu Lys His Arg Ile Thr Ala
115 120 125
Thr Ala Phe Phe Val Glu Leu Leu Gln Met Glu Gln Val Arg Arg Ile
130 135 140
Pro Glu Glu Tyr Ser Leu Gly Arg Met Ala Glu Gly Leu Ser His His
145 150 155 160
Asp Pro Ile Met Lys Val Leu Ser Ile Arg Gly Leu Val Ile Leu Ala
165 170 175
Arg Arg Ser Glu Lys Thr Ala Lys Val Lys Ala Leu Leu Pro Ser Met
180 185 190
Val Lys Gly Leu Lys Asn Met Asp Gly Met Leu Val Val Glu Ala Val
195 200 205
His Asn Leu Lys Ala Val Phe Lys Gly Arg Asp Gln Lys Leu Met Asp

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    210                 215                 220
Ser Ala Val Tyr Val Glu Met Leu Gln Ile Leu Leu Pro His Phe Ser
225                 230                 235                 240
Asp Ala Arg Glu Val Val Arg Ser Ser Cys Ile Asn Leu Tyr Gly Lys
                245                 250                 255
Val Val Gln Lys Leu Arg Ala Pro Arg Thr Gln Ala Met Glu Glu Gln
            260                 265                 270
Leu Val Ser Thr Leu Val Pro Leu Leu Leu Thr Met Gln Glu Gly Asn
        275                 280                 285
Ser Lys Val Ser Gln Lys Cys Val Lys Thr Leu Leu Arg Cys Ser Tyr
    290                 295                 300
Phe Met Ala Trp Glu Leu Pro Lys Arg Ala Tyr Ser Arg Lys Pro Trp
305                 310                 315                 320
Asp Asn Gln Gln Gln Thr Val Ala Lys Ile Cys Lys Cys Leu Val Asn
                325                 330                 335
Thr His Arg Asp Ser Ala Phe Ile Phe Leu Ser Gln Ser Leu Glu Tyr
            340                 345                 350
Ala Lys Asn Ser Arg Ala Ser Leu Arg Lys Cys Ser Val Met Phe Ile
        355                 360                 365
Gly Ser Leu Val Pro Cys Met Glu Ser Ile Met Thr Glu Asp Arg Leu
    370                 375                 380
Asn Glu Val Lys Ala Ala Leu Asp Asn Leu Arg His Asp Pro Glu Ala
385                 390                 395                 400
Ser Val Cys Ile Tyr Ala Ala Gln Val Gln Asp His Ile Leu Ala Ser
                405                 410                 415
Cys Trp Gln Asn Ser Trp Leu Pro His Gly Asn Ser Trp Val Cys Tyr
            420                 425                 430
Ser Ala Thr Thr His Arg Trp Ser Pro Ser Cys Glu Asn Leu Pro Thr
        435                 440                 445
Ser His Gln Arg Arg Ser Trp Ile Met Gln Ala Leu Gly Ser Trp Lys
    450                 455                 460
Met Ser Leu Lys Lys
465
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<210> 4943
<211> 1020
<212> DNA
<213> Homo sapiens

<400> 4943

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tagggcgaat ccacttcatt agtgaccagc tcgggcggtt cacgtgcatc acacaaataa
180
cttggccttt ttctgcctca gttgggggat ttcttaaacg tagaataccc gcgtttccgc
240
tgccgtaatt tcctctcagg cgcaattact ctcttccata ttggttaaca gtagaaggct
300
cagtttctct gctcatcaca cggccttcgg cactgtagct ttgggtggtg ggctgcagat
360
taattttgta accaccttaa gaaaaatacg gaactctaac tccttgccac tcaagaaatg
420
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tcctcccttt cagaatatgc cttccgcatg tctcgtctca gtgcccggct atttggtgaa
480
gtcaccaggc ctactaattc caagtctatg aaagtggtga aactgtttag tgaactgccc
540
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600
atgcagacgc tccgatttct tggactctac agagatgagc atcaggattt tatggatgag
660
caaaaacgac taaagaagct tcgtggaaag gagaaaccaa agaaaggaga agggaaaaga
720
gcagcaaaaa ggaaatagtg ttggtccctc aagagggaga ctttcttcct cagtggcgga
780
gagaagaaag tgcatttatt gtctttccac atattggagg aatgtcatct tcctaaatga
840
agtttatttg gaggaacaca gtcatctcct tggtgaaatc taatccggtt acattgtggc
900
tggtttcttg aacacattct aactgtgcaa aattatcttg gccttggccg tgtaatgtga
960
ggtttacctg attctctaat gaaataaata cctaagttat aaaaaaaaaa aaaaaaaaaa
1020

<210> 4944
<211> 106
<212> PRT
<213> Homo sapiens

<400> 4944
Met Ser Ser Leu Ser Glu Tyr Ala Phe Arg Met Ser Arg Leu Ser Ala
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Arg Leu Phe Gly Glu Val Thr Arg Pro Thr Asn Ser Lys Ser Met Lys
20 25 30
Val Val Lys Leu Phe Ser Glu Leu Pro Leu Ala Lys Lys Lys Glu Thr
35 40 45
Tyr Asp Trp Tyr Pro Asn His His Thr Tyr Ala Glu Leu Met Gln Thr
50 55 60
Leu Arg Phe Leu Gly Leu Tyr Arg Asp Glu His Gln Asp Phe Met Asp
65 70 75 80
Glu Gln Lys Arg Leu Lys Lys Leu Arg Gly Lys Glu Lys Pro Lys Lys
85 90 95
Gly Glu Gly Lys Arg Ala Ala Lys Arg Lys
100 105

<210> 4945
<211> 1792
<212> DNA
<213> Homo sapiens

<400> 4945
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aagcaggaat tctggcaaca gtgtgtctca ttcattcctc caggccagga gtaccgcatg
120
tacaacacat atgatgtcca cttttatgct tcctttgccc tcatcatgct ctggcccaaa
180

cttgagctca gcctacagta tgacatggct ctggccactc tcagggagga cctgacacgg
240
cgacggtacc tgatgagtgg ggtgatggca cctgtgaaaa ggaggaacgt catcccccat
300
gatattgggg acccagatga tgaaccatgg ctccgcgtca atgcatattt aatccatgat
360
actgctgatt ggaaggacct gaacctgaag tttgtgctgc aggtttatcg ggactattac
420
ctcacgggtg atcaaaactt cctgaaggac atgtggcctg tgtgtctagt aagggatgca
480
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540
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660
agacctatga tggatgggtg accacaggcc ccaggttagc gggtaggggt ttccaggagg
720
cctgaggtga gaaactgggc aacaagggat tgtagggctc aagaaagaat gactcattgt
780
ctattacacg gcatgggagc agctggagct gccagtctga cccccaaacc catgtccctg
840
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900
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960
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1080
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1140
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1320
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1380
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1440
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1620
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1680
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1792

<210> 4946
<211> 197
<212> PRT
<213> Homo sapiens

<400> 4946
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1 5 10 15
Gly Leu Lys Gly Lys Gln Glu Phe Trp Gln Gln Cys Val Ser Phe Ile
20 25 30
Pro Pro Gly Gln Glu Tyr Arg Met Tyr Asn Thr Tyr Asp Val His Phe
35 40 45
Tyr Ala Ser Phe Ala Leu Ile Met Leu Trp Pro Lys Leu Glu Leu Ser
50 55 60
Leu Gln Tyr Asp Met Ala Leu Ala Thr Leu Arg Glu Asp Leu Thr Arg
65 70 75 80
Arg Arg Tyr Leu Met Ser Gly Val Met Ala Pro Val Lys Arg Arg Asn
85 90 95
Val Ile Pro His Asp Ile Gly Asp Pro Asp Asp Glu Pro Trp Leu Arg
100 105 110
Val Asn Ala Tyr Leu Ile His Asp Thr Ala Asp Trp Lys Asp Leu Asn
115 120 125
Leu Lys Phe Val Leu Gln Val Tyr Arg Asp Tyr Tyr Leu Thr Gly Asp
130 135 140
Gln Asn Phe Leu Lys Asp Met Trp Pro Val Cys Leu Val Arg Asp Ala
145 150 155 160
His Ala Val Ala Ser Val Pro Gly Val Trp Leu Val Ser Gly Lys Ser
165 170 175
Leu Ala Gly Cys Cys Leu Ser Ser Val Pro Arg Ser Ser Thr Ser Trp
180 185 190
Ser Leu Ser Arg Leu
195

<210> 4947
<211> 2060
<212> DNA
<213> Homo sapiens

<400> 4947
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120
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180
atgtgatgct tggggactgg catattcgtt gcaaggggtt ttttcacctt ttctgaagct
240
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300
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360
tggaagacta ctaagcacgt agtttcagtc attcagttga tagacatttg aacacttatg
420

gtggtgccta accccaggcc gagtgtgact cattccacct tgcagttaaa gcagtggaag
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600
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720
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1020
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1320
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1560
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1620
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1740
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1920
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1980
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2040

aaaaaaaaaa aaaaaaaaaa
2060

<210> 4948
<211> 127
<212> PRT
<213> Homo sapiens

<400> 4948
Ala Glu Leu Thr Pro Leu Pro Phe Ser Leu Gln Ala Leu Ser Ile Leu
1 5 10 15
Met Leu Pro His Asn Ile Pro Ser Ser Leu Ser Leu Leu Thr Ser Met
20 25 30
Val Asp Asp Met Trp His Tyr Ala Gly Asp Gln Ser Thr Asp Phe Asn
35 40 45
Trp Tyr Thr Arg Arg Ala Met Leu Ala Ala Ile Tyr Asn Thr Thr Glu
50 55 60
Leu Val Met Met Gln Asp Ser Ser Pro Asp Phe Glu Asp Thr Trp Arg
65 70 75 80
Phe Leu Glu Asn Arg Val Asn Asp Ala Met Asn Met Gly His Thr Ala
85 90 95
Lys Gln Val Lys Ser Thr Gly Glu Ala Leu Val Gln Gly Leu Met Gly
100 105 110
Ala Ala Val Thr Leu Lys Asn Leu Thr Xaa Leu Asn Gln Arg Arg
115 120 125

<210> 4949
<211> 1259
<212> DNA
<213> Homo sapiens

<400> 4949
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120
gcttgggagg aaaagacgct gtccaagtac gagtccagcg agattcgcct gctggagatc
180
ctggaggggc tgtgcgagag cagcgacttc gaatgcaatc agatgctaga ggcgcaggag
240
gagcacctgg aggcctggtg gctgcagctg aagagcgaat atcctgactt attcgagtgg
300
ttttgtgtga agacactgaa agtgtgctgc tctccaggaa cctacggtcc cgactgtctc
360
gcatgccagg gcggatccca gaggccctgc agcgggaatg gccactgcag cggagatggg
420
agcagacagg gcgacgggtc ctgccggtgc cacatggggt accagggccc gctgtgcact
480
gactgcatgg acggctactt cagctcgctc cggaacgaga cccacagcat ctgcacagcc
540
tgtgacgagt cctgcaagac gtgctcgggc ctgaccaaca gagactgcgg cgagtgtgaa
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gtgggctggg tgctggacga gggcgcctgt gtggatgtgg acgagtgtgc ggccgagccg
660

cctccctgca gcgctgcgca gttctgtaag aacgccaacg gctcctacac gtgcgaagag
720
tgtgactcca gctgtgtggg ctgcacaggg gaaggcccag gaaactgtaa agagtgtatc
780
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900
tgtcctgacg gcttcgaaga anacggaaga tgcctgtgtg ccgccggcag aggctgaagc
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cacagaagga gaaagcccga cacagctgcc ctcccgcgaa gacctgtaat gtgccggact
1020
taccctttaa attattcaga aggatgtccc gtggaaaatg tggccctgag gatgccgtct
1080
cctgcagtgg acagcggcgg ggagaggctg cctgctctct aacggttgat tctcatttgt
1140
cccttaaaca gctgcatttc ttggttgttc ttaaacagac ttgtatattt tgatacagtt
1200
ctttgtaata aaattgacca ttgtaggtaa tcaggaggaa aaaaaaaaaa aaaaaaaaa
1259

<210> 4950
<211> 318
<212> PRT
<213> Homo sapiens

<400> 4950
Xaa Pro Ala Cys Pro Pro Gly Tyr Leu Thr Ala Pro Cys His Arg Cys
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Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr Ala Lys
            20   25   30
Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr Leu Ser
        35   40   45
Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu Gly Leu
    50   55   60
Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala Gln Glu
65   70   75   80
Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr Pro Asp
                85   90   95
Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys Ser Pro
            100   105   110
Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser Gln Arg
        115   120   125
Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg Gln Gly
    130   135   140
Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu Cys Thr
145   150   155   160
Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr His Ser
                165   170   175
Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly Leu Thr
            180   185   190
Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp Glu Gly
        195   200   205
Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro Cys Ser

```
    210                 215                 220
Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys Glu Glu
225                 230                 235                 240
Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly Asn Cys
                245                 250                 255
Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys Ala Asp
            260                 265                 270
Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys Asn Glu
        275                 280                 285
Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro Asp Gly
    290                 295                 300
Phe Glu Glu Xaa Gly Arg Cys Leu Cys Ala Ala Gly Arg Gly
305                 310                 315
```

<210> 4951
<211> 1835
<212> DNA
<213> Homo sapiens

<400> 4951
ngagctctgg cgctcagctg gcccccacca ctctcacctg ccgcctgggc tcgctcccgg
60
cttctctcca gccgtcgact ccacgcctcg cgcctctcgc gagaggagga ggctccacgg
120
agcgacgact tccgccctcc ttagggccgt ggtcccgtag ctaccggtcg cgtcgccgtg
180
ggcgacgtgc ccgcttccaa aatggcggcg gcggcggtat ctggtgcgct tggccgggcg
240
ggctggaggc tcctgcagct gcgatgcctg cccgtggccc gttgccgaca agccctggtg
300
ccgcgtgcct tccatgcttc agctgtgggg ctaaggtctt cagatgagca gaagcagcag
360
cctcccaact cattttctca gcagcattct gagacacagg gggcagaaaa acctgatcca
420
gagtcttctc attcaccccc caggtataca gaccagggcg gcgaggagga ggaggactat
480
gaaagtgagg agcagttgca gcaccgcatc ctgacggcag cccttgagtt tgtgcccgcc
540
cacgggtgga cagcagaggc gattgcagaa ggagcccagt ctctgggtct ctccagtgca
600
gcagccagca tgtttggaag gatgggcagt gagctaatac tgcattttgt gacccagtgc
660
aatacccggc tcacacgtgt gctagaagag gagcagaagc tggtacagtt gggccaggcg
720
gagaagagga agacagacca gttcctgagg gatgcagtgg aaaccagact gagaatgctg
780
atcccataca ttgagcactg gccccgggcc ctcagcatcc tcatgctccc tcacaacatc
840
ccgtccagcc tgagcctgct caccagcatg gtggatgaca tgtggcatta cgctggggac
900
cagtccactg attttaactg gtacacccgc cgagccatgc tggctgccat ctacaacaca
960
acagagctgg tgatgatgca ggactcctct ccagactttg aggacacttg gcgcttcctg
1020

gaaaaccggg ttaatgatgc aatgaacatg ggccacactg ccaagcaggt aaagtccaca
1080
ggagaggcac tggtgcaagg actcatgggt gcagcagtga cgctcaagaa cttgacaggt
1140
ctaaaccagc gtcggtgaga ggaaggggta taagctacaa tgcctagaag agaatgagcg
1200
gacagattga aagagctttg aaaagtataa ggtgccatcc acataacctg gtgttcacga
1260
gaacacacta aaggactcct gagtcactac cacagccacc tggaaaccac aaggcatttg
1320
atgctaccgt tctggtcagg gattgggctg cttcttcagt tcctaatacc agaccaagcc
1380
tcctgatgcc tttctgcact gcaactgtgt gattgaaaaa tgagatgttc atccaagcag
1440
tcaagccaca gaaacccagc atgtccctgt cacaatctca tgggcacctt gatcatgtct
1500
taaccttccc ttaaccttgg ggctcccaag ccagagtcaa ggtctgacgc cacctcaagg
1560
tgacagctca tctccagcac agcacaggcg tgtgcacaca gaggtgttcc ttgcagcccc
1620
ctccctctca ggtgtcctga gatgctgctc ctgggagccc cctcagaaaa ctgcctcacc
1680
tgagacaagt gcctgctgga cagaggtgtg attccaggcc tggtgtcaca tgacaccagc
1740
atgcattgca ggattattag tgtattttga gtctgtaaaa ataataaata tgtttgaagt
1800
agttaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa
1835

<210> 4952
<211> 318
<212> PRT
<213> Homo sapiens

<400> 4952
Met Ala Ala Ala Ala Val Ser Gly Ala Leu Gly Arg Ala Gly Trp Arg
 1   5   10   15
Leu Leu Gln Leu Arg Cys Leu Pro Val Ala Arg Cys Arg Gln Ala Leu
            20   25   30
Val Pro Arg Ala Phe His Ala Ser Ala Val Gly Leu Arg Ser Ser Asp
        35   40   45
Glu Gln Lys Gln Gln Pro Pro Asn Ser Phe Ser Gln Gln His Ser Glu
    50   55   60
Thr Gln Gly Ala Glu Lys Pro Asp Pro Glu Ser Ser His Ser Pro Pro
65   70   75   80
Arg Tyr Thr Asp Gln Gly Gly Glu Glu Glu Glu Asp Tyr Glu Ser Glu
                85   90   95
Glu Gln Leu Gln His Arg Ile Leu Thr Ala Ala Leu Glu Phe Val Pro
            100   105   110
Ala His Gly Trp Thr Ala Glu Ala Ile Ala Glu Gly Ala Gln Ser Leu
        115   120   125
Gly Leu Ser Ser Ala Ala Ala Ser Met Phe Gly Arg Met Gly Ser Glu
    130   135   140
Leu Ile Leu His Phe Val Thr Gln Cys Asn Thr Arg Leu Thr Arg Val

```
145                 150                 155                 160
Leu Glu Glu Glu Gln Lys Leu Val Gln Leu Gly Gln Ala Glu Lys Arg
                165                 170                 175
Lys Thr Asp Gln Phe Leu Arg Asp Ala Val Glu Thr Arg Leu Arg Met
            180                 185                 190
Leu Ile Pro Tyr Ile Glu His Trp Pro Arg Ala Leu Ser Ile Leu Met
        195                 200                 205
Leu Pro His Asn Ile Pro Ser Ser Leu Ser Leu Leu Thr Ser Met Val
    210                 215                 220
Asp Asp Met Trp His Tyr Ala Gly Asp Gln Ser Thr Asp Phe Asn Trp
225                 230                 235                 240
Tyr Thr Arg Arg Ala Met Leu Ala Ala Ile Tyr Asn Thr Thr Glu Leu
                245                 250                 255
Val Met Met Gln Asp Ser Ser Pro Asp Phe Glu Asp Thr Trp Arg Phe
            260                 265                 270
Leu Glu Asn Arg Val Asn Asp Ala Met Asn Met Gly His Thr Ala Lys
        275                 280                 285
Gln Val Lys Ser Thr Gly Glu Ala Leu Val Gln Gly Leu Met Gly Ala
    290                 295                 300
Ala Val Thr Leu Lys Asn Leu Thr Gly Leu Asn Gln Arg Arg
305                 310                 315
```

<210> 4953
<211> 355
<212> DNA
<213> Homo sapiens

<400> 4953
gtgcacgcag gaaatggcgg gtgggaggca ggacaggaga gcccaggcct ggacaccact
60
gtcagcctgg ggatgcttgg cggcttctcc agtcctggga gcaggcatca cctggccgcg
120
ggtgcccccc ggtggcagct tgaaggaagg acgggcagtg ggtcgcagcc agcggggacc
180
taccccgcaa aacgcacata aaagctggaa tcagcttgtt acagctgcag gtccctctcg
240
tccgatttgg atagaccctc ttgggaccca ctgcaccagg gaaccccaaa tgcagctcag
300
cagcatggga ggagccctgt ctgctggggg tgtctgggat cgtcggagag aggct
355

<210> 4954
<211> 114
<212> PRT
<213> Homo sapiens

<400> 4954
```
Met Ala Gly Gly Arg Gln Asp Arg Arg Ala Gln Ala Trp Thr Pro Leu
 1               5                  10                  15
Ser Ala Trp Gly Cys Leu Ala Ala Ser Pro Val Leu Gly Ala Gly Ile
            20                  25                  30
Thr Trp Pro Arg Val Pro Pro Gly Gly Ser Leu Lys Glu Gly Arg Ala
        35                  40                  45
Val Gly Arg Ser Gln Arg Gly Pro Thr Pro Gln Asn Ala His Lys Ser
```

```
    50                  55                  60
Trp Asn Gln Leu Val Thr Ala Ala Gly Pro Ser Arg Pro Ile Trp Ile
65                  70                  75                  80
Asp Pro Leu Gly Thr His Cys Thr Arg Glu Pro Gln Met Gln Leu Ser
                85                  90                  95
Ser Met Gly Gly Ala Leu Ser Ala Gly Gly Val Trp Asp Arg Arg Arg
            100                 105                 110
Glu Ala
```

<210> 4955
<211> 364
<212> DNA
<213> Homo sapiens

<400> 4955
agatctaagg ccctcgggag agatgggaac tgagcacctg ggtcttagac cggaggagca
60
aactgcaaga cagggtggcc ggggacacca gcctccgccc ttctgtgaca taaggacaag
120
agctcagcct gcccaggaac aactctgggc aagagatgtg gaaagaaaga gctcanggg
180
gggcacgcat ggcatcctgg ggggacatct gagggcaccc ccacccacta ttcctccctc
240
caaggtggcc tctgagtgtg aaggcagggg gaagcagaca cctgcccctc actctccctc
300
cctaccacat agctaccggg tgggggggcgt ccctgggatg attcctgagg gcaggatcca
360
gggg
364

<210> 4956
<211> 114
<212> PRT
<213> Homo sapiens

<400> 4956
```
Met Gly Thr Glu His Leu Gly Leu Arg Pro Glu Glu Gln Thr Ala Arg
 1               5                  10                  15
Gln Gly Gly Arg Gly His Gln Pro Pro Pro Phe Cys Asp Ile Arg Thr
            20                  25                  30
Arg Ala Gln Pro Ala Gln Glu Gln Leu Trp Ala Arg Asp Val Glu Arg
        35                  40                  45
Lys Ser Ser Xaa Gly Gly Thr His Gly Ile Leu Gly Gly His Leu Arg
    50                  55                  60
Ala Pro Pro Pro Thr Ile Pro Pro Ser Lys Val Ala Ser Glu Cys Glu
65                  70                  75                  80
Gly Arg Gly Lys Gln Thr Pro Ala Pro His Ser Pro Ser Leu Pro His
                85                  90                  95
Ser Tyr Arg Val Gly Gly Val Pro Gly Met Ile Pro Glu Gly Arg Ile
            100                 105                 110
Gln Gly
```

<210> 4957
<211> 872
<212> DNA
<213> Homo sapiens

<400> 4957
nttcatattt ttttttttt ttggacacaa catgatatta ggctttattt gaatttaaaa
60
tcttgattcc atccagggac attttttacc gaagcgtctc agagactggc tcagggtatt
120
tcttgacaag actgtacagg gcttctcatc atacacaaac cctccacagc ccacggctcc
180
aacccacagc acctcctgca gtcctggagg gaaaagggac agtaacatga agtgtctgaa
240
gatccatttc acctcttttc catgtgaatc atgacgcttt caatgcattt cttgacagga
300
ttctattttg aaagaatgat gctcaatctg taccttttat gcttcttgtt tcttctccat
360
caataatatg tcagtcaact gcttgtcaga gacacttagc tgctgacagg tcctcataac
420
ctgactcagg taaactgcca agagatgctt gcacaggatg ctgtcactct tccgtagcac
480
tgagaatgca aatgcaggac atgaacagta atgacaagaa gccaaacatg tgtatgtttt
540
actggaactt ccaaggacct ggtaaacacg ccttccactg ggtgatgaga ttaaggtgat
600
ggactgtcga tcaactaggt ccaaggcctg ggtggctgat gagccaaaga gaaacttcag
660
cgataacaga tattcatcag gaattcggtc ccgtacttcg cgcgctctcc tgcaccgccg
720
ccgccatctc gctcaggagc tcctccacaa ccgccggcaa ctacggccat cgcgccgcag
780
gacacgccct ccacgacgcg gaccgcgcga cgctccagct gactgcgcct acctgtggag
840
gatcctgacc ccccgccggc ctcgttccga at
872

<210> 4958
<211> 51
<212> PRT
<213> Homo sapiens

<400> 4958
Gln Ile Phe Ile Arg Asn Ser Val Pro Tyr Phe Ala Arg Ser Pro Ala
 1   5   10   15
Pro Pro Pro Pro Ser Arg Ser Gly Ala Pro Pro Gln Pro Pro Ala Thr
            20   25   30
Thr Ala Ile Ala Pro Gln Asp Thr Pro Ser Thr Thr Arg Thr Ala Arg
        35   40   45
Arg Ser Ser
    50

<210> 4959
<211> 449

<212> DNA
<213> Homo sapiens

<400> 4959
acgcgtgtca aggctgggaa tgcaaatggt agtggtggtt tcctttgctg ggggttgatg
60
cagtggttgg gggggcttcc atttgcagtt gagggccagg tgtttgggtc cttccatgtg
120
gcagggataa agaggagagc tggcatctgg agtcatgatc tgtctgagag gcagtgcctc
180
cggccaccgt aggatggagg ccagcttcca gccctggctg atgggggaga agcagcgaat
240
tctccagatg tggtatggca gacctttgga agattcactc ggcctccact taaccttgtg
300
agaccaaagg ccacagcccc atgtgttctg cgtgctgttg aacatgtttg tatttcattg
360
gcgtggatga taatttggtt gaaaggagag atggtcacca gtggactcag tttaggaagg
420
cacaaaggtc aacccctttcc gtttctaga
449

<210> 4960
<211> 115
<212> PRT
<213> Homo sapiens

<400> 4960
Met Phe Asn Ser Thr Gln Asn Thr Trp Gly Cys Gly Leu Trp Ser His
 1   5   10   15
Lys Val Lys Trp Arg Pro Ser Glu Ser Ser Lys Gly Leu Pro Tyr His
            20   25   30
Ile Trp Arg Ile Arg Cys Phe Ser Pro Ile Ser Gln Gly Trp Lys Leu
        35   40   45
Ala Ser Ile Leu Arg Trp Pro Glu Ala Leu Pro Leu Arg Gln Ile Met
    50   55   60
Thr Pro Asp Ala Ser Ser Pro Leu Tyr Pro Cys His Met Glu Gly Pro
65   70   75   80
Lys His Leu Ala Leu Asn Cys Lys Trp Lys Pro Pro Gln Pro Leu His
                85   90   95
Gln Pro Pro Ala Lys Glu Thr Thr Thr Thr Ile Cys Ile Pro Ser Leu
            100   105   110
Asp Thr Arg
        115

<210> 4961
<211> 4737
<212> DNA
<213> Homo sapiens

<400> 4961
gcggccgcca cacccagcac cacaggcacc aagtccaaca cgcccacatc ctccgtgccc
60
tcggccgccg tcacacccct caacgagagc ctgcagcccc tgggggacta tggcgtgggc
120

tccaagaaca gcaagcgtgc ccgggagaag cgcgacagcc gcaacatgga agtacaggtc
180
acccaggaga tgcgcaacgt cagtataggc atgggcagca gtgacgagtg gtctgatgtt
240
caagacatta ttgactccac gccagagctg gacatgtgtc cagagacccg cctggaccgc
300
acaggaagca gcccaaccca gggcatcgtg aacaaagctt tcggcatcaa caccgactcc
360
ctgtaccatg agctgtcgac ggcagggtct gaggtcatcg gggatgtgga cgaaggggcc
420
gacctcctag gggagttctc aggaatgggc aaagaagtgg ggaatctgct actggaaaac
480
tcacagcttc tggaaaccaa aaacgccttg aatgtggtga agaatgacct gattgccaag
540
gtcgaccagc tgtccgggga gcaggaggtg ctgaggggcg agttggaggc tgctaagcag
600
gccaaagtca agctggaaaa ccgtatcaag gagctggaag aggaactgaa aagagtgaag
660
tccgaggcca tcatcgcccg ccgtgaaccc aaagaagagg cggaggatgt aagcagctat
720
ctctgtacag aatcggacaa aatccccatg gcccagcgcc gccgcttcac gcgggtggag
780
atggcccgtg tgctcatgga gcggaaccag tacaaggagc ggctgatgga gctgcaggag
840
gctgtgcggt ggactgagat gatcagagcg tcccgagagc acccatccgt ccaggagaag
900
aagaagtcga ccatctggca gttcttcagc cgcctcttca gctcttcctc cagcccccct
960
ccggccaagc gcccctatcc ctcggtgaac atccactaca agtcacccac cactgccggc
1020
ttcagccagc gccgcaacca tgccatgtgc ccgatctcgg caggcagccg gcccctggaa
1080
ttcttccctg acgacgactg cacgtcctcc gcccgtcgag agcagaagcg cgagcagtac
1140
cgccaggtgc gtgagcacgt gcgtaacgac gacggccgtc tgcaggcctg cggctggagc
1200
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1260
aacgtgccgg tgccggtgta ctgccgccct ctggtggaga aggaccccac catgaagctg
1320
tggtgtgccg cgggcgtcaa cctgagcggg tggaggccca atgaggacga cgctgggaat
1380
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1440
cccaagagcg cccacgcgtc tcccgagaag aagaaggcca aggagctccc tgaaatggac
1500
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1560
atcgacgcca accagccggg cacggtggtg gaccagttca ccgtctgcaa cgcgcacgtg
1620
ctgtgcatct ccagcatccc cgcggccagc gacagcgact accctcccgg ggagatgttc
1680
ctggacagcg acgtgaaccc agaggacccg ggcgcagatg gcgtgctggc cggtatcacc
1740

ctggtgggct gtgccacccg ctgcaacgtg ccgcggagca actgctcctc ccgaggggac
1800
accccagtgc tagacaaggg gcaggggggag gtggccacca tcgccaacgg gaaggtcaac
1860
ccgtcccagt ccacagagga ggccacagag gccacggagg tgccagaccc tgggcccagc
1920
gagccagaga cagccacatt gcggcccggg cctctcacag agcacgtctt cactgaccca
1980
gccccgaccc cgtcctctgg cccccagcct ggcagcgaga acgggccaga gcctgacagc
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agcagcacac ggccagagcc agagcccagc ggggacccca cgggagcagg cagcagtgct
2100
gcacccacca tgtggctggg agcccagaac ggctggctct atgtgcactc ggctgtggcc
2160
aactggaaga agtgcctgca ctccatcaag ctgaaggatt ctgtgctgag cctggtgcat
2220
gtcaaaggcc gtgtgctggt ggctctggcg gacgggaccc tggccatctt ccaccgtggt
2280
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2340
tccatccgct gcatggctgt tgtgtacgac cgcgtgtggt gtggctacaa gaacaaggtg
2400
cacgtcatcc agcccaagac catgcagata gagaagtcat ttgacgccca cccgcggcgg
2460
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2700
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2760
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2880
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3240
ataggacccc cgaccacctg acccccgccc ggcccgcggg gtagccagcc aggcgccgcc
3300
gcccctcttc taacctctca acctgcagct ttcacctgag tctggccccc ccagcgggca
3360

gggagtgcgg ggatgcggat cagctgggag gaggagggga ggggtgcttc cacccgaggg
3420
gaagatgctc tcgggacagt ttcccgggca gctcctggcc agcttccagc ccagagtcct
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3660
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3720
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3780
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3960
accttggagg agtgggccct ggagtcctgt ccctcccaga agcccccagg gtgggatttc
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4140
tgcctcctgc acggggctcc acggagccca gctcccagac acgctactaa gtgcctaggg
4200
ttgcccgctg tggcctgctc ccagggagca acagagaggc caccaagcag aggcccgtgg
4260
ggctgaggat ggagccgccc ccagccgact ccaagcccgc agagggcaga cgccaccctg
4320
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4380
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4440
gaagcacaga tcttggggag ctgccccaca agccccgctg gccaccgagg gctgcagccg
4500
ctgcgctgcc ggcttctccc caccaccctg ccacctccac tgtgatgtat gtccgctccc
4560
tcgtctgttc ccccaggatc tcgaagtgac tccgggctga gcagtggggc ggctggggga
4620
ggggtgacga ttctcctcag gctttggccc tgcaagcaaa cccacatatc tgctctgtat
4680
gtaataaatg tcttaacgtc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa
4737

<210> 4962
<211> 1069
<212> PRT
<213> Homo sapiens

<400> 4962
Ala Ala Ala Thr Pro Ser Thr Thr Gly Thr Lys Ser Asn Thr Pro Thr

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 1               5                  10                  15
Ser Ser Val Pro Ser Ala Ala Val Thr Pro Leu Asn Glu Ser Leu Gln
            20                  25                  30
Pro Leu Gly Asp Tyr Gly Val Gly Ser Lys Asn Ser Lys Arg Ala Arg
        35                  40                  45
Glu Lys Arg Asp Ser Arg Asn Met Glu Val Gln Val Thr Gln Glu Met
    50                  55                  60
Arg Asn Val Ser Ile Gly Met Gly Ser Ser Asp Glu Trp Ser Asp Val
65                  70                  75                  80
Gln Asp Ile Ile Asp Ser Thr Pro Glu Leu Asp Met Cys Pro Glu Thr
                85                  90                  95
Arg Leu Asp Arg Thr Gly Ser Ser Pro Thr Gln Gly Ile Val Asn Lys
            100                 105                 110
Ala Phe Gly Ile Asn Thr Asp Ser Leu Tyr His Glu Leu Ser Thr Ala
        115                 120                 125
Gly Ser Glu Val Ile Gly Asp Val Asp Glu Gly Ala Asp Leu Leu Gly
    130                 135                 140
Glu Phe Ser Gly Met Gly Lys Glu Val Gly Asn Leu Leu Leu Glu Asn
145                 150                 155                 160
Ser Gln Leu Leu Glu Thr Lys Asn Ala Leu Asn Val Val Lys Asn Asp
                165                 170                 175
Leu Ile Ala Lys Val Asp Gln Leu Ser Gly Glu Gln Glu Val Leu Arg
            180                 185                 190
Gly Glu Leu Glu Ala Ala Lys Gln Ala Lys Val Lys Leu Glu Asn Arg
        195                 200                 205
Ile Lys Glu Leu Glu Glu Glu Leu Lys Arg Val Lys Ser Glu Ala Ile
    210                 215                 220
Ile Ala Arg Arg Glu Pro Lys Glu Glu Ala Glu Asp Val Ser Ser Tyr
225                 230                 235                 240
Leu Cys Thr Glu Ser Asp Lys Ile Pro Met Ala Gln Arg Arg Arg Phe
                245                 250                 255
Thr Arg Val Glu Met Ala Arg Val Leu Met Glu Arg Asn Gln Tyr Lys
            260                 265                 270
Glu Arg Leu Met Glu Leu Gln Glu Ala Val Arg Trp Thr Glu Met Ile
        275                 280                 285
Arg Ala Ser Arg Glu His Pro Ser Val Gln Glu Lys Lys Lys Ser Thr
    290                 295                 300
Ile Trp Gln Phe Phe Ser Arg Leu Phe Ser Ser Ser Ser Ser Pro Pro
305                 310                 315                 320
Pro Ala Lys Arg Pro Tyr Pro Ser Val Asn Ile His Tyr Lys Ser Pro
                325                 330                 335
Thr Thr Ala Gly Phe Ser Gln Arg Arg Asn His Ala Met Cys Pro Ile
            340                 345                 350
Ser Ala Gly Ser Arg Pro Leu Glu Phe Phe Pro Asp Asp Asp Cys Thr
        355                 360                 365
Ser Ser Ala Arg Arg Glu Gln Lys Arg Glu Gln Tyr Arg Gln Val Arg
    370                 375                 380
Glu His Val Arg Asn Asp Asp Gly Arg Leu Gln Ala Cys Gly Trp Ser
385                 390                 395                 400
Leu Pro Ala Lys Tyr Lys Gln Leu Ser Pro Asn Gly Gly Gln Glu Asp
                405                 410                 415
Thr Arg Met Lys Asn Val Pro Val Pro Val Tyr Cys Arg Pro Leu Val
            420                 425                 430
Glu Lys Asp Pro Thr Met Lys Leu Trp Cys Ala Ala Gly Val Asn Leu
```

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        435                 440                 445
Ser Gly Trp Arg Pro Asn Glu Asp Asp Ala Gly Asn Gly Val Lys Pro
    450                 455                 460
Ala Pro Gly Arg Asp Pro Leu Thr Cys Asp Arg Glu Gly Asp Gly Glu
465                 470                 475                 480
Pro Lys Ser Ala His Ala Ser Pro Glu Lys Lys Lys Ala Lys Glu Leu
                485                 490                 495
Pro Glu Met Asp Ala Thr Ser Ser Arg Val Trp Ile Leu Thr Ser Thr
            500                 505                 510
Leu Thr Thr Ser Lys Val Val Ile Ile Asp Ala Asn Gln Pro Gly Thr
        515                 520                 525
Val Val Asp Gln Phe Thr Val Cys Asn Ala His Val Leu Cys Ile Ser
    530                 535                 540
Ser Ile Pro Ala Ala Ser Asp Ser Asp Tyr Pro Pro Gly Glu Met Phe
545                 550                 555                 560
Leu Asp Ser Asp Val Asn Pro Glu Asp Pro Gly Ala Asp Gly Val Leu
                565                 570                 575
Ala Gly Ile Thr Leu Val Gly Cys Ala Thr Arg Cys Asn Val Pro Arg
            580                 585                 590
Ser Asn Cys Ser Ser Arg Gly Asp Thr Pro Val Leu Asp Lys Gly Gln
        595                 600                 605
Gly Glu Val Ala Thr Ile Ala Asn Gly Lys Val Asn Pro Ser Gln Ser
    610                 615                 620
Thr Glu Glu Ala Thr Glu Ala Thr Glu Val Pro Asp Pro Gly Pro Ser
625                 630                 635                 640
Glu Pro Glu Thr Ala Thr Leu Arg Pro Gly Pro Leu Thr Glu His Val
                645                 650                 655
Phe Thr Asp Pro Ala Pro Thr Pro Ser Ser Gly Pro Gln Pro Gly Ser
            660                 665                 670
Glu Asn Gly Pro Glu Pro Asp Ser Ser Ser Thr Arg Pro Glu Pro Glu
        675                 680                 685
Pro Ser Gly Asp Pro Thr Gly Ala Gly Ser Ser Ala Ala Pro Thr Met
    690                 695                 700
Trp Leu Gly Ala Gln Asn Gly Trp Leu Tyr Val His Ser Ala Val Ala
705                 710                 715                 720
Asn Trp Lys Lys Cys Leu His Ser Ile Lys Leu Lys Asp Ser Val Leu
                725                 730                 735
Ser Leu Val His Val Lys Gly Arg Val Leu Val Ala Leu Ala Asp Gly
            740                 745                 750
Thr Leu Ala Ile Phe His Arg Gly Glu Asp Gly Gln Trp Asp Leu Ser
        755                 760                 765
Asn Tyr His Leu Met Asp Leu Gly His Pro His His Ser Ile Arg Cys
    770                 775                 780
Met Ala Val Val Tyr Asp Arg Val Trp Cys Gly Tyr Lys Asn Lys Val
785                 790                 795                 800
His Val Ile Gln Pro Lys Thr Met Gln Ile Glu Lys Ser Phe Asp Ala
                805                 810                 815
His Pro Arg Arg Glu Ser Gln Val Arg Gln Leu Ala Trp Ile Gly Asp
            820                 825                 830
Gly Val Trp Val Ser Ile Arg Leu Asp Ser Thr Leu Arg Leu Tyr His
        835                 840                 845
Ala His Thr His Gln His Leu Gln Asp Val Asp Ile Glu Pro Tyr Val
    850                 855                 860
Ser Lys Met Leu Gly Thr Gly Lys Leu Gly Phe Ser Phe Val Arg Ile
```

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865                 870                 875                 880
Thr Ala Leu Leu Val Ala Gly Ser Arg Leu Trp Val Gly Thr Gly Asn
                885                 890                 895
Gly Val Val Ile Ser Ile Pro Leu Thr Glu Thr Val Val Leu His Arg
            900                 905                 910
Gly Gln Leu Leu Gly Leu Arg Ala Asn Lys Thr Ser Pro Thr Ser Gly
        915                 920                 925
Glu Gly Ala Arg Pro Gly Gly Ile Ile His Val Tyr Gly Asp Asp Ser
    930                 935                 940
Ser Asp Arg Ala Ala Ser Ser Phe Ile Pro Tyr Cys Ser Met Ala Gln
945                 950                 955                 960
Ala Gln Leu Cys Phe His Gly His Arg Asp Ala Val Lys Phe Phe Val
                965                 970                 975
Ser Val Pro Gly Asn Val Leu Ala Thr Leu Asn Gly Ser Val Leu Asp
            980                 985                 990
Ser Pro Ala Glu Gly Pro Gly Pro Ala Ala Pro Ala Ser Glu Val Glu
        995                 1000                1005
Gly Gln Lys Leu Arg Asn Val Leu Val Leu Ser Gly Gly Glu Gly Tyr
    1010                1015                1020
Ile Asp Phe Arg Ile Gly Asp Gly Glu Asp Asp Glu Thr Glu Glu Gly
1025                1030                1035                1040
Ala Gly Asp Met Ser Gln Val Lys Pro Val Leu Ser Lys Ala Glu Arg
                1045                1050                1055
Ser His Ile Ile Val Trp Gln Val Ser Tyr Thr Pro Glu
            1060                1065
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<210> 4963
<211> 1575
<212> DNA
<213> Homo sapiens

<400> 4963
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gagtacagca ctcaccagct cttcagccag ctcacgctgc tacagcagga gttgtttcaa
120
aagtgccacc cggtccactt cctgaactca cgggccctgg gcgtcatgga caagagcact
180
gccatcccca aagccagctc ttctgagtct ctttcggcca aaacctgcag cttatttctg
240
cccaattacg ttcaggacaa gtatctgtta cagcttctaa gaaacgcaga tgacgtcagc
300
acctgggtgg ctgcagagat tgtgaccagc cacacctcca agctgcaggt gaacttgctg
360
tccaaatttn tgctgattgc aaaatcttgc tatgagcaga gaaacttcgc gacagccatg
420
cagatcctga gcgggctgga gcacctggcc gtgaggcagt cccctgcctg gagaattctg
480
cctgcaaaga tagcagaggt catggaggag ctgaaagccg tggaggtctt cctgaagagc
540
gacagcctgt gtctgatgga agggcggcgc ttccgggcgc agcccaccct gccctcggcc
600
cacctcctgg ccatgcacat ccagcagctg gagacaggcg gcttcaccat gaccaacggg
660

gcccacaggt ggagcaagct caggaacatc gcaaaggtgg tgagccaggt gcacgcgttc
720
caggagaacc cttacacctt cagccccgac cccaagctcc agtcgtacct caagcagagg
780
attgcccgct tcagcggtgc cgacatttcc acactcgccg cagatagcag ggccaacttc
840
caccaggtct ccagcgagaa gcactcacgg aagattcagg acaagctacg gaggatgaag
900
gctacattcc agtagccgag ctcgggcctg gtgtggaatt ccagatccga atccgactgt
960
gggggggcggg ctgggaggtg ggagccgcgt ctcaggcccg gccgttatca aggcccctcc
1020
gcccccgaac cctggggagc tggaccagga ggtggaggct caggggaccc catggggaca
1080
ggcagagctg gtctcctccc agcagacgga gccaggacgg gcacaagagt cttggaggtt
1140
tgcgtgtttc tgctagaatt aaaaagttaa atttaaaaat gaaaatgaaa gacagcttcc
1200
caggagtttt gtgcctgtct gcgcctctca cacacagata agtggctctt acccagctct
1260
cagtgactcc cccacaaaac agcaacagcc tccaccgcca actcaacaaa cttcagagta
1320
gctcctccct gagcaggttt ctgagccagc ctcggttggc tgagcaacga agggccaaag
1380
ctgacctctg agtggccaac tgcagctccc agggactccg agacctccgg tccgagaccc
1440
tgcctgggtt caccccccac aacccagacc cagaaccgct ctccccttcc ctgcccagtg
1500
cccctcttcc ccagcccaga cccccaggtg cccaaggcct gctgctggag caggcacctt
1560
gggctggggc tgctc
1575

<210> 4964
<211> 304
<212> PRT
<213> Homo sapiens

<400> 4964
Leu Glu Asp Phe Tyr Gly Pro Cys Ala Lys Thr Ser Glu Lys Gly Pro
1 5 10 15
Tyr Phe Leu Thr Glu Tyr Ser Thr His Gln Leu Phe Ser Gln Leu Thr
20 25 30
Leu Leu Gln Gln Glu Leu Phe Gln Lys Cys His Pro Val His Phe Leu
35 40 45
Asn Ser Arg Ala Leu Gly Val Met Asp Lys Ser Thr Ala Ile Pro Lys
50 55 60
Ala Ser Ser Ser Glu Ser Leu Ser Ala Lys Thr Cys Ser Leu Phe Leu
65 70 75 80
Pro Asn Tyr Val Gln Asp Lys Tyr Leu Leu Gln Leu Leu Arg Asn Ala
85 90 95
Asp Asp Val Ser Thr Trp Val Ala Ala Glu Ile Val Thr Ser His Thr
100 105 110
Ser Lys Leu Gln Val Asn Leu Leu Ser Lys Phe Xaa Leu Ile Ala Lys

```
        115                 120                 125
Ser Cys Tyr Glu Gln Arg Asn Phe Ala Thr Ala Met Gln Ile Leu Ser
    130                 135                 140
Gly Leu Glu His Leu Ala Val Arg Gln Ser Pro Ala Trp Arg Ile Leu
145                 150                 155                 160
Pro Ala Lys Ile Ala Glu Val Met Glu Glu Leu Lys Ala Val Glu Val
                165                 170                 175
Phe Leu Lys Ser Asp Ser Leu Cys Leu Met Glu Gly Arg Arg Phe Arg
            180                 185                 190
Ala Gln Pro Thr Leu Pro Ser Ala His Leu Leu Ala Met His Ile Gln
        195                 200                 205
Gln Leu Glu Thr Gly Gly Phe Thr Met Thr Asn Gly Ala His Arg Trp
    210                 215                 220
Ser Lys Leu Arg Asn Ile Ala Lys Val Val Ser Gln Val His Ala Phe
225                 230                 235                 240
Gln Glu Asn Pro Tyr Thr Phe Ser Pro Asp Pro Lys Leu Gln Ser Tyr
                245                 250                 255
Leu Lys Gln Arg Ile Ala Arg Phe Ser Gly Ala Asp Ile Ser Thr Leu
            260                 265                 270
Ala Ala Asp Ser Arg Ala Asn Phe His Gln Val Ser Ser Glu Lys His
        275                 280                 285
Ser Arg Lys Ile Gln Asp Lys Leu Arg Arg Met Lys Ala Thr Phe Gln
    290                 295                 300
```

<210> 4965
<211> 1474
<212> DNA
<213> Homo sapiens

<400> 4965

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aaagcattca aagggagcag caggtctctc cccacgcctt gcagagacgg tcaggagaga
120
ccccaagcag agagcacgct gctcagggac agagctgggc ttgtgaccat gtgtcgccct
180
ggcgctgtgc ttccaggtcc tcgcctggag ggcagctgta ttctcagaga gccagccttt
240
cctacagccc ttttagtgac caggggcatt tcctaccctc acttgatctc aaagccacgg
300
tcggtaggaa caaaaaggtg ggttttctag caggctggaa atggccagca ggggagcaag
360
ccgcggctgc ctgggagtgt cgggtggtca ggtcaggctg tagatgtatc ctgtagactc
420
aaggccgctt ctcaggagtc cagagtccca taaaccacca tgagtgccct cctgggatct
480
cattctgctc agaaactcat tgattttact ctgaagcacc cacgaatgac agattcccag
540
gaggggcaga gaaggctgag cggcaccacg tggggctggc cgcgggttgt gggcatgagc
600
acgcctggag aggccatggg gctggtgaca agctctggcc agaagacccc aagaaggtct
660
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720
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agacgtggaa ggagccagtg tccgcagccg tctcaggacg tcagagagct cggtggcctg
780
tctccagcag catgctctcc agatgcagcc tactgtcgct ctccacatag ggctggtgca
840
gccacatgga caggtagctc agggtgaggt cgggatcccc ggtgtgggca agctccttgg
900
ccaccgtgcg cttcaggagc agctccttcc tgtacatctc caagagctta tgcgaaacct
960
catagaaatg ggttgtaggc cacgtgtgga acagaggggg tcgtttactc tcctccccat
1020
aatggtagtt ttctagttca caaattccct tggtagttga agacagcttt tccattttca
1080
cctgtatttt ggtcaaccca tccaaggtgg cctgcagttc ctcacacagc ttctccagtt
1140
cctcgttata ttccagacac acctttttctt cattttcctt cgaggctggg ctgctgctgt
1200
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1260
tggtaaaacc tgcatcattg agggtttccc acttcaggat taaattgtgc caatcagccg
1320
cattgtcctt aatttttctt gcactgacag ataagacagg ttttctgggc gttacagttc
1380
caagagtctt tgcttccata aggtccacag atatccgtag aaggagctgc tcctgaagcg
1440
cacggtggac aggtagctca gggtgaggtc gcga
1474

<210> 4966
<211> 212
<212> PRT
<213> Homo sapiens

<400> 4966
Met Glu Ala Lys Thr Leu Gly Thr Val Thr Pro Arg Lys Pro Val Leu
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Ser Val Ser Ala Arg Lys Ile Lys Asp Asn Ala Ala Asp Trp His Asn
20 25 30
Leu Ile Leu Lys Trp Glu Thr Leu Asn Asp Ala Gly Phe Thr Thr Ala
35 40 45
Asn Asn Ile Ala Asn Leu Lys Ile Ser Leu Leu Asn Lys Asp Lys Ile
50 55 60
Glu Leu Asp Ser Ser Ser Pro Ala Ser Lys Glu Asn Glu Glu Lys Val
65 70 75 80
Cys Leu Glu Tyr Asn Glu Glu Leu Glu Lys Leu Cys Glu Glu Leu Gln
85 90 95
Ala Thr Leu Asp Gly Leu Thr Lys Ile Gln Val Lys Met Glu Lys Leu
100 105 110
Ser Ser Thr Thr Lys Gly Ile Cys Glu Leu Glu Asn Tyr His Tyr Gly
115 120 125
Glu Glu Ser Lys Arg Pro Pro Leu Phe His Thr Trp Pro Thr Thr His
130 135 140
Phe Tyr Glu Val Ser His Lys Leu Leu Glu Met Tyr Arg Lys Glu Leu
145 150 155 160
Leu Leu Lys Arg Thr Val Ala Lys Glu Leu Ala His Thr Gly Asp Pro

```
                165                 170                 175
Asp Leu Thr Leu Ser Tyr Leu Ser Met Trp Leu His Gln Pro Tyr Val
            180                 185                 190
Glu Ser Asp Ser Arg Leu His Leu Glu Ser Met Leu Leu Glu Thr Gly
        195                 200                 205
His Arg Ala Leu
    210

<210> 4967
<211> 550
<212> DNA
<213> Homo sapiens

<400> 4967
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atgctgtggc acaattatag ctcactgcag cctcgaactc ctggcctcaa gcaatccttc
120
cgccttgacc tccaaaatag ctggngttac acgcgtgagc ccccatgccc agcttcccag
180
taagacattt attctgagga gttggctcac atgagtaagg aggctgagaa gttccacaat
240
ctgaacattc aggagaaagc tggtgatgta atttggtctg agtcccaatg cctgagaacc
300
agagaagccg atggtataaa tcccagtgca aaggcaggag aagacccatg tcccagctca
360
gaaggcaggc aggaagcaaa aggggcaaat ttctccgtcc tctgcctctt ttttttctat
420
tcaggctctc agaggcttgg atgatgtcca ttcacattgg gcagggctag gtacttttct
480
gagtccaccg actgaaatac taatctcatc cagaaacacc tgcacagaca cacaaataaa
540
tgtttaatct
550

<210> 4968
<211> 51
<212> PRT
<213> Homo sapiens

<400> 4968
Glu Thr Gly Ser His Ser Val Ile Gln Ala Gly Met Leu Trp His Asn
 1               5                  10                  15
Tyr Ser Ser Leu Gln Pro Arg Thr Pro Gly Leu Lys Gln Ser Phe Arg
            20                  25                  30
Leu Asp Leu Gln Asn Ser Trp Xaa Tyr Thr Arg Glu Pro Pro Cys Pro
        35                  40                  45
Ala Ser Gln
    50

<210> 4969
<211> 2911
<212> DNA
<213> Homo sapiens
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<400> 4969
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cctaccctta caacttcagt aacttggccg ctcccggttg ctctcaacat ggtcctacct
120
gatgagaagg gtgcgggggc ccttcccttc ctaccagggg tctttggcta cgcagtgaat
180
cctcaagcag cacccccctgc cccaccaaca ccacctcccc caactcttcc tccaccaatt
240
ccccctaagg gagaagggga aagggcaggg gttgagagaa cccagaaggg cgatgtgggg
300
ntgaaccctg gggctcaatc ccccctttcac cagatgccac cctccctgaa ccccccacca
360
ctaccagctc cctggcctcc ctgccccttg ggagcccctt cacactcttg tgcagggact
420
tgggggcccc tggagctcag gggtcaggct gctttgtgtg agatgtagtt ttcccatctc
480
ctgggaaggg atctttcgag gttcccctct cagtcttcct ccagggaatg gcctccatga
540
ggggcagggc cagcttccat cccttctcca gcccttgggg caactgagca atatacttaa
600
cctgaatctc tactcacagc ccccaccagc tctgaatgtc taacctgctc ccctgattcg
660
taaacctagg ggaaaccatc tctctcacct aatgacccgc cttgttctga agctttctct
720
aagcccttcc cagttgcttc ctagcacatt ccattctttg tggcccaggg ctggaccaga
780
ccattgtgat acctgacccc gcccacctgg gagtgtggct ttgggtttca tccttcccca
840
gcgtgggtct ctacgtccct gtttcccttg tatcaagaca ccttcctcag cttccatgcc
900
tttggatctt ccatgttcct ccccatattc ctggacttcg gagatggcct ctcccaagcc
960
aggtcaagga ggtttggggg agggttgccc ctctgccccct ctgttctgtg gctgagcact
1020
ttcccagtcc agggcaggga aatattggcc ctatcttgac ccccaaatcc agtgagctcc
1080
agattcttcc aaggcaaaag aggtaagcag atcacacctc tttctgcctc tacatatggc
1140
ctattctggg ctagaccaga tttgggggcc aggagggaag aactccatat gggatggaga
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1260
agccagaaaa atgatagggg tcggatgggt gggtaagccc aggatttgca catgaccttc
1320
catccttacc tgtattccca tctccccagt gtcactcccc tcaccaatca ctccagatgg
1380
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1440
tcaaaatagc accttacacc ccatctttga ctcagttccc cacacccaaa gatcccagcc
1500
tagggatggg gtacagggac tttaaatagt ccctaatccc taatttgcac tagttaaccc
1560

tggtcagggt ccctgtattt ccttccagtg ggggagataa atgtttgctc ctaattctct
1620
ttgaaaactg ggcctccctg ctctgtgatt ggataaatat ttcccatccc acccacctcc
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1740
attagaggag tgcagtttta aaaggaaaag ttgctgtcat caaaatggca gccttttccc
1800
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1860
tcatggcttt tggagggagg tgagtttagg gagggccagg accatcctcc tacccctcat
1920
accctcccag catatacaaa aggggaggtt ttagacaggc tccctgaatg ttaaccacag
1980
aggagtcact ccttcattcc tcctctgtct ctttgcactt ttcttggtct tggccacagc
2040
ctgagtgacg aatttcctac tgaatgtacc aagttccaat ttttaagggg gggaaaggtt
2100
tcaaatgggg aaaaacacac aaaaaaaaaa tcactaaaaa ttcccacaaa tcttgtttct
2160
ggcactttag aaaaactgca aaaaaatacg taataaagaa tacatatata tatatctaca
2220
cacaaattat atatctatct atctatacag cggaaccaca agagagactg aggaaggcct
2280
ggaggcaggg gcagaggtga cgacagtgcc cctatatcct taacccatac tcctctgagg
2340
caaacaggca tgggaaaatg gaagggttga ggatggaccg gagaattgga acttcagaat
2400
aggtcaaaat tccaaaacca tggacatttt tttttgggag aattgagatt gtagacattt
2460
tttttttctt aaatatgatc aaggaaaata gcttccagaa tgtggtggtt ctgggcaaca
2520
aatgagattg tggcgacgtg gagattaaaa tatatgtatt tgagctgggg aatttgaata
2580
ttgtgagttt cagatgttgg aaatttggga ttttgcagtt ttgtcttttg aaaatgatca
2640
agtcttgtca gttcgtgccc tctttcccca tgttccctgg gaagacgggt ggtggcagag
2700
tgagaaggcc actggttctg tgccgcagca cgcaaaattt agaattctac agactagctc
2760
tatacgtagt gaggacccag atttagagaa actgaccaat atttatctcc gcatttgtgt
2820
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2880
aaaaaaaaaa aatgtctaca atctcaattc t
2911

<210> 4970
<211> 155
<212> PRT
<213> Homo sapiens

<400> 4970
Pro Xaa Ser Leu Ser Thr Leu Ser Pro Thr Arg Ser Ser Met Ala Pro

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 1               5                  10                  15
Ser Ser Leu Pro Pro Thr Leu Thr Thr Ser Val Thr Trp Pro Leu Pro
            20                  25                  30
Val Ala Leu Asn Met Val Leu Pro Asp Glu Lys Gly Ala Gly Ala Leu
        35                  40                  45
Pro Phe Leu Pro Gly Val Phe Gly Tyr Ala Val Asn Pro Gln Ala Ala
    50                  55                  60
Pro Pro Ala Pro Pro Thr Pro Pro Pro Pro Thr Leu Pro Pro Pro Ile
65                  70                  75                  80
Pro Pro Lys Gly Glu Gly Glu Arg Ala Gly Val Glu Arg Thr Gln Lys
                85                  90                  95
Gly Asp Val Gly Xaa Asn Pro Gly Ala Gln Ser Pro Phe His Gln Met
            100                 105                 110
Pro Pro Ser Leu Asn Pro Pro Pro Leu Pro Ala Pro Trp Pro Pro Cys
        115                 120                 125
Pro Leu Gly Ala Pro Ser His Ser Cys Ala Gly Thr Trp Gly Pro Leu
    130                 135                 140
Glu Leu Arg Gly Gln Ala Ala Leu Cys Glu Met
145                 150                 155
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<210> 4971
<211> 2939
<212> DNA
<213> Homo sapiens

<400> 4971
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120
gcagtcttta atctgataaa gcggttatct cgtcttgagt cccaggtgcc gagtcaatcc
180
ccatacacag ccgccgccat tgcctcgagt ccttgtgtct gactgtctgt tcctgctgct
240
gtatgacaca gcacctcgag gcaaggaaat aagaaaactg cctctgatcc aagcagagaa
300
ggtcagtgag aaggtctgcc tgtagatctg ctgtagggct tgtcaccatt ggaagcaagg
360
tcctacttca gtggcagatc tggtggcctt ggagtggctg aagaccacca ccctccacag
420
ggctgggccc atgcacagcc atccttccct accttgagtg agcttcctct gcatgttttc
480
tatatcactg gcagagcctg tagttggaaa ggggacagag tgactactgg actttgtgtg
540
aaaacaccaa ccgggacaaa acttcagtca aggctgagac gggtgggggt atataacttg
600
tccttacgtt aaacttggaa catggttgac tctgggacag aagcaagggc tagaggaaag
660
gctgaggctg gcctgcaaga tggaatcagt ggtcctgcca ctgctagagt gaatggtaaa
720
acccaggccg aggcagtggc tgaggcagaa ctgaaaacag aatcagtgac ccaggccaaa
780
gctggtgatg gagcaatgac caggacacat acagtgacct acagggaggc tatggctgtg
840

acaagggaag tgatcaaggt ggaagataca actaagacta gagtcatggt tgagactaag
900
acaaaacccc tggcagaacg cagtatagtg ccacaaacca agtcaaaggc catgcctatg
960
tctagggtca gtactgtaac caagtctgaa gtcaaggttg ttgctgtcat tgaggcaaat
1020
attaggtcct atgccaagtc acatgataag gccaatactg ggtccagacc tgacagaagg
1080
gaagagacca gcattgggat gaaatccagt gatgaggatg aagaaaatat atgctcctgg
1140
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Val Thr Tyr Arg Glu Ala Met Ala Val Thr Arg Glu Val Ile Lys Val
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115 120 125
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Lys Ser Ser Asp Glu Asp Glu Glu Asn Ile Cys Ser Trp Phe Trp Thr
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Gly Glu Glu Pro Ser Val Gly Ser Trp Phe Trp Pro Glu Glu Glu Thr
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Ser Leu Gln Val Tyr Lys Pro Leu Pro Lys Ile Gln Glu Lys Pro Lys
195 200 205
Pro Thr His Lys Pro Thr Leu Thr Ile Lys Gln Lys Val Ile Ala Trp
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Ser Arg Ala Arg Tyr Ile Val Leu Val Pro Val Glu Gly Gly Glu Gln
225 230 235 240
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Leu Thr Lys Asp Pro Phe Ile His Glu Ile Ala Thr Met Ile Met Gly
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Ile Ser Pro Ala Tyr Pro Phe Thr Gln Asp Ile Ile His Asp Val Gly
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Ile Thr Val Met Ile Glu Asn Leu Val Asn Asn Pro Asn Val Lys Glu
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His Pro Gly Ala Leu Ser Met Val Asp Asp Ser Ser Glu Ser Ser Glu
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Glu Pro Lys Ser Gly Glu Ser Tyr Ile His Gln Val Cys Lys Gly Ile
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Lys Phe Tyr Val Leu Lys Val Phe Ser Cys Leu Ser Lys Asn His Ala
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465                 470                 475                 480
Pro Phe Asn Lys Asn Glu Ser Lys Ala Asn Ile Leu Asn Ile Ile Glu
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<212> DNA
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<213> Homo sapiens

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Gly Thr Arg Ile Ile Glu Val Ser Gly Gln Lys Ile Lys Leu Gln Ile
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Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Ala Val Thr Arg Ser Tyr
65 70 75 80
Tyr Arg Gly Ala Ala Gly Ala Leu Met Val Tyr Asp Ile Thr Arg Arg
85 90 95
Ser Thr Tyr Asn His Leu Ser Ser Trp Leu Thr Asp Ala Arg Asn Leu
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Thr Asn Pro Asn Thr Val Ile Ile Leu Ile Gly Asn Lys Ala Asp Leu
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Glu Ala Gln Arg Asp Val Thr Tyr Glu Glu Ala Lys Gln Phe Ala Glu
130 135 140
Glu Asn Gly Leu Leu Phe Leu Glu Ala Ser Ala Lys Thr Gly Glu Asn
145 150 155 160
Val Glu Asp Ala Phe Leu Glu Ala Ala Lys Lys Ile Tyr Gln Asn Ile
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Gln Asp Gly Ser Leu Asp Leu Asn Ala Ala Glu Ser Gly Val Gln His
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Pro Thr Leu Gln Thr Asp Leu Leu Pro Lys Met Lys Gly Lys Lys Asn
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Asp Arg Lys Arg Thr Trp Leu Gly Leu Leu Glu Glu Ala Tyr Thr Leu
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Val Gln His Gln Val Ser Glu Gly Leu Ser Ala Leu Lys Glu Glu Cys
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Arg Ala Leu Thr Lys Gly Leu Glu Gly Thr Ile Arg Ser Asp Met Asp
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Arg Leu Met Asn Leu Pro Leu His Ser Val Lys Met Glu Pro Cys Tyr
        195                 200                 205
Thr Lys Val Asn Leu Leu His Glu Arg Leu Gln Asp Leu Lys Ser Arg
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Phe Arg Phe Pro His Ile Asp Leu Val Val Gln Arg Thr Gln Asn Tyr
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Met Gln Glu Leu Met Glu Asn Ala Val Phe Thr Phe Glu Gln Leu Leu
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Ser Pro His Leu Gln Gly Glu Ala Ser Lys Thr Ala Phe Ser Ile Glu
            260                 265                 270
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3309

<210> 4978
<211> 792
<212> PRT
<213> Homo sapiens

<400> 4978
Met Ala Gln Glu Ala Pro Gln Glu Asp Thr Ser Pro Met Ala Leu Met
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Glu Thr Thr Thr Ser Thr Ile Ile Thr Thr Thr Val Ile Thr Thr Glu
35 40 45
Gln Ala Pro Ala Leu Cys Ser Val Ser Phe Ser Asn Pro Glu Gly Tyr
50 55 60
Ile Asp Ser Ser Asp Tyr Pro Leu Leu Pro Leu Asn Asn Phe Leu Glu
65 70 75 80
Cys Thr Tyr Asn Val Thr Val Tyr Thr Gly Tyr Gly Val Glu Leu Gln
85 90 95
Val Lys Ser Val Asn Leu Ser Asp Gly Glu Leu Leu Ser Ile Arg Gly
100 105 110
Val Asp Gly Pro Thr Leu Thr Val Leu Ala Asn Gln Thr Leu Leu Val

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        115                 120                 125
Glu Gly Gln Val Ile Arg Ser Pro Thr Asn Thr Ile Ser Val Tyr Phe
    130                 135                 140
Arg Thr Phe Gln Asp Asp Gly Leu Gly Thr Phe Gln Leu His Tyr Gln
145                 150                 155                 160
Ala Phe Met Leu Ser Cys Asn Phe Pro Arg Arg Pro Asp Ser Gly Asp
                165                 170                 175
Val Thr Val Met Asp Leu His Ser Gly Gly Val Ala His Phe His Cys
            180                 185                 190
His Leu Gly Tyr Glu Leu Gln Gly Ala Lys Met Leu Thr Cys Ile Asn
        195                 200                 205
Ala Ser Lys Pro His Trp Ser Ser Gln Glu Pro Ile Cys Ser Ala Pro
    210                 215                 220
Cys Gly Gly Ala Val His Asn Ala Thr Ile Gly Arg Val Leu Ser Pro
225                 230                 235                 240
Ser Tyr Pro Glu Asn Thr Asn Gly Ser Gln Phe Cys Ile Trp Thr Ile
                245                 250                 255
Glu Ala Pro Glu Gly Gln Lys Leu His Leu His Phe Glu Arg Leu Leu
            260                 265                 270
Leu His Asp Lys Asp Arg Met Thr Val His Ser Gly Gln Thr Asn Lys
        275                 280                 285
Ser Ala Leu Leu Tyr Asp Ser Leu Gln Thr Glu Ser Val Pro Phe Glu
    290                 295                 300
Gly Leu Leu Ser Glu Gly Asn Thr Ile Arg Ile Glu Phe Thr Ser Asp
305                 310                 315                 320
Gln Ala Arg Ala Ala Ser Thr Phe Asn Ile Arg Phe Glu Ala Phe Glu
                325                 330                 335
Lys Gly His Cys Tyr Glu Pro Tyr Ile Gln Asn Gly Asn Phe Thr Thr
            340                 345                 350
Ser Asp Pro Thr Tyr Asn Ile Gly Thr Ile Val Glu Phe Thr Cys Asp
        355                 360                 365
Pro Gly His Ser Leu Glu Gln Gly Pro Ala Ile Ile Glu Cys Ile Asn
    370                 375                 380
Val Arg Asp Pro Tyr Trp Asn Asp Thr Glu Pro Leu Cys Arg Ala Met
385                 390                 395                 400
Cys Gly Gly Glu Leu Ser Ala Val Ala Gly Val Val Leu Ser Pro Asn
                405                 410                 415
Trp Pro Glu Pro Tyr Val Glu Gly Glu Asp Cys Ile Trp Lys Ile His
            420                 425                 430
Val Gly Glu Glu Lys Arg Ile Phe Leu Asp Ile Gln Phe Leu Asn Leu
        435                 440                 445
Ser Asn Ser Asp Ile Leu Thr Ile Tyr Asp Gly Asp Glu Val Met Pro
    450                 455                 460
His Ile Leu Gly Gln Tyr Leu Gly Asn Ser Gly Pro Gln Lys Leu Tyr
465                 470                 475                 480
Ser Ser Thr Pro Asp Leu Thr Ile Gln Phe His Ser Asp Pro Ala Gly
                485                 490                 495
Leu Ile Phe Gly Lys Gly Gln Gly Phe Ile Met Asn Tyr Ile Glu Val
            500                 505                 510
Ser Arg Asn Asp Ser Cys Ser Asp Leu Pro Glu Ile Gln Asn Gly Trp
        515                 520                 525
Lys Thr Thr Ser His Thr Glu Leu Val Arg Gly Ala Arg Ile Thr Tyr
    530                 535                 540
Gln Cys Asp Pro Gly Tyr Asp Ile Val Gly Ser Asp Thr Leu Thr Cys
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545                 550                 555                 560
Gln Trp Asp Leu Ser Trp Ser Ser Asp Pro Pro Phe Cys Glu Lys Ile
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Met Tyr Cys Thr Asp Pro Gly Glu Val Asp His Ser Thr Arg Leu Ile
            580                 585                 590
Ser Asp Pro Val Leu Leu Val Gly Thr Thr Ile Gln Tyr Thr Cys Asn
        595                 600                 605
Pro Gly Phe Val Leu Glu Gly Ser Ser Leu Leu Thr Cys Tyr Ser Arg
    610                 615                 620
Glu Thr Gly Thr Pro Ile Trp Thr Ser Arg Leu Pro His Cys Val Ser
625                 630                 635                 640
Glu Glu Ser Leu Ala Cys Asp Asn Pro Gly Leu Pro Glu Asn Gly Tyr
                645                 650                 655
Gln Ile Leu Tyr Lys Arg Leu Tyr Leu Pro Gly Glu Ser Leu Thr Phe
            660                 665                 670
Met Cys Tyr Glu Gly Phe Glu Leu Met Gly Glu Val Thr Ile Arg Cys
        675                 680                 685
Ile Leu Gly Gln Pro Ser His Trp Asn Gly Pro Leu Pro Val Cys Lys
    690                 695                 700
Val Asn Gln Asp Ser Phe Glu His Ala Leu Glu Ala Glu Ala Ala Ala
705                 710                 715                 720
Glu Thr Ser Leu Glu Gly Gly Asn Met Ala Leu Ala Ile Phe Ile Pro
                725                 730                 735
Val Leu Ile Ile Ser Leu Leu Leu Gly Gly Ala Tyr Ile Tyr Ile Thr
            740                 745                 750
Arg Cys Arg Tyr Tyr Ser Asn Leu Arg Leu Pro Leu Met Tyr Ser His
        755                 760                 765
Pro Tyr Ser Gln Ile Thr Val Glu Thr Glu Phe Asp Asn Pro Ile Tyr
    770                 775                 780
Glu Thr Gly Gly Thr Gln Lys Val
785                 790
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<210> 4979
<211> 1865
<212> DNA
<213> Homo sapiens

<400> 4979
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120
cgagccgtca gtccccgggt gcgagtccct gctgtcttcc acacccttcc tccctccagg
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240
gcaggtgtgg ggggcgtgcg gggtggcacg agacaaaagg ggcacggggg taagcccgcc
300
atggcctccc ggagcctggg gggcctgagc gggatccgcg gcggtggcgg cggaggcggc
360
aagaaaagcc tgagcgcccg caatgctgcg gtggagagga ggaacctgat caccgtgtgc
420
aggttttctg tgaagaccct gattgatcgg tcttgctttg agacaattga tgattcttct
480

cctgaattta acaattttgc agctattttg gaacagattt taagccaccg gctaaaaggt
540
caagtaacct ggtttggtta tgaaagtcct cgtagcttct gggactatat cagagtggct
600
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660
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720
tacatctcta cagctctgag agacttcaaa acaaccagga gattttatga agatggagca
780
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840
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900
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1020
ttcctcatgg atgagaacag ttggttcaac aagtgtaaga gagttaaaca aaagtatcag
1080
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1140
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1200
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1260
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1320
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1380
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1440
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1560
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1620
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1680
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ttaca
1865

<210> 4980
<211> 266
<212> PRT
<213> Homo sapiens

<400> 4980
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Leu Lys Tyr Ile Gln Ser Ser Asp Ser Ile Ser Ser Asp Glu Glu Glu
20 25 30
Leu Arg Thr Leu Gly Ser Ser Gly Ser Glu Ser Ser Thr Pro Glu Asn
35 40 45
Val Gly Pro Pro Phe Leu Met Asp Glu Asn Ser Trp Phe Asn Lys Cys
50 55 60
Lys Arg Val Lys Gln Lys Tyr Gln Leu Thr Leu Glu Gln Lys Gly Tyr
65 70 75 80
Leu Glu Glu Leu Leu Arg Leu Arg Glu Asn Gln Leu Ser Glu Ser Val
85 90 95
Ser Gln Asn Lys Ile Leu Leu Gln Arg Ile Glu Asp Ser Asp Leu Ala
100 105 110
His Lys Leu Glu Lys Glu Gln Leu Glu Tyr Ile Ile Val Glu Leu Gln
115 120 125
Asp Gln Leu Thr Val Leu Lys Asn Asn Asp Leu Arg Ser Arg Gln Glu
130 135 140
Leu Thr Ala His Leu Thr Asn Gln Trp Pro Ser Pro Gly Ala Leu Asp
145 150 155 160
Val Asn Ala Val Ala Leu Asp Thr Leu Leu Tyr Arg Lys His Asn Lys
165 170 175
Gln Trp Lys Ser Tyr Gln Ser Leu Asp Gln Leu Ser Ala Glu Val Ser
180 185 190
Leu Ser Gln Thr Ser Leu Asp Pro Gly Gln Ser Gln Glu Gly Asp Gly
195 200 205
Lys Gln Asp Thr Leu Asn Val Met Ser Glu Gly Lys Glu Asp Thr Pro
210 215 220
Ser Leu Leu Gly Leu Cys Gly Ser Leu Thr Ser Val Ala Ser Tyr Lys
225 230 235 240
Ser Leu Thr Ser Leu Lys Ser Asn Asp Tyr Leu Ala Ser Pro Thr Thr
245 250 255
Glu Met Thr Ser Pro Gly Leu Thr Pro Ser
260 265

<210> 4981
<211> 1902
<212> DNA
<213> Homo sapiens

<400> 4981
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120
tcctctccag atctgccggt tcattatata cctgtggcac ctgactctaa tacctgagcc
180
aagaatggaa gtttgtgagg agacggactc tatgttgccc aggctgttat ggaactcctg
240
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300
acatccagcc tacacgtatt tgttaatatc taacatagga ctaaccagcc actgccctct
360

cttaggcccc tcatttaaaa acggttatac tataaaatct gcttttcaca ctgggtgata
420
ataacttgga caaattctat gtgtattttg ttttgttttg ctttgctttg ttttgagacg
480
gagtctcgct ctgtcatcca ggctggagtg cagtggcatg atctcggctc actgcaaccc
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600
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720
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780
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aaggcctggg ctttcccacc ctccctcctt agcaggtgcc gtgctgggac accatacggg
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1260
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1380
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1500
cagcatctgc tcacaggttc gagccacatc actgagcttg aggcgggcat agtccactcg
1560
cttcagagcc atctgacagt ccttcctcga agagtagctg gagccctcat ggggctgccc
1620
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1680
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1740
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1800
ttccagagcg cgtagtctct cgttcgccag gctgtaggta gccattatca ctctgggaat
1860
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1902

<210> 4982

<211> 73
<212> PRT
<213> Homo sapiens

<400> 4982
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Arg Ser Val Ile Gln Ala Gly Val Gln Trp His Asp Leu Gly Ser Leu
20 25 30
Gln Pro Pro Ser Pro Arg Phe Lys Arg Phe Ser Cys Leu Leu Leu Ser
35 40 45
Ser Trp Asp Tyr Arg Cys Ser Pro Pro His Pro Ala Asn Phe Cys Ile
50 55 60
Phe Ser Arg Asp Gly Val Ser Pro Cys
65 70

<210> 4983
<211> 1418
<212> DNA
<213> Homo sapiens

<400> 4983
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120
catgaaattc tggagcttat tattgaaaaa ctactcaagt tggatgtgaa tgcatcccgg
180
cagggtattg aagatgctga agaaacagca actcaaactt ttggtgggac agattccacg
240
gaaggattgt ttaatatgga tgaagatgaa gaaactgaac atgaaacaaa ggctggtcct
300
gaacggctcg accagatggt gcatcctgta gccgagcgcc tggacatcct gatgtctttg
360
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420
aaggatctat atcgcgacct gataaacatc tttgacaaac tcctgttgcc cacccatgcc
480
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540
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660
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720
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780
caagctgtgt tctacacctt tgtttttaga cacaagcagc ttttgagcgg aaacctgaaa
840
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cccctgaaga tttgcctgcc ctcagtggtt aacttttttg ctgcaatcac aaataagtac
960

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1020
aggagtaccg ctggaggaga ctcagtgcag acctgcacaa acccactgga caccttcttc
1080
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1140
tgggaagaca tgagtgctga agagctacag gagttcaaga aacccatgaa aaaggacata
1200
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1260
ggggtctttg tgggttggga agtagtttta atgtagaaag acatttacat ataagtctgt
1320
ttaatttcaa aggagtttgt gaaaaaaaat ccatggtgaa aatgaaacaa tgacatggtt
1380
aatctggaac ttacgttctt ataccaataa aaggtacc
1418

<210> 4984
<211> 256
<212> PRT
<213> Homo sapiens

<400> 4984
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20 25 30
Gly Ser Phe Leu Ala Arg Ala Lys Phe Ile Pro Leu Ile Thr Val Lys
35 40 45
Ser Cys Leu Asp Leu Leu Val Asn Trp Leu His Ile Tyr Leu Asn Asn
50 55 60
Gln Asp Ser Gly Thr Lys Ala Phe Cys Asp Val Ala Leu His Gly Pro
65 70 75 80
Phe Tyr Ser Ala Cys Gln Ala Val Phe Tyr Thr Phe Val Phe Arg His
85 90 95
Lys Gln Leu Leu Ser Gly Asn Leu Lys Glu Gly Leu Gln Tyr Leu Gln
100 105 110
Ser Leu Asn Phe Glu Arg Ile Val Met Ser Gln Leu Asn Pro Leu Lys
115 120 125
Ile Cys Leu Pro Ser Val Val Asn Phe Phe Ala Ala Ile Thr Asn Lys
130 135 140
Tyr Gln Leu Val Phe Cys Tyr Thr Ile Ile Glu Arg Asn Asn Arg Gln
145 150 155 160
Met Leu Pro Val Ile Arg Ser Thr Ala Gly Gly Asp Ser Val Gln Thr
165 170 175
Cys Thr Asn Pro Leu Asp Thr Phe Phe Pro Phe Asp Pro Cys Val Leu
180 185 190
Lys Arg Ser Lys Lys Phe Ile Asp Pro Ile Tyr Gln Val Trp Glu Asp
195 200 205
Met Ser Ala Glu Glu Leu Gln Glu Phe Lys Lys Pro Met Lys Lys Asp
210 215 220
Ile Val Glu Asp Glu Asp Asp Asp Phe Leu Lys Gly Glu Ile Pro Gln
225 230 235 240
Lys Leu Val Val Ser Gly Val Phe Val Gly Trp Glu Val Val Leu Met

245 250 255

<210> 4985
<211> 5695
<212> DNA
<213> Homo sapiens

<400> 4985
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240
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300
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360
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420
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480
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720
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780
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1380

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2820
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2940
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3000

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<211> 1239
<212> PRT
<213> Homo sapiens

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35 40 45
Lys Ile Phe Leu Pro Lys Lys Leu Leu Glu Cys Leu Pro Arg Cys Pro
50 55 60
Leu Leu Pro Pro Glu Arg Leu Arg Trp Asn Thr Asn Glu Glu Ile Ala
65 70 75 80
Ser Tyr Leu Ile Thr Phe Glu Lys His Asp Glu Trp Leu Ser Cys Ala

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Pro Lys Thr Arg Pro Gln Asn Gly Ser Ile Ile Leu Tyr Asn Arg Lys
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Lys Val Lys Tyr Arg Lys Asp Gly Tyr Leu Trp Lys Lys Arg Lys Asp
        115                 120                 125
Gly Lys Thr Thr Arg Glu Asp His Met Lys Leu Lys Val Gln Gly Met
    130                 135                 140
Glu Pro Val Ser Trp Gln Cys Leu Tyr Gly Cys Tyr Val His Ser Ser
145                 150                 155                 160
Ile Val Pro Thr Phe His Arg Arg Cys Tyr Trp Leu Leu Gln Asn Pro
                165                 170                 175
Asp Ile Val Leu Val His Tyr Leu Asn Val Pro Ala Leu Glu Asp Cys
            180                 185                 190
Gly Lys Gly Cys Ser Pro Ile Phe Cys Ser Ile Ser Ser Asp Arg Arg
        195                 200                 205
Glu Trp Leu Lys Trp Ser Arg Glu Glu Leu Leu Gly Gln Leu Lys Pro
    210                 215                 220
Met Phe His Gly Ile Lys Trp Ser Cys Gly Asn Gly Thr Glu Glu Phe
225                 230                 235                 240
Ser Val Glu His Leu Val Gln Gln Ile Leu Asp Thr His Pro Thr Lys
                245                 250                 255
Pro Ala Pro Arg Thr His Ala Cys Leu Cys Ser Gly Gly Leu Gly Ser
            260                 265                 270
Gly Ser Leu Thr His Lys Cys Ser Ser Thr Lys His Arg Ile Ile Ser
        275                 280                 285
Pro Lys Val Glu Pro Arg Ala Leu Thr Leu Thr Ser Ile Pro His Pro
    290                 295                 300
His Pro Pro Glu Pro Pro Pro Leu Ile Ala Pro Leu Pro Pro Glu Leu
305                 310                 315                 320
Pro Lys Ala His Thr Ser Pro Ser Ser Ser Ser Ser Ser Ser Ser Ser
                325                 330                 335
Gly Phe Ala Glu Pro Leu Glu Ile Arg Pro Ser Pro Pro Thr Ser Arg
            340                 345                 350
Gly Gly Ser Ser Arg Gly Gly Thr Ala Ile Leu Leu Leu Thr Gly Leu
        355                 360                 365
Glu Gln Arg Ala Gly Gly Leu Thr Pro Thr Arg His Leu Ala Pro Gln
    370                 375                 380
Ala Asp Pro Arg Pro Ser Met Ser Leu Ala Val Val Val Gly Thr Glu
385                 390                 395                 400
Pro Ser Ala Pro Pro Ala Pro Pro Ser Pro Ala Phe Asp Pro Asp Arg
                405                 410                 415
Phe Leu Asn Ser Pro Gln Arg Gly Gln Thr Tyr Gly Gly Gly Gln Gly
            420                 425                 430
Val Ser Pro Asp Phe Pro Glu Ala Glu Ala Ala His Thr Pro Cys Ser
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Ala Leu Glu Pro Ala Ala Ala Leu Glu Pro Gln Ala Ala Ala Arg Gly
    450                 455                 460
Pro Pro Pro Gln Ser Val Ala Gly Gly Arg Arg Gly Asn Cys Phe Phe
465                 470                 475                 480
Ile Gln Asp Asp Asp Ser Gly Glu Glu Leu Lys Gly His Gly Ala Ala
                485                 490                 495
Pro Pro Ile Pro Ser Pro Pro Pro Ser Pro Pro Pro Ser Pro Ala Pro
            500                 505                 510
Leu Glu Pro Ser Ser Arg Val Gly Arg Gly Glu Ala Leu Phe Gly Gly
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Pro Val Gly Ala Ser Glu Leu Glu Pro Phe Ser Leu Ser Ser Phe Pro
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Asp Leu Met Gly Glu Leu Ile Ser Asp Glu Ala Pro Ser Ile Pro Ala
545                 550                 555                 560
Pro Thr Pro Gln Leu Ser Pro Ala Leu Ser Thr Ile Thr Asp Phe Ser
                565                 570                 575
Pro Glu Trp Ser Tyr Pro Glu Gly Gly Val Lys Val Leu Ile Thr Gly
            580                 585                 590
Pro Trp Thr Glu Ala Ala Glu His Tyr Ser Cys Val Phe Asp His Ile
        595                 600                 605
Ala Val Pro Ala Ser Leu Val Gln Pro Gly Val Leu Arg Cys Tyr Cys
    610                 615                 620
Pro Ala His Glu Val Gly Leu Val Ser Leu Gln Val Ala Gly Arg Glu
625                 630                 635                 640
Gly Pro Leu Ser Ala Ser Val Leu Phe Glu Tyr Arg Ala Arg Arg Phe
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Leu Ser Leu Pro Ser Thr Gln Leu Asp Trp Leu Ser Leu Asp Asp Asn
            660                 665                 670
Gln Phe Arg Met Ser Ile Leu Glu Arg Leu Glu Gln Met Glu Lys Arg
        675                 680                 685
Met Ala Glu Ile Ala Ala Ala Gly Gln Val Pro Cys Gln Gly Pro Asp
    690                 695                 700
Ala Pro Pro Val Gln Asp Glu Gly Gln Gly Pro Gly Phe Glu Ala Arg
705                 710                 715                 720
Val Val Val Leu Val Glu Ser Met Ile Pro Arg Ser Thr Trp Lys Gly
                725                 730                 735
Pro Glu Arg Leu Ala His Gly Ser Pro Phe Arg Gly Met Ser Leu Leu
            740                 745                 750
His Leu Ala Ala Ala Gln Gly Tyr Ala Arg Leu Ile Glu Thr Leu Ser
        755                 760                 765
Gln Trp Arg Ser Val Glu Thr Gly Ser Leu Asp Leu Glu Gln Glu Val
    770                 775                 780
Asp Pro Leu Asn Val Asp His Phe Ser Cys Thr Pro Leu Met Trp Ala
785                 790                 795                 800
Cys Ala Leu Gly His Leu Glu Ala Ala Val Leu Leu Phe Arg Trp Asn
                805                 810                 815
Arg Gln Ala Leu Ser Ile Pro Asp Ser Leu Gly Arg Leu Pro Leu Ser
            820                 825                 830
Val Ala His Ser Arg Gly His Val Arg Leu Ala Arg Cys Leu Glu Glu
        835                 840                 845
Leu Gln Arg Gln Glu Pro Ser Val Glu Pro Pro Phe Ala Leu Ser Pro
    850                 855                 860
Pro Ser Ser Ser Pro Asp Thr Gly Leu Ser Ser Val Ser Ser Pro Ser
865                 870                 875                 880
Glu Leu Ser Asp Gly Thr Phe Ser Val Thr Ser Ala Tyr Ser Ser Ala
                885                 890                 895
Pro Asp Gly Ser Pro Pro Pro Ala Pro Leu Pro Ala Ser Glu Met Thr
            900                 905                 910
Met Glu Asp Met Ala Pro Gly Gln Leu Ser Ser Gly Val Pro Glu Ala
        915                 920                 925
Pro Leu Leu Leu Met Asp Tyr Glu Ala Thr Asn Ser Lys Gly Pro Leu
    930                 935                 940
Ser Ser Leu Pro Ala Leu Pro Pro Ala Ser Asp Asp Gly Ala Ala Pro
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945 950 955 960
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965 970 975
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980 985 990
Arg Glu Asp Phe Val Gly Leu Pro Glu Ala Gly Ala Ser Met Arg Glu
995 1000 1005
Arg Thr Gly Ala Val Gly Leu Ser Glu Thr Met Ser Trp Leu Ala Ser
1010 1015 1020
Tyr Leu Glu Asn Val Asp His Phe Pro Ser Ser Thr Pro Pro Ser Glu
1025 1030 1035 1040
Leu Pro Phe Glu Arg Gly Arg Leu Ala Val Pro Ser Ala Pro Ser Trp
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Ala Glu Phe Leu Ser Ala Ser Thr Ser Gly Lys Met Glu Ser Asp Phe
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Ala Leu Leu Thr Leu Ser Asp His Glu Gln Arg Glu Leu Tyr Glu Ala
1075 1080 1085
Ala Arg Val Ile Gln Thr Ala Phe Arg Lys Tyr Lys Gly Arg Arg Leu
1090 1095 1100
Lys Glu Gln Gln Glu Val Ala Ala Ala Val Ile Gln Arg Cys Tyr Arg
1105 1110 1115 1120
Lys Tyr Lys Gln Leu Thr Trp Ile Ala Leu Lys Phe Ala Leu Tyr Lys
1125 1130 1135
Lys Met Thr Gln Ala Ala Ile Leu Ile Gln Ser Lys Phe Arg Ser Tyr
1140 1145 1150
Tyr Glu Gln Lys Arg Phe Gln Gln Ser Arg Arg Ala Ala Val Leu Ile
1155 1160 1165
Gln Gln His Tyr Arg Ser Tyr Arg Arg Arg Pro Gly Pro Pro His Arg
1170 1175 1180
Thr Ser Ala Thr Leu Pro Ala Arg Asn Lys Gly Ser Phe Leu Thr Lys
1185 1190 1195 1200
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<211> 357
<212> DNA
<213> Homo sapiens

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ccccttgtgg aaacgcagtt ccaagaaaac aaagaggaaa tgctgcgaag agccacaagg
240
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357

<210> 4988
<211> 105
<212> PRT
<213> Homo sapiens

<400> 4988
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20 25 30
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35 40 45
Pro Leu Glu Ala Lys Gly Leu Ala Thr Gln Gly Ala Ser Leu Pro Leu
50 55 60
Leu Pro Thr Val Thr Cys Val Ser Ile Lys Ser Trp Lys Met Glu Cys
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Gln Leu Leu Gln Ala Pro Trp Pro Arg
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<212> DNA
<213> Homo sapiens

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<211> 54
<212> PRT
<213> Homo sapiens

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Arg Thr Ser Ile Ser Gly
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<210> 4991
<211> 828
<212> DNA
<213> Homo sapiens

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<211> 69
<212> PRT
<213> Homo sapiens

<400> 4992
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35 40 45
Cys Ser Thr Leu Gly Lys Asp Cys Glu Met Tyr Lys His Arg Met Asn
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Thr Val Met Leu Gln
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<210> 4993
<211> 837
<212> DNA
<213> Homo sapiens

<400> 4993

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<211> 133
<212> PRT
<213> Homo sapiens

<400> 4994
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Glu Glu Asp Ser Asp Gly Glu Leu Asn Thr Trp Glu Leu Ser Glu Gly
35 40 45
Thr Asn Cys Pro Pro Lys Glu Gln Pro Gly Asp Leu Phe Asn Glu Asp
50 55 60
Trp Asp Ser Glu Leu Lys Ala Asp Gln Gly Asn Pro Tyr Asp Ala Asp
65 70 75 80
Asp Ile Gln Glu Ser Ile Ser Gln Glu Leu Lys Pro Trp Val Cys Cys
85 90 95
Ala Pro Gln Gly Asp Met Ile Tyr Asp Pro Ser Trp His His Pro Pro
100 105 110
Pro Leu Ile Pro Tyr Tyr Ser Lys Met Val Phe Glu Thr Gly Gln Phe
115 120 125
Asp Asp Ala Glu Asp
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<210> 4995
<211> 1595
<212> DNA
<213> Homo sapiens

<400> 4995
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1440

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<210> 4996
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<212> PRT
<213> Homo sapiens

<400> 4996
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35 40 45
Val Met Asp Gly Val Ile Ser Asp His Glu Cys Gln Glu Leu Gln Arg
50 55 60
Leu Thr Asn Val Ala Ala Thr Ser Gly Asp Gly Tyr Arg Gly Gln Thr
65 70 75 80
Ser Pro His Thr Pro Asn Glu Lys Phe Tyr Gly Val Thr Val Phe Lys
85 90 95
Ala Leu Lys Leu Gly Gln Glu Gly Lys Val Pro Leu Gln Ser Ala His
100 105 110
Leu Tyr Tyr Asn Val Thr Glu Lys Val Arg Arg Ile Met Glu Ser Tyr
115 120 125
Phe Arg Leu Asp Thr Pro Leu Tyr Phe Ser Tyr Ser His Leu Val Cys
130 135 140
Arg Thr Ala Ile Glu Glu Val Gln Ala Glu Arg Lys Asp Asp Ser His
145 150 155 160
Pro Val His Val Asp Asn Cys Ile Leu Asn Ala Glu Thr Leu Val Cys
165 170 175
Val Lys Glu Pro Pro Ala Tyr Thr Phe Arg Asp Tyr Ser Ala Ile Leu
180 185 190
Tyr Leu Asn Gly Asp Phe Asp Gly Gly Asn Phe Tyr Phe Thr Glu Leu
195 200 205
Asp Ala Lys Thr Val Thr Ala Glu Val
210 215

<210> 4997
<211> 1688
<212> DNA
<213> Homo sapiens

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120
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180

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480
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1888

<210> 4998
<211> 464
<212> PRT
<213> Homo sapiens

<400> 4998
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35 40 45
Cys Pro Glu Glu Gln Pro His Val Gly Asn Tyr Arg Leu Leu Arg Thr
50 55 60
Ile Gly Lys Gly Asn Phe Ala Lys Val Lys Leu Ala Arg His Ile Leu
65 70 75 80
Thr Gly Arg Glu Val Ala Ile Lys Ile Ile Asp Lys Thr Gln Leu Asn
85 90 95
Pro Ser Ser Leu Gln Lys Leu Phe Arg Glu Val Arg Ile Met Lys Gly
100 105 110
Leu Asn His Pro Asn Ile Val Lys Leu Phe Glu Val Ile Glu Thr Glu
115 120 125
Lys Thr Leu Tyr Leu Val Met Glu Tyr Ala Ser Ala Gly Glu Pro Pro
130 135 140
Thr Leu Ser Ala Leu Pro Leu Cys His Leu Pro Leu Pro Leu His Leu
145 150 155 160
Thr Leu Thr Pro Leu Gly Leu Cys Pro Ala Gly Glu Val Phe Asp Tyr
165 170 175
Leu Val Ser His Gly Arg Met Lys Glu Lys Glu Ala Arg Ala Lys Phe
180 185 190
Arg Gln Ile Val Ser Ala Val His Tyr Cys His Gln Lys Asn Ile Val
195 200 205
His Arg Asp Leu Lys Ala Glu Asn Leu Leu Leu Asp Ala Glu Ala Asn
210 215 220
Ile Lys Ile Ala Asp Phe Gly Phe Ser Asn Glu Phe Thr Leu Gly Ser
225 230 235 240
Lys Leu Asp Thr Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu
245 250 255
Phe Gln Gly Lys Lys Tyr Asp Gly Pro Glu Val Asp Ile Trp Ser Leu
260 265 270
Gly Val Ile Leu Tyr Thr Leu Val Ser Gly Ser Leu Pro Phe Asp Gly
275 280 285
His Asn Leu Lys Glu Leu Arg Glu Arg Val Leu Lys Gly Lys Tyr Arg
290 295 300
Val Pro Phe Tyr Met Ser Thr Asp Cys Glu Ser Ile Leu Arg Arg Phe
305 310 315 320
Leu Val Leu Asn Pro Ala Lys Arg Cys Thr Leu Glu Gln Ile Met Lys
325 330 335
Asp Lys Trp Ile Asn Ile Gly Tyr Glu Gly Glu Glu Leu Lys Pro Tyr

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            340                 345                 350
Thr Glu Pro Glu Glu Asp Phe Gly Asp Thr Lys Arg Ile Glu Val Met
        355                 360                 365
Val Gly Met Gly Tyr Thr Arg Glu Glu Ile Lys Glu Ser Leu Thr Ser
    370                 375                 380
Gln Lys Tyr Asn Glu Val Thr Ala Thr Tyr Leu Leu Leu Gly Arg Lys
385                 390                 395                 400
Thr Glu Pro Asp Glu His Gly Gly Gly Gly Ala Glu Gly Gly Ala Ala
                405                 410                 415
Ala Arg Pro Glu Gly Glu Leu Gln His Arg Gly Glu Trp Glu Ser Arg
            420                 425                 430
Ala Ala Pro Leu Gln Pro His Gly Gln Gln Arg Pro Gln Pro Gln Gln
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Gly Arg Asp Pro Arg Ala Ala Glu Gly Gln His Glu His Pro Arg Glu
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<210> 4999
<211> 1630
<212> DNA
<213> Homo sapiens

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<210> 5000
<211> 307
<212> PRT
<213> Homo sapiens

<400> 5000
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35 40 45
Gly Ala Glu Asp Lys Met Thr Ser Gly Asp Val Leu Ser Asn Arg Lys
50 55 60
Met Phe Tyr Leu Leu Lys Thr Ala Phe Pro Ser Val Gln Ile Asn Thr
65 70 75 80
Glu Glu His Val Asp Ala Ala Asp Gln Glu Val Ile Leu Trp Asp His
85 90 95
Lys Ile Pro Glu Asp Ile Leu Lys Glu Val Thr Thr Pro Lys Glu Val
100 105 110
Pro Ala Glu Ser Val Thr Val Trp Ile Asp Pro Leu Asp Ala Thr Gln
115 120 125
Glu Tyr Thr Glu Asp Leu Arg Lys Tyr Val Thr Thr Met Val Cys Val
130 135 140
Ala Val Asn Gly Lys Pro Met Leu Gly Val Ile His Lys Pro Phe Ser
145 150 155 160
Glu Tyr Thr Ala Trp Ala Met Val Asp Gly Gly Ser Asn Val Lys Ala
165 170 175
Arg Ser Ser Tyr Asn Glu Lys Thr Pro Arg Ile Val Val Ser Arg Ser

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            180                 185                 190
His Ser Gly Met Val Lys Gln Val Ala Leu Gln Thr Phe Gly Asn Gln
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Thr Thr Ile Ile Pro Ala Gly Gly Ala Gly Tyr Lys Val Leu Ala Leu
    210                 215                 220
Leu Asp Val Pro Asp Lys Ser Gln Glu Lys Ala Asp Leu Tyr Ile His
225                 230                 235                 240
Val Thr Tyr Ile Lys Lys Trp Asp Ile Cys Ala Gly Asn Ala Ile Leu
                245                 250                 255
Lys Ala Leu Gly Gly His Met Thr Thr Leu Ser Gly Glu Glu Ile Ser
            260                 265                 270
Tyr Thr Gly Ser Asp Gly Ile Glu Gly Gly Leu Leu Ala Ser Ile Arg
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<210> 5001
<211> 3427
<212> DNA
<213> Homo sapiens

<400> 5001

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180
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720
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<210> 5002
<211> 335
<212> PRT
<213> Homo sapiens

<400> 5002
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Ile Val Leu Ile Val Glu Gly Thr Glu Phe Pro Cys His Lys Met Val
35 40 45
Leu Ala Thr Cys Ser Ser Tyr Phe Arg Ala Met Phe Met Ser Gly Leu
50 55 60
Ser Glu Ser Lys Gl Thr His Val His Leu Arg Asn Val Asp Ala Ala
65 70 75 80
Thr Leu Gln Ile Ile Ile Thr Tyr Ala Tyr Thr Gly Asn Leu Ala Met
85 90 95
Asn Asp Ser Thr Val Glu Gln Leu Tyr Glu Thr Ala Cys Phe Leu Gln
100 105 110
Val Glu Asp Val Leu Gln Arg Cys Arg Glu Tyr Leu Ile Lys Lys Ile

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Asn Ala Glu Asn Cys Val Arg Leu Leu Ser Phe Ala Asp Leu Phe Ser
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Cys Glu Glu Leu Lys Gln Ser Ala Lys Arg Met Val Glu His Lys Phe
145                 150                 155                 160
Thr Ala Val Tyr His Gln Asp Ala Phe Met Gln Leu Leu His Asp Leu
                165                 170                 175
Leu Ile Asp Ile Leu Ser Ser Asp Asn Leu Asn Val Glu Lys Glu Glu
            180                 185                 190
Thr Val Arg Glu Ala Ala Met Leu Trp Leu Glu Tyr Asn Thr Glu Ser
        195                 200                 205
Arg Ser Gln Tyr Leu Ser Ser Val Leu Ser Gln Ile Arg Ile Asp Ala
    210                 215                 220
Leu Ser Glu Val Thr Gln Arg Ala Trp Phe Gln Gly Leu Pro Pro Asn
225                 230                 235                 240
Asp Lys Ser Val Val Val Gln Gly Leu Tyr Lys Ser Met Pro Lys Phe
                245                 250                 255
Phe Lys Pro Arg Leu Gly Met Thr Lys Glu Glu Met Met Ile Phe Ile
            260                 265                 270
Glu Ala Ser Ser Glu Asn Pro Cys Ser Leu Tyr Ser Ser Val Cys Tyr
        275                 280                 285
Ser Pro Gln Ala Glu Lys Val Tyr Lys Leu Cys Ser Pro Pro Ala Asp
    290                 295                 300
Leu His Lys Val Gly Thr Val Val Thr Pro Asp Asn Asp Ile Tyr Ile
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<210> 5003
<211> 3729
<212> DNA
<213> Homo sapiens

<400> 5003

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600
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<211> 642
<212> PRT
<213> Homo sapiens

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35 40 45
Leu Gln Arg Ser Leu Asn Glu Leu Asp Gly Leu Lys Ile Pro Ser Glu
50 55 60
Ser Gly Glu Lys Leu Lys Val Val Asn Glu Arg Ala Thr Leu Phe Arg
65 70 75 80
Ile Thr Ser Asn Ala Met Ile Asn Ala Cys Arg Asp Phe Leu Glu Leu
85 90 95
Ala Glu Ile His Ser Arg Lys Trp Gln Arg Ala Leu Gln Tyr Glu Gln
100 105 110
Glu Gln Arg Val His Leu Glu Glu Thr Ile Glu Gln Leu Ala Lys Gln
115 120 125
His Asn Ser Leu Glu Arg Ala Phe His Ser Ala Pro Gly Arg Pro Ala
130 135 140
Asn Pro Ser Lys Ser Phe Ile Glu Gly Ser Leu Leu Thr Pro Lys Gly
145 150 155 160
Glu Asp Ser Glu Glu Asp Glu Asp Thr Glu Tyr Phe Asp Ala Met Glu
165 170 175
Asp Ser Thr Ser Phe Ile Thr Val Ile Thr Glu Ala Lys Glu Asp Ser
180 185 190
Arg Lys Ala Glu Gly Ser Thr Gly Thr Ser Ser Val Asp Trp Ser Ser
195 200 205
Ala Asp Asn Val Leu Asp Gly Ala Ser Leu Val Pro Lys Gly Ser Ser
210 215 220
Lys Val Lys Arg Arg Val Arg Ile Pro Asn Lys Pro Asn Tyr Ser Leu
225 230 235 240
Asn Leu Trp Ser Ile Met Lys Asn Cys Ile Gly Arg Glu Leu Ser Arg
245 250 255
Ile Pro Met Pro Val Asn Phe Asn Glu Pro Leu Ser Met Leu Gln Arg
260 265 270
Leu Thr Glu Asp Leu Glu Tyr His His Leu Leu Asp Lys Ala Val His
275 280 285
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290 295 300
Ser Ser Tyr Ser Thr Thr Val His Arg Ile Ala Lys Pro Phe Asn Pro
305 310 315 320
Met Leu Gly Glu Thr Phe Glu Leu Asp Arg Leu Asp Asp Met Gly Leu
325 330 335
Arg Ser Leu Cys Glu Gln Val Ser His His Pro Pro Ser Ala Ala His
340 345 350
Tyr Val Phe Ser Lys His Gly Trp Ser Leu Trp Gln Glu Ile Thr Ile
355 360 365
Ser Ser Lys Phe Arg Gly Lys Tyr Ile Ser Ile Met Pro Leu Gly Ala
370 375 380
Ile His Leu Glu Phe Gln Ala Ser Gly Asn His Tyr Val Trp Arg Lys

385 390 395 400
Ser Thr Ser Thr Val His Asn Ile Ile Val Gly Lys Leu Trp Ile Asp
405 410 415
Gln Ser Gly Asp Ile Glu Ile Val Asn His Lys Thr Asn Asp Arg Cys
420 425 430
Gln Leu Lys Phe Leu Pro Tyr Ser Tyr Phe Ser Lys Glu Ala Ala Arg
435 440 445
Lys Val Thr Gly Val Val Ser Asp Ser Gln Gly Lys Ala His Tyr Val
450 455 460
Leu Ser Gly Ser Trp Asp Glu Gln Met Glu Cys Ser Lys Val Met His
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485 490 495
Gln Thr Leu Ser Ala Lys Leu Leu Trp Lys Lys Tyr Pro Leu Pro Glu
500 505 510
Asn Ala Glu Asn Met Tyr Tyr Phe Ser Glu Leu Ala Leu Thr Leu Asn
515 520 525
Glu His Glu Glu Gly Val Ala Pro Thr Asp Ser Arg Leu Arg Pro Asp
530 535 540
Gln Arg Leu Met Glu Lys Gly Arg Trp Asp Glu Ala Asn Thr Glu Lys
545 550 555 560
Gln Arg Leu Glu Glu Lys Gln Arg Leu Ser Arg Arg Arg Arg Leu Glu
565 570 575
Ala Cys Gly Pro Gly Ser Ser Cys Ser Ser Glu Glu Gly Glu Ala Gly
580 585 590
Arg Glu Gly Arg Pro Gly Gly Glu Glu Arg Gly Ala Arg Val Gly Val
595 600 605
Pro Gln Gly Arg Ile Pro Gly Glu Gln Ala Thr Ser Pro Pro Thr Ser
610 615 620
Pro Leu Cys Leu Pro Ser Arg Glu Gly Gly Gly Cys Leu His Ala Thr
625 630 635 640
Val Val

<210> 5005
<211> 1120
<212> DNA
<213> Homo sapiens

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420

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<211> 165
<212> PRT
<213> Homo sapiens

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35 40 45
Ser Glu Phe Pro Ser Ser Leu Thr Gly Lys Val Ala Pro Glu Glu Phe
50 55 60
Lys Ala Ser Ile Asn Arg Val Asn Ser Cys Leu Lys Lys Asn Leu Pro
65 70 75 80
Val Asn Val Arg Trp Leu Leu Cys Gly Cys Leu Cys Cys Cys Cys Thr
85 90 95
Leu Gly Cys Ser Met Trp Pro Val Ile Cys Leu Ser Lys Arg Thr Arg
100 105 110
Arg Ser Ile Glu Lys Leu Leu Glu Trp Glu Asn Asn Arg Leu Tyr His
115 120 125
Lys Leu Cys Leu His Trp Arg Leu Ser Lys Arg Lys Cys Glu Thr Asn
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Ile Phe Arg Pro Asp
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<211> 2165
<212> DNA
<213> Homo sapiens

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<211> 487
<212> PRT
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35 40 45
Met Cys Tyr Ile His Ile Ala Ala Leu Ile Ala Glu Tyr Leu Lys Arg
50 55 60
Lys Gly Met Phe Ser Met Gly Trp Pro Ala Val Leu Ser Ile Thr Pro
65 70 75 80
Asn Ile Lys Glu Glu Gly Ala Met Lys Glu Asp Ser Gly Met Gln Asp
85 90 95
Thr Pro Tyr Asn Glu Asn Ile Leu Val Glu Gln Leu Tyr Met Cys Val
100 105 110
Glu Phe Leu Trp Lys Ser Glu Arg Tyr Glu Xaa Ser Leu Leu Met Ser
115 120 125
Thr Ser Pro Ser Leu Leu Ser Leu Arg Asn Asn Glu Thr Ser Lys Asn
130 135 140
Ser Asp Leu Tyr Tyr Asp Ile His Arg Ser Tyr Leu Lys Val Ala Glu
145 150 155 160
Val Val Asn Ser Glu Ala Ala Val Trp Ser Leu Leu Ser Cys Gly Ile

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Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly Lys Glu Tyr Ile Tyr
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Lys Glu Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Gln Arg Leu Leu
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Lys Leu Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val Lys Ile Ile Gln
    210                 215                 220
Asp Ser Asn Lys Val Asn Pro Lys Asp Leu Asp Pro Lys Tyr Ala Tyr
225                 230                 235                 240
Ile Gln Val Thr Tyr Val Thr Pro Phe Phe Glu Glu Lys Glu Ile Glu
                245                 250                 255
Asp Arg Lys Thr Asp Phe Glu Met His His Asn Ile Asn Arg Phe Val
            260                 265                 270
Phe Glu Thr Pro Phe Thr Leu Ser Gly Lys Lys His Gly Gly Val Ala
        275                 280                 285
Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Thr Ser His Leu Phe Pro
    290                 295                 300
Tyr Val Lys Lys Arg Ile Gln Val Ile Ser Gln Ser Ser Thr Glu Leu
305                 310                 315                 320
Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val Ser Glu
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Leu Asn Gln Leu Cys Thr Met Glu Glu Val Asp Met Ile Arg Leu Gln
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Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn Ala Gly Pro Met
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Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala Lys Lys Tyr Pro
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Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg Gln Phe Ala Asp
385                 390                 395                 400
Ala Cys Gly Gln Ala Leu Asp Val Asn Glu Arg Leu Ile Lys Glu Asp
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Gln Leu Glu Tyr Gln Glu Glu Leu Arg Ser His Tyr Lys Asp Met Leu
            420                 425                 430
Ser Glu Leu Ser Thr Val Met Asn Glu Gln Leu Cys Arg Gly Pro Cys
        435                 440                 445
Leu Tyr Ser Phe Cys Ser Ser Val Ser Ser Ile Ser Leu Ser Thr Val
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<211> 426
<212> DNA
<213> Homo sapiens

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180

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<210> 5010
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            20   25   30
Asn Leu Pro Gly Arg Val His Gln Phe Phe Ile Ser Pro Leu Phe Ile
        35   40   45
Leu Ser Phe Glu Val Ile Leu Ile His Phe Leu His Leu Gln Pro Pro
    50   55   60
Val Leu Leu Asp Leu Ala Pro Asn Leu Leu Leu Pro Phe Gly Thr Glu
65   70   75   80
Glu Lys Leu Leu Ser Ser Pro Cys Phe Ala Asp Ile Ser Lys Gly Lys
                85   90   95
Glu Ser Thr Gly Pro Phe Ile Ser Cys Pro Arg Pro Ser Gln Gly Ala
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Val Ile Met Pro Lys Pro Tyr
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<211> 3431
<212> DNA
<213> Homo sapiens

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2700
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2820
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2880
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2940
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3120
tgaatttatt attgcttata aaacacattt gatggaatag gagtactggt ttttcataat
3180
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3240
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3300
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3431

<210> 5012
<211> 950
<212> PRT
<213> Homo sapiens

<400> 5012
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20 25 30
Lys Ile Pro Val Asp Ala Ser Lys Pro Asn Pro Asn Asp Val Glu Phe
35 40 45
Asp Asn Leu Tyr Leu Asp Met Asn Gly Ile Ile His Pro Cys Thr His
50 55 60
Pro Glu Asp Lys Pro Ala Pro Lys Asn Glu Asp Glu Met Met Val Ala
65 70 75 80
Ile Phe Glu Tyr Ile Asp Arg Leu Phe Ser Ile Val Arg Pro Arg Arg
85 90 95
Leu Leu Tyr Met Ala Ile Asp Gly Val Ala Pro Arg Val Lys Met Asn
100 105 110
Gln Gln Arg Ser Arg Arg Phe Arg Ala Ile Lys Glu Gly Met Glu Ala
115 120 125
Ala Val Glu Lys Gln Arg Val Arg Glu Glu Ile Leu Ala Lys Gly Gly
130 135 140
Phe Leu Pro Pro Glu Glu Ile Lys Glu Arg Phe Asp Ser Asn Cys Ile
145 150 155 160
Thr Pro Gly Thr Glu Phe Met Asp Asn Leu Ala Lys Cys Leu Arg Tyr
165 170 175
Tyr Ile Ala Asp Arg Leu Asn Asn Asp Pro Gly Trp Lys Asn Leu Thr
180 185 190
Val Ile Leu Ser Asp Ala Ser Ala Pro Gly Glu Gly Glu His Lys Ile
195 200 205
Met Asp Tyr Ile Arg Arg Gln Arg Ala Gln Pro Asn His Asp Pro Asn
210 215 220
Thr His His Cys Leu Cys Gly Ala Asp Ala Asp Leu Ile Met Leu Gly
225 230 235 240
Leu Ala Thr His Glu Pro Asn Phe Thr Ile Ile Arg Glu Glu Phe Lys
245 250 255
Pro Asn Lys Pro Lys Pro Cys Gly Leu Cys Asn Gln Phe Gly His Glu
260 265 270
Val Lys Asp Cys Glu Gly Leu Pro Arg Glu Lys Lys Gly Lys His Asp
275 280 285
Glu Leu Ala Asp Ser Leu Pro Cys Ala Glu Gly Glu Phe Ile Phe Leu
290 295 300
Arg Leu Asn Val Leu Arg Glu Tyr Leu Glu Arg Glu Leu Thr Met Ala
305 310 315 320
Ser Leu Pro Phe Thr Phe Asp Val Glu Arg Ser Ile Asp Asp Trp Val
325 330 335
Phe Met Cys Phe Phe Val Gly Asn Asp Phe Leu Pro His Leu Pro Ser
340 345 350
Leu Glu Ile Arg Glu Asn Ala Ile Asp Arg Leu Val Asn Ile Tyr Lys
355 360 365
Asn Val Val His Lys Thr Gly Gly Tyr Leu Thr Glu Ser Gly Tyr Val
370 375 380
Asn Leu Gln Arg Val Gln Met Ile Met Leu Ala Val Gly Glu Val Glu
385 390 395 400
Asp Ser Ile Phe Lys Lys Arg Lys Asp Asp Glu Asp Ser Phe Arg Arg
405 410 415
Arg Gln Lys Glu Lys Arg Lys Arg Met Lys Arg Asp Gln Pro Ala Phe

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            420                 425                 430
Thr Pro Ser Gly Ile Leu Thr Pro His Ala Leu Gly Ser Arg Asn Ser
        435                 440                 445
Pro Gly Ser Gln Val Ala Ser Asn Pro Arg Gln Ala Ala Tyr Glu Met
    450                 455                 460
Arg Met Gln Asn Asn Ser Ser Pro Ser Ile Ser Pro Asn Thr Ser Phe
465                 470                 475                 480
Thr Ser Asp Gly Ser Pro Ser Pro Leu Gly Gly Ile Lys Arg Lys Ala
                485                 490                 495
Glu Asp Ser Asp Ser Glu Pro Glu Pro Glu Asp Asn Val Arg Leu Trp
            500                 505                 510
Glu Ala Gly Trp Lys Gln Arg Tyr Tyr Lys Asn Lys Phe Asp Val Asp
        515                 520                 525
Ala Ala Asp Glu Lys Phe Arg Arg Lys Val Val Gln Ser Tyr Val Glu
    530                 535                 540
Gly Leu Cys Trp Val Leu Arg Tyr Tyr Tyr Gln Gly Cys Ala Ser Trp
545                 550                 555                 560
Lys Trp Tyr Tyr Pro Phe His Tyr Ala Pro Phe Ala Ser Asp Phe Glu
                565                 570                 575
Gly Ile Ala Asp Met Pro Ser Asp Phe Glu Lys Gly Thr Lys Pro Phe
            580                 585                 590
Lys Pro Leu Glu Gln Leu Met Gly Val Phe Pro Ala Ala Ser Gly Asn
        595                 600                 605
Phe Leu Pro Pro Ser Trp Arg Lys Leu Met Ser Asp Pro Asp Ser Ser
    610                 615                 620
Ile Ile Asp Phe Tyr Pro Glu Asp Phe Ala Ile Asp Leu Asn Gly Lys
625                 630                 635                 640
Lys Tyr Ala Trp Gln Gly Val Ala Leu Leu Pro Phe Val Asp Glu Arg
                645                 650                 655
Arg Leu Arg Ala Ala Leu Glu Glu Val Tyr Pro Asp Leu Thr Pro Glu
            660                 665                 670
Glu Thr Arg Arg Asn Ser Leu Gly Gly Asp Val Leu Phe Val Gly Lys
        675                 680                 685
His His Pro Leu His Asp Phe Ile Leu Glu Leu Tyr Gln Thr Gly Ser
    690                 695                 700
Thr Glu Pro Val Glu Val Pro Pro Glu Leu Cys His Gly Ile Gln Gly
705                 710                 715                 720
Lys Phe Ser Leu Asp Glu Glu Ala Ile Leu Pro Asp Gln Ile Val Cys
                725                 730                 735
Ser Pro Val Pro Met Leu Arg Asp Leu Thr Gln Asn Thr Val Val Ser
            740                 745                 750
Ile Asn Phe Lys Asp Pro Gln Phe Ala Glu Asp Tyr Ile Phe Lys Ala
        755                 760                 765
Val Met Leu Pro Gly Ala Arg Lys Pro Ala Ala Val Leu Lys Pro Ser
    770                 775                 780
Asp Trp Glu Lys Ser Ser Asn Gly Arg Gln Trp Lys Pro Gln Leu Gly
785                 790                 795                 800
Phe Asn Arg Asp Arg Arg Pro Val His Leu Asp Gln Ala Ala Phe Arg
                805                 810                 815
Thr Leu Gly His Val Met Pro Arg Gly Ser Gly Thr Gly Ile Tyr Ser
            820                 825                 830
Asn Ala Ala Pro Pro Pro Val Thr Tyr Gln Gly Asn Leu Tyr Arg Pro
        835                 840                 845
Leu Leu Arg Gly Gln Ala Gln Ile Pro Lys Leu Met Ser Asn Met Arg
```

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    850                 855                 860
Pro Gln Asp Ser Trp Arg Gly Pro Pro Pro Leu Phe Gln Gln Gln Arg
865                 870                 875                 880
Phe Asp Arg Gly Val Gly Ala Glu Pro Leu Leu Pro Trp Asn Arg Met
                885                 890                 895
Leu Gln Thr Gln Asn Ala Ala Phe Gln Pro Asn Gln Tyr Gln Met Leu
            900                 905                 910
Ala Gly Pro Gly Gly Tyr Pro Pro Arg Arg Asp Asp Arg Gly Gly Arg
        915                 920                 925
Gln Gly Tyr Pro Arg Glu Gly Arg Lys Tyr Pro Leu Pro Pro Pro Ser
    930                 935                 940
Gly Arg Tyr Asn Trp Asn
945                 950
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<210> 5013
<211> 2480
<212> DNA
<213> Homo sapiens

<400> 5013
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120
tgccttctgc gcgcctggga tcccggagcc tgcctaggtt ctgtgcgctc ccgcccaggc
180
cggtgcccgc cgcccgcctg cgccccaggc aggtcccagg cctccggctg ctcccggccg
240
aaggtgggga caggcagtgg caggcaccac tagcgagggc gtttgggaac ccagggtgac
300
cacggcgcag ccatggggac cgcgcttgtg taccatgagg acatgacggc cacccggctg
360
ctctgggacg accccgagtg cgagatcgag cgtcctgagc gcctgaccgc agccctggat
420
cgcctgcggc agcgcggcct ggaacagagg tgtctgcggt tgtcagcccg cgaggcctcg
480
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540
gtcctaggca aggaggagct gcaggcgctg tccggacagt tcgacgccat ctacttccac
600
ccgagtacct ttcactgcgc gcggctggcc gcaggggctg gactgcagct ggtggacgct
660
gtgctcactg gagctgtgca aaatgggctt gccctggtga ggcctcccgg gcaccatggc
720
cagagggcgg ctgccaacgg gttctgtgtg ttcaacaacg tggccatagc agctgcacat
780
gccaagcaga aacacgggct acacaggatc ctcgtcgtgg actgggatgt gcaccatggc
840
caggggatcc agtatctctt tgaggatgac cccagcgtcc tttacttctc ctggcaccgc
900
tatgagcatg ggcgcttctg gcctttcctg cgagagtcag atgcagacgc agtggggcgg
960
ggacagggcc tcggcttcac tgtcaacctg ccctggaacc aggttgggat gggaaacgct
1020

gactacgtgg ctgccttcct gcacctgctg ctcccactgg cctttgagtt tgaccctgag
1080
ctggtgctgg tctcggcagg atttgactca gccatcgggg accctgaggg gcaaatgcag
1140
gccacgccag agtgcttcgc ccacctcaca cagctgctgc aggtgctggc cggcggccgg
1200
gtctgtgccg tgctggaggg cggctaccac ctggagtcac tggcggagtc agtgtgcatg
1260
acagtacaga cgctgctggg tgacccggcc ccacccctgt cagggccaat ggcgccatgt
1320
cagaggtgcg aggggagtgc cctagagtcc atccagagtg cccgtgctgc ccaggccccg
1380
cactggaaga gcctccagca gcaagatgtg accgctgtgc cgatgagccc cagcagccac
1440
tccccagagg ggaggcctcc acctctgctg cctgggggtc cagtgtgtaa ggcagctgca
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tctgcaccga gctccctcct ggaccagccg tgcctctgcc ccgcaccctc tgtccgcacc
1560
gctgttgccc tgacaacgcc ggatatcaca ttggttctgc cccctgacgt catccaacag
1620
gaagcgtcag ccctgaggga ggagacagaa gcctgggcca ggccacacga gtccctggcc
1680
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1800
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1920
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1980
ggtggtttcc tgagctgcat cttgggcttg gtgctgcccc tggcctatgg cttccagcct
2040
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2100
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2160
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2220
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2280
gaatggagag gcacctccta gcctaggccc ttcctctgtg gcctccccag aggacgtcca
2340
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2460
acgccagcgc cccgcggccg
2480

<210> 5014
<211> 675
<212> PRT

<213> Homo sapiens

<400> 5014

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Ala Leu Val Tyr His Glu Asp Met Thr Ala Thr Arg Leu Leu Trp Asp
            20                  25                  30
Asp Pro Glu Cys Glu Ile Glu Arg Pro Glu Arg Leu Thr Ala Ala Leu
        35                  40                  45
Asp Arg Leu Arg Gln Arg Gly Leu Glu Gln Arg Cys Leu Arg Leu Ser
    50                  55                  60
Ala Arg Glu Ala Ser Glu Glu Glu Leu Gly Leu Val His Ser Pro Glu
65                  70                  75                  80
Tyr Val Ser Leu Val Arg Glu Thr Gln Val Leu Gly Lys Glu Glu Leu
                85                  90                  95
Gln Ala Leu Ser Gly Gln Phe Asp Ala Ile Tyr Phe His Pro Ser Thr
            100                 105                 110
Phe His Cys Ala Arg Leu Ala Ala Gly Ala Gly Leu Gln Leu Val Asp
        115                 120                 125
Ala Val Leu Thr Gly Ala Val Gln Asn Gly Leu Ala Leu Val Arg Pro
    130                 135                 140
Pro Gly His His Gly Gln Arg Ala Ala Ala Asn Gly Phe Cys Val Phe
145                 150                 155                 160
Asn Asn Val Ala Ile Ala Ala Ala His Ala Lys Gln Lys His Gly Leu
                165                 170                 175
His Arg Ile Leu Val Val Asp Trp Asp Val His His Gly Gln Gly Ile
            180                 185                 190
Gln Tyr Leu Phe Glu Asp Asp Pro Ser Val Leu Tyr Phe Ser Trp His
        195                 200                 205
Arg Tyr Glu His Gly Arg Phe Trp Pro Phe Leu Arg Glu Ser Asp Ala
    210                 215                 220
Asp Ala Val Gly Arg Gly Gln Gly Leu Gly Phe Thr Val Asn Leu Pro
225                 230                 235                 240
Trp Asn Gln Val Gly Met Gly Asn Ala Asp Tyr Val Ala Ala Phe Leu
                245                 250                 255
His Leu Leu Leu Pro Leu Ala Phe Glu Phe Asp Pro Glu Leu Val Leu
            260                 265                 270
Val Ser Ala Gly Phe Asp Ser Ala Ile Gly Asp Pro Glu Gly Gln Met
        275                 280                 285
Gln Ala Thr Pro Glu Cys Phe Ala His Leu Thr Gln Leu Leu Gln Val
    290                 295                 300
Leu Ala Gly Gly Arg Val Cys Ala Val Leu Glu Gly Gly Tyr His Leu
305                 310                 315                 320
Glu Ser Leu Ala Glu Ser Val Cys Met Thr Val Gln Thr Leu Leu Gly
                325                 330                 335
Asp Pro Ala Pro Pro Leu Ser Gly Pro Met Ala Pro Cys Gln Arg Cys
            340                 345                 350
Glu Gly Ser Ala Leu Glu Ser Ile Gln Ser Ala Arg Ala Ala Gln Ala
        355                 360                 365
Pro His Trp Lys Ser Leu Gln Gln Gln Asp Val Thr Ala Val Pro Met
    370                 375                 380
Ser Pro Ser Ser His Ser Pro Glu Gly Arg Pro Pro Pro Leu Leu Pro
385                 390                 395                 400
Gly Gly Pro Val Cys Lys Ala Ala Ala Ser Ala Pro Ser Ser Leu Leu
```

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                405                 410                 415
Asp Gln Pro Cys Leu Cys Pro Ala Pro Ser Val Arg Thr Ala Val Ala
            420                 425                 430
Leu Thr Thr Pro Asp Ile Thr Leu Val Leu Pro Pro Asp Val Ile Gln
        435                 440                 445
Gln Glu Ala Ser Ala Leu Arg Glu Glu Thr Glu Ala Trp Ala Arg Pro
    450                 455                 460
His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu
465                 470                 475                 480
Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile
                485                 490                 495
Ala Ala Thr Pro Ala Ser Ala Ala Ala Ala Thr Leu Asp Val Ala Val
            500                 505                 510
Arg Arg Gly Leu Ser His Gly Ala Gln Arg Leu Leu Cys Val Ala Leu
        515                 520                 525
Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu
    530                 535                 540
Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His
545                 550                 555                 560
Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile
                565                 570                 575
Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val
            580                 585                 590
Leu Val Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Ala Ala
        595                 600                 605
Leu Leu Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala
    610                 615                 620
Leu Leu Glu Glu Val Ser Trp Ala Gly Trp Arg Cys Cys Gly Val Gly
625                 630                 635                 640
Arg Gly Glu Gly Pro Val Thr Ala Ser Val Phe Ala Pro Gly Pro Glu
                645                 650                 655
Leu His Thr Pro Ala Ser Arg Asp Pro Gly Pro Gly Ala Glu Trp Arg
            660                 665                 670
Gly Thr Ser
        675
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<210> 5015
<211> 1360
<212> DNA
<213> Homo sapiens

<400> 5015
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ccgcaggtcc ctcccctctc cgcaggcccc gccgccgccg ccatctttgt tgggggcagc
120
caggcctggc tcgagatgcc gaagtcgtgc gcggcccggc agtgctgcaa ccgctacagc
180
agccgcagga agcagctcac cttccaccgg tttccgttca gccgcccgga gctgctgaag
240
gaatgggtgc tgaacatcgg ccggggcaac ttcaagccca agcagcacac ggtcatctgc
300
tccgagcact tccggccaga gtgcttcagc gcctttggaa accgcaagaa cctaaagcac
360

aatgccgtgc ccacggtgtt cgcctttcag gaccccacac agcaggtgag ggagaacaca
420
gaccctgcca gtgagagagg aaatgccagc tcttctcaga aagaaaaggt cctccctgag
480
gcgggggccg gagaggacag tcctgggaga aacatggaca ctgcacttga agagcttcag
540
ttgcccccaa atgccgaagg ccacgtaaaa caggtctcgc cacggaggcc gcaagcaaca
600
gaggctgttg gccggccgac tggccctgca ggcctgagaa ggacccccaa caagcagcca
660
tctgatcaca gctatgccct tttggactta gattccctga agaaaaaact cttcctcact
720
ctgaaggaaa atgaaaagct ccggaagcgc ttgcaggccc agaggctggt gatgcgaagg
780
atgtccagcc gcctccgtgc ttgcaaaggg caccggggac tccaggccag acttgggcca
840
gagcagcaga gctgagcccc acaggctccg gacgcagagg tggcagtggc accagggccg
900
gcagagcttt ggagctctgg ctgtggacat ttttgtctgc tgtggacact gagaaagttg
960
gccatgaggc ctgcttggcc ggggatcgag acagtagcca agctccccgg cgagagcccc
1020
aatgccgtct gggggacgtt tagaggcgtg gcactaggag tgcacatctg tgagcatgac
1080
aagcttatcc tcccatggta acagaagtcc aggctgaggc tgattctgga cgctgtcctt
1140
tcagcacacg cagagcaaag atcgttggaa gccccagtgt gggagatgct cctcagggag
1200
gaagccatgt gaggggggctg gctctgtggc gggtgagtgg tcccctcctc catcagcctg
1260
gacagccgct cggggttcta aggagtgact cctgtcccgg cctggtgtga gtgggcagtg
1320
taataaagtg tctttctata cggaaaaaaa aaaaaaaaaa
1360

<210> 5016
<211> 284
<212> PRT
<213> Homo sapiens

<400> 5016
Met Ser Ala Pro Trp Arg Arg Ala Arg Pro Val Thr Thr Ser Gln Arg
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Pro Arg Pro Ser Pro Gln Val Pro Pro Leu Ser Ala Gly Pro Ala Ala
20 25 30
Ala Ala Ile Phe Val Gly Gly Ser Gln Ala Trp Leu Glu Met Pro Lys
35 40 45
Ser Cys Ala Ala Arg Gln Cys Cys Asn Arg Tyr Ser Ser Arg Arg Lys
50 55 60
Gln Leu Thr Phe His Arg Phe Pro Phe Ser Arg Pro Glu Leu Leu Lys
65 70 75 80
Glu Trp Val Leu Asn Ile Gly Arg Gly Asn Phe Lys Pro Lys Gln His
85 90 95
Thr Val Ile Cys Ser Glu His Phe Arg Pro Glu Cys Phe Ser Ala Phe

```
            100                 105                 110
Gly Asn Arg Lys Asn Leu Lys His Asn Ala Val Pro Thr Val Phe Ala
        115                 120                 125
Phe Gln Asp Pro Thr Gln Gln Val Arg Glu Asn Thr Asp Pro Ala Ser
    130                 135                 140
Glu Arg Gly Asn Ala Ser Ser Ser Gln Lys Glu Lys Val Leu Pro Glu
145                 150                 155                 160
Ala Gly Ala Gly Glu Asp Ser Pro Gly Arg Asn Met Asp Thr Ala Leu
                165                 170                 175
Glu Glu Leu Gln Leu Pro Pro Asn Ala Glu Gly His Val Lys Gln Val
            180                 185                 190
Ser Pro Arg Arg Pro Gln Ala Thr Glu Ala Val Gly Arg Pro Thr Gly
        195                 200                 205
Pro Ala Gly Leu Arg Arg Thr Pro Asn Lys Gln Pro Ser Asp His Ser
    210                 215                 220
Tyr Ala Leu Leu Asp Leu Asp Ser Leu Lys Lys Lys Leu Phe Leu Thr
225                 230                 235                 240
Leu Lys Glu Asn Glu Lys Leu Arg Lys Arg Leu Gln Ala Gln Arg Leu
                245                 250                 255
Val Met Arg Arg Met Ser Ser Arg Leu Arg Ala Cys Lys Gly His Arg
            260                 265                 270
Gly Leu Gln Ala Arg Leu Gly Pro Glu Gln Gln Ser
        275                 280
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<210> 5017
<211> 785
<212> DNA
<213> Homo sapiens

<400> 5017
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120
ggggtggggt ggggggcgga gggcccgccc agcatagctg cagtgtcaca aagccatggc
180
agaaggtcct agcggcgcca ccctgcccca gcctgaggag gagggagagg gaggaacaac
240
cctgggcaga cggggcctca gggacctgtg tccttccgcc tccagagctg cccagccacg
300
ggctctcagg gtgctggggc agccccaggt cccctcttga actcagctgg ggccaggggc
360
cctcagaatg aaggcaggca ccaggcagga gcagcatccc cctccttgac ggtgctggca
420
ggagggccgc gccatgctga ctgcttgaac ctctgctgac ctgacagtgc tggcgggagg
480
gccgcaccat gctgactgcc tgaatctctg ctgaggctgc ctgcctgccg ggcccagctc
540
agcgccctct ccactgcgaa tcagtggcga tcatgtgatt tctatttctg ccccacaggg
600
taagggacga gtcttctgga aggctctgcc atggacattt gtcctcgggc tcagaggccc
660
caccctgccc cacacctgcc cctaatcact gcagtgtcca gcccagtgtt gaacagattg
720

tagcgttctg tctcattacg agcaaataaa tagactttca ttggaaaaaa aaaaaaaaaa
780
aaaaa
785

<210> 5018
<211> 63
<212> PRT
<213> Homo sapiens

<400> 5018
Gly Pro Ser Ala Ser Glu Gly Arg Asp Ala Val Ser Ala Ala Gly Ala
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Ser His Thr Ser Ser Ile Leu Ser Thr Leu His Ser Lys Cys Cys Leu
            20   25   30
Leu Pro Ala Leu Pro Ser Asp Ala Gly Val Gly Trp Gly Ala Glu Gly
        35   40   45
Pro Pro Ser Ile Ala Ala Val Ser Gln Ser His Gly Arg Arg Ser
    50   55   60

<210> 5019
<211> 2766
<212> DNA
<213> Homo sapiens

<400> 5019
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120
cgccgaatgc cagatggagg ttatcctcat ggtcctccag gcccattagg ccttctggga
180
gtccgaccag gcatgcctcc tcagcctcag gggcctgcac ccttacgtcg tcctgactca
240
tctgatgacc gttatgtaat gacaaaacat gccaccattt atccaactga agaggagtta
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420
gacagagctt tgaaaggagt tttgcgagtg ggagtatttg caaaaggatt acttctccga
480
ggagatagaa atgtcaacct tgttttgctg tgctcagaga aaccttcaaa gacattatta
540
agccgtattg cagaaaacct acccaaacag cttgctttta taagccctga gaagtatgac
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ataaaatgtg ctgtatctga agcggcaata attttgaatt catgtgtgga acccaaaatg
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720
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780
gctctggctg ctctacgcca cgctaagtgg ttccaggcta gagctaatgg tctgcagtcc
840

tgtgtgatta tcatacgcat tcttcgagac ctctgtcagc gagttccaac ttggtctgat
900
tttccaagct gggctatgga gttactagta gagaaagcaa tcagcagtgc ttctagccct
960
cagagccctg gggatgcact gagaagagtt tttgaatgca tttcttcagg gattattctt
1020
aaaggtagtc ctggacttct ggatccttgt gaaaaggatc cctttgatac cttggcaaca
1080
atgactgacc agcagcgtga agacatcaca tccagtgcac agtttgcatt gagactcctt
1140
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1200
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<210> 5020
<211> 433
<212> PRT
<213> Homo sapiens

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20 25 30
Glu Gln His His Trp Asp Asp Arg Arg Arg Met Pro Asp Gly Gly Tyr
35 40 45
Pro His Gly Pro Pro Gly Pro Leu Gly Leu Leu Gly Val Arg Pro Gly
50 55 60
Met Pro Pro Gln Pro Gln Gly Pro Ala Pro Leu Arg Arg Pro Asp Ser
65 70 75 80
Ser Asp Asp Arg Tyr Val Met Thr Lys His Ala Thr Ile Tyr Pro Thr
85 90 95
Glu Glu Glu Leu Gln Ala Val Gln Lys Ile Val Ser Ile Thr Glu Arg
100 105 110
Ala Leu Lys Leu Val Ser Asp Ser Leu Ser Glu His Glu Lys Asn Lys
115 120 125
Asn Lys Glu Gly Asp Asp Lys Lys Glu Gly Gly Lys Asp Arg Ala Leu
130 135 140
Lys Gly Val Leu Arg Val Gly Val Phe Ala Lys Gly Leu Leu Leu Arg
145 150 155 160
Gly Asp Arg Asn Val Asn Leu Val Leu Leu Cys Ser Glu Lys Pro Ser
165 170 175
Lys Thr Leu Leu Ser Arg Ile Ala Glu Asn Leu Pro Lys Gln Leu Ala
180 185 190
Phe Ile Ser Pro Glu Lys Tyr Asp Ile Lys Cys Ala Val Ser Glu Ala
195 200 205
Ala Ile Ile Leu Asn Ser Cys Val Glu Pro Lys Met Gln Val Thr Ile
210 215 220
Thr Leu Thr Ser Pro Ile Ile Arg Glu Glu Asn Met Arg Glu Gly Asp
225 230 235 240
Val Thr Ser Gly Met Val Lys Asp Pro Pro Asp Val Leu Asp Arg Gln
245 250 255
Lys Cys Leu Asp Ala Leu Ala Ala Leu Arg His Ala Lys Trp Phe Gln
260 265 270
Ala Arg Ala Asn Gly Leu Gln Ser Cys Val Ile Ile Ile Arg Ile Leu

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        275                 280                 285
Arg Asp Leu Cys Gln Arg Val Pro Thr Trp Ser Asp Phe Pro Ser Trp
    290                 295                 300
Ala Met Glu Leu Leu Val Glu Lys Ala Ile Ser Ser Ala Ser Ser Pro
305                 310                 315                 320
Gln Ser Pro Gly Asp Ala Leu Arg Arg Val Phe Glu Cys Ile Ser Ser
                325                 330                 335
Gly Ile Ile Leu Lys Gly Ser Pro Gly Leu Leu Asp Pro Cys Glu Lys
            340                 345                 350
Asp Pro Phe Asp Thr Leu Ala Thr Met Thr Asp Gln Gln Arg Glu Asp
        355                 360                 365
Ile Thr Ser Ser Ala Gln Phe Ala Leu Arg Leu Leu Ala Phe Arg Gln
    370                 375                 380
Ile His Lys Val Leu Gly Met Asp Pro Leu Pro Gln Met Ser Gln Arg
385                 390                 395                 400
Phe Asn Ile His Asn Asn Arg Lys Arg Arg Arg Asp Ser Asp Gly Val
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Phe
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<210> 5021
<211> 494
<212> DNA
<213> Homo sapiens

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120
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240
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300
gagcctgtct ataattggag aacggtaatt aacagtgctg cggacttcta ttttgaagga
360
aatattcatc aatctctgca gaacataact gaaaaccagc tggtacaacc cactattctc
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480
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494

<210> 5022
<211> 124
<212> PRT
<213> Homo sapiens

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            20                  25                  30
Asp Tyr Lys Asn Tyr Leu Ala Leu Ile Asn His Arg Pro His Val Lys
        35                  40                  45
Gly Asn Ser Ser Cys Tyr Gly Val Leu Pro Thr Glu Glu Pro Val Tyr
    50                  55                  60
Asn Trp Arg Thr Val Ile Asn Ser Ala Ala Asp Phe Tyr Phe Glu Gly
65                  70                  75                  80
Asn Ile His Gln Ser Leu Gln Asn Ile Thr Glu Asn Gln Leu Val Gln
                85                  90                  95
Pro Thr Ile Leu Gln Gln Lys Gly Gly Lys Gly Arg Lys Lys Leu Arg
            100                 105                 110
Leu Phe Glu Tyr Leu His Glu Ser Leu Cys Asn Pro
        115                 120
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<210> 5023
<211> 3482
<212> DNA
<213> Homo sapiens

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120
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240
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300
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420
aagacaaatt ttggaatttt attttctaca agttcatttt catctttggt gtgctgaatg
480
tccagacagt ggaagaggtg gtcatgtggt gcctctggtt tgccggactt gtctttctgc
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<210> 5024
<211> 323
<212> PRT
<213> Homo sapiens

<400> 5024
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Gln Ala Arg Lys Arg Phe Leu Asn Lys Ser Ser Glu Asp Asp Ala Ala
20 25 30
Ser Glu Ser Phe Leu Pro Ser Glu Gly Ala Ser Ser Asp Pro Val Thr
35 40 45
Leu Arg Arg Arg Met Leu Ala Ala Ala Arg Asn Gly Gly Phe Arg Ser
50 55 60
Ser Arg Pro Pro Ser Ala Pro Leu Pro Ser Ser Ala Ala Ser Cys Ala
65 70 75 80
Leu Cys Pro Thr Asp Trp Arg Arg Pro Val Pro Ile Leu Pro Leu His
85 90 95
Gly Lys Ala Gly Leu Thr Ala Leu Pro Leu Tyr Lys Ala Cys Gly Leu
100 105 110
Ile Val Phe Gly Gln Leu Ile Asn Leu Ile Leu Leu Cys Asn Thr Phe

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        115                 120                 125
Asn Val Thr Phe Leu Phe Pro Leu Glu Thr Leu Gln Ile Leu Thr Val
    130                 135                 140
Gly Met Ile Ser Ser Gly Val Asp Trp Thr Ala Trp Gly Gly Gly Arg
145                 150                 155                 160
Ser Gly Gly Ser Glu Xaa Val Ala Cys Leu Gln Gln Ala Ala Ser Thr
                165                 170                 175
Pro Ala Ser Cys Ile Arg Pro Thr Asn Ala Gly Val Leu Ser Thr Thr
            180                 185                 190
Pro Ser Gly Lys Ser Val Gly Glu Ala His Ser Val Ser Pro Pro Pro
        195                 200                 205
Arg Arg Gly Val Thr Ser Val Ile Lys Leu Leu Ser Leu Leu Trp Lys
    210                 215                 220
His Val Asp Cys Ala Arg Ala Arg Pro Thr Gly Ser Cys Thr Pro Glu
225                 230                 235                 240
Gln Gln Gly Ile Leu Glu Lys Glu Leu Leu Val Arg Tyr Leu Glu Gln
                245                 250                 255
Arg Arg Gly Lys Ser Arg Ala Ile Gly Cys Asp Glu Val Thr Pro Phe
            260                 265                 270
Cys Pro Thr Thr Ser Gly Thr Asp Phe Pro Ser Leu Gln Ser Lys Ala
        275                 280                 285
Gly Leu Ile Ser Val Asn Ser Gly Ala Pro Ala Ser His Glu Cys Ala
    290                 295                 300
Pro Trp Val Pro Ser Pro Leu Ser Ile Ser Leu Ser Arg Leu Asp Leu
305                 310                 315                 320
Gly Ser Gly
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<210> 5025
<211> 2596
<212> DNA
<213> Homo sapiens

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<210> 5026
<211> 136
<212> PRT
<213> Homo sapiens

<400> 5026
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Leu Leu Phe Cys Lys Arg His Arg Ser Leu Val Arg Gln Glu His Pro
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Arg Leu Asp Asn Arg Gly Ala Thr Lys Ile Leu Ala Asp Trp Trp Ala
        35   40   45
Val Leu Asp Pro Lys Glu Lys Gln Lys Tyr Thr Asp Met Ala Lys Glu
    50   55   60
Tyr Lys Asp Ala Phe Met Lys Ala Asn Pro Gly Tyr Lys Trp Cys Pro
65   70   75   80
Thr Thr Asn Lys Pro Val Lys Ser Pro His Pro Leu Ser Ile His Glu
                85   90   95
Arg Asn Phe Gly Pro Ser His Leu Thr Leu Gln Glu Thr Cys Gln Ala
            100   105   110
Pro Arg Lys Gln Arg Leu Lys Lys Cys Leu Ser Leu Thr Leu Glu Trp
        115   120   125
Leu Ile Leu Leu Lys Trp Glu Ala
    130   135

<210> 5027
<211> 359
<212> DNA
<213> Homo sapiens

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120
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240

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359

<210> 5028
<211> 68
<212> PRT
<213> Homo sapiens

<400> 5028
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Gln Gly Gln Gln Gln Arg Ala Gln Arg Gly His Gly Gly Ser Ala Gly
20 25 30
Lys Thr His Lys Phe Ser Ala Gly Thr Tyr Pro Arg Leu Glu Glu Tyr
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Arg Arg Gly Ile Leu Gly Asp Trp Ser Asn Ala Ile Ser Ala Leu Tyr
50 55 60
Cys Arg Cys Ser
65

<210> 5029
<211> 1440
<212> DNA
<213> Homo sapiens

<400> 5029
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840
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900
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960
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caaggcaagt tcattgctct cttttatact gttgttacac ctagtcttaa ccctctaatc
1080
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1140
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1200
ctgttcattt atcaaccatt cttttattca ctcactctgt tagcacttgc tgagcatgta
1260
ctctaacaaa gtcgtggaga tcctggtaac aggtaggaat aaaacacatt cagcttaaat
1320
accattcact tttggagaaa acagctgtgt aaaatcaaga taaaacatct atagtgatgt
1380
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1440

<210> 5030
<211> 188
<212> PRT
<213> Homo sapiens

<400> 5030
Met Asn Asp Asp Gly Lys Val Asn Ala Ser Ser Glu Gly Tyr Phe Ile
1 5 10 15
Leu Val Gly Phe Ser Asn Trp Pro Tyr Leu Glu Val Val Leu Phe Val
20 25 30
Val Ile Leu Ile Phe Cys Leu Met Thr Leu Ile Gly Asn Leu Phe Ile
35 40 45
Ile Ile Leu Thr Tyr Leu Asp Ser His Leu His Thr Pro Leu Tyr Phe
50 55 60
Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser
65 70 75 80
Ile Pro Gln Leu Leu Val Ser Leu Trp Gly Val Glu Lys Thr Ile Ser
85 90 95
Tyr Ala Gly Cys Met Val Gln Leu Tyr Phe Phe Leu Thr Leu Gly Thr
100 105 110
Thr Glu Cys Val Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Ala
115 120 125
Val Cys Arg Pro Leu His Tyr Thr Val Leu Met His Ser Arg Phe Cys
130 135 140
His Leu Leu Ala Val Ala Ser Trp Val Ser Gly Phe Thr Asn Pro Ala
145 150 155 160
Leu His Ser Ser Phe Thr Phe Trp Val Pro Leu Cys Gly His Arg Gln
165 170 175
Ile Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu
180 185

<210> 5031
<211> 505
<212> DNA
<213> Homo sapiens

<400> 5031
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gaatggggtg gaccgacgtt ccctgcagcg ttcagcaagg ctggctctag aagtgctgga
120
gagggccaag aggagggcgg tggactggca tgccctggag cgtcccaaag gctgcatggg
180
ggtccttgcc cgggaggcgc cccacctaga gaaacagccg gcagccggcc cgcagcgcgt
240
tctcccggga gagagagaag agagaccccc aacccttagt gcttccttca gaacaatggc
300
tgaattcatg gactatactt caagtcagtg tgggaaatat tattcatctg tgccagagga
360
aggaggggca acccatgtct atcgttatca cagaggcgag tcgaagctgc acatgtgctt
420
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480
ctatcaaata tcagagcatg ctcca
505

<210> 5032
<211> 158
<212> PRT
<213> Homo sapiens

<400> 5032
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Ser Leu Gln Arg Ser Ala Arg Leu Ala Leu Glu Val Leu Glu Arg Ala
            20   25   30
Lys Arg Arg Ala Val Asp Trp His Ala Leu Glu Arg Pro Lys Gly Cys
        35   40   45
Met Gly Val Leu Ala Arg Glu Ala Pro His Leu Glu Lys Gln Pro Ala
    50   55   60
Ala Gly Pro Gln Arg Val Leu Pro Gly Glu Arg Glu Glu Arg Pro Pro
65   70   75   80
Thr Leu Ser Ala Ser Phe Arg Thr Met Ala Glu Phe Met Asp Tyr Thr
                85   90   95
Ser Ser Gln Cys Gly Lys Tyr Tyr Ser Ser Val Pro Glu Glu Gly Gly
            100   105   110
Ala Thr His Val Tyr Arg Tyr His Arg Gly Glu Ser Lys Leu His Met
        115   120   125
Cys Leu Asp Ile Gly Asn Gly Gln Arg Lys Asp Arg Lys Lys Thr Ser
    130   135   140
Leu Gly Pro Gly Gly Ser Tyr Gln Ile Ser Glu His Ala Pro
145   150   155

<210> 5033
<211> 2888

<212> DNA
<213> Homo sapiens

<400> 5033
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120
tcccactgca gcgtctgtga caactgtgta gaggtgactg ggaagttccg cgggggtgtg
180
aacccctttca cccgaggctg ctgtgggaat gtggagcacg tgctgtgtag ccccctggcg
240
ccccggtacg tggtggagcc accccggctg ccgctcgcgg tgagtttgaa gccgcctttc
300
cttaggcctg aactcctgga ccgagctgca ccgctcaagg tcaagcttag tgacaacggg
360
ctgaaggctg gcctgggccg tagcaagtcc aagggcagcc tggaccggct ggatgagaag
420
ccactggact tggggccacc actgcccccc aagatagagg ctggcacgtt cagcagtgac
480
ctgcagaccc cgcgcccagg cagtgctgag agtgccctgt cggtgcagag gaccagcccc
540
ccgacacctg ccatgtacaa gtttaggccg gctttcccca cgggtcccaa ggtgcccttc
600
tgtggaccag gcgagcaggt tccaggccct gattccctga ccctggggga cgacaacatc
660
cgtagcctgg actttgtgtc cgagccgagc ctggacctcc ctgactatgg gccagggggc
720
ctgcatgcag cctacccgcc atccccaccg ctcagcgcct ctgatgcctt ctcgggcgct
780
ttgcgctccc tgagcctcaa ggcctcgagc cggcggggcg gggatcatgt ggccctgcag
840
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900
ctgcccaacc gcaacggcag cctgtcctat gacagcctgc tcaatcctgg ctcgcctggt
960
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1080
ggcccccgcc cccgggagcc ctcgcctgtg cgctacgaca acctgtccag gaccatcatg
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1200
gactcactct tcggcgactc aggcgtctat gacgctccca gctcctacag cctgcagcag
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gccagtgtgc tgtccgaggg cccccgaggt cccgcgctgc gctatggctc cagagacgac
1320
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1380
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1440
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1500

acgccagggc ctgccctccc cgcccggcac tccccactca ccatcctacg cgggccccaa
1560
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1620
ggaccaccct cagctgaaga ctcccccaag taagcttaat gggcagtccc cgggcctggc
1680
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1740
ggttaagaag gtgtccggcg tgggtgggac cacctacgag atctcggtgt gaggactgac
1800
tgccacacat ccgccatggt gccacgggga ccaggacccc gcagcgcacc ccccctcccc
1860
accaacttct ctgccccagg gacccgaggc caccccagcc tggtgtggac ccatcggcgg
1920
gagagagtgc cacgcctcca cagcttgccc caagcgctct gcctgcccgt ccactcatct
1980
gcccatgggg aagtcggctc actgggacaa gggccactgg gctggtctgt gtctgggcct
2040
gtcccatggc tggggcagtg agggggccca gtcagcctct ttggggcacc ctctctcagc
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2160
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2220
tgacacagcc tgtgggctcc cggaccgagt gtcccccgcc aggctactcc taactaacgc
2280
gttgcctttc acggaccccg ctggaagctt gtagcttggc aaggctgatg cttctgccct
2340
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2400
gggcccggct ccatgtgtcc cgtgtctgtg tgctgtgctg ccgcgccgtg tctgatgtgt
2460
cagtgctccg gccgccgctg tcccctttcat caaagcctta acctttgctt tatgctcttg
2520
tgggaggcga cgggggggca ggcgggagca ggcacggggg tgatgctgcc acaggggget
2580
ggtgacaccc agagcccccct ccccagccct caggccctcc ctgccaaact ggagaacccc
2640
accccaaggc atgccacgtc cgcagccccg gcctggctgc ggtgctcgcg ccgtgggaaa
2700
gcacactggg gaggggtcag tgcttccctt ggtgtcaggg acctgagagt aagcacatga
2760
cagcgtctgc ttgcgttgtg tctgttttat gtttttatat ctacatctat atatctataa
2820
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2880
aaaaaaaa
2888

<210> 5034
<211> 550
<212> PRT
<213> Homo sapiens

<400> 5034
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Val Asp Val Arg Gly Ile Gln Val Arg Met Lys Trp Cys Ala Thr Cys
20 25 30
His Phe Tyr Arg Pro Pro Arg Cys Ser His Cys Ser Val Cys Asp Asn
35 40 45
Cys Val Glu Val Thr Gly Lys Phe Arg Gly Gly Val Asn Pro Phe Thr
50 55 60
Arg Gly Cys Cys Gly Asn Val Glu His Val Leu Cys Ser Pro Leu Ala
65 70 75 80
Pro Arg Tyr Val Val Glu Pro Pro Arg Leu Pro Leu Ala Val Ser Leu
85 90 95
Lys Pro Pro Phe Leu Arg Pro Glu Leu Leu Asp Arg Ala Ala Pro Leu
100 105 110
Lys Val Lys Leu Ser Asp Asn Gly Leu Lys Ala Gly Leu Gly Arg Ser
115 120 125
Lys Ser Lys Gly Ser Leu Asp Arg Leu Asp Glu Lys Pro Leu Asp Leu
130 135 140
Gly Pro Pro Leu Pro Pro Lys Ile Glu Ala Gly Thr Phe Ser Ser Asp
145 150 155 160
Leu Gln Thr Pro Arg Pro Gly Ser Ala Glu Ser Ala Leu Ser Val Gln
165 170 175
Arg Thr Ser Pro Pro Thr Pro Ala Met Tyr Lys Phe Arg Pro Ala Phe
180 185 190
Pro Thr Gly Pro Lys Val Pro Phe Cys Gly Pro Gly Glu Gln Val Pro
195 200 205
Gly Pro Asp Ser Leu Thr Leu Gly Asp Asp Asn Ile Arg Ser Leu Asp
210 215 220
Phe Val Ser Glu Pro Ser Leu Asp Leu Pro Asp Tyr Gly Pro Gly Gly
225 230 235 240
Leu His Ala Ala Tyr Pro Pro Ser Pro Pro Leu Ser Ala Ser Asp Ala
245 250 255
Phe Ser Gly Ala Leu Arg Ser Leu Ser Leu Lys Ala Ser Ser Arg Arg
260 265 270
Gly Gly Asp His Val Ala Leu Gln Pro Leu Arg Ser Glu Gly Gly Pro
275 280 285
Pro Thr Pro His Arg Ser Ile Phe Ala Pro His Ala Leu Pro Asn Arg
290 295 300
Asn Gly Ser Leu Ser Tyr Asp Ser Leu Leu Asn Pro Gly Ser Pro Gly
305 310 315 320
Gly His Ala Cys Pro Ala His Pro Ala Val Gly Val Ala Gly Tyr His
325 330 335
Ser Pro Tyr Leu His Pro Gly Ala Thr Gly Asp Pro Pro Arg Pro Leu
340 345 350
Pro Arg Ser Phe Ser Pro Val Leu Gly Pro Arg Pro Arg Glu Pro Ser
355 360 365
Pro Val Arg Tyr Asp Asn Leu Ser Arg Thr Ile Met Ala Ser Ile Gln
370 375 380
Glu Arg Lys Asp Arg Glu Glu Arg Glu Arg Leu Leu Arg Ser Gln Ala
385 390 395 400
Asp Ser Leu Phe Gly Asp Ser Gly Val Tyr Asp Ala Pro Ser Ser Tyr
405 410 415
Ser Leu Gln Gln Ala Ser Val Leu Ser Glu Gly Pro Arg Gly Pro Ala

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            420                 425                 430
Leu Arg Tyr Gly Ser Arg Asp Asp Leu Val Ala Gly Pro Gly Phe Gly
        435                 440                 445
Gly Ala Arg Asn Pro Ala Leu Gln Thr Ser Leu Ser Ser Leu Ser Ser
    450                 455                 460
Ser Val Ser Arg Ala Pro Arg Thr Ser Ser Ser Ser Leu Gln Ala Asp
465                 470                 475                 480
Gln Ala Ser Ser Asn Ala Pro Gly Ala Pro Ala Gln Gln Trp Leu Thr
                485                 490                 495
Gln Val Thr Cys Thr Pro Gly Pro Ala Leu Pro Ala Arg His Ser Pro
            500                 505                 510
Leu Thr Ile Leu Arg Gly Pro Gln Ser Cys Arg Leu His Pro His Gly
        515                 520                 525
Pro Pro Arg Ala Thr Ala Leu Ala Asp Arg Ala Glu Gly Pro Pro Ser
    530                 535                 540
Ala Glu Asp Ser Pro Lys
545                 550
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<210> 5035
<211> 2002
<212> DNA
<213> Homo sapiens

<400> 5035
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120
cttgatgccc actttgaaaa ccttctggcc cgggcagaca gcaccaagaa ctggacagag
180
aagatcttga ggcagacaga ggtgctgctg cagcccaacc ccagtgcccg agtggaggag
240
ttcctgtatg agaagctgga caggaaggtc ccctcaaggg tcaccaacgg ggagctgctg
300
gctcagtaca tggcagacgc ggccagtgag ctggggccga ccacccccta tgggaagaca
360
ctgatcaagg tggcagaagc tgaaaagcaa ctgggagccg cggagaggga ttttatccac
420
acggcctcca tcagcttcct cacacccttg cgcaacttcc tggaggggga ctggaagacc
480
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aggctgaaga aggccaaggc tgcagaagcc aaagccacgc tctggaatga tgaagtggac
600
aaggccgagc aggagctccg cgtggcccag acagagtttg accggcaagc agaagtgacc
660
cgtctcttgc tggagggaat cagtagcact cacgtgaacc acctgcgctg cctccacgag
720
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780
aagcagctgg gcagctccca gggtgccata tcccggcacc ttcgtgggca ccacagagcc
840
cgcctcccac ccctgagcag cacctcaccc accactgctg cggccactat gcctgtggtg
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ccctctgtgg ccagcctggc ccctccgggg gaggcctcgc tctgcctgga agaggtggcc
960
ccccctgcca gtgggacccg caaagctcgg gtgctctatg actacgaggc agccgacagc
1020
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1080
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1140
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1260
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1320
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1380
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1500
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aggcacacag ggctctggca gcccctgggg actgggcgct gcccctggga ggggagagcc
1620
tggccagggc tggtgttggg cccggagcag catcttccgg tgctatcctc ccctcccacc
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1740
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1800
agcgcaaagc tcgggtgctc tatgactacg aggcagccga cagcagtgag ctggccctgc
1860
tggctgatga gctcatcact gtctacagcc tgcctggcat ggaccctgac tggctcattg
1920
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1980
caggtgcccc catccccccc gc
2002

<210> 5036
<211> 384
<212> PRT
<213> Homo sapiens

<400> 5036
Arg Pro Cys Gly His Ala Met Asp Phe Asn Met Lys Lys Leu Ala Ser
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Asp Ala Gly Ile Phe Phe Thr Arg Ala Val Gln Phe Thr Glu Glu Lys
20 25 30
Phe Gly Gln Ala Glu Lys Thr Glu Leu Asp Ala His Phe Glu Asn Leu
35 40 45
Leu Ala Arg Ala Asp Ser Thr Lys Asn Trp Thr Glu Lys Ile Leu Arg
50 55 60
Gln Thr Glu Val Leu Leu Gln Pro Asn Pro Ser Ala Arg Val Glu Glu

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65                  70                  75                  80
Phe Leu Tyr Glu Lys Leu Asp Arg Lys Val Pro Ser Arg Val Thr Asn
                85                  90                  95
Gly Glu Leu Leu Ala Gln Tyr Met Ala Asp Ala Ala Ser Glu Leu Gly
            100                 105                 110
Pro Thr Thr Pro Tyr Gly Lys Thr Leu Ile Lys Val Ala Glu Ala Glu
        115                 120                 125
Lys Gln Leu Gly Ala Ala Glu Arg Asp Phe Ile His Thr Ala Ser Ile
    130                 135                 140
Ser Phe Leu Thr Pro Leu Arg Asn Phe Leu Glu Gly Asp Trp Lys Thr
145                 150                 155                 160
Ile Ser Lys Glu Ser Arg Leu Leu Gln Asn Arg Arg Leu Asp Leu Asp
                165                 170                 175
Ala Cys Lys Ala Arg Leu Lys Lys Ala Lys Ala Ala Glu Ala Lys Ala
            180                 185                 190
Thr Leu Trp Asn Asp Glu Val Asp Lys Ala Glu Gln Glu Leu Arg Val
        195                 200                 205
Ala Gln Thr Glu Phe Asp Arg Gln Ala Glu Val Thr Arg Leu Leu Leu
    210                 215                 220
Glu Gly Ile Ser Ser Thr His Val Asn His Leu Arg Cys Leu His Glu
225                 230                 235                 240
Phe Val Lys Ser Gln Thr Thr Tyr Tyr Ala Gln Cys Tyr Arg His Met
                245                 250                 255
Leu Asp Leu Gln Lys Gln Leu Gly Ser Ser Gln Gly Ala Ile Ser Arg
            260                 265                 270
His Leu Arg Gly His His Arg Ala Arg Leu Pro Pro Leu Ser Ser Thr
        275                 280                 285
Ser Pro Thr Thr Ala Ala Ala Thr Met Pro Val Val Pro Ser Val Ala
    290                 295                 300
Ser Leu Ala Pro Pro Gly Glu Ala Ser Leu Cys Leu Glu Glu Val Ala
305                 310                 315                 320
Pro Pro Ala Ser Gly Thr Arg Lys Ala Arg Val Leu Tyr Asp Tyr Glu
                325                 330                 335
Ala Ala Asp Ser Ser Glu Leu Ala Leu Leu Ala Asp Glu Leu Ile Thr
            340                 345                 350
Val Tyr Ser Leu Pro Gly Met Asp Pro Asp Trp Leu Ile Gly Glu Arg
        355                 360                 365
Gly Asn Lys Lys Gly Lys Val Pro Val Thr Tyr Leu Glu Leu Leu Ser
    370                 375                 380
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<210> 5037
<211> 2102
<212> DNA
<213> Homo sapiens

<400> 5037
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agtcttcagg ttttctttag aaaacttgaa gatctggcca cagctggcat cctggcagcg
120
gtttgctgga gttgagggtc agccgtccct ctgcagggtg ggtcaccctc ctgttaacca
180
cgccctgccc cgccccgctt cctccctctc gtgcgtcatc aagcatttgc tgttgttttc
240

ctcatagtag tgataagaga aaagtgaaat atctttgtct ccctgtctct gtcaaaagtg
300
ggaaaacgca agatagacca ggagggccgt gtgtttcaag aaaagtggga gagagcgtat
360
ttcttcgtgg aagtacagaa tattccaaca tgtctcatat gcaaacaaag catgtctgtg
420
tccaaagaat ataacctaag acgccactat caaaccaatc acagcaagca ttatgaccag
480
tatacggaaa gaatgcgtga cgagaagctt cacgagctga aaaaagggct caggaagtat
540
ctcttaggct catcagacac cgagtgtccc gagcaaaaac aagtgtttgc aaacccaagt
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ccaacccaga aatcccccgt gcagcctgta gaggacctag ctgggaactt atgggagaag
660
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720
ataaataata ccacccagtt ggccatattc atccgtggtg tcgatgagaa tttcgatgtg
780
tccgaagaac ttctggacac ggtgcccatg acgggtacaa aatctggcaa cgagatcttt
840
tcgcgtgttg agaagagcct gaaaaagttc tgtatcgact ggtcgaaatt agtaagcgtg
900
gcctccactg gcaccccagc gatggtggat gccaataacg ggcttgtcac aaaactgaag
960
tccagggtgg cgacgttctg caagggtgcg gaactgaagt ccatctgttg tataattcat
1020
ccggaatcac tctgtgctca gaagttgaag atggaccacg tcatggacgt ggtagtgaag
1080
tccgtgaact ggatatgctc ccggggactg aaccacagcg agttcacaac cttgctctat
1140
gagctggaca gccagtatgg tagcctcctg tactacacgg agattaagtg gctcagtcgc
1200
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1320
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1380
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1620
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1740
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1800
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1860

aaggattccc agtgggattc tgtactccac atcgcaacgt gatggagaga aaactcctgg
1920
cagggcccta tggtgggaaa ggctggagtc ttctagtccc aagggattgg gagatgacaa
1980
aatgaatttt ttttttcttt ttgagatgga gtcttgctct gtcgcccagg ttggagtgca
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2100
ca
2102

<210> 5038
<211> 533
<212> PRT
<213> Homo sapiens

<400> 5038
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Glu Arg Ala Tyr Phe Phe Val Glu Val Gln Asn Ile Pro Thr Cys Leu
20 25 30
Ile Cys Lys Gln Ser Met Ser Val Ser Lys Glu Tyr Asn Leu Arg Arg
35 40 45
His Tyr Gln Thr Asn His Ser Lys His Tyr Asp Gln Tyr Thr Glu Arg
50 55 60
Met Arg Asp Glu Lys Leu His Glu Leu Lys Lys Gly Leu Arg Lys Tyr
65 70 75 80
Leu Leu Gly Ser Ser Asp Thr Glu Cys Pro Glu Gln Lys Gln Val Phe
85 90 95
Ala Asn Pro Ser Pro Thr Gln Lys Ser Pro Val Gln Pro Val Glu Asp
100 105 110
Leu Ala Gly Asn Leu Trp Glu Lys Leu Arg Glu Lys Ile Arg Ser Phe
115 120 125
Val Ala Tyr Ser Ile Ala Ile Asp Glu Ile Thr Asp Ile Asn Asn Thr
130 135 140
Thr Gln Leu Ala Ile Phe Ile Arg Gly Val Asp Glu Asn Phe Asp Val
145 150 155 160
Ser Glu Glu Leu Leu Asp Thr Val Pro Met Thr Gly Thr Lys Ser Gly
165 170 175
Asn Glu Ile Phe Ser Arg Val Glu Lys Ser Leu Lys Lys Phe Cys Ile
180 185 190
Asp Trp Ser Lys Leu Val Ser Val Ala Ser Thr Gly Thr Pro Ala Met
195 200 205
Val Asp Ala Asn Asn Gly Leu Val Thr Lys Leu Lys Ser Arg Val Ala
210 215 220
Thr Phe Cys Lys Gly Ala Glu Leu Lys Ser Ile Cys Cys Ile Ile His
225 230 235 240
Pro Glu Ser Leu Cys Ala Gln Lys Leu Lys Met Asp His Val Met Asp
245 250 255
Val Val Val Lys Ser Val Asn Trp Ile Cys Ser Arg Gly Leu Asn His
260 265 270
Ser Glu Phe Thr Thr Leu Leu Tyr Glu Leu Asp Ser Gln Tyr Gly Ser
275 280 285
Leu Leu Tyr Tyr Thr Glu Ile Lys Trp Leu Ser Arg Gly Leu Val Leu

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    290                 295                 300
Lys Arg Phe Phe Glu Ser Leu Glu Glu Ile Asp Ser Phe Met Ser Ser
305                 310                 315                 320
Arg Gly Lys Pro Leu Pro Gln Leu Ser Ser Ile Asp Trp Ile Arg Asp
                325                 330                 335
Leu Ala Phe Leu Val Asp Met Thr Met His Leu Asn Ala Leu Asn Ile
            340                 345                 350
Ser Leu Gln Gly His Ser Gln Ile Val Thr Gln Met Tyr Asp Leu Ile
        355                 360                 365
Arg Ala Phe Leu Ala Lys Leu Cys Leu Trp Glu Thr His Leu Thr Arg
    370                 375                 380
Asn Asn Leu Ala His Phe Pro Thr Leu Lys Leu Ala Ser Arg Asn Glu
385                 390                 395                 400
Ser Asp Gly Leu Asn Tyr Ile Pro Lys Ile Ala Glu Leu Lys Thr Glu
                405                 410                 415
Phe Gln Lys Arg Leu Ser Asp Phe Lys Leu Tyr Glu Ser Glu Leu Thr
            420                 425                 430
Leu Phe Ser Ser Pro Phe Ser Thr Lys Ile Asp Ser Val His Glu Glu
        435                 440                 445
Leu Gln Met Glu Val Ile Asp Leu Gln Cys Asn Thr Val Leu Lys Thr
    450                 455                 460
Lys Tyr Asp Lys Val Gly Ile Pro Glu Phe Tyr Lys Tyr Leu Trp Gly
465                 470                 475                 480
Ser Tyr Pro Lys Tyr Lys His His Cys Ala Lys Ile Leu Ser Met Phe
                485                 490                 495
Gly Ser Thr Tyr Ile Cys Glu Gln Leu Phe Ser Ile Met Lys Leu Ser
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Lys Thr Lys Tyr Cys Ser Gln Leu Lys Asp Ser Gln Trp Asp Ser Val
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Leu His Ile Ala Thr
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<210> 5039
<211> 3059
<212> DNA
<213> Homo sapiens

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300
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420
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2100

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3059

<210> 5040
<211> 616
<212> PRT
<213> Homo sapiens

<400> 5040
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Tyr Leu Gly Ser Gly Gly Trp Arg Phe Ile Arg Val Phe Ile Lys Thr
35 40 45
Ile Arg Arg Asp Ile Phe Gly Gly Leu Val Leu Leu Lys Val Lys Ala
50 55 60
Lys Val Arg Gln Cys Leu Gln Glu Arg Arg Thr Val Pro Ile Leu Phe
65 70 75 80
Ala Ser Thr Val Arg Arg His Pro Asp Lys Thr Ala Leu Ile Phe Glu
85 90 95
Gly Thr Asp Thr His Trp Thr Phe Arg Gln Leu Asp Glu Tyr Ser Ser
100 105 110
Ser Val Ala Asn Phe Leu Gln Ala Arg Gly Leu Ala Ser Gly Asp Val

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        115                 120                 125
Ala Ala Ile Phe Met Glu Asn Arg Asn Glu Phe Val Gly Leu Trp Leu
    130                 135                 140
Gly Met Ala Lys Leu Gly Val Glu Ala Ala Leu Ile Asn Thr Asn Leu
145                 150                 155                 160
Arg Arg Asp Ala Leu Leu His Cys Leu Thr Thr Ser Arg Ala Arg Ala
                165                 170                 175
Leu Val Phe Gly Ser Glu Met Ala Ser Ala Ile Cys Glu Val His Ala
            180                 185                 190
Ser Pro Asp Pro Ser Leu Ser Leu Phe Cys Ser Gly Ser Trp Glu Pro
        195                 200                 205
Gly Ala Val Pro Pro Ser Thr Glu His Leu Asp Pro Leu Leu Lys Asp
    210                 215                 220
Ala Pro Lys His Leu Pro Ser Cys Pro Asp Lys Gly Phe Thr Asp Lys
225                 230                 235                 240
Leu Phe Tyr Ile Tyr Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala Ala
                245                 250                 255
Ile Val Val His Ser Arg Tyr Tyr Arg Met Ala Ala Leu Val Tyr Tyr
            260                 265                 270
Gly Phe Arg Met Arg Pro Asn Asp Ile Val Tyr Asp Cys Leu Pro Leu
        275                 280                 285
Tyr His Ser Ala Gly Asn Ile Val Gly Ile Gly Gln Cys Leu Leu His
    290                 295                 300
Gly Met Thr Val Val Ile Arg Lys Lys Phe Ser Ala Ser Arg Phe Trp
305                 310                 315                 320
Asp Asp Cys Ile Lys Tyr Asn Cys Thr Ile Val Gln Tyr Ile Gly Glu
                325                 330                 335
Leu Cys Arg Tyr Leu Leu Asn Gln Pro Pro Arg Glu Ala Glu Asn Gln
            340                 345                 350
His Gln Val Arg Met Ala Leu Gly Asn Ala Ser Gly Ser Pro Ser Gly
        355                 360                 365
Pro Thr Phe Pro Ala Ala Ser Thr Tyr Pro Arg Trp Leu Ser Ser Thr
    370                 375                 380
Gly Pro Glu Cys Asn Cys Ser Leu Gly Asn Phe Asp Ser Gln Val Gly
385                 390                 395                 400
Ala Cys Gly Phe Asn Ser Arg Ile Leu Ser Phe Val Tyr Pro Ile Arg
                405                 410                 415
Leu Val Arg Val Asn Glu Asp Thr Met Glu Leu Ile Arg Gly Pro Asp
            420                 425                 430
Gly Val Cys Ile Pro Cys Gln Pro Gly Glu Pro Gly Gln Leu Val Gly
        435                 440                 445
Arg Ile Ile Gln Lys Asp Pro Leu Arg Arg Phe Asp Gly Tyr Leu Asn
    450                 455                 460
Gln Gly Ala Asn Asn Lys Lys Ile Ala Lys Asp Val Phe Lys Lys Gly
465                 470                 475                 480
Asp Gln Ala Tyr Leu Thr Gly Asp Val Leu Val Met Asp Glu Leu Gly
                485                 490                 495
Tyr Leu Tyr Phe Arg Asp Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly
            500                 505                 510
Glu Asn Val Ser Thr Thr Glu Val Glu Gly Thr Leu Ser Arg Leu Leu
        515                 520                 525
Asp Met Ala Asp Val Ala Val Tyr Gly Val Glu Val Pro Gly Thr Glu
    530                 535                 540
Gly Arg Ala Gly Met Ala Ala Val Ala Ser Pro Thr Gly Asn Cys Asp
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545                 550                 555                 560
Leu Glu Arg Phe Ala Gln Val Leu Glu Lys Glu Leu Pro Leu Tyr Ala
                565                 570                 575
Arg Pro Ile Phe Leu Arg Leu Leu Pro Glu Leu His Lys Thr Gly Thr
            580                 585                 590
Tyr Lys Phe Gln Lys Thr Glu Leu Arg Lys Glu Ala Phe Asp Pro Ala
        595                 600                 605
Ile Val Lys Thr Arg Cys Ser Ile
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<210> 5041
<211> 2461
<212> DNA
<213> Homo sapiens

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240
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360
cccgagtgcg agatcgagcg tcctgagcgc ctgaccgcag ccctggatcg cctgcggcag
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480
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c
2461

<210> 5042
<211> 686
<212> PRT
<213> Homo sapiens

<400> 5042
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Asp Pro Glu Cys Glu Ile Glu Arg Pro Glu Arg Leu Thr Ala Ala Leu
        35                  40                  45
Asp Arg Leu Arg Gln Arg Gly Leu Glu Gln Arg Cys Leu Arg Leu Ser
    50                  55                  60
Ala Arg Glu Ala Ser Glu Glu Glu Leu Gly Leu Val His Ser Pro Glu
65                  70                  75                  80
Tyr Val Ser Leu Val Arg Glu Thr Gln Val Leu Gly Lys Glu Glu Leu
                85                  90                  95
Gln Ala Leu Ser Gly Gln Phe Asp Ala Ile Tyr Phe His Pro Ser Thr
            100                 105                 110
Phe His Cys Ala Arg Leu Ala Ala Gly Ala Gly Leu Gln Leu Val Asp
        115                 120                 125
Ala Val Leu Thr Gly Ala Val Gln Asn Gly Leu Ala Leu Val Arg Pro
    130                 135                 140
Pro Gly His His Gly Gln Arg Ala Ala Ala Asn Gly Phe Cys Val Phe
145                 150                 155                 160
Asn Asn Val Ala Ile Ala Ala Ala His Ala Lys Gln Lys His Gly Leu
                165                 170                 175
His Arg Ile Leu Val Val Asp Trp Asp Val His His Gly Gln Gly Ile
            180                 185                 190
Gln Tyr Leu Phe Glu Asp Asp Pro Ser Val Leu Tyr Phe Ser Trp His
        195                 200                 205
Arg Tyr Glu His Gly Arg Phe Trp Pro Phe Leu Arg Glu Ser Asp Ala
    210                 215                 220
Asp Ala Val Gly Arg Gly Gln Gly Leu Gly Phe Thr Val Asn Leu Pro
225                 230                 235                 240
Trp Asn Gln Val Gly Met Gly Asn Ala Asp Tyr Val Ala Ala Phe Leu
                245                 250                 255
His Leu Leu Leu Pro Leu Ala Phe Glu Phe Asp Pro Glu Leu Val Leu
            260                 265                 270
Val Ser Ala Gly Phe Asp Ser Ala Ile Gly Asp Pro Glu Gly Gln Met
        275                 280                 285
Gln Ala Thr Pro Glu Cys Phe Ala His Leu Thr Gln Leu Leu Gln Val
    290                 295                 300
Leu Ala Gly Gly Arg Val Cys Ala Val Leu Glu Gly Gly Tyr His Leu
305                 310                 315                 320
Glu Ser Leu Ala Glu Ser Val Cys Met Thr Val Gln Thr Leu Leu Gly
                325                 330                 335
Asp Pro Ala Pro Pro Leu Ser Gly Pro Met Ala Pro Cys Gln Arg Cys
            340                 345                 350
Glu Gly Ser Ala Leu Glu Ser Ile Gln Ser Ala Arg Ala Ala Gln Ala
        355                 360                 365
Pro His Trp Lys Ser Leu Gln Gln Gln Asp Val Thr Ala Val Pro Met
    370                 375                 380
Ser Pro Ser Ser His Ser Pro Glu Gly Arg Pro Pro Pro Leu Leu Pro
385                 390                 395                 400
Gly Gly Pro Val Cys Lys Ala Ala Ala Ser Ala Pro Ser Ser Leu Leu
                405                 410                 415
Asp Gln Pro Cys Leu Cys Pro Ala Pro Ser Val Arg Thr Ala Val Ala
            420                 425                 430
Leu Thr Thr Pro Asp Ile Thr Leu Val Leu Pro Pro Asp Val Ile Gln
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        435                 440                 445
Gln Glu Ala Ser Ala Leu Arg Glu Glu Thr Glu Ala Trp Ala Arg Pro
    450                 455                 460
His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu
465                 470                 475                 480
Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile
                485                 490                 495
Ala Ala Thr Pro Ala Ser Ala Ala Ala Ala Thr Leu Asp Val Ala Val
            500                 505                 510
Arg Arg Gly Leu Ser His Gly Ala Gln Arg Leu Leu Cys Val Ala Leu
        515                 520                 525
Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu
    530                 535                 540
Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His
545                 550                 555                 560
Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile
                565                 570                 575
Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val
            580                 585                 590
Leu Val Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Ala Ala
        595                 600                 605
Leu Leu Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala
    610                 615                 620
Leu Leu Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg
625                 630                 635                 640
Val Leu Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala
                645                 650                 655
Ser Pro Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu
            660                 665                 670
Pro Gln Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala
        675                 680                 685
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<210> 5043
<211> 1824
<212> DNA
<213> Homo sapiens

<400> 5043
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240
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300
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360
aaaccactga gtaagcaaaa atcagaggaa gagctcaagg acaagaacca gctgttagaa
420
gccgtcaaca agcagttgca ccagaagttg actgaaactc agggagagct gaaggacctg
480

acccagaagg tagagctgct ggagaagttt cgggacaact gtttggcaat tttggagagc
540
aagggccttg atccagcttt aggcagtgag accctggcat cacgacaaga atccactact
600
gatcacatgg actctatgtt gctgttagaa actttgcaag aggagctgaa gctttttaac
660
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720
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1020
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1140
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1200
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1260
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1320
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1380
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1440
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1500
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1560
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1620
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1680
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1800
aaaatagttg aaatggcaaa cttt
1824

<210> 5044
<211> 273
<212> PRT
<213> Homo sapiens

<400> 5044
Ala Gly Gly Thr Thr Val Ala Ala Gly Asn Leu Leu Asn Glu Ser Glu

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            20                  25                  30
Leu Val Thr Met Thr Ser Val Val Lys Thr Val Tyr Ser Leu Gln Pro
        35                  40                  45
Pro Ser Ala Leu Ser Gly Gly Gln Pro Ala Asp Thr Gln Thr Arg Ala
    50                  55                  60
Thr Ser Lys Ser Leu Leu Pro Val Arg Ser Lys Glu Val Asp Val Ser
65                  70                  75                  80
Lys Gln Leu His Ser Gly Gly Pro Glu Asn Asp Val Thr Lys Ile Thr
                85                  90                  95
Lys Leu Arg Arg Glu Asn Gly Gln Met Lys Ala Thr Asp Thr Ala Thr
            100                 105                 110
Arg Arg Asn Val Arg Lys Gly Tyr Lys Pro Leu Ser Lys Gln Lys Ser
        115                 120                 125
Glu Glu Glu Leu Lys Asp Lys Asn Gln Leu Leu Glu Ala Val Asn Lys
    130                 135                 140
Gln Leu His Gln Lys Leu Thr Glu Thr Gln Gly Glu Leu Lys Asp Leu
145                 150                 155                 160
Thr Gln Lys Val Glu Leu Leu Glu Lys Phe Arg Asp Asn Cys Leu Ala
                165                 170                 175
Ile Leu Glu Ser Lys Gly Leu Asp Pro Ala Leu Gly Ser Glu Thr Leu
            180                 185                 190
Ala Ser Arg Gln Glu Ser Thr Thr Asp His Met Asp Ser Met Leu Leu
        195                 200                 205
Leu Glu Thr Leu Gln Glu Glu Leu Lys Leu Phe Asn Glu Thr Ala Lys
    210                 215                 220
Lys Gln Met Glu Glu Leu Gln Ala Leu Lys Val Lys Leu Glu Met Lys
225                 230                 235                 240
Glu Glu Arg Val Arg Phe Leu Glu Gln Gln Thr Leu Cys Asn Asn Gln
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Val Asn Asp Leu Thr Thr Ala Leu Lys Glu Met Glu Gln Leu Leu Glu
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Met
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<210> 5045
<211> 462
<212> DNA
<213> Homo sapiens

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360

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462

<210> 5046
<211> 92
<212> PRT
<213> Homo sapiens

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            20   25   30
Ser Leu Arg Leu Thr Ala Pro Ser Leu Trp Gly Gly Ser Val Ala Arg
        35   40   45
Asp Met Val Ala Cys Cys Leu Phe Ser Cys Ser Ser Lys His Tyr Pro
    50   55   60
Leu Tyr Ser Leu Asn Val Ala Ser Met Trp Leu Lys Leu Gly Arg Leu
65   70   75   80
Tyr Met Gly Leu Glu His Lys Ala Ala Arg Asp Glu
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<210> 5047
<211> 3380
<212> DNA
<213> Homo sapiens

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120
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180
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240
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720

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2280
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2340

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2520
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2760
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<210> 5048
<211> 429
<212> PRT
<213> Homo sapiens

<400> 5048
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            20   25   30
Pro Ala Tyr Ala Tyr Val Leu Thr Val Asn Glu Arg Gly Asn His Cys
        35   40   45
Glu Tyr Cys Phe Thr Arg Lys Glu Gly Leu Ser Lys Cys Gly Arg Cys
    50   55   60
Lys Gln Ala Phe Tyr Cys Asn Val Glu Cys Gln Lys Glu Asp Trp Pro
65   70   75   80
Met His Lys Leu Glu Cys Ser Pro Met Val Val Phe Gly Glu Asn Trp

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Asn Pro Ser Glu Thr Val Arg Leu Thr Ala Arg Ile Leu Ala Lys Gln
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Lys Ile His Pro Glu Arg Thr Pro Ser Glu Lys Leu Leu Ala Val Lys
        115                 120                 125
Glu Phe Glu Ser His Leu Asp Lys Leu Asp Asn Glu Lys Lys Asp Leu
    130                 135                 140
Ile Gln Ser Asp Ile Ala Ala Leu His His Phe Tyr Ser Lys His Leu
145                 150                 155                 160
Glu Phe Pro Asp Asn Asp Ser Leu Val Val Leu Phe Ala Gln Val Asn
                165                 170                 175
Cys Asn Gly Phe Thr Ile Glu Asp Glu Glu Leu Ser His Leu Gly Ser
            180                 185                 190
Ala Ile Phe Pro Asp Val Ala Leu Met Asn His Ser Cys Cys Pro Asn
        195                 200                 205
Val Ile Val Thr Tyr Lys Gly Thr Leu Ala Glu Val Arg Ala Val Gln
    210                 215                 220
Glu Ile Lys Pro Gly Glu Glu Val Phe Thr Ser Tyr Ile Asp Leu Leu
225                 230                 235                 240
Tyr Pro Thr Glu Asp Arg Asn Asp Arg Leu Arg Asp Ser Tyr Phe Phe
                245                 250                 255
Thr Cys Glu Cys Gln Glu Cys Thr Thr Lys Asp Lys Asp Lys Ala Lys
            260                 265                 270
Val Glu Ile Arg Lys Leu Ser Asp Pro Pro Lys Ala Glu Ala Ile Arg
        275                 280                 285
Asp Met Val Arg Tyr Ala Arg Asn Val Ile Glu Glu Phe Arg Arg Ala
    290                 295                 300
Lys His Tyr Lys Ser Pro Ser Glu Leu Leu Glu Ile Cys Glu Leu Ser
305                 310                 315                 320
Gln Glu Lys Met Ser Ser Val Phe Glu Asp Ser Asn Val Tyr Met Leu
                325                 330                 335
His Met Met Tyr Gln Ala Met Gly Val Cys Leu Tyr Met Gln Asp Trp
            340                 345                 350
Glu Gly Ala Leu Gln Tyr Gly Gln Lys Ile Ile Lys Pro Tyr Ser Lys
        355                 360                 365
His Tyr Pro Leu Tyr Ser Leu Asn Val Ala Ser Met Trp Leu Lys Leu
    370                 375                 380
Gly Arg Leu Tyr Met Gly Leu Glu His Lys Ala Ala Gly Glu Lys Ala
385                 390                 395                 400
Leu Lys Lys Ala Ile Ala Ile Met Glu Val Ala His Gly Lys Asp His
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Pro Tyr Ile Ser Glu Ile Lys Gln Glu Ile Glu Ser His
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<212> DNA
<213> Homo sapiens

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<211> 619
<212> PRT
<213> Homo sapiens

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Gln His Val Cys Glu Thr Ile Ile Arg Ile Phe Lys Arg His Gly Ala
        35   40   45
Val Gln Leu Cys Thr Pro Leu Leu Leu Pro Arg Asn Arg Gln Ile Tyr
    50   55   60
Glu His Asn Glu Ser Ala Leu Phe Met Asp His Ser Gly Met Leu Val
65   70   75   80
Met Leu Pro Phe Asp Leu Arg Ile Pro Phe Ala Arg Tyr Val Ala Arg
                85   90   95
Asn Asn Ile Leu Asn Leu Lys Arg Tyr Cys Ile Glu Arg Val Phe Arg
            100   105   110
Pro Arg Lys Leu Asp Arg Phe His Pro Lys Glu Leu Leu Glu Cys Ala
        115   120   125
Phe Asp Ile Val Thr Ser Thr Thr Asn Ser Phe Leu Pro Thr Ala Glu
    130   135   140
Ile Ile Tyr Thr Ile Tyr Glu Ile Ile Gln Glu Phe Pro Ala Leu Gln
145   150   155   160
Glu Arg Asn Tyr Ser Ile Tyr Leu Asn His Thr Met Leu Leu Lys Ala
                165   170   175
Ile Leu Leu His Cys Gly Ile Pro Glu Asp Lys Leu Ser Gln Val Tyr

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            180                 185                 190
Ile Ile Leu Tyr Asp Ala Val Thr Glu Lys Leu Thr Arg Arg Glu Val
        195                 200                 205
Glu Ala Lys Phe Cys Asn Leu Ser Val Ser Ser Asn Ser Xaa Val Ser
    210                 215                 220
Thr Leu Gln Xaa Leu Leu Asn Arg Arg Glu Ile Xaa Ala Arg Ser Tyr
225                 230                 235                 240
Ala Asn Asn Xaa Asn Ser Leu Ile Lys Gln Lys Thr Gly Ile Ala Gln
                245                 250                 255
Leu Val Lys Tyr Gly Leu Lys Asp Leu Glu Glu Val Val Gly Leu Leu
            260                 265                 270
Lys Lys Leu Gly Ile Lys Leu Gln Val Leu Ile Asn Leu Gly Leu Val
        275                 280                 285
Tyr Lys Val Gln Gln His Asn Gly Ile Ile Phe Gln Phe Val Ala Phe
    290                 295                 300
Ile Lys Arg Arg Gln Arg Ala Val Pro Glu Ile Leu Ala Ala Gly Gly
305                 310                 315                 320
Arg Tyr Asp Leu Leu Ile Pro Gln Phe Arg Gly Pro Gln Ala Leu Gly
                325                 330                 335
Pro Val Pro Thr Ala Ile Gly Val Ser Ile Ala Ile Asp Lys Ile Ser
            340                 345                 350
Ala Ala Val Leu Asn Met Glu Glu Ser Val Thr Ile Ser Ser Cys Asp
        355                 360                 365
Leu Leu Val Val Ser Val Gly Gln Met Ser Met Ser Arg Ala Ile Asn
    370                 375                 380
Leu Thr Gln Lys Leu Trp Thr Ala Gly Ile Thr Ala Glu Ile Met Tyr
385                 390                 395                 400
Asp Trp Ser Gln Ser Gln Glu Glu Leu Gln Glu Tyr Cys Arg His His
                405                 410                 415
Glu Ile Thr Tyr Val Ala Leu Val Ser Asp Lys Glu Gly Ser His Val
            420                 425                 430
Lys Val Lys Ser Phe Glu Lys Glu Arg Gln Thr Glu Lys Arg Val Leu
        435                 440                 445
Glu Thr Glu Leu Val Asp His Val Leu Gln Lys Leu Arg Thr Lys Val
    450                 455                 460
Thr Asp Glu Arg Asn Gly Arg Glu Ala Ser Asp Asn Leu Ala Val Gln
465                 470                 475                 480
Asn Leu Lys Gly Ser Phe Ser Asn Ala Ser Gly Leu Phe Glu Ile His
                485                 490                 495
Gly Ala Thr Val Val Pro Ile Val Ser Val Leu Ala Pro Glu Lys Leu
            500                 505                 510
Ser Ala Ser Thr Arg Arg Arg Tyr Glu Thr Gln Val Gln Thr Arg Leu
        515                 520                 525
Gln Thr Ser Leu Ala Asn Leu His Gln Lys Ser Ser Glu Ile Glu Ile
    530                 535                 540
Leu Ala Val Asp Leu Pro Lys Glu Thr Ile Leu Gln Phe Leu Ser Leu
545                 550                 555                 560
Glu Trp Asp Ala Asp Glu Gln Ala Phe Asn Thr Thr Val Lys Gln Leu
                565                 570                 575
Leu Ser Arg Leu Pro Lys Gln Arg Tyr Leu Lys Leu Val Cys Asp Glu
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Ile Tyr Asn Ile Lys Val Glu Lys Lys Val Ser Val Leu Phe Leu Tyr
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Ser Tyr Arg Asp Asp Tyr Tyr Arg Ile Leu Phe
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610 615

<210> 5051
<211> 4125
<212> DNA
<213> Homo sapiens

<400> 5051
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3960
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4125

<210> 5052
<211> 433
<212> PRT
<213> Homo sapiens

<400> 5052
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Glu Ser Gly Asp Glu Phe Thr Tyr Gly Asp Val Pro Val Glu Asn Gly
35 40 45
Met Ala Pro Phe Phe Glu Met Lys Leu Lys His Tyr Lys Ile Phe Glu
50 55 60
Gly Met Pro Val Thr Phe Thr Cys Arg Val Ala Gly Asn Pro Lys Pro

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65                  70                  75                  80
Lys Ile Tyr Trp Phe Lys Asp Gly Lys Gln Ile Ser Pro Lys Ser Asp
                85                  90                  95
His Tyr Thr Ile Gln Arg Asp Leu Asp Gly Thr Cys Ser Leu His Thr
            100                 105                 110
Thr Ala Ser Thr Leu Asp Asp Asp Gly Asn Tyr Thr Ile Met Ala Ala
        115                 120                 125
Asn Pro Gln Gly Arg Ile Ser Cys Thr Gly Arg Leu Met Val Gln Ala
    130                 135                 140
Val Asn Gln Arg Gly Arg Ser Pro Arg Ser Pro Ser Gly His Pro His
145                 150                 155                 160
Val Arg Arg Pro Arg Ser Arg Ser Arg Asp Ser Gly Asp Glu Asn Glu
                165                 170                 175
Pro Ile Gln Glu Arg Phe Phe Arg Pro His Phe Leu Gln Ala Pro Gly
            180                 185                 190
Asp Leu Thr Val Gln Glu Gly Lys Leu Cys Arg Met Asp Cys Lys Val
        195                 200                 205
Ser Gly Leu Pro Thr Pro Asp Leu Ser Trp Gln Leu Asp Gly Lys Pro
    210                 215                 220
Val Arg Pro Asp Ser Ala His Lys Met Leu Val Arg Glu Asn Gly Val
225                 230                 235                 240
His Ser Leu Ile Ile Glu Pro Val Thr Ser Arg Asp Ala Gly Ile Tyr
                245                 250                 255
Thr Cys Ile Ala Thr Asn Arg Ala Gly Gln Asn Ser Phe Ser Leu Glu
            260                 265                 270
Leu Val Val Ala Ala Lys Glu Ala His Lys Pro Pro Val Phe Ile Glu
        275                 280                 285
Lys Leu Gln Asn Thr Gly Val Ala Asp Gly Tyr Pro Val Arg Leu Glu
    290                 295                 300
Cys Arg Val Leu Gly Val Pro Pro Pro Gln Ile Phe Trp Lys Lys Glu
305                 310                 315                 320
Asn Glu Ser Leu Thr His Ser Thr Asp Arg Val Ser Met His Gln Asp
                325                 330                 335
Asn His Gly Tyr Ile Cys Leu Leu Ile Gln Gly Ala Thr Lys Glu Asp
            340                 345                 350
Ala Gly Trp Tyr Thr Val Ser Ala Lys Asn Glu Ala Gly Ile Val Ser
        355                 360                 365
Cys Thr Ala Arg Leu Asp Val Tyr Thr Gln Trp His Gln Gln Ser Gln
    370                 375                 380
Ser Thr Lys Pro Lys Lys Val Arg Pro Ser Ala Ser Arg Tyr Ala Ala
385                 390                 395                 400
Leu Ser Asp Gln Gly Leu Asp Ile Lys Ala Ala Phe Gln Pro Glu Ala
                405                 410                 415
Asn Pro Ser His Leu Thr Leu Asn Thr Ala Leu Val Glu Ser Glu Asp
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<210> 5053
<211> 781
<212> DNA
<213> Homo sapiens

<400> 5053

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180
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240
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360
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420
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480
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540
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600
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<210> 5054
<211> 156
<212> PRT
<213> Homo sapiens

<400> 5054
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Val Gly Pro Cys Pro Lys Met Ser Pro Leu Arg Pro Leu Leu Leu Ala
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Leu Ala Leu Ala Ser Val Pro Cys Ala Gln Gly Ala Cys Pro Ala Ser
35 40 45
Ala Asp Leu Lys His Ser Asp Gly Thr Arg Thr Cys Ala Lys Leu Tyr
50 55 60
Asp Lys Ser Asp Pro Tyr Tyr Glu Asn Cys Cys Gly Gly Ala Glu Leu
65 70 75 80
Ser Leu Glu Ser Gly Ala Asp Leu Pro Tyr Leu Pro Ser Asn Trp Ala
85 90 95
Asn Thr Ala Ser Ser Leu Val Val Ala Pro Arg Cys Glu Leu Thr Val
100 105 110
Trp Ser Arg Gln Gly Lys Ala Gly Lys Thr His Lys Phe Ser Ala Gly
115 120 125
Thr Tyr Pro Arg Leu Glu Glu Tyr Arg Arg Gly Ile Leu Gly Asp Trp
130 135 140
Ser Asn Ala Ile Ser Ala Leu Tyr Cys Arg Cys Ser

145 150 155

<210> 5055
<211> 2520
<212> DNA
<213> Homo sapiens

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240
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420
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480
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540
gcagagcttg gtgtcccatt gtcacaggtt aaaagcatct caggtacagc gcaggatggt
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660
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720
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780
gatgtcattt tttgctccga gattctgccc acaaaggaga ctttgccgag taataacaca
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1140
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1320
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1380

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2340
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2400
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<210> 5056
<211> 672
<212> PRT
<213> Homo sapiens

<400> 5056
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20 25 30
Asp Val Thr Val Ile Val Glu Asp Arg Lys Phe Arg Ala His Lys Asn
35 40 45
Ile Leu Ser Ala Ser Ser Thr Tyr Phe His Gln Leu Phe Ser Val Ala
50 55 60
Gly Gln Val Val Glu Leu Ser Phe Ile Arg Ala Glu Ile Phe Ala Glu

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65                  70                  75                  80
Ile Leu Asn Tyr Ile Tyr Ser Ser Lys Ile Val Arg Val Arg Ser Asp
                85                  90                  95
Leu Leu Asp Glu Leu Ile Lys Ser Gly Gln Leu Leu Gly Val Lys Phe
            100                 105                 110
Ile Ala Glu Leu Gly Val Pro Leu Ser Gln Val Lys Ser Ile Ser Gly
        115                 120                 125
Thr Ala Gln Asp Gly Asn Thr Glu Pro Leu Pro Pro Asp Ser Gly Asp
    130                 135                 140
Lys Asn Leu Val Ile Gln Lys Ser Lys Asp Glu Ala Gln Asp Asn Gly
145                 150                 155                 160
Ala Thr Ile Met Pro Ile Ile Thr Glu Ser Phe Ser Leu Ser Ala Glu
                165                 170                 175
Asp Tyr Glu Met Lys Lys Ile Ile Val Thr Asp Ser Asp Asp Asp Asp
            180                 185                 190
Asp Asp Val Ile Phe Cys Ser Glu Ile Leu Pro Thr Lys Glu Thr Leu
        195                 200                 205
Pro Ser Asn Asn Thr Val Ala Gln Val Gln Ser Asn Pro Gly Pro Val
    210                 215                 220
Ala Ile Ser Asp Val Ala Pro Ser Ala Ser Asn Asn Ser Pro Pro Leu
225                 230                 235                 240
Thr Asn Ile Thr Pro Thr Gln Lys Leu Pro Thr Pro Val Asn Gln Ala
                245                 250                 255
Thr Leu Ser Gln Thr Gln Gly Ser Glu Lys Leu Leu Val Ser Ser Ala
            260                 265                 270
Pro Thr His Leu Thr Pro Asn Ile Ile Leu Leu Asn Gln Thr Pro Leu
        275                 280                 285
Ser Thr Pro Pro Asn Val Ser Ser Ser Leu Pro Asn His Met Pro Ser
    290                 295                 300
Ser Ile Asn Leu Leu Val Gln Asn Gln Gln Thr Pro Asn Ser Ala Ile
305                 310                 315                 320
Leu Thr Gly Asn Lys Ala Asn Glu Glu Glu Glu Glu Glu Ile Ile Asp
                325                 330                 335
Asp Asp Asp Asp Thr Ile Ser Ser Ser Pro Asp Ser Ala Val Ser Asn
            340                 345                 350
Thr Ser Leu Val Pro Gln Ala Asp Thr Ser Gln Asn Thr Ser Phe Asp
        355                 360                 365
Gly Ser Leu Ile Gln Lys Met Gln Ile Pro Thr Leu Leu Gln Glu Pro
    370                 375                 380
Leu Ser Asn Ser Leu Lys Ile Ser Asp Ile Ile Thr Arg Asn Thr Asn
385                 390                 395                 400
Asp Pro Gly Val Gly Ser Lys His Leu Met Glu Gly Gln Lys Ile Ile
                405                 410                 415
Thr Leu Asp Thr Ala Thr Glu Ile Glu Gly Leu Ser Thr Gly Cys Lys
            420                 425                 430
Val Tyr Ala Asn Ile Gly Glu Asp Thr Tyr Asp Ile Val Ile Pro Val
        435                 440                 445
Lys Asp Asp Pro Asp Glu Gly Glu Ala Arg Leu Glu Asn Glu Ile Pro
    450                 455                 460
Lys Thr Ser Gly Ser Glu Met Ala Asn Lys Arg Met Lys Val Lys His
465                 470                 475                 480
Asp Asp His Tyr Glu Leu Ile Val Asp Gly Arg Val Tyr Tyr Ile Cys
                485                 490                 495
Ile Val Cys Lys Arg Ser Tyr Val Cys Leu Thr Ser Leu Arg Arg His
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Phe Asn Ile His Ser Trp Glu Lys Lys Tyr Pro Cys Arg Tyr Cys Glu
        515                 520                 525
Lys Val Phe Pro Leu Ala Glu Tyr Arg Thr Lys His Glu Ile His His
    530                 535                 540
Thr Gly Glu Arg Arg Tyr Gln Cys Leu Ala Cys Gly Lys Ser Phe Ile
545                 550                 555                 560
Asn Tyr Gln Phe Met Ser Ser His Ile Lys Ser Val His Ser Gln Asp
                565                 570                 575
Pro Ser Gly Asp Ser Lys Leu Tyr Arg Leu His Pro Cys Arg Ser Leu
            580                 585                 590
Gln Ile Arg Gln Tyr Ala Tyr His Ser Asp Arg Ser Ser Thr Ile Pro
        595                 600                 605
Ala Met Lys Asp Asp Gly Ile Gly Tyr Lys Val Asp Thr Gly Lys Glu
    610                 615                 620
Pro Pro Val Gly Thr Thr Thr Ser Thr Gln Asn Lys Pro Met Thr Trp
625                 630                 635                 640
Glu Asp Ile Phe Ile Gln Gln Glu Asn Asp Ser Ile Phe Lys Gln Asn
                645                 650                 655
Val Thr Asp Gly Ser Thr Glu Phe Glu Phe Ile Ile Pro Glu Ser Tyr
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<210> 5057
<211> 673
<212> DNA
<213> Homo sapiens

<400> 5057
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180
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240
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300
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420
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480
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673

<210> 5058

<211> 122
<212> PRT
<213> Homo sapiens

<400> 5058
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20 25 30
Ser Cys Pro Lys Val Asn Ser Val Tyr Val Leu Val Arg Gln Lys Ala
35 40 45
Gly Gln Thr Pro Gln Glu Arg Val Glu Glu Val Leu Ser Gly Lys Leu
50 55 60
Phe Asp Arg Leu Arg Asp Glu Asn Pro Asp Phe Arg Glu Lys Ile Ile
65 70 75 80
Ala Ile Asn Ser Glu Leu Thr Gln Pro Lys Leu Ala Leu Ser Glu Glu
85 90 95
Asp Lys Glu Val Ile Ile Asp Ser Thr Asn Ile Ile Phe His Cys Ala
100 105 110
Ala Thr Val Arg Phe Asn Glu Asn Leu Arg
115 120

<210> 5059
<211> 480
<212> DNA
<213> Homo sapiens

<400> 5059
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120
cagctgtgag tctttctcca gggacagtcg gcagccggcc ctaggtgcag agccgatgac
180
aaggacccag gctctcagca ggtcttccaa gcagtgtggt agaaaggcag gcagggtgtg
240
gggaagtgga gccaggccac cagtcatgat gtcaagactg agccaggaag caaaggcagg
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480

<210> 5060
<211> 114
<212> PRT
<213> Homo sapiens

<400> 5060
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Leu Pro His Thr Leu Pro Ala Phe Leu Pro His Cys Leu Glu Asp Leu
        35                  40                  45
Leu Arg Ala Trp Val Leu Val Ile Gly Ser Ala Pro Arg Ala Gly Cys
    50                  55                  60
Arg Leu Ser Leu Glu Lys Asp Ser Gln Leu Val Ser Leu Cys Ile His
65                  70                  75                  80
Ala Leu Cys Pro Glu Arg Pro Ser Gln Ser Ala Arg Ala Val Ile Thr
                85                  90                  95
Arg Tyr His Ala Leu Gly Gly Leu Thr His Arg Glu Cys Leu Ser Val
            100                 105                 110
Leu Glu
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<210> 5061
<211> 2462
<212> DNA
<213> Homo sapiens

<400> 5061
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180
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960
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2340
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2462

<210> 5062
<211> 136
<212> PRT

<213> Homo sapiens

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35 40 45
Arg Asn Trp Arg Lys Asp Ile Lys Leu Ser Ala Val Asp Leu Ser Ala
50 55 60
Glu Ile Phe Pro Glu Ser Met Val Val Leu Asn Tyr Leu His Val Ser
65 70 75 80
Ser Ile Phe Asn Ser Gly Val Gly Leu Phe Leu Ile Ser Ser Gln Lys
85 90 95
Cys Ser Ala Leu Gly Glu Gly Thr Ser Pro Leu Ala Cys His Phe Pro
100 105 110
Gly Val Leu Tyr His Phe Asp Gly Thr Leu Trp Ser Ala Glu Asn Ala
115 120 125
Leu Ser Trp His Ala Ser Arg Leu
130 135

<210> 5063
<211> 561
<212> DNA
<213> Homo sapiens

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300
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420
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561

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<211> 110
<212> PRT
<213> Homo sapiens

<400> 5064
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Ala Arg Lys Tyr Trp Leu Thr Cys Phe Glu Glu Ala Leu Asp Gly Val
35 40 45
Val Lys Arg Ala Val Ala Ser Gln Pro Asp Ser Val Asp Ala Ala Glu
50 55 60
Arg Ala Glu Lys Phe Arg Gln Lys Tyr Trp Asn Lys Leu Gln Thr Leu
65 70 75 80
Arg Gln Gln Pro Phe Ala Tyr Gly Thr Leu Thr Val Arg Ser Leu Leu
85 90 95
Asp Thr Arg Glu His Cys Leu Asn Glu Phe Asn Phe Pro Asp
100 105 110

<210> 5065
<211> 370
<212> DNA
<213> Homo sapiens

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120
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acgtctgagg acaacatgac agacatggtg acccacatgc ctgaccgcta caagatcgtg
240
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370

<210> 5066
<211> 123
<212> PRT
<213> Homo sapiens

<400> 5066
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Asp Leu Pro Gly His Tyr Tyr Glu Thr Leu Lys Phe Leu Val Gly His
20 25 30
Leu Lys Thr Ile Ala Asp His Ser Glu Lys Asn Lys Met Glu Pro Arg
35 40 45
Asn Leu Ala Leu Val Phe Gly Pro Thr Leu Val Arg Thr Ser Glu Asp
50 55 60
Asn Met Thr Asp Met Val Thr His Met Pro Asp Arg Tyr Lys Ile Val
65 70 75 80
Glu Thr Leu Ile Gln His Ser Asp Trp Phe Phe Ser Asp Glu Glu Asp

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                85                  90                  95
Lys Gly Glu Arg Ile Leu Pro Pro Val Val Gln Ser Ser Pro Arg Val
            100                 105                 110
Arg Gly Pro Pro Arg Arg Ser Arg Thr Pro Gly
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<210> 5067
<211> 2023
<212> DNA
<213> Homo sapiens

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cgaatacgaa gcctgttgga acgtcaagcc agagagattg aagcttttga ctctgaaagc
180
atgagactag gttttagtaa tatggtcctt tctaatctct cccctgaggc attcagccac
240
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360
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600
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1020
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1080
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1140
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1200
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1260

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1920
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2023

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<211> 179
<212> PRT
<213> Homo sapiens

<400> 5068
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Ala Leu Gln Asn Glu Arg Thr Glu Arg Ile Arg Ser Leu Leu Glu Arg
        35   40   45
Gln Ala Arg Glu Ile Glu Ala Phe Asp Ser Glu Ser Met Arg Leu Gly
    50   55   60
Phe Ser Asn Met Val Leu Ser Asn Leu Ser Pro Glu Ala Phe Ser His
65   70   75   80
Ser Tyr Pro Gly Ala Ser Gly Trp Ser His Asn Pro Thr Gly Gly Pro
                85   90   95
Gly Pro His Trp Gly His Pro Met Gly Gly Pro Pro Gln Ala Trp Gly
            100   105   110
His Pro Met Gln Gly Gly Pro Gln Pro Trp Gly His Pro Ser Gly Pro
        115   120   125
Met Gln Gly Val Pro Arg Gly Ser Ser Met Gly Val Arg Asn Ser Pro
    130   135   140
Gln Ala Leu Arg Arg Thr Ala Ser Gly Gly Arg Thr Glu Gln Gly Met
145   150   155   160
Ser Arg Ser Thr Ser Val Thr Ser Gln Ile Ser Asn Gly Ser His Met

165 170 175
Ser Tyr Thr

<210> 5069
<211> 3655
<212> DNA
<213> Homo sapiens

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180
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240
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<210> 5070
<211> 255
<212> PRT
<213> Homo sapiens

<400> 5070
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Arg Ser Arg Ser Arg Ser Phe Ser Arg Ser Ser Arg Ser His Ser Arg
35 40 45
Val Ser Ser Arg Phe Ser Ser Arg Ser Arg Arg Ser Lys Ser Arg Ser
50 55 60
Arg Ser Arg Arg Arg His Gln Arg Lys Tyr Arg Arg Tyr Ser Arg Ser
65 70 75 80
Tyr Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Arg Tyr Arg Glu Arg
85 90 95
Arg Tyr Gly Phe Thr Arg Arg Tyr Tyr Arg Ser Pro Ser Arg Tyr Arg
100 105 110
Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Gly Arg Ser Tyr Cys Gly
115 120 125
Arg Ala Tyr Ala Ile Ala Arg Gly Gln Arg Tyr Tyr Gly Phe Gly Arg
130 135 140
Thr Val Tyr Pro Glu Glu His Ser Arg Trp Arg Asp Arg Ser Arg Thr
145 150 155 160
Arg Ser Arg Ser Arg Thr Pro Phe Arg Leu Ser Glu Lys Gly Gly Trp
165 170 175
Val Ile Tyr Leu Ser Ile Cys Gly Asn Val Trp Trp Gln Tyr Met Ser

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Arg Leu Gly Asn Gln Arg Cys Cys Val Val Ser Ile Leu Val Pro Leu
        195                 200                 205
Val Pro Glu Ile Phe Leu Glu Glu Arg Gly Arg Thr Leu Pro Val Phe
    210                 215                 220
Lys Trp Thr Ala Phe Ser Leu Gly Leu Lys Val Asn Trp Lys Leu Asn
225                 230                 235                 240
Gly Ser Gly Cys Arg Glu Leu Phe Phe Leu Leu Ala Asp Cys Ser
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<211> 2196
<212> DNA
<213> Homo sapiens

<400> 5071
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1920
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2040
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2196

<210> 5072
<211> 76
<212> PRT
<213> Homo sapiens

<400> 5072
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Gly Ser Leu Gln Pro Pro Pro Pro Arg Phe Lys Gln Phe Ser His Leu
20 25 30
Ser Leu Gln Ser Ser Trp Asp Tyr Arg His Ala Gln Pro Cys Pro Ala
35 40 45
Asn Phe Cys Asn Phe Ser Arg Asp Gly Phe Ser Leu Ser Arg Asp Gly
50 55 60
Cys Leu Pro Gly Trp Ser Arg Thr Pro Asp Leu Arg
65 70 75

<210> 5073
<211> 1712
<212> DNA
<213> Homo sapiens

<400> 5073
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180
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240
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<210> 5074
<211> 240
<212> PRT
<213> Homo sapiens

<400> 5074
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Met Asp Lys Glu Thr Phe Glu Phe Lys Phe Gly Lys Glu Leu Thr Phe
35 40 45
Thr Thr Val Leu Ser Asp Gln Gln Val Val Glu Leu Ile Pro Gly Gly
50 55 60
Ala Gly Ile Val Val Gly Tyr Gly Asp Arg Ser Arg Phe Ile Gln Leu
65 70 75 80
Val Gln Lys Ala Arg Leu Glu Glu Ser Lys Glu Gln Val Ala Ala Met
85 90 95
Gln Ala Gly Leu Leu Lys Val Val Pro Gln Ala Val Leu Asp Leu Leu
100 105 110
Thr Trp Gln Glu Leu Glu Lys Lys Val Cys Gly Asp Pro Glu Val Thr
115 120 125
Val Asp Ala Leu Arg Lys Leu Thr Arg Phe Glu Asp Phe Glu Pro Ser
130 135 140
Asp Ser Arg Val Gln Tyr Phe Trp Glu Ala Leu Asn Asn Phe Thr Asn
145 150 155 160
Glu Asp Arg Ser Arg Phe Leu Arg Phe Val Thr Gly Arg Ser Arg Leu
165 170 175
Pro Ala Arg Xaa Ser Thr Ser Thr Gln Thr Ser Trp Ala Thr Arg Pro
180 185 190
Xaa Asp Ala Leu Pro Glu Ser Ser Thr Cys Ser Ser Thr Leu Phe Leu
195 200 205
Pro His Tyr Ala Ser Ala Lys Val Cys Glu Glu Lys Leu Arg Tyr Ala
210 215 220
Ala Tyr Asn Cys Val Ala Ile Asp Thr Asp Met Ser Pro Trp Glu Glu
225 230 235 240

<210> 5075
<211> 444
<212> DNA
<213> Homo sapiens

<400> 5075

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<210> 5076
<211> 90
<212> PRT
<213> Homo sapiens

<400> 5076
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Ile Arg Lys Gln Gln Val Asn Cys Ser Pro Arg Trp Gln Trp Glu Ala
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Cys Trp Asp Gly Gly Gly Ser Gly Asn Phe Ser Ser Pro Gly Thr Leu
35 40 45
Arg Glu Thr Glu Val Ile Thr Ala Val Leu Glu Leu Gly Arg Gly Gly
50 55 60
Asp Gln Val Thr Ala Asp Gln Lys Ser Leu Asn Ile Asn Ala Met Glu
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Arg Glu Leu Ala Leu Ser Leu Arg Val Ala
85 90

<210> 5077
<211> 2352
<212> DNA
<213> Homo sapiens

<400> 5077
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1980

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2160
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2352

<210> 5078
<211> 558
<212> PRT
<213> Homo sapiens

<400> 5078
Met Ala Glu Leu Asn Thr His Val Asn Val Lys Glu Lys Ile Tyr Ala
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Val Arg Ser Val Val Pro Asn Lys Ser Asn Asn Glu Ile Val Leu Val
20 25 30
Leu Gln Gln Phe Asp Phe Asn Val Asp Lys Ala Val Gln Ala Phe Val
35 40 45
Asp Gly Ser Ala Ile Gln Val Leu Lys Glu Trp Asn Met Thr Gly Lys
50 55 60
Lys Lys Asn Asn Lys Arg Lys Arg Ser Lys Ser Lys Gln His Gln Gly
65 70 75 80
Asn Lys Asp Ala Lys Asp Lys Val Glu Arg Pro Glu Ala Gly Pro Leu
85 90 95
Gln Pro Gln Pro Pro Gln Ile Gln Asn Gly Pro Met Asn Gly Cys Glu
100 105 110
Lys Asp Ser Ser Ser Thr Asp Ser Ala Asn Glu Lys Pro Ala Leu Ile
115 120 125
Pro Arg Glu Lys Lys Ile Ser Ile Leu Glu Glu Pro Ser Lys Ala Leu
130 135 140
Arg Gly Val Thr Glu Gly Asn Arg Leu Leu Gln Gln Lys Leu Ser Leu
145 150 155 160
Asp Gly Asn Pro Lys Pro Ile His Gly Thr Thr Glu Arg Ser Asp Gly
165 170 175
Leu Gln Trp Ser Ala Glu Gln Pro Cys Asn Pro Ser Lys Pro Lys Ala
180 185 190
Lys Thr Ser Pro Val Lys Ser Asn Thr Pro Ala Ala His Leu Glu Ile
195 200 205
Lys Pro Asp Glu Leu Ala Lys Lys Arg Gly Pro Asn Ile Glu Lys Ser
210 215 220
Val Lys Asp Leu Gln Arg Cys Thr Val Ser Leu Thr Arg Tyr Arg Val
225 230 235 240
Met Ile Lys Glu Glu Val Asp Ser Ser Val Lys Lys Ile Lys Ala Ala
245 250 255
Phe Ala Glu Leu His Asn Cys Ile Ile Asp Lys Glu Val Ser Leu Met

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            260                 265                 270
Ala Glu Met Asp Lys Val Lys Glu Glu Ala Met Glu Ile Leu Thr Ala
        275                 280                 285
Arg Gln Lys Lys Ala Glu Glu Leu Lys Arg Leu Thr Asp Leu Ala Ser
    290                 295                 300
Gln Met Ala Glu Met Gln Leu Ala Glu Leu Arg Ala Glu Ile Lys His
305                 310                 315                 320
Phe Val Ser Glu Arg Lys Tyr Asp Glu Glu Leu Gly Lys Ala Ala Arg
                325                 330                 335
Phe Ser Cys Asp Ile Glu Gln Leu Lys Ala Gln Ile Met Leu Cys Gly
            340                 345                 350
Glu Ile Thr His Pro Lys Asn Asn Tyr Ser Ser Arg Thr Pro Cys Ser
        355                 360                 365
Ser Leu Leu Pro Leu Leu Asn Ala His Ala Ala Thr Ser Gly Lys Gln
    370                 375                 380
Ser Asn Phe Ser Arg Lys Ser Ser Thr His Asn Lys Pro Ser Glu Gly
385                 390                 395                 400
Lys Ala Ala Asn Pro Lys Met Val Ser Ser Leu Pro Ser Thr Ala Asp
                405                 410                 415
Pro Ser His Gln Thr Met Pro Ala Asn Lys Gln Asn Gly Ser Ser Asn
            420                 425                 430
Gln Arg Arg Arg Phe Asn Pro Gln Tyr His Asn Asn Arg Leu Asn Gly
        435                 440                 445
Pro Ala Lys Ser Gln Gly Ser Gly Asn Glu Ala Glu Pro Leu Gly Lys
    450                 455                 460
Gly Asn Ser Arg His Glu His Arg Arg Gln Pro His Asn Gly Phe Arg
465                 470                 475                 480
Pro Lys Asn Lys Gly Gly Ala Lys Asn Gln Glu Ala Ser Leu Gly Met
                485                 490                 495
Lys Thr Pro Glu Ala Pro Ala His Ser Glu Lys Pro Arg Arg Arg Gln
            500                 505                 510
His Ala Ala Asp Thr Ser Glu Ala Arg Pro Phe Arg Gly Ser Val Gly
        515                 520                 525
Arg Val Ser Gln Cys Asn Leu Cys Pro Thr Arg Ile Glu Val Ser Thr
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Asp Ala Ala Val Leu Ser Val Pro Ala Val Thr Leu Val Ala
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<210> 5079
<211> 1338
<212> DNA
<213> Homo sapiens

<400> 5079
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240
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300
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420
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480
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540
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1320
aaaaaaaaaa aaaaaaaa
1338

<210> 5080
<211> 165
<212> PRT
<213> Homo sapiens

<400> 5080
Gly Ala Gly Pro Trp Glu Ala Phe Pro Asp Gly Ile Gly Arg Arg Ser
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Arg Arg Ala Arg Leu Pro Gln Tyr Lys Arg Pro Pro Gly Arg Val Gly
20 25 30
Gly Gly Asp Ser Gly Arg Arg Asn Met Ala Val Ala Asp Leu Ala Leu
35 40 45
Ile Pro Asp Val Asp Ile Asp Ser Asp Gly Val Phe Lys Tyr Val Leu
50 55 60
Ile Arg Val His Ser Ala Pro Arg Ser Gly Ala Pro Ala Ala Glu Ser
65 70 75 80
Lys Glu Ile Val Arg Gly Tyr Lys Trp Ala Glu Tyr His Ala Asp Ile

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                85                  90                  95
Tyr Asp Lys Val Ser Gly Asp Met Gln Lys Gln Gly Cys Asp Cys Glu
            100                 105                 110
Cys Leu Gly Gly Gly Arg Ile Ser His Gln Ser Gln Asp Lys Lys Ile
        115                 120                 125
His Val Tyr Gly Tyr Ser Met Val Ser Arg Ser Pro Val Pro Pro Cys
    130                 135                 140
Arg Arg Pro Gln Tyr Gln Leu Arg Gly Pro Pro Glu Pro Ala Ala Leu
145                 150                 155                 160
Thr Arg Gly Pro Ser
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<210> 5081
<211> 561
<212> DNA
<213> Homo sapiens

<400> 5081
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240
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300
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420
gccaacaggg atgaattcta cagccgaccc tccaagttag ctgacttctg ggggaacaac
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aacgagatcc tcagtgggct ggacatggag gaaggcaagg aaggaggcac atggctgggc
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atcagcacac gtggcaagct g
561

<210> 5082
<211> 111
<212> PRT
<213> Homo sapiens

<400> 5082
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Ala Ala Gln Ala Trp His Cys Pro Pro Gly Gln Gly His Ser Val Trp
            20                  25                  30
Asp Ala Val Arg Met Pro Leu Gly Ala Gly Thr Pro Val Asn Val Gln
        35                  40                  45
Arg Arg Glu Asp Ser Ala Thr Glu Gly Ser His Arg Leu Ile Leu Ala
    50                  55                  60
Ala Asn Arg Asp Glu Phe Tyr Ser Arg Pro Ser Lys Leu Ala Asp Phe
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65 70 75 80
Trp Gly Asn Asn Asn Glu Ile Leu Ser Gly Leu Asp Met Glu Glu Gly
85 90 95
Lys Glu Gly Gly Thr Trp Leu Gly Ile Ser Thr Arg Gly Lys Leu
100 105 110

<210> 5083
<211> 1856
<212> DNA
<213> Homo sapiens

<400> 5083
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120
ccatggcaga gccagaccga ctcagattca gactctgagg gaggagccgc tggtggagaa
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1856

<210> 5084
<211> 396
<212> PRT
<213> Homo sapiens

<400> 5084
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Asp Ser Glu Gly Gly Ala Ala Gly Gly Glu Ala Asp Met Asp Phe Leu
35 40 45
Arg Asn Leu Phe Ser Gln Thr Leu Ser Leu Gly Ser Gln Lys Glu Arg
50 55 60
Leu Leu Asp Glu Leu Thr Leu Glu Gly Val Ala Arg Tyr Met Gln Ser
65 70 75 80
Glu Arg Cys Arg Arg Val Ile Cys Leu Val Gly Ala Gly Ile Ser Thr
85 90 95
Ser Ala Gly Ile Pro Asp Phe Arg Ser Pro Ser Thr Gly Leu Tyr Asp
100 105 110
Asn Leu Glu Lys Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe Glu Ile
115 120 125
Ser Tyr Phe Lys Lys His Pro Glu Pro Phe Phe Ala Leu Ala Lys Glu
130 135 140
Leu Tyr Pro Gly Gln Phe Lys Pro Thr Ile Cys His Tyr Phe Met Arg
145 150 155 160
Leu Leu Lys Asp Lys Gly Leu Leu Leu Arg Cys Tyr Thr Gln Asn Ile
165 170 175
Asp Thr Leu Glu Arg Ile Ala Gly Leu Glu Gln Glu Asp Leu Val Glu
180 185 190
Ala His Gly Thr Phe Tyr Thr Ser His Cys Val Ser Ala Ser Cys Arg
195 200 205
His Glu Tyr Pro Leu Ser Trp Met Lys Glu Lys Ile Phe Ser Glu Val

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    210                 215                 220
Thr Pro Lys Cys Glu Asp Cys Gln Ser Leu Val Lys Pro Asp Ile Val
225                 230                 235                 240
Phe Phe Gly Glu Ser Leu Pro Ala Arg Phe Phe Ser Cys Met Gln Ser
                245                 250                 255
Asp Phe Leu Lys Val Asp Leu Leu Leu Val Met Gly Thr Ser Leu Gln
            260                 265                 270
Val Gln Pro Phe Ala Ser Leu Ile Ser Lys Ala Pro Leu Ser Thr Pro
        275                 280                 285
Arg Leu Leu Ile Asn Lys Glu Lys Ala Gly Gln Ser Asp Pro Phe Leu
    290                 295                 300
Gly Met Ile Met Gly Leu Gly Gly Gly Met Asp Phe Asp Ser Lys Lys
305                 310                 315                 320
Ala Tyr Arg Asp Val Ala Trp Leu Gly Glu Cys Asp Gln Gly Cys Leu
                325                 330                 335
Ala Leu Ala Glu Leu Leu Gly Trp Lys Lys Glu Leu Glu Asp Leu Val
            340                 345                 350
Arg Arg Glu His Ala Ser Ile Asp Ala Gln Ser Gly Ala Gly Val Pro
        355                 360                 365
Asn Pro Ser Thr Ser Ala Ser Pro Lys Lys Ser Pro Pro Pro Ala Lys
    370                 375                 380
Asp Glu Ala Arg Thr Thr Glu Arg Glu Lys Pro Gln
385                 390                 395
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<210> 5085
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<212> DNA
<213> Homo sapiens

<400> 5085

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Glu Thr Gly Trp Phe Asp Asn Leu Leu Leu Asp Ile Asp Lys Ala Asp
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Ala Ile Val Lys Met Leu Asp Ala Ala Val Ile Lys Met Glu Gly Gly
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Glu Ser Glu Ser Gly Gln Ala Glu Glu Glu Lys Glu Glu Ala Glu Glu
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Ala Leu Lys Glu Lys Glu Lys Pro Lys Glu Glu Glu Trp Glu Lys Pro
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Lys Asp Ala Ala Gly Leu Glu Cys Lys Pro Arg Pro Leu His Lys Thr
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Cys Ser Leu Phe Met Arg Asn Ile Ala Pro Asn Ile Ser Arg Ala Glu
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Ala Lys Arg Pro Ala Leu Pro Glu Ile Lys Pro Ala Gln Pro Pro Gly
675 680 685
Pro Ala Gln Ile Leu Pro Pro Gly Leu Thr Pro Gly Leu Pro Tyr Pro
690 695 700
His Gln Thr Pro Gln Gly Leu Met Pro Tyr Gly Gln Pro Arg Pro Pro
705 710 715 720
Ile Leu Gly Tyr Gly Ala Gly Ala Val Arg Pro Ala Val Pro Thr Gly
725 730 735
Gly Pro Pro Tyr Pro His Ala Pro Tyr Gly Ala Gly Arg Gly Asn Tyr
740 745 750
Asp Ala Phe Arg Gly Gln Gly Gly Tyr Pro Gly Lys Pro Arg Asn Arg
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<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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Gln Gly Arg Ser Cys Pro Gly Thr Pro Asp Ile Ala Asp Val Ala Glu
35 40 45
Leu Arg Val Glu Leu Thr His Gly Ala Glu Thr Leu Thr Leu Trp Gln
50 55 60
Ser Thr Gly Pro Trp Xaa Pro Trp Xaa Trp Gln Glu Leu Ala Val Thr
65 70 75 80
Thr Gly Arg Ile Arg Gly Asp Phe Arg Val Thr Phe Ser Ala Thr Arg
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Asn Ala Thr His Arg Gly Ala Val Ala Leu Asp Asp Leu Glu Phe Trp
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Asp Cys Gly Leu Pro Thr Pro Gln Ala Asn Cys Pro Pro Gly His His

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Arg His Ile Ala Thr Asp Phe Glu Thr Gly Leu Gly Pro Trp Asn Arg
                165                 170                 175
Ser Glu Gly Trp Ser Arg Asn His Arg Ala Gly Gly Pro Glu Arg Pro
            180                 185                 190
Ser Trp Pro Arg Arg Asp His Ser Arg Asn Ser Ala Xaa Arg Leu Val
        195                 200                 205
Phe Tyr Gln Tyr Leu Ser Gly Ser Glu Ala Gly Cys Leu Gln Leu Phe
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Leu Gln Thr Leu Gly Pro Gly Ala Pro Arg Ala Pro Val Leu Leu Arg
225                 230                 235                 240
Arg Arg Arg Gly Glu Leu Gly Thr Ala Trp Val Arg Asp Arg Val Asp
                245                 250                 255
Ile Gln Ser Ala Tyr Pro Phe Gln Ile Leu Leu Ala Gly Gln Thr Gly
            260                 265                 270
Pro Gly Gly Val Val Gly Leu Asp Asp Leu Ile Leu Ser Asp His Cys
        275                 280                 285
Arg Pro Val Ser Glu Val Ser Thr Leu Gln Pro Leu Pro Pro Gly Pro
    290                 295                 300
Arg Ala Pro Ala Pro Gln Pro Leu Pro Pro Ser Ser Arg Leu Gln Asp
305                 310                 315                 320
Ser Cys Lys Gln Gly His Leu Ala Cys Gly Asp Leu Cys Val Pro Pro
                325                 330                 335
Glu Gln Leu Cys Asp Phe Glu Glu Gln Cys Ala Gly Gly Glu Asp Glu
            340                 345                 350
Gln Ala Cys Gly Thr Thr Asp Phe Glu Ser Pro Glu Ala Gly Gly Trp
        355                 360                 365
Glu Asp Ala Ser Val Gly Arg Leu Gln Trp Arg Arg Val Ser Ala Gln
    370                 375                 380
Glu Ser Gln Gly Ser Ser Ala Ala Ala Ala Gly His Phe Leu Ser Leu
385                 390                 395                 400
Gln Arg Ala Trp Gly Gln Leu Gly Ala Glu Ala Arg Val Leu Thr Pro
                405                 410                 415
Leu Leu Gly Pro Ser Gly Pro Ser Cys Glu Leu His Leu Ala Tyr Tyr
            420                 425                 430
Leu Gln Ser Gln Pro Arg Ala Gly Phe Val Gly Leu Val Asp Leu Asp
        435                 440                 445
Gly Pro Asp Gln Gln Xaa Ser Trp Gly Gly Gln Arg Asp Pro Glu Gly
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Leu
465
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<211> 793
<212> DNA
<213> Homo sapiens

<400> 5089
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<212> PRT
<213> Homo sapiens

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Asp Ser Ser Pro Gly Phe Ser Lys Glu Ile Ala Ala Ala Leu Ala Gly
        35   40   45
Val Pro Gly Phe Glu Val Ser Ala Ala Gly Leu Glu Leu Gly Leu Gly
    50   55   60
Leu Glu Asp Glu Leu Arg Met Glu Pro Leu Gly Leu Glu Gly Leu Asn
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<210> 5091
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<212> DNA
<213> Homo sapiens

<400> 5091

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<211> 632
<212> PRT
<213> Homo sapiens

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Arg Asp Pro Ile Ser Leu Asp Cys Gly His Asp Phe Cys Ile Arg Cys
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Phe Ser Thr His Arg Leu Pro Gly Cys Glu Pro Pro Cys Cys Pro Glu
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Cys Arg Lys Ile Cys Lys Gln Lys Arg Gly Leu Arg Ser Leu Gly Glu
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Lys Met Lys Leu Leu Pro Gln Arg Pro Leu Pro Pro Ala Leu Gln Glu
115 120 125
Thr Cys Pro Val Arg Ala Glu Pro Leu Leu Leu Val Arg Ile Asn Ala
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145 150 155 160
His Pro Leu Ala Arg Asp Thr Pro Val Cys Leu Leu Ala Val Leu Gly
165 170 175
Glu Gln His Ser Gly Lys Ser Phe Leu Leu Asn His Leu Leu Gln Gly
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Leu Pro Gly Leu Glu Ser Gly Glu Gly Gly Arg Pro Arg Gly Gly Glu
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Ala Ser Leu Gln Gly Cys Arg Trp Gly Ala Asn Gly Leu Ala Gly Gly
210 215 220
Ile Trp Met Trp Ser His Pro Phe Leu Leu Gly Lys Glu Gly Lys Lys
225 230 235 240
Val Ala Val Phe Leu Val Asp Thr Gly Asp Ala Met Ser Pro Glu Leu
245 250 255
Ser Arg Glu Thr Arg Ile Lys Leu Cys Ala Leu Thr Thr Met Leu Ser
260 265 270
Ser Tyr Gln Ile Leu Ser Thr Ser Gln Glu Leu Lys Asp Thr Asp Leu
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Tyr Gly Met Val Pro Ile Gln His Leu Asp Leu Leu Val Arg Asp Ser
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Ser His Pro Asn Lys Ala Gly Gln Gly His Val Gly Asn Ile Phe Gln
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Lys Asn Leu Ser Gly Trp Met Gly Arg Thr Gly Pro Gly Phe Thr Ser
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450 455 460
Ala Lys Arg Glu Phe Glu Glu Tyr Val Arg Gln Gln Asp Val Ala Thr
465 470 475 480
Lys Arg Ile Phe Ser Ala Leu Arg Val Leu Pro Asp Thr Met Arg Asn
485 490 495
Leu Leu Ser Thr Gln Lys Asp Ala Ile Leu Ala Arg His Gly Val Ala
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Leu Leu Cys Lys Gly Arg Asp Gln Thr Leu Glu Ala Leu Glu Ala Glu
515 520 525
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Gly Leu Ala Gly Gly Val Val Gly Ala Gly Met Ala Ala Ala Ala Leu
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Gly Ala Ala Val Val Gly Gly Gly Val Gly Ala Gly Leu Ala Ala Thr
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<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

<400> 5094
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Glu Leu Met Pro Ser Ser Arg Leu Trp Ser Leu Ser Tyr Thr Lys Leu

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Pro Ser Leu Ser Tyr Thr Lys Trp Lys Cys Leu Leu Tyr Cys Asn Gly
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Val Leu Glu Pro Leu Tyr Leu Cys Pro Asn Gly Ala Arg Cys Ala Thr
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Trp Phe Gln Asp Pro Thr Arg Phe Thr Gly Thr Met Asp Ala Phe Val
            100                 105                 110
Lys Ile Val Arg His Glu Gly Thr Arg Thr Leu Trp Ser Gly Leu Pro
        115                 120                 125
Ala Thr Leu Val Met Thr Val Pro Ala Thr Ala Ile Tyr Phe Thr Ala
    130                 135                 140
Tyr Asp Gln Leu Lys Ala Phe Leu Cys Gly Arg Ala Leu Thr Ser Asp
145                 150                 155                 160
Leu Tyr Ala Pro Met Val Ala Gly Ala Leu Ala Arg Leu Gly Thr Val
                165                 170                 175
Thr Val Ile Ser Pro Leu Glu Leu Met Arg Thr Lys Leu Gln Ala Gln
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His Val Ser Tyr Arg Glu Leu Gly Ala Cys Val Arg Thr Ala Val Ala
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Gln Gly Gly Trp Arg Ser Leu Trp Leu Gly Trp Gly Pro Thr Ala Leu
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Arg Asp Val Pro Phe Ser Val His Pro Pro Pro Gln Ala Leu Tyr Trp
225                 230                 235                 240
Phe Asn Tyr Glu Leu Val Lys Ser Trp Leu Asn Gly Leu Arg Pro Lys
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Asp Gln Thr Ser Val Gly Met Ser Phe Val Ala Gly Gly Ile Ser Gly
            260                 265                 270
Thr Val Ala Ala Val Leu Thr Leu Pro Phe Asp Val Val Lys Thr Gln
        275                 280                 285
Arg Gln Val Ala Leu Gly Ala Met Glu Ala Val Arg Val Asn Pro Leu
    290                 295                 300
His Val Asp Ser Thr Trp Leu Leu Leu Arg Arg Ile Arg Ala Glu Ser
305                 310                 315                 320
Gly Thr Lys Gly Leu Phe Ala Gly Phe Leu Pro Arg Ile Ile Lys Ala
                325                 330                 335
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<212> DNA
<213> Homo sapiens

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<211> 153
<212> PRT
<213> Homo sapiens

<400> 5096
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35 40 45
Gln Gln His Phe Pro Val Gly Thr Ala Pro Gly Asn Pro Val Pro Ser
50 55 60
Glu Gln Gly Gly Arg Thr His Pro Ser Leu Ile Arg Ile Trp Ala Arg
65 70 75 80
Arg Ala Gln Gln Gly Arg Leu Leu Arg Leu Pro Thr Ser Gln His Arg
85 90 95
Leu Ser Gly Leu Asn Pro Ser Val Leu Phe Pro Ser Trp Leu Ile Gly
100 105 110
Arg Pro Phe Ala Gly Thr His Cys Phe Asn Leu Thr Leu Pro Pro Pro
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Pro Phe Asn Lys Ser Tyr Ala Gln Met
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<210> 5097
<211> 3074
<212> DNA
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atgggatttt cacagatgct gcagacgggg gcgaatttcc tgtagaagtc gtccaggcag
2220
tacacctcgt tctggctgcc cagggcaaag ctctcatccc caatgcaccg ggcgcaggtc
2280
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2340
accacctcgc cacacttgcc gcacctctcc agtgtgtcct ggtagcaggg ttcgcagagg
2400
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2460
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3060
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3074

<210> 5098
<211> 114
<212> PRT
<213> Homo sapiens

<400> 5098
Met Ala Val Pro Gln Leu Gly Pro Ile Pro Val His Val Arg Thr Lys
1 5 10 15
Gly Val Phe Ala Ile Met Leu Pro Thr Lys Ser Lys Glu Cys Trp Phe

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            20                  25                  30
Pro Ser Phe Gln Pro Gln His Phe Gln Lys Ala Leu Phe Phe Leu Glu
        35                  40                  45
Thr Glu Ser Arg Cys Val Ser Gln Ala Gly Val Gln Arg Gly Asp Leu
    50                  55                  60
Ser Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Gln Phe Ser Cys Leu
65                  70                  75                  80
Ser Leu Pro Ser Ser Trp Asp Tyr Arg Cys Val Pro Pro His Pro Ala
                85                  90                  95
Asn Phe Cys Ile Phe Ser Arg Asn Gly Val Ser Pro His Trp Pro Gly
            100                 105                 110
Trp Ser
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<210> 5099
<211> 801
<212> DNA
<213> Homo sapiens

<400> 5099
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ttgcatcttt acccactaga cttctgcact gacccagggg ctggagcgaa tcccagacca
180
gctcggctac ctggtactga gtgaaggtgc agtgctggcg ggcagcaagt gtgaagacag
240
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420
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480
cccattgatg tctgagcctg ccggagggcg agggtcggag aagcggattg ggtcctgggc
540
ctctgtgatg aggcaggcac acctgtcggt cttggcttgc tgctagaact agggccttct
600
gctcgcccac ctcccacccc tacctggacg ggcccaggct tggggactct gagctgtgtt
660
aaggagaaca agggcaagga gacctccctt tgtgctccct cactccctaa taaacatgag
720
tctgatgttc tccaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
780
aaaaaaaaaa aaaaaaaaaa a
801

<210> 5100
<211> 102
<212> PRT
<213> Homo sapiens

<400> 5100
Ala Cys Arg Arg Ala Arg Val Gly Glu Ala Asp Trp Val Leu Gly Leu
1 5 10 15
Cys Asp Glu Ala Gly Thr Pro Val Gly Leu Gly Leu Leu Leu Glu Leu
20 25 30
Gly Pro Ser Ala Arg Pro Pro Pro Thr Pro Thr Trp Thr Gly Pro Gly
35 40 45
Leu Gly Thr Leu Ser Cys Val Lys Glu Asn Lys Gly Lys Glu Thr Ser
50 55 60
Leu Cys Ala Pro Ser Leu Pro Asn Lys His Glu Ser Asp Val Leu Gln
65 70 75 80
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
85 90 95
Lys Lys Lys Lys Lys Lys
100

<210> 5101
<211> 1711
<212> DNA
<213> Homo sapiens

<400> 5101
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120
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180
tatcagcccc gtgccctgga gaaacatgct gacagcatcc tggcactggc ttcagtattc
240
tggtccatct cttattactc ctctcccttc gccttcttct acttgtacag gaaaggttac
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360
gcaggtgtgg cctgcctccg aggcattggc cgctggacca acccccagta ccggcagttc
420
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480
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540
cggaaggagt ctcgaggggg cccttcccgc cggggtgtgg ccctgcttcg cccagagccc
600
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720
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gccaatgcca tggatgtggt ggttcagttt gccatccacc gcctgggctt ccagccccag
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1260
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1320
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1380
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1440
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1560
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1620
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1680
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1711

<210> 5102
<211> 436
<212> PRT
<213> Homo sapiens

<400> 5102
Met Ala Lys Leu Leu Ser Cys Val Leu Gly Pro Arg Leu Tyr Lys Ile
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Tyr Arg Glu Arg Asp Ser Glu Arg Ala Pro Ala Ser Val Pro Glu Thr
20 25 30
Pro Thr Ala Val Thr Ala Pro His Ser Ser Ser Trp Asp Thr Tyr Tyr
35 40 45
Gln Pro Arg Ala Leu Glu Lys His Ala Asp Ser Ile Leu Ala Leu Ala
50 55 60
Ser Val Phe Trp Ser Ile Ser Tyr Tyr Ser Ser Pro Phe Ala Phe Phe
65 70 75 80
Tyr Leu Tyr Arg Lys Gly Tyr Leu Ser Leu Ser Lys Val Val Pro Phe
85 90 95
Ser His Tyr Ala Gly Thr Leu Leu Leu Leu Leu Ala Gly Val Ala Cys
100 105 110
Leu Arg Gly Ile Gly Arg Trp Thr Asn Pro Gln Tyr Arg Gln Phe Ile
115 120 125
Thr Ile Leu Glu Ala Thr His Arg Asn Gln Ser Ser Glu Asn Lys Arg
130 135 140
Gln Leu Ala Asn Tyr Asn Phe Asp Phe Arg Ser Trp Pro Val Asp Phe
145 150 155 160
His Trp Glu Glu Pro Ser Ser Arg Lys Glu Ser Arg Gly Gly Pro Ser

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                165                 170                 175
Arg Arg Gly Val Ala Leu Leu Arg Pro Glu Pro Leu His Arg Gly Thr
            180                 185                 190
Ala Asp Thr Leu Leu Asn Arg Val Lys Lys Leu Pro Cys Gln Ile Thr
        195                 200                 205
Ser Tyr Leu Val Ala His Thr Leu Gly Arg Arg Met Leu Tyr Pro Gly
    210                 215                 220
Ser Val Tyr Leu Leu Gln Lys Ala Leu Met Pro Ala Leu Leu Gln Gly
225                 230                 235                 240
Gln Ala Arg Leu Val Glu Glu Cys Asn Gly Arg Arg Ala Lys Leu Leu
                245                 250                 255
Ala Cys Asp Gly Asn Glu Ile Asp Thr Met Phe Val Asp Arg Arg Gly
            260                 265                 270
Thr Ala Glu Pro Gln Gly Gln Lys Leu Val Ile Cys Cys Glu Gly Asn
        275                 280                 285
Ala Gly Phe Tyr Glu Val Gly Cys Val Ser Thr Pro Leu Glu Ala Gly
    290                 295                 300
Tyr Ser Val Leu Gly Trp Asn His Pro Gly Phe Ala Gly Ser Thr Gly
305                 310                 315                 320
Val Pro Phe Pro Gln Asn Glu Ala Asn Ala Met Asp Val Val Val Gln
                325                 330                 335
Phe Ala Ile His Arg Leu Gly Phe Gln Pro Gln Asp Ile Val Ile Tyr
            340                 345                 350
Ala Trp Ser Ile Gly Gly Phe Thr Ala Thr Trp Ala Ala Met Ser Tyr
        355                 360                 365
Pro Asp Val Ser Ala Met Ile Leu Asp Ala Ser Phe Asp Asp Leu Val
    370                 375                 380
Pro Leu Ala Leu Lys Val Met Pro Asp Ser Trp Arg Gly Leu Val Thr
385                 390                 395                 400
Arg Thr Val Arg Gln His Leu Asn Leu Asn Asn Ala Glu Gln Leu Cys
                405                 410                 415
Arg Tyr Gln Gly Pro Val Leu Leu Ile Arg Arg Thr Lys Asp Glu Ile
            420                 425                 430
Ile Thr Thr Thr
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<210> 5103
<211> 1982
<212> DNA
<213> Homo sapiens

<400> 5103

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120
aatttaggcc aatacataac tagatttgaa taaagtcaga tgaagcaata attcctcctc
180
tgtgtttgaa aggaatgagt gtggttacaa agtcacagga tgagtccctg ggatctgggg
240
tgggagaagg ggtggatcaa gaatgacttg ggtttgtcac tccctagcag gctgagggcg
300
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360
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480
gaaaactggg gaggggggaac agggagacag aatcttcatc ttcttccttt tgtgaactgg
540
ggaggagggt gcttggtgac attttcctga gtataaagaa ggaatacagg tttgaaaggt
600
ttgtaattgt atatgaaaac aggtattgaa aaccaatact gggggaaaaa aggcattgta
660
aacacttcta tttaaaatga agatttctgg aacaactata ctatatagtg gtatcacaag
720
tctttagctg gtaagatcta gcactgaaac aactcttaat ttttaacttg tgagggttct
780
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900
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960
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1020
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1140
tggaaccagt tttaacaatc tctgaaaact ttaaattcta gacatgttta ttttgaaaca
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1620
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1680
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1740
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1800
tctattgctt tcctctccag ctcctgatcc tcttccatcg ctggggcggt ttctggatcc
1860
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1920
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1980

gg
1982

<210> 5104
<211> 167
<212> PRT
<213> Homo sapiens

<400> 5104
Met Phe Ile Leu Lys His Thr Ser Lys Gln Asp Lys Gln Gln Tyr Val
1 5 10 15
Ser Leu Leu His Cys Arg Ser Ser Leu Asn Leu Pro Arg His Pro Pro
20 25 30
Leu His Leu Phe Pro Gln Glu Leu Leu Gly His Phe Phe Cys Leu Trp
35 40 45
Pro Ala Ala Ser Leu Lys Thr Thr Lys Asp Leu Met Ser Lys Ser Leu
50 55 60
Ser Gly Val Cys Pro Ala Ser Ser Gly Leu Leu Arg Thr Pro His Pro
65 70 75 80
Glu Gly Ala Arg Arg Pro Ala Gly Leu Ala Gly Pro Gly Ser Ser Leu
85 90 95
Thr Ala Gly Trp Thr Ala Phe Arg Thr Cys Pro Gly Cys Ser Ala Phe
100 105 110
Val Ala Gly Ser Asn Trp Arg Asn Leu Glu Arg Gly Ser Cys Ala Cys
115 120 125
Lys Asp Gly Phe Cys Val Ser Ser Gly Phe Leu Leu Ser Gly Pro Gly
130 135 140
Ser Ser Leu Val Pro Tyr Arg Pro Leu Phe Val His Gly Leu Ala Leu
145 150 155 160
Tyr Glu Arg Ala Met Cys Phe
165

<210> 5105
<211> 1359
<212> DNA
<213> Homo sapiens

<400> 5105
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180
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240
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420
caacaacgag atcctcagtg ggctggacat ggaggaaggc aaggaaggag gcacatggct
480

gggcatcagc acacgtggca agctggcagc actcaccaac tacctgcagc cgcagctgga
540
ctggcaggcc cgagggcgag cacagcaaag ggagacgtca tttgctacta tgggaaccga
600
ggggagcctg atcctatcgt tttgacgccc ggcacgtacg ggctgagcaa cgcgctgctg
660
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720
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780
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840
ctgagcaagt acgcggctgt gtgcgtgcgc tgccctggct acggcaccag aaccaacact
900
atcatcctgg tagatgcgga cggccacgtg accttcactg agcgtagcat gatggacaag
960
gacctctccc actgggagac cagaacctat gagttcacac tgcagagcta accccacctc
1020
tgggcctggc cagtgggctc ctgggggcc ctgccttgag gggcactgtg gacaggaaac
1080
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1140
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1200
gccagtgagg agcagcagag tctgatacta ggtctaggac cggccgaggt ataccatgaa
1260
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1320
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1359

<210> 5106
<211> 178
<212> PRT
<213> Homo sapiens

<400> 5106
Met Ala Gly His Gln His Thr Trp Gln Ala Gly Ser Thr His Gln Leu
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Pro Ala Ala Ala Ala Gly Leu Ala Gly Pro Arg Ala Ser Thr Ala Lys
20 25 30
Gly Asp Val Ile Cys Tyr Tyr Gly Asn Arg Gly Glu Pro Asp Pro Ile
35 40 45
Val Leu Thr Pro Gly Thr Tyr Gly Leu Ser Asn Ala Leu Leu Glu Thr
50 55 60
Pro Trp Arg Lys Leu Cys Phe Gly Lys Gln Leu Phe Leu Glu Ala Val
65 70 75 80
Glu Arg Ser Gln Ala Leu Pro Lys Asp Val Leu Ile Ala Ser Leu Leu
85 90 95
Asp Val Leu Asn Asn Glu Glu Ala Gln Leu Pro Asp Pro Ala Ile Glu
100 105 110
Asp Gln Gly Gly Glu Tyr Val Gln Pro Met Leu Ser Lys Tyr Ala Ala
115 120 125
Val Cys Val Arg Cys Pro Gly Tyr Gly Thr Arg Thr Asn Thr Ile Ile

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    130                 135                 140
Leu Val Asp Ala Asp Gly His Val Thr Phe Thr Glu Arg Ser Met Met
145                 150                 155                 160
Asp Lys Asp Leu Ser His Trp Glu Thr Arg Thr Tyr Glu Phe Thr Leu
                165                 170                 175
Gln Ser
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<210> 5107
<211> 1207
<212> DNA
<213> Homo sapiens

<400> 5107
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120
acagggatga ccaccacctg gaacggggac agccacagtg gccatttccc cccgcagctt
180
tctgccagca ctcccaacag tctttccaca gaaccgagca ctgctcggtg aatgaggact
240
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300
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420
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600
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660
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720
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780
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840
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1080
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1200

ggccggc
1207

<210> 5108
<211> 83
<212> PRT
<213> Homo sapiens

<400> 5108
Met Arg Thr Gly Arg Ser Arg Ala Pro Ala Pro Val Cys Ile Tyr Leu
1 5 10 15
Phe Ile Tyr Leu Phe Arg Asp Arg Val Ser Leu Cys Arg Xaa Arg Gly
20 25 30
Val Gln Trp Arg Asn Leu Ser Ser Leu Gln Pro Pro Pro Pro Gly Phe
35 40 45
Lys Arg Phe Ser Cys Leu Ser Leu Leu Ser Ser Trp Asp Tyr Arg Arg
50 55 60
Val Pro Pro Cys Pro Ala Asn Phe Cys Ile Phe Ser Arg Asp Arg Val
65 70 75 80
Ser Pro Cys

<210> 5109
<211> 651
<212> DNA
<213> Homo sapiens

<400> 5109
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ctgcagnatg cgcagtggac ttttgaatca gctgtgcaag agaatatcag cattaatggg
120
caagcatggc aggaagcttc agataattgt tttatggatt ctgacatcaa agtacttgaa
180
gatcagtttg atgaaatcat agtagatata gccacaaaac gtaagcagta tcccagaaag
240
atcctggaat gtgtcatcaa aaccataaaa gcaaaacaag aaattctgaa gcagtaccac
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480
agtgaagcca tgaagtcctt gcctgcatta attgaacaag gagagggatt ttcccaagtt
540
ctcaggatgc agcctgttat ccacctccag aggattcacc aagaagtctt ttccagttgt
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651

<210> 5110
<211> 206
<212> PRT

<213> Homo sapiens

<400> 5110

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            20                  25                  30
Gln Glu Ala Ser Asp Asn Cys Phe Met Asp Ser Asp Ile Lys Val Leu
        35                  40                  45
Glu Asp Gln Phe Asp Glu Ile Ile Val Asp Ile Ala Thr Lys Arg Lys
    50                  55                  60
Gln Tyr Pro Arg Lys Ile Leu Glu Cys Val Ile Lys Thr Ile Lys Ala
65                  70                  75                  80
Lys Gln Glu Ile Leu Lys Gln Tyr His Pro Val Val His Pro Leu Asp
                85                  90                  95
Leu Lys Tyr Asp Pro Asp Pro Val Leu Asn Gly Asn Ala Phe Asn Phe
            100                 105                 110
Ser Pro Phe Asn Met Met Leu Ala Val Asp Leu Ser Tyr Met Val Phe
        115                 120                 125
Ile Thr Ser Ala Pro His Met Glu Asn Leu Lys Cys Arg Gly Glu Thr
    130                 135                 140
Val Ala Lys Glu Ile Ser Glu Ala Met Lys Ser Leu Pro Ala Leu Ile
145                 150                 155                 160
Glu Gln Gly Glu Gly Phe Ser Gln Val Leu Arg Met Gln Pro Val Ile
                165                 170                 175
His Leu Gln Arg Ile His Gln Glu Val Phe Ser Ser Cys His Arg Lys
            180                 185                 190
Pro Asp Ala Lys Pro Glu Asn Phe Ile Thr Gln Ile Glu Thr
        195                 200                 205
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<210> 5111
<211> 2247
<212> DNA
<213> Homo sapiens

<400> 5111

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120
tggtgcgcag gcgcgggccg ccgcggcccg gctctcttgc gcaagcgcgc tgtccgcttc
180
ttctgggcgg acgctctgga ggcaaaacat ttccctgctg ggggcggcga ccaccgtgag
240
cgtcccggaa ggggcggcaa agacgcctcc gtcgcgcacg aggtggcctc gttggcttta
300
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360
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420
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480
tctatcggct gcacgccaac atcaacacag gcgaagatgg tctccaagcg cattgcccag
540
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gagacctttg atgcagctgt gcgcgagaac atcgaggagt ttgcgatggg gccagaggag
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660
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780
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960
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1080
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1140
caccacactg acgtggtcag ggaagcctgc tgggccctgc gtgtcatgac cttcgatgac
1200
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1260
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1320
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1440
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1560
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1620
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1680
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1740
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1920
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1980
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2040
tcccccttcac aatgagaagt gttttctggc aggccctagg taaagggtcg ggggaggggg
2100
gagccttgta gggaggcctc tacacagaag aaagcagccc ccatgtccca gccacttctg
2160

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2220
cagaggggggc aaagggcacg tcccatc
2247

<210> 5112
<211> 581
<212> PRT
<213> Homo sapiens

<400> 5112
Ala Lys His Phe Pro Ala Gly Gly Gly Asp His Arg Glu Arg Pro Gly
1 5 10 15
Arg Gly Gly Lys Asp Ala Ser Val Ala His Glu Val Ala Ser Leu Ala
20 25 30
Leu Pro Trp Phe Ala Val Val Leu Gly Tyr Arg Glu Arg Pro Arg Val
35 40 45
Ser Gly Arg Pro Ser Leu Gly Ala Pro Gln Arg Leu Arg Ala Tyr Gly
50 55 60
Gly Arg Lys Gly Leu Glu Ala Ala Pro Trp Val Thr Thr Ala Arg Pro
65 70 75 80
Thr Phe Pro His Val Ala Ala Lys Thr Gly Ser Gly Ala Ser Ile Gly
85 90 95
Cys Thr Pro Thr Ser Thr Gln Ala Lys Met Val Ser Lys Arg Ile Ala
100 105 110
Gln Glu Thr Phe Asp Ala Ala Val Arg Glu Asn Ile Glu Glu Phe Ala
115 120 125
Met Gly Pro Glu Glu Ala Val Lys Glu Ala Val Glu Gln Phe Glu Ser
130 135 140
Gln Gly Val Asp Leu Ser Asn Ile Val Lys Thr Ala Pro Lys Val Ser
145 150 155 160
Ala Asp Gly Ser Gln Glu Pro Thr His Asp Ile Leu Gln Met Leu Ser
165 170 175
Asp Leu Gln Glu Ser Val Ala Ser Ser Arg Pro Gln Glu Val Ser Ala
180 185 190
Tyr Leu Thr Arg Phe Cys Asp Gln Cys Lys Gln Asp Lys Ala Cys Arg
195 200 205
Phe Leu Ala Ala Gln Lys Gly Ala Tyr Pro Ile Ile Phe Thr Ala Arg
210 215 220
Lys Leu Ala Thr Ala Gly Asp Gln Gly Leu Leu Leu Gln Ser Leu Asn
225 230 235 240
Ala Leu Ser Val Leu Thr Asp Gly Gln Pro Asp Leu Leu Asp Ala Gln
245 250 255
Gly Leu Gln Leu Leu Val Ala Thr Leu Thr Gln Asn Ala Asp Glu Ala
260 265 270
Asp Leu Thr Cys Ser Gly Ile Arg Cys Val Arg His Ala Cys Leu Lys
275 280 285
His Glu Gln Asn Arg Gln Asp Leu Val Lys Ala Gly Val Leu Pro Leu
290 295 300
Leu Thr Gly Ala Ile Thr His His Gly His His Thr Asp Val Val Arg
305 310 315 320
Glu Ala Cys Trp Ala Leu Arg Val Met Thr Phe Asp Asp Asp Ile Arg
325 330 335
Val Pro Phe Gly His Ala His Asn His Ala Lys Met Ile Val Gln Glu

```
            340                 345                 350
Asn Lys Gly Leu Lys Val Leu Ile Glu Ala Thr Lys Ala Phe Leu Asp
        355                 360                 365
Asn Pro Gly Ile Leu Ser Glu Leu Cys Gly Thr Leu Ser Arg Leu Ala
    370                 375                 380
Ile Arg Asn Glu Phe Cys Gln Glu Val Val Asp Leu Gly Gly Leu Ser
385                 390                 395                 400
Ile Leu Val Ser Leu Leu Ala Asp Cys Asn Asp His Gln Met Arg Asp
                405                 410                 415
Gln Ser Gly Val Gln Glu Leu Val Lys Gln Val Leu Ser Thr Leu Arg
            420                 425                 430
Ala Ile Ala Gly Asn Asp Asp Val Lys Asp Ala Ile Val Arg Ala Gly
        435                 440                 445
Gly Thr Glu Ser Ile Val Ala Ala Met Thr Gln His Leu Thr Ser Pro
    450                 455                 460
Gln Val Trp Glu Gln Ser Cys Ala Ala Leu Cys Phe Leu Ala Leu Arg
465                 470                 475                 480
Lys Pro Asp Asn Ser Arg Ile Ile Val Glu Gly Gly Gly Ala Val Ala
                485                 490                 495
Ala Leu Gln Ala Met Lys Ala His Pro Gln Lys Ala Gly Val Gln Lys
            500                 505                 510
Gln Ala Cys Met Leu Ile Arg Asn Leu Val Ala His Gly Gln Ala Phe
        515                 520                 525
Ser Lys Pro Ile Leu Asp Leu Gly Ala Glu Ala Leu Ile Met Gln Ala
    530                 535                 540
Arg Ser Ala His Arg Asp Cys Glu Asp Val Ala Lys Ala Ala Leu Arg
545                 550                 555                 560
Asp Leu Gly Cys His Val Glu Leu Arg Glu Leu Trp Thr Gly Gln Arg
                565                 570                 575
Gly Asn Leu Ala Pro
            580
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<210> 5113
<211> 472
<212> DNA
<213> Homo sapiens

<400> 5113
cagactatgg tccagcctct gctccatgtg ccccctgtgg gtctttgtga tctcagtcct
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ggcaccttga cccgctgctt gttctgctct cctttaaact ccatgcacct gacacctgta
120
attggcacgc agcgcggagc ctggcacctg cagtgtagac acactggcca ccgctcagtg
180
caagagggcc cctttgctaa tgtgcacagc tctttatgcc ttttttccta tgccttttg
240
gattggagca agagattttt ttttccaagt aaagaacaat ttatgttcct aaatactttt
300
tttccttgac atgatgaagt tgagcaaggt ggctatagaa ctttttttct taattttatt
360
gcccaagtaa tgttctttac aaagtaggga aatacagata cataaaaaga agactgccaa
420
tcccccgtaa tcccaccagt cgcatcccta cccgctctta ggagattccg ga
472

<210> 5114
<211> 100
<212> PRT
<213> Homo sapiens

<400> 5114
Met Val Gln Pro Leu Leu His Val Pro Pro Val Gly Leu Cys Asp Leu
1 5 10 15
Ser Pro Gly Thr Leu Thr Arg Cys Leu Phe Cys Ser Pro Leu Asn Ser
20 25 30
Met His Leu Thr Pro Val Ile Gly Thr Gln Arg Gly Ala Trp His Leu
35 40 45
Gln Cys Arg His Thr Gly His Arg Ser Val Gln Glu Gly Pro Phe Ala
50 55 60
Asn Val His Ser Ser Leu Cys Leu Phe Ser Tyr Ala Phe Leu Asp Trp
65 70 75 80
Ser Lys Arg Phe Phe Phe Pro Ser Lys Glu Gln Phe Met Phe Leu Asn
85 90 95
Thr Phe Phe Pro
100

<210> 5115
<211> 1003
<212> DNA
<213> Homo sapiens

<400> 5115
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ttttatttac aaaatatata ctgaatacta tacatctggc cccatcacca tggaaacaac
120
tccaaagcct gcctggggat ttgtgcccaa gcccagccca ggagggctag agaaagcaaa
180
ggtgtctacc agccgccgcc atcccagaag gaaagcctct tcccatgagt gcctgtgggt
240
gggcggtgag ctcaacaccc acaaagggca gaaggcctgg gggcagtgag gtgatggtga
300
gggcatggga agcagatgct gctgagggtg ggtggaggga gaaatggaga cccagcaccc
360
agcaggggga gccaggtgac agcaggggaa gcagatggca gggccccagg cagtccagga
420
ccccaggctc tgaagggtgg ggcaaggggg tcaggtcacg tcttgacatc cagcagtggc
480
tccgcttgtg ctggtagccc actctgccca gccatgtccc accttggggt ctcccatgtc
540
agagagcagc tcctgctcag catcatgcag ttcctcagct gggtcatagc tgtacatggg
600
gagcaggtgc atgcgcagcc ggtccacccg ctttttcttc tgtacataca ttaccacagc
660
caccaccacc ccgaccaggg tgatgaggaa gaagggcccc aacacatagc ccaccatgga
720
gtcgctgttg gcctgggggg cattgggcac agtggtgtta ctcatgacat cagcagccgg
780

agggctgggt ggtcagcatg ggcagtggcg cttcgggagg gcgcctccac tgggctcccc
840
agtcgtatgc tcatcgtccc aggtcaaggg ggcatgccag ggtggggagg gcgtcaggcc
900
gctgctagga tgcgggccag caacagcgga ncaggaggtg gttcccacgg cgctgggnag
960
gctcacgccg gaggtggggg tgttggggga tgctgatggg tcg
1003

<210> 5116
<211> 226
<212> PRT
<213> Homo sapiens

<400> 5116
Met Leu Leu Arg Val Gly Gly Gly Arg Asn Gly Asp Pro Ala Pro Ser
 1   5   10   15
Arg Gly Ser Gln Val Thr Ala Gly Glu Ala Asp Gly Arg Ala Pro Gly
            20   25   30
Ser Pro Gly Pro Gln Ala Leu Lys Gly Gly Ala Arg Gly Ser Gly His
        35   40   45
Val Leu Thr Ser Ser Ser Gly Ser Ala Cys Ala Gly Ser Pro Leu Cys
    50   55   60
Pro Ala Met Ser His Leu Gly Val Ser His Val Arg Glu Gln Leu Leu
65   70   75   80
Leu Ser Ile Met Gln Phe Leu Ser Trp Val Ile Ala Val His Gly Glu
                85   90   95
Gln Val His Ala Gln Pro Val His Pro Leu Phe Leu Leu Tyr Ile His
            100   105   110
Tyr His Ser His His His Pro Asp Gln Gly Asp Glu Glu Glu Gly Pro
        115   120   125
Gln His Ile Ala His His Gly Val Ala Val Gly Leu Gly Gly Ile Gly
    130   135   140
His Ser Gly Val Thr His Asp Ile Ser Ser Arg Arg Ala Gly Trp Ser
145   150   155   160
Ala Trp Ala Val Ala Leu Arg Glu Gly Ala Ser Thr Gly Leu Pro Ser
                165   170   175
Arg Met Leu Ile Val Pro Gly Gln Gly Gly Met Pro Gly Trp Gly Gly
            180   185   190
Arg Gln Ala Ala Ala Arg Met Arg Ala Ser Asn Ser Gly Xaa Gly Gly
        195   200   205
Gly Ser His Gly Ala Gly Xaa Ala His Ala Gly Gly Gly Gly Val Gly
    210   215   220
Gly Cys
225

<210> 5117
<211> 1180
<212> DNA
<213> Homo sapiens

<400> 5117
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gtgagcatgg ctgagagtga ggaccgctcc ctgaggatcg ttctggtagg gaaaactgga
120
agtgggaaaa gtgcaacagc gaacaccatc cttggagagg aaatctttga ttctagaatt
180
gctgcccaag ctgttaccaa gaactgtcaa aaagcatccc gggaatggca ggggagagac
240
cttcttgttg tagacactcc agggctcttt gacaccaagg agagcctgga caccacctgc
300
aaggaaatca gccgctgcat catctcctcc tgcccagggc cccatgctat tgtcctagtt
360
ctgctgctgg gccgctacac agaggaggag cagaaaaccg ttgcattgat caaggctgtc
420
tttgggaagt cagccatgaa gcacatggtc atcttgttca ctcgcaaaga agagttggag
480
ggccagagct tccatgactt catagcagat gcggatgtgg gcctaaaaag catcgtcaag
540
gagtgcggga accgctgctg tgcctttagc aacagcaaga aaaccagtaa ggcagagaag
600
gaaagtcaag tgcaggagtt ggtggagctg atagagaaaa tggtgcagtg caacgaaggg
660
gcttactttt ctgatgacat atacaaggac acagaggaaa ggctgaaaca acgggaagag
720
gttttgagga aaatctacac tgaccaatta aatgaagaaa ttaaactagt agaagaggat
780
aagcataaat cagaggaaga aaaggagaaa gaaattaaat tactaaaatt aaaatatgat
840
gaaaaaataa aaaatataag ggaagaagct gagagaaata tatttaaaga tgtttttaat
900
aggatttgga agatgctttc agaaatatgg cataggtttt tgtcgaaatg taagttttat
960
tcttcctaat ttactgtgat ttgttaatgg atgaattgta ttttgcaaag atagttagag
1020
aaatacctcc ttccccttag ctttattaag gtatcattga taaataaaaa taaaatatgt
1080
ttaatgtata taatgtgatt tttaaatata tatatatata tatacacaca ttgtgaaata
1140
atgaaataaa ggtaattaac acatctaaaa aaaaaaaaaa
1180

<210> 5118
<211> 300
<212> PRT
<213> Homo sapiens

<400> 5118
Met Ala Glu Ser Glu Asp Arg Ser Leu Arg Ile Val Leu Val Gly Lys
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Thr Gly Ser Gly Lys Ser Ala Thr Ala Asn Thr Ile Leu Gly Glu Glu
20 25 30
Ile Phe Asp Ser Arg Ile Ala Ala Gln Ala Val Thr Lys Asn Cys Gln
35 40 45
Lys Ala Ser Arg Glu Trp Gln Gly Arg Asp Leu Leu Val Val Asp Thr
50 55 60
Pro Gly Leu Phe Asp Thr Lys Glu Ser Leu Asp Thr Thr Cys Lys Glu

```
65                  70                  75                  80
Ile Ser Arg Cys Ile Ile Ser Ser Cys Pro Gly Pro His Ala Ile Val
                85                  90                  95
Leu Val Leu Leu Leu Gly Arg Tyr Thr Glu Glu Glu Gln Lys Thr Val
            100                 105                 110
Ala Leu Ile Lys Ala Val Phe Gly Lys Ser Ala Met Lys His Met Val
        115                 120                 125
Ile Leu Phe Thr Arg Lys Glu Glu Leu Glu Gly Gln Ser Phe His Asp
    130                 135                 140
Phe Ile Ala Asp Ala Asp Val Gly Leu Lys Ser Ile Val Lys Glu Cys
145                 150                 155                 160
Gly Asn Arg Cys Cys Ala Phe Ser Asn Ser Lys Lys Thr Ser Lys Ala
                165                 170                 175
Glu Lys Glu Ser Gln Val Gln Glu Leu Val Glu Leu Ile Glu Lys Met
            180                 185                 190
Val Gln Cys Asn Glu Gly Ala Tyr Phe Ser Asp Asp Ile Tyr Lys Asp
        195                 200                 205
Thr Glu Glu Arg Leu Lys Gln Arg Glu Glu Val Leu Arg Lys Ile Tyr
    210                 215                 220
Thr Asp Gln Leu Asn Glu Glu Ile Lys Leu Val Glu Glu Asp Lys His
225                 230                 235                 240
Lys Ser Glu Glu Glu Lys Glu Lys Glu Ile Lys Leu Leu Lys Leu Lys
                245                 250                 255
Tyr Asp Glu Lys Ile Lys Asn Ile Arg Glu Glu Ala Glu Arg Asn Ile
            260                 265                 270
Phe Lys Asp Val Phe Asn Arg Ile Trp Lys Met Leu Ser Glu Ile Trp
        275                 280                 285
His Arg Phe Leu Ser Lys Cys Lys Phe Tyr Ser Ser
    290                 295                 300
```

<210> 5119
<211> 1450
<212> DNA
<213> Homo sapiens

<400> 5119
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cagctggtga aaatcttatc cttgagtaga aaggaatcaa acaagtcata taccacccgt
120
cttcctgtct gtactggaac catcacaggc ttttgaggaa ctacttttga accgttcccc
180
agagaggcat ttgccccagt agctatgatt ataatttgca atgacagcca cagtgatttc
240
atccttctgg gcttctctaa caagccacat ttggagaaga tacttttttng gatcattttt
300
atttttttatt ttttgactct tgcaggaaat atggtcatag ttcttgtgtc cttgaaggat
360
ccaaaactcc acatccctat gtatttcttt ctttccaacc tttccttggt agacctctgt
420
ttgaccagca gctgtgttcc acagatgttg attaacttct ggggcccaga aaagaccatc
480
agctacattg gctgtgccat tcaactctat gtttttttgt ggcttggggc cacggaatat
540

gtccttcttg ttgtcatggc tgtggattgt tatgtagcag tgtgtcatcc actgcaaaat
600
accatgatca tgcacccaaa actttgtctg cagctggcta tcttggcatg ggggactggc
660
ttggcccagt ctctgatcca gtcccctgcc accctccggt tacccttctg ctcccagcgg
720
atggtggatg atgttgtttg tgaagtccca gctctgattc agctctccag tactgatact
780
acctacagtg aaattcagat gtctatcgcc agtgttgtcc tcctggtgat gcccttgatc
840
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900
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960
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1020
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1080
aggaacaagg aggtaaaggg agcactaata agattgggga ggaggacctg ggattcccag
1140
aataactaac aaggttaaca tatgtttacc tttgcttaac ctaagaatag agaacaacct
1200
catcacaaaa agctggagat acacctccta agccaaaagt aggagagaaa gagctgcatt
1260
ctgttcaggt tgagatttca gtttccttca tcaatcaatt gggcccttaa attcttcata
1320
ttgtggattt agacacagta tggtataaaa attaatatat ttaatagcta ttgtcttgaa
1380
aaggacacaa tgcaattgaa tgggggagga ggagaagaca caagaaacac attacttgca
1440
aaataaaata
1450

<210> 5120
<211> 314
<212> PRT
<213> Homo sapiens

<400> 5120
Met Ile Ile Ile Cys Asn Asp Ser His Ser Asp Phe Ile Leu Leu Gly
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Phe Ser Asn Lys Pro His Leu Glu Lys Ile Leu Phe Xaa Ile Ile Phe
            20   25   30
Ile Phe Tyr Phe Leu Thr Leu Ala Gly Asn Met Val Ile Val Leu Val
        35   40   45
Ser Leu Lys Asp Pro Lys Leu His Ile Pro Met Tyr Phe Phe Leu Ser
    50   55   60
Asn Leu Ser Leu Val Asp Leu Cys Leu Thr Ser Ser Cys Val Pro Gln
65   70   75   80
Met Leu Ile Asn Phe Trp Gly Pro Glu Lys Thr Ile Ser Tyr Ile Gly
                85   90   95
Cys Ala Ile Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Tyr
            100   105   110
Val Leu Leu Val Val Met Ala Val Asp Cys Tyr Val Ala Val Cys His

```
        115                 120                 125
Pro Leu Gln Asn Thr Met Ile Met His Pro Lys Leu Cys Leu Gln Leu
    130                 135                 140
Ala Ile Leu Ala Trp Gly Thr Gly Leu Ala Gln Ser Leu Ile Gln Ser
145                 150                 155                 160
Pro Ala Thr Leu Arg Leu Pro Phe Cys Ser Gln Arg Met Val Asp Asp
                165                 170                 175
Val Val Cys Glu Val Pro Ala Leu Ile Gln Leu Ser Ser Thr Asp Thr
            180                 185                 190
Thr Tyr Ser Glu Ile Gln Met Ser Ile Ala Ser Val Val Leu Leu Val
        195                 200                 205
Met Pro Leu Ile Ile Ile Leu Ser Ser Ser Gly Ala Ile Ala Lys Ala
    210                 215                 220
Val Leu Arg Ile Lys Ser Thr Ala Gly Gln Lys Lys Ala Phe Gly Thr
225                 230                 235                 240
Cys Ile Ser His Leu Leu Val Val Ser Leu Phe Tyr Gly Thr Val Thr
                245                 250                 255
Gly Val Tyr Leu Gln Pro Lys Asn His Tyr Pro His Glu Trp Gly Lys
            260                 265                 270
Phe Leu Thr Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Leu
        275                 280                 285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Ile Arg Leu
    290                 295                 300
Gly Arg Arg Thr Trp Asp Ser Gln Asn Asn
305                 310
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<210> 5121
<211> 944
<212> DNA
<213> Homo sapiens

<400> 5121
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cgggggcgac gcggctgagg gcttctcgtc ggggtcgggg ctgcagccgt catgccgggg
120
atagtggagc tgcccactct agaggagctg aaagtagatg aggtgaaaat tagttctgct
180
gtgcttaaag ctgcggccca tcactatgga gctcaatgtg ataagcccaa caaggagttt
240
atgctctgcc gctgggaaga gaaagatccg aggcggtgtt tagaggaagg caaactggtc
300
aacaagtgtg ctttggactt ctttaggcag ataaaacgtc actgtgcaga gccttttaca
360
gaatattgga cttgcattga ttatactggc cagcagttat ttcgtcactg tcgcaaacag
420
caggcaaagt ttgacgagtg tgtgctggac aaactgggct gggtgcggcc tgacctggga
480
gaactgtcaa aggtcaccaa agtgaaaaca gatcgacctt taccggagaa tcccctatcac
540
tcaagaccaa gaccggatcc cagccctgag atcgagggag atctgcagcc tgccacacat
600
ggcagccgct tttatttctg gaccaagtaa agatgggtcc gtggcccaca ctcggtcatg
660

tgctcagaca acgactgatg aaaacgccca tgcggtttgc atcgactgat agtgtgttct
720
ttccgggatc acaaacatta acaaaaaagt taacttatgt gacttggcag ttattctata
780
ccatttcctg tccattaaaa tttttaaagg aaacggttgt attttattat gttttatgtg
840
acctttggc ctttaaagat gacttcccct tgctttttc ttcttgtggt cctgcctgtt
900
cctcttgctt tgctttaggc actcgctcat gtggctgggg atcc
944

<210> 5122
<211> 172
<212> PRT
<213> Homo sapiens

<400> 5122
Met Pro Gly Ile Val Glu Leu Pro Thr Leu Glu Glu Leu Lys Val Asp
1 5 10 15
Glu Val Lys Ile Ser Ser Ala Val Leu Lys Ala Ala Ala His His Tyr
20 25 30
Gly Ala Gln Cys Asp Lys Pro Asn Lys Glu Phe Met Leu Cys Arg Trp
35 40 45
Glu Glu Lys Asp Pro Arg Arg Cys Leu Glu Glu Gly Lys Leu Val Asn
50 55 60
Lys Cys Ala Leu Asp Phe Phe Arg Gln Ile Lys Arg His Cys Ala Glu
65 70 75 80
Pro Phe Thr Glu Tyr Trp Thr Cys Ile Asp Tyr Thr Gly Gln Gln Leu
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Phe Arg His Cys Arg Lys Gln Gln Ala Lys Phe Asp Glu Cys Val Leu
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Asp Lys Leu Gly Trp Val Arg Pro Asp Leu Gly Glu Leu Ser Lys Val
115 120 125
Thr Lys Val Lys Thr Asp Arg Pro Leu Pro Glu Asn Pro Tyr His Ser
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Arg Pro Arg Pro Asp Pro Ser Pro Glu Ile Glu Gly Asp Leu Gln Pro
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Ala Thr His Gly Ser Arg Phe Tyr Phe Trp Thr Lys
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<211> 1139
<212> DNA
<213> Homo sapiens

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<210> 5124
<211> 101
<212> PRT
<213> Homo sapiens

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Gln Ala Cys Met Leu Ile Arg Asn Leu Val Ala His Gly Gln Ala Phe
35 40 45
Ser Lys Pro Ile Leu Asp Leu Gly Ala Glu Ala Leu Ile Met Gln Ala
50 55 60
Arg Ser Ala His Arg Asp Cys Glu Asp Val Ala Lys Ala Ala Leu Arg
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Asp Leu Gly Cys His Val Glu Leu Arg Glu Leu Trp Thr Gly Gln Arg
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Gly Asn Leu Ala Pro
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<210> 5125
<211> 6244

<212> DNA
<213> Homo sapiens

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6244

<210> 5126

<211> 117
<212> PRT
<213> Homo sapiens

<400> 5126
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1 5 10 15
Thr Phe Ser Gly Leu Val Ser Thr Phe Glu Val Val Leu Trp Leu Asn
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Phe Ser Cys Ser Phe Cys Val Val Phe Arg Gly Gly Ser Pro His Ala
35 40 45
Glu Ile Leu Cys Met Gln Pro Thr Gly Lys Arg Pro Pro Gly Ser Gln
50 55 60
Asp Phe Ser Phe Ser Cys Leu Cys Pro Ala Thr Cys Ser Leu Pro Leu
65 70 75 80
Phe Arg Cys Gln Arg Gly Asp Phe Arg Ala Val Cys Phe Asn Pro Gly
85 90 95
Arg Ser Asp Thr Leu Val Ser Phe Phe Gln Glu Thr Ile Ala Phe Thr
100 105 110
Asp Val Leu Val Val
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<210> 5127
<211> 400
<212> DNA
<213> Homo sapiens

<400> 5127
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180
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400

<210> 5128
<211> 55
<212> PRT
<213> Homo sapiens

<400> 5128
Gly Thr Ala Pro Met Pro Leu Gly Arg Pro Cys Gly Pro Ala Leu Gly
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Cys Val Phe Pro Ser Ser Ser Ser Thr Cys Trp Thr Cys Thr Gly Pro
20 25 30
Trp Gly Trp Thr Phe Thr Gly Thr Met Ser Ala Gly Ser Ala Ala Pro

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Ala Ser Ser Thr Thr Ile Ser
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<210> 5129
<211> 745
<212> DNA
<213> Homo sapiens

<400> 5129
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745

<210> 5130
<211> 111
<212> PRT
<213> Homo sapiens

<400> 5130
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Trp Ala Leu Ala Gly Ala Arg Gln Leu Phe Leu Ala Pro Gln Gln Ile
            20                  25                  30
Ser Arg Gln Leu His Phe Arg Leu Leu Glu Glu Arg Gln Gly Val Gly
        35                  40                  45
Gly Val Gly Leu Ser Ala Lys Gly Gly Lys His Pro Gln Asp Arg Asn
    50                  55                  60
Leu Ala Ala Val Gly Pro Glu Val Gln Ala Cys Gly Trp Ala Arg Pro
65                  70                  75                  80
Asp Pro Ala Cys Ala Gly Gly Gln Val Ala Gly Gly Gly Glu Pro Gly
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85 90 95
Val Val Gln Ala Ala Trp Met Ser Arg Gln Leu Gly Leu Cys Pro
100 105 110

<210> 5131
<211> 789
<212> DNA
<213> Homo sapiens

<400> 5131
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180
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<211> 263
<212> PRT
<213> Homo sapiens

<400> 5132
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Ile Gly Glu Val Leu Val Ser Val Asn Pro Tyr Gln Glu Leu Pro Leu
20 25 30
Tyr Gly Pro Glu Ala Ile Ala Gln Tyr Gln Gly Arg Glu Leu Tyr Glu
35 40 45
Arg Pro Pro His Leu Tyr Ala Val Ala Asn Ala Ala Tyr Lys Ala Met
50 55 60
Lys His Arg Ser Arg Asp Thr Cys Ile Val Ile Ser Gly Glu Ser Gly

65 70 75 80
Ala Gly Lys Thr Glu Ala Ser Lys His Ile Met Gln Tyr Ile Ala Ala
85 90 95
Val Thr Asn Pro Ser Gln Arg Ala Glu Val Glu Arg Val Lys Asp Val
100 105 110
Leu Leu Lys Ser Thr Cys Val Leu Glu Ala Phe Gly Asn Ala Arg Thr
115 120 125
Asn Arg Asn His Asn Ser Ser Arg Phe Gly Lys Tyr Met Asp Ile Asn
130 135 140
Phe Asp Phe Lys Gly Asp Pro Ile Gly Gly His Ile His Ser Tyr Leu
145 150 155 160
Leu Glu Lys Ser Arg Val Leu Lys Gln His Val Gly Glu Arg Asn Phe
165 170 175
His Ala Phe Tyr Gln Leu Leu Arg Gly Ser Glu Asp Lys Gln Leu His
180 185 190
Glu Leu His Leu Glu Arg Asn Pro Ala Val Tyr Asn Phe Thr His Gln
195 200 205
Gly Ala Gly Leu Asn Met Thr Val His Ser Ala Leu Asp Ser Asp Glu
210 215 220
Gln Ser His Gln Ala Val Thr Glu Ala Met Arg Val Ile Gly Phe Ser
225 230 235 240
Pro Glu Glu Val Glu Ser Val His Arg Ile Leu Ala Ala Ile Leu His
245 250 255
Leu Gly Asn Ile Glu Phe Val
260

<210> 5133
<211> 581
<212> DNA
<213> Homo sapiens

<400> 5133
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480
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<210> 5134

<211> 157
<212> PRT
<213> Homo sapiens

<400> 5134
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His Leu Ser His Pro Asp His Tyr His His His Gly Lys Ser Asp Leu
35 40 45
Ser Arg Gly Ser Pro Tyr Arg Glu Ser Pro Leu Gly His Phe Glu Ser
50 55 60
Tyr Gly Gly Met Pro Phe Phe Gln Ala Gln Lys Met Phe Val Asp Val
65 70 75 80
Pro Glu Asn Thr Val Ile Leu Asp Glu Met Thr Leu Arg His Met Val
85 90 95
Gln Asp Cys Thr Ala Val Lys Thr Gln Leu Leu Lys Leu Lys Arg Leu
100 105 110
Leu His Gln His Asp Gly Ser Gly Ser Leu His Asp Ile Gln Leu Ser
115 120 125
Leu Pro Ser Ser Pro Glu Pro Glu Asp Gly Asp Lys Val Tyr Lys Asn
130 135 140
Glu Asp Leu Leu Asn Glu Ile Lys Gln Leu Lys Asp Glu
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<210> 5135
<211> 1696
<212> DNA
<213> Homo sapiens

<400> 5135
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cggaagtgtt ccgtcttcca cctgttcgtg gcctgcctct cgctgggctt cttctcccta
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420
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540
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660

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720
gaggacgacg agttctaccg gcgcattaag ggagctgggc tccagctttt ccgcccctcg
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1320
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1696

<210> 5136
<211> 341
<212> PRT
<213> Homo sapiens

<400> 5136
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Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser Val Phe His Leu
35 40 45
Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp Leu Gln
50 55 60
Leu Ser Cys Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln Gly Gln
65 70 75 80
Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro Pro Glu

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                85                  90                  95
His Trp Glu Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala Val Leu
            100                 105                 110
Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val Pro His
        115                 120                 125
Met Arg Arg Phe Leu Ser Arg Lys Lys Ile Arg His His Ile Tyr Val
    130                 135                 140
Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn
145                 150                 155                 160
Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His
                165                 170                 175
Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro
            180                 185                 190
Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr
        195                 200                 205
His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His
    210                 215                 220
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly Arg
225                 230                 235                 240
Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu Gln Leu
                245                 250                 255
Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg His Leu
            260                 265                 270
His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala Ala Gln
        275                 280                 285
Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn Thr Val
    290                 295                 300
Lys Tyr His Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly Ala Pro
305                 310                 315                 320
Cys Thr Val Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala Thr Pro
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Trp Cys Thr Phe Ser
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<210> 5137
<211> 3090
<212> DNA
<213> Homo sapiens

<400> 5137
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120
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180
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240
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300
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360
aggcctacag ctggcctggg gctcgtgtct gggcttcgga cgttggggcc cggtggccca
420

ccctttccgt agttgtccca aatggagctg gaattggatg ctggtgacca agacctgctg
480
gccttcctgc tagaggaaag tggagatttg gggacggcac ccgatgaggc cgtgagggcc
540
ccactggact gggcgctgcc gctttctgag gtaccgagcg actgggaagt agatgatttg
600
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660
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720
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780
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tatgttgggg gtttagagag cagggtcttg aaatacacag cccagaatat ggagcttcag
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1080
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1440
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1740
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1800
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1980
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2040

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2160
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2280
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2340
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2700
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2760
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2880
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2940
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3000
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3090

<210> 5138
<211> 371
<212> PRT
<213> Homo sapiens

<400> 5138
Met Glu Leu Glu Leu Asp Ala Gly Asp Gln Asp Leu Leu Ala Phe Leu
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20 25 30
Ala Pro Leu Asp Trp Ala Leu Pro Leu Ser Glu Val Pro Ser Asp Trp
35 40 45
Glu Val Asp Asp Leu Leu Cys Ser Leu Leu Ser Pro Pro Ala Ser Leu
50 55 60
Asn Ile Leu Ser Ser Ser Asn Pro Cys Leu Val His His Asp His Thr
65 70 75 80
Tyr Ser Leu Pro Arg Glu Thr Val Ser Met Asp Leu Glu Ser Glu Ser

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                85                  90                  95
Cys Arg Lys Glu Gly Thr Gln Met Thr Pro Gln His Met Glu Glu Leu
            100                 105                 110
Ala Glu Gln Glu Ile Ala Arg Leu Val Leu Thr Asp Glu Glu Lys Ser
        115                 120                 125
Leu Leu Glu Lys Glu Gly Leu Ile Leu Pro Glu Thr Leu Pro Leu Thr
    130                 135                 140
Lys Thr Glu Glu Gln Ile Leu Lys Arg Val Arg Arg Lys Ile Arg Asn
145                 150                 155                 160
Lys Arg Ser Ala Gln Glu Ser Arg Arg Lys Lys Lys Val Tyr Val Gly
                165                 170                 175
Gly Leu Glu Ser Arg Val Leu Lys Tyr Thr Ala Gln Asn Met Glu Leu
            180                 185                 190
Gln Asn Lys Val Gln Leu Leu Glu Glu Gln Asn Leu Ser Leu Leu Asp
        195                 200                 205
Gln Leu Arg Lys Leu Gln Ala Met Val Ile Glu Ile Ser Asn Lys Thr
    210                 215                 220
Ser Ser Ser Ser Thr Cys Ile Leu Val Leu Leu Val Ser Phe Cys Leu
225                 230                 235                 240
Leu Leu Val Pro Ala Met Tyr Ser Ser Asp Thr Arg Gly Ser Leu Pro
                245                 250                 255
Ala Glu His Gly Val Leu Ser Arg Gln Leu Arg Ala Leu Pro Ser Glu
            260                 265                 270
Asp Pro Tyr Gln Leu Glu Leu Pro Ala Leu Gln Ser Glu Val Pro Lys
        275                 280                 285
Asp Ser Thr His Gln Trp Leu Asp Gly Ser Asp Cys Val Leu Gln Ala
    290                 295                 300
Pro Gly Asn Thr Ser Cys Leu Leu His Tyr Met Pro Gln Ala Pro Ser
305                 310                 315                 320
Ala Glu Pro Pro Leu Glu Trp Pro Phe Pro Asp Leu Phe Ser Glu Pro
                325                 330                 335
Leu Cys Arg Gly Pro Ile Leu Pro Leu Gln Ala Asn Leu Thr Arg Lys
            340                 345                 350
Gly Gly Trp Leu Pro Thr Gly Ser Pro Ser Val Ile Leu Gln Asp Arg
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Tyr Ser Gly
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<210> 5139
<211> 1968
<212> DNA
<213> Homo sapiens

<400> 5139
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180
cgggttgtaa tatttcaacg agagcaggag agtaaaaatc aggttcatcg taggggtgaa
240
tacaatgttt acagcacatt ccagagccat gaacccgagt tcgattacct gaagagttta
300

gaaatagaag aaaaaatcaa taaaataaga tggctccccc agcagaatgc agcttacttt
360
cttctgtcta ctaatgataa aactgtgaag ctgtggaaag tcagcgagcg tgataagagg
420
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600
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720
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780
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1860
caggctcagg cggccccact cacccacagc atccgccgcc acccccttcgg gtgtgagcgc
1920

tcaataaaaa caacacacta taaagtgttt ttaaatccaa aaaaaaaa
1968

<210> 5140
<211> 443
<212> PRT
<213> Homo sapiens

<400> 5140
Met Glu Glu Asp Ile Asp Thr Arg Lys Ile Asn Asn Ser Phe Leu Arg
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20 25 30
Asn His Thr Gly Glu Leu Leu Ala Thr Gly Asp Lys Gly Gly Arg Val
35 40 45
Val Ile Phe Gln Arg Glu Gln Glu Ser Lys Asn Gln Val His Arg Arg
50 55 60
Gly Glu Tyr Asn Val Tyr Ser Thr Phe Gln Ser His Glu Pro Glu Phe
65 70 75 80
Asp Tyr Leu Lys Ser Leu Glu Ile Glu Glu Lys Ile Asn Lys Ile Arg
85 90 95
Trp Leu Pro Gln Gln Asn Ala Ala Tyr Phe Leu Leu Ser Thr Asn Asp
100 105 110
Lys Thr Val Lys Leu Trp Lys Val Ser Glu Arg Asp Lys Arg Pro Glu
115 120 125
Gly Tyr Asn Leu Lys Asp Glu Glu Gly Arg Leu Arg Asp Pro Ala Thr
130 135 140
Ile Thr Thr Leu Arg Val Pro Val Leu Arg Pro Met Asp Leu Met Val
145 150 155 160
Glu Ala Thr Pro Arg Arg Val Phe Ala Asn Ala His Thr Tyr His Ile
165 170 175
Asn Ser Ile Ser Val Asn Ser Asp Tyr Glu Thr Tyr Met Ser Ala Asp
180 185 190
Asp Leu Arg Ile Asn Leu Trp Asn Phe Glu Ile Thr Asn Gln Ser Phe
195 200 205
Asn Ile Val Asp Ile Lys Pro Ala Asn Met Glu Glu Leu Thr Glu Val
210 215 220
Ile Thr Ala Ala Glu Phe His Pro His His Cys Asn Thr Phe Val Tyr
225 230 235 240
Ser Ser Ser Lys Gly Thr Ile Arg Leu Cys Asp Met Arg Ala Ser Ala
245 250 255
Leu Cys Asp Arg His Thr Lys Phe Phe Glu Glu Pro Glu Asp Pro Ser
260 265 270
Asn Arg Ser Phe Phe Ser Glu Ile Ile Ser Ser Ile Ser Asp Val Lys
275 280 285
Phe Ser His Ser Gly Arg Tyr Ile Met Thr Arg Asp Tyr Leu Thr Val
290 295 300
Lys Val Trp Asp Leu Asn Met Glu Ser Arg Pro Val Glu Thr His Gln
305 310 315 320
Val His Asp Tyr Leu Arg Ser Lys Leu Cys Ser Leu Tyr Glu Asn Asp
325 330 335
Cys Ile Phe Asp Lys Phe Glu Cys Val Trp Asn Gly Ser Asp Ser Val
340 345 350
Ile Met Thr Gly Ser Tyr Asn Asn Phe Phe Arg Met Phe Asp Arg Asp

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        355                 360                 365
Thr Lys Arg Asp Val Thr Leu Glu Ala Ser Arg Glu Asn Ser Lys Pro
    370                 375                 380
Arg Ala Ile Leu Lys Pro Arg Lys Val Cys Val Gly Gly Lys Arg Arg
385                 390                 395                 400
Lys Asp Glu Ile Ser Val Asp Ser Leu Asp Phe Ser Lys Lys Ile Leu
                405                 410                 415
His Thr Ala Trp His Pro Val Asp Asn Val Ile Ala Val Ala Ala Thr
            420                 425                 430
Asn Asn Leu Tyr Ile Phe Gln Asp Lys Ile Asn
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<210> 5141
<211> 928
<212> DNA
<213> Homo sapiens

<400> 5141
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120
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180
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240
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360
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420
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720
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780
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900
gggccactcg ccctctccct tcacgcgt
928

<210> 5142
<211> 227
<212> PRT

<213> Homo sapiens

<400> 5142
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Glu Arg Leu Ile His Cys Tyr Asp Glu Glu Val Val Lys Glu Leu Met
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Pro Leu Val Val Asn Val Leu Glu Asn Leu Asp Ser Val Leu Ser Glu
35 40 45
Asn Gln Glu His Glu Val Glu Leu Glu Leu Leu Arg Glu Asp Asn Glu
50 55 60
Gln Leu Leu Thr Gln Tyr Glu Arg Glu Lys Ala Leu Arg Arg Gln Ala
65 70 75 80
Glu Glu Lys Phe Ile Glu Phe Glu Asp Ala Leu Glu Gln Glu Lys Lys
85 90 95
Glu Leu Gln Ile Gln Val Glu His Tyr Glu Phe Gln Thr Arg Gln Leu
100 105 110
Glu Leu Lys Ala Lys Asn Tyr Ala Asp Gln Ile Ser Arg Leu Glu Glu
115 120 125
Arg Glu Ser Glu Met Lys Lys Glu Tyr Asn Ala Leu His Gln Arg His
130 135 140
Thr Glu Met Ile Gln Thr Tyr Val Glu His Ile Glu Arg Ser Lys Met
145 150 155 160
Gln Gln Val Gly Gly Asn Ser Gln Thr Glu Ser Ser Leu Pro Gly Arg
165 170 175
Ser Arg Lys Glu Arg Pro Thr Ser Leu Asn Val Phe Pro Leu Ala Asp
180 185 190
Gly Thr Val Arg Ala Gln Ile Gly Gly Lys Leu Val Pro Ala Gly Asp
195 200 205
His Trp His Leu Ser Asp Leu Gly Gln Leu Gln Ser Ser Ser Ser Tyr
210 215 220
Gln Val Leu
225

<210> 5143
<211> 1666
<212> DNA
<213> Homo sapiens

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120
cgagaagact ttcgggtgcg ctgcacctcg aagcgggctg tgaccgaaat gctacaactg
180
tgcggccgct tcgtgcaaaa gctcggggac gctctgccgg aggagattcg ggagcccgct
240
ctgcgagatg cgcagtggac ttttgaatca gctgtgcaag agaatatcag cattaatggg
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caagcatggc aggaagcttc agataattgt tttatggatt ctgacatcaa agtacttgaa
360
gatcagtttg atgaaatcat agtagatata gccacaaaac gtaagcagta tcccagaaag
420

atcctggaat gtgtcatcaa aaccataaaa gcaaaacaag aaattctgaa gcagtaccac
480
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540
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600
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660
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960
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1200
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1260
gctgtataat gatttttcgt ttacatgctg aaaagtaatt atcagttctg cacagcagca
1320
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1380
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1440
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1560
cataatttga cttggaacta atggtttctt tttagggttt cttatttatt tctttacaaa
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1666

<210> 5144
<211> 218
<212> PRT
<213> Homo sapiens

<400> 5144
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Phe Glu Ser Ala Val Gln Glu Asn Ile Ser Ile Asn Gly Gln Ala Trp
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Gln Glu Ala Ser Asp Asn Cys Phe Met Asp Ser Asp Ile Lys Val Leu

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        35                  40                  45
Glu Asp Gln Phe Asp Glu Ile Ile Val Asp Ile Ala Thr Lys Arg Lys
    50                  55                  60
Gln Tyr Pro Arg Lys Ile Leu Glu Cys Val Ile Lys Thr Ile Lys Ala
65                  70                  75                  80
Lys Gln Glu Ile Leu Lys Gln Tyr His Pro Val Val His Pro Leu Asp
                85                  90                  95
Leu Lys Tyr Asp Pro Asp Pro Ala Pro His Met Glu Asn Leu Lys Cys
            100                 105                 110
Arg Gly Glu Thr Val Ala Lys Glu Ile Ser Glu Ala Met Lys Ser Leu
        115                 120                 125
Pro Ala Leu Ile Glu Gln Gly Glu Gly Phe Ser Gln Val Leu Arg Met
    130                 135                 140
Gln Pro Val Ile His Leu Gln Arg Ile His Gln Glu Val Phe Ser Ser
145                 150                 155                 160
Cys His Arg Lys Pro Asp Ala Lys Pro Glu Asn Phe Ile Thr Gln Ile
                165                 170                 175
Glu Thr Thr Pro Thr Glu Thr Ala Ser Arg Lys Thr Ser Asp Met Val
            180                 185                 190
Leu Lys Arg Lys Gln Thr Lys Asp Cys Pro Gln Arg Lys Trp Tyr Pro
        195                 200                 205
Leu Arg Pro Lys Lys Ile Asn Leu Asp Thr
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<210> 5145
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 5145

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540
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600
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ggacgtggag ctgggccgaa ccacgtgtac caagacccag cccaacttgg acaactgccc
720
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840
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1440
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1740
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1885

<210> 5146
<211> 312
<212> PRT
<213> Homo sapiens

<400> 5146
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Cys Ala Leu Ala Gly His Asn Asp Leu Val Glu Ile His Leu Ser Gly
20 25 30
Arg Leu Gly Val Cys Thr Gly Leu Ala Cys Ala Tyr His Leu Leu Cys
35 40 45
Thr Pro Pro Thr Pro Cys Ile Pro Thr Pro Gly Leu Val Ala Pro Ala

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    50                  55                  60
Leu Gly Lys Val Ser Pro Cys Ala Cys Thr Arg Arg Gln Thr Glu Lys
65                  70                  75                  80
Ala Ala Gly Gly Leu Cys Cys Ser Ala Arg Gly Ser Ala Leu Pro Pro
                85                  90                  95
Ser Phe Leu Leu Leu Ile Ala Pro Val Cys Gly Ala Tyr Thr Pro Thr
            100                 105                 110
Ser Cys Asn Lys Ile Val Ala Ser Ala Lys Lys Pro Gly Ile Arg Thr
        115                 120                 125
Gly Ile Gln Gly Leu Lys Gly Asp Gln Gly Glu Pro Gly Pro Ser Gly
    130                 135                 140
Asn Pro Gly Lys Val Gly Tyr Pro Gly Pro Ser Gly Pro Leu Gly Ala
145                 150                 155                 160
Arg Gly Ile Pro Gly Ile Lys Gly Thr Lys Gly Ser Pro Gly Asn Ile
                165                 170                 175
Lys Asp Gln Pro Arg Pro Ala Phe Ser Ala Ile Arg Arg Asn Pro Pro
            180                 185                 190
Met Gly Gly Asn Val Val Ile Phe Asp Thr Val Ile Thr Asn Gln Glu
        195                 200                 205
Glu Pro Tyr Gln Asn His Ser Gly Arg Phe Val Cys Thr Val Pro Gly
    210                 215                 220
Tyr Tyr Tyr Phe Thr Phe Gln Val Leu Ser Gln Trp Glu Ile Cys Leu
225                 230                 235                 240
Ser Ile Val Ser Ser Ser Arg Gly Gln Val Arg Arg Ser Leu Gly Phe
                245                 250                 255
Cys Asp Thr Thr Asn Lys Gly Leu Phe Gln Val Val Ser Gly Gly Met
            260                 265                 270
Val Leu Gln Leu Gln Gln Gly Asp Gln Val Trp Val Glu Lys Asp Pro
        275                 280                 285
Lys Lys Gly His Ile Tyr Gln Gly Ser Glu Ala Asp Ser Val Phe Ser
    290                 295                 300
Gly Phe Leu Ile Phe Pro Ser Ala
305                 310
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<210> 5147
<211> 2943
<212> DNA
<213> Homo sapiens

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360
accaaacatc ttagggcaga taatgccttt atgttactta ctcaggctcg attatttgat
420

gaacctcagc ttgctagtct ttgtctagat acaatagaca aaagcacaat ggatgcaata
480
agtgcagaag ggtttactga tattgatata gatacactct gtgcagtttt agagagagac
540
acactcagta ttcgagaaag tcgacttttt ggagctgttg tacgctgggc agaagcagaa
600
tgtcagagac aacaattacc tgtgactttt gggaataaac aaaaagttct aggaaaagca
660
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720
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780
aaaccccgag ttgaatacat tgaccgacca agatgctgtc tcaggggaaa ggaatgctgc
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1380
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2280
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2340
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2400
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2520
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2580
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2700
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2940
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2943

<210> 5148
<211> 296
<212> PRT
<213> Homo sapiens

<400> 5148
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20 25 30
Ile Asp Ile Asp Thr Leu Cys Ala Val Leu Glu Arg Asp Thr Leu Ser
35 40 45
Ile Arg Glu Ser Arg Leu Phe Gly Ala Val Val Arg Trp Ala Glu Ala
50 55 60
Glu Cys Gln Arg Gln Gln Leu Pro Val Thr Phe Gly Asn Lys Gln Lys
65 70 75 80
Val Leu Gly Lys Ala Leu Ser Leu Ile Arg Phe Pro Leu Met Thr Ile
85 90 95
Glu Glu Phe Ala Ala Gly Pro Ala Gln Ser Gly Ile Leu Ser Asp Arg
100 105 110
Glu Val Val Asn Leu Phe Leu His Phe Thr Val Asn Pro Lys Pro Arg

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        115                 120                 125
Val Glu Tyr Ile Asp Arg Pro Arg Cys Cys Leu Arg Gly Lys Glu Cys
    130                 135                 140
Cys Ile Asn Arg Phe Gln Gln Val Glu Ser Arg Trp Gly Tyr Ser Gly
145                 150                 155                 160
Thr Ser Asp Arg Ile Arg Phe Thr Val Asn Arg Arg Ile Ser Ile Val
                165                 170                 175
Gly Phe Gly Leu Tyr Gly Ser Ile His Gly Pro Thr Asp Tyr Gln Val
            180                 185                 190
Asn Ile Gln Ile Ile Glu Tyr Glu Lys Lys Gln Thr Leu Gly Gln Asn
        195                 200                 205
Asp Thr Gly Phe Ser Cys Asp Gly Thr Ala Asn Thr Phe Arg Val Met
    210                 215                 220
Phe Lys Glu Pro Ile Glu Ile Leu Pro Asn Val Cys Tyr Thr Ala Cys
225                 230                 235                 240
Ala Thr Leu Lys Gly Pro Asp Ser His Tyr Gly Thr Lys Gly Leu Lys
                245                 250                 255
Lys Val Val His Glu Thr Pro Ala Ala Ser Lys Thr Val Phe Phe Phe
            260                 265                 270
Phe Ser Ser Pro Gly Asn Asn Asn Gly Thr Ser Ile Glu Asp Gly Gln
        275                 280                 285
Ile Pro Glu Ile Ile Phe Tyr Thr
    290                 295
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<210> 5149
<211> 533
<212> DNA
<213> Homo sapiens

<400> 5149
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180
cagctcctac cagaggacct cagaaaggag ctctatgaac tttgggaaga gtacgagacc
240
caatctagtg cagaagccaa atttgtgaag cagctagacc aatgtgaaat gattcttcaa
300
gcatctgaat atgaagacct tgaacacaaa cctgggagac tgcaagactt ctatgattcc
360
acagcaggaa aattcaatca ccctgagata gtccagcttg tttctgaact tgaggcagaa
420
agaagcacta acatagctgc agctgccagt gagccacact cctgagacac tctctaaatt
480
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533

<210> 5150
<211> 154
<212> PRT
<213> Homo sapiens

<400> 5150
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20 25 30
Ile Val Gly Asp Ile Ala Pro Ala Asp Asn Ile Pro Lys Glu Glu Lys
35 40 45
His Arg Arg Glu Glu Glu Ala Met Lys Gln Ile Thr Gln Leu Leu Pro
50 55 60
Glu Asp Leu Arg Lys Glu Leu Tyr Glu Leu Trp Glu Glu Tyr Glu Thr
65 70 75 80
Gln Ser Ser Ala Glu Ala Lys Phe Val Lys Gln Leu Asp Gln Cys Glu
85 90 95
Met Ile Leu Gln Ala Ser Glu Tyr Glu Asp Leu Glu His Lys Pro Gly
100 105 110
Arg Leu Gln Asp Phe Tyr Asp Ser Thr Ala Gly Lys Phe Asn His Pro
115 120 125
Glu Ile Val Gln Leu Val Ser Glu Leu Glu Ala Glu Arg Ser Thr Asn
130 135 140
Ile Ala Ala Ala Ala Ser Glu Pro His Ser
145 150

<210> 5151
<211> 2273
<212> DNA
<213> Homo sapiens

<400> 5151
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cgagagtctg agtcgcgggg cagctccggt cgcgtcaagc gggagcgaga tcgggagcgg
120
gagcctgagg cggcgagctc ccggggcagc cctgtgcgcg tgaagcggga gttcgagccg
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gcgagcgcgc gcgaggcccc ggcttctgtt gtcccgtttg tgcgggtgaa gcgggagcgc
240
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720
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780

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2273

<210> 5152
<211> 324
<212> PRT

<213> Homo sapiens

<400> 5152
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Lys Pro Thr Phe Thr Lys Gln Gln Ile Ala Asn Leu Asp Lys Gln Ala
35 40 45
Lys Leu Ser Arg Ala Tyr Asp Gly Thr Thr Tyr Leu Pro Gly Ile Val
50 55 60
Gly Leu Asn Asn Ile Lys Ala Asn Asp Tyr Ala Asn Ala Val Leu Gln
65 70 75 80
Ala Leu Ser Asn Val Pro Pro Leu Arg Asn Tyr Phe Leu Glu Glu Asp
85 90 95
Asn Tyr Lys Asn Ile Lys Arg Pro Pro Gly Asp Ile Met Phe Leu Leu
100 105 110
Val Gln Arg Phe Gly Glu Leu Met Arg Lys Leu Trp Asn Pro Arg Asn
115 120 125
Phe Lys Ala His Val Ser Pro His Glu Met Leu Gln Ala Val Val Leu
130 135 140
Cys Ser Lys Lys Thr Phe Gln Ile Thr Lys Gln Gly Asp Gly Val Asp
145 150 155 160
Phe Leu Ser Trp Phe Leu Asn Ala Leu His Ser Ala Leu Gly Gly Thr
165 170 175
Lys Lys Lys Lys Lys Thr Ile Val Thr Asp Val Phe Gln Gly Ser Met
180 185 190
Arg Ile Phe Thr Lys Lys Leu Pro His Pro Asp Leu Pro Ala Glu Glu
195 200 205
Lys Glu Gln Leu Leu His Asn Asp Glu Tyr Gln Glu Thr Met Val Glu
210 215 220
Ser Thr Phe Met Tyr Leu Thr Leu Asp Leu Pro Thr Ala Pro Leu Tyr
225 230 235 240
Lys Asp Glu Lys Glu Gln Leu Ile Ile Pro Gln Val Pro Leu Phe Asn
245 250 255
Ile Leu Ala Lys Phe Asn Gly Ile Thr Glu Lys Glu Tyr Lys Thr Tyr
260 265 270
Lys Glu Asn Phe Leu Lys Arg Phe Gln Leu Thr Lys Leu Pro Pro Tyr
275 280 285
Leu Ile Phe Cys Ile Lys Ile Phe Thr Lys Asn Asn Phe Phe Val Glu
290 295 300
Lys Asn Pro Thr Ser Cys Gln Phe Pro Tyr Tyr Lys Cys Gly Ser Glu
305 310 315 320
Arg Ile Leu Val

<210> 5153
<211> 640
<212> DNA
<213> Homo sapiens

<400> 5153
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gggtccacgt tgggagggac aggtgagctg gcctttggtg ctgacacact cctgactttg
180
ccctttctcc tgcaggggct gccattcccg cagaatgagg ctaatgccat ggatgtggtg
240
gtccagtttg ccatccaccg cctgggcttc cagccccagg acatcatcat ctacgcctgg
300
tccatcggcg gcttcactgc cacgtgggca gccatgtcct acccagatgt tagtgccatg
360
atcctggatg cctcctttga tgacctggtg cccttggcct tgaaggtcat gccagacagc
420
tggagtgagt gcagctccca ggcctgccct tcctgggaag gggtgggctg gaactgggaa
480
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540
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<210> 5154
<211> 162
<212> PRT
<213> Homo sapiens

<400> 5154
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20 25 30
Ala Cys His Arg Trp Leu Gln Glu Gly Ser Thr Leu Gly Gly Thr Gly
35 40 45
Glu Leu Ala Phe Gly Ala Asp Thr Leu Leu Thr Leu Pro Phe Leu Leu
50 55 60
Gln Gly Val Pro Phe Pro Gln Asn Glu Ala Asn Ala Met Asp Val Val
65 70 75 80
Val Gln Phe Ala Ile His Arg Leu Gly Phe Gln Pro Gln Asp Ile Ile
85 90 95
Ile Tyr Ala Trp Ser Ile Gly Gly Phe Thr Ala Thr Trp Ala Ala Met
100 105 110
Ser Tyr Pro Asp Val Ser Ala Met Ile Leu Asp Ala Ser Phe Asp Asp
115 120 125
Leu Val Pro Leu Ala Leu Lys Val Met Pro Asp Ser Trp Ser Glu Cys
130 135 140
Ser Ser Gln Ala Cys Pro Ser Trp Glu Gly Val Gly Trp Asn Trp Glu
145 150 155 160
Leu Phe

<210> 5155
<211> 1402
<212> DNA
<213> Homo sapiens

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120
tgacattgac ttctccactg caaccatcga gttcattgtc tcctaaacct tgccatggag
180
gcctgtggca cctgagccag ccattatcat caccagcact tccatgagct acaagctgga
240
cccactgcag tcctcctgac acactgaaat cagagcctgc acacagagca gcagatgctt
300
caatgtaaag gtcatttcca ggtccttgac aggcgtgcat ctgggccaga tccatggcaa
360
taaccttcag gttgaggcta gagggcttca gatgggcagc ttcgaatgac aggagcaagg
420
aacaagaggc cggaaaggga gggtgacatt ttcagcatct ataagatcaa ctttagaaat
480
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540
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720
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780
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900
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960
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1020
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1080
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1140
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1200
ggccttcctg ataagaacat gaccagatcc agctggtttg caacaagatg aacttcagtg
1260
ctgagctttc accaagtttt tctcactaca atctcattgt aatactaaaa tctccaccca
1320
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1380
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1402

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<211> 118
<212> PRT

<213> Homo sapiens

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20 25 30
Ser Gly Gly Leu Gln Trp Val Gln Leu Val Ala His Gly Ser Ala Gly
35 40 45
Asp Asp Asn Gly Trp Leu Arg Cys His Arg Pro Pro Trp Gln Gly Leu
50 55 60
Gly Asp Asn Glu Leu Asp Gly Cys Ser Gly Glu Val Asn Val Ser Gln
65 70 75 80
Asp Phe Val Lys Thr Leu Leu Arg Ile Cys Asn Ala Ile Pro Ser Phe
85 90 95
Arg Gly Leu Leu Glu Ser Cys Met Phe Gly Cys Arg Ala Arg Val Thr
100 105 110
Arg Asn Phe Trp Thr Leu
115

<210> 5157
<211> 1310
<212> DNA
<213> Homo sapiens

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120
cggggcaggg gaattgcatc tgcaggaaag agatgcagca tgctcctcac tcctgagtgc
180
ccacctgtcc tgcttctctg caggtgaaaa ctctgggggа tgctgatcaa tagagcttgg
240
tcccaagctc tactgggccc ttggaggtag caaggccact gggttgctat cctcttgctg
300
gggatagcaa ccactggttt gcaaccactg ggttgctatc cttttgctat cctcttgctc
360
atgaccagcc atatggtgag gctggggagt tcacatcctc aggcaggaac tagcagttgt
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660
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720
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780
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840

gtccatttct gtgactaagc tgtgcagagg ttgacagcag ggcaagttat attgatattc
900
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1020
aacagctcag tgctgtcctg ggagtcctct gactcagaac cctcgaagca tcctgcattg
1080
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1140
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1200
ctcagacagc ccagcagtgt gaacacacaa tgccaggcca gggaactggg gaccaccatc
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<210> 5158
<211> 82
<212> PRT
<213> Homo sapiens

<400> 5158
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Thr Ser Ser Cys Leu Ser Ser Asn Ala Ser Arg Met Leu His Cys Ser
20 25 30
Gln Glu Leu Ala Ile Arg Tyr Val Leu Cys Gly Gln Ser Ala Ser Gln
35 40 45
Thr His Arg Cys Ser Pro Ala Trp Leu Ser Trp Asp Leu Asn Leu Leu
50 55 60
Val Lys Ser Phe Ser Leu Ser Glu Val Pro Ser Leu Gln Met Leu Asn
65 70 75 80
Leu Ala

<210> 5159
<211> 3233
<212> DNA
<213> Homo sapiens

<400> 5159
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120
gcaaaagtga tcagggaaga tttcctgatg gaggggggag tccaaccggg gtcttcttgg
180
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240
agttgcattt ctggacatga gagcagtgtt gtgaaactta gatgatgcat atagagaagg
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cagcgagtgt gtttgaggat agtgagcgaa cagtttgtct gttcacggac atctgtccag
360

agtggcaagc acatagtggg taaccagaat gggcctcttc cctttccttt ttggttaccc
420
cacaactcag tataggtact gactgccaaa tctccacatt tgtatatttc ttagcgtaat
480
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720
atgtttttgt tgggggggtgt cattcagatg gaacatcgac atcggaagaa agacaccccg
780
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1980

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2820
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3120
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3233

<210> 5160
<211> 849
<212> PRT
<213> Homo sapiens

<400> 5160
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Thr His Asp Arg Met Lys Asp Val Lys Arg His Ile Thr Ala Arg Leu
20 25 30
Asp Trp Gly Asn Glu Gln Leu Gly Leu Asp Leu Val Pro Arg Lys Glu

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        35                  40                  45
Tyr Ala Met Val Asp Pro Glu Asp Ile Ser Ile Thr Glu Leu Tyr Arg
    50                  55                  60
Leu Ser Met Leu Ile Met Phe Leu Leu Gly Gly Val Ile Gln Met Glu
65                  70                  75                  80
His Arg His Arg Lys Lys Asp Thr Pro Val Gln Ala Ser Ser His His
                85                  90                  95
Leu Phe Val Gln Met Lys Ser Leu Met Cys Ser Asn Leu Gly Glu Glu
            100                 105                 110
Leu Glu Val Ile Phe Ser Leu Phe Asp Ser Lys Glu Asn Arg Pro Ile
        115                 120                 125
Ser Glu Arg Phe Phe Leu Arg Leu Asn Arg Asn Gly Leu Pro Lys Ala
    130                 135                 140
Pro Asp Lys Pro Glu Arg His Cys Ser Leu Phe Val Asp Leu Gly Ser
145                 150                 155                 160
Ser Glu Leu Arg Lys Asp Ile Tyr Ile Thr Val His Ile Ile Arg Ile
                165                 170                 175
Gly Arg Met Gly Ala Gly Glu Lys Lys Asn Ala Cys Ser Val Gln Tyr
            180                 185                 190
Arg Arg Pro Phe Gly Cys Ala Val Leu Ser Ile Ala Asp Leu Leu Thr
        195                 200                 205
Gly Glu Thr Lys Asp Asp Leu Ile Leu Lys Val Tyr Met Cys Asn Thr
    210                 215                 220
Glu Ser Glu Trp Tyr Gln Ile His Glu Asn Ile Ile Lys Lys Leu Asn
225                 230                 235                 240
Ala Arg Tyr Asn Leu Thr Gly Ser Asn Ala Gly Leu Ala Val Ser Leu
                245                 250                 255
Gln Leu Leu His Gly Asp Ile Glu Gln Ile Arg Arg Glu Tyr Ser Ser
            260                 265                 270
Val Phe Ser His Gly Val Ser Ile Thr Arg Lys Leu Gly Phe Ser Asn
        275                 280                 285
Ile Ile Met Pro Gly Glu Met Arg Asn Asp Leu Tyr Ile Thr Ile Glu
    290                 295                 300
Arg Gly Glu Phe Glu Lys Gly Gly Lys Ser Val Ala Arg Asn Val Glu
305                 310                 315                 320
Val Thr Met Phe Ile Val Asp Ser Ser Gly Gln Thr Leu Lys Asp Phe
                325                 330                 335
Ile Ser Phe Gly Ser Gly Glu Pro Pro Ala Ser Glu Tyr His Ser Phe
            340                 345                 350
Val Leu Tyr His Asn Asn Ser Pro Arg Trp Ser Glu Leu Leu Lys Leu
        355                 360                 365
Pro Ile Pro Val Asp Lys Phe Arg Gly Ala His Ile Arg Phe Glu Phe
    370                 375                 380
Arg His Cys Ser Thr Lys Glu Lys Gly Glu Lys Lys Leu Phe Gly Phe
385                 390                 395                 400
Ser Phe Val Pro Leu Met Gln Glu Asp Gly Arg Thr Leu Pro Asp Gly
                405                 410                 415
Thr His Glu Leu Ile Val His Lys Cys Glu Glu Asn Thr Asn Leu Gln
            420                 425                 430
Asp Thr Thr Arg Tyr Leu Lys Leu Pro Phe Ser Lys Gly Ile Phe Leu
        435                 440                 445
Gly Asn Asn Asn Gln Ala Met Lys Ala Thr Lys Glu Ser Phe Cys Ile
    450                 455                 460
Thr Ser Phe Leu Cys Ser Thr Lys Leu Thr Gln Asn Gly Asp Met Leu
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465                 470                 475                 480
Asp Leu Leu Lys Trp Arg Thr His Pro Asp Lys Ile Thr Gly Cys Leu
                485                 490                 495
Ser Lys Leu Lys Glu Ile Asp Gly Ser Glu Ile Val Lys Phe Leu Gln
            500                 505                 510
Asp Thr Leu Asp Thr Leu Phe Gly Ile Leu Asp Glu Asn Ser Gln Lys
        515                 520                 525
Tyr Gly Ser Lys Val Phe Asp Ser Leu Val His Ile Ile Asn Leu Leu
    530                 535                 540
Gln Asp Ser Lys Phe His His Phe Lys Pro Val Met Asp Thr Tyr Ile
545                 550                 555                 560
Glu Ser His Phe Ala Gly Ala Leu Ala Tyr Arg Asp Leu Ile Lys Val
                565                 570                 575
Leu Lys Trp Tyr Val Asp Arg Ile Thr Glu Ala Glu Arg Gln Glu His
            580                 585                 590
Ile Gln Glu Val Leu Lys Ala Gln Glu Tyr Ile Phe Lys Tyr Ile Val
        595                 600                 605
Gln Ser Arg Arg Leu Phe Ser Leu Ala Thr Gly Gly Gln Asn Glu Glu
    610                 615                 620
Glu Phe Arg Cys Cys Ile Gln Glu Leu Leu Met Ser Val Arg Phe Phe
625                 630                 635                 640
Leu Ser Gln Glu Ser Lys Gly Ser Gly Ala Leu Ser Gln Ser Gln Ala
                645                 650                 655
Val Phe Leu Ser Ser Phe Pro Ala Val Tyr Ser Glu Leu Leu Lys Leu
            660                 665                 670
Phe Asp Val Arg Glu Val Ala Asn Leu Val Gln Asp Thr Leu Gly Ser
        675                 680                 685
Leu Pro Thr Ile Leu His Val Asp Asp Ser Leu Gln Ala Ile Lys Leu
    690                 695                 700
Gln Cys Ile Gly Lys Thr Val Glu Ser Gln Leu Tyr Thr Asn Pro Asp
705                 710                 715                 720
Ser Arg Tyr Ile Leu Leu Pro Val Val Leu His His Leu His Ile His
                725                 730                 735
Leu Gln Glu Gln Lys Asp Leu Ile Met Cys Ala Arg Ile Leu Ser Asn
            740                 745                 750
Val Phe Cys Leu Ile Lys Lys Asn Ser Ser Glu Lys Ser Val Leu Glu
        755                 760                 765
Glu Ile Asp Val Ile Val Ala Ser Leu Leu Asp Ile Leu Leu Arg Thr
    770                 775                 780
Ile Leu Glu Ile Thr Ser Arg Pro Gln Pro Ser Ser Ser Ala Met Arg
785                 790                 795                 800
Phe Gln Phe Gln Asp Val Thr Gly Glu Phe Val Ala Cys Leu Leu Ser
                805                 810                 815
Leu Leu Arg Gln Met Thr Asp Arg His Tyr Gln Gln Leu Leu Asp Ser
            820                 825                 830
Phe Asn Thr Lys Glu Glu Leu Arg Val Ser Asp Ile Leu Lys Cys Phe
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Leu
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<210> 5161
<211> 1645
<212> DNA
<213> Homo sapiens

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180
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240
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300
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360
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420
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480
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720
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<210> 5162
<211> 207
<212> PRT
<213> Homo sapiens

<400> 5162
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Lys Thr Gly Leu Arg Leu Arg Lys Val Asp Gln Gly Leu Phe Val Gln
35 40 45
Leu Val Gln Ala Asn Thr Pro Ala Ser Leu Val Gly Leu Arg Phe Gly
50 55 60
Asp Gln Leu Leu Gln Ile Asp Gly Arg Asp Cys Ala Gly Trp Ser Ser
65 70 75 80
His Lys Ala His Gln Val Val Lys Lys Ala Ser Gly Asp Lys Ile Val
85 90 95
Val Val Val Arg Asp Arg Pro Phe Gln Arg Thr Val Thr Met His Lys
100 105 110
Asp Ser Met Gly His Val Gly Phe Val Ile Lys Lys Gly Lys Ile Val
115 120 125
Ser Leu Val Lys Gly Ser Ser Ala Ala Cys Asn Gly Leu Leu Thr Asn
130 135 140
His Tyr Val Cys Glu Val Asp Gly Gln Asn Val Ile Gly Leu Lys Asp
145 150 155 160
Lys Lys Ile Met Glu Ile Leu Ala Thr Ala Gly Asn Val Val Thr Leu
165 170 175
Thr Ile Ile Pro Ser Val Ile Tyr Glu His Met Val Lys Lys Leu Pro
180 185 190
Pro Val Leu Leu His His Thr Met Asp His Ser Ile Pro Asp Ala
195 200 205

<210> 5163
<211> 1187
<212> DNA
<213> Homo sapiens

<400> 5163
nngtagagac ggggctctcc gtgttgctca ggctggctgc tgcacttcga ttcctgtgct
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tgttctggct gaaggcgccg gccgctcaag cgtgtttcgg cagatatttt tgagaacatt
120
tttttatttt taaatacatg tatagcatga gtgatggagc caaacacaag ttttgaagcc
180
aagctcttgg ttctgagaaa caggcccaac actgcacagt gtcattcgca gtcaacccaa
240
ccactgtctg agttcacgtg acgatttctc ctgccaggtc acgggaagtt gttatttaaa
300

gatggcagtt attacgaagg ggcgtttgtg gacggagaga tcacgggaga aggccgccgg
360
cactgggcct ggtcaggaga caccttctct ggacagtttg ttctgggaga gcctcaaggc
420
tacggcgtca tggagtacaa agccggcgga tgttatgaag gggaggtctc ccacggcatg
480
cgggaaggac acgggtttct ggtggaccgg gatggacaag tgtaccaggg ctccttccat
540
gacaacaaga ggcacggccc tgggcagatg ctctttcaga acggtgacaa gtacgacggc
600
gactgggtcc gggaccggcg tcagggacac ggggtgctgc gctgcgccga cggctccacc
660
tacaagggac agtggcacag cgacgtcttc agtggactgg gcagcatggc ccactgctca
720
ggggtcacct attatgggtt gtggatcaat ggccacccag cagaacaagc tacgaggatc
780
gtgatcttgg gtccggaggt gatggaagtg gcccaagggt ctcccttctc ggtgaacgtt
840
cagctgctgc aggaccacgg ggaaattgcc aagagtaagc atctccaggg ggagatgacc
900
taacgtttcc aaaagagaaa caggcagcag gttcttaagc agtgaagatg cggacgagat
960
gttgcatgtg gctcctgagg cacagcagtg acttcgtgcc cagagcctgg cagagaggtc
1020
gcaggtgtgc cagcttccct gccagtcagg gcagccttgg gtgtgtgtgc aagcatgtgt
1080
gcacatattg tgtgatgtgc gtgctcctgt atgtgtgtgc atatgtgtgt atgccttgca
1140
caggtgtgca caggtctgaa tgtgtatacg tgtgggggggg cacgcgt
1187

<210> 5164
<211> 213
<212> PRT
<213> Homo sapiens

<400> 5164
Arg Phe Leu Leu Pro Gly His Gly Lys Leu Leu Phe Lys Asp Gly Ser
1 5 10 15
Tyr Tyr Glu Gly Ala Phe Val Asp Gly Glu Ile Thr Gly Glu Gly Arg
20 25 30
Arg His Trp Ala Trp Ser Gly Asp Thr Phe Ser Gly Gln Phe Val Leu
35 40 45
Gly Glu Pro Gln Gly Tyr Gly Val Met Glu Tyr Lys Ala Gly Gly Cys
50 55 60
Tyr Glu Gly Glu Val Ser His Gly Met Arg Glu Gly His Gly Phe Leu
65 70 75 80
Val Asp Arg Asp Gly Gln Val Tyr Gln Gly Ser Phe His Asp Asn Lys
85 90 95
Arg His Gly Pro Gly Gln Met Leu Phe Gln Asn Gly Asp Lys Tyr Asp
100 105 110
Gly Asp Trp Val Arg Asp Arg Arg Gln Gly His Gly Val Leu Arg Cys
115 120 125
Ala Asp Gly Ser Thr Tyr Lys Gly Gln Trp His Ser Asp Val Phe Ser

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    130                 135                 140
Gly Leu Gly Ser Met Ala His Cys Ser Gly Val Thr Tyr Tyr Gly Leu
145                 150                 155                 160
Trp Ile Asn Gly His Pro Ala Glu Gln Ala Thr Arg Ile Val Ile Leu
                165                 170                 175
Gly Pro Glu Val Met Glu Val Ala Gln Gly Ser Pro Phe Ser Val Asn
            180                 185                 190
Val Gln Leu Leu Gln Asp His Gly Glu Ile Ala Lys Ser Lys His Leu
        195                 200                 205
Gln Gly Glu Met Thr
    210
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<210> 5165
<211> 2370
<212> DNA
<213> Homo sapiens

<400> 5165
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cgtggagcca ccatggaccc cgcaggggca gcagacccct cagtgcctcc caatcctttg
120
actcacctga gcctgcagga cagatcagag atgcagctgc agagcgaagc cgacaggcgg
180
agcctcccgg gcacttggac caggtcatcc ccagagcaca ccaccattct gaggggaggc
240
gtgcgcaggt gcctgcagca acagtgtgaa cagactgtgc ggatcctgca tgccaaggtg
300
gcccagaaat catacggaaa tgagaagcgg ttcttctgcc ccccgccctg tgtctacctc
360
tcggggcctg gctggagggt gaagccaggg caggatcaag ctcaccaggc gggggaaacg
420
gggcccacgg tctgcggtta catgggactg gacagcgcgt ccggcagcgc cactgagacg
480
cagaagctga atttcgagca gcagccggac tccagggaat tcggctgcgc caagaccctg
540
tacatctcag atgcagacaa gaggaagcac tttcggctgg tgctgcggct ggtgctgcgc
600
gggggccggg agctgggtac cttccacagc cgccttatca aggtcatctc gaagccctcg
660
cagaagaagc agtcgctgaa aaacaccgat ctgtgcatat cctccggctc aaaggtctcc
720
ctcttcaacc gcctgcgctc tcagacggtc tccacacgct acctctctgt ggaggatggg
780
gcctttgtgg ccagtgcacg acagtgggct gccttcacgc tccacctggc tgatgggcac
840
tctgcccaag gagacttccc accgcgagag ggctacgttc gctatggctc cctggtgcag
900
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960
cagtgtgcgc tccttgatgt ggatgagccc atctcccagc tgcacaagtg tgcattccag
1020
tttccaggca gtcccccagg agggggtggc acctacttat gccttgccac agagaaggtg
1080

gtgcaatttc aggcctctcc ctgccccaag gaggcgaaca gggctctgct taacgacagc
1140
tcttgctgga ccatcatcgg caccgagtcg gtggaatttt ccttcagcac cagcctggcg
1200
tgtaccctgg agccggtcac tccggtgcct ctcatcagca ccctagagct gagcggcggg
1260
ggcgacgtgg ccacgctgga gctccacgga gagaacttcc acgcggggct caaggtgtgg
1320
tttggggacg tggaggcaga aaccatgtac aggtacgggg tgnngagccc gcggtccctg
1380
gtgtgcgtgg tgccggacgt ggcggccttc tgcagcgact ggcgctggct gcgcgctccc
1440
atcacaatcc ccatgagcct ggtgcgcgcc gacgggctct tctaccctag tgccttctcc
1500
ttcacctaca ccccggaata cagcgtgcgg ccgggtcacc ccggcgtccc cgagcccgcc
1560
accgacgccg acgcgctcct ggagagcatc catcaggagt tcacgcgcac caacttccac
1620
ctcttcatcc agacttaggc gcgcccggta gccccggctg cccaccctgg agggctgcgc
1680
ccgcgccagg cgcggggacg tgtttctggg ttctaggccc tgcttccttg ccccttttgct
1740
gcagaagggc agctgaaggc tcaccctaga aaccgggcct ggtgggtctt acccggctca
1800
ctccctccct tgtccttaca catacaggaa gacaagacct gagtggtgct gtctttgtgt
1860
ccgtcgtgta tggctctccc tgtcttcatt tcttctcact ctgtctctaa acctctctct
1920
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1980
ccttttctct cttcagctct ccctgcctct cacacacaat tttacatgcc ccgaggagcc
2040
aagtttggga catttaccct ccaggcatct atgtcccctc ttgaagagaa aacacacagc
2100
ttcacacatc caggcatagg gggcaagctc ttggggcatc aggaccctgg agcaccaggt
2160
ccttcctgga atattagatc cacctggaga accgggtctc tctaagtctc acctggggaa
2220
ttcggtccca cctggggcac cagttcccac ctagagcact gtgtcctgcc ctagagcaca
2280
aagacctgct cctcccgaga ctctctctga ctgcagccag gcatagtacc cttgcctgtg
2340
tttgctccct ggtccacaga tttggtggct
2370

<210> 5166
<211> 521
<212> PRT
<213> Homo sapiens

<400> 5166
Met Asp Pro Ala Gly Ala Ala Asp Pro Ser Val Pro Pro Asn Pro Leu
1 5 10 15
Thr His Leu Ser Leu Gln Asp Arg Ser Glu Met Gln Leu Gln Ser Glu

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            20                  25                  30
Ala Asp Arg Arg Ser Leu Pro Gly Thr Trp Thr Arg Ser Ser Pro Glu
        35                  40                  45
His Thr Thr Ile Leu Arg Gly Gly Val Arg Arg Cys Leu Gln Gln Gln
    50                  55                  60
Cys Glu Gln Thr Val Arg Ile Leu His Ala Lys Val Ala Gln Lys Ser
65                  70                  75                  80
Tyr Gly Asn Glu Lys Arg Phe Phe Cys Pro Pro Pro Cys Val Tyr Leu
                85                  90                  95
Ser Gly Pro Gly Trp Arg Val Lys Pro Gly Gln Asp Gln Ala His Gln
            100                 105                 110
Ala Gly Glu Thr Gly Pro Thr Val Cys Gly Tyr Met Gly Leu Asp Ser
        115                 120                 125
Ala Ser Gly Ser Ala Thr Glu Thr Gln Lys Leu Asn Phe Glu Gln Gln
    130                 135                 140
Pro Asp Ser Arg Glu Phe Gly Cys Ala Lys Thr Leu Tyr Ile Ser Asp
145                 150                 155                 160
Ala Asp Lys Arg Lys His Phe Arg Leu Val Leu Arg Leu Val Leu Arg
                165                 170                 175
Gly Gly Arg Glu Leu Gly Thr Phe His Ser Arg Leu Ile Lys Val Ile
            180                 185                 190
Ser Lys Pro Ser Gln Lys Lys Gln Ser Leu Lys Asn Thr Asp Leu Cys
        195                 200                 205
Ile Ser Ser Gly Ser Lys Val Ser Leu Phe Asn Arg Leu Arg Ser Gln
    210                 215                 220
Thr Val Ser Thr Arg Tyr Leu Ser Val Glu Asp Gly Ala Phe Val Ala
225                 230                 235                 240
Ser Ala Arg Gln Trp Ala Ala Phe Thr Leu His Leu Ala Asp Gly His
                245                 250                 255
Ser Ala Gln Gly Asp Phe Pro Pro Arg Glu Gly Tyr Val Arg Tyr Gly
            260                 265                 270
Ser Leu Val Gln Leu Val Cys Thr Val Thr Gly Ile Thr Leu Pro Pro
        275                 280                 285
Met Ile Ile Arg Lys Val Ala Lys Gln Cys Ala Leu Leu Asp Val Asp
    290                 295                 300
Glu Pro Ile Ser Gln Leu His Lys Cys Ala Phe Gln Phe Pro Gly Ser
305                 310                 315                 320
Pro Pro Gly Gly Gly Gly Thr Tyr Leu Cys Leu Ala Thr Glu Lys Val
                325                 330                 335
Val Gln Phe Gln Ala Ser Pro Cys Pro Lys Glu Ala Asn Arg Ala Leu
            340                 345                 350
Leu Asn Asp Ser Ser Cys Trp Thr Ile Ile Gly Thr Glu Ser Val Glu
        355                 360                 365
Phe Ser Phe Ser Thr Ser Leu Ala Cys Thr Leu Glu Pro Val Thr Pro
    370                 375                 380
Val Pro Leu Ile Ser Thr Leu Glu Leu Ser Gly Gly Gly Asp Val Ala
385                 390                 395                 400
Thr Leu Glu Leu His Gly Glu Asn Phe His Ala Gly Leu Lys Val Trp
                405                 410                 415
Phe Gly Asp Val Glu Ala Glu Thr Met Tyr Arg Tyr Gly Val Xaa Ser
            420                 425                 430
Pro Arg Ser Leu Val Cys Val Val Pro Asp Val Ala Ala Phe Cys Ser
        435                 440                 445
Asp Trp Arg Trp Leu Arg Ala Pro Ile Thr Ile Pro Met Ser Leu Val
```

```
    450                 455                 460
Arg Ala Asp Gly Leu Phe Tyr Pro Ser Ala Phe Ser Phe Thr Tyr Thr
465                 470                 475                 480
Pro Glu Tyr Ser Val Arg Pro Gly His Pro Gly Val Pro Glu Pro Ala
                485                 490                 495
Thr Asp Ala Asp Ala Leu Leu Glu Ser Ile His Gln Glu Phe Thr Arg
            500                 505                 510
Thr Asn Phe His Leu Phe Ile Gln Thr
        515                 520
```

<210> 5167
<211> 878
<212> DNA
<213> Homo sapiens

<400> 5167
gggccccgga ccaggcgctg gggacacagc agtgaaaata ctaacattgt ttctgccctc
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acggagctca cagtgtaaca gggagacaaa tagacctgtc agtagataac atgaaaataa
120
ttggactgtg tgctgcagac acaatatccc aggtctatga gaatgtcaat acagacttca
180
cgtgggaaat ggtgaggcaa taaggatcgt ttcccttgat gaaatggagc ttgcagaaga
240
aggcagggtc agttgtgggg agctctgggt ggaggtggag ggagtgcatt ccaagctgag
300
ccaagctatg acacctgagt ttcctgcctc tgtgctgcct ccctgttttc cattcccggt
360
tctcagcttc acttgtgggc tgagagtccc tgcgtgggtt atttttctgc ctttctcagg
420
gccttgggtt ccccaaatgt cacatgggca cagtaacacc catgtcctag ggttgaagat
480
ggcatgatat gatgtatgta aaatgcttgg cacaaggttt ctcaccgaag tctggaggag
540
ctgtccaggg ttctggagac gaaacggagc ccgctgggaa ctgtcctgag ccccggtgct
600
gaaacagatc gcggttctct tctcggacct cccgagaggc gctgtccgga tatttggtgc
660
tcccaagcag tcagccctgc tggtctctgc tttccagacc gtcaaacttc gccatctctg
720
tccctttttg ggaaaatgtc catgcgccaa cctgcaaacc agcctcattc ccggcatccc
780
acgtccctca gaccaccccc cctcccacgc agctgcggga ctccccctct gtgtgcctca
840
cctgcttcca gtcttgttgg cagatgcagg tgtcccgt
878

<210> 5168
<211> 199
<212> PRT
<213> Homo sapiens

<400> 5168
Met Pro Gly Met Arg Leu Val Cys Arg Leu Ala His Gly His Phe Pro

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 1               5                  10                  15
Lys Lys Gly Gln Arg Trp Arg Ser Leu Thr Val Trp Lys Ala Glu Thr
            20                  25                  30
Ser Arg Ala Asp Cys Leu Gly Ala Pro Asn Ile Arg Thr Ala Pro Leu
        35                  40                  45
Gly Arg Ser Glu Lys Arg Thr Ala Ile Cys Phe Ser Thr Gly Ala Gln
    50                  55                  60
Asp Ser Ser Gln Arg Ala Pro Phe Arg Leu Gln Asn Pro Gly Gln Leu
65                  70                  75                  80
Leu Gln Thr Ser Val Arg Asn Leu Val Pro Ser Ile Leu His Thr Ser
                85                  90                  95
Tyr His Ala Ile Phe Asn Pro Arg Thr Trp Val Leu Leu Cys Pro Cys
            100                 105                 110
Asp Ile Trp Gly Thr Gln Gly Pro Glu Lys Gly Arg Lys Ile Thr His
        115                 120                 125
Ala Gly Thr Leu Ser Pro Gln Val Lys Leu Arg Thr Gly Asn Gly Lys
    130                 135                 140
Gln Gly Gly Ser Thr Glu Ala Gly Asn Ser Gly Val Ile Ala Trp Leu
145                 150                 155                 160
Ser Leu Glu Cys Thr Pro Ser Thr Ser Thr Gln Ser Ser Pro Gln Leu
                165                 170                 175
Thr Leu Pro Ser Ser Ala Ser Ser Ile Ser Ser Arg Glu Thr Ile Leu
            180                 185                 190
Ile Ala Ser Pro Phe Pro Thr
        195
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<210> 5169
<211> 609
<212> DNA
<213> Homo sapiens

<400> 5169
accggtggct ttgcactcta cccgctgctc aacgaggctg cgccgttggc gctgggggcc
60
ggtttggtgc ctgaggagct gccaccatcc cgcgggggcc tgggtgaggc actgggtgcc
120
gtggagctta gcctcagcga gttcctgcta ctcttcacca ctgctggcat ctacgtggat
180
ggcgcaggcc gcaagtctcg tggccacgag ctgttgtggc cagcagcgcc catgggctgg
240
gggtatgcgg ccccctacct gacagtgttc agcgagaact ccatcgatgt gtttgacgtg
300
aggagggcag aatgggtgca gaccgtgccg ctcaagaagg tgcggcccct caatccagag
360
ggctccctgt tcctctacgg caccgagaag gtccgcctga cctacctcag gaaccagctg
420
gcagagaagg acgagttcga catcccggac ctcaccgaca acagccggcg ccagctgttc
480
ctcaccaaga gcaagcgccg cttctttttc cgcgtgtcgg aggagcagca gaagcagcag
540
cgcagggaga tgctgaagga ccctttgtg cgctccaagc tcatctcgcc gcctaccaac
600
ttcaaccac
609

<210> 5170
<211> 203
<212> PRT
<213> Homo sapiens

<400> 5170
Thr Gly Gly Phe Ala Leu Tyr Pro Leu Leu Asn Glu Ala Ala Pro Leu
1 5 10 15
Ala Leu Gly Ala Gly Leu Val Pro Glu Glu Leu Pro Pro Ser Arg Gly
20 25 30
Gly Leu Gly Glu Ala Leu Gly Ala Val Glu Leu Ser Leu Ser Glu Phe
35 40 45
Leu Leu Leu Phe Thr Thr Ala Gly Ile Tyr Val Asp Gly Ala Gly Arg
50 55 60
Lys Ser Arg Gly His Glu Leu Leu Trp Pro Ala Ala Pro Met Gly Trp
65 70 75 80
Gly Tyr Ala Ala Pro Tyr Leu Thr Val Phe Ser Glu Asn Ser Ile Asp
85 90 95
Val Phe Asp Val Arg Arg Ala Glu Trp Val Gln Thr Val Pro Leu Lys
100 105 110
Lys Val Arg Pro Leu Asn Pro Glu Gly Ser Leu Phe Leu Tyr Gly Thr
115 120 125
Glu Lys Val Arg Leu Thr Tyr Leu Arg Asn Gln Leu Ala Glu Lys Asp
130 135 140
Glu Phe Asp Ile Pro Asp Leu Thr Asp Asn Ser Arg Arg Gln Leu Phe
145 150 155 160
Leu Thr Lys Ser Lys Arg Arg Phe Phe Phe Arg Val Ser Glu Glu Gln
165 170 175
Gln Lys Gln Gln Arg Arg Glu Met Leu Lys Asp Pro Phe Val Arg Ser
180 185 190
Lys Leu Ile Ser Pro Pro Thr Asn Phe Asn His
195 200

<210> 5171
<211> 2060
<212> DNA
<213> Homo sapiens

<400> 5171
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ctctagtgtc tgactttgag atgcattata tttttaacac ataaatgagg ggatccatat
120
cacattcttt cttgtggacc accaaattga aggctttctt gtaattcaca agcagcagct
180
ctccagcatc tctccgtagc ctgggtgaag tcccagaagc tggtgtgcat cattttccaa
240
ggtggcagag ctgcttgctc tgcagatcat tcctttgaga gaggagtaca agtgaagaaa
300
caaggaggca cttcctgtag gagcactgat gtgccttgtc cacactcccc tctgagcttt
360
actggtaaga gagctccgac tgaacatgct gagcagttga gcacttttcc atcagcaaca
420

acagcgagga tggaaatgga aaggaaccga actaaaatgc atttcccttt gcagggcaga
480
gagctaagct cttaggaata gtgttataga aataagcacc ctaacttcaa ttcctgaaaa
540
tgttggttaa tggagagaat tttggagttt cacttaatat tttcccatcg gtcgccataa
600
ataagtcttc aggcgctcct agaagagtcc cagcccaagg ctcgattaag gaccacactg
660
caggtctgag gctcactgct ctgagtcctg aacaccagag ccctgcagag agtggtgata
720
acacatcatc tctgcaaaga ggaacctctc ccccggccgc cacttcactc aggcttctac
780
tgagcagcaa ggacagcctg ggtttcaaat gccacttccc ctgctttagg gatccaggtg
840
tcctgatagc gtgaccctgc tgaggcaagg tatcaactcc gagagtgact gagtcactga
900
gcgtggcaca tgaacaaacg tcatgacaaa gattctctga gtgaagttaa caccacgtat
960
tttacctttg caaaaaacaa actggcaccc tgagttctaa ctacggacgg acgatatctt
1020
tgcctccaca cccagattcc tggaaatggc taacgtttcc tttctagggg aagggtcgag
1080
gaatactcaa gtgctagctt agcagctttg ttcagtccag atcagagctg ttaggtaaag
1140
gcctaaccac ctccctgcag tctcttatat ctcaagcttt aggaacccat ttctaaatgt
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1320
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1380
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1440
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1500
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1560
ccacctacca gattctggaa atgccgtctt ctagaaaacg atggcgtttg tggtggtctt
1620
cttttgaaag gaacagtaat ttgtgtggat attgttaaag tgtttaaaga atattttgac
1680
aattaagttt acattttaca attgctttat tttttattaa aatagttgta tataaatatt
1740
accctatttc actgttgttc aagtaaatct aaaccttgta gacaagtgag tcacctgata
1800
tgtatagaag ctgtgatata tagagtacat ttattgtgta aatgtttatg aatataattg
1860
ttcctgtgtt tttataagtt ggggatattt tgttgtttta cggcaacaaa atttattgca
1920
tttaaatggt ttttatgtaa tagaaatcac gcaaaatagt gaaggattta aaatatgtat
1980
atgatacatg taaatgtaca aactttagaa agaaataaat ccaacaaatt tcaaaaaaaa
2040

aaaaaaaaaa aaaaaaaaaa
2060

<210> 5172
<211> 104
<212> PRT
<213> Homo sapiens

<400> 5172
Met Leu Val Asn Gly Glu Asn Phe Gly Val Ser Leu Asn Ile Phe Pro
1 5 10 15
Ser Val Ala Ile Asn Lys Ser Ser Gly Ala Pro Arg Arg Val Pro Ala
20 25 30
Gln Gly Ser Ile Lys Asp His Thr Ala Gly Leu Arg Leu Thr Ala Leu
35 40 45
Ser Pro Glu His Gln Ser Pro Ala Glu Ser Gly Asp Asn Thr Ser Ser
50 55 60
Leu Gln Arg Gly Thr Ser Pro Pro Ala Ala Thr Ser Leu Arg Leu Leu
65 70 75 80
Leu Ser Ser Lys Asp Ser Leu Gly Phe Lys Cys His Phe Pro Cys Phe
85 90 95
Arg Asp Pro Gly Val Leu Ile Ala
100

<210> 5173
<211> 557
<212> DNA
<213> Homo sapiens

<400> 5173
ctttgatgcc tttattgatt caacacatgc ttattatatg cttgctgtgt gccgggcccc
60
agaccaggcg ctggagacac agcagtgaaa atactaacat tgtttctgcc ctcacggagc
120
tcacagtgta acagggagac aaatagacct gtcagtagat aacatgaaaa taattggact
180
atgtgctgca gacacaatat cccaggtcta tgagaatgtc aatacagact tcacgtggga
240
aatggtgagg caataaggat cgtttccctt gatgaaatgg agcttgcaga agaaggcagg
300
gtcagttgtg gggagctctg gttggaggtg gagggagtgc attccaagct ggaggagctg
360
tccagggttc tggagactaa acggagcccg ctgggaactg tcctgagccc cggtgctgaa
420
acagatcgcg gttctcttct cggacctccc gagaagcgct gtccggatat ttggtgctcc
480
caagcagtca gccctgctgg tctctgcttt ccagaccggc aaacttcgcc gtctctgtcc
540
ctttctggga aaatggc
557

<210> 5174
<211> 93
<212> PRT

<213> Homo sapiens

<400> 5174
Met Glu Leu Ala Glu Glu Gly Arg Val Ser Cys Gly Glu Leu Trp Leu
1 5 10 15
Glu Val Glu Gly Val His Ser Lys Leu Glu Glu Leu Ser Arg Val Leu
20 25 30
Glu Thr Lys Arg Ser Pro Leu Gly Thr Val Leu Ser Pro Gly Ala Glu
35 40 45
Thr Asp Arg Gly Ser Leu Leu Gly Pro Pro Glu Lys Arg Cys Pro Asp
50 55 60
Ile Trp Cys Ser Gln Ala Val Ser Pro Ala Gly Leu Cys Phe Pro Asp
65 70 75 80
Arg Gln Thr Ser Pro Ser Leu Ser Leu Ser Gly Lys Met
85 90

<210> 5175
<211> 272
<212> DNA
<213> Homo sapiens

<400> 5175
ccatggcagc tccagagacc aggtggaggg gaaatcaccc cacgctcccg agcagagagc
60
ttcggagcca gccagcctca ctgtgcgtgg cccacaacag ctgtctccat gtgtcacgtg
120
agggctgccc aacaccaggt agggcagcaa cgcccacgcc ctcgccgggc acagcctccc
180
agaggtcact gccatgccgc actgaccgga gagagggcag tggtgagagg tgcatgccac
240
cccaggcttg ttccgaaggc ccnnnnnncc nc
272

<210> 5176
<211> 90
<212> PRT
<213> Homo sapiens

<400> 5176
Met Ala Ala Pro Glu Thr Arg Trp Arg Gly Asn His Pro Thr Leu Pro
1 5 10 15
Ser Arg Glu Leu Arg Ser Gln Pro Ala Ser Leu Cys Val Ala His Asn
20 25 30
Ser Cys Leu His Val Ser Arg Glu Gly Cys Pro Thr Pro Gly Arg Ala
35 40 45
Ala Thr Pro Thr Pro Ser Pro Gly Thr Ala Ser Gln Arg Ser Leu Pro
50 55 60
Cys Arg Thr Asp Arg Arg Glu Gly Ser Gly Glu Arg Cys Met Pro Pro
65 70 75 80
Gln Ala Cys Ser Glu Gly Pro Xaa Xaa Xaa
85 90

<210> 5177
<211> 637

<212> DNA
<213> Homo sapiens

<400> 5177
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<211> 92
<212> PRT
<213> Homo sapiens

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            20   25   30
Asn Ser Gln Ile Arg Ser Arg Ser Ser Ser Ser Ser Ser Gly Gly Gly
        35   40   45
Leu Leu Pro Tyr Pro Arg Arg Arg Pro Pro His Ser Ala Arg Gly Gly
    50   55   60
Gly Ser Gly Gly Gly Gly Gly Ser Ser Ser Ser Ser Ser Ser Ser Gln
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Gln Gln Leu Arg Asn Phe Ser Arg Ser Arg His Ala
                85   90

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<211> 1527
<212> DNA
<213> Homo sapiens

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1527

<210> 5180
<211> 444
<212> PRT

<213> Homo sapiens

<400> 5180

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Phe Asp Gly His Asp Ile Pro Tyr Asp Ala Met Trp Leu Asp Ile Glu
        35                  40                  45
His Thr Glu Gly Lys Arg Tyr Phe Thr Trp Asp Lys Asn Arg Phe Pro
    50                  55                  60
Asn Pro Lys Arg Met Gln Glu Leu Leu Arg Asn Lys Lys Arg Lys Leu
65                  70                  75                  80
Val Val Ile Ser Asp Pro His Ile Lys Ile Glu Pro Asp Tyr Ser Val
                85                  90                  95
Tyr Val Lys Ala Lys Asp Gln Gly Phe Phe Val Lys Asn Gln Glu Gly
            100                 105                 110
Glu Asp Phe Glu Gly Val Cys Trp Pro Gly Leu Ser Ser Tyr Leu Asp
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Phe Thr Asn Pro Lys Val Arg Glu Trp Tyr Ser Ser Leu Phe Ala Phe
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Pro Val Tyr Gln Gly Ser Thr Asp Ile Leu Phe Leu Trp Asn Asp Met
145                 150                 155                 160
Asn Glu Pro Ser Val Phe Arg Gly Pro Glu Gln Thr Met Gln Lys Asn
                165                 170                 175
Ala Ile His His Gly Asn Trp Glu His Arg Glu Leu His Asn Ile Tyr
            180                 185                 190
Gly Phe Tyr His Gln Met Ala Thr Ala Glu Gly Leu Ile Lys Arg Ser
        195                 200                 205
Lys Gly Lys Glu Arg Pro Phe Val Leu Thr Arg Ser Phe Phe Ala Gly
    210                 215                 220
Ser Gln Lys Tyr Gly Ala Val Trp Thr Gly Asp Asn Thr Ala Glu Trp
225                 230                 235                 240
Ser Asn Leu Lys Ile Ser Ile Pro Met Leu Leu Thr Leu Ser Ile Thr
                245                 250                 255
Gly Ile Ser Phe Cys Gly Ala Asp Ile Gly Gly Phe Ile Gly Asn Pro
            260                 265                 270
Glu Thr Glu Leu Leu Val Arg Trp Tyr Gln Ala Gly Ala Tyr Gln Pro
        275                 280                 285
Phe Phe Arg Gly His Ala Thr Met Asn Thr Lys Arg Arg Glu Pro Trp
    290                 295                 300
Leu Phe Gly Glu Glu His Thr Arg Leu Ile Arg Glu Ala Ile Arg Glu
305                 310                 315                 320
Arg Tyr Gly Leu Leu Pro Tyr Trp Tyr Ser Leu Phe Tyr His Ala His
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Val Ala Ser Gln Pro Val Met Arg Pro Leu Trp Val Glu Phe Pro Asp
            340                 345                 350
Glu Leu Lys Thr Phe Asp Met Glu Asp Glu Tyr Met Leu Gly Ser Ala
        355                 360                 365
Leu Leu Val His Pro Val Thr Glu Pro Lys Ala Thr Thr Val Asp Val
    370                 375                 380
Phe Leu Pro Gly Ser Asn Glu Val Trp Tyr Asp Tyr Lys Thr Phe Ala
385                 390                 395                 400
His Trp Glu Gly Gly Cys Thr Val Lys Ile Pro Val Ala Leu Asp Thr
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<210> 5181
<211> 4961
<212> DNA
<213> Homo sapiens

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4961

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<211> 697
<212> PRT
<213> Homo sapiens

<400> 5182
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Met Gly Ala Leu Ala Ala Ile Leu Ala Tyr Trp Phe Thr His Arg Pro
35 40 45
Lys Ala Leu Gln Pro Pro Cys Asn Leu Leu Met Gln Ser Glu Glu Val
50 55 60
Glu Asp Ser Gly Gly Ala Arg Arg Ser Val Ile Gly Ser Gly Pro Gln
65 70 75 80
Leu Leu Thr His Tyr Tyr Asp Asp Ala Arg Thr Met Tyr Gln Val Phe
85 90 95
Arg Arg Gly Leu Ser Ile Ser Gly Asn Gly Pro Cys Leu Gly Phe Arg
100 105 110
Lys Pro Lys Gln Pro Tyr Gln Trp Leu Ser Tyr Gln Glu Val Ala Asp
115 120 125
Arg Ala Glu Phe Leu Gly Ser Gly Leu Leu Gln His Asn Cys Lys Ala
130 135 140
Cys Thr Asp Gln Phe Ile Gly Val Phe Ala Gln Asn Arg Pro Glu Trp
145 150 155 160
Ile Ile Val Glu Leu Ala Cys Tyr Thr Tyr Ser Met Val Val Val Pro
165 170 175
Leu Tyr Asp Thr Leu Gly Pro Gly Ala Ile Arg Tyr Ile Ile Asn Thr
180 185 190
Ala Asp Ile Ser Thr Val Ile Val Asp Lys Pro Gln Lys Ala Val Leu
195 200 205
Leu Leu Glu His Val Glu Arg Lys Glu Thr Pro Gly Leu Lys Leu Ile
210 215 220
Ile Leu Met Asp Pro Phe Glu Glu Ala Leu Lys Glu Arg Gly Gln Lys
225 230 235 240
Cys Gly Val Val Ile Lys Ser Met Gln Ala Val Glu Asp Cys Gly Gln

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Glu Asn His Gln Ala Pro Val Pro Pro Gln Pro Asp Asp Leu Ser Ile
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Val Cys Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Ala Met Leu
        275                 280                 285
Thr His Gly Asn Val Val Ala Asp Phe Ser Gly Phe Leu Lys Val Thr
    290                 295                 300
Glu Ser Gln Trp Ala Pro Thr Cys Ala Asp Val His Ile Ser Tyr Leu
305                 310                 315                 320
Pro Leu Ala His Met Phe Glu Arg Met Val Gln Ser Val Val Tyr Cys
                325                 330                 335
His Gly Gly Arg Val Gly Phe Phe Gln Gly Asp Ile Arg Leu Leu Ser
            340                 345                 350
Asp Asp Met Lys Ala Leu Cys Pro Thr Ile Phe Pro Val Val Pro Arg
        355                 360                 365
Leu Leu Asn Arg Met Tyr Asp Lys Ile Phe Ser Gln Ala Asn Thr Pro
    370                 375                 380
Leu Lys Arg Trp Leu Leu Glu Phe Ala Ala Lys Arg Lys Gln Ala Glu
385                 390                 395                 400
Val Arg Ser Gly Ile Ile Arg Asn Asp Ser Ile Trp Asp Glu Leu Phe
                405                 410                 415
Phe Asn Lys Ile Gln Ala Ser Leu Gly Gly Cys Val Arg Met Ile Val
            420                 425                 430
Thr Gly Ala Ala Pro Ala Ser Pro Thr Val Leu Gly Phe Leu Arg Ala
        435                 440                 445
Ala Leu Gly Cys Gln Val Tyr Glu Gly Tyr Gly Gln Thr Glu Cys Thr
    450                 455                 460
Ala Gly Cys Thr Phe Thr Thr Pro Gly Asp Trp Thr Ser Gly His Val
465                 470                 475                 480
Gly Ala Pro Leu Pro Cys Asn His Ile Lys Leu Val Asp Val Glu Glu
                485                 490                 495
Leu Asn Tyr Trp Ala Cys Lys Gly Glu Gly Glu Ile Cys Val Arg Gly
            500                 505                 510
Pro Asn Val Phe Lys Gly Tyr Leu Lys Asp Pro Asp Arg Thr Lys Glu
        515                 520                 525
Ala Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Lys Trp
    530                 535                 540
Leu Pro Ala Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys His Ile Phe
545                 550                 555                 560
Lys Leu Ala Gln Gly Glu Tyr Val Ala Pro Glu Lys Ile Glu Asn Ile
                565                 570                 575
Tyr Ile Arg Ser Gln Pro Val Ala Gln Ile Tyr Val His Gly Asp Ser
            580                 585                 590
Leu Lys Ala Phe Leu Val Gly Ile Val Val Pro Asp Pro Glu Val Met
        595                 600                 605
Pro Ser Trp Ala Gln Lys Arg Gly Ile Glu Gly Thr Tyr Ala Asp Leu
    610                 615                 620
Cys Thr Asn Lys Asp Leu Lys Lys Ala Ile Leu Glu Asp Met Val Arg
625                 630                 635                 640
Leu Gly Lys Glu Ser Gly Leu His Ser Phe Glu Gln Val Lys Ala Ile
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His Ile His Ser Asp Met Phe Ser Val Gln Asn Gly Leu Leu Thr Pro
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Thr Leu Lys Ala Lys Arg Pro Glu Leu Arg Glu Tyr Phe Lys Lys Gln
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Ile Glu Glu Leu Tyr Ser Ile Ser Met
690 695

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<211> 2466
<212> DNA
<213> Homo sapiens

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1920
acagctgaat gttcctaaag aactgctgcc ccacagtgag ggtgggagca gcggaacagg
1980
gaatgccaga cacaggctcg ctgctgctgg aaggcggggt gggacttcct tcctctgtcc
2040
ggagaggcac aggtgtcacc agttccagcc aaaggctcct cacaggcgct gtgaattttt
2100
gtacaagtct tgtaattatc gaatcaacaa cttgtttcaa tttaataaaa atgctcatgg
2160
gaaggcgggc gcggaggcgg ctagaaggtg accgcggatc ccagcttcct gcagtcagcc
2220
ctgaaggatg gctgccatat tgggagacac catcatggtg gctaaaggcc ttgtcaagct
2280
gacccctgcg ctccgaggac ccctcaggga agaaggccgt gctgggttcc agtcctttcc
2340
tgtccgaggc caatgcagag cggatcgtgc gcacgctctg caaggtgcgt ggtgcggcac
2400
tcaagctggg ccagatgctg agcatccagg atgatgcctt tatcaacccc cacctggcta
2460
agatct
2466

<210> 5184
<211> 395
<212> PRT
<213> Homo sapiens

<400> 5184
Pro Phe Leu Ser Glu Ala Asn Ala Glu Arg Ile Val Arg Thr Leu Cys
1 5 10 15
Lys Val Arg Gly Ala Ala Leu Lys Leu Gly Gln Met Leu Ser Ile Gln
20 25 30
Asp Asp Ala Phe Ile Asn Pro His Leu Ala Lys Ile Phe Glu Arg Val
35 40 45
Arg Gln Ser Ala Asp Phe Met Pro Leu Lys Gln Met Met Lys Thr Leu

```
   50                  55                  60
Asn Asn Asp Leu Gly Pro Asn Trp Arg Asp Lys Leu Glu Tyr Phe Glu
65                  70                  75                  80
Glu Arg Pro Phe Ala Ala Ala Ser Ile Gly Gln Val His Leu Ala Arg
                85                  90                  95
Met Lys Gly Gly Arg Glu Val Ala Met Lys Ile Gln Tyr Pro Gly Val
            100                 105                 110
Ala Gln Ser Ile Asn Ser Asp Val Asn Asn Leu Met Ala Val Leu Asn
        115                 120                 125
Met Ser Asn Met Leu Pro Glu Gly Leu Phe Pro Glu His Leu Ile Asp
    130                 135                 140
Val Leu Arg Arg Glu Leu Ala Leu Glu Cys Asp Tyr Gln Arg Glu Ala
145                 150                 155                 160
Ala Cys Ala Arg Lys Phe Arg Asp Leu Leu Lys Gly His Pro Phe Phe
                165                 170                 175
Tyr Val Pro Glu Ile Val Asp Glu Leu Cys Ser Pro His Val Leu Thr
            180                 185                 190
Thr Glu Leu Val Ser Gly Phe Pro Leu Asp Gln Ala Glu Gly Leu Ser
        195                 200                 205
Gln Glu Ile Arg Asn Glu Ile Cys Tyr Asn Ile Leu Val Leu Cys Leu
    210                 215                 220
Arg Glu Leu Phe Glu Phe His Phe Met Gln Thr Asp Pro Asn Trp Ser
225                 230                 235                 240
Asn Phe Phe Tyr Asp Pro Gln Gln His Lys Val Ala Leu Leu Asp Phe
                245                 250                 255
Gly Ala Thr Arg Glu Tyr Asp Arg Ser Phe Thr Asp Leu Tyr Ile Gln
            260                 265                 270
Ile Ile Arg Ala Ala Ala Asp Arg Asp Arg Glu Thr Val Arg Ala Lys
        275                 280                 285
Ser Ile Glu Met Lys Phe Leu Thr Gly Tyr Glu Val Lys Val Met Glu
    290                 295                 300
Asp Ala His Leu Asp Ala Ile Leu Ile Leu Gly Glu Ala Phe Ala Ser
305                 310                 315                 320
Asp Glu Pro Phe Asp Phe Gly Thr Gln Ser Thr Thr Glu Lys Ile His
                325                 330                 335
Asn Leu Ile Pro Val Met Leu Arg His Arg Leu Val Pro Pro Pro Glu
            340                 345                 350
Glu Thr Tyr Ser Leu His Arg Lys Met Gly Gly Ser Phe Leu Ile Cys
        355                 360                 365
Ser Lys Leu Lys Ala Arg Phe Pro Cys Lys Ala Met Phe Glu Glu Ala
    370                 375                 380
Tyr Ser Asn Tyr Cys Lys Arg Gln Ala Gln Gln
385                 390                 395
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<210> 5185
<211> 1657
<212> DNA
<213> Homo sapiens

<400> 5185
gtgcactcac agaatctgct gcttcccagg tcttttggat gtgaaatgaa accccaagga
60
ctgctttaac aaggggcaaa aacacatgca accaaagcca gcagttatgc cgaagcatcc
120

cggattccca tgagaaactc tctggatcta gttcctctac gtcacatgag tgtgcaaaca
180
ggagactaca agagtttaaa aatactggga ctgctggaga tttccctggc catatatagt
240
tcacttgttt cacagatctc actctgtcac ccaggctgga gtacagtggt gcgatctcaa
300
cttactgcaa cctccgcctc ccggttcaag cgattcgcct gcctctgcct tagctatgtc
360
cctttcagaa aaattctact tcaagagaag atttggtttc aggatgtctc ctggactgga
420
gggcatgtac ctagagtccc acgaactggc tgggtataca gaaatgtcca gaggccggag
480
agcgtttcag atcacatgta ccggatggca gttatggcta tggtgatcaa agatgaccgt
540
cttaacaaag acncggaagc tatgaagcag ataacccagc tcctaccaga ggacctcaga
600
aaggagctct atgaactttg ggaagagtac gagacccaat ctagtgcaga agccaaattt
660
gtgaagcagc tagaccaatg tgaaatgatt cttcaagcat ctgaatatga agaccttgaa
720
cacaaacctg ggagactgca agacttctat gattccacag caggaaaatt caatcaccct
780
gagatagtcc agcttgtttc tgaacttgag gcagaaagaa gcactaacat agctgcagct
840
gccagtgagc cacactcctg agacactctc taaattgctg cactcctgta acaaacatta
900
tttttccatt tcattgtatt gtgttttgcc attgttggtc tgttgatttc cctagatgtg
960
agtctgtttg ttttcaattg tctgaacttc agcaagaaat gtgatacaac ttgggcacta
1020
aaagaagcca cagaacagga agcggtcatg aaagtgccat ggatgaacac tggaggtggc
1080
agtgcctgtt tatgaactaa ataaataaat attaaacacc taaaatatta gaatatttat
1140
tggagattta aaatcatctt attctgactt aattaccgat atccccgaag gctaggttca
1200
ttgaataata gaaaatttca ttatgattgc ttttaagaac agattcttca gctgatttag
1260
tgataagaat ccagaaaaga aaatgtacta gtgatgtatt ctctccccag atgaaattgc
1320
tgccttattc agatttactc tcttgagcca gattttgaat ttcactgcag actgcttcag
1380
acttctaatc ataggcttgt aaacctacta ataggctctg cccctcttcc caatactttt
1440
tgtcatttag agatataaac cggggcatat aaaaatgcaa cttgtattcc tttgtatatt
150.
tttccctgtc tgacttataa atcttgagac ctttattgta aaagcattta tcatcaggtg
1560
agaaatataa ataggaactg gggtcattga gcctcaggta gggaatatat caacccgatt
1620
tcttcctctc ttttcccttt tataggataa ataatcc
1657

<210> 5186

<211> 243
<212> PRT
<213> Homo sapiens

<400> 5186
Met Arg Asn Ser Leu Asp Leu Val Pro Leu Arg His Met Ser Val Gln
1 5 10 15
Thr Gly Asp Tyr Lys Ser Leu Lys Ile Leu Gly Leu Leu Glu Ile Ser
20 25 30
Leu Ala Ile Tyr Ser Ser Leu Val Ser Gln Ile Ser Leu Cys His Pro
35 40 45
Gly Trp Ser Thr Val Val Arg Ser Gln Leu Thr Ala Thr Ser Ala Ser
50 55 60
Arg Phe Lys Arg Phe Ala Cys Leu Cys Leu Ser Tyr Val Pro Phe Arg
65 70 75 80
Lys Ile Leu Leu Gln Glu Lys Ile Trp Phe Gln Asp Val Ser Trp Thr
85 90 95
Gly Gly His Val Pro Arg Val Pro Arg Thr Gly Trp Val Tyr Arg Asn
100 105 110
Val Gln Arg Pro Glu Ser Val Ser Asp His Met Tyr Arg Met Ala Val
115 120 125
Met Ala Met Val Ile Lys Asp Asp Arg Leu Asn Lys Asp Xaa Glu Ala
130 135 140
Met Lys Gln Ile Thr Gln Leu Leu Pro Glu Asp Leu Arg Lys Glu Leu
145 150 155 160
Tyr Glu Leu Trp Glu Glu Tyr Glu Thr Gln Ser Ser Ala Glu Ala Lys
165 170 175
Phe Val Lys Gln Leu Asp Gln Cys Glu Met Ile Leu Gln Ala Ser Glu
180 185 190
Tyr Glu Asp Leu Glu His Lys Pro Gly Arg Leu Gln Asp Phe Tyr Asp
195 200 205
Ser Thr Ala Gly Lys Phe Asn His Pro Glu Ile Val Gln Leu Val Ser
210 215 220
Glu Leu Glu Ala Glu Arg Ser Thr Asn Ile Ala Ala Ala Ala Ser Glu
225 230 235 240
Pro His Ser

<210> 5187
<211> 1712
<212> DNA
<213> Homo sapiens

<400> 5187
nttttgtctt gtcggctcct gtgtgtagga gggatttcgg cctgagagcg ggccgaggag
60
attggcgacg gtgtcgcccg tgttttcgtt ggcgggtgcc tgggctggtg ggaacagccg
120
cccgaaggaa gcaccatgat ttcggccgcg cagttgttgg atgagttaat gggccgggac
180
cgaaacctag ccccggacga gaagcgcagc aacgtgcggt gggaccacga gagcgtttgt
240
aaatattatc tctgtggttt ttgtcctgcg gaattgttca caaatacacg ttctgatctt
300

ggtccgtgtg aaaaaattca tgatgaaaat ctacgaaaac agtatgagaa gagctctcgt
360
ttcatgaaag ttggctatga gagagatttt ttgcgatact tacagagctt acttgcagaa
420
gtagaacgta ggatcagacg aggccatgct cgtttggcat tatctcaaaa ccagcagtct
480
tctggggccg ctggcccaac aggcaaaaat gaagaaaaaa ttcaggttct aacagacaaa
540
attgatgtac ttctgcaaca gattgaagaa ttagggtctg aaggaaaagt agaagaagcc
600
caggggatga tgaaattagt tgagcaatta aaagaagaga gagaactgct aaggtccaca
660
acgtcgacaa ttgaaagctt tgctgcacaa gaaaaacaaa tggaagtttg tgaagtatgt
720
ggagcctttt taatagtagg agatgcccag tcccgggtag atgaccattt gatgggaaaa
780
caacacatgg gctatgccaa aattaaagct actgtagaag aattaaaaga aaagttaagg
840
aaaagaaccg aagaacctga tcgtgatgag cgtctaaaaa aggagaagca agaaagagaa
900
gaaagagaaa aagaacggga gagagaaagg gaagaaagag aaaggaaaag acgaagggaa
960
gaggaagaaa gagaaaaaga aagggctcgt gacagagaaa gaagaaagag aagtcgttca
1020
cgaagtagac actcaagccg aacatcagac agaagatgca gcaggtctcg ggaccacaaa
1080
aggtcacgaa gtagagaaag aaggcggagc agaagtagag atcgacgaag aagcagaagc
1140
catgatcgat cagaaagaaa acacagatct cgaagtcggg atcgaagaag atcaaaaagc
1200
cgggatcgaa agtcatataa gcacaggagc aaaagtcggg acagagaaca agatagaaaa
1260
tccaaggaga aagaaaagag gggatctgat gataaaaaaa gtagtgtgaa gtccggtagt
1320
cgagaaaagc agagtgaaga cacaaacact gaatcgaagg aaagtgatac taagaatgag
1380
gtcaatggga ccagtgaaga cattaaatct gaagtgcagc gtaagtatgc acagatgaag
1440
atggaactaa gccgagtaag aagacataca aaagcctctt ctgaaggaaa agacagtgta
1500
gtcctgcaaa acattttgag gtacattgtt ttgtctcagc tattttgtag cagactcgtg
1560
cccccattag tgtgcctctt tggaaattat cgcccacatt tgtaatatag tcgccattga
1620
aaagttaatt atccttttt tagggatttt gatgtcgttt ctttttttt ttaatacaaa
1680
ggttgaactg ttttttttt ccttttttgg tt
1712

<210> 5188
<211> 489
<212> PRT
<213> Homo sapiens

<400> 5188
Met Ile Ser Ala Ala Gln Leu Leu Asp Glu Leu Met Gly Arg Asp Arg
1 5 10 15
Asn Leu Ala Pro Asp Glu Lys Arg Ser Asn Val Arg Trp Asp His Glu
20 25 30
Ser Val Cys Lys Tyr Tyr Leu Cys Gly Phe Cys Pro Ala Glu Leu Phe
35 40 45
Thr Asn Thr Arg Ser Asp Leu Gly Pro Cys Glu Lys Ile His Asp Glu
50 55 60
Asn Leu Arg Lys Gln Tyr Glu Lys Ser Ser Arg Phe Met Lys Val Gly
65 70 75 80
Tyr Glu Arg Asp Phe Leu Arg Tyr Leu Gln Ser Leu Leu Ala Glu Val
85 90 95
Glu Arg Arg Ile Arg Arg Gly His Ala Arg Leu Ala Leu Ser Gln Asn
100 105 110
Gln Gln Ser Ser Gly Ala Ala Gly Pro Thr Gly Lys Asn Glu Glu Lys
115 120 125
Ile Gln Val Leu Thr Asp Lys Ile Asp Val Leu Leu Gln Gln Ile Glu
130 135 140
Glu Leu Gly Ser Glu Gly Lys Val Glu Glu Ala Gln Gly Met Met Lys
145 150 155 160
Leu Val Glu Gln Leu Lys Glu Glu Arg Glu Leu Leu Arg Ser Thr Thr
165 170 175
Ser Thr Ile Glu Ser Phe Ala Ala Gln Glu Lys Gln Met Glu Val Cys
180 185 190
Glu Val Cys Gly Ala Phe Leu Ile Val Gly Asp Ala Gln Ser Arg Val
195 200 205
Asp Asp His Leu Met Gly Lys Gln His Met Gly Tyr Ala Lys Ile Lys
210 215 220
Ala Thr Val Glu Glu Leu Lys Glu Lys Leu Arg Lys Arg Thr Glu Glu
225 230 235 240
Pro Asp Arg Asp Glu Arg Leu Lys Lys Glu Lys Gln Glu Arg Glu Glu
245 250 255
Arg Glu Lys Glu Arg Glu Arg Glu Arg Glu Glu Arg Glu Arg Lys Arg
260 265 270
Arg Arg Glu Glu Glu Glu Arg Glu Lys Glu Arg Ala Arg Asp Arg Glu
275 280 285
Arg Arg Lys Arg Ser Arg Ser Arg Ser Arg His Ser Ser Arg Thr Ser
290 295 300
Asp Arg Arg Cys Ser Arg Ser Arg Asp His Lys Arg Ser Arg Ser Arg
305 310 315 320
Glu Arg Arg Arg Ser Arg Ser Arg Asp Arg Arg Arg Ser Arg Ser His
325 330 335
Asp Arg Ser Glu Arg Lys His Arg Ser Arg Ser Arg Asp Arg Arg Arg
340 345 350
Ser Lys Ser Arg Asp Arg Lys Ser Tyr Lys His Arg Ser Lys Ser Arg
355 360 365
Asp Arg Glu Gln Asp Arg Lys Ser Lys Glu Lys Glu Lys Arg Gly Ser
370 375 380
Asp Asp Lys Lys Ser Ser Val Lys Ser Gly Ser Arg Glu Lys Gln Ser
385 390 395 400
Glu Asp Thr Asn Thr Glu Ser Lys Glu Ser Asp Thr Lys Asn Glu Val
405 410 415
Asn Gly Thr Ser Glu Asp Ile Lys Ser Glu Val Gln Arg Lys Tyr Ala

```
            420                 425                 430
Gln Met Lys Met Glu Leu Ser Arg Val Arg Arg His Thr Lys Ala Ser
        435                 440                 445
Ser Glu Gly Lys Asp Ser Val Val Leu Gln Asn Ile Leu Arg Tyr Ile
    450                 455                 460
Val Leu Ser Gln Leu Phe Cys Ser Arg Leu Val Pro Pro Leu Val Cys
465                 470                 475                 480
Leu Phe Gly Asn Tyr Arg Pro His Leu
                485
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<210> 5189
<211> 323
<212> DNA
<213> Homo sapiens

<400> 5189
acgcgtgaag ggattacagg catgagccac tgcacctggc caggagaaat tgtttttata
60
acgtatgaca aatgcttgag taattcctgg cttgaaagtg ggctcacaat aaataactgg
120
aatccaaaaa taacaaaatg tttagcaatt caggtaatgt caagcagtat tcaaacacat
180
gaagttaatc attccttaat tcctgtttat ttatatttca tttttgcttt ctttttactc
240
catgtgttat tcctacagaa gtcacaagtt aaatgttttt ggggaacttt gggggggggg
300
gacaaacatc catgtgctgc taa
323

<210> 5190
<211> 100
<212> PRT
<213> Homo sapiens

<400> 5190
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Met Ser His Cys Thr Trp Pro Gly Glu Ile Val Phe Ile Thr Tyr Asp
 1               5                  10                  15
Lys Cys Leu Ser Asn Ser Trp Leu Glu Ser Gly Leu Thr Ile Asn Asn
            20                  25                  30
Trp Asn Pro Lys Ile Thr Lys Cys Leu Ala Ile Gln Val Met Ser Ser
        35                  40                  45
Ser Ile Gln Thr His Glu Val Asn His Ser Leu Ile Pro Val Tyr Leu
    50                  55                  60
Tyr Phe Ile Phe Ala Phe Phe Leu Leu His Val Leu Phe Leu Gln Lys
65                  70                  75                  80
Ser Gln Val Lys Cys Phe Trp Gly Thr Leu Gly Gly Gly Asp Lys His
                85                  90                  95
Pro Cys Ala Ala
            100
```

<210> 5191
<211> 1632
<212> DNA
<213> Homo sapiens

<400> 5191
tcccgcattt tagaggtgac tggagaactc tcacgtaggc ggccgcccca atttcccgcc
60
cgggtcatcg gggagcccct tcccaagccc cgcaaacacc tgcatgcaaa gaggcaggct
120
tccttctgac agcagataac atgtcgcctg cggcgtcagc aagaggcgca tgcgccttgc
180
cgtgggaggc cgggtgcgca ggactggaac gcggttcctc cttcttcccc gccccgcccc
240
gcttccggcg gaagcggcct caacaaggga aactttattg ttcccgtggg gcagtcgagg
300
atgtcggtga attacgcggc ggggctgtcg ccgtacgcgg acaagggcaa gtgcggcctc
360
ccggagatct tcgacccccc ggaggagctg gagcggaagg tgtgggaact ggcgaggctg
420
gtctggcagt cttccagtgt ggtgttccac acgggtgccg gcatcagcac tgcctctggc
480
atccccgact tcaggggtcc ccacggagtc tggaccatgg aggagcgagg tctggccccc
540
aagttcgaca ccacctttga gagcgcgcgg cccacgcaga cccacatggc gctggtgcag
600
ctggagcgcg tgggcctcct ccgcttcctg gtcagccaga acgtggacgg gctccatgtg
660
cgctcaggct tccccaggga caaactggca gagctccacg ggaacatgtt tgtggaagaa
720
tgtgccaagt gtaagacgca gtacgtccga gacacagtcg tgggcaccat gggcctgaag
780
gccacgggcc ggctctgcac cgtggctaag gcaaggggc tgcgagcctg caggggaggc
840
tgcgaggccc ctgaggactc tcctcagctt cctcattgca ggggagagct gagggacacc
900
atcctagact gggaggactc cctgcccgac cgggacctgg cactcgccga tgaggccagc
960
aggaacgccg acctgtccat cacgctgggt acatcgctgc agatccggcc cagcgggaac
1020
ctgccgctgg ctaccaagcg ccggggaggc cgcctggtca tcgtcaacct gcagcccacc
1080
aagcacgacc gccatgctga cctccgcatc catggctacg ttgacgaggt catgacccgg
1140
ctcatgaagc acctggggct ggagatcccc gcctgggacg gcccccgtgt gctggagagg
1200
gcgctgccac ccctgccccg cccgcccacc cccaagctgg agcccaagga ggaatctccc
1260
acccggatca acggctctat ccccgccagc cccaagcagg agccctgcgc ccagcacaac
1320
ggctcagagc ccgccagccc caaacgggag cggcccacca gccctgcccc ccacagaccc
1380
cccaaaaggg ggcctctggt gcggttccgg gaagaagcca caccccagag gtgacagctg
1440
agcccctgcc acaccccagc ctctgacttg ctgtgttgtc cagaggtgag gctgggccct
1500
ccctggtctc cagcttaaac aggagtgaac tccctctgtc cccagggcct cccttctggg
1560

cccccctacag cccaccctac ccctcctcca tgggccctgc aggaggggag acccaccttg
1620
aagtgggggа tc
1632

<210> 5192
<211> 377
<212> PRT
<213> Homo sapiens

<400> 5192
Met Ser Val Asn Tyr Ala Ala Gly Leu Ser Pro Tyr Ala Asp Lys Gly
 1   5   10   15
Lys Cys Gly Leu Pro Glu Ile Phe Asp Pro Pro Glu Glu Leu Glu Arg
            20   25   30
Lys Val Trp Glu Leu Ala Arg Leu Val Trp Gln Ser Ser Ser Val Val
        35   40   45
Phe His Thr Gly Ala Gly Ile Ser Thr Ala Ser Gly Ile Pro Asp Phe
    50   55   60
Arg Gly Pro His Gly Val Trp Thr Met Glu Glu Arg Gly Leu Ala Pro
65   70   75   80
Lys Phe Asp Thr Thr Phe Glu Ser Ala Arg Pro Thr Gln Thr His Met
                85   90   95
Ala Leu Val Gln Leu Glu Arg Val Gly Leu Leu Arg Phe Leu Val Ser
            100   105   110
Gln Asn Val Asp Gly Leu His Val Arg Ser Gly Phe Pro Arg Asp Lys
        115   120   125
Leu Ala Glu Leu His Gly Asn Met Phe Val Glu Glu Cys Ala Lys Cys
    130   135   140
Lys Thr Gln Tyr Val Arg Asp Thr Val Val Gly Thr Met Gly Leu Lys
145   150   155   160
Ala Thr Gly Arg Leu Cys Thr Val Ala Lys Ala Arg Gly Leu Arg Ala
                165   170   175
Cys Arg Gly Gly Cys Glu Ala Pro Glu Asp Ser Pro Gln Leu Pro His
            180   185   190
Cys Arg Gly Glu Leu Arg Asp Thr Ile Leu Asp Trp Glu Asp Ser Leu
        195   200   205
Pro Asp Arg Asp Leu Ala Leu Ala Asp Glu Ala Ser Arg Asn Ala Asp
    210   215   220
Leu Ser Ile Thr Leu Gly Thr Ser Leu Gln Ile Arg Pro Ser Gly Asn
225   230   235   240
Leu Pro Leu Ala Thr Lys Arg Arg Gly Gly Arg Leu Val Ile Val Asn
                245   250   255
Leu Gln Pro Thr Lys His Asp Arg His Ala Asp Leu Arg Ile His Gly
            260   265   270
Tyr Val Asp Glu Val Met Thr Arg Leu Met Lys His Leu Gly Leu Glu
        275   280   285
Ile Pro Ala Trp Asp Gly Pro Arg Val Leu Glu Arg Ala Leu Pro Pro
    290   295   300
Leu Pro Arg Pro Pro Thr Pro Lys Leu Glu Pro Lys Glu Glu Ser Pro
305   310   315   320
Thr Arg Ile Asn Gly Ser Ile Pro Ala Gly Pro Lys Gln Glu Pro Cys
                325   330   335
Ala Gln His Asn Gly Ser Glu Pro Ala Ser Pro Lys Arg Glu Arg Pro

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            340                 345                 350
Thr Ser Pro Ala Pro His Arg Pro Pro Lys Arg Gly Pro Leu Val Arg
        355                 360                 365
Phe Arg Glu Glu Ala Thr Pro Gln Arg
    370                 375
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<210> 5193
<211> 554
<212> DNA
<213> Homo sapiens

<400> 5193
acgcgtccct tcccgaggtt ccaggcggac gtgtcccttc ccgaggttct aggcggacat
60
gtcttttgag agggcctcag gttaacccac tactgtgtct gaatctgtcc cttccccaag
120
cagcagctct gtgtcccggc atggccactg tggggcagag acacagcagg tcccacatct
180
ctgtgccctg cagacccgtc agccctgggg atgctggtct gggacggacc cctagatatc
240
acacagccga gaggtaggtc agcgctttaa gatgctgata ccgctggttc agctcctgga
300
gcagaattct cagggtggat ttccagcaac gcctcctggg agggtcagca ggggctgggg
360
tccgtggggt ggtctccggg aggtttgcct gtgtcaggcc tgtgctgctt ctggcggagg
420
cgcttgtcca gcctcatcca gcctggtgtc tccggtgcca cgcgctaaca ccttcagtgc
480
acgctcggga acgcgcctgg aaggccctgc cctgccccgc cccaggctcc agccagatgc
540
tgccagcacc cggg
554

<210> 5194
<211> 94
<212> PRT
<213> Homo sapiens

<400> 5194
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Met Leu Ile Pro Leu Val Gln Leu Leu Glu Gln Asn Ser Gln Gly Gly
 1               5                  10                  15
Phe Pro Ala Thr Pro Pro Gly Arg Val Ser Arg Gly Trp Gly Pro Trp
            20                  25                  30
Gly Gly Leu Arg Glu Val Cys Leu Cys Gln Ala Cys Ala Ala Ser Gly
        35                  40                  45
Gly Gly Ala Cys Pro Ala Ser Ser Ser Leu Val Ser Pro Val Pro Arg
    50                  55                  60
Ala Asn Thr Phe Ser Ala Arg Ser Gly Thr Arg Leu Glu Gly Pro Ala
65                  70                  75                  80
Leu Pro Arg Pro Arg Leu Gln Pro Asp Ala Ala Ser Thr Arg
                85                  90
```

<210> 5195
<211> 964

<212> DNA
<213> Homo sapiens

<400> 5195
gggcccaggc tcacagaggt gtgaaagagg caagcacacc gcaggggcct ctgagcccag
60
ccagcctcgc ttcaatgctg ggaggctgac gtcttccttt ttgtcttctg cccaggccag
120
ctgcgggccg tccagcggct gtgccacttc tacagcgccg tcatgcccag cgaggcccag
180
tgtgtcatct accatgagct ccagctctcc ctggcctgca aggtggccga caaggtgctg
240
gaggggcagc tcctggagac catcagccag ctctacctgt ccctgggcac cgagcgggcc
300
tacaaatccg cactggacta caccaaacga agtctgggga ttttcattga cctccagaag
360
aaagagaagg aggcgcatgc ctggctgcaa gcagggaaga tctattacat cttgcggcag
420
agcgagctgg tggacctcta catccaggtg gcacagaacg tggccctgta cacaggcgac
480
cccaacctgg ggctggagct gtttgaggcg gctggagaca tcttcttcga cggggcctgg
540
gagcgggaga aagctgtgtc cttctaccgg gaccgggccc tgcccctggc agtgactacg
600
ggcaaccgca aggcggagct gcggctgtgc aacaagctgg tggcactgct ggccacgctg
660
gaggagcccc aggagggctt ggagtttgcc cacatggccc tagcactcag catcactctg
720
ggggaccggc tgaacgagcg cgtggcctac caccggctgg ccgccctgca acaccgactg
780
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840
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900
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964

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<211> 267
<212> PRT
<213> Homo sapiens

<400> 5196
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Leu Ala Cys Lys Val Ala Asp Lys Val Leu Glu Gly Gln Leu Leu Glu
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Thr Ile Ser Gln Leu Tyr Leu Ser Leu Gly Thr Glu Arg Ala Tyr Lys
        35   40   45
Ser Ala Leu Asp Tyr Thr Lys Arg Ser Leu Gly Ile Phe Ile Asp Leu
    50   55   60
Gln Lys Lys Glu Lys Glu Ala His Ala Trp Leu Gln Ala Gly Lys Ile

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65                  70                  75                  80
Tyr Tyr Ile Leu Arg Gln Ser Glu Leu Val Asp Leu Tyr Ile Gln Val
                85                  90                  95
Ala Gln Asn Val Ala Leu Tyr Thr Gly Asp Pro Asn Leu Gly Leu Glu
            100                 105                 110
Leu Phe Glu Ala Ala Gly Asp Ile Phe Phe Asp Gly Ala Trp Glu Arg
        115                 120                 125
Glu Lys Ala Val Ser Phe Tyr Arg Asp Arg Ala Leu Pro Leu Ala Val
    130                 135                 140
Thr Thr Gly Asn Arg Lys Ala Glu Leu Arg Leu Cys Asn Lys Leu Val
145                 150                 155                 160
Ala Leu Leu Ala Thr Leu Glu Glu Pro Gln Glu Gly Leu Glu Phe Ala
                165                 170                 175
His Met Ala Leu Ala Leu Ser Ile Thr Leu Gly Asp Arg Leu Asn Glu
            180                 185                 190
Arg Val Ala Tyr His Arg Leu Ala Ala Leu Gln His Arg Leu Gly His
        195                 200                 205
Gly Glu Leu Ala Glu His Phe Tyr Leu Lys Ala Leu Ser Leu Cys Asn
    210                 215                 220
Ser Pro Leu Glu Phe Asp Glu Glu Thr Leu Tyr Tyr Val Lys Val Tyr
225                 230                 235                 240
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Ala Ala Gly Tyr Tyr Gln Leu Ala Leu Ala Ala
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420
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<211> 283
<212> PRT
<213> Homo sapiens

<400> 5198
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Glu Glu Glu Glu Glu Val Val Lys Asp Gly Arg Pro Lys Trp Asn Ser
35 40 45
Trp Asp Pro Arg Arg Gln Arg Gln Leu Ser Met Ser Ser Ala Asp Ser
50 55 60
Ala Asp Ala Lys Arg Thr Arg Glu Glu Gly Lys Asp Trp Ala Glu Ala
65 70 75 80
Val Gly Ala Ser Arg Val Val Arg Lys Ala Pro Asp Pro Gln Pro Pro
85 90 95
Pro Arg Lys Leu His Gly Trp Ala Pro Gly Pro Asp Tyr Gln Lys Ser
100 105 110
Ser Met Gly Ser Met Phe Arg Gln Gln Ser Ile Glu Asp Lys Glu Asp
115 120 125
Lys Pro Pro Pro Arg Gln Lys Phe Ile Gln Ser Glu Met Ser Glu Ala
130 135 140
Val Glu Arg Ala Arg Lys Arg Arg Glu Glu Glu Glu Arg Arg Ala Arg
145 150 155 160
Glu Glu Arg Leu Ala Ala Cys Ala Ala Lys Leu Lys Gln Leu Asp Gln
165 170 175
Lys Cys Lys Gln Ala Arg Lys Ala Gly Glu Ala Arg Lys Gln Ala Glu
180 185 190
Lys Glu Val Pro Trp Ser Pro Ser Ala Glu Lys Ala Ser Pro Gln Glu
195 200 205
Asn Gly Pro Ala Val His Lys Gly Ser Pro Glu Phe Pro Ala Gln Glu
210 215 220
Thr Pro Thr Thr Phe Pro Glu Glu Ala Pro Thr Val Ser Pro Ala Val
225 230 235 240
Ala Gln Ser Asn Ser Ser Glu Glu Glu Ala Arg Glu Ala Gly Ser Pro
245 250 255
Ala Gln Glu Phe Lys Tyr Gln Lys Ser Leu Pro Pro Arg Phe Gln Arg

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275 280

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<212> DNA
<213> Homo sapiens

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180
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240
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420
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480
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1332

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<212> PRT
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<400> 5200
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35 40 45
Gln Gly Ala Asp Asp Val Thr Ser Val Leu Phe Ser Pro Ser Cys Pro
50 55 60
Thr Lys Leu Tyr Ala Ser His Gly Glu Thr Ile Ser Val Leu Asp Val
65 70 75 80
Arg Ser Leu Lys Asp Ser Leu Asp His Phe His Val Asn Glu Glu Glu
85 90 95
Ile Asn Cys Leu Ser Leu Asn Gln Thr Glu Asn Leu Leu Ala Ser Ala
100 105 110
Asp Asp Ser Gly Ala Ile Lys Ile Leu Asp Leu Glu Asn Lys Lys Val
115 120 125
Ile Arg Ser Leu Lys Arg His Ser Asn Ile Cys Ser Ser Val Ala Phe
130 135 140
Arg Pro Gln Arg Pro Gln Ser Leu Val Ser Cys Gly Leu Asp Met Gln
145 150 155 160
Val Met Leu Trp Ser Leu Gln Lys Ala Arg Pro Leu Trp Ile Thr Asn
165 170 175
Leu Gln Glu Asp Glu Thr Glu Glu Met Glu Gly Pro Gln Ser Pro Gly
180 185 190
Gln Leu Leu Asn Pro Ala Leu Ala His Ser Ile Ser Val Ala Ser Cys
195 200 205
Gly Asn Ile Phe Ser Cys Gly Ala Glu Asp Gly Lys Val Arg Ile Phe
210 215 220
Arg Val Met Gly Val Lys Cys Glu Gln Glu Leu Gly Phe Lys Gly His
225 230 235 240
Thr Ser Gly Val Ser Gln Val Cys Phe Leu Pro Glu Ser Tyr Leu Leu
245 250 255
Leu Thr Gly Gly Asn Asp Gly Lys Ile Thr Leu Trp Asp Ala Asn Ser
260 265 270
Glu Val Glu Lys Lys Gln Lys Ser Pro Thr Lys Arg Thr His Arg Lys
275 280 285
Lys Pro Lys Arg Gly Thr Cys Thr Lys Gln Gly Gly Asn Thr Asn Ala
290 295 300
Ser Val Thr Asp Glu Glu Glu His Gly Asn Ile Leu Pro Lys Leu Asn
305 310 315 320
Ile Glu His Gly Glu Lys Val Asn Trp Leu Leu Gly Thr Lys Ile Lys
325 330 335
Gly His Gln Asn Ile Leu Val Ala Asp Gln Thr Ser Cys Ile Ser Val
340 345 350
Tyr Pro Leu Asn Glu Phe

355

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<211> 6104
<212> DNA
<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Ser Gln Gly Ser Leu Glu Arg Gly Leu Ala Gly Leu Gly Gly His Arg
35 40 45
Pro His Ser Gly Leu Pro Ala Gln Gly Arg Arg Pro Glu Pro Val Trp
50 55 60
Pro Cys Ser Pro Gly Gln Ser Trp Ala Cys Arg Val Phe Leu Pro Gly
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Arg Cys Arg Cys Trp Pro Ser Ala Gly Gly Arg Arg Trp Glu Ser Trp
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Ile Phe Cys Phe Phe Leu Ser Phe Phe Phe Leu Arg
100 105

<210> 5203
<211> 1863
<212> DNA
<213> Homo sapiens

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900

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1320
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1680
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1740
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1863

<210> 5204
<211> 249
<212> PRT
<213> Homo sapiens

<400> 5204
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20 25 30
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35 40 45
Asn Leu Ala Ala Val Ala Gly Ala Arg Asp Thr Tyr Cys Lys Ser Met
50 55 60
Glu Gln Val Cys Gly Gly Asp Lys Pro Tyr Ile Ala Pro Ser Asp Leu
65 70 75 80
Glu Arg Lys His Leu Asp Leu Lys Glu Val Ala Ile Lys Gln Phe Arg
85 90 95
Ser Val Lys Lys Met Gly Gly Asp Glu Phe Cys Arg Arg Tyr Gln Asp

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Gln Leu Glu Ala Glu Ile Glu Glu Thr Tyr Ala Asn Phe Ile Lys His
        115                 120                 125
Asn Asp Gly Lys Asn Ile Phe Tyr Ala Ala Arg Thr Pro Ala Thr Leu
    130                 135                 140
Phe Ala Val Met Phe Ala Met Tyr Ile Ile Ser Gly Leu Thr Gly Phe
145                 150                 155                 160
Ile Gly Leu Asn Ser Ile Ala Val Leu Cys Asn Leu Val Met Gly Leu
                165                 170                 175
Ala Leu Ile Phe Leu Cys Thr Trp Ala Tyr Val Lys Tyr Ser Gly Glu
            180                 185                 190
Phe Arg Glu Ile Gly Thr Val Ile Asp Gln Ile Ala Glu Thr Leu Trp
        195                 200                 205
Glu Gln Val Leu Lys Pro Leu Gly Asp Asn Leu Met Glu Glu Asn Ile
    210                 215                 220
Arg Gln Ser Val Thr Asn Ser Ile Lys Ala Gly Leu Thr Asp Gln Val
225                 230                 235                 240
Ser His His Ala Arg Leu Lys Thr Asp
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<210> 5205
<211> 2011
<212> DNA
<213> Homo sapiens

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240
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360
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420
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480
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540
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660
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840

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1560
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1860
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2011

<210> 5206
<211> 248
<212> PRT
<213> Homo sapiens

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20 25 30
Asp Arg Arg Lys Leu Arg Ala Asp Val Thr Thr Ala Phe Pro Thr Leu
35 40 45
Gly Thr Asp Gln Val Ser Glu Leu Val Pro Gly Lys Glu Glu Leu Asn

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Ile Val Lys Leu Tyr Ala His Lys Gly Asp Ala Val Thr Val Tyr Val
65                  70                  75                  80
Ser Gly Gly Asn Pro Ile Leu Phe Glu Leu Glu Lys Asn Leu Tyr Pro
                85                  90                  95
Thr Val Tyr Thr Leu Trp Ser Tyr Pro Asp Leu Leu Pro Thr Phe Thr
            100                 105                 110
Thr Trp Pro Leu Val Leu Glu Lys Leu Val Gly Gly Ala Asp Leu Met
        115                 120                 125
Leu Pro Gly Leu Val Met Pro Pro Ala Gly Leu Pro Gln Val Gln Lys
    130                 135                 140
Gly Asp Leu Cys Ala Ile Ser Leu Val Gly Asn Arg Ala Pro Val Ala
145                 150                 155                 160
Ile Gly Val Ala Ala Met Ser Thr Ala Glu Met Leu Thr Ser Gly Leu
                165                 170                 175
Lys Gly Arg Gly Phe Ser Val Leu His Thr Tyr Gln Asp His Leu Trp
            180                 185                 190
Arg Ser Gly Asn Lys Ser Ser Pro Pro Ser Ile Ala Pro Leu Ala Leu
        195                 200                 205
Asp Ser Ala Asp Leu Ser Glu Glu Lys Gly Ser Val Gln Met Asp Ser
    210                 215                 220
Thr Leu Gln Gly Asp Met Arg His Met Thr Leu Glu Gly Glu Glu Glu
225                 230                 235                 240
Asn Gly Glu Val His Gln Gly Thr
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<210> 5207
<211> 594
<212> DNA
<213> Homo sapiens

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240
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300
cgccgccttt acctgcctgc tgtcgtcatg aacggccacg tgcacgacct ccagatcctc
360
gactttccac ccatcagcgc cttcccrqtc aatacgctcc aggagtgggc agacacctgc
420
tgcaggggac tccggagtgt ccacgcctac atcctggtct acgacatctg ctgctttgac
480
agctttgagt acgtcaagac catccgccag cagatcctgg agacgagggt gatcggaacc
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594

<210> 5208

<211> 136
<212> PRT
<213> Homo sapiens

<400> 5208
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Lys Ser Ala Ile Val Arg Gln Phe Leu Tyr Asn Glu Phe Ser Glu Val
20 25 30
Cys Val Pro Thr Thr Ala Arg Arg Leu Tyr Leu Pro Ala Val Val Met
35 40 45
Asn Gly His Val His Asp Leu Gln Ile Leu Asp Phe Pro Pro Ile Ser
50 55 60
Ala Phe Pro Val Asn Thr Leu Gln Glu Trp Ala Asp Thr Cys Cys Arg
65 70 75 80
Gly Leu Arg Ser Val His Ala Tyr Ile Leu Val Tyr Asp Ile Cys Cys
85 90 95
Phe Asp Ser Phe Glu Tyr Val Lys Thr Ile Arg Gln Gln Ile Leu Glu
100 105 110
Thr Arg Val Ile Gly Thr Ser Glu Thr Pro Ile Ile Ile Val Gly Asn
115 120 125
Lys Arg Asp Leu Gln Arg Gly Arg
130 135

<210> 5209
<211> 1592
<212> DNA
<213> Homo sapiens

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240
agtgtggagg aggagtgagc cggatgcccc acacaccgcc agtgtcatac caaagagctg
300
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360
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420
ccattccccc tgcctgtcct tgcggccctg tcttctgagg ttctctgtct ggggttggct
480
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600
cttccctctg ctgctgcctt ggcttcctcc taatgctcgt gctctcctgt ccttctgaag
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720

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1440
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<210> 5210
<211> 85
<212> PRT
<213> Homo sapiens

<400> 5210
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20 25 30
Ala Leu Leu Ile Leu Tyr Ala Leu Leu Ser Arg Leu Thr Gly Ser Arg
35 40 45
Ala Ser Gly Ala Gln Leu Glu Ala Lys Val Arg Gly Leu Glu Arg Gln
50 55 60
Val Glu Glu Leu Arg Trp Arg Gln Arg Arg Ala Ala Lys Gly Ala Arg
65 70 75 80
Ser Val Glu Glu Glu
85

<210> 5211
<211> 602
<212> DNA
<213> Homo sapiens

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gcacaggacc agacaacaag tttttaaaaa tgatgccaga gcattagaag cagccagaat
180
aaagataaat gaagaattca aaaataataa aagtgaaact tcttctaaga aaatagaaga
240
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480
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602

<210> 5212
<211> 104
<212> PRT
<213> Homo sapiens

<400> 5212
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            20   25   30
Arg Ile Lys Ile Asn Glu Glu Phe Lys Asn Asn Lys Ser Glu Thr Ser
        35   40   45
Ser Lys Lys Ile Glu Glu Leu Met Lys Ile Gly Ser Asp Val Glu Leu
    50   55   60
Leu Leu Arg Thr Ser Val Ile Gln Gly Ile His Thr Asp His Asn Thr
65   70   75   80
Leu Lys Leu Val Pro Arg Lys Asp Leu Leu Val Glu Asn Val Pro Tyr
                85   90   95
Cys Asp Ala Pro Thr Gln Lys Gln
            100

<210> 5213
<211> 4387
<212> DNA
<213> Homo sapiens

<400> 5213
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gagacgcaac tgcagagcat tttcgaagag gtggtgaaaa cggaagttat agaagaggct
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<210> 5214
<211> 1364
<212> PRT
<213> Homo sapiens

<400> 5214
Met Glu Thr Gln Leu Gln Ser Ile Phe Glu Glu Val Val Lys Thr Glu
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Val Ile Glu Glu Ala Phe Pro Gly Met Phe Met Asp Thr Pro Glu Asp
20 25 30
Glu Lys Thr Lys Leu Ile Ser Cys Leu Gly Ala Phe Arg Gln Phe Trp
35 40 45
Gly Gly Leu Ser Gln Glu Ser His Glu Gln Cys Ile Gln Trp Ile Val
50 55 60
Lys Phe Ile His Gly Gln His Ser Pro Lys Arg Ile Ser Phe Leu Tyr

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65                  70                  75                  80
Asp Cys Leu Ala Met Ala Val Glu Thr Gly Leu Leu Pro Pro Arg Leu
                85                  90                  95
Val Cys Glu Ser Leu Ile Asn Ser Asp Thr Leu Glu Trp Glu Arg Thr
            100                 105                 110
Gln Leu Trp Ala Leu Thr Phe Lys Leu Val Arg Lys Ile Ile Gly Gly
        115                 120                 125
Val Asp Tyr Lys Gly Val Arg Asp Leu Leu Lys Val Ile Leu Glu Lys
    130                 135                 140
Ile Leu Thr Ile Pro Asn Thr Val Ser Ser Ala Val Val Gln Gln Leu
145                 150                 155                 160
Leu Ala Ala Arg Glu Val Ile Ala Tyr Ile Leu Glu Arg Asn Ala Cys
                165                 170                 175
Leu Leu Pro Ala Tyr Phe Ala Val Thr Glu Ile Arg Lys Leu Tyr Pro
            180                 185                 190
Glu Gly Lys Leu Pro His Trp Leu Leu Gly Asn Leu Val Ser Asp Phe
        195                 200                 205
Val Asp Thr Phe Arg Pro Thr Ala Arg Ile Asn Ser Ile Cys Gly Arg
    210                 215                 220
Cys Ser Leu Leu Pro Val Val Asn Asn Ser Gly Ala Ile Cys Asn Ser
225                 230                 235                 240
Trp Lys Leu Asp Pro Ala Thr Leu Arg Phe Pro Leu Lys Gly Leu Leu
                245                 250                 255
Pro Tyr Asp Lys Asp Leu Phe Glu Pro Gln Thr Ala Leu Leu Arg Tyr
            260                 265                 270
Val Leu Glu Gln Pro Tyr Ser Arg Asp Met Val Cys Asn Met Leu Gly
        275                 280                 285
Leu Asn Lys Gln His Lys Gln Arg Cys Pro Val Leu Glu Asp Gln Leu
    290                 295                 300
Val Asp Leu Val Val Tyr Ala Met Glu Arg Ser Glu Thr Glu Glu Lys
305                 310                 315                 320
Phe Asp Asp Gly Gly Thr Ser Gln Leu Leu Trp Gln His Leu Ser Ser
                325                 330                 335
Gln Leu Ile Phe Phe Val Leu Phe Gln Phe Ala Ser Phe Pro His Met
            340                 345                 350
Val Leu Ser Leu His Gln Lys Leu Ala Gly Arg Gly Leu Ile Lys Gly
        355                 360                 365
Arg Asp His Leu Met Trp Val Leu Leu Gln Phe Ile Ser Gly Ser Ile
    370                 375                 380
Gln Lys Asn Ala Leu Ala Asp Phe Leu Pro Val Met Lys Leu Phe Asp
385                 390                 395                 400
Leu Leu Tyr Pro Glu Lys Glu Tyr Ile Pro Val Pro Asp Ile Asn Lys
                405                 410                 415
Pro Gln Ser Thr His Ala Phe Ala Met Thr Cys Ile Trp Ile His Leu
            420                 425                 430
Asn Arg Lys Ala Gln Asn Asp Asn Ser Lys Leu Gln Ile Pro Ile Pro
        435                 440                 445
His Ser Leu Arg Leu His His Glu Phe Leu Gln Gln Ser Leu Arg His
    450                 455                 460
Lys Ser Leu Gln Met Asn Asp Tyr Lys Ile Ala Leu Leu Cys Asn Ala
465                 470                 475                 480
Tyr Ser Thr Asn Ser Glu Cys Val Thr Leu Pro Met Gly Ala Leu Val
                485                 490                 495
Glu Thr Ile Tyr Gly Asn Gly Ile Met Arg Leu Pro Leu Pro Gly Thr
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            500                 505                 510
Asn Cys Met Ala Ser Ala Ser Ile Thr Pro Leu Pro Met Asn Leu Leu
        515                 520                 525
Asp Ser Leu Thr Val His Ala Lys Met Ser Leu Ile His Ser Ile Ala
    530                 535                 540
Thr Arg Val Ile Lys Leu Ala His Ala Lys Ser Ser Val Ala Leu Ala
545                 550                 555                 560
Pro Ala Leu Val Glu Thr Tyr Ser Arg Leu Leu Val Tyr Met Glu Ile
                565                 570                 575
Glu Ser Leu Gly Ile Lys Gly Phe Ile Ser Gln Leu Leu Pro Thr Val
            580                 585                 590
Phe Lys Ser His Ala Trp Gly Ile Leu His Thr Leu Leu Glu Met Phe
        595                 600                 605
Ser Tyr Arg Met His His Ile Gln Pro His Tyr Arg Val Gln Leu Leu
    610                 615                 620
Ser His Leu His Thr Leu Ala Ala Val Ala Gln Thr Asn Gln Asn Gln
625                 630                 635                 640
Leu His Leu Cys Val Glu Ser Thr Ala Leu Arg Leu Ile Thr Ala Leu
                645                 650                 655
Gly Ser Ser Glu Val Gln Pro Gln Phe Thr Arg Phe Leu Ser Asp Pro
            660                 665                 670
Lys Thr Val Leu Ser Ala Glu Ser Glu Glu Leu Asn Arg Ala Leu Ile
        675                 680                 685
Leu Thr Leu Ala Arg Ala Thr His Val Thr Asp Phe Phe Thr Gly Ser
    690                 695                 700
Asp Ser Ile Gln Gly Thr Trp Cys Lys Asp Ile Leu Gln Thr Ile Met
705                 710                 715                 720
Ser Phe Thr Pro His Asn Trp Ala Ser His Thr Leu Ser Cys Phe Pro
                725                 730                 735
Gly Pro Leu Gln Ala Phe Phe Lys Gln Asn Asn Val Pro Gln Glu Ser
            740                 745                 750
Arg Phe Asn Leu Lys Lys Asn Val Glu Glu Glu Tyr Arg Lys Trp Lys
        755                 760                 765
Ser Met Ser Asn Glu Asn Asp Ile Ile Thr His Phe Ser Met Gln Gly
    770                 775                 780
Ser Pro Pro Leu Phe Leu Cys Leu Leu Trp Lys Met Leu Leu Glu Thr
785                 790                 795                 800
Asp His Ile Asn Gln Ile Gly Tyr Arg Val Leu Glu Arg Ile Gly Ala
                805                 810                 815
Arg Ala Leu Val Ala His Val Arg Thr Phe Ala Asp Phe Leu Val Tyr
            820                 825                 830
Glu Phe Ser Thr Ser Ala Gly Gly Gln Gln Leu Asn Lys Cys Ile Glu
        835                 840                 845
Ile Leu Asn Asp Met Val Trp Lys Tyr Asn Ile Val Thr Leu Asp Arg
    850                 855                 860
Leu Ile Leu Cys Leu Ala Met Arg Ser His Glu Gly Asn Glu Ala Gln
865                 870                 875                 880
Val Cys Tyr Phe Ile Ile Gln Leu Leu Leu Leu Lys Pro Asn Asp Phe
                885                 890                 895
Arg Asn Arg Val Ser Asp Phe Val Lys Glu Asn Ser Pro Glu His Trp
            900                 905                 910
Leu Gln Asn Asp Trp His Thr Lys His Met Asn Tyr His Lys Lys Tyr
        915                 920                 925
Pro Glu Lys Leu Tyr Phe Glu Gly Leu Ala Glu Gln Val Asp Pro Pro
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    930                 935                 940
Val Gln Ile Gln Ser Pro Tyr Leu Pro Ile Tyr Phe Gly Asn Val Cys
945                 950                 955                 960
Leu Arg Phe Leu Pro Val Phe Asp Ile Val Ile His Arg Phe Leu Glu
                965                 970                 975
Leu Leu Pro Val Ser Lys Ser Leu Glu Thr Leu Leu Asp His Leu Gly
            980                 985                 990
Gly Leu Tyr Lys Phe His Asp Arg Pro Val Thr Tyr Leu Tyr Asn Thr
        995                 1000                1005
Leu His Tyr Tyr Glu Met His Leu Arg Asp Arg Ala Phe Leu Lys Arg
    1010                1015                1020
Lys Leu Val His Ala Ile Ile Gly Ser Leu Lys Asp Asn Arg Pro Gln
1025                1030                1035                1040
Gly Trp Cys Leu Ser Asp Thr Tyr Leu Lys Cys Ala Met Asn Ala Arg
                1045                1050                1055
Glu Glu Asn Pro Trp Val Pro Asp Asp Thr Tyr Tyr Cys Arg Leu Ile
            1060                1065                1070
Gly Arg Leu Val Asp Thr Met Ala Gly Lys Ser Pro Gly Pro Phe Pro
        1075                1080                1085
Asn Cys Asp Trp Arg Phe Asn Glu Phe Pro Asn Pro Ala Ala His Ala
    1090                1095                1100
Leu His Val Thr Cys Val Glu Leu Met Ala Leu Ala Val Ser Gly Lys
1105                1110                1115                1120
Glu Val Gly Asn Ala Leu Leu Asn Val Val Leu Lys Ser Gln Pro Leu
                1125                1130                1135
Val Pro Arg Glu Asn Ile Thr Ala Trp Met Asn Ala Ile Gly Leu Ile
            1140                1145                1150
Ile Thr Ala Leu Pro Glu Pro Tyr Trp Ile Val Leu His Asp Arg Ile
        1155                1160                1165
Val Ser Val Ile Ser Ser Pro Ser Leu Thr Ser Glu Thr Glu Trp Val
    1170                1175                1180
Gly Tyr Pro Phe Arg Leu Phe Asp Phe Thr Ala Cys His Gln Ser Tyr
1185                1190                1195                1200
Ser Glu Met Ser Cys Ser Tyr Thr Leu Ala Leu Ala His Ala Val Trp
                1205                1210                1215
His His Ser Ser Ile Gly Gln Leu Ser Leu Ile Pro Lys Phe Leu Thr
            1220                1225                1230
Glu Val Leu Leu Pro Ile Val Lys Thr Glu Phe Gln Leu Leu Tyr Val
        1235                1240                1245
Tyr His Leu Val Gly Pro Phe Leu Gln Arg Phe Gln Gln Glu Arg Thr
    1250                1255                1260
Arg Cys Met Ile Glu Ile Gly Val Ala Phe Tyr Asp Met Leu Leu Asn
1265                1270                1275                1280
Val Asp Gln Cys Ser Thr His Leu Asn Tyr Met Asp Pro Ile Cys Asp
                1285                1290                1295
Phe Leu Tyr His Met Lys Tyr Met Phe Thr Gly Asp Ser Val Lys Glu
            1300                1305                1310
Gln Val Glu Lys Ile Ile Cys Asn Leu Lys Pro Ala Leu Lys Leu Arg
        1315                1320                1325
Leu Arg Phe Ile Thr His Ile Ser Lys Met Glu Pro Ala Ala Val Pro
    1330                1335                1340
Pro Gln Ala Met Asn Ser Gly Ser Pro Ala Pro Gln Ser Asn Gln Val
1345                1350                1355                1360
Asp Thr Leu Thr
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<210> 5215
<211> 548
<212> DNA
<213> Homo sapiens

<400> 5215
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180
gctgtctcgc gagaaaactt taacacgtga ggagttgcct ctgaagggtg agcaggggag
240
ttgcttcagt tgcgctctag tcccagtgaa gattctgtga acctgggggt aatgaggaca
300
aagaacttgg aacagcccgg aacctcggtt gatgaagccg cggccgggnt tgagaggacc
360
gactgcagtt ctgaaagacg ttctgctgtg ggttcaatgc tatcagacag catcacgccc
420
cacagagaaa tctttcatga aaggaagagt ccatcgctgt ggccaacttt tttgtggtca
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540
acattgag
548

<210> 5216
<211> 83
<212> PRT
<213> Homo sapiens

<400> 5216
Ala Gly Glu Leu Leu Gln Leu Arg Ser Ser Pro Ser Glu Asp Ser Val
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Asn Leu Gly Val Met Arg Thr Lys Asn Leu Glu Gln Pro Gly Thr Ser
20 25 30
Val Asp Glu Ala Ala Ala Gly Xaa Glu Arg Thr Asp Cys Ser Ser Glu
35 40 45
Arg Arg Ser Ala Val Gly Ser Met Leu Ser Asp Ser Ile Thr Pro His
50 55 60
Arg Glu Ile Phe His Glu Arg Lys Ser Pro Ser Leu Trp Pro Thr Phe
65 70 75 80
Leu Trp Ser

<210> 5217
<211> 4189
<212> DNA
<213> Homo sapiens

<400> 5217

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120
ccccactggc gcaggctgcc ccaggccctg tgcagacaca ccaggccctc agccgcagcc
180
catggacctg cgggtgccag cggcccccag tggagccccc accagagccc acattgctgg
240
ccctgcagcg tccccagcgc ctgcaccacc acctcttcct agcaggcctg cagcagcagc
300
gctcggtgga gcccatgagg ctctccatgg acacgccgat gcccgagttg caggtgggac
360
cccaggaaca acagctgcgg cagcttctcc acaaggacaa gagcaagcga agtgctgtag
420
ccagcagcgt ggtcaagcag aagctagcgg aggtgattct gaaaaaacag caggcggccc
480
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540
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660
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720
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840
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1980
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2340
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3540
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3720
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3780
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4080
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4189

<210> 5218
<211> 541
<212> PRT
<213> Homo sapiens

<400> 5218
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Ser Trp Ala Met Gly Ser Leu Arg Pro Glu Ala Pro Leu Leu Ser Ser
20 25 30
Ser Thr Leu Arg Cys Cys Ser Gly Asn Ser Ser Asp Trp Leu Gly Gly
35 40 45
Ser Pro Gly Ala Ala Pro Gly Thr Leu Cys Cys Phe Leu Trp Pro Arg
50 55 60
Val Gly Thr Gly Leu Cys Pro Gly Leu Ser Leu Pro Gln Pro His Leu
65 70 75 80
Pro His Cys Gln Pro Gln Ser Leu Pro Ala Xaa Ala Arg Val Leu Ser
85 90 95
Ser Ser Glu Thr Pro Ala Arg Thr Leu Pro Phe Thr Thr Gly Leu Ile
100 105 110
Tyr Asp Ser Val Met Leu Lys His Gln Cys Ser Cys Gly Asp Asn Ser

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        115                 120                 125
Arg His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg Leu
    130                 135                 140
Gln Glu Arg Gly Leu Arg Ser Gln Cys Glu Cys Leu Arg Gly Arg Lys
145                 150                 155                 160
Ala Ser Leu Glu Glu Leu Gln Ser Val His Ser Glu Arg His Val Leu
                165                 170                 175
Leu Tyr Gly Thr Asn Pro Leu Ser Arg Leu Lys Leu Asp Asn Gly Lys
            180                 185                 190
Leu Ala Gly Leu Leu Ala Gln Arg Met Phe Val Met Leu Pro Cys Gly
        195                 200                 205
Gly Val Gly Val Asp Thr Asp Thr Ile Trp Asn Glu Leu His Ser Ser
    210                 215                 220
Asn Ala Ala Arg Trp Ala Ala Gly Ser Val Thr Asp Leu Ala Phe Lys
225                 230                 235                 240
Val Ala Ser Arg Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro
                245                 250                 255
Gly His His Ala Asp His Ser Thr Ala Met Gly Phe Cys Phe Phe Asn
            260                 265                 270
Ser Val Ala Ile Ala Cys Arg Gln Leu Gln Gln Gln Ser Lys Ala Ser
        275                 280                 285
Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Ala Thr Gln
    290                 295                 300
Gln Thr Phe Tyr Gln Asp Pro Ser Val Leu Tyr Ile Ser Leu His Arg
305                 310                 315                 320
His Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Val Asp Glu Val
                325                 330                 335
Gly Ala Gly Ser Gly Glu Gly Phe Asn Val Asn Val Ala Trp Ala Gly
            340                 345                 350
Gly Leu Asp Pro Pro Met Gly Asp Pro Glu Tyr Leu Ala Ala Phe Arg
        355                 360                 365
Ile Val Val Met Pro Ile Ala Arg Glu Phe Ser Pro Asp Leu Val Leu
    370                 375                 380
Val Ser Ala Gly Phe Asp Ala Ala Glu Gly His Pro Ala Pro Leu Gly
385                 390                 395                 400
Gly Tyr His Val Ser Ala Lys Cys Phe Gly Tyr Met Thr Gln Gln Leu
                405                 410                 415
Met Asn Leu Ala Gly Gly Ala Val Val Leu Ala Leu Glu Gly Gly His
            420                 425                 430
Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ala Ala Leu
        435                 440                 445
Leu Gly Asn Arg Val Asp Pro Leu Ser Glu Glu Gly Trp Lys Gln Lys
    450                 455                 460
Pro Asn Leu Asn Ala Ile Arg Ser Leu Glu Ala Val Ile Arg Val His
465                 470                 475                 480
Ser Lys Tyr Trp Gly Cys Met Gln Arg Leu Ala Ser Cys Pro Asp Ser
                485                 490                 495
Trp Val Pro Arg Val Pro Gly Ala Asp Lys Glu Glu Val Glu Ala Val
            500                 505                 510
Thr Ala Leu Ala Ser Leu Ser Val Gly Ile Leu Ala Glu Asp Arg Pro
        515                 520                 525
Ser Glu Gln Leu Val Glu Glu Glu Glu Pro Met Asn Leu
    530                 535                 540
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<210> 5219
<211> 1212
<212> DNA
<213> Homo sapiens

<400> 5219
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120
aacgtctccc tgctcacccc acccccgcgc agacgcagtg ctgagcacac agctaccgga
180
caaagagtga cgcccggagc tggagttatg gcggctacgg agccgatctt ggcggccact
240
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300
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360
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420
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720
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840
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attgggttta ttttaccaag cctgtttcct accgcctttc tggctggtgg cgaaacgaag
960
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1020
aacctaggtt atccctctac cacacatggg aagtttttca cctgggctcc caaggaccca
1080
cttgggtttc ttacacgcaa aatagctggc tctattaaat gctcacttaa ctggctacct
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1200
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1212

<210> 5220
<211> 179
<212> PRT
<213> Homo sapiens

<400> 5220
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Val Pro Pro Glu Lys Leu Glu Gly Ala Gly Ser Ser Ser Ala Pro Glu
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Arg Asn Cys Val Gly Ser Ser Leu Pro Glu Ala Ser Pro Pro Ala Pro
35 40 45
Glu Pro Ser Ser Pro Asn Ala Ala Val Pro Glu Ala Ile Pro Thr Pro
50 55 60
Arg Ala Ala Ala Ser Ala Ala Leu Glu Leu Pro Leu Gly Pro Ala Pro
65 70 75 80
Val Ser Val Ala Pro Gln Ala Glu Ala Glu Ala Arg Ser Thr Pro Gly
85 90 95
Pro Ala Gly Ser Arg Leu Gly Pro Glu Thr Phe Arg Gln Arg Phe Arg
100 105 110
Gln Phe Arg Tyr Gln Asp Ala Ala Gly Pro Arg Glu Ala Phe Arg Gln
115 120 125
Leu Arg Glu Leu Ser Arg Gln Trp Leu Arg Pro Asp Ile Arg Thr Lys
130 135 140
Glu Gln Ile Val Glu Met Leu Val Gln Glu Gln Leu Leu Ala Ile Leu
145 150 155 160
Pro Glu Ala Ala Arg Ala Arg Arg Ile Arg Arg Arg Thr Asp Val Arg
165 170 175
Ile Thr Gly

<210> 5221
<211> 497
<212> DNA
<213> Homo sapiens

<400> 5221
ntccggaccc tccaagtgga gaccctggtg gagcccccag aaccatgtgc cgagcccgct
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gcttttggag acacgcttca catacactac acgggaagct tggtagatgg acgtattatt
120
gacacctccc tgaccagaga ccctctggtt atagaacttg gccaaaagca ggtgattcca
180
ggtctggagc agagtcttct cgacatgtgt gtgggagaga agcgaagggc aatcattcct
240
tctcacttgg cctatggaaa acggggattt ccaccatctg tcccagggac taaagacaac
300
ctgatgaggc cacctggcat gacctccagc agccagtaac ttgttaggga agagacctgc
360
ttgggccaca tgggtctgct gcctgtgrca ccacctttcc cagaacactg gacttctttc
420
ctgccctttt ctacaactct acgctgtgtc agctgtacag ccacccccca ccccttcctt
480
tcagccacca tctgtcc
497

<210> 5222
<211> 112
<212> PRT

<213> Homo sapiens

<400> 5222
Xaa Arg Thr Leu Gln Val Glu Thr Leu Val Glu Pro Pro Glu Pro Cys
 1   5   10   15
Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu His Ile His Tyr Thr Gly
            20   25   30
Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser Leu Thr Arg Asp Pro
        35   40   45
Leu Val Ile Glu Leu Gly Gln Lys Gln Val Ile Pro Gly Leu Glu Gln
    50   55   60
Ser Leu Leu Asp Met Cys Val Gly Glu Lys Arg Arg Ala Ile Ile Pro
65   70   75   80
Ser His Leu Ala Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val Pro Gly
                85   90   95
Thr Lys Asp Asn Leu Met Arg Pro Pro Gly Met Thr Ser Ser Ser Gln
            100   105   110

<210> 5223
<211> 637
<212> DNA
<213> Homo sapiens

<400> 5223
ngcaccattt tcgacaatga agccaaagac gtggagagag aagtttgctt tattgatatt
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gcctgcgatg aaattccaga gcgctactac aaagaatctg aggatcctaa gcacttcaag
120
tcagagaaga caggacgggg acagttgagg gaaggctgga gagatagtca tcagcctatc
180
atgtgctcct acaagctggt gactgtgaag tttgaggtct gggggcttca gaccagagtg
240
gaacaatttg tacacaaggt ggtccgagac attctgctga ttggacatag acaggctttt
300
gcatgggttg atgagtggta tgatatgaca atggatgatg ttcgggaata cgagaaaaac
360
atgcatgaac aaaccaacat aaaagtttgc aatcagcatt cctcccctgt ggatgacata
420
gagagtcatg cccaaacaag tacatgacaa tggatgaagt ccgagaattt gaacgagcca
480
ctcaggaagc caccaacaag aaaatcggca ttttcccacc tgcaatttct atctccagca
540
tccccctgct gccttcttcc gtccgcagtg cgccttctag tgctccatcc acccctctct
600
ccacagacgc acccgaattt ctgtccgttc ccaaaga
637

<210> 5224
<211> 148
<212> PRT
<213> Homo sapiens

<400> 5224
Xaa Thr Ile Phe Asp Asn Glu Ala Lys Asp Val Glu Arg Glu Val Cys

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 1               5                  10                  15
Phe Ile Asp Ile Ala Cys Asp Glu Ile Pro Glu Arg Tyr Tyr Lys Glu
            20                  25                  30
Ser Glu Asp Pro Lys His Phe Lys Ser Glu Lys Thr Gly Arg Gly Gln
        35                  40                  45
Leu Arg Glu Gly Trp Arg Asp Ser His Gln Pro Ile Met Cys Ser Tyr
    50                  55                  60
Lys Leu Val Thr Val Lys Phe Glu Val Trp Gly Leu Gln Thr Arg Val
65                  70                  75                  80
Glu Gln Phe Val His Lys Val Val Arg Asp Ile Leu Leu Ile Gly His
                85                  90                  95
Arg Gln Ala Phe Ala Trp Val Asp Glu Trp Tyr Asp Met Thr Met Asp
            100                 105                 110
Asp Val Arg Glu Tyr Glu Lys Asn Met His Glu Gln Thr Asn Ile Lys
        115                 120                 125
Val Cys Asn Gln His Ser Ser Pro Val Asp Asp Ile Glu Ser His Ala
    130                 135                 140
Gln Thr Ser Thr
145
```

<210> 5225
<211> 394
<212> DNA
<213> Homo sapiens

<400> 5225
acgcgtgaag gggctggggt gggcaatcag ggaggacttc ctggaggcgg cagctgaggc
60
tggggcagag aaggacccag ggcactggaa ggggaaggag aaacgtaagc agagtcttgg
120
caggcctggt cagacggaca tgcccaaggg aacagatagt accaggacag gggaccctgg
180
tctgaagggg cgatagcctg gcccccagtg gaaacagccc ctcccaaccc tggcggcaga
240
cagggagggt cggcaggtat gtgagatgca aacctggggg actgcccatc ccccagtgga
300
tgtgaggaca cggtgggttc aggaagtgga gtgacaaatg ggctgtgctg gacttgcttt
360
ccccacatga aggttaggaa ccaagagaac ggcc
394

<210> 5226
<211> 113
<212> PRT
<213> Homo sapiens

<400> 5226
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Met Trp Gly Lys Gln Val Gln His Ser Pro Phe Val Thr Pro Leu Pro
 1               5                  10                  15
Glu Pro Thr Val Ser Ser His Pro Leu Gly Asp Gly Gln Ser Pro Arg
            20                  25                  30
Phe Ala Ser His Ile Pro Ala Asp Pro Pro Cys Leu Pro Pro Gly Leu
        35                  40                  45
Gly Gly Ala Val Ser Thr Gly Gly Gln Ala Ile Ala Pro Ser Asp Gln
```

```
    50                  55                  60
Gly Pro Leu Ser Trp Tyr Tyr Leu Phe Pro Trp Ala Cys Pro Ser Asp
65                  70                  75                  80
Gln Ala Cys Gln Asp Ser Ala Tyr Val Ser Pro Ser Pro Ser Ser Ala
                85                  90                  95
Leu Gly Pro Ser Leu Pro Gln Pro Gln Leu Pro Pro Pro Gly Ser Pro
            100                 105                 110
Pro
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<210> 5227
<211> 2366
<212> DNA
<213> Homo sapiens

<400> 5227
tcgcgaacag gccacccagg cacacgtgga tgttctttag ctccttggcg ccaccagatg
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cagctgccag tgagatgttc tgcagctgtt tgatcctctc gctgaagtcg gacacccact
120
ggatgacggt catgccggca ggcaccgtgt agaaggccag tgtggtaacc ttacctgtct
180
acctgaactt cacccgtgca gacctcatct tcaccgtgga cttcgaaatt gctacaaagg
240
aggatcctcg cagcttctac gagcggggtg tcgcagtctt gtgcacagag taaacttttc
300
tagctgcccc tttctgtaat agtgaaagtt ggtatttaac atttattcat ttttaaaata
360
tttggaaggt ctgagcttgt gaaaagaaag tggttggtct gaggttggag gaagctgaat
420
ggaatctgac ggttgggagt ggtggaaatt ggaaggatac caggaggtat ttgggaaaac
480
cttacggagc tgccctcgtc tactggagca gaagaaatag acctaatttt cctcaaggga
540
attatggaga atcctattgt aaaatcactt gctaaggctc gtgagaggct agaagattcc
600
aaactagaag ctgtcagtga caataacttg gaattagtca atgaaattct tgaagacatc
660
actcctctaa taaatgtgga tgaaaatgtg gcagaattgg ttggtatact caaagaacct
720
cacttccagt cactgttgga ggcccatgat attgtggcat caaagtgtta tgattcacct
780
ccatcaagcc cagaaatgaa taattcttct atcaataatc agttattacc agtagatgcc
840
attcgtattc ttggtattca caaaagagct ggggaaccac tgggtgtgac atttagggtt
900
gaaaataatg atctggtaat tgcccgaatc ctccatgggg gaatgataga tcgacaaggt
960
ctacttcatg tgggagatat aattaaagaa gtcaatggcc atgaggttgg aaataatcca
1020
aaggaattac aagaattact gaaaaatatt agtggaagtg tcaccctaaa aatcttacca
1080
agttatagag ataccattac tcctcaacag gtatttgtga agtgtcattt tgattataat
1140

ccatacaatg acaacctaat accttgcaaa gaagcaggat tgaagtttc caaaggagag
1200
attcttcaga ttgtaaatag agaagatcca aattggtggc aggctagcca tgtaaaagag
1260
ggaggaagcg ctggtctcat tccaagccag ttcctggaag agaagagaaa ggcatttgtt
1320
agaagagact gggacaattc aggacctttt tgtggaacta taagtagcaa aaaaaagaaa
1380
aagatgatgt atctcacaac cagaaatgca gaatttgatc gtcatgaaat ccagatatat
1440
gaggaggtag ccaaaatgcc tcccttccag agaaaaacat tagtattgat aggagctcaa
1500
ggtgtaggcc gaagaagctt gaaaaacagg ttcatagtat tgaatcccac tagatttgga
1560
actacggtgc catttacttc acggaaacca agggaagatg aaaaagatgg ccaggcatat
1620
aagtttgtgt cacgatctga gatggaagca gatattaaag ctggaaagta tttggaacat
1680
ggggaatatg aaggaaatct ctatggaacc aaaattgatt ctattcttga ggttgtccaa
1740
actggacgga cttgcattct ggatgtcaac ccacaagcac tgaaagtatt gaggacatca
1800
gagtttatgc cctatgtggt atttattgcg gctccggagc tagagacgtt acgtgccatg
1860
cacaaggctg tggtggatgc aggaatcact accaagcttc tgaccgactc tgacttgaag
1920
aaaacagtgg atgaaagtgc acggattcag agagcataca accactattt tgatttgatc
1980
atcataaatg ataatctaga caaagccttt gaaaaactgc aaactgccat agagaaactg
2040
agaatggaac cacagtgggt cccaatcagc tgggtttact gatgattcag taaggttaac
2100
aatgaaaatt aaactcttaa aaagtgactg caacaaataa accttctact gagaaaatac
2160
atcacagata gaagattatc tgctaagtcc aggcattttt atggtgtaga ttgaaataat
2220
agtacacttc tgaattttta tataaaatgt ggttggaagg tgtactaata tataatttat
2280
cttaattttt ctaactttgt atggataatc tttctattca tatcacataa agaaatgcgt
2340
tgaagcaaaa aaaaaaaaaa aaaaaa
2366

<210> 5228
<211> 550
<212> PRT
<213> Homo sapiens

<400> 5228
Arg Leu Gly Val Val Glu Ile Gly Arg Ile Pro Gly Gly Ile Trp Glu
1 5 10 15
Asn Leu Thr Glu Leu Pro Ser Ser Thr Gly Ala Glu Glu Ile Asp Leu
20 25 30
Ile Phe Leu Lys Gly Ile Met Glu Asn Pro Ile Val Lys Ser Leu Ala

```
        35                  40                  45
Lys Ala Arg Glu Arg Leu Glu Asp Ser Lys Leu Glu Ala Val Ser Asp
    50                  55                  60
Asn Asn Leu Glu Leu Val Asn Glu Ile Leu Glu Asp Ile Thr Pro Leu
65                  70                  75                  80
Ile Asn Val Asp Glu Asn Val Ala Glu Leu Val Gly Ile Leu Lys Glu
                85                  90                  95
Pro His Phe Gln Ser Leu Leu Glu Ala His Asp Ile Val Ala Ser Lys
            100                 105                 110
Cys Tyr Asp Ser Pro Pro Ser Ser Pro Glu Met Asn Asn Ser Ser Ile
        115                 120                 125
Asn Asn Gln Leu Leu Pro Val Asp Ala Ile Arg Ile Leu Gly Ile His
    130                 135                 140
Lys Arg Ala Gly Glu Pro Leu Gly Val Thr Phe Arg Val Glu Asn Asn
145                 150                 155                 160
Asp Leu Val Ile Ala Arg Ile Leu His Gly Gly Met Ile Asp Arg Gln
                165                 170                 175
Gly Leu Leu His Val Gly Asp Ile Ile Lys Glu Val Asn Gly His Glu
            180                 185                 190
Val Gly Asn Asn Pro Lys Glu Leu Gln Glu Leu Leu Lys Asn Ile Ser
        195                 200                 205
Gly Ser Val Thr Leu Lys Ile Leu Pro Ser Tyr Arg Asp Thr Ile Thr
    210                 215                 220
Pro Gln Gln Val Phe Val Lys Cys His Phe Asp Tyr Asn Pro Tyr Asn
225                 230                 235                 240
Asp Asn Leu Ile Pro Cys Lys Glu Ala Gly Leu Lys Phe Ser Lys Gly
                245                 250                 255
Glu Ile Leu Gln Ile Val Asn Arg Glu Asp Pro Asn Trp Trp Gln Ala
            260                 265                 270
Ser His Val Lys Glu Gly Gly Ser Ala Gly Leu Ile Pro Ser Gln Phe
        275                 280                 285
Leu Glu Glu Lys Arg Lys Ala Phe Val Arg Arg Asp Trp Asp Asn Ser
    290                 295                 300
Gly Pro Phe Cys Gly Thr Ile Ser Ser Lys Lys Lys Lys Lys Met Met
305                 310                 315                 320
Tyr Leu Thr Thr Arg Asn Ala Glu Phe Asp Arg His Glu Ile Gln Ile
                325                 330                 335
Tyr Glu Glu Val Ala Lys Met Pro Pro Phe Gln Arg Lys Thr Leu Val
            340                 345                 350
Leu Ile Gly Ala Gln Gly Val Gly Arg Arg Ser Leu Lys Asn Arg Phe
        355                 360                 365
Ile Val Leu Asn Pro Thr Arg Phe Gly Thr Thr Val Pro Phe Thr Ser
    370                 375                 380
Arg Lys Pro Arg Glu Asp Glu Lys Asp Gly Gln Ala Tyr Lys Phe Val
385                 390                 395                 400
Ser Arg Ser Glu Met Glu Ala Asp Ile Lys Ala Gly Lys Tyr Leu Glu
                405                 410                 415
His Gly Glu Tyr Glu Gly Asn Leu Tyr Gly Thr Lys Ile Asp Ser Ile
            420                 425                 430
Leu Glu Val Val Gln Thr Gly Arg Thr Cys Ile Leu Asp Val Asn Pro
        435                 440                 445
Gln Ala Leu Lys Val Leu Arg Thr Ser Glu Phe Met Pro Tyr Val Val
    450                 455                 460
Phe Ile Ala Ala Pro Glu Leu Glu Thr Leu Arg Ala Met His Lys Ala
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465                 470                 475                 480
Val Val Asp Ala Gly Ile Thr Thr Lys Leu Leu Thr Asp Ser Asp Leu
                485                 490                 495
Lys Lys Thr Val Asp Glu Ser Ala Arg Ile Gln Arg Ala Tyr Asn His
            500                 505                 510
Tyr Phe Asp Leu Ile Ile Ile Asn Asp Asn Leu Asp Lys Ala Phe Glu
        515                 520                 525
Lys Leu Gln Thr Ala Ile Glu Lys Leu Arg Met Glu Pro Gln Trp Val
    530                 535                 540
Pro Ile Ser Trp Val Tyr
545                 550
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<210> 5229
<211> 1031
<212> DNA
<213> Homo sapiens

<400> 5229
acgcgtgtgc tgtggttaca tccgtggaac agacagacag cagctgcccc tgcaaatgtc
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agcgccagcc cagtcaaaag agcttgaaac ctaccaagcc ggaggactgt gctgtgcctc
120
tctcgcccac attttcccca agcactctca ggaacctggc aacagtgtcc ccttgtggcc
180
aagcctggaa catcacatct gtacgttgca atctgtggat cagctacgag actgagagaa
240
aggaatgaaa ggatggaaga attacaagat caggcactgc tgtctgtctg ttccacggat
300
gtaaccacag cacacgcgtg gctcacggta ctagtgtgat aaatgcttgt tacatgaagg
360
cgtgaacagg gatgagaaga gacttcctgg agaaacaaaa ggactaacaa tcaggaaggg
420
gaggtgatcg gggcaggagt aaagtggaca cctcagcaaa gccattcgct gtgatctctg
480
attgtgcagt gtcatgtcct gtcaccagag ccccctcgtg tttgatgttg gccaatgccg
540
ccagcatgat ctagcaggcc aaatcctaat ctaccattct ctgacaccag ctggtccccc
600
ggggtcgtcc acccgatgtc ccccattctc cccacttggc ctcccccaca ggctctcggc
660
aaaggaccgt gggaggcacc tgtgacactg ccctttttcct gtgcagctgt ttttcttctt
720
cattcttttc actcctcgtt actctttttt ttttcactct cagcccacac aaaactagga
780
actttgttat tctacttatt tttctgtact ctgtctgttt gcacacagat ggatatctga
840
gagccagcga actttcttta cctcctagta tcatttcatg aaaattagta gcacctgcac
900
aatggggcct tggagacagg aataaaagga aaaatctgga atggaatcac atgacgcaac
960
aggctatgaa gactccctgc ccggctgcta tatgtctggt aaacagaata aatagtactt
1020
gagcatccct g
1031

<210> 5230
<211> 102
<212> PRT
<213> Homo sapiens

<400> 5230
Met Ile Leu Gly Gly Lys Glu Ser Ser Leu Ala Leu Arg Tyr Pro Ser
1 5 10 15
Val Cys Lys Gln Thr Glu Tyr Arg Lys Ile Ser Arg Ile Thr Lys Phe
20 25 30
Leu Val Leu Cys Gly Leu Arg Val Lys Lys Lys Arg Val Thr Arg Ser
35 40 45
Glu Lys Asn Glu Glu Glu Lys Gln Leu His Arg Lys Arg Ala Val Ser
50 55 60
Gln Val Pro Pro Thr Val Leu Cys Arg Glu Pro Val Gly Glu Ala Lys
65 70 75 80
Trp Gly Glu Trp Gly Thr Ser Gly Gly Arg Pro Gln Gly Thr Ser Trp
85 90 95
Cys Gln Arg Met Val Asp
100

<210> 5231
<211> 845
<212> DNA
<213> Homo sapiens

<400> 5231
tccggatctt ggagggtaca gagggcgccc ctcggcctcc tccctttcgg aggtggggac
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aaggtggagg aagggctgca ggaggaggag ctctagcatc gcgacccgcc ccgtcccgtc
120
cagtctggcc tgggcgccgc gggaacgctg tcctggctgc cgccacccga acagcctgtc
180
ctggtgcccc ggctccctgc cccgcgccca gtcatgaccc tgcgcccctc actcctcccg
240
ctccatctgc tgctgctgct gctgctcagt gcggcggtgt gccgggctga ggctgggctc
300
gaaaccgaaa gtcccgtccg gaccctccaa gtggagaccc tggtggagcc cccagaacca
360
tgtgccgagc ccgctgcttt tggagacacg cttcacatac actacacggg aagcttggta
420
gatggacgta ttattgacac ctccctgacc agagaccctc tggttataga acttggccaa
480
aagcaggtga ttccaggtct ggagcagagt cttctcgaca tgtgtgtggg agagaagcga
540
agggcaatca ttccttctca cttggcctat ggaaaacggg gatttccacc atctgtccca
600
gcggatgcag tggtgcagta tgacgtggag ctgattgcac taatccgagc caactactgg
660
ctaaagctgg tgaagggcat tttgcctctg gtagggatgg ccatggtgcc agccctcctg
720
ggcctcattg ggtatcacct atacagaaag gccaatagac ccaaagtctc caaaaagaag
780

ctcaaggaag agaaacgaaa caagagcaaa aagaaataat aaataataaa ttttaaaaaa
840
cttaa
845

<210> 5232
<211> 201
<212> PRT
<213> Homo sapiens

<400> 5232
Met Thr Leu Arg Pro Ser Leu Leu Pro Leu His Leu Leu Leu Leu Leu
 1   5   10   15
Leu Leu Ser Ala Ala Val Cys Arg Ala Glu Ala Gly Leu Glu Thr Glu
            20   25   30
Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu Pro Pro Glu
        35   40   45
Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu His Ile His Tyr
    50   55   60
Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser Leu Thr Arg
65   70   75   80
Asp Pro Leu Val Ile Glu Leu Gly Gln Lys Gln Val Ile Pro Gly Leu
                85   90   95
Glu Gln Ser Leu Leu Asp Met Cys Val Gly Glu Lys Arg Arg Ala Ile
            100   105   110
Ile Pro Ser His Leu Ala Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val
        115   120   125
Pro Ala Asp Ala Val Val Gln Tyr Asp Val Glu Leu Ile Ala Leu Ile
    130   135   140
Arg Ala Asn Tyr Trp Leu Lys Leu Val Lys Gly Ile Leu Pro Leu Val
145   150   155   160
Gly Met Ala Met Val Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu
                165   170   175
Tyr Arg Lys Ala Asn Arg Pro Lys Val Ser Lys Lys Lys Leu Lys Glu
            180   185   190
Glu Lys Arg Asn Lys Ser Lys Lys Lys
        195   200

<210> 5233
<211> 2801
<212> DNA
<213> Homo sapiens

<400> 5233
agatctcaat tcacacatga ctacctttca gctaatgact gtctccagaa aataactgtg
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ccccaagaag tgctccagat ttgcaaggaa tagccccaag agaataccaa gacaagcagg
120
ctgttccctg gaaaaaatct aatgcaagga gggctagttc acagcaaatt cactgcctcc
180
tcccatgcac gtggtagaga gtaccagtat caacatggcc ctgttttctg ctaaaaccag
240
attttgagga atcagagacc cccaacacta ctcactcagt agctagcagc cccttccttt
300

caactgggag tgttattaga atgaaaagta attagttaga agggcataca tctcagtggc
360
atgagcattg tggaatatcc tttcctaggc acatttgtcc actaagggaa cagcctcaga
420
aactggtaca gcaatgggtg agatgagatc ctggagagag aacacagcca tcccctatag
480
aaaggcacag cttttgggct tctctggcct gaatgccttc tggggtattt ccatatgcaa
540
cagcccagag tcatagcctt gggcaaccac acatagaggt ttccttctca cttcagacac
600
atacatcact ttcacaccac ttggggatgg aaatacctac aagagtgaag gtcaagggcc
660
ctccccaggc atctcattca ttactcagct tccttcctga ccaagtctgc caaccaatgg
720
ccagctatgc gcctcatcct cattgcttct gcctccacgt aaatgaaacc aaaggcctca
780
gcatatcctg ggaggactgg gggctgttac ctaatggtcc tctctgtccc attataggtg
840
caaggcaccc catccacaca tttgcaccac tactccaaga tagtattttt cttttcacac
900
aatctcttta cagcagaatc cagagttggg ttgtagttta ccttcctgga aagctcatta
960
tctttgtttg aattaacatt tcagcatgga actaactggg cggaggaagg atcgttatac
1020
gtcttcagaa agttctcatt gccccagctg cctagtacta tacaagaagc tctactttga
1080
tggcagatct aagaaggcta taggcctttg tttgtaggaa gcagtgtcat tacattcaag
1140
cttcacttct ctgattggct tccaaccact gggattcaaa gagaatccaa ggttctgcct
1200
atgtctgatg acataaggaa aacttggctt cctctgctca aggttcccct ctgctcatcc
1260
ctcctcattc agacatcctc caccatacca gtgtttagaa gcaaaacatg aagggctagc
1320
gccaccagga tagttagcag aaatattgtc tgtaaagcta ggcagatgag cccagaagaa
1380
tggtcccaga gaaagcagac tggctccaat agatatcagg cagcaatccc aataaattct
1440
gacatgtcct tggcaatgga agcctgggtt ggagatcctg aggcagctgt gcctactgtt
1500
ccccacctca gaagcttcct gcccagagag ccagcagcct tgggatacta atgaggatgc
1560
aactggctta ttggtatgaa atagaaggtg gctttgtagg ggcaagcagg caaagagtac
1620
tatccacatg gcaggcaggt ggctttgtgt ctggaaagct ttgcctagcc agtacagctg
1680
tgagcagagg ctggttataa atttgaactc cctcagccca tttgcaactc tgcctctgtt
1740
cccttgcatt ctgtttggtt gccctttagt ttcctagtaa atgctccttt tgaaaaactc
1800
caaccttgtc ttatttaact tgggggaagg ggattctcca atgtcttttc caggataaag
1860
aaggaaatta aaataccatg aaaaaatgga catggcagta gaaaggaaac attctgatca
1920

gaccttggga aaagctggtg ccgagagagg gagaggccag gtgtcccccc acccaactgg
1980
cactgattct cagccccttc ctcttacttc tgttggcttc aaggagacct gcccttgatg
2040
tgtgttgctg ctgaagcacc ctcccagcca gtgagttgga catatgcagc aggcactttg
2100
atgtccagga agtacactgg tacatgacag gagcaagggt cagggagggg aggggaaagg
2160
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2220
tagggctggg tgcagtgact cacacctgta atctcagcac tttgggaggc caaggcggga
2280
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2340
tcaaaagaga ccccccccgcc cccccggcta atttttaaaa aattagcagt acctgtagtc
2400
ccagctactt aggaagctga gataggagaa tcgcctgagt ccaagagctt gaggctacag
2460
cgagccaaga ttgcaacact gcatttcagc ctgggtgaca gagcaaggcc ctgtctctct
2520
aaaaaagaaa aaaaaggtat tgtttagttc acatggccat cagtagaact acatttcata
2580
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2640
gtatggaaaa tggcttgcta ttttcatggc caccctgtcc tgcaatgcgg ggggtgggag
2700
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2760
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2801

<210> 5234
<211> 57
<212> PRT
<213> Homo sapiens

<400> 5234
Leu Thr Pro Val Ile Ser Ala Leu Trp Glu Ala Lys Ala Gly Gly Ser
1 5 10 15
Leu Asp Thr Arg Ser Ser Arg Pro Val Trp Gln Arg Gly Glu Thr Thr
20 25 30
Ile Ile Ser Lys Glu Thr Pro Pro Pro Pro Arg Leu Ile Phe Lys Lys
35 40 45
Leu Ala Val Pro Val Val Pro Ala Thr
50 55

<210> 5235
<211> 3017
<212> DNA
<213> Homo sapiens

<400> 5235
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cccattccta ctaaaaatat gttggaggaa agcaaagtac ttccaattat tcaacgctgg
120
tctcagacta agactgctgt ccctccgttg agtgaaggag atgggtattc tagtgagaat
180
acatcgcgtg ctcatacacc actcaacaca cctgatcctt ccaccaagct gagcacagaa
240
gctgacacag acactcccaa gaaactaatg tttcgcagac tgaaaattat aagtgaaaat
300
agcatggaca gtgcaatctc tgatgcaacc agtgagctag aaggcaagga tggcaaagag
360
gatcttgatc aattagaaaa tgtccctgta gaggaagagg aagaattgca gtcacaacag
420
ctactcccac aacagctgcc tgaatgcaaa gttgatagtg aaaccaacat agaagctagt
480
aagctaccta catctgaacc agaagctgac gctgaaatag agcccaaaga gagcaacggc
540
acaaaactag aagaacctat taatgaagaa acaccatccc aagatgaaga ggagggtgtg
600
tctgatgtgg agagtgaaag gagccaagaa cagccagata aaacagtgga tataagtgat
660
ttggccacca aactcctgga cagttggaaa gacctaaagg aggtatatcg aattccaaag
720
aaaagtcaaa ctgaaaagga aaacacaaca actgaacgag gaagggatgc tgttggcttc
780
agagatcaaa cacctgcccc gaagactcct aataggtcaa gagagagaga cccagacaag
840
caaactcaaa ataaagagaa aaggaaacga agaagctccc tctcaccacc ctcttctgcc
900
tatgagcggg gaacaaaaag gccagatgac agatatgata caccaacttc taaaaagaaa
960
gtacgaatta aagaccgcaa taaactttct acagaggaac gccggaagtt gtttgagcaa
1020
gaggtggctc aacgggaggc tcagaaacaa cagcaacaga tgcagaacct gggaatgaca
1080
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1140
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1200
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1260
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1320
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1380
gtacaccaag actccagcgt tgctgtcttg ccagtgccgg cccccggccc agttcaggga
1440
cagaattata gtgtttggga ttcaaaccaa cagtctgtca gtgtacagca gcagtactct
1500
cctgcacagt ctcaagcaac catatattat caaggacaga catgtccaac agtctatggt
1560
gtgacatcac cttattcaca gacaactcca ccaattgtac agagttatgc ccagccaagt
1620
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1680

ccagccgcag cagtgactac aatagttgca ccagggcagc ctcagccctt gcagccatct
1740
gaaatggttg tgacaaataa tctcttggat ctgccgcccc cctctcctcc caaaccaaaa
1800
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1860
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1920
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1980
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2040
aagaaaagca aagaagtatt cagaaaagag atgtcccagt tcatcgtcca gtgcctgaac
2100
ccttaccgga aacctgactg caaagtggga agaattacca caactgaaga ctttaaacat
2160
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2220
gaggacctgg agtgcaatga gaatgtgaaa cacaaaacca aggagtacat taagaagtac
2280
atgcagaagt ttggggctgt ttacaaaccc aaagaggaca ctgaattaga atgactgttg
2340
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2400
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2460
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2520
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2580
acctggccag acctgactcc actcttaaac ctgggtcttc tccttggcgg tgctgtcagc
2640
gcacagaccc atgcgcatcc ccacccacaa ccctttaccc tgatgatctg tattatattt
2700
taatgtatat gtgaatatat tgaaaataat ttgtttttc ctggtttttg tttggttttc
2760
gttttgcttt tagcctctac atgctaggat cacaggaaga ctttgtaagg acagtttaag
2820
ttctcctgca aggtttaatt tgttatcatg taaatattcc aaagcaggct gccttgtggt
2880
tttggccagc cttgtgctat gttgataaga ttgatttact gcttaaaatc actttacttt
2940
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3000
aaaaaaaaaa aaaaaaa
3017

<210> 5236
<211> 178
<212> PRT
<213> Homo sapiens

<400> 5236
Lys Thr Ile Val Leu Pro Pro Asn Trp Lys Thr Ala Arg Asp Pro Glu

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 1               5                  10                  15
Gly Lys Ile Tyr Tyr Tyr His Val Ile Thr Arg Gln Thr Gln Trp Asp
            20                  25                  30
Pro Pro Thr Trp Glu Ser Pro Gly Asp Asp Ala Ser Leu Glu His Glu
        35                  40                  45
Ala Glu Met Asp Leu Gly Thr Pro Thr Tyr Asp Glu Asn Pro Met Lys
    50                  55                  60
Ala Ser Lys Lys Pro Lys Thr Ala Glu Ala Asp Thr Ser Ser Glu Leu
65                  70                  75                  80
Ala Lys Lys Ser Lys Glu Val Phe Arg Lys Glu Met Ser Gln Phe Ile
                85                  90                  95
Val Gln Cys Leu Asn Pro Tyr Arg Lys Pro Asp Cys Lys Val Gly Arg
            100                 105                 110
Ile Thr Thr Thr Glu Asp Phe Lys His Leu Ala Arg Lys Leu Thr His
        115                 120                 125
Gly Val Met Asn Lys Glu Leu Lys Tyr Cys Lys Asn Pro Glu Asp Leu
    130                 135                 140
Glu Cys Asn Glu Asn Val Lys His Lys Thr Lys Glu Tyr Ile Lys Lys
145                 150                 155                 160
Tyr Met Gln Lys Phe Gly Ala Val Tyr Lys Pro Lys Glu Asp Thr Glu
                165                 170                 175
Leu Glu
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<210> 5237
<211> 1238
<212> DNA
<213> Homo sapiens

<400> 5237
ntagaagaca aggcgtcgtt tgaataactt gcctgatttt tcttcctacc gagtagcatt
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tctttttttt tcaccatatc tttccctaag gcagctcctt attctgtagg aattgccaat
120
gttgatgtgt tattgttagg tatttatatc attcacaggg ctgtcagaaa tcccgatgat
180
cttgaagcaa ggtctcatat gcacttggca agtgcttttg ctggcatcgg ctttggaaat
240
gctggtgttc atctgtgcca tggaatgtct tacccaattt caggtttagt gaagatgtat
300
aaagcaaagg attacaatgt ggatcaccca ctggtgcccc atggcctttc tgtggtgctc
360
acgtccccag cggtgttcac tttcacggcc cagatgtttc cagagcgaca cctggagatg
420
gcagaaatac tgggagccga cacccgcact gccaggatcc aagatgcagg gctggtgttg
480
gcagacacgc tccggaaatt cttattcgat ctggatgttg atgatggcct agcagctgtt
540
ggttactcca aagctgatat ccccgcacta gtgaaaggaa cgctgcccca ggaaagggtc
600
accaagcttg caccccgtcc ccagtcagaa gaggatctgg ctgctctgtt tgaagcttca
660
atgaaactgt attaattgtc attttaactg aaagaattac cgctggccat tgtagtgctg
720

agagcaagag ctgatctagc tagggctttg tcttttcatc tttgtgcata acttacctgt
780
taccagtata ggtgggatat acatttatct tgcaggaaat tccccaaagc tcagagtcca
840
gttccttcca taaaacaggc tggacaaatg accactatgt tagaccccca ggctcgactt
900
caggggtcag tgttcctgtc ccaaacccca cacagaatac tctgcctctg cttcatgtag
960
caaatgagca aaaactcagt atctatcaaa agtgtaaatt atatttccta tgcctagtaa
1020
ttcacttcat gtctaaaaat ttatctgata gaaacactag caccagtaca tacagaagca
1080
tggcaaggat gtttctggca gcacttttct aataataaaa gatttgaaac aaccttaagt
1140
attcattatt ggtatataga tcacttatag tatactagac agtggaatac tatggtactg
1200
ttaataaaga tgaagtaaat ctcttggaaa aaaaaaaa
1238

<210> 5238
<211> 212
<212> PRT
<213> Homo sapiens

<400> 5238
Phe Phe Phe Leu Pro Ser Ser Ile Ser Phe Phe Phe Thr Ile Ser Phe
1 5 10 15
Pro Lys Ala Ala Pro Tyr Ser Val Gly Ile Ala Asn Val Asp Val Leu
20 25 30
Leu Leu Gly Ile Tyr Ile Ile His Arg Ala Val Arg Asn Pro Asp Asp
35 40 45
Leu Glu Ala Arg Ser His Met His Leu Ala Ser Ala Phe Ala Gly Ile
50 55 60
Gly Phe Gly Asn Ala Gly Val His Leu Cys His Gly Met Ser Tyr Pro
65 70 75 80
Ile Ser Gly Leu Val Lys Met Tyr Lys Ala Lys Asp Tyr Asn Val Asp
85 90 95
His Pro Leu Val Pro His Gly Leu Ser Val Val Leu Thr Ser Pro Ala
100 105 110
Val Phe Thr Phe Thr Ala Gln Met Phe Pro Glu Arg His Leu Glu Met
115 120 125
Ala Glu Ile Leu Gly Ala Asp Thr Arg Thr Ala Arg Ile Gln Asp Ala
130 135 140
Gly Leu Val Leu Ala Asp Thr Leu Arg Lys Phe Leu Phe Asp Leu Asp
145 150 155 160
Val Asp Asp Gly Leu Ala Ala Val Gly Tyr Ser Lys Ala Asp Ile Pro
165 170 175
Ala Leu Val Lys Gly Thr Leu Pro Gln Glu Arg Val Thr Lys Leu Ala
180 185 190
Pro Arg Pro Gln Ser Glu Glu Asp Leu Ala Ala Leu Phe Glu Ala Ser
195 200 205
Met Lys Leu Tyr
210

<210> 5239
<211> 2061
<212> DNA
<213> Homo sapiens

<400> 5239
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120
taaaaacaaa agaggtgagt gagaatcgtc acctttctgc tttccttcct cacttggcca
180
ggctctagta ctccaccttt gagctgccat gcccaatagg ggaagtccaa aattaaaaat
240
acaaccggtg tagaagaaaa taaatgggga gtgaaataga agaaaagatg agggagggga
300
gtgctaatat ttacactaga gttttataga caactgtccc attccatccc aattccaatc
360
ctgacccaga aagtgatggt ggcaggtcca agagacagag attatgtgtc gggacacaga
420
cagcctccca tccccaaccg taatggattc aatttcaagt ccacagagtg gggaggaagg
480
atagggtggg aaagtgagac actcattttc aaacaagtct cccttgagaa ttcctgcctt
540
gaagtgcaga cagtatccaa gctccagggg ataggctgag gaccctgagg ctcagttccc
600
aaatcatgtt gtcatttgga agttccaggc taaagttggt gccatcaggg ctctccagat
660
ttgggaggcc cccctaaccg ccgggcctct ggcctcagtt ccttgcattt ctggcaataa
720
aagaagtcgg ggacgttggt cttcttaatc ttagcacagg agaggtggat ccacgtccca
780
cacaggctgc actcaatcat gggccgccct gcaaagggct ttcgacagta acatgtgatc
840
agatcccatg agtcatcacc tgattctacc atgatgtcct cgtccatgac ccgcatctcg
900
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960
tcactgtcag caggagggac tccttcaggg tgcactgtgg caggggcct aggagcctca
1020
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1080
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1140
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1260
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1320
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1440

tcaaagagag agtccttgag cttcatcttc tcaagcaagg tagcactgtc gggggcctgc
1500
agacgagaga aagtggacct tgggggtcct ggctgggtgg gacctgcttg agctgccctt
1560
ctcttggatg actttgcttt cttaacaaaa gtctggatgg ttcgaagatc tgaggggggcc
1620
gagtcccagc catcactgtc ggccgcactc tctcctcgca atggagagct ggagccagag
1680
gctggccagt cactttcctc tttgctaggg ggaatgtaac cagcatatgc caaaacaaaa
1740
ctgcagaatt tgttgaaatc ctcaattgtt ctccgccgtt tctctggtgg ctgagtctct
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1860
ccctcccctc ctcccggtcc ggcgcccccc tccccggagc cggggatccc ggtgccgcct
1920
ctagtgctcg atgctcccac tgcttcgctc cacagaagtg tccgcctcag cccggttgag
1980
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2040
ccgggccccc tccccccgcg g
2061

<210> 5240
<211> 226
<212> PRT
<213> Homo sapiens

<400> 5240
Met Met Ser Ser Ser Met Thr Arg Ile Ser Pro Ser Leu Glu Leu Ala
1 5 10 15
Ser Pro Ser Trp Leu Val Ser Val Leu Pro Thr Ser Leu Leu Ser Leu
20 25 30
Ser Ala Gly Gly Thr Pro Ser Gly Cys Thr Val Ala Gly Gly Leu Gly
35 40 45
Ala Ser Gly Gly Val Gly Ser Thr Gly Thr Gly Ala Ser Pro Pro Thr
50 55 60
Thr Val Ala Ile Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
65 70 75 80
Ser Ser Glu Ser Val Ser Leu Gly Gly Ala Trp Gly Gly Pro Gly Gly
85 90 95
Gly Ser Leu Ser Pro Arg Ser Ala Phe Phe Asn Phe Arg Phe Leu Leu
100 105 110
Phe Leu Ile Arg Asp Leu Phe Ser Pro Ser Pro Gly Val Gly Arg Gly
115 120 125
Leu Arg Ser Thr Pro Lys Pro Ala Pro Ala Pro Gly Pro Asn Phe Arg
130 135 140
Phe Phe Arg Ser Phe Phe Arg Gly Gly Trp Glu Arg Ser Pro Trp Glu
145 150 155 160
Arg Gly Thr Gly Val Arg Ala Ala Gly Gly Arg Glu Val Cys Val Arg
165 170 175
Asp Val Gly Asp Lys Gly Asp Ala Thr Leu Gly Pro Ser Arg Ser Lys
180 185 190
Arg Glu Ser Leu Ser Phe Ile Phe Ser Ser Lys Val Ala Leu Ser Gly

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        195                 200                 205
Ala Cys Arg Arg Glu Lys Val Asp Leu Gly Gly Pro Gly Trp Val Gly
    210                 215                 220
Pro Ala
225
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<210> 5241
<211> 461
<212> DNA
<213> Homo sapiens

<400> 5241
gcggcccccg atttgcagcc catggatgca tttatcacgt ttgttcctct gcgtgcctcc
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ccctcaatat gccgggggtg tacccatttc caagggatga cagcagggcc ccacagcgag
120
ccccaggctg atccggagcc ctcttcatcc ccgtccaggg ccgtttgcac tgctcccggc
180
atcggcacac cttgttctgg ttgtgctggg acggcagcgc cccgtgaggt cagagggttg
240
ctgtcacatc tgccacccag tgtggtctcc tggagatttc agtggttcgg tgcttcgctt
300
ctcacctggc cagctctgag ttcagcctct cgcctgtggg gacccctgca tcctggcggc
360
agaaggagga ggaagaagcc accagaggtt gccaggaacc cagtggcagg ggaggtgggg
420
ctgagccagg cccgcccgct gtgccgggag ttcccacgcg g
461

<210> 5242
<211> 146
<212> PRT
<213> Homo sapiens

<400> 5242

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Met Asp Ala Phe Ile Thr Phe Val Pro Leu Arg Ala Ser Pro Ser Ile
 1               5                  10                  15
Cys Arg Gly Cys Thr His Phe Gln Gly Met Thr Ala Gly Pro His Ser
            20                  25                  30
Glu Pro Gln Ala Asp Pro Glu Pro Ser Ser Ser Pro Ser Arg Ala Val
        35                  40                  45
Cys Thr Ala Pro Gly Ile Gly Thr Pro Cys Ser Gly Cys Ala Gly Thr
    50                  55                  60
Ala Ala Pro Arg Glu Val Arg Gly Leu Leu Ser His Leu Pro Pro Ser
65                  70                  75                  80
Val Val Ser Trp Arg Phe Gln Trp Phe Gly Ala Ser Leu Leu Thr Trp
                85                  90                  95
Pro Ala Leu Ser Ser Ala Ser Arg Leu Trp Gly Pro Leu His Pro Gly
            100                 105                 110
Gly Arg Arg Arg Arg Lys Lys Pro Pro Glu Val Ala Arg Asn Pro Val
        115                 120                 125
Ala Gly Glu Val Gly Leu Ser Gln Ala Arg Pro Leu Cys Arg Glu Phe
    130                 135                 140
Pro Arg
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145

<210> 5243
<211> 344
<212> DNA
<213> Homo sapiens

<400> 5243
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tggctggacc ttacagacga gccatttggt cagaaggtaa ctgtggaccc tgacaactca
120
aattgcagtg aagaaagtgc taggttgtct ttgaagcttg gtgatgctgg aaaccccaga
180
agtcttgcta taagattcat ccttaccaat tacaacaagt tgtccatcca gagttggttt
240
agtttgcgcc gagtcgagat catttccaac aattcaatcc aagcagtctt taacccaact
300
ggcgtatatg ctcccctctgg ttactcctac cgctgccaac gcgt
344

<210> 5244
<211> 114
<212> PRT
<213> Homo sapiens

<400> 5244
Xaa Ile Pro Cys Ile Leu Phe Trp Ala Lys Arg Ile Met Ile Lys Phe
 1   5   10   15
Lys Asn Gln Thr Trp Leu Asp Leu Thr Asp Glu Pro Phe Gly Gln Lys
            20   25   30
Val Thr Val Asp Pro Asp Asn Ser Asn Cys Ser Glu Glu Ser Ala Arg
        35   40   45
Leu Ser Leu Lys Leu Gly Asp Ala Gly Asn Pro Arg Ser Leu Ala Ile
    50   55   60
Arg Phe Ile Leu Thr Asn Tyr Asn Lys Leu Ser Ile Gln Ser Trp Phe
65   70   75   80
Ser Leu Arg Arg Val Glu Ile Ile Ser Asn Asn Ser Ile Gln Ala Val
                85   90   95
Phe Asn Pro Thr Gly Val Tyr Ala Pro Ser Gly Tyr Ser Tyr Arg Cys
            100   105   110
Gln Arg

<210> 5245
<211> 483
<212> DNA
<213> Homo sapiens

<400> 5245
nngccatgga aacgaaagcg gccaagtaga gctccgtcct gacgcgccgc ctcccgtggg
60
ctccggccgg ctaagccgcg gcggacaact atgctgaaag ccaagatcct cttcgtgggg
120

ccttgcgaga gtggaaaaac tgttttggcc aactttctga cagaatcttc tgacatcact
180
gaatacagcc caacccaagg agtgaggttt gagtcctgct ggccggccct gatgaaggat
240
gctcatggag tggtgatcgt cttcaatgct gacatcccaa gccaccggaa ggaaatggag
300
atgtggtatt cctgctttgt ccaacagccg tccttacagg acacacagtg tatgctaatt
360
gcacaccaca aaccaggctc tggagatgat aaaggaagcc tgtctttgtc gccacccttg
420
aacaagctga agctggtgca ctcaaacctg gaagatgacc ctgaggagat ccggatggaa
480
ttc
483

<210> 5246
<211> 131
<212> PRT
<213> Homo sapiens

<400> 5246
Met Leu Lys Ala Lys Ile Leu Phe Val Gly Pro Cys Glu Ser Gly Lys
 1   5   10   15
Thr Val Leu Ala Asn Phe Leu Thr Glu Ser Ser Asp Ile Thr Glu Tyr
            20   25   30
Ser Pro Thr Gln Gly Val Arg Phe Glu Ser Cys Trp Pro Ala Leu Met
        35   40   45
Lys Asp Ala His Gly Val Val Ile Val Phe Asn Ala Asp Ile Pro Ser
    50   55   60
His Arg Lys Glu Met Glu Met Trp Tyr Ser Cys Phe Val Gln Gln Pro
65   70   75   80
Ser Leu Gln Asp Thr Gln Cys Met Leu Ile Ala His His Lys Pro Gly
                85   90   95
Ser Gly Asp Asp Lys Gly Ser Leu Ser Leu Ser Pro Pro Leu Asn Lys
            100   105   110
Leu Lys Leu Val His Ser Asn Leu Glu Asp Asp Pro Glu Glu Ile Arg
        115   120   125
Met Glu Phe
    130

<210> 5247
<211> 1004
<212> DNA
<213> Homo sapiens

<400> 5247
nngccatgga aacgaaagcg gccaagtaga gctccgtcct gacgcgccgc ctcccgtggg
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ctccggccgg ctaagccgcg gcggacaact atgctgaaag ccaagatcct cttcgtgggg
120
ccttgcgaga gtggaaaaac tgttttggcc aactttctga cagaatcttc tgacatcact
180
gaatacagcc caacccaagg agtgaggatc ctagaatttg agaacccgca tgttaccagc
240

aacaacaaag gcacgggctg tgaattcgag ctatgggact gtggtggcga tgctaagttt
300
gagtcctgct ggccggccct gatgaaggat gctcatggag tggtgatcgt cttcaatgct
360
gacatcccaa gccaccggaa ggaaatggag atgtggtatt cctgctttgt ccaacagccg
420
tccttacagg acacacagtg tatgctaatt gcacaccaca aaccaggctc tggagatgat
480
aaaggaagcc tgtctttgtc gccacccttg aacaagctga agctggtgca ctcaaacctg
540
gaagatgacc ctgaggagat ccggatggaa ttcataaagt atttaaaaag cataatcaac
600
tccatgtctg agagcagaga cagggaggag atgtcaatta tgacctagcc agccttcacc
660
tgggactgcc acatccccag tgaaatcagc atgtttctcg gtgcagatct gaaatcacat
720
ccagctcctg atgttttctt ctccctctga ctgcagagga agtgttccta cctgcaggaa
780
ggcacctgtc acacagggcg ttcactcaga ccatctgtgc tctgccctga gttcagttga
840
gaaaatccta ttatcaaatt tggatttcct ggccccagaa cttcccaaag acctgtaaaa
900
tggagggatt taccacctca catatgtcca gttaaacagt ttgtggactt gtaaccgtcg
960
cagcccaatg atacaacagt agtttaatca cgtgaaaaaa aaaa
1004

<210> 5248
<211> 185
<212> PRT
<213> Homo sapiens

<400> 5248
Met Leu Lys Ala Lys Ile Leu Phe Val Gly Pro Cys Glu Ser Gly Lys
1 5 10 15
Thr Val Leu Ala Asn Phe Leu Thr Glu Ser Ser Asp Ile Thr Glu Tyr
20 25 30
Ser Pro Thr Gln Gly Val Arg Ile Leu Glu Phe Glu Asn Pro His Val
35 40 45
Thr Ser Asn Asn Lys Gly Thr Gly Cys Glu Phe Glu Leu Trp Asp Cys
50 55 60
Gly Gly Asp Ala Lys Phe Glu Ser Cys Trp Pro Ala Leu Met Lys Asp
65 70 75 80
Ala His Gly Val Val Ile Val Phe Asn Ala Asp Ile Pro Ser His Arg
85 90 95
Lys Glu Met Glu Met Trp Tyr Ser Cys Phe Val Gln Gln Pro Ser Leu
100 105 110
Gln Asp Thr Gln Cys Met Leu Ile Ala His His Lys Pro Gly Ser Gly
115 120 125
Asp Asp Lys Gly Ser Leu Ser Leu Ser Pro Pro Leu Asn Lys Leu Lys
130 135 140
Leu Val His Ser Asn Leu Glu Asp Asp Pro Glu Glu Ile Arg Met Glu
145 150 155 160
Phe Ile Lys Tyr Leu Lys Ser Ile Ile Asn Ser Met Ser Glu Ser Arg

165 170 175
Asp Arg Glu Glu Met Ser Ile Met Thr
180 185

<210> 5249
<211> 653
<212> DNA
<213> Homo sapiens

<400> 5249
nnacgcgtgc gcgccaccgg cccggcaggt gctgtcctta ttcccagccc agtcaagagc
60
taccggggct ggctagtcat gggggagccc agtagagagg agtataaaat ccagtccttt
120
gatgcagaga cccagcagct gctgaagaca gcactcaaag atccgggtgc tgtggacttg
180
gagaaagtgg ccaatgtgat tgtggaccat tctctgcagg actgtgtgtt cagcaaggaa
240
gcaggacgca tgtgctacgc catcattcag gcagagagta aacaagcagg ccagagtgtc
300
ttccgacgtg gactcctcaa ccggctgcag caggagtacc aggctcggga gcagctgcga
360
gcacgctccc tgcagggctg ggtctgctat gtcaccttta tctgcaacat ctttgactac
420
ctgagggtga acaacatgcc catgatggcc ctggtgaacc ctgtctatga ctgcctcttc
480
cggctggccc agccagacag tttgagcaag gaggaggagg tggactgttt ggtgctgcag
540
ctgcaccggg ttggggagca gctggagaaa atgaatgggc agcgcatgga tgagctcttt
600
gtgctgatcc gggatggctt cctgctccca actggcctca gctccctggc cca
653

<210> 5250
<211> 217
<212> PRT
<213> Homo sapiens

<400> 5250
Xaa Arg Val Arg Ala Thr Gly Pro Ala Gly Ala Val Leu Ile Pro Ser
1 5 10 15
Pro Val Lys Ser Tyr Arg Gly Trp Leu Val Met Gly Glu Pro Ser Arg
20 25 30
Glu Glu Tyr Lys Ile Gln Ser Phe Asp Ala Glu Thr Gln Gln Leu Leu
35 40 45
Lys Thr Ala Leu Lys Asp Pro Gly Ala Val Asp Leu Glu Lys Val Ala
50 55 60
Asn Val Ile Val Asp His Ser Leu Gln Asp Cys Val Phe Ser Lys Glu
65 70 75 80
Ala Gly Arg Met Cys Tyr Ala Ile Ile Gln Ala Glu Ser Lys Gln Ala
85 90 95
Gly Gln Ser Val Phe Arg Arg Gly Leu Leu Asn Arg Leu Gln Gln Glu
100 105 110
Tyr Gln Ala Arg Glu Gln Leu Arg Ala Arg Ser Leu Gln Gly Trp Val

```
        115                 120                 125
Cys Tyr Val Thr Phe Ile Cys Asn Ile Phe Asp Tyr Leu Arg Val Asn
    130                 135                 140
Asn Met Pro Met Met Ala Leu Val Asn Pro Val Tyr Asp Cys Leu Phe
145                 150                 155                 160
Arg Leu Ala Gln Pro Asp Ser Leu Ser Lys Glu Glu Glu Val Asp Cys
                165                 170                 175
Leu Val Leu Gln Leu His Arg Val Gly Glu Gln Leu Glu Lys Met Asn
            180                 185                 190
Gly Gln Arg Met Asp Glu Leu Phe Val Leu Ile Arg Asp Gly Phe Leu
        195                 200                 205
Leu Pro Thr Gly Leu Ser Ser Leu Ala
    210                 215
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<210> 5251
<211> 372
<212> DNA
<213> Homo sapiens

<400> 5251
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caccccagcg ggacggcact tcattatgac gatgtcccgt gcatcaacgg ctcgggggaa
120
ccggaagacg gctttcctgc tttctgcagc agaagcttgg gagaagaagg ggcttttgaa
180
aacccaggcc tgtacgataa ctggccgcct ccgcacatct ttgcccgcta ctctcctgct
240
gacagaaagg cctctaggct gtctgctgac aagctgtcct ctaaccatta caaataccct
300
gcctctgctc agtctgtcac taatacctct tctgtgggga gggcgtctct cgggctcaac
360
tcgcagcctc ag
372

<210> 5252
<211> 124
<212> PRT
<213> Homo sapiens

<400> 5252
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Met Asn Arg Arg Val Ile Ser Ala Asn Pro Tyr Leu Gly Gly Thr Ser
 1               5                  10                  15
Asn Gly Tyr Ala His Pro Ser Gly Thr Ala Leu His Tyr Asp Asp Val
            20                  25                  30
Pro Cys Ile Asn Gly Ser Gly Glu Pro Glu Asp Gly Phe Pro Ala Phe
        35                  40                  45
Cys Ser Arg Ser Leu Gly Glu Glu Gly Ala Phe Glu Asn Pro Gly Leu
    50                  55                  60
Tyr Asp Asn Trp Pro Pro Pro His Ile Phe Ala Arg Tyr Ser Pro Ala
65                  70                  75                  80
Asp Arg Lys Ala Ser Arg Leu Ser Ala Asp Lys Leu Ser Ser Asn His
                85                  90                  95
Tyr Lys Tyr Pro Ala Ser Ala Gln Ser Val Thr Asn Thr Ser Ser Val
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100 105 110
Gly Arg Ala Ser Leu Gly Leu Asn Ser Gln Pro Gln
115 120

<210> 5253
<211> 898
<212> DNA
<213> Homo sapiens

<400> 5253
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ccacagtgca tttccagtcc agcaaatgga aatctgggga gtctatactt tgctcacaac
120
tcatctcaat gccatccttg tggagagcca cagtgtagtg caaggttcca tccaattcac
180
tgtggacaag gtcttggagc aacatcacca ggctgccaag gctcagcaga aactacaggc
240
ctcactctca gtggctgtga actccatcat gagtattctg actggaagca ctaggagcag
300
cttccgaaag atgtgtctcc agacccttca agcagctgac acacaagagt tcaggaccaa
360
actgcacaaa gtatttcgtg agatcaccca acaccaattt cttcaccact gctcatgtga
420
ggtgaagcag cagctaaccc tagaaaaaaa ggactcagcc cagggcactg aggacgcacc
480
tgataacagc agcctggagc tcctagcaga taccagcggg caagcagaaa acaagaggct
540
caagaggggc agcccccgca tagaggagat gcgagctctg cgctctgcca gggccccgag
600
cccgtcagag gccgccccgc gccgcccgga agccaccgcg gccccctca ctcctagagg
660
aagggagcac cgcgaggctc acggcagggc cctggcgccg ggcagggcga gcctcggaag
720
ccgcctggag gacgtgctgt ggctgcagga ggtctccaac ctgtcagagt ggctgagtcc
780
cagccctggg ccctgagccg ggtccccttc cgcaagcgcc caccgatccg gaggctgcgg
840
gcagccgtta tcccgtggtt taataaagct gccgcgcgct caaaaaaaaa aaaaaaaa
898

<210> 5254
<211> 56
<212> PRT
<213> Homo sapiens

<400> 5254
Gln Gln Pro Gly Ala Pro Ser Arg Tyr Gln Arg Ala Ser Arg Lys Gln
1 5 10 15
Glu Ala Gln Glu Gly Gln Pro Pro His Arg Gly Asp Ala Ser Ser Ala
20 25 30
Leu Cys Gln Gly Pro Glu Pro Val Arg Gly Arg Pro Ala Pro Pro Gly
35 40 45
Ser His Arg Gly Pro Pro His Ser

50 55

<210> 5255
<211> 1410
<212> DNA
<213> Homo sapiens

<400> 5255
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caaccccaga tccccatgcc tcgagccctg gatctccaag ctcagctgct ggattctgga
120
tgtcaacaaa cctcaccact ggatcctgac aaccacaatg cctggatcct ggggcccccа
180
tcactggatc ccagatcccc tcactccacc cactggattc ctgcattggt ttttggtttt
240
ttgttttttt ttaacctcga cactgggtct cagatccttc tgctgactgc cagatccctg
300
catttcaagc actacgcctt ccacccccag gcactggatc ccagattccc aagccttcac
360
ccaccagatt ctggctccta aaacaagtgc gggggcccca gtggcacagc aagtggatcc
420
tggcaactgc agctgctgga ttccagattc tgggtcccca atccctctgc ccagtccctc
480
aatgttgaaa cctcatctct tgaaggcaga tcctgatatt ccaaggcact gaatcccaag
540
ccctgaatcc ccggtttctg atctgaatct tccaggcgcc gggtcccaaa tgttcaggcc
600
ccaagtctag atcctggcag cccagtcaca gagtatccca cacacactgg tgcccagagc
660
cggcttctca tgacatgaaa ttgcatggtc gagggagtct gtggggaagg aagcccaggt
720
cctggctgca acctgcacgg atgctggatt ccccctcacc ccacctctgc atggccaccc
780
cctcccagcc ctgtggggaa actgttccct ggaaccactc cactccctgc atccccacac
840
ttcacagcat cttccatccc cctcccacct tctaggcgaa tagtccccag agctgtgttc
900
ctccaagggg tccgaggaat cactcactcc tggaggctgg caaggagaca gtctgaggcc
960
agggacacat gaagggatgt ccccacccca gcactatcag ggcctcccca ggcttccaga
1020
gttgaaagcc aggagaaaat cggcaaagac cacccttccc taaacccaag cacccaatga
1080
tgcaaaaaac aaaaacaaaa aaaaccacca aatccccaaa ttcattccag atctatttтt
1140
ctaccagaga gaggagcaaa gtcctcctcc cctgcgccct tacattctgc acttcatagt
1200
tggattctga gcttaggatc atctggagac cccatggagg gacttggaaa ggggaactgg
1260
gatttgggga ggggctggag gacttccgca cgcttccacc tccttcgacc tccactgcgc
1320
cccacctccc tgcctgtgtg tgttatttca aaggaaaaga acaaaaggaa taaatttтct
1380

aagctcttta aaaaaaaaaa aaaaaaaaaa
1410

<210> 5256
<211> 95
<212> PRT
<213> Homo sapiens

<400> 5256
Met Val Glu Gly Val Cys Gly Glu Gly Ser Pro Gly Pro Gly Cys Asn
1 5 10 15
Leu His Gly Cys Trp Ile Pro Pro His Pro Thr Ser Ala Trp Pro Pro
20 25 30
Pro Pro Ser Pro Val Gly Lys Leu Phe Pro Gly Thr Thr Pro Leu Pro
35 40 45
Ala Ser Pro His Phe Thr Ala Ser Ser Ile Pro Leu Pro Pro Ser Arg
50 55 60
Arg Ile Val Pro Arg Ala Val Phe Leu Gln Gly Val Arg Gly Ile Thr
65 70 75 80
His Ser Trp Arg Leu Ala Arg Arg Gln Ser Glu Ala Arg Asp Thr
85 90 95

<210> 5257
<211> 1366
<212> DNA
<213> Homo sapiens

<400> 5257
ncaggctctg tgttggttgg agcgagcatg tgggtctgca gtaccctgtg gcgggtgcga
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accccgcccg gcagtggcgg gggcctgctc ccagcttctg gctgtcacgg acctgccgcc
120
tcctcctact ccgcatccgc cgagcctgcc cgggtccgcg gccttgtcta tgggcaccac
180
ggggatccag ccaaggtcgt cgaactcaag aacctggagc tagctgctgt gagaggatca
240
gatgtccgtg tgaagatgct ggcggcccct atcaatccat ctgacataaa tatgatccaa
300
ggaaactacg gactccttcc tgaactgcct gctgttggag ggaacgaagg tgttgcacag
360
gtggtagcgg tgggcagcaa tgtgaccggg ctgaagccag gagactgggt gattccagca
420
aatgctggtt tagactcagg aacctggcgg accgaggctg tgttcagcga ggaagcactg
480
atccaagttc cgagtgacat ccctcttcag agcgctgcca ccctgggtgt caatccctgc
540
acagcctaca ggatgttgat ggacttcgag caactgcagc caggggattc tgtcatccag
600
aatgcatcca acagcggagt ggggcaagca gtcatccaga tcgccgcagc cctgggccta
660
agaaccatca atgtggtccg agacagacct gatatccaga agctgagtga cagactgaag
720
agtctggggg ctgagcatgt catcacagaa gaggagctaa gaaggcccga aatgaaaaac
780

ttctttaagg acatgcccca gccacggctt gctctcaact gtgttggtgg gaaaagctcc
840
acagagctgc tgcggcagtt agcgcgtgga ggaaccatgg taacctatgg ggggatggcc
900
aagcagcccg tcgtagcctc tgtgagcctg ctcattttta aggatctcaa acttcgaggc
960
ttttggttgt cccagtggaa gaaggatcac agtccagacc agttcaagga gctgatcctc
1020
acactgtgcg atctcatccg ccgaggccag ctcacagccc ctgcctgctc ccaggtcccg
1080
ctgcaggact accagtctgc cttggaagcc tccatgaagc ccttcatatc ttcaaagcag
1140
attctcacca tgtgatcatc ccaaaagagc tggagtgaca tgggagggga ggcggatctg
1200
aggggctggg tgcaggcccc tcagttgggg ctcccacctt ccccagacta ctgttctcct
1260
cactgcctct tcctattagg aggatggtga agccagccac ggttttcccc agggccagcc
1320
ttaaggtatc taataaagtc tgaactctcc cttccaaaaa aaaaaa
1366

<210> 5258
<211> 375
<212> PRT
<213> Homo sapiens

<400> 5258
Met Trp Val Cys Ser Thr Leu Trp Arg Val Arg Thr Pro Pro Gly Ser
1 5 10 15
Gly Gly Gly Leu Leu Pro Ala Ser Gly Cys His Gly Pro Ala Ala Ser
20 25 30
Ser Tyr Ser Ala Ser Ala Glu Pro Ala Arg Val Arg Gly Leu Val Tyr
35 40 45
Gly His His Gly Asp Pro Ala Lys Val Val Glu Leu Lys Asn Leu Glu
50 55 60
Leu Ala Ala Val Arg Gly Ser Asp Val Arg Val Lys Met Leu Ala Ala
65 70 75 80
Pro Ile Asn Pro Ser Asp Ile Asn Met Ile Gln Gly Asn Tyr Gly Leu
85 90 95
Leu Pro Glu Leu Pro Ala Val Gly Gly Asn Glu Gly Val Ala Gln Val
100 105 110
Val Ala Val Gly Ser Asn Val Thr Gly Leu Lys Pro Gly Asp Trp Val
115 120 125
Ile Pro Ala Asn Ala Gly Leu Asp Ser Gly Thr Trp Arg Thr Glu Ala
130 135 140
Val Phe Ser Glu Glu Ala Leu Ile Gln Val Pro Ser Asp Ile Pro Leu
145 150 155 160
Gln Ser Ala Ala Thr Leu Gly Val Asn Pro Cys Thr Ala Tyr Arg Met
165 170 175
Leu Met Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser Val Ile Gln Asn
180 185 190
Ala Ser Asn Ser Gly Val Gly Gln Ala Val Ile Gln Ile Ala Ala Ala
195 200 205
Leu Gly Leu Arg Thr Ile Asn Val Val Arg Asp Arg Pro Asp Ile Gln

```
    210                 215                 220
Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu His Val Ile Thr
225                 230                 235                 240
Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe Phe Lys Asp Met
                245                 250                 255
Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly Lys Ser Ser Thr
            260                 265                 270
Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met Val Thr Tyr Gly
        275                 280                 285
Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser Leu Leu Ile Phe
    290                 295                 300
Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln Trp Lys Lys Asp
305                 310                 315                 320
His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr Leu Cys Asp Leu
                325                 330                 335
Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser Gln Val Pro Leu
            340                 345                 350
Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys Pro Phe Ile Ser
        355                 360                 365
Ser Lys Gln Ile Leu Thr Met
    370                 375
```

<210> 5259
<211> 306
<212> DNA
<213> Homo sapiens

<400> 5259
ctgaattgct gtgagggcag aacacccaag gagacaatag aaaatttgtt gcacagaatg
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actgaagaga agacgctgac tgctgagggt ttggtaaaac tcctccaggc tgtgaagacg
120
actttcccaa acctgggcct tctgctagag aagttgcaga aatcagccac tttgccaagc
180
accacagtcc aaccaagccc tgatgattat gggactgagc tattgagacg ctatcatgaa
240
aacctctctg agattttcac agacaaccag attttattaa agatgatctc acacatgaca
300
agttta
306

<210> 5260
<211> 83
<212> PRT
<213> Homo sapiens

<400> 5260
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Met Thr Glu Glu Lys Thr Leu Thr Ala Glu Gly Leu Val Lys Leu Leu
 1               5                  10                  15
Gln Ala Val Lys Thr Thr Phe Pro Asn Leu Gly Leu Leu Leu Glu Lys
            20                  25                  30
Leu Gln Lys Ser Ala Thr Leu Pro Ser Thr Thr Val Gln Pro Ser Pro
        35                  40                  45
Asp Asp Tyr Gly Thr Glu Leu Leu Arg Arg Tyr His Glu Asn Leu Ser
```

50 55 60
Glu Ile Phe Thr Asp Asn Gln Ile Leu Leu Lys Met Ile Ser His Met
65 70 75 80
Thr Ser Leu

<210> 5261
<211> 2394
<212> DNA
<213> Homo sapiens

<400> 5261
ncggccgcca tggcgacccc ggccaggccc ggcgaggccg aggacgcggc cgagcggccc
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ctccaggatg agccggcggc ggcggcggca ggcccgggca agggtcgctt cctcgtccgc
120
atctgtttcc agggagacga gggcgcctgc ccgacccggg acttcgtggt aggagcgctt
180
atcctgcgct ccatcggcat ggacccgagc gacatctacg cggtcatcca gatcccgggc
240
agccgcgaat tcgacgtgag cttccgctca gcggagaagc tggccctgtt cctacgcgtc
300
tacgaggaga agcgggagca ggaggactgc tgggagaact ttgtggtgct ggggcggagc
360
aagtccagct tgaagacgct cttcatcctc ttccggaacg agacggtgga cgtggaggac
420
attgtgactt ggctcaagcg ccactgcgac gtgctggccg tgccggtgaa agtgaccgac
480
aggtttggga tctggaccgg ggagtacaaa tgcgagatcg agctgcgcca gggggagggc
540
ggggtcaggc acttgccagg ggccttcttc ctgggggccg agaggggcta cagctggtac
600
aaggggcagc ccaagacatg ctttaaatgt ggttcccgga cccacatgag cggcagctgc
660
acgcaggaca ggtgcttcag gtgcggggag gaggggcacc tgagccctta ctgccggaag
720
ggcatcgtgt gcaacctctg tggcaagcga ggacacgcct ttgcccagtg tcccaaagca
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840
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900
catttttat cgtttttgaa ggagatcttt ttaaaaccta caagagacat ctctctatgc
960
cttcttaaac cgagtttact ccatttcagc ctgttctgaa ttggtgactc tgtcaccaat
1020
aacgactgcg gagaactgta gcgtgcagat gtgttgcccc tccctttttaa aattttattt
1080
tcgtttttct attgggtatt tgttttgttt cttgtacttt ttctctctct ccttgccccc
1140
ctcccgccct ccccgcccca taccttttct tcccctggat tttcaccctt tgggctgcct
1200
tgctcatctt tatgccccag cactaggtac ggggcccaac acgtggtagg cactccatca
1260

gtgtttgctg aattgaaaac attgttgact gtggcttcta tcagagtgtc tacctttgc
1320
agctcttccc ctccctcatt taatttgctg cttttaatct acgtggtctg agaatttgtg
1380
aaaccagtgt tgttagaagt gtatataatc tgaatcaata agctctgaat ggtggccaag
1440
ggcctctctt atggcacaaa gatgcatgga cttcatgaca gctcttttgg tggctcagaa
1500
gccatttttt atagaatcat ggaatctaga atattcctgc tggaaagaac ctgagagttg
1560
gtttggacca attccctggt tttccagcag atgaaacagg cccaaagagg ttaaatgact
1620
gggtgaaaat cacatagctg tctggtgcca gagccagcct atagtagagt cccctgaccc
1680
caagcccggt gctcattcca ctacctctca cacttcacaa caatttcctc aacacttgag
1740
ggcccagaaa gtctgatctc tccagaatga tcagcccaga ggaatgctga gaaatcacct
1800
ggaggaggga gcagaaagag aaggttttta aggaggggct tctgaatact tgggagatac
1860
ggaacggacc aaggaccaca ctccagggtg cattcgttgc tccctggggc accacttctg
1920
gattacagtg tgccaggtcc tttggaggcc ctacccccttc cccattcatt gccaccagtg
1980
agaaatgggg gtgcccctgt gtaaagaaac ctaccaaagg tttacatttg caccttagcc
2040
tcaatagcta cgaaccctag agaagcagct agctggagct catgtgcaac tcctgattct
2100
caggagaaag atggatttta acccaaaatt atgagtgagc tgttaactct aaaatgtact
2160
tgggagatag gccaagcgag aggtcatggg ccaactaagt gttatccagt agaaaagaca
2220
gtacactgct tttcttttag tgtttgcttt tcctttgcta tatgttttgc tatttccttg
2280
tggcttagaa tgtaaaattg attgttaaaa gttttgttct gaataaatat ttatcttttg
2340
tattgccaaa aaacacttga gggcccagaa agtctgatct ctccagaatg atca
2394

<210> 5262
<211> 275
<212> PRT
<213> Homo sapiens

<400> 5262
Xaa Ala Ala Met Ala Thr Pro Ala Arg Pro Gly Glu Ala Glu Asp Ala
1 5 10 15
Ala Glu Arg Pro Leu Gln Asp Glu Pro Ala Ala Ala Ala Ala Gly Pro
20 25 30
Gly Lys Gly Arg Phe Leu Val Arg Ile Cys Phe Gln Gly Asp Glu Gly
35 40 45
Ala Cys Pro Thr Arg Asp Phe Val Val Gly Ala Leu Ile Leu Arg Ser
50 55 60

```
Ile Gly Met Asp Pro Ser Asp Ile Tyr Ala Val Ile Gln Ile Pro Gly
70                  75                  80
Ser Arg Glu Phe Asp Val Ser Phe Arg Ser Ala Glu Lys Leu Ala Leu
                85                  90                  95
Phe Leu Arg Val Tyr Glu Glu Lys Arg Glu Gln Glu Asp Cys Trp Glu
            100                 105                 110
Asn Phe Val Val Leu Gly Arg Ser Lys Ser Ser Leu Lys Thr Leu Phe
        115                 120                 125
Ile Leu Phe Arg Asn Glu Thr Val Asp Val Glu Asp Ile Val Thr Trp
    130                 135                 140
Leu Lys Arg His Cys Asp Val Leu Ala Val Pro Val Lys Val Thr Asp
145                 150                 155                 160
Arg Phe Gly Ile Trp Thr Gly Glu Tyr Lys Cys Glu Ile Glu Leu Arg
                165                 170                 175
Gln Gly Glu Gly Gly Val Arg His Leu Pro Gly Ala Phe Phe Leu Gly
            180                 185                 190
Ala Glu Arg Gly Tyr Ser Trp Tyr Lys Gly Gln Pro Lys Thr Cys Phe
        195                 200                 205
Lys Cys Gly Ser Arg Thr His Met Ser Gly Ser Cys Thr Gln Asp Arg
    210                 215                 220
Cys Phe Arg Cys Gly Glu Glu Gly His Leu Ser Pro Tyr Cys Arg Lys
225                 230                 235                 240
Gly Ile Val Cys Asn Leu Cys Gly Lys Arg Gly His Ala Phe Ala Gln
                245                 250                 255
Cys Pro Lys Ala Val His Asn Ser Val Ala Ala Gln Leu Thr Gly Val
            260                 265                 270
Ala Gly His
        275
```

<210> 5263
<211> 319
<212> DNA
<213> Homo sapiens

<400> 5263
tctagaacaa atgagaacca gtatcagaag gtgacacagg agagtttgtg acagtgccga
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tttcagctga cgaattacca gaagatccag cattgctgtc gtttccatca aaagtagctg
120
gaagtagata cacattattt tctgacaggg gggaagtatc agaagaaagc atgttggttg
180
tgccttggaa aatctttttt ggttgatatt gaaatgccat ttcaccagtt tcaagccttc
240
ttcccaagag tgacttatct gtatcttact ttgtagcttc cattcagaca ttgttgctct
300
atttattaaa tccatggct
319

<210> 5264
<211> 105
<212> PRT
<213> Homo sapiens

<400> 5264

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Met Asp Leu Ile Asn Arg Ala Thr Met Ser Glu Trp Lys Leu Gln Ser
 1               5                  10                  15
Lys Ile Gln Ile Ser His Ser Trp Glu Glu Gly Leu Lys Leu Val Lys
            20                  25                  30
Trp His Phe Asn Ile Asn Gln Lys Arg Phe Ser Lys Ala Gln Pro Thr
        35                  40                  45
Cys Phe Leu Leu Ile Leu Pro Pro Cys Gln Lys Ile Met Cys Ile Tyr
    50                  55                  60
Phe Gln Leu Leu Leu Met Glu Thr Thr Ala Met Leu Asp Leu Leu Val
65                  70                  75                  80
Ile Arg Gln Leu Lys Ser Ala Leu Ser Gln Thr Leu Leu Cys His Leu
                85                  90                  95
Leu Ile Leu Val Leu Ile Cys Ser Arg
            100                 105
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<210> 5265
<211> 3203
<212> DNA
<213> Homo sapiens

<400> 5265
cgcccgggca ggtcggagac ggaggaaagg tggcagccag attacttaga gaggcacaga
60
ggagagagat cggggtgagt cgccatgggg actcccaggg cccagcaccc gccgcctccc
120
cagctgctgt tcctaattct gctgagctgt ccctggatcc agggtctgcc cctgaaggag
180
gaggagatat tgccagagcc tggaagtgag acccccacgg tggcctctga ggccctggct
240
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<211> 853
<212> PRT
<213> Homo sapiens

<400> 5266
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Glu Glu Ile Leu Pro Glu Pro Gly Ser Glu Thr Pro Thr Val Ala Ser
        35   40   45
Glu Ala Leu Ala Glu Leu Leu His Gly Ala Leu Leu Arg Arg Gly Pro
    50   55   60
Glu Met Gly Tyr Leu Pro Gly Pro Pro Leu Gly Pro Glu Gly Gly Glu
65   70   75   80
Glu Glu Thr Thr Thr Thr Ile Ile Thr Thr Thr Thr Val Thr Thr Thr
                85   90   95
Val Thr Ser Pro Val Leu Cys Asn Asn Asn Ile Ser Glu Gly Glu Gly
            100   105   110
Tyr Val Glu Ser Pro Asp Leu Gly Ser Pro Val Ser Arg Thr Leu Gly
        115   120   125
Leu Leu Asp Cys Thr Tyr Ser Ile His Val Tyr Pro Gly Tyr Gly Ile
    130   135   140
Glu Ile Gln Val Gln Thr Leu Asn Leu Ser Gln Glu Glu Glu Leu Leu
145   150   155   160
Val Leu Ala Gly Gly Gly Ser Pro Gly Leu Ala Pro Arg Leu Leu Ala
                165   170   175
Asn Ser Ser Met Leu Gly Glu Gly Gln Val Leu Arg Ser Pro Thr Asn
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Arg Leu Leu Leu His Phe Gln Ser Pro Arg Val Pro Arg Gly Gly Gly

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Phe Arg Ile His Tyr Gln Ala Tyr Leu Leu Ser Cys Gly Phe Pro Pro
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225                 230                 235                 240
Thr Ala Thr Phe His Cys Asp Ser Gly Tyr Gln Leu Gln Gly Glu Glu
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Thr Leu Ile Cys Leu Asn Gly Thr Arg Pro Ser Trp Asn Gly Glu Thr
            260                 265                 270
Pro Ser Cys Met Ala Ser Cys Gly Gly Thr Ile His Asn Ala Thr Leu
        275                 280                 285
Gly Arg Ile Val Ser Pro Glu Pro Gly Gly Ala Val Gly Pro Asn Leu
    290                 295                 300
Thr Cys Arg Trp Val Ile Glu Ala Ala Glu Gly Arg Arg Leu His Leu
305                 310                 315                 320
His Phe Glu Arg Val Ser Leu Asp Glu Asp Asn Asp Arg Leu Met Val
                325                 330                 335
Arg Ser Gly Gly Ser Pro Leu Ser Pro Val Ile Tyr Asp Ser Asp Met
            340                 345                 350
Asp Asp Val Pro Glu Arg Gly Leu Ile Ser Asp Ala Gln Ser Leu Tyr
        355                 360                 365
Val Glu Leu Leu Ser Glu Thr Pro Ala Asn Pro Leu Leu Leu Ser Leu
    370                 375                 380
Arg Phe Glu Ala Phe Glu Glu Asp Arg Cys Phe Ala Pro Phe Leu Ala
385                 390                 395                 400
His Gly Asn Val Thr Thr Thr Asp Pro Glu Tyr Arg Pro Gly Ala Leu
                405                 410                 415
Ala Thr Phe Ser Cys Leu Pro Gly Tyr Ala Leu Glu Pro Pro Gly Pro
            420                 425                 430
Pro Asn Ala Ile Glu Cys Val Asp Pro Thr Glu Pro His Trp Asn Asp
        435                 440                 445
Thr Glu Pro Ala Cys Lys Ala Met Cys Gly Gly Glu Leu Ser Glu Pro
    450                 455                 460
Ala Gly Val Val Leu Ser Pro Asp Trp Pro Gln Ser Tyr Ser Pro Gly
465                 470                 475                 480
Gln Asp Cys Val Trp Gly Val His Val Gln Glu Glu Lys Arg Ile Leu
                485                 490                 495
Leu Gln Val Glu Ile Leu Asn Val Arg Glu Gly Asp Met Leu Thr Leu
            500                 505                 510
Phe Asp Gly Asp Gly Pro Ser Ala Arg Val Leu Ala Gln Leu Arg Gly
        515                 520                 525
Pro Gln Pro Arg Arg Arg Leu Leu Ser Ser Gly Pro Asp Leu Thr Leu
    530                 535                 540
Gln Phe Gln Ala Pro Pro Gly Pro Pro Asn Pro Gly Leu Gly Gln Gly
545                 550                 555                 560
Phe Val Leu His Phe Lys Glu Val Pro Arg Asn Asp Thr Cys Pro Glu
                565                 570                 575
Leu Pro Pro Pro Glu Trp Gly Trp Arg Thr Ala Ser His Gly Asp Leu
            580                 585                 590
Ile Arg Gly Thr Val Leu Thr Tyr Gln Cys Glu Pro Gly Tyr Glu Leu
        595                 600                 605
Leu Gly Ser Asp Ile Leu Thr Cys Gln Trp Asp Leu Ser Trp Ser Ala
    610                 615                 620
Ala Pro Pro Ala Cys Gln Lys Ile Met Thr Cys Ala Asp Pro Gly Glu
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625 630 635 640
Ile Ala Asn Gly His Arg Thr Ala Ser Asp Ala Gly Phe Pro Val Gly
645 650 655
Ser His Val Gln Tyr Arg Cys Leu Pro Gly Tyr Ser Leu Glu Gly Ala
660 665 670
Ala Met Leu Thr Cys Tyr Ser Arg Asp Thr Gly Thr Pro Lys Trp Ser
675 680 685
Asp Arg Val Pro Lys Cys Ala Leu Lys Tyr Glu Pro Cys Leu Asn Pro
690 695 700
Gly Val Pro Glu Asn Gly Tyr Gln Thr Leu Tyr Lys His His Tyr Gln
705 710 715 720
Ala Gly Glu Ser Leu Arg Phe Phe Cys Tyr Glu Gly Phe Glu Leu Ile
725 730 735
Gly Glu Val Thr Ile Thr Cys Val Pro Gly His Pro Ser Gln Trp Thr
740 745 750
Ser Gln Pro Pro Leu Cys Lys Val Ala Tyr Glu Glu Leu Leu Asp Asn
755 760 765
Arg Lys Leu Glu Val Thr Gln Thr Thr Asp Pro Ser Arg Gln Leu Glu
770 775 780
Gly Gly Asn Leu Ala Leu Ala Ile Leu Leu Pro Leu Gly Leu Val Ile
785 790 795 800
Val Leu Gly Ser Gly Val Tyr Ile Tyr Tyr Thr Lys Leu Gln Gly Lys
805 810 815
Ser Leu Phe Gly Phe Ser Gly Ser His Ser Tyr Ser Pro Ile Thr Val
820 825 830
Glu Ser Asp Phe Ser Asn Pro Leu Tyr Glu Ala Gly Asp Thr Arg Glu
835 840 845
Tyr Glu Val Ser Ile
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<210> 5267
<211> 885
<212> DNA
<213> Homo sapiens

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120
attcccagtc ttcatttccc agccaccaaa ggacatctca gcaacagagc cattatccga
180
gcccccttctg ttagagaaat ttacatgaat gtacctgtag gggctgcggg agtgagagga
240
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300
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360
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420
cagaaaaata actggggaca gccagtgtac cagctgcact ctgctattgg acaagaccaa
480
agacagctat tcttgtacaa aataactatt cctgctctag ccagccagaa tcctgcaatc
540

caccctttca cacctccaaa gctgagtgcc tttgtggatg aagcaaagac gtatgcagcc
600
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720
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780
tatgaggtct acccaacttt tgcagtgact gcccgagggg atggatatgg caccttctga
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<210> 5268
<211> 279
<212> PRT
<213> Homo sapiens

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Tyr Ala Pro Gln Thr Tyr Ala Ala Ile Pro Ser Leu His Phe Pro Ala
35 40 45
Thr Lys Gly His Leu Ser Asn Arg Ala Ile Ile Arg Ala Pro Ser Val
50 55 60
Arg Glu Ile Tyr Met Asn Val Pro Val Gly Ala Ala Gly Val Arg Gly
65 70 75 80
Leu Gly Gly Arg Gly Tyr Leu Ala Tyr Thr Gly Leu Gly Arg Gly Tyr
85 90 95
Gln Val Lys Gly Asp Lys Arg Glu Asp Lys Leu Tyr Asp Ile Leu Pro
100 105 110
Gly Met Glu Leu Thr Pro Met Asn Pro Val Thr Leu Lys Pro Gln Gly
115 120 125
Ile Lys Leu Ala Pro Gln Ile Leu Glu Glu Ile Cys Gln Lys Asn Asn
130 135 140
Trp Gly Gln Pro Val Tyr Gln Leu His Ser Ala Ile Gly Gln Asp Gln
145 150 155 160
Arg Gln Leu Phe Leu Tyr Lys Ile Thr Ile Pro Ala Leu Ala Ser Gln
165 170 175
Asn Pro Ala Ile His Pro Phe Thr Pro Pro Lys Leu Ser Ala Phe Val
180 185 190
Asp Glu Ala Lys Thr Tyr Ala Ala Glu Tyr Thr Leu Gln Thr Leu Gly
195 200 205
Ile Pro Thr Asp Gly Gly Asp Gly Thr Met Ala Thr Ala Ala Ala Ala
210 215 220
Ala Thr Ala Phe Pro Gly Tyr Ala Val Pro Asn Ala Thr Ala Pro Val
225 230 235 240
Ser Ala Ala Gln Leu Lys Gln Ala Val Thr Leu Gly Gln Asp Leu Ala
245 250 255
Ala Tyr Thr Thr Tyr Glu Val Tyr Pro Thr Phe Ala Val Thr Ala Arg
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Gly Asp Gly Tyr Gly Thr Phe

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<211> 1177
<212> DNA
<213> Homo sapiens

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120
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180
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240
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300
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<212> PRT
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Gln Pro Ile Ser Glu Glu Glu Ala Ile Gln Ile Ile Ala Asp Pro Pro
35 40 45
Leu Pro Pro Ala Ser Phe Thr Leu Arg Asp Tyr Val Asp His Ser Glu
50 55 60
Thr Leu Gln Lys Leu Val Leu Leu Gly Val Asp Leu Ser Lys Ile Glu
65 70 75 80
Lys His Pro Glu Ala Ala Asn Leu Leu Leu Arg Leu Asp Phe Glu Lys
85 90 95
Asp Ile Lys Gln Met Leu Leu Phe Leu Lys Asp Val Gly Ile Glu Asp
100 105 110
Asn Gln Leu Gly Ala Phe Leu Thr Lys Asn His Ala Ile Phe Ser Glu
115 120 125
Asp Leu Glu Asn Leu Lys Thr Arg Val Ala Tyr Leu His Ser Lys Asn
130 135 140
Phe Ser Lys Ala Asp Val Ala Gln Met Val Arg Lys Ala Pro Phe Leu
145 150 155 160
Leu Asn Phe Ser Val Glu Arg Leu Asp Asn Arg Leu Gly Phe Phe Gln
165 170 175
Lys Glu Leu Glu Leu Ser Val Lys Lys Thr Arg Asp Leu Val Val Arg
180 185 190
Leu Pro Arg Leu Leu Thr Gly Ser Leu Glu Pro Val Lys Glu Asn Met
195 200 205
Lys Val Tyr Arg Leu Glu Leu Gly Phe Lys His Asn Glu Ile Gln His
210 215 220
Met Ile Thr Arg Ile Pro Lys Met Leu Thr Ala Asn Lys Met Lys Leu
225 230 235 240
Thr Glu Thr Phe Asp Phe Val His Asn Val Met Ser Ile Pro His His
245 250 255
Ile Ile Val Lys Phe Pro Gln Val Phe Asn Thr Arg Leu Phe Lys Val
260 265 270
Lys Glu Arg His Leu Phe Leu Thr Tyr Leu Gly Arg Ala Gln Tyr Asp
275 280 285
Pro Ala Lys Pro Asn Tyr Ile Ser Leu Asp Lys Leu Val Ser Ile Pro
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Asp Glu Ile Phe Cys Glu Glu Ile Ala Lys Ala Ser Val Gln Asp Phe
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Glu Lys Phe Leu Lys Thr Leu
325

<210> 5271
<211> 1185
<212> DNA
<213> Homo sapiens

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120

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<210> 5272
<211> 385
<212> PRT
<213> Homo sapiens

<400> 5272
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Glu Cys Gly Asn Val Thr Gly Ala Ser Ser Pro Ser Arg Thr Pro Phe
35 40 45
Gln Asn Pro Ser Leu Leu Leu Val His Lys Gln Lys Leu Ala Lys Trp
50 55 60
Val Ala Ile Gln Ser Val Ser Ala Trp Pro Glu Lys Arg Gly Glu Ile
65 70 75 80
Arg Arg Met Met Glu Val Ala Ala Ala Asp Val Lys Gln Leu Gly Gly

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Ser Val Glu Leu Val Asp Ile Gly Lys Gln Lys Leu Pro Asp Gly Ser
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Glu Ile Pro Leu Pro Pro Ile Leu Leu Gly Arg Leu Gly Ser Asp Pro
        115                 120                 125
Gln Lys Lys Thr Val Cys Ile Tyr Gly His Leu Asp Val Gln Pro Ala
    130                 135                 140
Ala Leu Glu Asp Gly Trp Asp Ser Glu Pro Phe Thr Leu Val Glu Arg
145                 150                 155                 160
Asp Gly Lys Leu Tyr Gly Arg Gly Ser Thr Asp Asp Lys Gly Pro Val
                165                 170                 175
Ala Gly Trp Ile Asn Ala Leu Glu Ala Tyr Gln Lys Thr Gly Gln Glu
            180                 185                 190
Ile Pro Val Asn Val Arg Phe Cys Leu Glu Gly Met Glu Glu Ser Gly
        195                 200                 205
Ser Glu Gly Leu Asp Glu Leu Ile Phe Ala Arg Lys Asp Thr Phe Phe
    210                 215                 220
Lys Asp Val Asp Tyr Val Cys Ile Ser Asp Asn Tyr Trp Leu Gly Lys
225                 230                 235                 240
Lys Lys Pro Cys Ile Thr Tyr Gly Leu Arg Gly Ile Cys Tyr Phe Phe
                245                 250                 255
Ile Glu Val Glu Cys Ser Asn Lys Asp Leu His Ser Gly Val Tyr Gly
            260                 265                 270
Gly Ser Val His Glu Ala Met Thr Asp Leu Ile Leu Leu Met Gly Ser
        275                 280                 285
Leu Val Asp Lys Arg Gly Asn Ile Leu Ile Pro Gly Ile Asn Glu Ala
    290                 295                 300
Val Ala Ala Val Thr Glu Glu Glu His Lys Leu Tyr Asp Asp Ile Asp
305                 310                 315                 320
Phe Asp Ile Glu Glu Phe Ala Lys Asp Val Gly Ala Gln Ile Leu Leu
                325                 330                 335
His Ser His Lys Lys Asp Ile Leu Met His Arg Trp Arg Tyr Pro Ser
            340                 345                 350
Leu Ser Leu His Gly Ile Glu Gly Ala Phe Ser Gly Ser Gly Ala Lys
        355                 360                 365
Thr Val Ile Pro Lys Lys Val Val Gly Lys Phe Ser Ile Arg Leu Val
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Pro
385
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<210> 5273
<211> 4580
<212> DNA
<213> Homo sapiens

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120
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180
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240

gcagcccttt caaagtaagc gctgaggttg aactcctgtg tgtcgttggc cttgatgccc
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360
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900
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960
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1020
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1080
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1140
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1200
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1320
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1380
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1440
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1920
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1980
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2040
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2100
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2160
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2220
ccagccctca catgtgtatg cacatttgcc agaatataag agttttgttt taaatacagt
2280
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2340
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2400
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2460
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2520
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2580
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2640
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2700
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2760
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2820
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2880
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3060
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3180
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3300
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3360
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3480

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3720
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3780
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3840
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4140
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4260
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4320
gtgaattttt ctggacagaa aagggagagc taccaaattg ttttttttctt tttaaaagga
4380
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4440
atgtcttaca ttacaaaggt aaaaaaaaaa aaaaaaaaaa cccaaaaatt ttttataccg
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4560
taattacacc attctcccat
4580

<210> 5274
<211> 185
<212> PRT
<213> Homo sapiens

<400> 5274
Met Ser Gly Ser Phe Glu Leu Ser Val Gln Asp Leu Asn Asp Leu Leu
1 5 10 15
Ser Asp Gly Ser Gly Cys Tyr Ser Leu Pro Ser Gln Pro Cys Asn Glu
20 25 30
Val Thr Pro Arg Ile Tyr Val Gly Asn Ala Ser Val Ala Gln Asp Ile
35 40 45
Pro Lys Leu Gln Lys Leu Gly Ile Thr His Val Leu Asn Ala Ala Glu
50 55 60
Gly Arg Ser Phe Met His Val Asn Thr Asn Ala Asn Phe Tyr Lys Asp

65 70 75 80
Ser Gly Ile Thr Tyr Leu Gly Ile Lys Ala Asn Asp Thr Gln Glu Phe
85 90 95
Asn Leu Ser Ala Tyr Phe Glu Arg Ala Ala Asp Phe Ile Asp Gln Ala
100 105 110
Leu Ala Gln Lys Asn Gly Arg Val Leu Val His Cys Arg Glu Gly Tyr
115 120 125
Ser Arg Ser Pro Thr Leu Val Ile Ala Tyr Leu Met Met Arg Gln Lys
130 135 140
Met Asp Val Lys Ser Ala Leu Ser Ile Val Arg Gln Asn Arg Glu Ile
145 150 155 160
Gly Pro Asn Asp Gly Phe Leu Ala Gln Leu Cys Gln Leu Asn Asp Arg
165 170 175
Leu Ala Lys Glu Gly Lys Leu Lys Pro
180 185

<210> 5275
<211> 810
<212> DNA
<213> Homo sapiens

<400> 5275
nntctcgctc aggctcggtt ttaccccgga gtctattcga agggggctgc tacgtcagcg
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cgtctcagcg taagacggcg ctattccgct gtaacagctt ccggcgggtc ctggatgttg
120
atgtcctgca tctaacgcgg tgtgaccccc gaagccgagc gagctccgga ggaatttcag
180
tatctgctac ggtaacttca tcagcccgcc aagatggcga tgcaagcggc caagagggcg
240
aacattcgac ttccacctga agtaaatcgg atattgtata taagaaattt gccatacaaa
300
atcacagctg aagaaatgta tgatatattt gggaaatatg gacctattcg tcaaatcaga
360
gtggggaaca cacctgaaac tagaggaaca gcttatgtgg tctatgagga catctttgat
420
gccaagaatg catgtgatca cctatcggga ttcaatgttt gtaacagata ccttgtggtt
480
ttgtactata atgccaacag ggcatttcag aagatggaca caaagaagaa ggaggaacag
540
ttgaagcttc tcaaggagaa atatggcatc aacacagatc caccaaaata aatgttttct
600
acattttcat ttggactaaa tcccacgaat gacaactacc acctttttt ccttttaat
660
taatactaaa tattgtgatt tcttatttga ggttcaaaat gacctgcttg aaactttgat
720
acatattgga atacattatg ttaataaact tgtagctttt tgtgaaacaa aaaaaaaaag
780
tcgacgcggc cggcaattta gtagtagtag
810

<210> 5276
<211> 125
<212> PRT

<213> Homo sapiens

<400> 5276
Met Ala Met Gln Ala Ala Lys Arg Ala Asn Ile Arg Leu Pro Pro Glu
1 5 10 15
Val Asn Arg Ile Leu Tyr Ile Arg Asn Leu Pro Tyr Lys Ile Thr Ala
20 25 30
Glu Glu Met Tyr Asp Ile Phe Gly Lys Tyr Gly Pro Ile Arg Gln Ile
35 40 45
Arg Val Gly Asn Thr Pro Glu Thr Arg Gly Thr Ala Tyr Val Val Tyr
50 55 60
Glu Asp Ile Phe Asp Ala Lys Asn Ala Cys Asp His Leu Ser Gly Phe
65 70 75 80
Asn Val Cys Asn Arg Tyr Leu Val Val Leu Tyr Tyr Asn Ala Asn Arg
85 90 95
Ala Phe Gln Lys Met Asp Thr Lys Lys Lys Glu Glu Gln Leu Lys Leu
100 105 110
Leu Lys Glu Lys Tyr Gly Ile Asn Thr Asp Pro Pro Lys
115 120 125

<210> 5277
<211> 612
<212> DNA
<213> Homo sapiens

<400> 5277
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gtggcggcca tcacggccac ggagctgctc atcgtggtga agtacgaccc ccacacgctc
120
accctgtccc tgcccttcta catctcccag tgctggaccc tcggctccgt cctggcgctc
180
acctggaccg tctggcgctt cttcctgcgg gacatcacat tgaggtacaa ggagacccgg
240
tggcagaagt ggcagaacaa ggatgaccag ggcagcaccg tcggcaacgg ggaccagcac
300
ccactggggc tggacgaaga cctgctgggg cctggggtgg ccgagggcga gggagcacca
360
actccaaact gacctgggcc gtggctgcct cgtgagcctc ccagagccca ggcctccgtg
420
gcctcctcct gtgtgagtcc caccaggagc cacgtgcccg gccttgccct caaggttttt
480
tgcttttctc ctgtgcacct ggcgaggctg aaggcgaggg gtggaggagg ccccagcaca
540
gcctcatctc catgtgtaca cgtgtgtacg tgtgtatgcg tgtgtgtacg tgtgtatgcg
600
tgtgtgtacg tg
612

<210> 5278
<211> 123
<212> PRT
<213> Homo sapiens

<400> 5278
Ile Tyr Asp Phe Met Asp Asp Pro Lys Pro His Lys Lys Leu Gly Pro
1 5 10 15
Gln Ala Trp Leu Val Ala Ala Ile Thr Ala Thr Glu Leu Leu Ile Val
20 25 30
Val Lys Tyr Asp Pro His Thr Leu Thr Leu Ser Leu Pro Phe Tyr Ile
35 40 45
Ser Gln Cys Trp Thr Leu Gly Ser Val Leu Ala Leu Thr Trp Thr Val
50 55 60
Trp Arg Phe Phe Leu Arg Asp Ile Thr Leu Arg Tyr Lys Glu Thr Arg
65 70 75 80
Trp Gln Lys Trp Gln Asn Lys Asp Asp Gln Gly Ser Thr Val Gly Asn
85 90 95
Gly Asp Gln His Pro Leu Gly Leu Asp Glu Asp Leu Leu Gly Pro Gly
100 105 110
Val Ala Glu Gly Glu Gly Ala Pro Thr Pro Asn
115 120

<210> 5279
<211> 1225
<212> DNA
<213> Homo sapiens

<400> 5279
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cctgactttc agctgcaggc catgattcag gcagcaggaa agcttgtgtt gattgataaa
120
ctactcccta agctgattgc aggtggccac aaagtactca tcttctccca gatggtgcgc
180
tgcctcgaca tcctagaaga ttatttaatc cagagaagat acacctatga acgtattgat
240
gggcgagtac ggggaaacct gcgccaggct gccatcgacc gcttcagcaa gcctgactca
300
gaccgctttg tcttcttact gtgcaccaga gcgggaggcc tggggatcaa tctcacagct
360
gctgatacct gcatcatatt tgattctgac tggaacccac aaaatgactt gcaggctcag
420
gcccgatgtc accgcatagg ccagagcaaa gctgtgaagg tgtatcgcct catcactcga
480
aattcctacg agcgcgagat gtttgacaag gccagcctaa agctggggct ggacaaggct
540
gttcttcaga catcaaccga aagggcggca ccaatgggta cagcactctc aaaaatggag
600
gtggaggacc tactccggaa aggtgcttat ggagccttaa tggatgaaga agatgaaggc
660
tccaagttct gtgaagaaga catagaccag attctgcaga ggcgaacgca caccatcacc
720
atccagtctg aggggaaagg gtccactttt gccaaggcta gctttgtggc ttcaggaaac
780
agaacagata tttccttaga tgatcctaac ttttggcaga aatgggctaa aatagctgaa
840
ctagacactg aagcaaagaa tgaaaaggaa agcttagtga tcgaccgacc tcgcgtgaga
900

aagcagacca aacactacaa ctcgtttgag gaagacgagc tcatggagtt ttcagagtta
960
gacagcgact cagacgaaag gcccacgaga tccaggcgcc tcaatgacaa agccaggcgc
1020
tacctccgag cggagtgctt ccgggtagag aagaacctgc tcatctttgg ctggggccgg
1080
tggaaggaca tcctgactca tggccgattc aagtggcatc tgaacgagaa ggacatggag
1140
atgatttgcc gtgccctcct ggtgtactgt gtcaagcatt ataaggggga cgagaagatc
1200
aagagtttca tttgggaact gatca
1225

<210> 5280
<211> 408
<212> PRT
<213> Homo sapiens

<400> 5280
Ile Asn Gly Ala Glu Glu Lys Ile Leu Glu Asp Phe Arg Lys Thr His
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Ser Pro Asp Ala Pro Asp Phe Gln Leu Gln Ala Met Ile Gln Ala Ala
20 25 30
Gly Lys Leu Val Leu Ile Asp Lys Leu Leu Pro Lys Leu Ile Ala Gly
35 40 45
Gly His Lys Val Leu Ile Phe Ser Gln Met Val Arg Cys Leu Asp Ile
50 55 60
Leu Glu Asp Tyr Leu Ile Gln Arg Arg Tyr Thr Tyr Glu Arg Ile Asp
65 70 75 80
Gly Arg Val Arg Gly Asn Leu Arg Gln Ala Ala Ile Asp Arg Phe Ser
85 90 95
Lys Pro Asp Ser Asp Arg Phe Val Phe Leu Leu Cys Thr Arg Ala Gly
100 105 110
Gly Leu Gly Ile Asn Leu Thr Ala Ala Asp Thr Cys Ile Ile Phe Asp
115 120 125
Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala Arg Cys His
130 135 140
Arg Ile Gly Gln Ser Lys Ala Val Lys Val Tyr Arg Leu Ile Thr Arg
145 150 155 160
Asn Ser Tyr Glu Arg Glu Met Phe Asp Lys Ala Ser Leu Lys Leu Gly
165 170 175
Leu Asp Lys Ala Val Leu Gln Thr Ser Thr Glu Arg Ala Ala Pro Met
180 185 190
Gly Thr Ala Leu Ser Lys Met Glu Val Glu Asp Leu Leu Arg Lys Gly
195 200 205
Ala Tyr Gly Ala Leu Met Asp Glu Glu Asp Glu Gly Ser Lys Phe Cys
210 215 220
Glu Glu Asp Ile Asp Gln Ile Leu Gln Arg Arg Thr His Thr Ile Thr
225 230 235 240
Ile Gln Ser Glu Gly Lys Gly Ser Thr Phe Ala Lys Ala Ser Phe Val
245 250 255
Ala Ser Gly Asn Arg Thr Asp Ile Ser Leu Asp Asp Pro Asn Phe Trp
260 265 270
Gln Lys Trp Ala Lys Ile Ala Glu Leu Asp Thr Glu Ala Lys Asn Glu

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        275                 280                 285
Lys Glu Ser Leu Val Ile Asp Arg Pro Arg Val Arg Lys Gln Thr Lys
    290                 295                 300
His Tyr Asn Ser Phe Glu Glu Asp Glu Leu Met Glu Phe Ser Glu Leu
305                 310                 315                 320
Asp Ser Asp Ser Asp Glu Arg Pro Thr Arg Ser Arg Arg Leu Asn Asp
                325                 330                 335
Lys Ala Arg Arg Tyr Leu Arg Ala Glu Cys Phe Arg Val Glu Lys Asn
            340                 345                 350
Leu Leu Ile Phe Gly Trp Gly Arg Trp Lys Asp Ile Leu Thr His Gly
        355                 360                 365
Arg Phe Lys Trp His Leu Asn Glu Lys Asp Met Glu Met Ile Cys Arg
    370                 375                 380
Ala Leu Leu Val Tyr Cys Val Lys His Tyr Lys Gly Asp Glu Lys Ile
385                 390                 395                 400
Lys Ser Phe Ile Trp Glu Leu Ile
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<210> 5281
<211> 336
<212> DNA
<213> Homo sapiens

<400> 5281
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aaatgcaaac cgcccaaaat aaataccagg agcttaagaa tatttgcagc tatagggctc
120
aggcattcct ggtactcaca ggtctgacag ccacagttgg agacacagct atttcttcag
180
aagagaaaac acaacgcatg tcattaatga gacatcacat gggacaatca ttgtccaaag
240
aagttgcaca tgtcctcacc aaacctggag cagatcacga ttgggaaaac ctagagaaag
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acttgagatt gctcattaat ggggattatg aagaag
336

<210> 5282
<211> 91
<212> PRT
<213> Homo sapiens

<400> 5282
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Met Gln Thr Ala Gln Asn Lys Tyr Gln Glu Leu Lys Asn Ile Cys Ser
 1               5                  10                  15
Tyr Arg Ala Gln Ala Phe Leu Val Leu Thr Gly Leu Thr Ala Thr Val
            20                  25                  30
Gly Asp Thr Ala Ile Ser Ser Glu Glu Lys Thr Gln Arg Met Ser Leu
        35                  40                  45
Met Arg His His Met Gly Gln Ser Leu Ser Lys Glu Val Ala His Val
    50                  55                  60
Leu Thr Lys Pro Gly Ala Asp His Asp Trp Glu Asn Leu Glu Lys Asp
65                  70                  75                  80
Leu Arg Leu Leu Ile Asn Gly Asp Tyr Glu Glu
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85 90

<210> 5283
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 5283
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ggcaagtgta acctacattc ccagcccacc agcctgacgc ccagccaggg agagagtacc
120
atggatggca tcattgaaca gaagagcatg ctggtgcaca gtaaaatcag tgatgctggc
180
aagaggaatg gtttaattaa caccagaaac ttgatggccg agagcagaga tggtctggtg
240
tctgtttacc cagcgcccca gtaccagagc caccgggtgg gggccagcac agtgccggcc
300
agcctggaca gcagcaggag tgagccgatg cagcagctgc tggaccccaa caccctgcag
360
cagtcagtgg agtcccgcta ccggcccaac atcatcctct attcagaggg cgtgctgcgc
420
tcctgggggg acggtgtggc cgccgactgc tgcgagacca ccttcatcga ggaccggtcg
480
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600
agcgactact caagcgacac agagagtgag gacaatttcc tcatgatgcc cccgcgggac
660
cacctgggcc tcagtgtctt ctccatgctc tgctgcttct ggcctctggg catcgcagcc
720
ttctacttgt cccatgagac caacaaagcc gtggccaagg gggacttgca ccaggccagc
780
accagctccc ggcgggccct attcctggca gtgctgtcca tcaccattgg gactggcgtc
840
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900
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960
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1020
ttcctaccca tggatttatt ttgtttttat cctttaattt catgttcaca gcactgtgta
1080
gagcaccaga cagacgggca ctgctaatcc ttccaaagga aagctccaaa gatcccagcc
1140
cgcaaggctg tctctggatg gattctggtg gatgaatggc aacgcggctc tctgcagcct
1200
gccagtgccc agagtgccac cgcattagca atatacaaac agtccaaaaa agtgtttatt
1260
ttttatggaa tacggtgcaa taggcagagg acaagggaca catcactctt ctgtctgtgg
1320
ccctgctgga gtcctttgtg ccccccggag tccacacgcc ttccctgcaa gacgagaatg
1380

gggctgggaa gaaagaggca acaccacggc tggcaggagc cccgctgcac tgctctgcag
1440
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1560
cacagctacc ccgcagcaat acgcactctt gggacctcgc tgatctagga tggggaggca
1620
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1680
ggcactgcag ctatgggcac tgcctcagcc taaagacaca ggggcgcctc ccaatcaccg
1740
cgctggcgga tgctcacccc gtcataagca gaaactagtg atcctggaaa tgagatgggc
1800
cttactctgt cgactaaatg aatagctatt ttcttgtcat tttttaaagt gcaactcttg
1860
cttcatgctg cttaagttac cagatgaatg ctgagaaata agtaatcaca gacattttaa
1920
taccatttca ttgctgtttt acgagtgttc attacttaac aaaaaattat cttttagctt
1980
tttcgctta
1989

<210> 5284
<211> 258
<212> PRT
<213> Homo sapiens

<400> 5284
Met Asp Gly Ile Ile Glu Gln Lys Ser Met Leu Val His Ser Lys Ile
1 5 10 15
Ser Asp Ala Gly Lys Arg Asn Gly Leu Ile Asn Thr Arg Asn Leu Met
20 25 30
Ala Glu Ser Arg Asp Gly Leu Val Ser Val Tyr Pro Ala Pro Gln Tyr
35 40 45
Gln Ser His Arg Val Gly Ala Ser Thr Val Pro Ala Ser Leu Asp Ser
50 55 60
Ser Arg Ser Glu Pro Met Gln Gln Leu Leu Asp Pro Asn Thr Leu Gln
65 70 75 80
Gln Ser Val Glu Ser Arg Tyr Arg Pro Asn Ile Ile Leu Tyr Ser Glu
85 90 95
Gly Val Leu Arg Ser Trp Gly Asp Gly Val Ala Ala Asp Cys Cys Glu
100 105 110
Thr Thr Phe Ile Glu Asp Arg Ser Pro Thr Lys Asp Ser Leu Glu Tyr
115 120 125
Pro Asp Gly Lys Phe Ile Asp Leu Ser Ala Asp Asp Ile Lys Ile His
130 135 140
Thr Leu Ser Tyr Asp Val Glu Glu Glu Glu Glu Phe Gln Glu Leu Glu
145 150 155 160
Ser Asp Tyr Ser Ser Asp Thr Glu Ser Glu Asp Asn Phe Leu Met Met
165 170 175
Pro Pro Arg Asp His Leu Gly Leu Ser Val Phe Ser Met Leu Cys Cys
180 185 190
Phe Trp Pro Leu Gly Ile Ala Ala Phe Tyr Leu Ser His Glu Thr Asn

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        195                 200                 205
Lys Ala Val Ala Lys Gly Asp Leu His Gln Ala Ser Thr Ser Ser Arg
    210                 215                 220
Arg Ala Leu Phe Leu Ala Val Leu Ser Ile Thr Ile Gly Thr Gly Val
225                 230                 235                 240
Tyr Val Gly Val Ala Val Ala Leu Ile Ala Tyr Leu Ser Lys Asn Asn
                245                 250                 255
His Leu
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<210> 5285
<211> 2155
<212> DNA
<213> Homo sapiens

<400> 5285
nnacgcgtgc agcaaagaat ggaggagtcg gaacccgaac ggaagcgggc tcgcaccgac
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gaggtgcctg ccggaggaag ccgctccgag gcggaagatg aggacgacga ggactacgtg
120
ccctatgtgc cgttacggca gcgccggcag ctactgctcc agaagctgct gcagcgaaga
180
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gacgacatcc cgctaggccc tcagtccaac gtcagcctcc tggatcagca ccagcacctt
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420
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840
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1140

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1320
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1380
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1860
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1920
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1980
cagctcagct ggcctggaat gggccaggct ggtcctggct gcctgttccc tgtgctcttc
2040
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2100
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa
2155

<210> 5286
<211> 628
<212> PRT
<213> Homo sapiens

<400> 5286
Xaa Arg Val Gln Gln Arg Met Glu Glu Ser Glu Pro Glu Arg Lys Arg
1 5 10 15
Ala Arg Thr Asp Glu Val Pro Ala Gly Gly Ser Arg Ser Glu Ala Glu
20 25 30
Asp Glu Asp Asp Glu Asp Tyr Val Pro Tyr Val Pro Leu Arg Gln Arg
35 40 45
Arg Gln Leu Leu Leu Gln Lys Leu Leu Gln Arg Arg Arg Lys Gly Ala
50 55 60
Ala Glu Glu Glu Gln Gln Asp Ser Gly Ser Glu Pro Arg Gly Asp Glu
65 70 75 80
Asp Asp Ile Pro Leu Gly Pro Gln Ser Asn Val Ser Leu Leu Asp Gln
85 90 95
His Gln His Leu Lys Glu Lys Ala Glu Ala Arg Lys Glu Ser Ala Lys

```
            100                 105                 110
Glu Lys Gln Leu Lys Glu Glu Glu Lys Ile Leu Glu Ser Val Ala Glu
        115                 120                 125
Gly Arg Ala Leu Met Ser Val Lys Glu Met Ala Lys Gly Ile Thr Tyr
    130                 135                 140
Asp Asp Pro Ile Lys Thr Ser Trp Thr Pro Pro Arg Tyr Val Leu Ser
145                 150                 155                 160
Met Ser Glu Glu Arg His Glu Arg Val Arg Lys Lys Tyr His Ile Leu
                165                 170                 175
Val Glu Gly Asp Gly Ile Pro Pro Pro Ile Lys Ser Phe Lys Glu Met
            180                 185                 190
Lys Phe Pro Ala Ala Ile Leu Arg Gly Leu Lys Lys Lys Gly Ile His
        195                 200                 205
His Pro Thr Pro Ile Gln Ile Gln Gly Ile Pro Thr Ile Leu Ser Gly
    210                 215                 220
Arg Asp Met Ile Gly Ile Ala Phe Thr Gly Ser Gly Lys Thr Leu Val
225                 230                 235                 240
Phe Thr Leu Pro Val Ile Met Phe Cys Leu Glu Gln Glu Lys Arg Leu
                245                 250                 255
Pro Phe Ser Lys Arg Glu Gly Pro Tyr Gly Leu Ile Ile Cys Pro Ser
            260                 265                 270
Arg Glu Leu Ala Arg Gln Thr His Gly Ile Leu Glu Tyr Tyr Cys Arg
        275                 280                 285
Leu Leu Gln Glu Asp Ser Ser Pro Leu Leu Arg Cys Ala Leu Cys Ile
    290                 295                 300
Gly Gly Met Ser Val Lys Glu Gln Met Glu Thr Ile Arg His Gly Val
305                 310                 315                 320
His Met Met Val Ala Thr Pro Gly Arg Leu Met Asp Leu Leu Gln Lys
                325                 330                 335
Lys Met Val Ser Leu Asp Ile Cys Arg Tyr Leu Ala Leu Asp Glu Ala
            340                 345                 350
Asp Arg Met Ile Asp Met Gly Phe Glu Gly Asp Ile Arg Thr Ile Phe
        355                 360                 365
Ser Tyr Phe Lys Gly Gln Arg Gln Thr Leu Leu Phe Ser Ala Thr Met
    370                 375                 380
Pro Lys Lys Ile Gln Asn Phe Ala Lys Ser Ala Leu Val Lys Pro Val
385                 390                 395                 400
Thr Ile Asn Val Gly Arg Ala Gly Ala Ala Ser Leu Asp Val Ile Gln
                405                 410                 415
Glu Val Glu Tyr Val Lys Glu Glu Ala Lys Met Val Tyr Leu Leu Glu
            420                 425                 430
Cys Leu Gln Lys Thr Pro Pro Pro Val Leu Ile Phe Ala Glu Lys Lys
        435                 440                 445
Ala Asp Val Asp Ala Ile His Glu Tyr Leu Leu Leu Lys Gly Val Glu
    450                 455                 460
Ala Val Ala Ile His Gly Gly Lys Asp Gln Glu Glu Arg Thr Lys Ala
465                 470                 475                 480
Ile Glu Ala Phe Arg Glu Gly Lys Lys Asp Val Leu Val Ala Thr Asp
                485                 490                 495
Val Ala Ser Lys Gly Leu Asp Phe Pro Ala Ile Gln His Val Ile Asn
            500                 505                 510
Tyr Asp Met Pro Glu Glu Ile Glu Asn Tyr Val His Arg Ile Gly Arg
        515                 520                 525
Thr Gly Arg Ser Gly Asn Thr Gly Ile Ala Thr Thr Phe Ile Asn Lys
```

```
    530                 535                 540
Ala Cys Asp Glu Ser Val Leu Met Asp Leu Lys Ala Leu Leu Leu Glu
545                 550                 555                 560
Ala Lys Gln Lys Val Pro Pro Val Leu Gln Val Leu His Cys Gly Asp
                565                 570                 575
Glu Ser Met Leu Asp Ile Gly Gly Glu Arg Gly Cys Ala Phe Cys Gly
            580                 585                 590
Gly Leu Gly His Arg Ile Thr Asp Cys Pro Lys Leu Glu Ala Met Gln
        595                 600                 605
Thr Lys Gln Val Ser Asn Ile Gly Arg Lys Asp Tyr Leu Ala His Ser
    610                 615                 620
Ser Met Asp Phe
625
```

<210> 5287
<211> 581
<212> DNA
<213> Homo sapiens

<400> 5287
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agccccgcgc cgcactccat ccccacaggc tggggacggg ccaggtgcgg ctgtgtgggt
120
tcgggagcgg agttgcagaa tccaaggacc cattttgttc tttctccgca ctgctttatg
180
ggaggcatta tggcccccaa agacataatg acaaatactc atgctaaatc catcctcaat
240
tcaatgaact ccctcaggaa gagcaatacc ctctgtgatg tgacattgag agtagagcag
300
aaagacttcc ctgcccatcg gattgtgctg gctgcctgta gtgattactt ctgtgccatg
360
ttcactagtg agctctcaga gaaggggaaa ccttatgttg acatccaagg tttgactgcc
420
tctaccatgg aaattttatt ggactttgtg tacacagaaa cggtacatgt gacagtggag
480
aatgtacaag aactgcttcc tgcagcctgt ctgcttcagt tgaaaggtgt gaaacaagcc
540
tgctgtgagt tcttagaaag tcagttggac ccttcacgcg t
581

<210> 5288
<211> 193
<212> PRT
<213> Homo sapiens

<400> 5288
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Xaa Glu Pro Pro Glu Pro Pro Gly Leu Gly Gly Ala Ser Ala Pro Pro
 1               5                  10                  15
Glu Pro Pro Ala Ser Pro Ala Pro His Ser Ile Pro Thr Gly Trp Gly
            20                  25                  30
Arg Ala Arg Cys Gly Cys Val Gly Ser Gly Ala Glu Leu Gln Asn Pro
        35                  40                  45
Arg Thr His Phe Val Leu Ser Pro His Cys Phe Met Gly Gly Ile Met
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```
    50                  55                  60
Ala Pro Lys Asp Ile Met Thr Asn Thr His Ala Lys Ser Ile Leu Asn
65                  70                  75                  80
Ser Met Asn Ser Leu Arg Lys Ser Asn Thr Leu Cys Asp Val Thr Leu
                85                  90                  95
Arg Val Glu Gln Lys Asp Phe Pro Ala His Arg Ile Val Leu Ala Ala
            100                 105                 110
Cys Ser Asp Tyr Phe Cys Ala Met Phe Thr Ser Glu Leu Ser Glu Lys
        115                 120                 125
Gly Lys Pro Tyr Val Asp Ile Gln Gly Leu Thr Ala Ser Thr Met Glu
    130                 135                 140
Ile Leu Leu Asp Phe Val Tyr Thr Glu Thr Val His Val Thr Val Glu
145                 150                 155                 160
Asn Val Gln Glu Leu Leu Pro Ala Ala Cys Leu Leu Gln Leu Lys Gly
                165                 170                 175
Val Lys Gln Ala Cys Cys Glu Phe Leu Glu Ser Gln Leu Asp Pro Ser
            180                 185                 190
Arg
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<210> 5289
<211> 361
<212> DNA
<213> Homo sapiens

<400> 5289
agatctctgt acacatgtta caccagacag ctatattcca tgccttgcag acctgtgcaa
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agcactatgg gaagttatgc tcagctatta taggactatg gaatggcatg aaaagcatga
120
caatgaggat actgcttcag cttctgaagg ggaagtatat gatagggtcc tgaagaaact
180
tattttgatc ggggctacat taaaaaagaa attagaacat ggacttacac gaatatggca
240
ggatgttcag ctaaaagtaa aaacctactt gcttggaact gatttgtcta tattcaaata
300
tgatgatttc atctttgttt tggatataat cagcaggttg atgcaagttg gagaagaatt
360
c
361

<210> 5290
<211> 95
<212> PRT
<213> Homo sapiens

<400> 5290
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Met Leu Ser Tyr Tyr Arg Thr Met Glu Trp His Glu Lys His Asp Asn
 1               5                  10                  15
Glu Asp Thr Ala Ser Ala Ser Glu Gly Glu Val Tyr Asp Arg Val Leu
            20                  25                  30
Lys Lys Leu Ile Leu Ile Gly Ala Thr Leu Lys Lys Lys Leu Glu His
        35                  40                  45
Gly Leu Thr Arg Ile Trp Gln Asp Val Gln Leu Lys Val Lys Thr Tyr
```

```
    50                  55                  60
Leu Leu Gly Thr Asp Leu Ser Ile Phe Lys Tyr Asp Asp Phe Ile Phe
65                  70                  75                  80
Val Leu Asp Ile Ile Ser Arg Leu Met Gln Val Gly Glu Glu Phe
                85                  90                  95
```

<210> 5291
<211> 767
<212> DNA
<213> Homo sapiens

<400> 5291
gtcgggaggt tctttgcgct gatagcaggg acgaagacca caccattgac caagaagatg
60
aagatggcca cgcagaagac tcccagcagg gcgtacatgc ccagctctag ctcagtgaca
120
tgctgagggg cagggaccat ctcctcctcc tcttcctcct cctccctggc tttggtctcc
180
tccttcctgg cctcctcctc tgcccgctca aacttgcccc tcacacctgt gttgcccccg
240
acactgcctg ccacctgccg tttaccaccc atggtggctt ctgtggctgg tgggctccaa
300
gcagggctgg atggggagag caggggctgg agtggaggca gggggcagcc ccacccaggc
360
ggtgccagag gccaaaggca cacggtggcg gccccggcgn gcagggctcg ggcgggtgca
420
gagccacatg cagcggcagc ccctcggcgc ctgccccact caccaccacc ccgagctggg
480
caccctgctc ctcagctggc aggatggcac caggctcctc ggctgaaacg gacagtccca
540
gtcaggcggt cgtagagctc agctgggcca cagtgtgatc agagaaggac agccataggg
600
agagggccac ctcctgtggg gcacacagac acaggcagag acatgcgagg gcacgcacgc
660
atgcacagag aaaccactcc cacagagaca ggccacatgg aggagagacc agagagaaaa
720
cagagacaca ggcagataga caaaacacag ggagagaggg gacgcgt
767

<210> 5292
<211> 142
<212> PRT
<213> Homo sapiens

<400> 5292
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Gly Ala Gly Thr Ile Ser Ser Ser Ser Ser Ser Ser Ser Leu Ala Leu
 1               5                  10                  15
Val Ser Ser Phe Leu Ala Ser Ser Ser Ala Arg Ser Asn Leu Pro Leu
            20                  25                  30
Thr Pro Val Leu Pro Pro Thr Leu Pro Ala Thr Cys Arg Leu Pro Pro
        35                  40                  45
Met Val Ala Ser Val Ala Gly Gly Leu Gln Ala Gly Leu Asp Gly Glu
    50                  55                  60
Ser Arg Gly Trp Ser Gly Gly Arg Gly Gln Pro His Pro Gly Gly Ala
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65 70 75 80
Arg Gly Gln Arg His Thr Val Ala Ala Pro Ala Xaa Arg Ala Arg Ala
85 90 95
Gly Ala Glu Pro His Ala Ala Ala Ala Pro Arg Arg Leu Pro His Ser
100 105 110
Pro Pro Pro Arg Ala Gly His Pro Ala Pro Gln Leu Ala Gly Trp His
115 120 125
Gln Ala Pro Arg Leu Lys Arg Thr Val Pro Val Arg Arg Ser
130 135 140

<210> 5293
<211> 1428
<212> DNA
<213> Homo sapiens

<400> 5293
tcagactgtg tgggtggttt ccccggccgc agctccgtac gggcttggat tgctgggcct
60
cggtgcaccc cagcctcccc cactcgggtt ctgagcttga gctggcggct ctttaactct
120
gcttcactgt tgctcttggc aacatccact tccgggagcg agtgccgttt cccccgctca
180
ccgcgggcta gggagcgtgg gattccggac tgtgagcggc tgttagtgcg tcgcagctgc
240
tggcgatccg gcgaccctcg gccggcagga cccgcgggcc acgcagccgg ggccttctca
300
acgcctcagt acctcggcgg gaccgccatg gttctgctgc acgtgaagcg gggcgacgag
360
agccagttcc tgctgcaggc gcctgggagt accgagctgg aggagctcac ggtgcaggtg
420
gcccgggtct ataatgggcg gctcaaggtg cagcgcctct gctcagaaat ggaagaatta
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540
gaattgaaat tgaaggatga atggggtgaa aaatgcgtac ccagcggagg tgcagtgttt
600
aaaaaggatg atattggacg aaggaatggg caagctccaa atgagaagat gaagcaagtg
660
ttaaagaaga ctatagaaga agccaaggca ataatatcta agaaacaagt ggaagccggt
720
gtctgtgtta ccatggagat ggtgaaagat gccttggacc agcttcgagg cgcggtgatg
780
attgtttacc ccatggggtt gccaccgtat gatcccatcc gcatggagtt tgaaaataag
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gaagacttgt cgggaacaca ggcagggctc aacgtcatta aagaggcaga ggcgcagctg
900
tggtgggcag ccaaggagct gagaagaacg aagaagcttt cagactacgt ggggaagaat
960
gaaaaaacca aaattatcgc caagattcag caaaggggac agggagctcc agcccgagag
1020
cctattatta gcagtgagga gcagaagcag ctgatgctgt actatcacag aagacaagag
1080
gagctcaaga gattggaaga aaatgatgat gatgcctatt taaactcacc atgggcggat
1140

aacactgctt tgaaaagaca ttttcatgga gtgaaagaca taaagtggag accaagatga
1200
agttcaccag ctgatgacac ttccaaagag attagctcac ctttctccta ggcaattata
1260
atttaaaaaa aaaaaaaagg ccacttactg ccctctgtaa aagatgttaa catttctagt
1320
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1380
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1428

<210> 5294
<211> 290
<212> PRT
<213> Homo sapiens

<400> 5294
Met Val Leu Leu His Val Lys Arg Gly Asp Glu Ser Gln Phe Leu Leu
1 5 10 15
Gln Ala Pro Gly Ser Thr Glu Leu Glu Glu Leu Thr Val Gln Val Ala
20 25 30
Arg Val Tyr Asn Gly Arg Leu Lys Val Gln Arg Leu Cys Ser Glu Met
35 40 45
Glu Glu Leu Ala Glu His Gly Ile Phe Leu Pro Pro Asn Met Gln Gly
50 55 60
Leu Thr Asp Asp Gln Ile Glu Glu Leu Lys Leu Lys Asp Glu Trp Gly
65 70 75 80
Glu Lys Cys Val Pro Ser Gly Gly Ala Val Phe Lys Lys Asp Asp Ile
85 90 95
Gly Arg Arg Asn Gly Gln Ala Pro Asn Glu Lys Met Lys Gln Val Leu
100 105 110
Lys Lys Thr Ile Glu Glu Ala Lys Ala Ile Ile Ser Lys Lys Gln Val
115 120 125
Glu Ala Gly Val Cys Val Thr Met Glu Met Val Lys Asp Ala Leu Asp
130 135 140
Gln Leu Arg Gly Ala Val Met Ile Val Tyr Pro Met Gly Leu Pro Pro
145 150 155 160
Tyr Asp Pro Ile Arg Met Glu Phe Glu Asn Lys Glu Asp Leu Ser Gly
165 170 175
Thr Gln Ala Gly Leu Asn Val Ile Lys Glu Ala Glu Ala Gln Leu Trp
180 185 190
Trp Ala Ala Lys Glu Leu Arg Arg Thr Lys Lys Leu Ser Asp Tyr Val
195 200 205
Gly Lys Asn Glu Lys Thr Lys Ile Ile Ala Lys Ile Gln Gln Arg Gly
210 215 220
Gln Gly Ala Pro Ala Arg Glu Pro Ile Ile Ser Ser Glu Glu Gln Lys
225 230 235 240
Gln Leu Met Leu Tyr Tyr His Arg Arg Gln Glu Glu Leu Lys Arg Leu
245 250 255
Glu Glu Asn Asp Asp Asp Ala Tyr Leu Asn Ser Pro Trp Ala Asp Asn
260 265 270
Thr Ala Leu Lys Arg His Phe His Gly Val Lys Asp Ile Lys Trp Arg
275 280 285
Pro Arg

290

<210> 5295
<211> 1451
<212> DNA
<213> Homo sapiens

<400> 5295
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aacacataag agttttgact tcacggcagt tcatactggg acctcagacc actgaaggca
120
gacagtaacg agcagtgctg gccgggcccc actttcagag ggggcggaag ggcatcttga
180
cacgtgtcat atggtaagag gcgcatccac tcacccaggc ctggtgcagg actctgcaag
240
gccctcctga gtaaagagtg gccacgaagg gctgctaggc agcacctact cttggaatca
300
agcagggaaa aagtgcaaaa ttggagctgg cgggaggtgt gtgtgcctgc cccacagatg
360
gctgtggtga gccacaaagc accaagattc tgttcttcat tcagcaacca cccatgagcc
420
tcctgcttta ttccaatcgc atggcaccag cctgaaaacc tctctccctt ctgagaggaa
480
tgctggaatg acactccact ctgcccctcc ctccctcctt ccttgctcag ggtccatgtg
540
aacagcaggc cattgttggg aagtgcctgt tgcagtcatt cttacacccc cacagccact
600
gccccacaca cccactggtg gctaccaagg cccgtcaata gatcttgtgt ccaccgagcc
660
ctggtgtcca ggtccagcag ccagacaggc tgaaggttcc ctcctgccat cacagagtag
720
ccaagcacta caaagaggtt ttcatggcca gattcctgac ggctggcccc ttacagggca
780
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840
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900
aagctcatcc tggttgaggg ggttcaagtt aaaacccttc agctccggtt tgccttgggc
960
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1020
cagatgatct tgatcttttt caatcatttc ctttgtctca gggtgaggca tcttgataaa
1080
catgttcccg aagcaaacca tcacatcttc agagaggctg agatccttct gcagggccct
1140
caggccctct cgattctgat tccttttagt gtccaggtcc acaatctgcc gcttgtccgc
1200
cagcacctcc tcggcgagct cctccacttc tacaaggtac cgcagcactc gctctgcctc
1260
gggtgatagc atagcgccca ccaactccgc ttgcggctct cgcgcgaccc cgggatctcc
1320
gcttcgggaa catgtttatc aagatgcctc accctgagac aaaggaaatg attgaaaaag
1380

atcaagatca tctggataaa gaaatagaaa aactgcggaa gcaacttaaa gtgaaggtcc
1440
ccttcacgcg t
1451

<210> 5296
<211> 133
<212> PRT
<213> Homo sapiens

<400> 5296
Met Leu Ser Pro Glu Ala Glu Arg Val Leu Arg Tyr Leu Val Glu Val
1 5 10 15
Glu Glu Leu Ala Glu Glu Val Leu Ala Asp Lys Arg Gln Ile Val Asp
20 25 30
Leu Asp Thr Lys Arg Asn Gln Asn Arg Glu Gly Leu Arg Ala Leu Gln
35 40 45
Lys Asp Leu Ser Leu Ser Glu Asp Val Met Val Cys Phe Gly Asn Met
50 55 60
Phe Ile Lys Met Pro His Pro Glu Thr Lys Glu Met Ile Glu Lys Asp
65 70 75 80
Gln Asp His Leu Asp Lys Glu Ile Glu Lys Leu Arg Lys Gln Leu Lys
85 90 95
Val Lys Val Asn Arg Leu Phe Glu Ala Gln Gly Lys Pro Glu Leu Lys
100 105 110
Gly Phe Asn Leu Asn Pro Leu Asn Gln Asp Glu Leu Lys Ala Leu Lys
115 120 125
Val Ile Leu Lys Gly
130

<210> 5297
<211> 5318
<212> DNA
<213> Homo sapiens

<400> 5297
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agcttcccat tgctgagagc tcctgctgtt gattgtggaa aaggacacct cttctgctgg
120
gagtgccttg gtgaagcaca tgagccttgt gactgccaaa catggaagaa ttggctgcaa
180
aaaataaccg aaatgaaacc agaagaactt gtgggagtta gtgaagccta cgaggatgcc
240
gccaattgtc tctggttatt aactaactcc aagccttgtg ccaactgtaa gtctccaata
300
cagaagaatg aaggctgcaa tcacatgcag tgtgctaagt gcaagtatga cttttgctgg
360
atttgccttg aagagtggaa aaaacatagt tcgtccactg gaggttatta cggatgtact
420
cgctatgaag tcattcaaca cgtggaggag caatccaagg aaatgactgt ggaggctgag
480
aaaaaacaca aacgatttca ggaacttgac agatttatgc actattatac aagatttaaa
540

aaccatgagc atagttatca gctagaacaa cgccttctta aaacagccaa agaaaagatg
600
gagcaattga gcagagctct caaagaaact gaaggaggct gtccagatac cactttcatt
660
gaagatgcag ttcatgtgct cttaaaaact cggcgcattc tcaagtgttc ttatccatat
720
ggatttttct tggaacctaa aagcacaaag aaagaaattt ttgaactaat gcaaacagac
780
ctagaaatgg tcactgaaga ccttgcccag aaagtcaata ggccttacct tcgcacaccc
840
cgccacaaga tcatcaaagc agcatgcctt gtacagcaga agaggcaaga attcctggca
900
tctgtggctc ggggagtagc tcctgcagac tcaccagaag ctccaaggcg cagctttgct
960
ggtggaacat gggattggga atatttagga tttgcatcac cagaggaata tgctgaattt
1020
cagtatcgga ggaggcacag acaacgtcgt cgaggagatg ttcacagtct actcagtaat
1080
cctccagacc ctgatgagcc aagtgaaagc actttagata ttccagaagg cggcagcagc
1140
agccgcaggc ctggcacatc cgtggtaagt tctgcatcta tgagtgtgct gcacagctct
1200
tccctgcgtg actacacccc tgccagtcgc tctgaaaacc aggactctct tcaggctctg
1260
agttccttgg atgaagacga tcccaatata cttcttgcaa tacagttatc actgcaagag
1320
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Met Lys Pro Glu Glu Leu Val Gly Val Ser Glu Ala Tyr Glu Asp Ala
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6300
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6360
taacatttac aaatgacata ttgaaagcaa aggctgtttt atttagccaa gatgattacc
6420
attaggagtt actttatgta ttgttgaaag caaattttaa acatgatgtt ttagaagtgt
6480
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6540
ggaaatttat tatttcttgc aattcccgtg atagctctgt tctttatgca ttgtctcaac
6600
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6660
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa
6712

<210> 5302
<211> 1339
<212> PRT
<213> Homo sapiens

<400> 5302
Ala Pro Pro Ala Gly Arg Arg Arg Met Gln Ala Ala Pro Arg Ala Gly
1 5 10 15
Cys Gly Ala Ala Leu Leu Leu Trp Ile Val Ser Ser Cys Leu Cys Arg
20 25 30
Ala Trp Thr Ala Pro Ser Thr Ser Gln Lys Cys Asp Glu Pro Leu Val
35 40 45
Ser Gly Leu Pro His Val Ala Phe Ser Ser Ser Ser Ser Ile Ser Gly

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    50                  55                  60
Ser Tyr Ser Pro Gly Tyr Ala Lys Ile Asn Lys Arg Gly Gly Ala Gly
65                  70                  75                  80
Gly Trp Ser Pro Ser Asp Ser Asp His Tyr Gln Trp Leu Gln Val Asp
                85                  90                  95
Phe Gly Asn Arg Lys Gln Ile Ser Ala Ile Ala Thr Gln Gly Arg Tyr
            100                 105                 110
Ser Ser Ser Asp Trp Val Thr Gln Tyr Arg Met Leu Tyr Ser Asp Thr
        115                 120                 125
Gly Arg Asn Trp Lys Pro Tyr His Gln Asp Gly Asn Ile Trp Ala Phe
    130                 135                 140
Pro Gly Asn Ile Asn Ser Asp Gly Val Val Arg His Glu Leu Gln His
145                 150                 155                 160
Pro Ile Ile Ala Arg Tyr Val Arg Ile Val Pro Leu Asp Trp Asn Gly
                165                 170                 175
Glu Gly Arg Ile Gly Leu Arg Ile Glu Val Tyr Gly Cys Ser Tyr Trp
            180                 185                 190
Ala Asp Val Ile Asn Phe Asp Gly His Val Val Leu Pro Tyr Arg Phe
        195                 200                 205
Arg Asn Lys Lys Met Lys Thr Leu Lys Asp Val Ile Ala Leu Asn Phe
    210                 215                 220
Lys Thr Ser Glu Ser Glu Gly Val Ile Leu His Gly Glu Gly Gln Gln
225                 230                 235                 240
Gly Asp Tyr Ile Thr Leu Glu Leu Lys Lys Ala Lys Leu Val Leu Ser
                245                 250                 255
Leu Asn Leu Gly Ser Asn Gln Leu Gly Pro Ile Tyr Gly His Thr Ser
            260                 265                 270
Val Met Thr Gly Ser Leu Leu Asp Asp His His Trp His Ser Val Val
        275                 280                 285
Ile Glu Arg Gln Gly Arg Ser Ile Asn Leu Thr Leu Asp Arg Ser Met
    290                 295                 300
Gln His Phe Arg Thr Asn Gly Glu Phe Asp Tyr Leu Asp Leu Asp Tyr
305                 310                 315                 320
Glu Ile Thr Phe Gly Gly Ile Pro Phe Ser Gly Lys Pro Ser Ser Ser
                325                 330                 335
Ser Arg Lys Asn Phe Lys Gly Cys Met Glu Ser Ile Asn Tyr Asn Gly
            340                 345                 350
Val Asn Ile Thr Asp Leu Ala Arg Arg Lys Lys Leu Glu Pro Ser Asn
        355                 360                 365
Val Gly Asn Leu Ser Phe Ser Cys Val Glu Pro Tyr Thr Val Pro Val
    370                 375                 380
Phe Phe Asn Ala Thr Ser Tyr Leu Glu Val Pro Gly Arg Leu Asn Gln
385                 390                 395                 400
Asp Leu Phe Ser Val Ser Phe Gln Phe Arg Thr Trp Asn Pro Asn Gly
                405                 410                 415
Leu Leu Val Phe Ser His Phe Ala Asp Asn Leu Gly Asn Val Glu Ile
            420                 425                 430
Asp Leu Thr Glu Ser Lys Val Gly Val His Ile Asn Ile Thr Gln Thr
        435                 440                 445
Lys Met Ser Gln Ile Asp Ile Ser Ser Gly Ser Gly Leu Asn Asp Gly
    450                 455                 460
Gln Trp His Glu Val Arg Phe Leu Ala Lys Glu Asn Phe Ala Ile Leu
465                 470                 475                 480
Thr Ile Asp Gly Asp Glu Ala Ser Ala Val Arg Thr Asn Ser Pro Leu
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                485                 490                 495
Gln Val Lys Thr Gly Glu Lys Tyr Phe Phe Gly Gly Phe Leu Asn Gln
            500                 505                 510
Met Asn Asn Ser Ser His Ser Val Leu Gln Pro Ser Phe Gln Gly Cys
        515                 520                 525
Met Gln Leu Ile Gln Val Asp Asp Gln Leu Val Asn Leu Tyr Glu Val
    530                 535                 540
Ala Gln Arg Lys Pro Gly Ser Phe Ala Asn Val Ser Ile Asp Met Cys
545                 550                 555                 560
Ala Ile Ile Asp Arg Cys Val Pro Asn His Cys Glu His Gly Gly Lys
                565                 570                 575
Cys Ser Gln Thr Trp Asp Ser Phe Lys Cys Thr Cys Asp Glu Thr Gly
            580                 585                 590
Tyr Ser Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Pro Ser Cys Glu
        595                 600                 605
Ala Tyr Lys His Leu Gly Gln Thr Ser Asn Tyr Tyr Trp Ile Asp Pro
    610                 615                 620
Asp Gly Ser Gly Pro Leu Gly Pro Leu Lys Val Tyr Cys Asn Met Thr
625                 630                 635                 640
Glu Asp Lys Val Trp Thr Ile Val Ser His Asp Leu Gln Met Gln Thr
                645                 650                 655
Pro Val Val Gly Tyr Asn Pro Glu Lys Tyr Ser Val Thr Gln Leu Val
            660                 665                 670
Tyr Ser Ala Ser Met Asp Gln Ile Ser Ala Ile Thr Asp Ser Ala Glu
        675                 680                 685
Tyr Cys Glu Gln Tyr Val Ser Tyr Phe Cys Lys Met Ser Arg Leu Leu
    690                 695                 700
Asn Thr Pro Asp Gly Ser Pro Tyr Thr Trp Trp Val Gly Lys Ala Asn
705                 710                 715                 720
Glu Lys His Tyr Tyr Trp Gly Gly Ser Gly Pro Gly Ile Gln Lys Cys
                725                 730                 735
Ala Cys Gly Ile Glu Arg Asn Cys Thr Asp Pro Lys Tyr Tyr Cys Asn
            740                 745                 750
Cys Asp Ala Asp Tyr Lys Gln Trp Arg Lys Asp Ala Gly Phe Leu Ser
        755                 760                 765
Tyr Lys Asp His Leu Pro Val Ser Gln Val Val Val Gly Asp Thr Asp
    770                 775                 780
Arg Gln Gly Ser Glu Ala Lys Leu Ser Val Gly Pro Leu Arg Cys Gln
785                 790                 795                 800
Gly Asp Arg Asn Tyr Trp Asn Ala Ala Ser Phe Pro Asn Pro Ser Ser
                805                 810                 815
Tyr Leu His Phe Ser Thr Phe Gln Gly Glu Thr Ser Ala Asp Ile Ser
            820                 825                 830
Phe Tyr Phe Lys Thr Leu Thr Pro Trp Gly Val Phe Leu Glu Asn Met
        835                 840                 845
Gly Lys Glu Asp Phe Ile Lys Leu Glu Leu Lys Ser Ala Thr Glu Val
    850                 855                 860
Ser Phe Ser Phe Asp Val Gly Asn Gly Pro Val Glu Ile Val Val Arg
865                 870                 875                 880
Ser Pro Thr Pro Leu Asn Asp Asp Gln Trp His Arg Val Thr Ala Glu
                885                 890                 895
Arg Asn Val Lys Gln Ala Ser Leu Gln Val Asp Arg Leu Pro Gln Gln
            900                 905                 910
Ile Arg Lys Ala Pro Thr Glu Gly His Thr Arg Leu Glu Leu Tyr Ser
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915 920 925
Gln Leu Phe Val Gly Gly Ala Gly Gly Gln Gln Gly Phe Leu Gly Cys
930 935 940
Ile Arg Ser Leu Arg Met Asn Gly Val Thr Leu Asp Leu Glu Glu Arg
945 950 955 960
Ala Lys Val Thr Ser Gly Phe Ile Ser Gly Cys Ser Gly His Cys Thr
965 970 975
Ser Tyr Gly Thr Asn Cys Glu Asn Gly Gly Lys Cys Leu Glu Arg Tyr
980 985 990
His Gly Tyr Ser Cys Asp Cys Ser Asn Thr Ala Tyr Asp Gly Thr Phe
995 1000 1005
Cys Asn Lys Asp Val Gly Ala Phe Phe Glu Glu Gly Met Trp Leu Arg
1010 1015 1020
Tyr Asn Phe Gln Ala Pro Ala Thr Asn Ala Arg Asp Ser Ser Ser Arg
1025 1030 1035 1040
Val Asp Asn Ala Pro Asp Gln Gln Asn Ser His Pro Asp Leu Ala Gln
1045 1050 1055
Glu Glu Ile Arg Phe Ser Phe Ser Thr Thr Lys Ala Pro Cys Ile Leu
1060 1065 1070
Leu Tyr Ile Ser Ser Phe Thr Thr Asp Phe Leu Ala Val Leu Val Lys
1075 1080 1085
Pro Thr Gly Ser Leu Gln Ile Arg Tyr Asn Leu Gly Gly Thr Arg Glu
1090 1095 1100
Pro Tyr Asn Ile Asp Val Asp His Arg Asn Met Ala Asn Gly Gln Pro
1105 1110 1115 1120
His Ser Val Asn Ile Thr Arg His Glu Lys Thr Ile Phe Leu Lys Leu
1125 1130 1135
Asp His Tyr Pro Ser Val Ser Tyr His Leu Pro Ser Ser Ser Asp Thr
1140 1145 1150
Leu Phe Asn Ser Pro Lys Ser Leu Phe Leu Gly Lys Val Ile Glu Thr
1155 1160 1165
Gly Lys Ile Asp Gln Glu Ile His Lys Tyr Asn Thr Pro Gly Phe Thr
1170 1175 1180
Gly Cys Leu Ser Arg Val Gln Phe Asn Gln Ile Ala Pro Leu Lys Ala
1185 1190 1195 1200
Ala Leu Arg Gln Thr Asn Ala Ser Ala His Val His Ile Gln Gly Glu
1205 1210 1215
Leu Val Glu Ser Asn Cys Gly Ala Ser Pro Leu Thr Leu Ser Pro Met
1220 1225 1230
Ser Ser Ala Thr Asp Pro Trp His Leu Asp His Leu Asp Ser Ala Ser
1235 1240 1245
Ala Asp Phe Pro Tyr Asn Pro Gly Gln Gly Gln Ala Ile Arg Asn Gly
1250 1255 1260
Val Asn Arg Asn Ser Ala Ile Ile Gly Gly Val Ile Ala Val Val Ile
1265 1270 1275 1280
Phe Thr Ile Leu Cys Thr Leu Val Phe Leu Ile Arg Tyr Met Phe Arg
1285 1290 1295
His Lys Gly Thr Tyr His Thr Asn Glu Ala Lys Gly Ala Glu Ser Ala
1300 1305 1310
Glu Ser Ala Asp Ala Ala Ile Met Asn Asn Asp Pro Asn Phe Thr Glu
1315 1320 1325
Thr Ile Asp Glu Ser Lys Lys Glu Trp Leu Ile
1330 1335

<210> 5303
<211> 334
<212> DNA
<213> Homo sapiens

<400> 5303
cgtacgcacg ccactgacag ccgcccagca gaagtacaag aagggcgatg tggtctgcac
60
acccagcgga atacgaaaga agttcaacgg caagccgggg cgcccggctg ggctcacgag
120
atggctgcat gaaggagtca cagcggcgag gctactgctc acgccacctg tccatgcgaa
180
ccaaagagat ggaaggcctg gcagacagtg ggcctggcgg ggcgggccgg cccgcggccg
240
tggcagcccg tgagggcagc acggagtttg actggggtga tgagacgtcg agggacagtg
300
gaggccagca gtgtggcgac tcgtggagac tcac
334

<210> 5304
<211> 95
<212> PRT
<213> Homo sapiens

<400> 5304
Met Trp Ser Ala His Pro Ala Glu Tyr Glu Arg Ser Ser Thr Ala Ser
 1   5   10   15
Arg Gly Ala Arg Leu Gly Ser Arg Asp Gly Cys Met Lys Glu Ser Gln
            20   25   30
Arg Arg Gly Tyr Cys Ser Arg His Leu Ser Met Arg Thr Lys Glu Met
        35   40   45
Glu Gly Leu Ala Asp Ser Gly Pro Gly Gly Ala Gly Arg Pro Ala Ala
    50   55   60
Val Ala Ala Arg Glu Gly Ser Thr Glu Phe Asp Trp Gly Asp Glu Thr
65   70   75   80
Ser Arg Asp Ser Gly Gly Gln Gln Cys Gly Asp Ser Trp Arg Leu
                85   90   95

<210> 5305
<211> 582
<212> DNA
<213> Homo sapiens

<400> 5305
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60
cctctgtccc ccaggatgtc ttgtggtggc ggtcggccgt tctgcccccc agggcacccc
120
ctgttgtagg cactggctag ggaggggcag gcctccttcc tgcccctcga gacactcttg
180
ggagatgcat tttccgtctg gctcacaggg ggagggtgag gctttgtacc ccagcccctg
240
cccaggccac tgtgagggtg ggtgctggct gagcccctgg ggcagaagga gtggggcagg
300

cggggtcttt gttctcggct cccacagcag agccaggtga ggggggggcct gccaggacta
360
gacagaagtg gggcggcctg aaccctgctt ccagccatgg ccaggggcca cggaacccgg
420
caggggtgtc tgaagccgcc ctgtcagctg gccggtccaa gcctgtggct ggagctggtg
480
tgtgtttatc taataaagtc ccacaggtgc ctcaaaaaaa aaaaaaaaaa aaaaaaaaaa
540
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa
582

<210> 5306
<211> 62
<212> PRT
<213> Homo sapiens

<400> 5306
Met Ala Arg Gly His Gly Thr Arg Gln Gly Cys Leu Lys Pro Pro Cys
 1   5   10   15
Gln Leu Ala Gly Pro Ser Leu Trp Leu Glu Leu Val Cys Val Tyr Leu
            20   25   30
Ile Lys Ser His Arg Cys Leu Lys Lys Lys Lys Lys Lys Lys Lys Lys
        35   40   45
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
    50   55   60

<210> 5307
<211> 1551
<212> DNA
<213> Homo sapiens

<400> 5307
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60
ataaaactga gtgaaggctg ctatgacctg tgttcactct ggttacaggg aggtgcaaac
120
cattctgtct cccagccttt cttctctctt tgtgtgctcc cagcacttcc ttcttttcta
180
acatggcctg gagagagtct ctctctcctt gtctctgtct cttaataata gtttttaacg
240
tggacatctc ttccttggta cagtggtttt taaatactga gaagaaccaa gtcaggtttt
300
ttaaagcaga ctaaaagcat gaaattgctt tcagaagaat gtatatcatc gggaaaagtt
360
cgggggcaga gtgggggaat caggctttat tcaaaagaaa cagttgaaaa catgggactt
420
tttctaccca atgcccattt cacgactcct ctgagactaa ttgggaaacg gggaaattct
480
tggaattttt tttttaagaa actttttttgt gttttttttta attttaggtc acttattagt
540
gaaacctcat tttagatctg acattggtag atagatggat ttaggcaaat atgatgcgtt
600
tgtggggaat ccacgtggtt gacgttagaa cctcccttct gcagactgtt gcctgtcatc
660

taagcgaatt ggaaatgctg agcttccata agtcagctga gttttaaagg taaacgttat
720
ggctgaagta gtaaagcacc tgaccacaaa acctcttgta aaaacagccc tgagtaggta
780
tttccagggc tccacaaagt tgcttatggg aatcctgagc tgcttttcac catctcaaga
840
agcctaagaa gttatatatt taatcaggta gacaaaacag ttcaaagcat aaggtccatg
900
gtggtggaaa atggatgcaa gtgattctaa gtttgtggat ttgtggatag cagagggatc
960
gggacctctt ggaggaaccc tgggtaccaa gctcccaggc ccttcctcta tcatggatgc
1020
tgggtgactt tgggaagtca ccacctcttc ccaagcctgt ttcccatatc acagatgtgg
1080
ggccatggcc tcgatgatgg tctccacagg tctttccacc tctgtgagtc caagtcaggt
1140
caatcagcaa ggacccatct ctgccctggg tcagctcctc agaaccaacc cccagcatct
1200
ctaaagcaaa agcctcacct caagggctgc tcagaagaga gcaccttcag catgagttgt
1260
tgctggaaga tctaataagc tgtgtttcct gggaagtggt gctttactta gccctgtgga
1320
caacttctct atgcatctgt gtgagcagat gatcattgta ttacctttta tcggtagtaa
1380
gcttggaaaa ataatttaag aatacaatgg agaaatgtaa ataagtatct atgtaaattt
1440
gtttaaaata aactgaatgt atttaatggt ccatttatat gttcttttat gtaacatgta
1500
gtttaataaa gttcctgttt atgagagtca tgtttcatct cagcttcttc c
1551

<210> 5308
<211> 112
<212> PRT
<213> Homo sapiens

<400> 5308
Met Leu Gly Val Gly Ser Glu Glu Leu Thr Gln Gly Arg Asp Gly Ser
1 5 10 15
Leu Leu Ile Asp Leu Thr Trp Thr His Arg Gly Gly Lys Thr Cys Gly
20 25 30
Asp His His Arg Gly His Gly Pro Thr Ser Val Ile Trp Glu Thr Gly
35 40 45
Leu Gly Arg Gly Gly Asp Phe Pro Lys Ser Pro Ser Ile His Asp Arg
50 55 60
Gly Arg Ala Trp Glu Leu Gly Thr Gln Gly Ser Ser Lys Arg Ser Arg
65 70 75 80
Ser Leu Cys Tyr Pro Gln Ile His Lys Leu Arg Ile Thr Cys Ile His
85 90 95
Phe Pro Pro Pro Trp Thr Leu Cys Phe Glu Leu Phe Cys Leu Pro Asp
100 105 110

<210> 5309
<211> 2078

<212> DNA
<213> Homo sapiens

<400> 5309
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60
aacgccggcc actctaggat cctcactcgg ggagaggagg catagctcgc ggggtcaccc
120
tccacccgca acgtactccg ggtcggcctt gcgctcgggg cctgagaggg gcggcggcgg
180
ggtcaggggc cgcacaaaga atgaaccagc agtggaagag aaaatactgt aagctggctg
240
actgctggtg aagaaaatgc tttatttttg tggcaggcat ctgtgggatc tgtaatagaa
300
atgatggctg gctgtggtga aattgatcat tcaataaaca tgcttcctac aaacaggaaa
360
gcgaacgagt cctgttctaa tactgcacct tctttaaccg tccctgaatg tgccatttgt
420
ctgcaaacat gtgttcatcc agtcagtctg ccctgtaagc acgttttctg ctatctatgt
480
gtaaaaggag cttcatggct tggaaagcgg tgtgctcttt gtcgacaaga aattcccgag
540
gatttccttg acaagccaac cttgttgtca ccagaagaac tcaaggcagc aagtagagga
600
aatggtgaat atgcatggta ttatgaagga agaaatgggt ggtggcagta cgatgagcgc
660
actagtagag agctggaaga tgctttttcc aaaggtaaaa agaacactga aatgttaatt
720
gctggctttc tgtatgtcgc tgatcttgaa aacatggttc aatataggag aaatgaacat
780
ggacgtcgca ggaagattaa gcgagatata atagatatac caaagaaggg agtagctgga
840
cttaggctag actgtgatgc taataccgta aacctagcaa gagagagctc tgctgacgga
900
gcggacagtg tatcagcaca gagtggagct tctgttcagc ccctagtgtc ttctgtaagg
960
cccctaacat cagtagatgg tcagttaaca agccctgcaa caccatcccc tgatgcaagc
1020
acttctctgg aagactcttt tgctcattta caactcagtg gagacaacac agctgaaagg
1080
agtcataggg gagaaggaga agaagatcat gaatcaccat cttcaggcag ggtaccagca
1140
ccagacacct ccattgaaga aactgaatca gatgccagta gtgatagtga ggatgtatct
1200
gcagttgttg cacagcactc cttgacccaa cagagacttt tggtttctaa tgcaaaccag
1260
acagtacccg atcgatcaga tcgatcggga actgatcgat cagtagcagg gggtggaaca
1320
gtgagtgtca gtgtcagatc tagaaggcct gatggacagt gcacagtaac tgaagtttaa
1380
ataaaaatgt cttcagctcc atgctcaagg ttgaaagggt tacctgtaaa tttctgccca
1440
cataacatta tactcatccc tagtagtgca ttttgggagt tggggtggga aggggtatgg
1500

gaaggataga ctcataatta aaatgtctaa catgtctctg ttgagaaatt tatttaatgt
1560
aaggaacttg ggtgttaata gttgagagct gtttagtaat aacccagttt tcttgaggtc
1620
tgtttacttt atacttttta aaaacttctg tagttctttt ggccagtgtg tttgtattat
1680
ctgtgcatta atggtcctca tctgactcct gcattgtgtc ttatttttct gcatggattg
1740
gcataagacc attactaaaa tttggcacct gtgagatgtt tgatattatg aacaggaaac
1800
ataatttaat gtatgaatag atgtgaattt gggatttcaa aatagatgaa taacaactat
1860
tttatagtaa agttattgaa atggaaatga aaacagccag taacttatgt ttcagaatgt
1920
ttgtaacaca cttcatggtg ttcccatagg ctttgctgtc tagtcttata gtttgaggtt
1980
tttttggtct gcatttttct ttttgattac aaaatttata atttaataaa tactagagtt
2040
tatcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa
2078

<210> 5310
<211> 359
<212> PRT
<213> Homo sapiens

<400> 5310
Met Met Ala Gly Cys Gly Glu Ile Asp His Ser Ile Asn Met Leu Pro
1 5 10 15
Thr Asn Arg Lys Ala Asn Glu Ser Cys Ser Asn Thr Ala Pro Ser Leu
20 25 30
Thr Val Pro Glu Cys Ala Ile Cys Leu Gln Thr Cys Val His Pro Val
35 40 45
Ser Leu Pro Cys Lys His Val Phe Cys Tyr Leu Cys Val Lys Gly Ala
50 55 60
Ser Trp Leu Gly Lys Arg Cys Ala Leu Cys Arg Gln Glu Ile Pro Glu
65 70 75 80
Asp Phe Leu Asp Lys Pro Thr Leu Leu Ser Pro Glu Glu Leu Lys Ala
85 90 95
Ala Ser Arg Gly Asn Gly Glu Tyr Ala Trp Tyr Tyr Glu Gly Arg Asn
100 105 110
Gly Trp Trp Gln Tyr Asp Glu Arg Thr Ser Arg Glu Leu Glu Asp Ala
115 120 125
Phe Ser Lys Gly Lys Lys Asn Thr Glu Met Leu Ile Ala Gly Phe Leu
130 135 140
Tyr Val Ala Asp Leu Glu Asn Met Val Gln Tyr Arg Arg Asn Glu His
145 150 155 160
Gly Arg Arg Arg Lys Ile Lys Arg Asp Ile Ile Asp Ile Pro Lys Lys
165 170 175
Gly Val Ala Gly Leu Arg Leu Asp Cys Asp Ala Asn Thr Val Asn Leu
180 185 190
Ala Arg Glu Ser Ser Ala Asp Gly Ala Asp Ser Val Ser Ala Gln Ser
195 200 205
Gly Ala Ser Val Gln Pro Leu Val Ser Ser Val Arg Pro Leu Thr Ser

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    210                 215                 220
Val Asp Gly Gln Leu Thr Ser Pro Ala Thr Pro Ser Pro Asp Ala Ser
225                 230                 235                 240
Thr Ser Leu Glu Asp Ser Phe Ala His Leu Gln Leu Ser Gly Asp Asn
                245                 250                 255
Thr Ala Glu Arg Ser His Arg Gly Glu Gly Glu Glu Asp His Glu Ser
            260                 265                 270
Pro Ser Ser Gly Arg Val Pro Ala Pro Asp Thr Ser Ile Glu Glu Thr
        275                 280                 285
Glu Ser Asp Ala Ser Ser Asp Ser Glu Asp Val Ser Ala Val Val Ala
    290                 295                 300
Gln His Ser Leu Thr Gln Gln Arg Leu Leu Val Ser Asn Ala Asn Gln
305                 310                 315                 320
Thr Val Pro Asp Arg Ser Asp Arg Ser Gly Thr Asp Arg Ser Val Ala
                325                 330                 335
Gly Gly Gly Thr Val Ser Val Ser Val Arg Ser Arg Arg Pro Asp Gly
            340                 345                 350
Gln Cys Thr Val Thr Glu Val
        355
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<210> 5311
<211> 572
<212> DNA
<213> Homo sapiens

<400> 5311
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ctccacttcg tgcaccaggc ctacctgcag cagtggatca agagctccga cacgcgctgc
120
tgcgagctct gcaagtatga gttcatcatg gagaccaagc tgaagccact gagaaaatgg
180
gagaagttgc agatgacgtc cagcgagcgc aggaagatca tgtgctcagt gacattccac
240
gtcattgcca tcacatgtgt ggtctggtcc ttgtatgtgc tcattgaccg tcctgctgag
300
gagatcaagc aggggcaggc aacaggaatc ctagaatggc ccttttggac taaattggtg
360
gttgtggcca tcggcttcac cagaggactt ctttttatgt atgttcagtg taaagtgtat
420
gtgcaattgt ggaagagact caaggcctat aatagagtga tctatgttca aaactgtcca
480
gaaacaagca aaaagaatat ttttgaaaaa tctccactaa cagagcccaa ctttgaaaat
540
aaacatggat atggaatctg tcattccgac ac
572

<210> 5312
<211> 190
<212> PRT
<213> Homo sapiens

<400> 5312
Cys His Cys Glu Gly Asp Asp Glu Ser Pro Leu Ile Thr Pro Cys His

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 1               5                  10                  15
Cys Thr Gly Ser Leu His Phe Val His Gln Ala Tyr Leu Gln Gln Trp
            20                  25                  30
Ile Lys Ser Ser Asp Thr Arg Cys Cys Glu Leu Cys Lys Tyr Glu Phe
        35                  40                  45
Ile Met Glu Thr Lys Leu Lys Pro Leu Arg Lys Trp Glu Lys Leu Gln
    50                  55                  60
Met Thr Ser Ser Glu Arg Arg Lys Ile Met Cys Ser Val Thr Phe His
65                  70                  75                  80
Val Ile Ala Ile Thr Cys Val Val Trp Ser Leu Tyr Val Leu Ile Asp
                85                  90                  95
Arg Pro Ala Glu Glu Ile Lys Gln Gly Gln Ala Thr Gly Ile Leu Glu
            100                 105                 110
Trp Pro Phe Trp Thr Lys Leu Val Val Val Ala Ile Gly Phe Thr Arg
        115                 120                 125
Gly Leu Leu Phe Met Tyr Val Gln Cys Lys Val Tyr Val Gln Leu Trp
    130                 135                 140
Lys Arg Leu Lys Ala Tyr Asn Arg Val Ile Tyr Val Gln Asn Cys Pro
145                 150                 155                 160
Glu Thr Ser Lys Lys Asn Ile Phe Glu Lys Ser Pro Leu Thr Glu Pro
                165                 170                 175
Asn Phe Glu Asn Lys His Gly Tyr Gly Ile Cys His Ser Asp
            180                 185                 190
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<210> 5313
<211> 322
<212> DNA
<213> Homo sapiens

<400> 5313
cggggccgcc gagaggaaga gggtgacaag cgcagcgttg ccccccagac tcgggtcctg
60
aaaggcgtca tgcgagtagg catcctggcg aaaggcctcc tcctgcgtgg ggacaggaac
120
gtgcgcctcg ctctgctctg ctccgagaag cccacgcaca gcctgctgcg gaggatcgcc
180
cagcagctgc cccggcaaca caggcaattc cacgttgtgt gcgactggcc tgtgcatatg
240
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<210> 5314
<211> 107
<212> PRT
<213> Homo sapiens

<400> 5314
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            20                  25                  30
Leu Leu Leu Arg Gly Asp Arg Asn Val Arg Leu Ala Leu Leu Cys Ser
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        35                  40                  45
Glu Lys Pro Thr His Ser Leu Leu Arg Arg Ile Ala Gln Gln Leu Pro
    50                  55                  60
Arg Gln His Arg Gln Phe His Val Val Cys Asp Trp Pro Val His Met
65                  70                  75                  80
Glu Val Phe Ser Asp Leu Ala Leu Asp Thr Pro Ala Asn Arg Thr His
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Thr Tyr Ser Leu Thr His Ile His Val His Thr
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<211> 2298
<212> DNA
<213> Homo sapiens

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420
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480
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<210> 5316
<211> 544
<212> PRT
<213> Homo sapiens

<400> 5316
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Gln Lys Leu Asn Cys Arg Gln Ile Pro Lys Leu Leu Arg Gln Leu Gln
            20   25   30
Glu Phe Thr Asp Leu Gly His Arg Leu Asp Cys Leu Asp Leu Lys Gly
        35   40   45
Glu Lys Leu Asp Tyr Lys Thr Cys Glu Ala Leu Glu Glu Val Phe Lys

```
    50                  55                  60
Arg Leu Gln Phe Lys Val Val Asp Leu Glu Gln Thr Asn Leu Asp Glu
65                  70                  75                  80
Asp Gly Ala Ser Ala Leu Phe Asp Met Ile Glu Tyr Tyr Glu Ser Ala
                85                  90                  95
Thr His Leu Asn Ile Ser Phe Asn Lys His Ile Gly Thr Arg Gly Trp
            100                 105                 110
Gln Ala Ala Ala His Met Met Arg Lys Thr Ser Cys Leu Gln Tyr Leu
        115                 120                 125
Asp Ala Arg Asn Thr Pro Leu Leu Asp His Ser Ala Pro Phe Val Ala
    130                 135                 140
Arg Ala Leu Arg Ile Arg Ser Ser Leu Ala Val Leu His Leu Glu Asn
145                 150                 155                 160
Ala Ser Leu Ser Gly Arg Pro Leu Met Leu Leu Ala Thr Ala Leu Lys
                165                 170                 175
Met Asn Met Asn Leu Arg Glu Leu Tyr Leu Ala Asp Asn Lys Leu Asn
            180                 185                 190
Gly Leu Gln Asp Ser Ala Gln Leu Gly Asn Leu Leu Lys Phe Asn Cys
        195                 200                 205
Ser Leu Gln Ile Leu Asp Leu Arg Asn Asn His Val Leu Asp Ser Gly
    210                 215                 220
Leu Ala Tyr Ile Cys Glu Gly Leu Lys Glu Gln Arg Lys Gly Leu Val
225                 230                 235                 240
Thr Leu Val Leu Trp Asn Asn Gln Leu Thr His Thr Gly Met Ala Phe
                245                 250                 255
Leu Gly Met Thr Leu Ser His Thr Gln Ser Leu Glu Thr Leu Asn Leu
            260                 265                 270
Gly His Asn Pro Ile Gly Asn Glu Gly Val Arg His Leu Lys Asn Gly
        275                 280                 285
Leu Ile Ser Asn Arg Ser Val Leu Arg Leu Gly Leu Ala Ser Thr Lys
    290                 295                 300
Leu Thr Cys Glu Gly Ala Val Ala Val Ala Glu Phe Ile Ala Glu Ser
305                 310                 315                 320
Pro Arg Leu Leu Arg Leu Asp Leu Arg Glu Asn Glu Ile Lys Thr Gly
                325                 330                 335
Gly Leu Met Ala Leu Ser Leu Ala Leu Lys Val Asn His Ser Leu Leu
            340                 345                 350
Arg Leu Asp Leu Asp Arg Glu Pro Lys Lys Glu Ala Val Lys Ser Phe
        355                 360                 365
Ile Glu Thr Gln Lys Ala Leu Leu Ala Glu Ile Gln Asn Gly Cys Lys
    370                 375                 380
Arg Asn Leu Val Leu Ala Arg Glu Arg Glu Glu Lys Glu Gln Pro Pro
385                 390                 395                 400
Gln Leu Ser Ala Ser Met Pro Glu Thr Thr Ala Thr Glu Pro Gln Pro
                405                 410                 415
Asp Asp Glu Pro Ala Ala Gly Val Gln Asn Gly Ala Pro Ser Pro Ala
            420                 425                 430
Pro Ser Pro Asp Ser Asp Ser Asp Ser Asp Ser Asp Gly Glu Glu Glu
        435                 440                 445
Glu Glu Glu Glu Gly Glu Arg Asp Glu Thr Pro Ser Gly Ala Ile Asp
    450                 455                 460
Thr Arg Asp Thr Gly Ser Ser Glu Pro Gln Pro Pro Pro Glu Pro Pro
465                 470                 475                 480
Arg Ser Gly Pro Pro Leu Pro Asn Gly Leu Lys Pro Glu Phe Ala Leu
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                485                 490                 495
Ala Leu Pro Pro Glu Pro Pro Pro Gly Pro Glu Val Lys Gly Gly Ser
            500                 505                 510
Cys Gly Leu Glu His Glu Leu Ser Cys Ser Lys Asn Glu Lys Glu Leu
        515                 520                 525
Glu Glu Leu Leu Leu Glu Ala Ser Gln Glu Ser Gly Gln Glu Thr Leu
    530                 535                 540
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<210> 5317
<211> 889
<212> DNA
<213> Homo sapiens

<400> 5317
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120
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180
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420
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480
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<210> 5318
<211> 132
<212> PRT
<213> Homo sapiens

<400> 5318
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Arg Gly Arg Pro Gly Ser Cys Ser Thr Arg Pro Ser Cys Gly Ala Arg
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Arg Pro Cys Val Ser Gly Thr Val Pro Ser Ser Cys Gln Leu Gly Gly
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            20                  25                  30
Pro Thr Ser Pro Thr Ser Ala Ala Ser Arg Ala Cys Gly Ser Arg Gly
        35                  40                  45
Ala Ala Thr Trp Trp Ser Arg Ser Ser Gly Ser Thr Thr Leu Arg Arg
    50                  55                  60
Pro Ser Trp Ala Ser Ser Ser Thr Arg Ala Ser Thr Gly Thr Arg Ser
65                  70                  75                  80
Pro Ala Ala Ala Ser Arg Arg Pro Cys Gly Ser Pro Ala Arg Gly Arg
                85                  90                  95
Thr Ser Trp Ser Ala Arg Tyr Thr Ser Pro Arg Met Trp Thr Lys Met
            100                 105                 110
Thr Cys Arg Arg Cys Arg Thr Ser Ala Trp Trp Trp Ala Trp Ser Ser
        115                 120                 125
Met Ser Arg Cys
    130
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<210> 5319
<211> 4231
<212> DNA
<213> Homo sapiens

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4231

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<211> 96
<212> PRT
<213> Homo sapiens

<400> 5320
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Arg Ser Leu Ala Leu Xaa Thr Gln Ala Gly Val Leu Trp Leu Asp Leu
35 40 45
Gly Ser Leu Gln Pro Pro Pro Pro Arg Phe Lys Gln Phe Ser Cys Pro
50 55 60
Ser Leu Pro Ser Ser Trp Asp Tyr Arg Cys Met Pro Pro Trp Leu Ala
65 70 75 80
Asn Phe Cys Ile Phe Ser Arg Asp Gly Val Ser Pro Tyr Trp Ser Gly
85 90 95

<210> 5321
<211> 6324
<212> DNA
<213> Homo sapiens

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720
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780

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1980
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6324

<210> 5322
<211> 209
<212> PRT
<213> Homo sapiens

<400> 5322
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Arg Gly Glu Leu Gln Gln Leu Ser Gly Ser Gln Leu His Gly Lys Ser
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Asp Ser Pro Asn Val Tyr Thr Glu Lys Lys Glu Ile Ala Ile Leu Arg
35 40 45
Glu Arg Leu Thr Glu Leu Glu Arg Lys Leu Thr Phe Glu Gln Gln Arg
50 55 60
Ser Asp Leu Trp Glu Arg Leu Tyr Val Glu Ala Lys Asp Gln Asn Gly
65 70 75 80
Lys Gln Gly Thr Asp Gly Lys Lys Lys Gly Gly Arg Gly Ser His Arg
85 90 95
Ala Lys Asn Lys Ser Lys Glu Thr Phe Leu Gly Ser Val Lys Glu Thr
100 105 110
Phe Asp Ala Met Lys Asn Ser Thr Lys Glu Phe Val Arg His His Lys
115 120 125
Glu Lys Ile Lys Gln Ala Lys Glu Ala Val Lys Glu Asn Leu Lys Lys
130 135 140
Phe Ser Asp Ser Val Lys Ser Thr Phe Arg His Phe Lys Asp Thr Thr
145 150 155 160
Lys Asn Ile Phe Asp Glu Lys Gly Asn Lys Arg Phe Gly Ala Thr Lys
165 170 175
Glu Ala Ala Glu Lys Pro Arg Thr Val Phe Ser Asp Tyr Leu His Pro

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            180                 185                 190
Gln Tyr Lys Ala Pro Thr Glu Asn His His Asn Arg Pro Tyr Tyr Ala
        195                 200                 205
Lys


<210> 5323
<211> 475
<212> DNA
<213> Homo sapiens

<400> 5323
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120
catagctgcc aggcctttct gcccacacca cgccacttat atggcctcct gccatgggca
180
gagtagggag gtgaggtgct cgtggtgccc agagtcctca tcaaggagtg aaaccagagt
240
gtggccatag ccagtaagaa cagcacgctg cagcccagcc catcagcctc aggcactgag
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ctctctgcac actccatgaa tgcagagcag catcaggctg gcctcagccc cttcccgtct
360
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475

<210> 5324
<211> 105
<212> PRT
<213> Homo sapiens

<400> 5324
Met Glu Cys Ala Glu Ser Ser Val Pro Glu Ala Asp Gly Leu Gly Cys
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Ser Val Leu Phe Leu Leu Ala Met Ala Thr Leu Trp Phe His Ser Leu
            20                  25                  30
Met Arg Thr Leu Gly Thr Thr Ser Thr Ser Pro Pro Tyr Ser Ala His
        35                  40                  45
Gly Arg Arg Pro Tyr Lys Trp Arg Gly Val Gly Arg Lys Ala Trp Gln
    50                  55                  60
Leu Trp Thr Ala Pro Arg Ser Leu Leu Leu Ser Val Gly Leu Ala Ser
65                  70                  75                  80
Leu Arg Arg Ala Ser Gln His Ala Val Met Leu Pro Gln Leu Leu Ala
                85                  90                  95
Val Ser Cys Leu Pro Asp Pro Gly Arg
            100                 105

<210> 5325
<211> 938
<212> DNA
<213> Homo sapiens
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<400> 5325
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120
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180
agtgagtcat ctcattcccc tccgtggatc agaggacttg gactagatag aagcatgtgg
240
tgtctcctac gaggcctggg ccggcctgga gccctggcac ggggagccct ggggcagcag
300
caatccctgg gtgcccgggc cctggccagc gcaggctctg agagccggga cgagtacagc
360
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420
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480
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540
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600
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720
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780
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840
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900
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938

<210> 5326
<211> 234
<212> PRT
<213> Homo sapiens

<400> 5326
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Gly Ala Leu Gly Gln Gln Gln Ser Leu Gly Ala Arg Ala Leu Ala Ser
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Ala Gly Ser Glu Ser Arg Asp Glu Tyr Ser Tyr Val Val Val Gly Ala
35 40 45
Gly Ser Ala Gly Cys Val Leu Ala Gly Arg Leu Thr Glu Asp Pro Ala
50 55 60
Glu Arg Val Leu Leu Leu Glu Ala Gly Pro Lys Asp Val Arg Ala Gly
65 70 75 80
Ser Lys Arg Leu Ser Trp Lys Ile His Met Pro Ala Ala Leu Val Ala
85 90 95
Asn Leu Cys Asp Asp Arg Tyr Asn Trp Cys Tyr His Thr Glu Val Gln

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            100                 105                 110
Arg Gly Leu Asp Gly Arg Val Leu Tyr Trp Pro Arg Gly Arg Val Trp
        115                 120                 125
Gly Gly Ser Ser Ser Leu Asn Ala Met Val Tyr Val Arg Gly His Ala
    130                 135                 140
Glu Asp Tyr Glu Arg Trp Gln Arg Gln Gly Ala Arg Gly Trp Asp Tyr
145                 150                 155                 160
Ala His Cys Leu Pro Tyr Phe Arg Lys Ala Gln Gly His Xaa Ala Gly
                165                 170                 175
Arg Gln Pro Val Pro Gly Arg Asp Gly Pro Leu Arg Val Ser Arg Gly
            180                 185                 190
Lys Thr Asn His Pro Leu His Cys Ala Phe Leu Glu Ala Thr Gln Gln
        195                 200                 205
Ala Gly Tyr Pro Leu Thr Glu Asp Met Asn Gly Phe Gln Gln Glu Gly
    210                 215                 220
Phe Gly Trp Met Asp Met Thr Ile His Glu
225                 230
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<210> 5327
<211> 2084
<212> DNA
<213> Homo sapiens

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120
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180
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240
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780
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840
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960
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<210> 5328
<211> 694
<212> PRT
<213> Homo sapiens

<400> 5328
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Lys Glu Val Ser Gln Phe Thr Pro Val Ala Phe Pro Ile Ala Lys Asp
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Arg Cys Val Val Ala Ala Phe Trp Ala Asp Val Asp Asn Arg Arg Ala
35 40 45
Gly Asp Val Tyr Tyr Arg Glu Ala Thr Asp Pro Ala Met Leu Arg Arg

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    50                  55                  60
Ala Thr Glu Asp Val Arg His Tyr Phe Pro Glu Leu Leu Asp Phe Asn
65                  70                  75                  80
Ala Thr Trp Val Phe Val Ala Thr Trp Tyr Arg Val Thr Phe Phe Gly
                85                  90                  95
Gly Ser Ser Ser Ser Pro Val Asn Thr Phe Gln Thr Val Leu Ile Thr
            100                 105                 110
Asp Gly Lys Leu Ser Phe Thr Ile Phe Asn Tyr Glu Ser Ile Val Trp
        115                 120                 125
Thr Thr Gly Thr His Ala Ser Ser Gly Gly Asn Ala Thr Gly Leu Gly
    130                 135                 140
Gly Ile Ala Ala Gln Ala Gly Phe Asn Ala Gly Asp Gly Gln Arg Tyr
145                 150                 155                 160
Phe Ser Ile Pro Gly Ser Arg Thr Ala Asp Met Ala Glu Val Glu Thr
                165                 170                 175
Thr Thr Asn Val Gly Val Pro Gly Arg Trp Ala Phe Arg Ile Asp Asp
            180                 185                 190
Ala Gln Val Arg Val Gly Gly Cys Gly His Thr Thr Ser Val Cys Leu
        195                 200                 205
Ala Leu Arg Pro Cys Leu Asn Gly Gly Lys Cys Ile Asp Asp Cys Val
    210                 215                 220
Thr Gly Asn Pro Ser Tyr Thr Cys Ser Cys Leu Ser Gly Phe Thr Gly
225                 230                 235                 240
Arg Arg Cys His Leu Asp Val Asn Glu Cys Ala Ser Gln Pro Cys Gln
                245                 250                 255
Asn Gly Gly Thr Cys Thr His Gly Ile Asn Ser Phe Arg Cys Gln Cys
            260                 265                 270
Pro Ala Gly Phe Gly Gly Pro Thr Cys Glu Thr Ala Gln Ser Pro Cys
        275                 280                 285
Asp Thr Lys Glu Cys Gln His Gly Gly Gln Cys Gln Val Glu Asn Gly
    290                 295                 300
Ser Ala Val Cys Val Cys Gln Ala Gly Tyr Thr Gly Ala Ala Cys Glu
305                 310                 315                 320
Met Asp Val Asp Asp Cys Ser Pro Asp Pro Cys Leu Asn Gly Gly Ser
                325                 330                 335
Cys Val Asp Leu Val Gly Asn Tyr Thr Cys Leu Cys Ala Glu Pro Phe
            340                 345                 350
Lys Gly Leu Arg Cys Glu Thr Gly Asp His Pro Val Pro His Ala Cys
        355                 360                 365
Leu Ser Ala Pro Cys His Asn Gly Gly Thr Cys Val Asp Ala Asp Gln
    370                 375                 380
Gly Tyr Val Cys Glu Cys Pro Glu Gly Phe Met Gly Leu Asp Cys Arg
385                 390                 395                 400
Glu Arg Val Xaa Pro Met Thr Val Ser Ala Ala Thr Glu Ala Asp Ala
                405                 410                 415
Trp Ala Pro Thr Pro Pro Ser Ala His Ala Pro Cys Gly Xaa Ser Leu
            420                 425                 430
Gly Phe Ser Val Asn Leu Lys Ser Gln Pro Xaa Pro Cys Asn Met Asn
        435                 440                 445
Thr Gln Cys Pro Asp Gly Gly Tyr Cys Met Glu His Gly Gly Ser Tyr
    450                 455                 460
Leu Cys Val Cys His Thr Asp His Asn Ala Ser His Ser Leu Pro Ser
465                 470                 475                 480
Pro Cys Asp Ser Asp Pro Cys Phe Asn Gly Gly Ser Cys Asp Ala His
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                485                 490                 495
Asp Asp Ser Tyr Thr Cys Glu Cys Pro Arg Gly Phe His Gly Lys His
            500                 505                 510
Cys Glu Lys Ala Arg Pro His Leu Cys Ser Ser Gly Pro Cys Arg Asn
        515                 520                 525
Gly Gly Thr Cys Lys Glu Ala Gly Gly Glu Tyr His Cys Ser Cys Pro
    530                 535                 540
Tyr Arg Phe Thr Gly Arg His Cys Glu Ile Gly Lys Pro Asp Ser Cys
545                 550                 555                 560
Ala Ser Gly Pro Cys His Asn Gly Gly Thr Cys Phe His Tyr Ile Gly
                565                 570                 575
Lys Tyr Lys Cys Asp Cys Pro Pro Gly Phe Ser Gly Arg His Cys Glu
            580                 585                 590
Ile Ala Pro Ser Pro Cys Phe Arg Ser Pro Cys Val Asn Gly Gly Thr
        595                 600                 605
Cys Glu Asp Arg Asp Thr Asp Phe Phe Cys His Cys Gln Ala Gly Tyr
    610                 615                 620
Met Gly Arg Arg Cys Gln Ala Glu Val Asp Cys Gly Pro Pro Glu Glu
625                 630                 635                 640
Val Lys His Ala Thr Leu Arg Phe Asn Gly Thr Arg Leu Gly Ala Val
                645                 650                 655
Ala Leu Tyr Ala Cys Asp Arg Gly Tyr Ser Leu Ser Ala Pro Ser Arg
            660                 665                 670
Ile Arg Val Cys Gln Pro His Gly Val Trp Ser Glu Pro Pro Gln Cys
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Leu Gly Asp Ser Val Gly
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<210> 5329
<211> 2582
<212> DNA
<213> Homo sapiens

<400> 5329

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600
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720
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780
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840
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<212> PRT
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Ala Leu Arg Lys Lys Glu Leu Asp Glu Glu Glu Ser Ile Arg Lys Lys
35 40 45
Ala Val Gln Phe Gly Thr Gly Glu Leu Cys Asp Ala Ile Ser Ala Val
50 55 60
Glu Glu Lys Val Ser Tyr Leu Arg Pro Leu Asp Phe Glu Glu Ala Arg
65 70 75 80
Glu Leu Phe Leu Leu Gly Gln His Tyr Val Phe Glu Ala Lys Glu Phe
85 90 95
Phe Gln Ile Asp Gly Tyr Val Thr Asp His Ile Glu Val Val Gln Asp
100 105 110
His Ser Ala Leu Phe Lys Val Leu Ala Phe Phe Glu Thr Asp Met Glu
115 120 125
Arg Arg Cys Lys Met His Lys Arg Arg Ile Ala Met Leu Glu Pro Leu
130 135 140
Thr Val Asp Leu Asn Pro Gln Tyr Tyr Leu Leu Val Asn Arg Gln Ile
145 150 155 160
Gln Phe Glu Ile Ala His Ala Tyr Tyr Asp Met Met Asp Leu Lys Val
165 170 175
Ala Ile Ala Asp Arg Leu Arg Asp Pro Asp Ser His Ile Val Lys Lys
180 185 190
Ile Asn Asn Leu Asn Lys Ser Ala Leu Lys Tyr Tyr Gln Leu Phe Leu
195 200 205
Asp Ser Leu Arg Asp Pro Asn Lys Val Phe Pro Glu His Ile Gly Glu
210 215 220
Asp Val Leu Arg Pro Ala Met Leu Ala Lys Phe Arg Val Ala Arg Leu
225 230 235 240
Tyr Gly Lys Ile Ile Thr Ala Asp Pro Lys Lys Glu Leu Glu Asn Leu
245 250 255
Ala Thr Ser Leu Glu His Tyr Lys Phe Ile Val Asp Tyr Cys Glu Lys

260 265 270
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<212> DNA
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<213> Homo sapiens

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Ser Gln Pro Gln Gly Leu Ser Tyr Ala Xaa Gly Arg Gly
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Ile Gln Ala Arg Met Gly Val Phe Ala Gln Ala Asp Gly Ser Ala Tyr
50 55 60
Ile Glu Gln Gly Asn Thr Lys Ala Leu Ala Val Val Tyr Gly Pro His
65 70 75 80
Glu Ile Arg Gly Ser Arg Ala Arg Ala Leu Pro Asp Arg Ala Leu Val
85 90 95
Asn Cys Gln Tyr Ser Ser Ala Thr Phe Ser Thr Gly Glu Arg Lys Arg
100 105 110
Arg Pro His Gly Asp Arg Lys Ser Cys Glu Met Gly Leu Gln Leu Arg
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Gln Thr Phe Glu Ala Ala Ile Leu Thr Gln Leu His Pro Arg Ser Gln
130 135 140
Ile Asp Ile Tyr Val Gln Val Leu Gln Ala Asp Gly Gly Thr Tyr Ala
145 150 155 160
Ala Cys Val Asn Ala Ala Thr Leu Ala Val Leu Asp Ala Gly Ile Pro
165 170 175
Met Arg Asp Phe Val Cys Ala Cys Ser Ala Gly Phe Val Asp Gly Thr
180 185 190
Ala Leu Ala Asp Leu Ser His Val Glu Glu Ala Ala Gly Gly Pro Gln
195 200 205
Leu Ala Leu Ala Leu Leu Pro Ala Ser Gly Gln Ile Ala Leu Leu Glu
210 215 220
Met Asp Ala Arg Leu His Glu Asp His Leu Glu Arg Val Leu Glu Ala
225 230 235 240
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<211> 4282
<212> DNA
<213> Homo sapiens

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Arg Leu Val Asn Glu Tyr Val Glu Leu Val Asn Ala Ala Cys Asn Phe
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Glu Pro His Glu Ser Phe Phe Ser Leu Phe Ser Asp Pro Arg Ser Thr
65 70 75 80
Arg Leu Thr Arg Ile His Leu Arg Glu Asp Leu Val Gln Asp Gln Asp
85 90 95
Leu Glu Ala Ile Arg Lys Gln Asp Leu Val Glu Leu Tyr Leu Thr Asn
100 105 110
Cys Glu Lys Leu Ser Ala Lys Ser Leu Gln Thr Leu Arg Ser Phe Ser
115 120 125
His Thr Leu Val Ser Leu Ser Leu Phe Gly Cys Thr Asn Ile Phe Tyr
130 135 140
Glu Glu Glu Asn Pro Gly Gly Cys Glu Asp Glu Tyr Leu Val Asn Pro
145 150 155 160
Thr Cys Gln Val Leu Val Lys Asp Phe Thr Phe Glu Gly Phe Ser Arg
165 170 175
Leu Arg Phe Leu Asn Leu Gly Arg Met Ile Asp Trp Val Pro Val Glu

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    210                 215                 220
Val Ser Leu Val Leu Tyr Asn Met Asp Leu Ser Asp Asp His Ile Arg
225                 230                 235                 240
Val Ile Val Gln Leu His Lys Leu Arg His Leu Asp Ile Ser Arg Asp
                245                 250                 255
Arg Leu Ser Ser Tyr Tyr Lys Phe Lys Leu Thr Arg Glu Val Leu Ser
            260                 265                 270
Leu Phe Val Gln Lys Leu Gly Asn Leu Met Ser Leu Asp Ile Ser Gly
        275                 280                 285
His Met Ile Leu Glu Asn Cys Ser Ile Ser Lys Met Glu Glu Glu Ala
    290                 295                 300
Gly Gln Thr Ser Ile Glu Pro Ser Lys Ser Ser Ile Ile Pro Phe Arg
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Ala Leu Lys Arg Pro Leu Gln Phe Leu Gly Leu Phe Glu Asn Ser Leu
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Cys Arg Leu Thr His Ile Pro Ala Tyr Lys Val Ser Gly Asp Lys Asn
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Glu Glu Gln Val Leu Asn Ala Ile Glu Ala Tyr Thr Glu His Arg Pro
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Glu Ile Thr Ser Arg Ala Ile Asn Leu Leu Phe Asp Ile Ala Arg Ile
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Glu Arg Cys Asn Gln Leu Leu Arg Ala Leu Lys Leu Val Ile Thr Ala
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Leu Lys Cys His Lys Tyr Asp Arg Asn Ile Gln Val Thr Gly Ser Ala
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Ala Leu Phe Tyr Leu Thr Asn Ser Glu Tyr Arg Ser Glu Gln Ser Val
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Lys Leu Arg Arg Gln Val Ile Gln Val Val Leu Asn Gly Met Glu Ser
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Tyr Gln Glu Val Thr Val Gln Arg Asn Cys Cys Leu Thr Leu Cys Asn
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Phe Ser Ile Pro Glu Glu Leu Glu Phe Gln Tyr Arg Arg Val Asn Glu
465                 470                 475                 480
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Cys Leu Lys Glu Phe Pro Glu Lys Gln Glu Leu His Arg Asn Met Leu
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Glu Glu Val Glu Glu Arg Met Trp Ala Ala Ile Gln Ser Trp Asp Ile
            660                 665                 670
Asn Ser Arg Arg Asn Ile Asn Tyr Arg Ser Phe Glu Pro Ile Leu Arg
        675                 680                 685
Leu Leu Pro Gln Gly Ile Ser Pro Val Ser Gln His Trp Ala Thr Trp
    690                 695                 700
Ala Leu Tyr Asn Leu Val Ser Val Tyr Pro Asp Lys Tyr Cys Pro Leu
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Leu Ile Lys Glu Gly Gly Met Pro Leu Leu Arg Asp Ile Ile Lys Met
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<212> DNA
<213> Homo sapiens

<400> 5337

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1140
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1200
gaccagtaga ttgttgaaag ttggtgaatc ggattataag cttctagcta acacaaggat
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1320
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1380
attgtacagt gggtggaaag ggcatttgga gctcattaga atgagacata gtacacccca
1440
atggccctgt ttattaaatg tagtggatta agtgtctgtc aacaaataca ccaaaaccat
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1560
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1620
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1680
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1740
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1800
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1860
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1920
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1980
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2040
acagcttagg catctgctta cctgcttagg catcaagagg tgccaaatta gaaaataggg
2100
cattaacaat caaaattttt aagctgaccc acatacttgc tactggtttc gcttatgttt
2160
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2220
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2280
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2340
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2400
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2460

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2520
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2580
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2640
ccatttttgt aagataaagg ccaagaaaac tttacatatg ctacaagttt attacagata
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2742

<210> 5338
<211> 139
<212> PRT
<213> Homo sapiens

<400> 5338
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20 25 30
Asn Ser Gln Met Lys Ile Val His Lys Lys Lys Glu Arg Gly His Gly
35 40 45
Tyr Asn Ser Ser Ala Ala Ala Trp Gln Ala Met Gln Asn Gly Gly Lys
50 55 60
Asn Lys Asn Phe Pro Asn Asn Gln Ser Trp Asn Ser Ser Leu Ser Gly
65 70 75 80
Pro Arg Leu Leu Phe Lys Ser Gln Ala Asn Gln Asn Tyr Ala Gly Ala
85 90 95
Lys Phe Ser Glu Pro Pro Ser Pro Ser Val Leu Pro Lys Pro Pro Ser
100 105 110
His Trp Val Pro Val Ser Phe Asn Pro Ser Asp Lys Glu Ile Met Thr
115 120 125
Phe Gln Leu Lys Thr Leu Leu Lys Val Gln Val
130 135

<210> 5339
<211> 847
<212> DNA
<213> Homo sapiens

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120
ttgtttgctc ccccttttta aaatatttaa tagcttatgt tcacttctca tagctccttt
180
ctttatgaaa aataacatga aaatagaaaa gttgttctaa gtatactttt tgtatatatt
240
ctagacttat cagatgtaga cttcctagat gattcttcaa cggagagttt gcttctgagt
300
ggggatgaat acaatcagga ctttgattca accaattttg aggaatctca ggatgaggat
360

gatgctctta atgaaattgt gcgatgtatt tgtgagatgg atgaggagaa tggcttcatg
420
atccagtgtg aagagtgctt gtgttggcaa cacagcgtgt gcatggggct gctggaggag
480
agcattccag agcagtacat ctgctatatc tgccgggacc caccaggtca gaggtggagt
540
gcaaaatatc gttatgataa ggagtggttg aataatggga gaatgtgcgg gttatcattt
600
ttcaaagaaa attattctca tctcaatgcc aaaaagatag tttctacaca tcacctgctt
660
gctgatgtct atggtgttac agaagtgcta cacgggctac agctgaagat tggaatacta
720
aagaataaac atcatcctga ccttcatctc tgggcttgtt ccgggaagcg aaaagaccaa
780
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840
aaaaaaa
847

<210> 5340
<211> 217
<212> PRT
<213> Homo sapiens

<400> 5340
His Glu Asn Arg Lys Val Val Leu Ser Ile Leu Phe Val Tyr Ile Leu
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Asp Leu Ser Asp Val Asp Phe Leu Asp Asp Ser Ser Thr Glu Ser Leu
            20   25   30
Leu Leu Ser Gly Asp Glu Tyr Asn Gln Asp Phe Asp Ser Thr Asn Phe
        35   40   45
Glu Glu Ser Gln Asp Glu Asp Asp Ala Leu Asn Glu Ile Val Arg Cys
    50   55   60
Ile Cys Glu Met Asp Glu Glu Asn Gly Phe Met Ile Gln Cys Glu Glu
65   70   75   80
Cys Leu Cys Trp Gln His Ser Val Cys Met Gly Leu Leu Glu Glu Ser
                85   90   95
Ile Pro Glu Gln Tyr Ile Cys Tyr Ile Cys Arg Asp Pro Pro Gly Gln
            100   105   110
Arg Trp Ser Ala Lys Tyr Arg Tyr Asp Lys Glu Trp Leu Asn Asn Gly
        115   120   125
Arg Met Cys Gly Leu Ser Phe Phe Lys Glu Asn Tyr Ser His Leu Asn
    130   135   140
Ala Lys Lys Ile Val Ser Thr His His Leu Leu Ala Asp Val Tyr Gly
145   150   155   160
Val Thr Glu Val Leu His Gly Leu Gln Leu Lys Ile Gly Ile Leu Lys
                165   170   175
Asn Lys His His Pro Asp Leu His Leu Trp Ala Cys Ser Gly Lys Arg
            180   185   190
Lys Asp Gln Asp Gln Ile Ile Ala Gly Val Glu Lys Lys Ile Ala Gln
        195   200   205
Asp Thr Val Asn Arg Glu Glu Lys Lys
    210   215

<210> 5341
<211> 2455
<212> DNA
<213> Homo sapiens

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240
ggcccctggg tgccccatgg gctgagcctg gcagctgcgg ccctggcact aaccctcctg
300
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360
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420
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480
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540
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720
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1020
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1080
taccacgtga tgggacttgt cgttgggatc ctcggctgct tagatctcgg agccacctgt
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1200
acagtgatcc tgtatgtggg cgagctcctg cggtacttgt gtaacattcc ccagcaacca
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1320
gagaccttcc agcagcgctt cggtcctatt cggatctggg aagtctacgg ctccacagaa
1380
ggcaacatgg gcttagtcaa ctatgtgggg cgctgcgggg ccctgggcaa gatgagctgc
1440

ctcctccgaa tgctgtcccc ctttgagctg gtgcagttcg acatggaggc ggcggagcct
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1980
gtcaccagca cgttcaaact gatgaagacc cggttggtgc gtgagggctt caatgtgggg
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2100
gcagaaatgt accaggctgt gtgtgaggga acctggaagc tctgatcacc tggccaaccc
2160
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2220
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2280
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2340
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2455

<210> 5342
<211> 690
<212> PRT
<213> Homo sapiens

<400> 5342
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Leu Trp Gly Leu Gly Gln Pro Val Trp Pro Val Ala Val Ala Leu Thr
            20   25   30
Leu Arg Trp Leu Leu Gly Asp Pro Thr Cys Cys Val Leu Leu Gly Leu
        35   40   45
Ala Met Leu Ala Arg Pro Trp Leu Gly Pro Trp Val Pro His Gly Leu
    50   55   60
Ser Leu Ala Ala Ala Ala Leu Ala Leu Thr Leu Leu Pro Ala Arg Leu
65   70   75   80
Pro Pro Gly Leu Arg Trp Leu Pro Ala Asp Val Ile Phe Leu Ala Lys
                85   90   95
Ile Leu His Leu Gly Leu Lys Ile Arg Gly Cys Leu Ser Arg Gln Pro

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                100                 105                 110
Pro Asp Thr Phe Val Asp Ala Phe Glu Arg Arg Ala Arg Ala Gln Pro
        115                 120                 125
Gly Arg Ala Leu Leu Val Trp Thr Gly Pro Gly Ala Gly Ser Val Thr
    130                 135                 140
Phe Gly Glu Leu Asp Ala Arg Ala Cys Gln Ala Ala Trp Ala Leu Lys
145                 150                 155                 160
Ala Glu Leu Gly Asp Pro Ala Ser Leu Cys Ala Gly Glu Pro Thr Ala
                165                 170                 175
Leu Leu Val Leu Ala Ser Gln Ala Val Pro Ala Leu Cys Met Trp Leu
            180                 185                 190
Gly Leu Ala Lys Leu Gly Cys Pro Thr Ala Trp Ile Asn Pro His Gly
        195                 200                 205
Arg Gly Met Pro Leu Ala His Ser Val Leu Ser Ser Gly Ala Arg Val
    210                 215                 220
Leu Val Val Asp Pro Asp Leu Arg Glu Ser Leu Glu Glu Ile Leu Pro
225                 230                 235                 240
Lys Leu Gln Ala Glu Asn Ile Arg Cys Phe Tyr Leu Ser His Thr Ser
                245                 250                 255
Pro Thr Pro Gly Val Gly Ala Leu Gly Ala Ala Leu Asp Ala Ala Pro
            260                 265                 270
Ser His Pro Val Pro Ala Asp Leu Arg Ala Gly Ile Thr Trp Arg Ser
        275                 280                 285
Pro Ala Leu Phe Ile Tyr Thr Ser Gly Thr Thr Gly Leu Pro Lys Pro
    290                 295                 300
Ala Ile Leu Thr His Glu Arg Val Leu Gln Met Ser Lys Met Leu Ser
305                 310                 315                 320
Leu Ser Gly Ala Thr Ala Asp Asp Val Val Tyr Thr Val Leu Pro Leu
                325                 330                 335
Tyr His Val Met Gly Leu Val Val Gly Ile Leu Gly Cys Leu Asp Leu
            340                 345                 350
Gly Ala Thr Cys Val Leu Ala Pro Lys Phe Ser Thr Ser Cys Phe Trp
        355                 360                 365
Asp Asp Cys Arg Gln His Gly Val Thr Val Ile Leu Tyr Val Gly Glu
    370                 375                 380
Leu Leu Arg Tyr Leu Cys Asn Ile Pro Gln Gln Pro Glu Asp Arg Thr
385                 390                 395                 400
His Thr Val Arg Leu Ala Met Gly Asn Gly Leu Arg Ala Asp Val Trp
                405                 410                 415
Glu Thr Phe Gln Gln Arg Phe Gly Pro Ile Arg Ile Trp Glu Val Tyr
            420                 425                 430
Gly Ser Thr Glu Gly Asn Met Gly Leu Val Asn Tyr Val Gly Arg Cys
        435                 440                 445
Gly Ala Leu Gly Lys Met Ser Cys Leu Leu Arg Met Leu Ser Pro Phe
    450                 455                 460
Glu Leu Val Gln Phe Asp Met Glu Ala Ala Glu Pro Val Arg Asp Asn
465                 470                 475                 480
Gln Gly Phe Cys Ile Pro Val Gly Leu Gly Glu Pro Gly Leu Leu Leu
                485                 490                 495
Thr Lys Val Val Ser Gln Gln Pro Phe Val Gly Tyr Arg Gly Pro Arg
            500                 505                 510
Glu Leu Ser Glu Arg Lys Leu Val Arg Asn Val Arg Gln Ser Gly Asp
        515                 520                 525
Val Tyr Tyr Asn Thr Gly Asp Val Leu Ala Met Asp Arg Glu Gly Phe
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    530                 535                 540
Leu Tyr Phe Arg Asp Arg Leu Gly Asp Thr Phe Arg Trp Lys Gly Glu
545                 550                 555                 560
Asn Val Ser Thr His Glu Val Glu Gly Val Leu Ser Gln Val Asp Phe
                565                 570                 575
Leu Gln Gln Val Asn Val Tyr Gly Val Cys Val Pro Gly Cys Glu Gly
            580                 585                 590
Lys Val Gly Met Ala Ala Val Gln Leu Ala Pro Gly Gln Thr Phe Asp
        595                 600                 605
Gly Glu Lys Leu Tyr Gln His Val Arg Ala Trp Leu Pro Ala Tyr Ala
    610                 615                 620
Thr Pro His Phe Ile Arg Ile Gln Asp Ala Met Glu Val Thr Ser Thr
625                 630                 635                 640
Phe Lys Leu Met Lys Thr Arg Leu Val Arg Glu Gly Phe Asn Val Gly
                645                 650                 655
Ile Val Val Asp Pro Leu Phe Val Leu Asp Asn Arg Ala Gln Ser Phe
            660                 665                 670
Arg Pro Leu Thr Ala Glu Met Tyr Gln Ala Val Cys Glu Gly Thr Trp
        675                 680                 685
Lys Leu
    690
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<210> 5343
<211> 752
<212> DNA
<213> Homo sapiens

<400> 5343
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120
cggcgggcag attttgtggc tggctctctg agtggacggg tcatagtggc tgggggactt
180
gggaatcaac ccactgtcct ggagacggcg gaagcattcc acccagggaa gaacaaatgg
240
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300
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420
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480
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540
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600
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752

<210> 5344
<211> 124
<212> PRT
<213> Homo sapiens

<400> 5344
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Arg Thr Met Asp Val Phe Asp Met Glu Gln Gly Gly Trp Leu Lys Met
20 25 30
Glu Arg Ser Phe Phe Leu Lys Lys Arg Arg Ala Asp Phe Val Ala Gly
35 40 45
Ser Leu Ser Gly Arg Val Ile Val Ala Gly Gly Leu Gly Asn Gln Pro
50 55 60
Thr Val Leu Glu Thr Ala Glu Ala Phe His Pro Gly Lys Asn Lys Trp
65 70 75 80
Glu Ile Leu Pro Ala Met Pro Thr Pro Arg Cys Ala Cys Ser Ser Ile
85 90 95
Val Val Lys Asn Cys Leu Leu Ala Val Gly Gly Val Asn Gln Gly Leu
100 105 110
Ser Asp Ala Val Glu Ala Leu Cys Val Ser Asp Ser
115 120

<210> 5345
<211> 1912
<212> DNA
<213> Homo sapiens

<400> 5345
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120
gactcttccc ctgccaagaa aactcgtaga tgccagagac aggagtcgaa aaagatgcct
180
gtggctggag gaaaagctaa taaggacagg acagaagaca agcaagatgg tatgccagga
240
aggtcatggg ccagcaaaag ggtctctgaa tctgtgaagg ccttgctgtt aaagggcaaa
300
gctcctgtgg acccagagtg tacagccaag gtggggaagg ctcatgtgta ttgtgaagga
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420
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ggccgagttg ggaaaatggg acagcacagc ctggtggctt gttcaggcaa tctcaacaag
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600
gaaaagtttg agaaggtgcc tggaaaatat gatatgctac agatggacta tgccaccaat
660
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720

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780
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1020
caattactag aggctttggg agacattgaa attgctatta agctggtgaa aacagagcta
1080
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1140
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1200
cccacacaca gcgactatac catgaccttg ctggatttgt ttgaagtgga gaaggatggt
1260
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1320
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1380
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1440
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1620
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1680
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1800
gagatctgat cttcaagcaa gaaaataagc agtgttgtac ttgtgaattt tgtgatattt
1860
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1912

<210> 5346
<211> 534
<212> PRT
<213> Homo sapiens

<400> 5346
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Gln Asp Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser Glu
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Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala Pro Val Asp Pro Glu
35 40 45
Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr Cys Glu Gly Asn Asp

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    50                  55                  60
Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu Gln Phe Asn Asn Asn
65                  70                  75                  80
Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp Ala Gln Arg Asn Phe
                85                  90                  95
Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys Met Gly Gln His Ser
            100                 105                 110
Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala Lys Glu Ile Phe Gln
        115                 120                 125
Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp Glu Asp Arg Glu Lys
    130                 135                 140
Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu Gln Met Asp Tyr Ala
145                 150                 155                 160
Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys Glu Glu Ser Leu Lys
                165                 170                 175
Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu Arg Val Gln Glu Leu
            180                 185                 190
Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu Glu Met Met Met Glu
        195                 200                 205
Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly Lys Leu Thr Val Ala
    210                 215                 220
Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys Ile Glu Asp Cys Ile
225                 230                 235                 240
Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu Ala Cys Asn Glu Phe
                245                 250                 255
Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg Thr Pro Pro Leu Ile
            260                 265                 270
Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln Leu Leu Glu Ala Leu
        275                 280                 285
Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys Thr Glu Leu Gln Ser
    290                 295                 300
Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn Leu His Cys Ala Leu
305                 310                 315                 320
Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys Val Ile Ser Gln Tyr
                325                 330                 335
Leu Gln Ser Thr His Ala Pro Thr His Ser Asp Tyr Thr Met Thr Leu
            340                 345                 350
Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu Lys Glu Ala Phe Arg
        355                 360                 365
Glu Asp Leu His Asn Arg Met Leu Leu Trp His Gly Ser Arg Met Ser
    370                 375                 380
Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile Ala Pro Pro Glu
385                 390                 395                 400
Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile Tyr Phe Ala Asp
                405                 410                 415
Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser Arg Leu Lys Asn
            420                 425                 430
Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu Gly Gln Cys Asn Glu
        435                 440                 445
Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu Gln Gly Lys His
    450                 455                 460
Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser Ala His Phe Val
465                 470                 475                 480
Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala Ser Asp Thr Gly
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                485                 490                 495
Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn Glu Tyr Ile Val
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Asn Phe Leu Gln Leu Trp
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<212> DNA
<213> Homo sapiens

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<211> 694
<212> PRT
<213> Homo sapiens

<400> 5348
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Tyr Leu Leu Leu Pro Pro Pro Thr Leu Leu Gln Asp Glu Leu Leu Phe
35 40 45
Leu Gly Gly Pro Ala Ser Ser Ala Tyr Ala Leu Ser Pro Phe Ser Ala
50 55 60
Ser Gly Gly Trp Gly Arg Ala Gly His Leu His Pro Lys Gly Arg Glu
65 70 75 80
Leu Asp Pro Ala Ala Pro Pro Glu Gly Gln Leu Leu Arg Glu Val Arg
85 90 95
Ala Leu Gly Val Pro Phe Val Pro Arg Thr Ser Val Asp Ala Trp Leu
100 105 110
Val His Ser Val Ala Ala Gly Ser Ala Asp Glu Ala His Gly Leu Leu
115 120 125
Gly Ala Ala Ala Ala Ser Ser Thr Gly Gly Ala Gly Ala Ser Val Asp
130 135 140
Gly Gly Ser Gln Ala Val Gln Gly Gly Cys Gly Asp Ser Arg Ala Ala
145 150 155 160
Arg Ser Gly Pro Leu Asp Ala Gly Glu Glu Glu Lys Ala Pro Ala Glu
165 170 175
Pro Thr Ala Gln Val Pro Asp Ala Gly Gly Cys Ala Ser Glu Glu Asn
180 185 190
Gly Val Leu Arg Glu Lys His Glu Ala Val Asp His Ser Ser Gln His
195 200 205
Glu Glu Asn Glu Glu Arg Val Ser Ala Gln Lys Glu Asn Ser Leu Gln
210 215 220
Gln Asn Asp Asp Asp Glu Asn Lys Ile Ala Glu Lys Pro Asp Trp Glu
225 230 235 240
Ala Glu Lys Thr Thr Glu Ser Arg Asn Glu Arg His Leu Asn Gly Thr
245 250 255
Asp Thr Ser Phe Ser Leu Glu Asp Leu Phe Gln Leu Leu Ser Ser Gln
260 265 270
Pro Glu Asn Ser Leu Glu Gly Ile Ser Leu Gly Asp Ile Pro Leu Pro
275 280 285
Gly Ser Ile Ser Asp Gly Met Asn Ser Ser Ala His Tyr His Val Asn
290 295 300
Phe Ser Gln Ala Ile Ser Gln Asp Val Asn Leu His Glu Ala Ile Leu
305 310 315 320
Leu Cys Pro Asn Asn Thr Phe Arg Arg Asp Pro Thr Ala Arg Thr Ser
325 330 335
Gln Ser Gln Glu Pro Phe Leu Gln Leu Asn Ser His Thr Thr Asn Pro

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            340                 345                 350
Glu Gln Thr Leu Pro Gly Thr Asn Leu Thr Gly Phe Leu Ser Pro Val
        355                 360                 365
Asp Asn His Met Arg Asn Leu Thr Ser Gln Asp Leu Leu Tyr Asp Leu
    370                 375                 380
Asp Ile Asn Ile Phe Asp Glu Ile Asn Leu Met Ser Leu Ala Thr Glu
385                 390                 395                 400
Asp Asn Phe Asp Pro Ile Asp Val Ser Gln Leu Phe Asp Glu Ser Asp
                405                 410                 415
Ser Asp Ser Gly Leu Ser Leu Asp Ser Ser His Asn Asn Thr Ser Val
            420                 425                 430
Ile Lys Ser Asn Ser Ser His Ser Val Cys Asp Glu Gly Ala Ile Gly
        435                 440                 445
Tyr Cys Thr Asp His Glu Ser Ser Ser His His Asp Leu Glu Gly Ala
    450                 455                 460
Val Gly Gly Tyr Tyr Pro Glu Pro Ser Lys Leu Cys His Leu Asp Gln
465                 470                 475                 480
Ser Asp Ser Asp Phe His Gly Asp Leu Thr Phe Gln His Val Phe His
                485                 490                 495
Asn His Thr Tyr His Leu Gln Pro Thr Ala Pro Glu Ser Thr Ser Glu
            500                 505                 510
Pro Phe Pro Trp Pro Gly Lys Ser Gln Lys Ile Arg Ser Arg Tyr Leu
        515                 520                 525
Glu Asp Thr Asp Arg Asn Leu Ser Arg Asp Glu Gln Arg Ala Lys Ala
    530                 535                 540
Leu His Ile Pro Phe Ser Val Asp Glu Ile Val Gly Met Pro Val Asp
545                 550                 555                 560
Ser Phe Asn Ser Met Leu Ser Arg Tyr Tyr Leu Thr Asp Leu Gln Val
                565                 570                 575Leu Ile Arg
Asp Ile Arg Arg Arg Gly Lys Asn Lys Val Ala Ala
            580                 585                 590
Gln Asn Cys Arg Lys Arg Lys Leu Asp Ile Ile Leu Asn Leu Glu Asp
        595                 600                 605
Asp Val Cys Asn Leu Gln Ala Lys Lys Glu Thr Leu Lys Arg Glu Gln
    610                 615                 620
Ala Gln Cys Asn Lys Ala Ile Asn Ile Met Lys Gln Lys Leu His Asp
625                 630                 635                 640
Leu Tyr His Asp Ile Phe Ser Arg Leu Arg Asp Asp Gln Gly Arg Pro
                645                 650                 655
Val Asn Pro Asn His Tyr Ala Leu Gln Cys Thr His Asp Gly Ser Ile
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Leu Ile Val Pro Lys Glu Leu Val Ala Ser Gly His Lys Lys Glu Thr
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Gln Lys Gly Lys Arg Lys
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<210> 5349
<211> 425
<212> DNA
<213> Homo sapiens

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120
tgggcaaaca ccacaccagc agggagcccc aagcccagcc caagccccac aaagtctcca
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gccaggaagg ggaaggcagg ataccactgc ctgggaaggc ggaagtgaga gaggcaggcc
240
aacccattcc tgtttctctt ctacttcttt ctccaaagaa agccctcact ctcctcgcta
300
cagcccaggg aggtcacgag gggctgggaa gactcctgtg gcaaagtggc ccactccagc
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<210> 5350
<211> 134
<212> PRT
<213> Homo sapiens

<400> 5350
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Val Thr Ala Cys His Ser Ser Pro Leu Pro Cys Gly Cys Gln Asp Asn
            20   25   30
Leu Gly Lys His His Thr Ser Arg Glu Pro Gln Ala Gln Pro Lys Pro
        35   40   45
His Lys Val Ser Ser Gln Glu Gly Glu Gly Arg Ile Pro Leu Pro Gly
    50   55   60
Lys Ala Glu Val Arg Glu Ala Gly Gln Pro Ile Pro Val Ser Leu Leu
65   70   75   80
Leu Leu Ser Pro Lys Lys Ala Leu Thr Leu Leu Ala Thr Ala Gln Gly
                85   90   95
Gly His Glu Gly Leu Gly Arg Leu Leu Trp Gln Ser Gly Pro Leu Gln
            100   105   110
Pro Arg Pro Glu Lys Lys Arg Thr Pro Lys Ser Phe Trp Leu Pro Val
        115   120   125
Ser Ser Ala Phe Thr Arg
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<210> 5351
<211> 343
<212> DNA
<213> Homo sapiens

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120
gctgaacagg ctgggtttcg agacggaccg agaaggcaag ttctgctgca ggcttttgga
180
cagagcgtct tggtgccaat caaaatcact cttgttgctg ccgtttcggg tgtcacagtt
240

cctcctctca ctattggaca gcttgaagcc aaggcccagg cctgaccagt aggaatccga
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343

<210> 5352
<211> 112
<212> PRT
<213> Homo sapiens

<400> 5352
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20 25 30
Asn Cys Asp Thr Arg Asn Gly Ser Asn Lys Ser Asp Phe Asp Trp His
35 40 45
Gln Asp Ala Leu Ser Lys Ser Leu Gln Gln Asn Leu Pro Ser Arg Ser
50 55 60
Val Ser Lys Pro Ser Leu Phe Ser Ser Val Gln Leu Tyr Arg Gln Ser
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<210> 5353
<211> 4217<212> DNA
<213> Homo sapiens

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360
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420
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480
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<210> 5354
<211> 605
<212> PRT
<213> Homo sapiens

<400> 5354
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35 40 45
Gln Val Cys Gln Phe Ser Asn Val Leu Arg Lys Gln Gly Ile Gln Lys
50 55 60
Gly Asp Arg Val Ala Ile Tyr Met Pro Met Ile Pro Glu Leu Val Val
65 70 75 80
Ala Met Leu Ala Cys Ala Arg Ile Gly Ala Leu His Ser Ile Val Phe
85 90 95
Ala Gly Phe Ser Ser Glu Ser Leu Cys Glu Arg Ile Leu Asp Ser Ser
100 105 110
Cys Ser Leu Leu Ile Thr Thr Asp Ala Phe Tyr Arg Gly Glu Lys Leu
115 120 125
Val Asn Leu Lys Glu Leu Ala Asp Glu Ala Leu Gln Lys Cys Gln Glu
130 135 140
Lys Gly Phe Pro Val Arg Cys Cys Ile Val Val Lys His Leu Gly Arg
145 150 155 160
Ala Glu Leu Gly Met Gly Thr Pro Pro Ala Ser Pro Pro Gln Leu Arg
165 170 175
Gly His Ala Asp Val Gln Ile Ser Trp Asn Gln Gly Ile Asp Leu Trp
180 185 190
Trp His Glu Leu Met Gln Glu Ala Gly Asp Glu Cys Glu Pro Glu Trp
195 200 205
Cys Asp Ala Glu Asp Pro Leu Phe Ile Leu Tyr Thr Ser Gly Ser Thr
210 215 220
Gly Lys Pro Lys Gly Val Val His Thr Val Gly Gly Tyr Met Leu Tyr
225 230 235 240
Val Ala Thr Thr Phe Lys Tyr Val Phe Asp Phe His Ala Glu Asp Val
245 250 255
Phe Trp Cys Thr Ala Asp Ile Gly Trp Ile Thr Gly His Ser Tyr Val
260 265 270
Thr Tyr Gly Pro Leu Ala Asn Gly Ala Thr Ser Val Leu Phe Glu Gly

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Ile Pro Thr Tyr Pro Asp Val Asn Arg Leu Trp Ser Ile Val Asp Lys
    290                 295                 300
Tyr Lys Val Thr Lys Phe Tyr Thr Ala Pro Thr Ala Ile Arg Leu Leu
305                 310                 315                 320
Met Lys Phe Gly Asp Glu Pro Val Thr Lys His Ser Arg Ala Ser Leu
                325                 330                 335
Gln Val Leu Gly Thr Val Gly Glu Pro Ile Asn Pro Glu Ala Trp Leu
            340                 345                 350
Trp Tyr His Arg Val Val Gly Ala Gln Arg Cys Pro Ile Val Asp Thr
        355                 360                 365
Phe Trp Gln Thr Glu Thr Gly Gly His Met Leu Thr Pro Leu Pro Val
    370                 375                 380
Pro Thr Pro Met Lys Pro Gly Ser Ala Thr Phe Pro Phe Phe Gly Val
385                 390                 395                 400
Ala Pro Ala Ile Leu Asn Glu Ser Gly Glu Glu Leu Glu Gly Glu Ala
                405                 410                 415
Glu Gly Tyr Leu Val Phe Lys Gln Pro Trp Pro Gly Ile Met Arg Thr
            420                 425                 430
Val Tyr Gly Asn His Glu Arg Phe Glu Thr Thr Tyr Ser Lys Lys Phe
        435                 440                 445
Pro Gly Tyr Tyr Val Thr Gly Asp Gly Cys Gln Arg Asp Gln Asp Gly
    450                 455                 460
Tyr Tyr Trp Ile Thr Gly Arg Ile Asp Asp Met Leu Asn Val Ser Gly
465                 470                 475                 480
His Leu Leu Ser Thr Ala Glu Val Glu Ser Ala Leu Val Glu His Glu
                485                 490                 495
Ala Val Ala Glu Ala Ala Val Val Gly His Pro His Pro Val Lys Gly
            500                 505                 510
Glu Cys Leu Tyr Cys Phe Val Thr Leu Cys Asp Gly His Thr Phe Ser
        515                 520                 525
Pro Lys Leu Thr Glu Glu Leu Lys Lys Gln Ile Arg Glu Lys Ile Gly
    530                 535                 540
Pro Ile Ala Thr Pro Asp Tyr Ile Gln Asn Ala Pro Gly Leu Pro Lys
545                 550                 555                 560
Thr Arg Ser Gly Lys Ile Met Arg Arg Val Leu Arg Lys Ile Ala Gln
                565                 570                 575
Asn Asp His Asp Leu Gly Asp Met Ser Thr Val Ala Asp Pro Ser Val
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Ile Ser His Leu Phe Ser His Arg Cys Leu Thr Ile Gln
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<210> 5355
<211> 1596
<212> DNA
<213> Homo sapiens

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1080
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1260
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<210> 5356
<211> 245
<212> PRT
<213> Homo sapiens

<400> 5356
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Cys Arg Phe His Ser Phe Lys Lys Val Leu Tyr Glu Met Gly Pro Glu
35 40 45
Tyr Ser Ser Asn Val Glu Leu Ala Ser Phe His Ser Thr Ser Lys Gly
50 55 60
Tyr Met Gly Glu Cys Gly Tyr Arg Gly Gly Tyr Met Glu Val Val Asn
65 70 75 80
Leu His Pro Glu Ile Lys Gly Gln Leu Val Lys Leu Leu Ser Val Arg
85 90 95
Leu Cys Pro Pro Val Ser Gly Gln Ala Ala Met Asp Ile Val Val Asn
100 105 110
Pro Pro Val Ala Gly Glu Glu Ser Phe Glu Gln Phe Ser Arg Glu Lys
115 120 125
Glu Ser Val Leu Gly Asn Leu Ala Lys Lys Ala Lys Leu Thr Glu Asp
130 135 140
Leu Phe Asn Gln Val Pro Gly Ile His Cys Asn Pro Leu Gln Gly Ala
145 150 155 160
Met Tyr Ala Phe Pro Arg Ile Phe Ile Pro Ala Lys Ala Val Glu Ala
165 170 175
Ala Gln Ala His Gln Met Ala Pro Asp Met Phe Tyr Cys Met Lys Leu
180 185 190
Leu Glu Glu Thr Gly Ile Cys Val Val Pro Gly Ser Gly Phe Gly Gln
195 200 205
Arg Glu Gly Thr Tyr His Phe Arg Met Thr Ile Leu Pro Pro Val Glu
210 215 220
Lys Leu Lys Thr Val Leu Gln Lys Val Lys Asp Phe His Ile Asn Phe
225 230 235 240
Leu Glu Lys Tyr Ala
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<210> 5357
<211> 1722
<212> DNA
<213> Homo sapiens

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180
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240
cgctttgccc tgcccaccgc ccaccacact ctggggctgc ctgtgggcaa acatatctac
300
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360
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420

tttcctgagg gagggaagat gtctcagtac ctggatagcc tgaaggttgg ggatgtggtg
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600
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960
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1020
aagcactata agccttagat tcctttcctc agagtttcag gtttttcag ttacatctag
1080
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1320
cagtctgtgc aatgggtttt acttaaactt cactgttcaa cctatgagca aatctgtatg
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1722

<210> 5358
<211> 321
<212> PRT
<213> Homo sapiens

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Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
        35                  40                  45
Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
    50                  55                  60
Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
65                  70                  75                  80
Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
                85                  90                  95
Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
            100                 105                 110
Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
        115                 120                 125
Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
    130                 135                 140
Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val
145                 150                 155                 160
Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
                165                 170                 175
Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala
            180                 185                 190
Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu
        195                 200                 205
Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys
    210                 215                 220
Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu
225                 230                 235                 240
Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp
                245                 250                 255
Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe
            260                 265                 270
Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp
        275                 280                 285
Val Leu Val Leu Leu Cys Gly Pro Pro Pro Met Val Gln Leu Ala Cys
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His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr
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Tyr
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<211> 5003
<212> DNA
<213> Homo sapiens

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<211> 1406
<212> PRT
<213> Homo sapiens

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Val Ser Gln Leu Arg Glu Val Tyr Ser Ser Cys Asp Thr Thr Gly Thr
35 40 45
Gly Phe Leu Asp Arg Gln Glu Leu Thr Gln Leu Cys Leu Lys Leu His
50 55 60
Leu Glu Gln Gln Leu Pro Val Leu Leu Gln Thr Leu Leu Gly Asn Asp
65 70 75 80
His Phe Ala Arg Val Asn Phe Glu Glu Phe Lys Glu Gly Phe Val Ala
85 90 95
Val Leu Ser Ser Asn Ala Gly Val Arg Pro Ser Asp Glu Asp Ser Ser
100 105 110
Ser Leu Glu Ser Ala Ala Ser Ser Ala Ile Pro Pro Lys Tyr Val Asn
115 120 125
Gly Ser Lys Trp Tyr Gly Arg Arg Ser Arg Pro Glu Leu Cys Asp Ala
130 135 140
Ala Thr Glu Ala Arg Arg Val Pro Glu Gln Gln Thr Gln Ala Ser Leu
145 150 155 160
Lys Ser His Leu Trp Arg Ser Ala Ser Leu Glu Ser Val Glu Ser Pro
165 170 175
Lys Ser Asp Glu Glu Ala Glu Ser Thr Lys Glu Ala Gln Asn Glu Leu
180 185 190
Phe Glu Ala Gln Gly Gln Leu Gln Thr Trp Asp Ser Glu Asp Phe Gly
195 200 205
Ser Pro Gln Lys Ser Cys Ser Pro Ser Phe Asp Thr Pro Glu Ser Gln
210 215 220
Ile Arg Gly Val Trp Glu Glu Leu Gly Val Gly Ser Ser Gly His Leu
225 230 235 240
Ser Glu Gln Glu Leu Ala Val Val Cys Gln Ser Val Gly Leu Gln Gly
245 250 255
Leu Glu Lys Glu Glu Leu Glu Asp Leu Phe Asn Lys Leu Asp Gln Asp
260 265 270
Gly Asp Gly Lys Val Ser Leu Glu Glu Phe Gln Leu Gly Leu Phe Ser
275 280 285
His Glu Pro Ala Leu Leu Leu Glu Ser Ser Thr Arg Val Lys Pro Ser
290 295 300
Lys Ala Trp Ser His Tyr Gln Val Pro Glu Glu Ser Gly Cys His Thr
305 310 315 320
Thr Thr Thr Ser Ser Leu Val Ser Leu Cys Ser Ser Leu Arg Leu Phe
325 330 335
Ser Ser Ile Asp Asp Gly Ser Gly Phe Ala Phe Pro Asp Gln Val Leu
340 345 350
Ala Met Trp Thr Gln Glu Gly Ile Gln Asn Gly Arg Glu Ile Leu Gln
355 360 365
Ser Leu Asp Phe Ser Val Asp Glu Lys Val Asn Leu Leu Glu Leu Thr
370 375 380
Trp Ala Leu Asp Asn Glu Leu Met Thr Val Asp Ser Ala Val Gln Gln

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Ala Ala Leu Ala Cys Tyr His Gln Glu Leu Ser Tyr Gln Gln Gly Gln
                405                 410                 415
Val Glu Gln Leu Ala Arg Glu Arg Asp Lys Ala Arg Gln Asp Leu Glu
            420                 425                 430
Arg Ala Glu Lys Arg Asn Leu Glu Phe Val Lys Glu Met Asp Asp Cys
        435                 440                 445
His Ser Thr Leu Glu Gln Leu Thr Glu Lys Lys Ile Lys His Leu Glu
    450                 455                 460
Gln Gly Tyr Arg Glu Arg Leu Ser Leu Leu Arg Ser Glu Val Glu Ala
465                 470                 475                 480
Glu Arg Glu Leu Phe Trp Glu Gln Ala His Arg Gln Arg Ala Ala Leu
                485                 490                 495
Glu Trp Asp Val Gly Arg Leu Gln Ala Glu Glu Ala Gly Leu Arg Glu
            500                 505                 510
Lys Leu Thr Leu Ala Leu Lys Glu Asn Ser Arg Leu Gln Lys Glu Ile
        515                 520                 525
Val Glu Val Val Glu Lys Leu Ser Asp Ser Glu Arg Leu Ala Leu Lys
    530                 535                 540
Leu Gln Lys Asp Leu Glu Phe Val Leu Lys Asp Lys Leu Glu Pro Gln
545                 550                 555                 560
Ser Ala Glu Leu Leu Ala Gln Glu Glu Arg Phe Ala Ala Val Leu Lys
                565                 570                 575
Glu Tyr Glu Leu Lys Cys Arg Asp Leu Gln Asp Arg Asn Asp Glu Leu
            580                 585                 590
Gln Ala Glu Leu Glu Gly Leu Trp Ala Arg Leu Pro Lys Asn Arg His
        595                 600                 605
Ser Pro Ser Trp Ser Pro Asp Gly Arg Arg Arg Gln Leu Pro Gly Leu
    610                 615                 620
Gly Pro Ala Gly Ile Ser Phe Leu Gly Asn Ser Ala Pro Val Ser Ile
625                 630                 635                 640
Glu Thr Glu Leu Met Met Glu Gln Val Lys Glu His Tyr Gln Asp Leu
                645                 650                 655
Arg Thr Gln Leu Glu Thr Lys Val Asn Tyr Tyr Glu Arg Glu Ile Ala
            660                 665                 670
Ala Leu Lys Arg Asn Phe Glu Lys Glu Arg Lys Asp Met Glu Gln Ala
        675                 680                 685
Arg Arg Arg Glu Val Ser Val Leu Glu Gly Gln Lys Ala Asp Leu Glu
    690                 695                 700
Glu Leu His Glu Lys Ser Gln Glu Val Ile Trp Gly Leu Gln Glu Gln
705                 710                 715                 720
Leu Gln Asp Thr Ala Arg Gly Pro Glu Pro Glu Gln Met Gly Leu Ala
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Pro Cys Cys Thr Gln Ala Leu Cys Gly Leu Ala Leu Arg His His Ser
            740                 745                 750
His Leu Gln Gln Ile Arg Arg Glu Ala Glu Ala Glu Leu Ser Gly Glu
        755                 760                 765
Leu Ser Gly Leu Gly Ala Leu Pro Ala Arg Arg Asp Leu Thr Leu Glu
    770                 775                 780
Leu Glu Glu Pro Pro Gln Gly Pro Leu Pro Arg Gly Ser Gln Arg Ser
785                 790                 795                 800
Glu Gln Leu Glu Leu Glu Arg Ala Leu Lys Leu Gln Pro Cys Ala Ser
                805                 810                 815
Glu Lys Arg Ala Gln Met Cys Val Ser Leu Ala Leu Glu Glu Glu Glu
```

820 825 830
Leu Glu Leu Ala Arg Gly Lys Arg Val Asp Gly Pro Ser Leu Glu Ala
835 840 845
Glu Met Gln Ala Leu Pro Lys Asp Gly Leu Val Ala Gly Ser Gly Gln
850 855 860
Glu Gly Thr Arg Gly Leu Leu Pro Leu Arg Pro Gly Cys Gly Glu Arg
865 870 875 880
Pro Leu Ala Trp Leu Ala Pro Gly Asp Gly Arg Glu Ser Glu Glu Ala
885 890 895
Ala Gly Ala Gly Pro Arg Arg Arg Gln Ala Gln Asp Thr Glu Ala Thr
900 905 910
Gln Ser Pro Ala Pro Ala Pro Ala Pro Ala Ser His Gly Pro Ser Glu
915 920 925
Arg Trp Ser Arg Met Gln Pro Cys Gly Val Asp Gly Asp Ile Val Pro
930 935 940
Lys Glu Pro Glu Pro Phe Gly Ala Ser Ala Ala Gly Leu Glu Gln Pro
945 950 955 960
Gly Ala Arg Glu Leu Pro Leu Leu Gly Thr Glu Arg Asp Ala Ser Gln
965 970 975
Thr Gln Pro Arg Met Trp Glu Pro Pro Leu Arg Pro Ala Ala Ser Cys
980 985 990
Arg Gly Gln Ala Glu Arg Leu Gln Ala Ile Gln Glu Glu Arg Ala Arg
995 1000 1005
Ser Trp Ser Arg Gly Thr Gln Glu Gln Ala Ser Glu Gln Gln Ala Arg
1010 1015 1020
Ala Glu Gly Ala Leu Glu Pro Gly Cys His Lys His Ser Val Glu Val
1025 1030 1035 1040
Ala Arg Arg Gly Ser Leu Pro Ser His Leu Gln Leu Ala Asp Pro Gln
1045 1050 1055
Gly Ser Trp Gln Glu Gln Leu Ala Ala Pro Glu Glu Gly Glu Thr Lys
1060 1065 1070
Ile Ala Leu Glu Arg Glu Lys Asp Asp Met Glu Thr Lys Leu Leu His
1075 1080 1085
Leu Glu Asp Val Val Arg Ala Leu Glu Lys His Val Asp Leu Arg Glu
1090 1095 1100
Asn Asp Arg Leu Glu Phe His Arg Leu Ser Glu Glu Asn Thr Leu Leu
1105 1110 1115 1120
Lys Asn Asp Leu Gly Arg Val Arg Gln Glu Leu Glu Ala Ala Glu Ser
1125 1130 1135
Thr His Asp Ala Gln Arg Lys Glu Ile Glu Val Leu Lys Lys Asp Lys
1140 1145 1150
Glu Lys Ala Cys Ser Glu Met Glu Val Leu Asn Arg Gln Asn Gln Asn
1155 1160 1165
Tyr Lys Asp Gln Leu Ser Gln Leu Asn Val Arg Val Leu Gln Leu Gly
1170 1175 1180
Gln Glu Ala Ser Thr His Gln Ala Gln Asn Glu Glu His Arg Val Thr
1185 1190 1195 1200
Ile Gln Met Leu Thr Gln Ser Leu Glu Glu Val Val Arg Ser Gly Gln
1205 1210 1215
Gln Gln Ser Asp Gln Ile Gln Lys Leu Arg Val Glu Leu Glu Cys Leu
1220 1225 1230
Asn Gln Glu His Gln Ser Leu Gln Leu Pro Trp Ser Glu Leu Thr Gln
1235 1240 1245
Thr Leu Glu Glu Ser Gln Asp Gln Val Gln Gly Ala His Leu Arg Leu

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    1250                1255                1260
Arg Gln Ala Gln Ala Gln His Leu Gln Glu Val Arg Leu Val Pro Gln
1265                1270                1275                1280
Asp Arg Val Ala Glu Leu His Arg Leu Leu Ser Leu Gln Gly Glu Gln
                1285                1290                1295
Ala Arg Arg Arg Leu Asp Ala Gln Arg Glu Glu His Glu Lys Gln Leu
            1300                1305                1310
Lys Ala Thr Glu Glu Arg Val Glu Glu Ala Glu Met Ile Leu Lys Asn
        1315                1320                1325
Met Glu Met Leu Leu Gln Glu Lys Val Asp Lys Leu Lys Glu Gln Phe
    1330                1335                1340
Glu Lys Asn Thr Lys Ser Asp Leu Leu Leu Lys Glu Leu Tyr Val Glu
1345                1350                1355                1360
Asn Ala His Leu Val Arg Ala Leu Gln Ala Thr Glu Glu Lys Gln Arg
                1365                1370                1375
Gly Ala Glu Lys Gln Ser Arg Leu Leu Glu Glu Lys Val Arg Ala Leu
            1380                1385                1390
Asn Lys Leu Val Ser Arg Ile Ala Pro Ala Ala Leu Ser Val
        1395                1400                1405
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<210> 5361
<211> 1080
<212> DNA
<213> Homo sapiens

<400> 5361
nngaattcct ctccaaagca gagtacgtca agttttccct ggtgtcagac agcatttcac
60
catgaaaccc taagacctgc ctcctgggct ccttccagct ggtgggcctg gtgtgaaggt
120
gggcttcctg ggcctccggc agatggagga tggcattaaa tgccaacaca gtcagcttac
180
catccacaag gccagcagct gccaacagct gccctagacc tatcaacaag acaacttcat
240
ggctcccaat gggaatggag gctgggcccg ccctacttag agcaggggaa agaacttttc
300
cctcaaagag ccggggcagg atgccagaat ctaactacat cctctcccgg tttgcagttc
360
taggaagtgg aatttgctgc cctaggcgtg gtctaaagga caagtttaga aatgattcaa
420
ctcaagttcc taaacagagt aagtgccagt tgatgtccca ccgtggatcc tttactccag
480
aaaaattgta atgatggctc ggccaccgcc ttggctagag tcccactgca cgcgtgtcgt
540
gagggccgat gggcaagtcc gtccggtttt ttttgttgtt gttgttgttt tttgagatgg
600
agtctcgccc tgnttgccca gactgaagtg caaaggcccg atctcaactc actgcaacct
660
ccgcctcctg ggttcaaagg attctcctgt ctcagcctcc tgagtagctg ggattacagg
720
cacccgccag cacgcccagc tttttttttgt atttttagta gagacggggt tttatcatgt
780
tggccaggct ggtctcgaac gcctgacctc atgnnatcca cccgccttgg cctcccaaat
840

tgctgggacc acaggcgtga gccaccgcgc ccggccgtct gtctggtttt caaaccaatc
900
aatgaacccg taagcctctt tggtatatat aacaatgaaa aaattcatta agccatgaaa
960
tctagaaata agtcatattt ctgagttgat aaaatgcttt tctgaacata cattttaggt
1020
atctgggcgt gctggcgggt gcctgtaatc ccagctactc ggggaggctt gagacaggga
1080

<210> 5362
<211> 165
<212> PRT
<213> Homo sapiens

<400> 5362
Cys Pro Thr Val Asp Pro Leu Leu Gln Lys Asn Cys Asn Asp Gly Ser
1 5 10 15
Ala Thr Ala Leu Ala Arg Val Pro Leu His Ala Cys Arg Glu Gly Arg
20 25 30
Trp Ala Ser Pro Ser Gly Phe Phe Cys Cys Cys Cys Cys Phe Leu Arg
35 40 45
Trp Ser Leu Ala Leu Xaa Ala Gln Thr Glu Val Gln Arg Pro Asp Leu
50 55 60
Asn Ser Leu Gln Pro Pro Pro Pro Gly Phe Lys Gly Phe Ser Cys Leu
65 70 75 80
Ser Leu Leu Ser Ser Trp Asp Tyr Arg His Pro Pro Ala Arg Pro Ala
85 90 95
Phe Phe Cys Ile Phe Ser Arg Asp Gly Val Leu Ser Cys Trp Pro Gly
100 105 110
Trp Ser Arg Thr Pro Asp Leu Met Xaa Ser Thr Arg Leu Gly Leu Pro
115 120 125
Asn Cys Trp Asp His Arg Arg Glu Pro Pro Arg Pro Ala Val Cys Leu
130 135 140
Val Phe Lys Pro Ile Asn Glu Pro Val Ser Leu Phe Gly Ile Tyr Asn
145 150 155 160
Asn Glu Lys Ile His
165

<210> 5363
<211> 894
<212> DNA
<213> Homo sapiens

<400> 5363
cggccggcgc gggcccctgg cgggcgggcg gtacagcccc aagcctgaga cccggacctg
60
agcatcgcag gttcgagtcc cgccccgcct ggggcgaagc cgggggtggc ggcgacctcg
120
cggcgttgca ccggctctgt gagcacctcc cctctgagca cttcccttgt gacaggccac
180
ttcccttgtg acaggcccag gacgaggtgg ccaggcggcc cccatggcgt ccctggtcta
240
ggcggagaac cgcctgggcg atgagtgaga acctcgacaa cgagggcccg aagcccatgg
300

agagctgtgg ccaggagagc agcagtgccc tgagctgccc taccgtctcg gtgccccctg
360
cagccccggc agccctggag gaggtggaga aagagggcgc tggggcggct acagggcncg
420
gggcctcagc ccgggctcta cagctacatc agggatgact tgtttacctc tgagatcttt
480
aaactggagc tgcagaacgc gcctcgccac gccagcttca gcgacgtccg gcgcttcctg
540
ggccgctttg gtctgcagcc ccacaaaacc aaactctttg ggcaaccacc ctgcgccttt
600
gtgacattcc gcagcgctgc agagagggac aaggccctgc gcgttttgca tggtgccctc
660
tggaaaggcc gcccactcag tgtggcctgg cccggcccaa ggccgacccc atggccagga
720
ggaggcngac aggagggtga gagtgagcca ccagtaacac gangtggccg acgtggtgac
780
ccctctatgg acagtgccct antgctgagc agcttgagcg gaagcagctg gagtgcgagc
840
aggtgctgca gaaacnttgc ccaggaaatc gggagcacca accgtgcctt gcgt
894

<210> 5364
<211> 187
<212> PRT
<213> Homo sapiens

<400> 5364
Ala Ala Leu Pro Ser Arg Cys Pro Leu Gln Pro Arg Gln Pro Trp Arg
1 5 10 15
Arg Trp Arg Lys Arg Ala Leu Gly Arg Leu Gln Gly Xaa Gly Pro Gln
20 25 30
Pro Gly Leu Tyr Ser Tyr Ile Arg Asp Asp Leu Phe Thr Ser Glu Ile
35 40 45
Phe Lys Leu Glu Leu Gln Asn Ala Pro Arg His Ala Ser Phe Ser Asp
50 55 60
Val Arg Arg Phe Leu Gly Arg Phe Gly Leu Gln Pro His Lys Thr Lys
65 70 75 80
Leu Phe Gly Gln Pro Pro Cys Ala Phe Val Thr Phe Arg Ser Ala Ala
85 90 95
Glu Arg Asp Lys Ala Leu Arg Val Leu His Gly Ala Leu Trp Lys Gly
100 105 110
Arg Pro Leu Ser Val Ala Trp Pro Gly Pro Arg Pro Thr Pro Trp Pro
115 120 125
Gly Gly Gly Xaa Gln Glu Gly Glu Ser Glu Pro Pro Val Thr Arg Xaa
130 135 140
Gly Arg Arg Gly Asp Pro Ser Met Asp Ser Ala Leu Xaa Leu Ser Ser
145 150 155 160
Leu Ser Gly Ser Ser Trp Ser Ala Ser Arg Cys Cys Arg Asn Xaa Ala
165 170 175
Gln Glu Ile Gly Ser Thr Asn Arg Ala Leu Arg
180 185

<210> 5365
<211> 1824

<212> DNA
<213> Homo sapiens

<400> 5365
cagcctttcc cggcagcgag cgctcggcca ggtgcactag gcgctgtgcg ggcccccctt
60
ccccgcgagt ccctcaagcg ggaacctgcc tcgtgtctcc caggagccat ggaggctgtg
120
gaactcgcca gaaaactgca ggaggaagct acgtgctcca tctgtctgga ttacttcaca
180
gaccctgtga tgaccacctg tggccacaac ttctgccgag cctgcatcca gctgagctgg
240
gaaaaggcga ggggcaagaa ggggaggcgg aagcggaagg gctccttccc ctgccccgag
300
tgcagagaga tgtccccgca gaggaacctg ctgcccaacc ggctgctgac caaggtggcc
360
gagatggcgc agcagcatcc tggtctgcag aagcaagacc tgtgccagga gcaccacgag
420
cccctcaagc ttttctgcca gaaggaccag agccccatct gtgtggtgtg cagggagtcc
480
cgggagcacc ggctgcacag ggtgctgccc gccgaggagg cagtgcaggg gtacaagttg
540
aagctggagg aggacatgga gtaccttcgg gagcagatca ccaggacagg gaatctgcag
600
gccagggagg agcagagctt agccgagtgg cagggcaagg tgaaggagcg gagagaacgc
660
attgtgctgg agtttgagaa gatgaacctc tacctggtgg aagaagagca gaggctcctc
720
caggctctgg agacggaaga agaggagact gccagcaggc tccgggagag cgtggcctgc
780
ctggaccggc agggtcactc tctggagctg ctgctgctgc agctggagga gcggagcaca
840
caggggcccc tccagatgct gcaggacatg aaggaacccc tgagcaggaa gaacaacgtg
900
agtgtgcagt gcccagaggt tgcccccca accagaccca ggactgtgtg cagagttccc
960
ggacagattg aagtgctaag aggctttcta gaggatgtgg tgcctgatgc cacctccgcg
1020
taccctacc tcctcctgta tgagagccgc cagaggcgct acctcggctc ttcgccggag
1080
ggcagtgggt tctgcagcaa ggaccgattt gtggcttacc cctgtgctgt gggccagacg
1140
gccttctcct ctgggaggca ctactgggag gtgggcatga acatcaccgg ggacgcgttg
1200
tgggccctgg gtgtgtgcag ggacaacgtg agccggaaag acagggtcct caagtgcccc
1260
gaaaacggct tctgggtggt gcagctgtcc aaggggacca agtacttatc caccttctct
1320
gccctaaccc cggtcatgct gatggagcct cccagccaca tgggcatctt cctggacttc
1380
gaagccgggg aagtgtcctt ctacagtgta agcgatgggt cccacctgca cacctactcc
1440
caggccacct tcccaggccc cctgcagcct ttcttctgcc tgggggctcc gaagtctggt
1500

cagatggtca tctccacagt gaccatgtgg gtgaaaggat agacacagac cgggggactc
1560
gggcactgct cctggctctg cagaaggtgt gggccttctg cttactgcag gccacctgcc
1620
agggttctct ggcatcacgc tggcagccat tagacacaca ggggggtttc tcaaattcta
1680
aatataattg tgattagaac tgtcaaacat taagagggta tactgacaga tgcttcctag
1740
aggaaacttt tgaaagcccc tgcgttctga gtggaccgat ttctaaatcc atacctacac
1800
accaaaaaaa aaaaaaagtc gagc
1824

<210> 5366
<211> 477
<212> PRT
<213> Homo sapiens

<400> 5366
Met Glu Ala Val Glu Leu Ala Arg Lys Leu Gln Glu Glu Ala Thr Cys
1 5 10 15
Ser Ile Cys Leu Asp Tyr Phe Thr Asp Pro Val Met Thr Thr Cys Gly
20 25 30
His Asn Phe Cys Arg Ala Cys Ile Gln Leu Ser Trp Glu Lys Ala Arg
35 40 45
Gly Lys Lys Gly Arg Arg Lys Arg Lys Gly Ser Phe Pro Cys Pro Glu
50 55 60
Cys Arg Glu Met Ser Pro Gln Arg Asn Leu Leu Pro Asn Arg Leu Leu
65 70 75 80
Thr Lys Val Ala Glu Met Ala Gln Gln His Pro Gly Leu Gln Lys Gln
85 90 95
Asp Leu Cys Gln Glu His His Glu Pro Leu Lys Leu Phe Cys Gln Lys
100 105 110
Asp Gln Ser Pro Ile Cys Val Val Cys Arg Glu Ser Arg Glu His Arg
115 120 125
Leu His Arg Val Leu Pro Ala Glu Glu Ala Val Gln Gly Tyr Lys Leu
130 135 140
Lys Leu Glu Glu Asp Met Glu Tyr Leu Arg Glu Gln Ile Thr Arg Thr
145 150 155 160
Gly Asn Leu Gln Ala Arg Glu Glu Gln Ser Leu Ala Glu Trp Gln Gly
165 170 175
Lys Val Lys Glu Arg Arg Glu Arg Ile Val Leu Glu Phe Glu Lys Met
180 185 190
Asn Leu Tyr Leu Val Glu Glu Glu Gln Arg Leu Leu Gln Ala Leu Glu
195 200 205
Thr Glu Glu Glu Glu Thr Ala Ser Arg Leu Arg Glu Ser Val Ala Cys
210 215 220
Leu Asp Arg Gln Gly His Ser Leu Glu Leu Leu Leu Leu Gln Leu Glu
225 230 235 240
Glu Arg Ser Thr Gln Gly Pro Leu Gln Met Leu Gln Asp Met Lys Glu
245 250 255
Pro Leu Ser Arg Lys Asn Asn Val Ser Val Gln Cys Pro Glu Val Ala
260 265 270
Pro Pro Thr Arg Pro Arg Thr Val Cys Arg Val Pro Gly Gln Ile Glu

```
        275                 280                 285
Val Leu Arg Gly Phe Leu Glu Asp Val Val Pro Asp Ala Thr Ser Ala
    290                 295                 300
Tyr Pro Tyr Leu Leu Leu Tyr Glu Ser Arg Gln Arg Arg Tyr Leu Gly
305                 310                 315                 320
Ser Ser Pro Glu Gly Ser Gly Phe Cys Ser Lys Asp Arg Phe Val Ala
                325                 330                 335
Tyr Pro Cys Ala Val Gly Gln Thr Ala Phe Ser Ser Gly Arg His Tyr
            340                 345                 350
Trp Glu Val Gly Met Asn Ile Thr Gly Asp Ala Leu Trp Ala Leu Gly
        355                 360                 365
Val Cys Arg Asp Asn Val Ser Arg Lys Asp Arg Val Leu Lys Cys Pro
    370                 375                 380
Glu Asn Gly Phe Trp Val Val Gln Leu Ser Lys Gly Thr Lys Tyr Leu
385                 390                 395                 400
Ser Thr Phe Ser Ala Leu Thr Pro Val Met Leu Met Glu Pro Pro Ser
                405                 410                 415
His Met Gly Ile Phe Leu Asp Phe Glu Ala Gly Glu Val Ser Phe Tyr
            420                 425                 430
Ser Val Ser Asp Gly Ser His Leu His Thr Tyr Ser Gln Ala Thr Phe
        435                 440                 445
Pro Gly Pro Leu Gln Pro Phe Phe Cys Leu Gly Ala Pro Lys Ser Gly
    450                 455                 460
Gln Met Val Ile Ser Thr Val Thr Met Trp Val Lys Gly
465                 470                 475
```

<210> 5367
<211> 549
<212> DNA
<213> Homo sapiens

<400> 5367
nntcctcttc cccctcattc tcttcccccc cgtcttcagg aggccggtgg gcaggagctg
60
ggatctcggg tggctgcatg cgtgtctcct tgggggaagt ctcgggggaa gtaggctgtg
120
gagtctcagg ggctggggat gctgcccccg aagcccccta cttttgggga gttcctgtcc
180
cagcacaaag ctgaggccag cagccgcaga aggagaaaga gcagtcggcc ccaggccaag
240
gcagcgccca gggcctacag tgaccatgat gaccgctggg agacaaaaga aggggcagca
300
tccccagccc ctgagactcc acagcctact tcccccgaga cttcccccaa ggagacaccc
360
atgcagccac ccgagatccc agctcctgcc caccggcctc ctgaagacga gggggaagag
420
aatgaggggg aagaggatga agaatgggag gacataagtg aggatgagga agaggaggag
480
atcgaggtgg aagaaggtga tgaggaggaa ccagcccaag accaccaagc cccagaggct
540
gcccccacc
549

<210> 5368

<211> 137
<212> PRT
<213> Homo sapiens

<400> 5368
Met Leu Pro Pro Lys Pro Pro Thr Phe Gly Glu Phe Leu Ser Gln His
1 5 10 15
Lys Ala Glu Ala Ser Ser Arg Arg Arg Arg Lys Ser Ser Arg Pro Gln
20 25 30
Ala Lys Ala Ala Pro Arg Ala Tyr Ser Asp His Asp Asp Arg Trp Glu
35 40 45
Thr Lys Glu Gly Ala Ala Ser Pro Ala Pro Glu Thr Pro Gln Pro Thr
50 55 60
Ser Pro Glu Thr Ser Pro Lys Glu Thr Pro Met Gln Pro Pro Glu Ile
65 70 75 80
Pro Ala Pro Ala His Arg Pro Pro Glu Asp Glu Gly Glu Glu Asn Glu
85 90 95
Gly Glu Glu Asp Glu Glu Trp Glu Asp Ile Ser Glu Asp Glu Glu Glu
100 105 110
Glu Glu Ile Glu Val Glu Glu Gly Asp Glu Glu Glu Pro Ala Gln Asp
115 120 125
His Gln Ala Pro Glu Ala Ala Pro Thr
130 135

<210> 5369
<211> 646
<212> DNA
<213> Homo sapiens

<400> 5369
ngggaggcgg gaggcgcggc cgccgctcca gctgcgagtc cgcccgccgc ccgccgccgc
60
cgccgccggc tcggtcccgc gcccgccatg gcccgcctga cggagagcga ggcgcgccgg
120
cagcagcagc agctcctgca gccgcggccc tcgcccgtgg gcagcagcgg gcccgagccc
180
cccgggggge agcccgacgg catgaaggac ctggacgcca tcaaactctt cgtgggccag
240
atcccgcggc acctggacga gaaggacctc aagccgctct tcgagcagtt cggccgcatc
300
tacgagctca cggtgctcaa agacccctac acggggatgc acaaaggtgg gcgcccggcc
360
ccctcccccc tctccccctc cctccgcctc ccaccccacc ttccggcatc ttctctcccc
420
catcaccatc cctcctctgc tcacctccct cctctgcctg cctctgccgg agcatcggtt
480
cttacccccc ccctcccacc cacccctcct cccctctctg ggggtgcagc tgacagatcc
540
gagcgggccc cctcccctcc tccgcccccc ctccctccct ccccaccttc cggcatctcc
600
tctctctctc cctctctctc tccctctctc tctccctttc tcttct
646

<210> 5370

<211> 148
<212> PRT
<213> Homo sapiens

<400> 5370
Met Lys Asp Leu Asp Ala Ile Lys Leu Phe Val Gly Gln Ile Pro Arg
1 5 10 15
His Leu Asp Glu Lys Asp Leu Lys Pro Leu Phe Glu Gln Phe Gly Arg
20 25 30
Ile Tyr Glu Leu Thr Val Leu Lys Asp Pro Tyr Thr Gly Met His Lys
35 40 45
Gly Gly Arg Pro Ala Pro Ser Pro Leu Ser Pro Ser Leu Arg Leu Pro
50 55 60
Pro His Leu Pro Ala Ser Ser Leu Pro His His His Pro Ser Ser Ala
65 70 75 80
His Leu Pro Pro Leu Pro Ala Ser Ala Gly Ala Ser Val Leu Thr Pro
85 90 95
Ser Leu Pro Pro Thr Pro Pro Pro Leu Ser Gly Gly Ala Ala Asp Arg
100 105 110
Ser Glu Arg Ala Pro Ser Pro Pro Pro Pro Pro Leu Pro Pro Ser Pro
115 120 125
Pro Ser Gly Ile Ser Ser Leu Ser Pro Ser Leu Ser Pro Ser Leu Ser
130 135 140
Pro Phe Leu Phe
145

<210> 5371
<211> 1177
<212> DNA
<213> Homo sapiens

<400> 5371
nnacacagtg ccagcgccct catgtaccac cggaacgaga gcctacagcc cagcctgcag
60
agcccgcaaa cggagctgcg gtcggacttc cagtgcgttg tgggcttcgg gggcattcac
120
tccacgccgt ccactgtcct cagcgaccag gccaagtatc taaacccctt actgggagag
180
tggaagcact tcactgcctc cctggccccc cgcatgtcca accagggcat cgcggtgctc
240
aacaacttcg tatacttgat tggaggggac aacaatgtcc aaggatttcg agcagagtcc
300
cgatgctgga ggtatgaccc acggcacaac cgctggnttc cagatccagt ccctgcagca
360
ggagcacgcc gacctgtcnn cgtgtgtg-t gtaggcaggt acatctacgc tgtggcgggc
420
cgtgactacc acaatgacct gaatgctgtg gagcgctacg accctgccac caactcctgg
480
gcatacgtgg ccccactcaa gagggaggtg tatgcccacg caggcgcgac gctggagggg
540
aagatgtata tcacctgcgg ccgcagaggg gaggattacc tgaaagagac acactgctac
600
gatccaggca gcaacacttg gcacacactg gctgatgggc ctgtgcggcg cgcctggcac
660

ggcatggcaa ccctcctcaa caagctgtat gtgatcgggg gcagcaacaa cgatgccgga
720
tacaggaggg acgtgcacca ggtggcctgc tacagctgca cgtctggaca gtggtcatct
780
gtctgcccac tccctgctgg gcacggtgag cctggcattg ctgtgctgga caacaggatc
840
tatgtgttag gtggccgctc acacaaccgc ggcagccgca caggctacgt gcacatttac
900
gatgtggaga aggactgctg ggaggaaggg ccccagctgg acaactccat ctcaggcctg
960
gcggcctgtg tgctcaccct gccccgctcc ctgctccttg agccgccccg cgggacccct
1020
gaccgcagcc aggccgaccc ggactttgcc tctgaggtga tgagtgtgtc tgactgggag
1080
gagtttgaca actccagtga ggactaggct ccctgtgcct ggcatcagag ggaagggagg
1140
ctggggctgc agggcagtga aacccacgca gcctagg
1177

<210> 5372
<211> 368
<212> PRT
<213> Homo sapiens

<400> 5372
Xaa His Ser Ala Ser Ala Leu Met Tyr His Arg Asn Glu Ser Leu Gln
1 5 10 15
Pro Ser Leu Gln Ser Pro Gln Thr Glu Leu Arg Ser Asp Phe Gln Cys
20 25 30
Val Val Gly Phe Gly Gly Ile His Ser Thr Pro Ser Thr Val Leu Ser
35 40 45
Asp Gln Ala Lys Tyr Leu Asn Pro Leu Leu Gly Glu Trp Lys His Phe
50 55 60
Thr Ala Ser Leu Ala Pro Arg Met Ser Asn Gln Gly Ile Ala Val Leu
65 70 75 80
Asn Asn Phe Val Tyr Leu Ile Gly Gly Asp Asn Asn Val Gln Gly Phe
85 90 95
Arg Ala Glu Ser Arg Cys Trp Arg Tyr Asp Pro Arg His Asn Arg Trp
100 105 110
Xaa Pro Asp Pro Val Pro Ala Ala Gly Ala Arg Arg Pro Val Xaa Val
115 120 125
Cys Val Val Gly Arg Tyr Ile Tyr Ala Val Ala Gly Arg Asp Tyr His
130 135 140
Asn Asp Leu Asn Ala Val Glu Arg Tyr Asp Pro Ala Thr Asn Ser Trp
145 150 155 160
Ala Tyr Val Ala Pro Leu Lys Arg Glu Val Tyr Ala His Ala Gly Ala
165 170 175
Thr Leu Glu Gly Lys Met Tyr Ile Thr Cys Gly Arg Arg Gly Glu Asp
180 185 190
Tyr Leu Lys Glu Thr His Cys Tyr Asp Pro Gly Ser Asn Thr Trp His
195 200 205
Thr Leu Ala Asp Gly Pro Val Arg Arg Ala Trp His Gly Met Ala Thr
210 215 220
Leu Leu Asn Lys Leu Tyr Val Ile Gly Gly Ser Asn Asn Asp Ala Gly

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225                 230                 235                 240
Tyr Arg Arg Asp Val His Gln Val Ala Cys Tyr Ser Cys Thr Ser Gly
                245                 250                 255
Gln Trp Ser Ser Val Cys Pro Leu Pro Ala Gly His Gly Glu Pro Gly
            260                 265                 270
Ile Ala Val Leu Asp Asn Arg Ile Tyr Val Leu Gly Gly Arg Ser His
        275                 280                 285
Asn Arg Gly Ser Arg Thr Gly Tyr Val His Ile Tyr Asp Val Glu Lys
    290                 295                 300
Asp Cys Trp Glu Glu Gly Pro Gln Leu Asp Asn Ser Ile Ser Gly Leu
305                 310                 315                 320
Ala Ala Cys Val Leu Thr Leu Pro Arg Ser Leu Leu Leu Glu Pro Pro
                325                 330                 335
Arg Gly Thr Pro Asp Arg Ser Gln Ala Asp Pro Asp Phe Ala Ser Glu
            340                 345                 350
Val Met Ser Val Ser Asp Trp Glu Glu Phe Asp Asn Ser Ser Glu Asp
        355                 360                 365
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<210> 5373
<211> 4221
<212> DNA
<213> Homo sapiens

<400> 5373

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<212> PRT
<213> Homo sapiens

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Asp Asp Ser Glu Val Pro Ser Ser Ser Gly Ile Asn Ser Thr Lys Ser
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Gln Asp Lys Asp Val Asn Glu Gly Glu Thr Ser Asp Gly Val Arg Lys
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Ser Val His Lys Val Phe Ala Ser Met Leu Gly Glu Asn Glu Asp Asp
85 90 95
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Thr
100 105 110
Pro Glu Gln Pro Thr Ala Gly Asp Val Phe Val Leu Glu Met Val Leu
115 120 125
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Leu Pro Arg Ala Leu Arg Gly Leu Met Gly Glu Ala Asn Ile Arg Phe
145 150 155 160
Ala Arg Gly Glu Arg Glu Glu Ala Ile Leu Met Cys Met Glu Ile Ile
165 170 175
Arg Gln Ala Pro Leu Ala Tyr Glu Pro Phe Ser Thr Leu Ala Met Ile
180 185 190
Tyr Glu Asp Gln Gly Asp Met Glu Lys Ser Leu Gln Phe Glu Leu Ile
195 200 205
Ala Ala His Leu Asn Pro Ser Asp Thr Glu Glu Trp Val Arg Leu Ala
210 215 220
Glu Met Ser Leu Glu Gln Asp Asn Ile Lys Gln Ala Ile Phe Cys Tyr
225 230 235 240
Thr Lys Ala Leu Lys Tyr Glu Pro Thr Asn Val Arg Tyr Leu Trp Glu
245 250 255
Arg Ser Ser Leu Tyr Glu Gln Met Gly Asp His Lys Met Ala Met Asp
260 265 270
Gly Tyr Arg Arg Ile Leu Asn Leu Leu Ser Pro Ser Asp Gly Glu Arg
275 280 285
Phe Met Gln Leu Ala Arg Asp Met Ala Lys Ser Tyr Tyr Glu Ala Asn
290 295 300
Asp Val Thr Ser Ala Ile Asn Ile Ile Asp Glu Ala Phe Ser Lys His
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Gln Gly Leu Val Ser Met Glu Asp Val Asn Ile Ala Ala Glu Leu Tyr
325 330 335
Ile Ser Asn Lys Gln Tyr Asp Lys Ala Leu Glu Ile Ile Thr Asp Phe

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Pro Ile Asp Ile Thr Val Lys Leu Met Val Cys Leu Val His Leu Asn
385                 390                 395                 400
Ile Leu Glu Pro Leu Asn Pro Leu Leu Thr Thr Leu Val Glu Gln Asn
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Pro Glu Asp Met Gly Asp Leu Tyr Leu Asp Val Ala Glu Ala Phe Leu
            420                 425                 430
Asp Val Gly Glu Tyr Asn Ser Ala Leu Pro Leu Leu Ser Ala Leu Val
        435                 440                 445
Cys Ser Glu Arg Tyr Asn Leu Ala Val Val Trp Leu Arg His Ala Glu
    450                 455                 460
Cys Leu Lys Ala Leu Gly Tyr Met Glu Arg Ala Ala Glu Ser Tyr Gly
465                 470                 475                 480
Lys Val Val Asp Leu Ala Pro Leu His Leu Asp Ala Arg Ile Ser Leu
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Ser Thr Leu Gln Gln Gln Leu Gly Gln Pro Glu Lys Ala Leu Glu Ala
            500                 505                 510
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Ala Gln Gln Glu Leu Lys Leu Leu Leu His Arg Ser Thr Leu Leu Phe
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Ser Gln Gly Lys Met Tyr Gly Tyr Val Asp Thr Leu Leu Thr Met Leu
545                 550                 555                 560
Ala Met Leu Leu Lys Val Ala Met Asn Arg Ala Gln Val Cys Leu Ile
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Ser Ser Ser Lys Ser Gly Glu Arg His Leu Tyr Leu Ile Lys Val Ser
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Arg Asp Lys Ile Ser Asp Ser Asn Asp Gln Glu Ser Ala Asn Cys Asp
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Ser Phe Tyr Asp Asp Arg Gln Lys Arg Lys Glu Leu Glu Tyr Phe Gly
            660                 665                 670
Leu Ser Ala Ala Ile Leu Asp Lys Asn Phe Arg Lys Ala Tyr Asn Tyr
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Ile Arg Ile Met Val Met Glu Asn Val Asn Lys Pro Gln Leu Trp Asn
    690                 695                 700
Ile Phe Asn Gln Val Thr Met His Ser Gln Asp Val Arg His His Arg
705                 710                 715                 720
Phe Cys Leu Arg Leu Met Leu Lys Asn Pro Glu Asn His Ala Leu Cys
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Val Leu Asn Gly His Asn Ala Phe Val Ser Gly Ser Phe Lys His Ala
            740                 745                 750
Leu Gly Gln Tyr Val Gln Ala Phe Arg Thr His Pro Asp Glu Pro Leu
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Tyr Ser Phe Cys Ile Gly Leu Thr Phe Ile His Met Ala Ser Gln Lys
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Tyr Val Leu Arg Arg His Ala Leu Ile Val Gln Gly Phe Ser Phe Leu
785                 790                 795                 800
Asn Arg Tyr Leu Ser Leu Arg Gly Pro Cys Gln Glu Ser Phe Tyr Asn
                805                 810                 815
Leu Gly Arg Gly Leu His Gln Leu Gly Leu Ile His Leu Ala Ile His
            820                 825                 830
Tyr Tyr Gln Lys Ala Leu Glu Leu Pro Pro Leu Val Val Glu Gly Ile
        835                 840                 845
Glu Leu Asp Gln Leu Asp Leu Arg Arg Asp Ile Ala Tyr Asn Leu Ser
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<213> Homo sapiens

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Arg Ala Ser Arg Val Leu Ser Gly Asn Asp Leu Ser Ser Ala Asn Gly
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Leu Gln Arg Ala Ala Ala Ser Ser Glu Ser Pro Val Ala Arg Thr Trp
        35                  40                  45
Val Gln Leu Lys Ser Ile Ser Leu Phe Ala Phe Ser Glu Ala Ser Pro
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Cys His Arg Pro Arg Thr Ile Ser Ile Phe Asn Pro Arg Asn His Thr
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<212> PRT
<213> Homo sapiens

<400> 5378
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Thr Pro Pro Arg Arg Ala Pro Asp Gln Ala Ala Glu Ile Gly Ser Arg
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65   70   75   80
Pro Ser Tyr Ala Lys Lys Val Ala Leu Trp Leu Ala Gly Leu Leu Gly
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Ala Gly Gly Thr Val Ser Val Val Tyr Ile Phe Gly Asn Asn Pro Val
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Asp Glu Asn Gly Ala Lys Ile Pro Asp Glu Phe Asp Asn Asp Pro Ile
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Leu Val Gln Gln Leu Arg Arg Thr Tyr Lys Tyr Phe Lys Asp Tyr Arg
    130   135   140
Gln Met Ile Ile Glu Pro Thr Ser Pro Cys Leu Leu Pro Asp Pro Leu
145   150   155   160
Gln Glu Pro Tyr Tyr Gln Pro Pro Tyr Thr Leu Val Leu Glu Leu Thr
                165   170   175
Gly Val Leu Leu His Pro Glu Trp Ser Leu Ala Thr Gly Trp Arg Phe
            180   185   190
Lys Lys Arg Pro Gly Ile Glu Thr Leu Phe Gln Gln Leu Ala Pro Leu
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Tyr Glu Ile Val Ile Phe Thr Ser Glu Thr Gly Met Thr Ala Phe Pro
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Leu Ile Asp Ser Val Asp Pro His Gly Phe Ile Ser Tyr Arg Leu Phe
225   230   235   240
Arg Asp Ala Thr Arg Tyr Met Asp Gly His His Val Lys Asp Ile Ser
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Cys Leu Asn Arg Asp Pro Ala Arg Val Val Val Asp Cys Lys Lys
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Glu Ala Phe Arg Leu Gln Pro Tyr Asn Gly Val Ala Leu Arg Pro Trp
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His Tyr Ala Leu Glu Asp Asp Pro Leu Ala Ala Phe Lys Gln Arg Gln
325 330 335
Ser Arg Leu Glu Gln Glu Glu Gln Gln Arg Leu Ala Glu Leu Ser Lys
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<212> DNA
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2520
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2580
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2640
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2700

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2940
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3000
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3120
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3213

<210> 5380
<211> 903
<212> PRT
<213> Homo sapiens

<400> 5380
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20 25 30
Ser Cys Ala Pro Ala Leu Leu Gly Ser Gly Cys Gly Ser Gly Glu Ser
35 40 45
Cys Asp Arg Gly Cys Leu Ala Ala Ile Leu Ala Ser Thr Ser Ala Thr
50 55 60
Gln Ala Arg Met Val Leu Arg Cys Cys Ser Glu Phe Ile Glu Ala His
65 70 75 80
Gly Val Val Asp Gly Ile Tyr Arg Leu Ser Gly Val Ser Ser Asn Ile
85 90 95
Gln Arg Leu Arg His Glu Phe Asp Ser Glu Arg Ile Pro Glu Leu Ser
100 105 110
Gly Pro Ala Phe Leu Gln Asp Ile His Ser Val Ser Ser Leu Cys Lys
115 120 125
Leu Tyr Phe Arg Glu Leu Pro Asn Pro Leu Leu Thr Tyr Gln Leu Tyr
130 135 140
Gly Lys Phe Ser Glu Ala Met Ser Val Pro Gly Glu Glu Glu Arg Leu
145 150 155 160
Val Arg Val His Asp Val Ile Gln Gln Leu Pro Pro Pro His Tyr Arg
165 170 175
Thr Leu Glu Tyr Leu Leu Arg His Leu Ala Arg Met Ala Arg His Ser
180 185 190
Ala Asn Thr Ser Met His Ala Arg Asn Leu Ala Ile Val Trp Ala Pro
195 200 205
Asn Leu Leu Arg Ser Met Glu Leu Glu Ser Val Gly Met Gly Gly Ala
210 215 220
Ala Ala Phe Arg Glu Val Arg Val Gln Ser Val Val Val Glu Phe Leu

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225                 230                 235                 240
Leu Thr His Val Asp Val Leu Phe Ser Asp Thr Phe Thr Ser Ala Gly
                245                 250                 255
Leu Asp Pro Ala Gly Arg Cys Leu Leu Pro Arg Pro Lys Ser Leu Ala
            260                 265                 270
Gly Ser Cys Pro Ser Thr Arg Leu Leu Thr Leu Glu Glu Ala Gln Ala
        275                 280                 285
Arg Thr Gln Gly Arg Leu Gly Thr Pro Thr Glu Pro Thr Thr Pro Lys
    290                 295                 300
Ala Pro Ala Ser Pro Ala Glu Arg Arg Lys Gly Glu Arg Gly Glu Lys
305                 310                 315                 320
Gln Arg Lys Pro Gly Gly Ser Ser Trp Lys Thr Phe Phe Ala Leu Gly
                325                 330                 335
Arg Gly Pro Ser Val Pro Arg Lys Lys Pro Leu Pro Trp Leu Gly Gly
            340                 345                 350
Thr Arg Ala Pro Pro Gln Pro Ser Ala Trp Leu Asp Asp Gly Asp Glu
        355                 360                 365
Leu Asp Phe Ser Pro Pro Arg Cys Leu Glu Gly Leu Arg Gly Leu Asp
    370                 375                 380
Phe Asp Pro Leu Thr Phe Arg Cys Ser Ser Pro Thr Pro Gly Asp Pro
385                 390                 395                 400
Ala Pro Pro Ala Ser Pro Ala Pro Pro Ala Pro Ala Ser Ala Phe Pro
                405                 410                 415
Pro Arg Val Thr Pro Gln Ala Ile Ser Pro Arg Gly Pro Thr Ser Pro
            420                 425                 430
Ala Ser Pro Ala Ala Leu Asp Ile Ser Glu Pro Leu Ala Val Ser Val
        435                 440                 445
Pro Pro Ala Val Leu Glu Leu Leu Gly Ala Gly Gly Ala Pro Ala Ser
    450                 455                 460
Ala Thr Pro Thr Pro Ala Leu Ser Pro Gly Arg Ser Leu Arg Pro His
465                 470                 475                 480
Leu Ile Pro Leu Leu Leu Arg Gly Ala Glu Ala Pro Leu Thr Asp Ala
                485                 490                 495
Cys Gln Gln Glu Met Cys Ser Lys Leu Arg Gly Ala Gln Gly Pro Leu
            500                 505                 510
Ala Arg Leu Met Ala Leu Ala Leu Ala Glu Arg Ala Gln Gln Val Ala
        515                 520                 525
Glu Gln Gln Ser Gln Gln Glu Cys Gly Gly Thr Pro Pro Ala Ser Gln
    530                 535                 540
Ser Pro Phe His Arg Ser Leu Ser Leu Glu Val Gly Gly Glu Pro Leu
545                 550                 555                 560
Gly Thr Ser Gly Ser Gly Pro Pro Pro Asn Ser Leu Ala His Pro Gly
                565                 570                 575
Ala Trp Val Pro Gly Pro Pro Pro Tyr Leu Pro Arg Gln Gln Ser Asp
            580                 585                 590
Gly Ser Leu Leu Arg Ser Gln Arg Pro Met Gly Thr Ser Arg Arg Gly
        595                 600                 605
Leu Arg Gly Pro Ala Gln Val Ser Ala Gln Leu Arg Ala Gly Gly Gly
    610                 615                 620
Gly Arg Asp Ala Pro Glu Ala Ala Ala Gln Ser Pro Cys Ser Val Pro
625                 630                 635                 640
Ser Gln Val Pro Thr Pro Gly Phe Phe Ser Pro Ala Pro Arg Glu Cys
                645                 650                 655
Leu Pro Pro Phe Leu Gly Val Pro Lys Pro Gly Leu Tyr Pro Leu Gly
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            660                 665                 670
Pro Pro Ser Phe Gln Pro Ser Ser Pro Ala Pro Val Trp Arg Ser Ser
        675                 680                 685
Leu Gly Pro Pro Ala Pro Leu Asp Arg Gly Glu Asn Leu Tyr Tyr Glu
    690                 695                 700
Ile Gly Ala Ser Glu Gly Ser Pro Tyr Ser Gly Pro Thr Arg Ser Trp
705                 710                 715                 720
Ser Pro Phe Arg Ser Met Pro Pro Asp Arg Leu Asn Ala Ser Tyr Gly
                725                 730                 735
Met Leu Gly Gln Ser Pro Pro Leu His Arg Ser Pro Asp Phe Leu Leu
            740                 745                 750
Ser Tyr Pro Pro Ala Pro Ser Cys Phe Pro Pro Asp His Leu Gly Tyr
        755                 760                 765
Ser Ala Pro Gln His Pro Ala Arg Arg Pro Thr Pro Pro Glu Pro Leu
    770                 775                 780
Tyr Val Asn Leu Ala Leu Gly Pro Arg Gly Pro Ser Pro Ala Ser Ser
785                 790                 795                 800
Ser Ser Ser Ser Pro Pro Ala His Pro Arg Ser Arg Ser Asp Pro Gly
                805                 810                 815
Pro Pro Val Pro Arg Leu Pro Gln Lys Gln Arg Ala Pro Trp Gly Pro
            820                 825                 830
Arg Thr Pro His Arg Val Pro Gly Pro Trp Gly Pro Pro Glu Pro Leu
        835                 840                 845
Leu Leu Tyr Arg Ala Ala Pro Pro Ala Tyr Gly Arg Gly Gly Glu Leu
    850                 855                 860
His Arg Gly Ser Leu Tyr Arg Asn Gly Gly Gln Arg Gly Glu Gly Ala
865                 870                 875                 880
Gly Pro Pro Pro Pro Tyr Pro Thr Pro Ser Trp Ser Leu His Ser Glu
                885                 890                 895
Gly Gln Thr Arg Ser Tyr Cys
            900
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<210> 5381
<211> 1576
<212> DNA
<213> Homo sapiens

<400> 5381
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120
gccaggacca tctatggcga ccaccagcga tttgtggacg cctacttcaa ggcctaccca
180
ggctattact tcactggaga cggggcttac cgaactgagg gcggctatta ccagatcaca
240
gggcggatgg atgatgtcat caacatcagt ggccaccggc tggggaccgc agagattgag
300
gacgccatcg ccgaccaccc tgcagtacca gaaagtgctg tcattggcta cccccacgac
360
atcaaaggag aagctgcctt tgccttcatt gtggtgaaag atagtgcggg tgactcagat
420
gtggtggtgc aggagctcaa gtccatggtg gccaccaaga tcgccaaata tgctgtgcct
480

gatgagatcc tggtggtgaa acgtcttcca aaaaccaggt ctgggaaggt catgcggcgg
540
ctcctgagga agatcatcac tagtgaggcc caggagctgg gagacactac caccttggag
600
gaccccagca tcatcgcaga gatcctgagt gtctaccaga agtgcaagga caagcaggct
660
gctgctaagt gagctggcac cttgtggggc tcttgggatg ggcgggcacc caagccctgg
720
cttgtccttc ccagaaggta cccctgaggt tggcgtcttc ctacgtccca gaagcagccc
780
ccaccccaca catgacccac accgccctca cgtgaagctg ggctgagagc cctttctccc
840
atccattgga ggtcccagga gtgtcaccca tggagaggct atgcgacatg gctagggctg
900
gttctgccat ctgagtttgg tttcctggaa tgaaaaggca ttgccatctc cattcctctg
960
ccctcttgag ccagcacagg aaggtgaggc cctgggatag cgcgcctgct cagataacac
1020
agagctagtt agctagtagc aaccgtgttt tctccagatc tgtctagata caaaggtcag
1080
aaatcttatt tttatacttt tatattgtgg aagaacagca tgcaacactc acatgtagtg
1140
tgtggattta cttgaacatg ttctttttaa catgtagtta tgaaaatctc ctttttgcc
1200
tctactggtg aggaaacatg aggatcagag gccacatttt taattattgt tagtgtattt
1260
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1320
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1380
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1440
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1576

<210> 5382
<211> 223
<212> PRT
<213> Homo sapiens

<400> 5382
Xaa Met Ala Met Arg Pro Phe Phe Gly Ile Val Pro Val Leu Met Asp
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Glu Lys Gly Ser Val Val Glu Gly Ser Asn Val Ser Gly Ala Leu Cys
20 25 30
Ile Ser Gln Ala Trp Pro Gly Met Ala Arg Thr Ile Tyr Gly Asp His
35 40 45
Gln Arg Phe Val Asp Ala Tyr Phe Lys Ala Tyr Pro Gly Tyr Tyr Phe
50 55 60
Thr Gly Asp Gly Ala Tyr Arg Thr Glu Gly Gly Tyr Tyr Gln Ile Thr

65 70 75 80
Gly Arg Met Asp Asp Val Ile Asn Ile Ser Gly His Arg Leu Gly Thr
85 90 95
Ala Glu Ile Glu Asp Ala Ile Ala Asp His Pro Ala Val Pro Glu Ser
100 105 110
Ala Val Ile Gly Tyr Pro His Asp Ile Lys Gly Glu Ala Ala Phe Ala
115 120 125
Phe Ile Val Val Lys Asp Ser Ala Gly Asp Ser Asp Val Val Val Gln
130 135 140
Glu Leu Lys Ser Met Val Ala Thr Lys Ile Ala Lys Tyr Ala Val Pro
145 150 155 160
Asp Glu Ile Leu Val Val Lys Arg Leu Pro Lys Thr Arg Ser Gly Lys
165 170 175
Val Met Arg Arg Leu Leu Arg Lys Ile Ile Thr Ser Glu Ala Gln Glu
180 185 190
Leu Gly Asp Thr Thr Thr Leu Glu Asp Pro Ser Ile Ile Ala Glu Ile
195 200 205
Leu Ser Val Tyr Gln Lys Cys Lys Asp Lys Gln Ala Ala Ala Lys
210 215 220

<210> 5383
<211> 2027
<212> DNA
<213> Homo sapiens

<400> 5383
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ccctgtaagg acagcagtca tgctggatca gggcccaccc tcatccacac aaccttgtct
120
taactcagta catctccagt ggccccattt ccaaagaagg ttgcgttctg gggttctggg
180
ggctgagact ccagcatatg aatttggggg ggacatgatg ggacccagcg cagtggcctt
240
ctcctccgag cagcgccggg caggccaggg catgacccac acctgtttgt ttcccttcag
300
atcgtctcga cccaggagaa ggagctggtg cagcccttca gctcgctgtt cccgaaggtg
360
gagtacatcg ccagggccgg cgcctgggcc atgttcctgg accggcccca gcagtggctc
420
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480
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540
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600
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660
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720
ggtgagcaga gcctgacgaa tgctatctgg gtcaatgagg agaccaagct ggtgtacttc
780
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840

ggcgagatcg tacgcctcac cacgcccggc ttctcccata gctgctccat gagccagaac
900
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960
aagctgagcg gccccgacga cgaccccctg cacaagcagc cccgcttctg ggctagcatg
1020
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1080
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1140
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1200
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1260
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1320
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1380
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1440
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1860
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1920
gtgaggcact ttgtcccgcc cagcgctggc cagccccgag gagccgctgc cttcaccgcc
1980
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2027

<210> 5384
<211> 508
<212> PRT
<213> Homo sapiens

<400> 5384
Ile Val Ser Thr Gln Glu Lys Glu Leu Val Gln Pro Phe Ser Ser Leu
1 5 10 15
Phe Pro Lys Val Glu Tyr Ile Ala Arg Ala Gly Ala Trp Ala Met Phe
20 25 30
Leu Asp Arg Pro Gln Gln Trp Leu Gln Leu Val Leu Leu Pro Pro Ala
35 40 45
Leu Phe Ile Pro Ser Thr Glu Asn Glu Glu Gln Arg Leu Ala Ser Ala

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    50                  55                  60
Arg Ala Val Pro Arg Asn Val Gln Pro Tyr Val Val Tyr Glu Glu Val
65                  70                  75                  80
Thr Asn Val Trp Ile Asn Val His Asp Ile Phe Tyr Pro Phe Pro Gln
                85                  90                  95
Ser Glu Gly Glu Asp Glu Leu Cys Phe Leu Arg Ala Asn Glu Cys Lys
            100                 105                 110
Thr Gly Phe Cys His Leu Tyr Lys Val Thr Ala Val Leu Lys Ser Gln
        115                 120                 125
Gly Tyr Asp Trp Ser Glu Pro Phe Ser Pro Gly Glu Gly Glu Gln Ser
    130                 135                 140
Leu Thr Asn Ala Ile Trp Val Asn Glu Glu Thr Lys Leu Val Tyr Phe
145                 150                 155                 160
Gln Gly Thr Lys Asp Thr Pro Leu Glu His His Leu Tyr Val Val Ser
                165                 170                 175
Tyr Glu Ala Ala Gly Glu Ile Val Arg Leu Thr Thr Pro Gly Phe Ser
            180                 185                 190
His Ser Cys Ser Met Ser Gln Asn Phe Asp Met Phe Val Ser His Tyr
        195                 200                 205
Ser Ser Val Ser Thr Pro Pro Cys Val His Val Tyr Lys Leu Ser Gly
    210                 215                 220
Pro Asp Asp Asp Pro Leu His Lys Gln Pro Arg Phe Trp Ala Ser Met
225                 230                 235                 240
Met Glu Ala Ala Lys Ile Phe His Phe His Thr Arg Ser Asp Val Arg
                245                 250                 255
Leu Tyr Gly Met Ile Tyr Lys Pro His Ala Leu Gln Pro Gly Lys Lys
            260                 265                 270
His Pro Thr Val Leu Phe Val Tyr Gly Gly Pro Gln Val Gln Leu Val
        275                 280                 285
Asn Asn Ser Phe Lys Gly Ile Lys Tyr Leu Arg Leu Asn Thr Leu Ala
    290                 295                 300
Ser Leu Gly Tyr Ala Val Val Val Ile Asp Gly Arg Gly Ser Cys Gln
305                 310                 315                 320
Arg Gly Leu Arg Phe Glu Gly Ala Leu Lys Asn Gln Met Gly Gln Val
                325                 330                 335
Glu Ile Glu Asp Gln Val Glu Gly Leu Gln Phe Val Ala Glu Lys Tyr
            340                 345                 350
Gly Phe Ile Asp Leu Ser Arg Val Ala Ile His Gly Trp Ser Tyr Gly
        355                 360                 365
Gly Phe Leu Ser Leu Met Gly Leu Ile His Lys Pro Gln Val Phe Lys
    370                 375                 380
Val Ala Ile Ala Gly Ala Pro Val Thr Val Trp Met Ala Tyr Asp Thr
385                 390                 395                 400
Gly Tyr Thr Glu Arg Tyr Met Asp Val Pro Glu Asn Asn Gln His Gly
                405                 410                 415
Tyr Glu Ala Gly Ser Val Ala Leu His Val Glu Lys Leu Pro Asn Glu
            420                 425                 430
Pro Asn Arg Leu Leu Ile Leu His Gly Phe Leu Asp Glu Asn Val His
        435                 440                 445
Phe Phe His Thr Asn Phe Leu Val Ser Gln Leu Ile Arg Ala Gly Lys
    450                 455                 460
Pro Tyr Gln Leu Gln Val Ala Leu Pro Pro Val Ser Pro Gln Ile Tyr
465                 470                 475                 480
Pro Asn Glu Arg His Ser Ile Arg Cys Pro Glu Ser Gly Glu His Tyr
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485 490 495
Glu Val Thr Leu Leu His Phe Leu Gln Glu Tyr Leu
500 505

<210> 5385
<211> 314
<212> DNA
<213> Homo sapiens

<400> 5385
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120
cctccccggg cccagccgct gggcagaggg ctgcatgctg gctggctggc caggctgggg
180
cagcctggcc tcctcggccc ctacgctgca cccaccttcc acttcctgga gatgcaccca
240
catctccagg aaaattgttt cagaaaatgc ctacaacaca gcagagagtg gaacaaacag
300
ggtcccaacg catg
314

<210> 5386
<211> 100
<212> PRT
<213> Homo sapiens

<400> 5386
Met Gly Thr Pro Ala Gly Thr Gly Trp His Phe Phe Phe Pro Cys Ser
1 5 10 15
Thr Trp Ser Ile Cys Cys Ser Trp Asn Arg Lys Glu Arg Ser Lys Lys
20 25 30
Ser Val Pro Ser Pro Pro Arg Ala Gln Pro Leu Gly Arg Gly Leu His
35 40 45
Ala Gly Trp Leu Ala Arg Leu Gly Gln Pro Gly Leu Leu Gly Pro Tyr
50 55 60
Ala Ala Pro Thr Phe His Phe Leu Glu Met His Pro His Leu Gln Glu
65 70 75 80
Asn Cys Phe Arg Lys Cys Leu Gln His Ser Arg Glu Trp Asn Lys Gln
85 90 95
Gly Pro Asn Ala
100

<210> 5387
<211> 375
<212> DNA
<213> Homo sapiens

<400> 5387
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60
accgccacgc accagtccat gggcaactgg tccatgttca cctggtgctt ctgcttctcc
120

atgaccctga tcatcctcat cgtggagctg tgcgggctcc aggcccgctt ccccctgtct
180
tggcgcaact tccccatcac cttcgcctgc tatgcggccc tcttctgcct ctcggcctcc
240
atcatctacc ccaccaccta tgtccagttc ctgtcccacg gccgttcgcg ggaccacgcc
300
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360
acccgggccc gggcc
375

<210> 5388
<211> 125
<212> PRT
<213> Homo sapiens

<400> 5388
Xaa Asp Ser Pro Arg Phe Ser Arg Met Ala Met Ala Ala Arg Met Lys
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Gln Met Ala Tyr Thr Ala Thr His Gln Ser Met Gly Asn Trp Ser Met
20 25 30
Phe Thr Trp Cys Phe Cys Phe Ser Met Thr Leu Ile Ile Leu Ile Val
35 40 45
Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe
50 55 60
Pro Ile Thr Phe Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser
65 70 75 80
Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser
85 90 95
Arg Asp His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val
100 105 110
Ala Tyr Ala Thr Glu Met Ala Trp Thr Arg Ala Arg Ala
115 120 125

<210> 5389
<211> 1711
<212> DNA
<213> Homo sapiens

<400> 5389
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120
aagcgcggag gatccggcga gaagaagcgt cagggagcct cggcggtgtc cccggggtcc
180
gccgaagcca cccggccgcc ggctggggcc cggggtggtg aggaagtgct ccgaggcctc
240
gccgaggcct agcgccggct ttgtgtccga ggcggcggcg gcggcggggg gaggcggagc
300
cgggggcggc ctgcgggaag gcctctcctc cgccgaccgc gcgttttcgg cctaggccgc
360
ggggccgctc gtggcctccg gggagcaggc gccaggggtt tgtgtgcggt gggggcctgg
420

gcctgggcct ggggaagctg acgccggtcg tccggaagcc aggaggaggc gtgaggccgc
480
tcgtggactc cgggcctagg ccctctcccc tcaaccttct cccggggcct gggtcacccc
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600
tggggtcgct cggactctta acgtgtggac tgaccgctac tgactgcacc gccaatcccc
660
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720
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780
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840
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900
ttttgctctt aaagtttata aatatacgta tattgagagt gtccacgtct cctcgctgaa
960
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1020
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1080
atggggagag agaagctgaa agctgccgac tgcgacctgc agatcaccaa tgcgcagacg
1140
aaagaagaat atactgatga taatgctctg attcctaaga attcttctgt aattgttaga
1200
agaattccta ttggaggtgt taaatctaca agcaagacat atgttataag tcgaactgaa
1260
ccagcgatgg caactacaaa agcagtatgt aaaaacacaa tctcacactt tttctacaca
1320
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1380
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1440
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1500
gtttcatatt aaatatgata gcattatccc tgtatgacac tgtgttgtac agttaatgta
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1620
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1711

<210> 5390
<211> 118
<212> PRT
<213> Homo sapiens

<400> 5390
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Val Thr Phe Asp Gly Leu His Ile Ser Leu Cys Asp Leu Lys Lys Gln

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Ile Met Gly Arg Glu Lys Leu Lys Ala Ala Asp Cys Asp Leu Gln Ile
        35                  40                  45
Thr Asn Ala Gln Thr Lys Glu Glu Tyr Thr Asp Asp Asn Ala Leu Ile
    50                  55                  60
Pro Lys Asn Ser Ser Val Ile Val Arg Arg Ile Pro Ile Gly Gly Val
65                  70                  75                  80
Lys Ser Thr Ser Lys Thr Tyr Val Ile Ser Arg Thr Glu Pro Ala Met
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<211> 797
<212> DNA
<213> Homo sapiens

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<211> 55
<212> PRT
<213> Homo sapiens

<400> 5392
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Thr Ile Lys Gly His Cys Asn Leu Ser Leu Asn Leu Leu Gly Ser Ser
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Asn Pro Pro Ala Ser Ala Ser
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<210> 5393
<211> 4837
<212> DNA
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<210> 5394
<211> 354
<212> PRT
<213> Homo sapiens

<400> 5394
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Phe Tyr Arg Leu Leu Arg His Pro Ser Asp Arg Met Gly Phe Pro Pro
35 40 45
Gly Ala Ala Gln Ala Leu Val Leu Gln Val Phe Lys Thr Phe Asp His
50 55 60
Met Ala Arg Gln Asp Asp Glu Lys Arg Arg Gln Glu Leu Glu Glu Lys
65 70 75 80
Ile Arg Arg Lys Glu Glu Glu Glu Ala Lys Thr Val Ser Ala Ala Ala
85 90 95
Ala Glu Lys Glu Pro Val Pro Val Pro Val Gln Glu Ile Glu Ile Asp
100 105 110
Ser Thr Thr Glu Leu Asp Gly His Gln Glu Val Glu Lys Val Gln Pro
115 120 125
Pro Gly Pro Val Lys Glu Met Ala His Gly Ser Gln Glu Ala Glu Ala
130 135 140
Pro Gly Ala Val Ala Gly Ala Ala Glu Val Pro Arg Glu Pro Pro Ile
145 150 155 160
Leu Pro Arg Ile Gln Glu Gln Phe Gln Lys Asn Pro Asp Ser Tyr Asn
165 170 175
Gly Ala Val Arg Glu Asn Tyr Thr Trp Ser Gln Asp Tyr Thr Asp Leu
180 185 190
Glu Val Arg Val Pro Val Pro Lys His Val Val Lys Gly Lys Gln Val
195 200 205
Ser Val Ala Leu Ser Ser Ser Ser Ile Arg Val Ala Met Leu Glu Glu
210 215 220
Asn Gly Glu Arg Val Leu Met Glu Gly Lys Leu Thr His Lys Ile Asn
225 230 235 240
Thr Glu Ser Ser Leu Trp Ser Leu Glu Pro Gly Lys Cys Val Leu Val

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Glu Glu Pro Ile Asp Ile Asp Lys Ile Asn Lys Glu Arg Ser Met Ala
        275                 280                 285
Thr Val Asp Glu Glu Glu Gln Ala Val Leu Asp Arg Leu Thr Phe Asp
    290                 295                 300
Tyr His Gln Lys Leu Gln Gly Lys Pro Gln Ser His Glu Leu Lys Val
305                 310                 315                 320
His Glu Met Leu Lys Lys Gly Trp Asp Ala Glu Gly Ser Pro Phe Arg
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<210> 5395
<211> 3711
<212> DNA
<213> Homo sapiens

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<210> 5396
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<212> PRT
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<400> 5396
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35 40 45
Asn Met Glu Lys Lys Arg Ser Asn Thr Glu Asn Leu Ser Gln His Phe
50 55 60
Arg Lys Gly Thr Leu Thr Val Leu Lys Lys Lys Trp Glu Asn Pro Gly

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                85                  90                  95
Ile Arg His Arg Ala Asp His Pro Pro Ala Glu Val Thr Ser His Ala
            100                 105                 110
Ala Ser Gly Ala Lys Ala Asp Gln Glu Glu Gln Ile His Pro Arg Ser
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Arg Leu Arg Ser Pro Pro Glu Ala Leu Val Gln Gly Arg Tyr Pro His
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Ile Lys Asp Gly Glu Asp Leu Lys Asp His Ser Thr Glu Ser Lys Lys
145                 150                 155                 160
Met Glu Asn Cys Leu Gly Glu Ser Arg His Glu Val Glu Lys Ser Glu
                165                 170                 175
Ile Ser Glu Asn Thr Asp Ala Ser Gly Lys Ile Glu Lys Tyr Asn Val
            180                 185                 190
Pro Leu Asn Arg Leu Lys Met Met Phe Glu Lys Gly Glu Pro Thr Gln
        195                 200                 205
Thr Lys Ile Leu Arg Ala Gln Ser Arg Ser Ala Ser Gly Arg Lys Ile
    210                 215                 220
Ser Glu Asn Ser Tyr Ser Leu Asp Asp Leu Glu Ile Gly Pro Gly Gln
225                 230                 235                 240
Leu Ser Ser Ser Thr Phe Asp Ser Glu Lys Asn Glu Ser Arg Arg Asn
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            260                 265                 270
Lys Tyr Gln Ala Ala Val Ser Lys Gln Ser Ser Ser Thr Asn Tyr Thr
        275                 280                 285
Asn Glu Leu Lys Ala Ser Gly Gly Glu Ile Lys Ile His Lys Met Glu
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Gln Lys Glu Asn Val Pro Pro Gly Pro Glu Val Cys Ile Thr His Gln
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Glu Gly Glu Lys Ile Ser Ala Asn Glu Asn Ser Leu Ala Val Arg Ser
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Thr Pro Ala Glu Asp Asp Ser Pro Gly Asp Ser Gln Val Lys Ser Glu
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Val Gln Gln Pro Val His Pro Lys Pro Leu Ser Pro Asp Ser Arg Ala
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Ser Ser Leu Ser Glu Ser Ser Pro Pro Lys Ala Met Lys Lys Phe Gln
    370                 375                 380
Ala Pro Ala Arg Glu Thr Cys Val Glu Cys Gln Lys Thr Val Tyr Pro
385                 390                 395                 400
Met Glu Arg Leu Leu Ala Asn Gln Gln Val Phe His Ile Ser Cys Phe
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Arg Cys Ser Tyr Cys Asn Asn Lys Leu Ser Leu Gly Thr Tyr Ala Ser
            420                 425                 430
Leu His Gly Arg Ile Tyr Cys Lys Pro His Phe Asn Gln Leu Phe Lys
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Ser Lys Gly Asn Tyr Asp Glu Gly Phe Gly His Arg Pro His Lys Asp
    450                 455                 460
Leu Trp Ala Ser Lys Asn Glu Asn Glu Glu Ile Leu Glu Arg Pro Ala
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Gln Leu Ala Asn Ala Arg Glu Thr Pro His Ser Pro Gly Val Glu Asp
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Ala Pro Ile Ala Lys Val Gly Val Leu Ala Ala Ser Met Glu Ala Lys
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Ala Leu Glu Glu Gly Ile Lys Met Ser Lys Pro Lys Trp Pro Pro Glu
545                 550                 555                 560
Asp Glu Ile Ser Lys Pro Glu Val Pro Glu Asp Val Asp Leu Asp Leu
                565                 570                 575
Lys Lys Leu Arg Arg Ser Ser Ser Leu Lys Glu Arg Ser Arg Pro Phe
            580                 585                 590
Thr Val Ala Ala Ser Phe Gln Ser Thr Ser Val Lys Ser Pro Lys Thr
        595                 600                 605
Val Ser Pro Pro Ile Arg Lys Gly Trp Ser Met Ser Glu Gln Ser Glu
    610                 615                 620
Glu Ser Val Gly Gly Arg Val Ala Glu Arg Lys Gln Val Glu Asn Ala
625                 630                 635                 640
Lys Ala Ser Lys Lys Asn Gly Asn Val Gly Lys Thr Thr Trp Gln Asn
                645                 650                 655
Lys Glu Ser Lys Gly Glu Thr Gly Lys Arg Ser Lys Glu Gly His Ser
            660                 665                 670
Leu Glu Met Glu Asn Glu Asn Leu Val Glu Asn Gly Ala Asp Ser Asp
        675                 680                 685
Glu Asp Asp Asn Ser Phe Leu Lys Gln Gln Ser Pro Gln Glu Pro Lys
    690                 695                 700
Ser Leu Asn Trp Ser Ser Phe Val Asp Asn Thr Phe Ala Glu Glu Phe
705                 710                 715                 720
Thr Thr Gln Asn Gln Lys Ser Gln Asp Val Glu Leu Trp Glu Gly Glu
                725                 730                 735
Val Val Lys Glu Leu Ser Val Glu Glu Gln Ile Lys Arg Asn Arg Tyr
            740                 745                 750
Tyr Asp Glu Asp Glu Asp Glu Glu
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<210> 5397
<211> 561
<212> DNA
<213> Homo sapiens

<400> 5397
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120
ccccagaaca taagacagga gggagagatg ccatccattc agcgggcact tatgcccacg
180
accagctgag ccagaccagc attcccattt caccacccct tactcctcaa gatgcaaatg
240
aagctcaggg ctgggcggaa gctggcaggg ctgtccacag ggaggacccc cgtgtgtctc
300
tcgggctgcc caggtggctc tgtccaccct tctgtctggg aggctcctta aggctgggga
360
gggcccagag ggaaggagat cctgaggggc tggcagattc aggccctccc tgcgagctga
420
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ggtttgaaga ggagagcaga ccacccagag tagtgggaga aagcaccggc agaaaagctg
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gcatatccac cgagggcctc tctgcttctt ttgacctttt tcagagtttc agagttatga
540
accaaatcgc cttcatgaga g
561

<210> 5398
<211> 154
<212> PRT
<213> Homo sapiens

<400> 5398
Met Ala Leu Gly Ser Thr Trp Thr Pro Glu His Lys Thr Gly Gly Arg
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Asp Ala Ile His Ser Ala Gly Thr Tyr Ala His Asp Gln Leu Ser Gln
20 25 30
Thr Ser Ile Pro Ile Ser Pro Pro Leu Thr Pro Gln Asp Ala Asn Glu
35 40 45
Ala Gln Gly Trp Ala Glu Ala Gly Arg Ala Val His Arg Glu Asp Pro
50 55 60
Arg Val Ser Leu Gly Leu Pro Arg Trp Leu Cys Pro Pro Phe Cys Leu
65 70 75 80
Gly Gly Ser Leu Arg Leu Gly Arg Ala Gln Arg Glu Gly Asp Pro Glu
85 90 95
Gly Leu Ala Asp Ser Gly Pro Pro Cys Glu Leu Arg Phe Glu Glu Glu
100 105 110
Ser Arg Pro Pro Arg Val Val Gly Glu Ser Thr Gly Arg Lys Ala Gly
115 120 125
Ile Ser Thr Glu Gly Leu Ser Ala Ser Phe Asp Leu Phe Gln Ser Phe
130 135 140
Arg Val Met Asn Gln Ile Ala Phe Met Arg
145 150

<210> 5399
<211> 835
<212> DNA
<213> Homo sapiens

<400> 5399
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120
atgggcagta accctcattc tcagcctcag cagagcagtc cgtacccagg aggttcctat
180
ggccctccag gcccacagcg gtatccaatt ggcatccagg gtcggactcc cggggccatg
240
gccggaatgc agtaccctca gcagcagatg ccacctcagt atggacagca aggtgtgagt
300
ggttactgcc agcagggcca acagccatat tacagccagc agccgcagcc cccgcacctc
360
ccaccccagg cgcagtatct gccgtcccag tcccagcaga ggtaccagcc gcagcaggac
420

atgtctcagg aaggctatgg aactagatct caacctcctc tggcccccgg aaaacctaac
480
catgaagact tgaacttaat acagcaagaa agaccatcaa gtttaccagt aagacattat
540
tgtgctgatt tggaaatgta atgagttaaa gacttttaga aagagctgtt gtttttgttt
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gttctacttt atattatgac atgattgaga agtttctaga cttcaggttt attttgtggt
660
caatttttca aggtttacct tttaggagct ctgtagtcct ggataagtct atttcatgtg
720
tatatatctc tgttgcagag tgtagacatc agttggaagg ttttatgcgg ctggtcgatt
780
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835

<210> 5400
<211> 186
<212> PRT
<213> Homo sapiens

<400> 5400
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Gly Pro Thr Met Gly Arg Ser Gln Gly Ser Pro Met Asp Pro Met Val
            20   25   30
Met Lys Arg Pro Gln Leu Tyr Gly Met Gly Ser Asn Pro His Ser Gln
        35   40   45
Pro Gln Gln Ser Ser Pro Tyr Pro Gly Gly Ser Tyr Gly Pro Pro Gly
    50   55   60
Pro Gln Arg Tyr Pro Ile Gly Ile Gln Gly Arg Thr Pro Gly Ala Met
65   70   75   80
Ala Gly Met Gln Tyr Pro Gln Gln Gln Met Pro Pro Gln Tyr Gly Gln
                85   90   95
Gln Gly Val Ser Gly Tyr Cys Gln Gln Gly Gln Gln Pro Tyr Tyr Ser
            100   105   110
Gln Gln Pro Gln Pro Pro His Leu Pro Pro Gln Ala Gln Tyr Leu Pro
        115   120   125
Ser Gln Ser Gln Gln Arg Tyr Gln Pro Gln Gln Asp Met Ser Gln Glu
    130   135   140
Gly Tyr Gly Thr Arg Ser Gln Pro Pro Leu Ala Pro Gly Lys Pro Asn
145   150   155   160
His Glu Asp Leu Asn Leu Ile Gln Gln Glu Arg Pro Ser Ser Leu Pro
                165   170   175
Val Arg His Tyr Cys Ala Asp Leu Glu Met
            180   185

<210> 5401
<211> 2674
<212> DNA
<213> Homo sapiens

<400> 5401
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180
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240
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300
tggcctagca gtgacataaa caccattcct ggagaactga ctgatgcttc tgcttgtaag
360
aacatactgc gctttattca atttgagcca gaagaagata taaaaagaaa attcatgaga
420
aagaaggaca aaaagttatc agacatgcat caaatagtaa atatagatct tatgctggaa
480
atgtcaacct ccctggcagc tgtaacgccc atcattgaaa gggaaagcgg aggacaccat
540
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600
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660
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720
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gcttatcgat ctctgcagac tatctgctct tggttcaaac atcagggata cacagagagg
1080
tccattccaa cacacagaga aattcagcag gctctagtcg atgccgggga caaaccagca
1140
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1200
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1320
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1380
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1440
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1500
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1560
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1620
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1740
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1800
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1920
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1980
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2040
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2160
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2340
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2400
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2460
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2520
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2674

<210> 5402
<211> 507
<212> PRT
<213> Homo sapiens

<400> 5402
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20 25 30
Pro Arg His Val Ala Asp Met Val Ile Ser Glu Ser Met Asp Ile Leu
35 40 45
Phe Arg Ile Arg Gly Gly Leu Asp Leu Ala Phe Gln Leu Ala Thr Pro
50 55 60
Asn Glu Ile Phe Leu Lys Lys Ala Leu Lys His Val Leu Ser Asp Leu
65 70 75 80
Ser Thr Lys Leu Ser Ser Asn Ala Leu Val Phe Arg Ile Cys His Ser
85 90 95
Ser Val Tyr Ile Trp Pro Ser Ser Asp Ile Asn Thr Ile Pro Gly Glu

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            100                 105                 110
Leu Thr Asp Ala Ser Ala Cys Lys Asn Ile Leu Arg Phe Ile Gln Phe
        115                 120                 125
Glu Pro Glu Glu Asp Ile Lys Arg Lys Phe Met Arg Lys Lys Asp Lys
    130                 135                 140
Lys Leu Ser Asp Met His Gln Ile Val Asn Ile Asp Leu Met Leu Glu
145                 150                 155                 160
Met Ser Thr Ser Leu Ala Ala Val Thr Pro Ile Ile Glu Arg Glu Ser
                165                 170                 175
Gly Gly His His Tyr Val Asn Met Thr Leu Pro Val Asp Ala Val Ile
            180                 185                 190
Ser Val Ala Pro Glu Glu Thr Trp Gly Lys Val Arg Lys Leu Leu Val
        195                 200                 205
Asp Ala Ile His Asn Gln Leu Thr Asp Met Glu Lys Cys Ile Leu Lys
    210                 215                 220
Tyr Met Lys Arg Thr Ser Ile Val Val Pro Glu Pro Leu His Phe Leu
225                 230                 235                 240
Leu Pro Gly Lys Lys Asn Leu Val Thr Ile Ser Tyr Pro Ser Gly Ile
                245                 250                 255
Pro Asp Gly Gln Leu Gln Ala Tyr Arg Lys Glu Leu His Asp Leu Phe
            260                 265                 270
Asn Leu Pro His Asp Arg Pro Tyr Phe Lys Arg Ser Asn Ala Tyr His
        275                 280                 285
Phe Pro Asp Glu Pro Tyr Lys Asp Gly Tyr Ile Arg Asn Pro His Thr
    290                 295                 300
Tyr Leu Asn Pro Pro Asn Met Glu Thr Gly Met Ile Tyr Val Val Gln
305                 310                 315                 320
Gly Ile Tyr Gly Tyr His His Tyr Met Gln Asp Arg Ile Asp Asp Asn
                325                 330                 335
Gly Trp Gly Cys Ala Tyr Arg Ser Leu Gln Thr Ile Cys Ser Trp Phe
            340                 345                 350
Lys His Gln Gly Tyr Thr Glu Arg Ser Ile Pro Thr His Arg Glu Ile
        355                 360                 365
Gln Gln Ala Leu Val Asp Ala Gly Asp Lys Pro Ala Thr Phe Val Gly
    370                 375                 380
Ser Arg Gln Trp Ile Gly Ser Ile Glu Val Gln Leu Val Leu Asn Gln
385                 390                 395                 400
Leu Ile Gly Ile Thr Ser Lys Ile Leu Phe Val Ser Gln Gly Ser Glu
                405                 410                 415
Ile Ala Ser Gln Gly Arg Glu Leu Ala Asn His Phe Gln Ser Glu Gly
            420                 425                 430
Thr Pro Val Met Ile Gly Gly Gly Val Leu Ala His Thr Ile Leu Gly
        435                 440                 445
Val Ala Trp Asn Glu Ile Thr Gly Gln Ile Lys Phe Leu Ile Leu Asp
    450                 455                 460
Pro His Tyr Thr Gly Ala Glu Asp Leu Gln Val Ile Leu Glu Lys Gly
465                 470                 475                 480
Trp Cys Gly Trp Lys Gly Pro Asp Phe Trp Asn Lys Asp Ala Tyr Tyr
                485                 490                 495
Asn Leu Cys Leu Pro Gln Arg Pro Asn Met Ile
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<210> 5403
<211> 451

<212> DNA
<213> Homo sapiens

<400> 5403
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120
tcatctttgg gggctctggg accttgggtg ggggctctgg agctgcctcg cctgcaggca
180
ccactctctc agccagggac gcacgctggg gctntggatc cacgccccag tctcaggaag
240
gccagtctcc gggcggcctc ccccgctgcc tcctcgtcgc cgtgggctcg ggtcccatgc
300
agccgggcca ggaggccaaa atctgctgag ctcctgcgta tccctggtac cagcacacgg
360
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420
ccagccggaa gggggccagg cccgcaagct t
451

<210> 5404
<211> 150
<212> PRT
<213> Homo sapiens

<400> 5404
Ala Pro Ser Pro Ser Thr Ala Pro Ala Pro Arg Pro Leu Ala Pro Gly
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Cys Ala Arg Pro His Ala Leu Val Arg Ala Ala Gly Ser Gly Ser Gly
            20   25   30
Ser Pro Ala Leu Thr Met Ala Pro Ser Ser Leu Gly Ala Leu Gly Pro
        35   40   45
Trp Val Gly Ala Leu Glu Leu Pro Arg Leu Gln Ala Pro Leu Ser Gln
    50   55   60
Pro Gly Thr His Ala Gly Ala Xaa Asp Pro Arg Pro Ser Leu Arg Lys
65   70   75   80
Ala Ser Leu Arg Ala Ala Ser Pro Ala Ala Ser Ser Ser Pro Trp Ala
                85   90   95
Arg Val Pro Cys Ser Arg Ala Arg Arg Pro Lys Ser Ala Glu Leu Leu
            100   105   110
Arg Ile Pro Gly Thr Ser Thr Arg Pro Lys Lys Glu Arg Gly Cys Pro
        115   120   125
Ser Pro Gly Leu Pro Ala Ala Gly Pro Gly Pro Ser Pro Ala Gly Arg
    130   135   140
Gly Pro Gly Pro Gln Ala
145   150

<210> 5405
<211> 1609
<212> DNA
<213> Homo sapiens

<400> 5405

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120
gtcattgaac cagacaaaaa cagaaaatat tgtagtgcaa aagcaaggca ttcgtggacc
180
aaagaccggc gtgcgatgag agtgatgtct attgaacgta agaagtggat gaacatccgt
240
cctctcccca caaagaaaca aatgccttta cagtttgatc tgtgcaacca tattgcttct
300
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360
gtttggactt acatgaagga gaatgggata caagatatgg agcaatttta cgaactatgg
420
ctcaagagtc aaaaaaatga aaaaagtgaa gacatagcca gtcagtcaaa caaggaaaat
480
ggaaaacaaa ttcacatgcc aacagattat gctgaagtta cagtggactt tcactgctgg
540
atgtgtggga aaaactgcaa cagtgagaag cagtggcagg gccacatctc ctccgagaag
600
cacaaagaga aggttttcca caccgaggac gaccagtact gctggcagca ccgcttccca
660
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720
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780
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840
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900
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1020
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1080
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1200
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1380
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1440
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1609

<210> 5406
<211> 291
<212> PRT
<213> Homo sapiens

<400> 5406
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Ala Gln Cys Leu Arg Asn Gly Gln Val Ile Glu Pro Asp Lys Asn Arg
35 40 45
Lys Tyr Cys Ser Ala Lys Ala Arg His Ser Trp Thr Lys Asp Arg Arg
50 55 60
Ala Met Arg Val Met Ser Ile Glu Arg Lys Lys Trp Met Asn Ile Arg
65 70 75 80
Pro Leu Pro Thr Lys Lys Gln Met Pro Leu Gln Phe Asp Leu Cys Asn
85 90 95
His Ile Ala Ser Gly Lys Lys Cys Gln Tyr Val Gly Asn Cys Ser Phe
100 105 110
Ala His Ser Pro Glu Glu Arg Glu Val Trp Thr Tyr Met Lys Glu Asn
115 120 125
Gly Ile Gln Asp Met Glu Gln Phe Tyr Glu Leu Trp Leu Lys Ser Gln
130 135 140
Lys Asn Glu Lys Ser Glu Asp Ile Ala Ser Gln Ser Asn Lys Glu Asn
145 150 155 160
Gly Lys Gln Ile His Met Pro Thr Asp Tyr Ala Glu Val Thr Val Asp
165 170 175
Phe His Cys Trp Met Cys Gly Lys Asn Cys Asn Ser Glu Lys Gln Trp
180 185 190
Gln Gly His Ile Ser Ser Glu Lys His Lys Glu Lys Val Phe His Thr
195 200 205
Glu Asp Asp Gln Tyr Cys Trp Gln His Arg Phe Pro Thr Gly Tyr Phe
210 215 220
Ser Ile Cys Asp Arg Tyr Met Asn Gly Thr Cys Pro Glu Gly Asn Ser
225 230 235 240
Cys Lys Phe Ala His Gly Asn Ala Glu Leu His Glu Trp Glu Glu Arg
245 250 255
Arg Asp Ala Leu Lys Met Lys Leu Asn Lys Ala Arg Lys Asp His Leu
260 265 270
Ile Gly Pro Asn Asp Asn Asp Phe Gly Lys Tyr Ser Phe Leu Phe Lys
275 280 285
Asp Leu Asn
290

<210> 5407
<211> 2010
<212> DNA
<213> Homo sapiens

<400> 5407
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60

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gagatggtgt tatctgaaaa ggttagtcag ctgatggaat ggactaacaa aagacctgta
180
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240
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1140
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1320
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1680

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2010

<210> 5408
<211> 335
<212> PRT
<213> Homo sapiens

<400> 5408
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Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr
35 40 45
Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu
50 55 60
Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile Val Met Phe Thr Ala
65 70 75 80
Leu Gln Leu His Arg Gln Cys Val Val Cys Lys Gln Ala Asp Glu Glu
85 90 95
Phe Gln Ile Leu Ala Asn Ser Trp Arg Tyr Ser Ser Ala Phe Thr Asn
100 105 110
Arg Ile Phe Phe Ala Met Val Asp Phe Asp Glu Gly Ser Asp Val Phe
115 120 125
Gln Met Leu Asn Met Asn Ser Ala Pro Thr Phe Ile Asn Phe Pro Ala
130 135 140
Lys Gly Lys Pro Lys Arg Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly
145 150 155 160
Phe Ser Ala Glu Gln Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val
165 170 175
Asn Ile Arg Val Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu
180 185 190
Gly Leu Leu Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser
195 200 205
Asn Met Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu
210 215 220
Cys Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
225 230 235 240
Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn Tyr
245 250 255
Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His Ile Val
260 265 270
Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu Leu Cys Glu

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        275                 280                 285
Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys Ile Met Cys Val
    290                 295                 300
Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser Trp Met Leu Ser Ile
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Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr Ser Phe Leu Met Ser
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<210> 5409
<211> 2019
<212> DNA
<213> Homo sapiens

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360
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420
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480
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600
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660
aactcttaac cccttgctcg acaggtttga gttcaagggg ttggatgctc caagcagagg
720
gccaaaccct gatttatgaa gcatgctagg tcaacagcca gtcagaccac tcccacaaag
780
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900
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1020
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1080
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1140
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1200

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1320
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1380
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1440
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1560
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1620
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1680
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1800
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1860
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1920
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2019

<210> 5410
<211> 198
<212> PRT
<213> Homo sapiens

<400> 5410
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Gln Ile Glu Gln Gly Met Asp Met Val Ile Ser Ser Val Ile Gly Glu
35 40 45
Ser Tyr Arg Leu Gln Ser Met Gln Cys Ser Ser Leu Phe Gln Phe Asp
50 55 60
Phe Gln Glu Ala Val Lys Asn Phe Phe Pro Pro Gly Asn Glu Val Val
65 70 75 80
Asn Gly Glu Asn Leu Ser Phe Ala Tyr Glu Phe Lys Ala Asp Ala Leu
85 90 95
Phe Asp Phe Phe Tyr Trp Phe Gly Leu Ser Asn Ser Val Val Lys Val
100 105 110
Asn Gly Lys Val Leu Asn Leu Ser Ser Thr Ser Pro Glu Lys Lys Glu
115 120 125
Thr Ile Lys Leu Phe Leu Glu Lys Met Ser Glu Pro Leu Ile Arg Arg
130 135 140
Ser Ser Phe Ser Asp Arg Lys Phe Ser Val Thr Ser Arg Gly Ser Ile

145 150 155 160
Asp Asp Val Phe Asn Cys Asn Leu Ser Pro Arg Ser Ser Leu Thr Glu
165 170 175
Pro Leu Leu Ala Glu Leu Pro Phe Pro Ser Val Leu Glu Ser Glu Glu
180 185 190
Thr Pro Asn Gln Phe Ile
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<210> 5411
<211> 2802
<212> DNA
<213> Homo sapiens

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120
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1980
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2520
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2580
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2640
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2700
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2760
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2802

<210> 5412
<211> 642
<212> PRT
<213> Homo sapiens

<400> 5412
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Gly Glu Ile Leu Tyr Asn Asn Phe Leu Phe Asp Ile Pro Lys Ile Leu
35 40 45
Asp Leu Cys Val Leu Phe Gly Lys Gly Asn Ser Pro Leu Leu Gln Lys
50 55 60
Met Ile Gly Asn Ile Phe Thr Gln Gln Pro Ser Tyr Tyr Ser Asp Leu
65 70 75 80
Asp Glu Thr Leu Pro Thr Ile Leu Gln Val Phe Ser Asn Ile Leu Gln
85 90 95
His Cys Gly Leu Gln Gly Asp Gly Ala Asn Thr Thr Pro Gln Lys Leu
100 105 110
Glu Glu Arg Gly Arg Leu Thr Pro Ser Asp Met Pro Leu Leu Glu Leu
115 120 125
Lys Asp Ile Val Leu Tyr Leu Cys Asp Thr Cys Thr Thr Leu Trp Ala
130 135 140
Phe Leu Asp Ile Phe Pro Leu Ala Cys Gln Thr Phe Gln Lys His Asp
145 150 155 160
Phe Cys Tyr Arg Leu Ala Ser Phe Tyr Glu Ala Ala Ile Pro Glu Met
165 170 175
Glu Ser Ala Ile Lys Lys Arg Arg Leu Glu Asp Ser Lys Leu Leu Gly
180 185 190
Asp Leu Trp Gln Arg Leu Ser His Ser Arg Lys Lys Leu Met Glu Ile
195 200 205
Phe His Ile Ile Leu Asn Gln Ile Cys Leu Leu Pro Ile Leu Glu Ser
210 215 220
Ser Cys Asp Asn Ile Gln Gly Phe Ile Glu Glu Phe Leu Gln Ile Phe
225 230 235 240
Ser Ser Leu Leu Gln Glu Lys Arg Phe Leu Arg Asp Tyr Asp Ala Leu
245 250 255
Phe Pro Val Ala Glu Asp Ile Ser Leu Leu Gln Gln Ala Ser Ser Val
260 265 270
Leu Asp Glu Thr Arg Thr Ala Tyr Ile Leu Gln Ala Val Glu Ser Ala
275 280 285
Trp Glu Gly Val Asp Arg Arg Lys Ala Thr Asp Ala Lys Asp Pro Ser
290 295 300
Val Ile Glu Glu Pro Asn Gly Glu Pro Asn Gly Val Thr Val Thr Ala
305 310 315 320
Glu Ala Val Ser Gln Ala Ser Ser His Pro Glu Asn Ser Glu Glu Glu
325 330 335
Glu Cys Met Gly Ala Ala Ala Ala Val Gly Pro Ala Met Cys Gly Val
340 345 350
Glu Leu Asp Ser Leu Ile Ser Gln Val Lys Asp Leu Leu Pro Asp Leu
355 360 365
Gly Glu Gly Phe Ile Leu Ala Cys Leu Glu Tyr Tyr His Tyr Asp Pro

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    370                 375                 380
Glu Gln Val Ile Asn Asn Ile Leu Glu Glu Arg Leu Ala Pro Thr Leu
385                 390                 395                 400
Ser Gln Leu Asp Arg Asn Leu Asp Arg Glu Met Lys Pro Asp Pro Thr
                405                 410                 415
Pro Leu Leu Thr Ser Arg His Asn Val Phe Gln Asn Asp Glu Phe Asp
            420                 425                 430
Val Phe Ser Arg Asp Ser Val Asp Leu Ser Arg Val His Lys Gly Lys
        435                 440                 445
Ser Thr Arg Lys Glu Glu Asn Thr Arg Ser Leu Leu Asn Asp Lys Arg
    450                 455                 460
Ala Val Ala Ala Gln Arg Gln Arg Tyr Glu Gln Tyr Ser Val Val Val
465                 470                 475                 480
Glu Glu Val Pro Leu Gln Pro Gly Glu Ser Leu Pro Tyr His Ser Val
                485                 490                 495
Tyr Tyr Glu Asp Glu Tyr Asp Asp Thr Tyr Asp Gly Asn Gln Val Gly
            500                 505                 510
Ala Asn Asp Ala Asp Ser Met Thr Ser Ser Ser Ala Ala Gly His Ser
        515                 520                 525
Pro Ser Gln Val Leu Arg Thr Lys Val Pro Arg Glu Gly Gln Glu Glu
    530                 535                 540
Asp Asp Asp Asp Glu Glu Asp Asp Ala Asp Glu Glu Ala Pro Lys Pro
545                 550                 555                 560
Asp His Phe Val Gln Asp Pro Ala Val Leu Arg Glu Lys Ala Glu Ala
                565                 570                 575
Arg Arg Met Ala Phe Leu Ala Lys Lys Gly Tyr Arg His Asp Ser Ser
            580                 585                 590
Thr Ala Val Ala Gly Ser Pro Arg Gly His Gly Gln Ser Arg Glu Thr
        595                 600                 605
Thr Gln Glu Arg Arg Lys Lys Glu Ala Asn Lys Ala Thr Arg Ala Asn
    610                 615                 620
His Asn Arg Arg Thr Met Ala Asp Arg Lys Arg Ser Lys Gly Met Ile
625                 630                 635                 640
Pro Ser
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<210> 5413
<211> 1677
<212> DNA
<213> Homo sapiens

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tgtgtgcagt catttataaa tcaatgacat ttctcttttt tgtcataaaa ctgtatactg
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240
cccactaaga agaatttcag cattctggcc agaaatttga atacaattca agttgaagaa
300
atgtctgcct gtaacattag catccagggt cccagcatat ataataagga gcctaaaaat
360

ataataaatc ctcatgaaaa agttcaaatg aagtcaattt gtgcaaattc tcctataaag
420
gcacaacagg atcaattaca agtaaaaaac aatataaaag caagtcttca caatgtcaaa
480
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540
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780
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1440
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1560
aggccttcaa tgaggaattg ataacctttc atgtatgaat cctaattgtt ccttgaattt
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1677

<210> 5414
<211> 426
<212> PRT
<213> Homo sapiens

<400> 5414
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Glu Pro Lys Asn Ile Ile Asn Pro His Glu Lys Val Gln Met Lys Ser

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Ile Cys Ala Asn Ser Pro Ile Lys Ala Gln Gln Asp Gln Leu Gln Val
        35                  40                  45
Lys Asn Asn Ile Lys Ala Ser Leu His Asn Val Lys Ser Ser Leu Pro
    50                  55                  60
Leu Phe Asn Thr Lys Ser Ser Thr Ser Val Gly Gln Leu Gln Ser Pro
65                  70                  75                  80
Thr Leu Asn Ser Pro Ile Tyr Met Gln Lys Gln Gly Lys Asn Glu His
                85                  90                  95
Leu Ala Phe Asn Thr Lys Ser Lys Ala Ser Thr Val Gly Ser Glu Leu
            100                 105                 110
Val Leu Val Ser Thr Thr Val Pro Thr Val His His Val Ser Asp Leu
        115                 120                 125
Glu Met Ser Ser Thr Leu Asp Cys Leu Pro Val Leu Ala Asp Trp Glu
    130                 135                 140
Asp Val Val Leu Leu Pro Ala Ser Gln Pro Glu Glu Asn Val Asp Cys
145                 150                 155                 160
Thr Val Pro Ile Ser Asp Ser Asp Leu Glu Ile Ser Phe Asn Ser Gly
                165                 170                 175
Glu Arg Leu Met Val Leu Lys Glu Leu Glu Met Ser Ser His Glu Asn
            180                 185                 190
Phe Gly Asp Ile Glu Glu Thr Pro Gln Lys Ser Glu Thr Ser Lys Ser
        195                 200                 205
Ile Val Tyr Lys Ser Pro His Thr Thr Ile Tyr Asn Val Lys Glu Ala
    210                 215                 220
Lys Asp Pro Gly Ser Asp Ile Ser Ala Phe Lys Leu Pro Glu His Lys
225                 230                 235                 240
Ser Ser Thr Phe Asn Arg Val Asn Ala Asn Met Ser His Pro Leu Val
                245                 250                 255
Leu Gly Lys His Pro Leu Leu Ser Gly Gly Thr Lys Arg Asn Pro Cys
            260                 265                 270
Ser Pro Gln Ala Phe Pro Pro Ala Lys Lys Gln Pro Phe Thr Ile His
        275                 280                 285
Glu Glu Lys Pro Thr Ser Ser Asp Cys Ser Pro Val Arg Ser Ser Ser
    290                 295                 300
Trp Arg Arg Leu Pro Ser Ile Leu Thr Ser Thr Val Asn Leu Gln Glu
305                 310                 315                 320
Pro Trp Lys Ser Gly Lys Met Thr Pro Pro Leu Cys Lys Cys Gly Arg
                325                 330                 335
Arg Ser Lys Arg Leu Val Val Ser Asn Asn Gly Pro Asn His Gly Lys
            340                 345                 350
Val Phe Tyr Cys Cys Pro Ile Gly Lys Tyr Gln Glu Asn Arg Lys Cys
        355                 360                 365
Cys Gly Tyr Phe Lys Trp Glu Gln Thr Leu Gln Lys Glu Arg Ala Asn
    370                 375                 380
Ser Met Val Pro Ser His Ser Thr Gly Gly Leu Thr Phe Ser Ser Pro
385                 390                 395                 400
Glu Thr Ser His Ile Cys Asp Arg Asn Leu Ser Ile Ser Thr Lys Asn
                405                 410                 415
Ser Leu Arg Leu Arg Pro Ser Met Arg Asn
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<210> 5415
<211> 1493

<212> DNA
<213> Homo sapiens

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tctccttctg aaaagctgga tccagcttgt ttgaagccct tgagctgatc ttagatccgg
180
cgcaggagac caacgcctgc catgctgttc cggctctcag agcactcctc accagaggag
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420
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540
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1020
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1080
ctggggaaag gaggtcctga gaaccttgag gtacccttag atccttttct acccactttc
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1493

<210> 5416
<211> 55
<212> PRT
<213> Homo sapiens

<400> 5416
Xaa Ser Leu Thr Glu Thr Gly Lys Glu Ala Gln Thr Lys Ala Pro Glu
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Arg Ser Pro Arg Pro Leu Trp Phe Pro Glu Pro Gln Leu Glu Val Gly
20 25 30
Gly Ala Cys Ser Ala Leu Ala Gln Ser Pro Ser Glu Lys Leu Asp Pro
35 40 45
Ala Cys Leu Lys Pro Leu Ser
50 55

<210> 5417
<211> 2087
<212> DNA
<213> Homo sapiens

<400> 5417
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aacctaccac cctcatggat aaagaaggtg gagagtgata aaggagactg ttctagataa
120
catggtcaga gaaggtctct ctgaagaggt gacttttag cagagacttg aaggagatga
180
gagaataagc catgccagca tctgagatga agagcattcc agacagaaag aacagcaagc
240
gcagaggccc tgaggtggcc catatctggc gtgttcaagg agtagccata ggaggccagg
300
atggctgcaa ttgatgagga aggagggaga gagataggag atgaagtcaa tatattggtg
360
aaggaacaga cacagttagg ggtcaagact ctcatgaggt tactcaagga accagagaaa
420
gaacgggact cagactcaga tttctcccct cttcagcaga ctgagggatg ccagcgaaga
480
gacaagcact tccgtcatgc agaaaacccc catcatcctc tcaaaacctc cagcagagcg
540
gcccctctgg agaagcccat cgttctcatg aagccacggg aggaggggaa ggggcctgtg
600
gccgtgacag gtgcctctac ccctgagggc accgccccac caccccctgc agcccctgcg
660
ccacccaagg gggagaagga ggggcagaga cccacacagc ctgtgtacca gatccagaac
720
cggggcatgg gcactgccgc accagcagcc atggaccctg tcgtgggtca ggccaaacta
780
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840
gacagtgcca tcgagtacct gttggatcag actgatgtgt tggtggttgg tgtcctgggc
900
ctccagggga caggcaagtc catggtcatg tcattgttgt cagccaacac tccagaggag
960

gaccagagga cttatgtttt ccgggcccag agcgctgaaa tgaaggaacg agggggcaac
1020
cagaccagtg gcatcgactt ctttattacc caagaacgga ttgttttcct ggacacacag
1080
cccatcctga gcccttctat cctagaccat ctcatcaata atgaccgcaa actgcctcca
1140
gagtacaacc ttccccacac ttacgttgaa atgcagtcac tccagattgc tgccttcctt
1200
ttcacggtct gccatgtggt gattgttgtc caggactggt tcacagacct cagtctctac
1260
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1320
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1380
agctcatcgg gctccgatga aggcaccgag tactaccccc acctagtctt cttgcagaac
1440
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1500
cagctcatgg cccactccca cctgcgttac aagggaactc tgtccatgtt acaatgcaat
1560
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1620
ttcatggaca gtgaagcaga gagtgaaaac ccaccaagag caggacctgg ttccagccca
1680
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1740
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1800
aagaactggt tccactacgc tgcccggatc tgggatgggg tgagaaagtc ctctgctctg
1860
gcagagtaca gccgcctgct ggcctgaggc caaggagagg aatgtcatgc aggggacctc
1920
ctgggtccgc agtgtactgc gagggagcac agatgtccat cccccgctgg ggtggagagc
1980
ggcagcaggc ctgatggatg agggatcgtg gcttcccggc ccagagacat gaggtgtcca
2040
gggccaggcc ccccaccctc agttggggct gttccggggg tgactgt
2087

<210> 5418
<211> 528
<212> PRT
<213> Homo sapiens

<400> 5418
Met Ala Ala Ile Asp Glu Glu Gly Gly Arg Glu Ile Gly Asp Glu Val
 1   5   10   15
Asn Ile Leu Val Lys Glu Gln Thr Gln Leu Gly Val Lys Thr Leu Met
            20   25   30
Arg Leu Leu Lys Glu Pro Glu Lys Glu Arg Asp Ser Asp Ser Asp Phe
        35   40   45
Ser Pro Leu Gln Gln Thr Glu Gly Cys Gln Arg Arg Asp Lys His Phe
    50   55   60
Arg His Ala Glu Asn Pro His His Pro Leu Lys Thr Ser Ser Arg Ala

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65                  70                  75                  80
Ala Pro Leu Glu Lys Pro Ile Val Leu Met Lys Pro Arg Glu Glu Gly
                85                  90                  95
Lys Gly Pro Val Ala Val Thr Gly Ala Ser Thr Pro Glu Gly Thr Ala
            100                 105                 110
Pro Pro Pro Pro Ala Ala Pro Ala Pro Pro Lys Gly Glu Lys Glu Gly
        115                 120                 125
Gln Arg Pro Thr Gln Pro Val Tyr Gln Ile Gln Asn Arg Gly Met Gly
    130                 135                 140
Thr Ala Ala Pro Ala Ala Met Asp Pro Val Val Gly Gln Ala Lys Leu
145                 150                 155                 160
Leu Pro Pro Glu Arg Met Lys His Ser Ile Lys Leu Val Asp Asp Gln
                165                 170                 175
Met Asn Trp Cys Asp Ser Ala Ile Glu Tyr Leu Leu Asp Gln Thr Asp
            180                 185                 190
Val Leu Val Val Gly Val Leu Gly Leu Gln Gly Thr Gly Lys Ser Met
        195                 200                 205
Val Met Ser Leu Leu Ser Ala Asn Thr Pro Glu Glu Asp Gln Arg Thr
    210                 215                 220
Tyr Val Phe Arg Ala Gln Ser Ala Glu Met Lys Glu Arg Gly Gly Asn
225                 230                 235                 240
Gln Thr Ser Gly Ile Asp Phe Phe Ile Thr Gln Glu Arg Ile Val Phe
                245                 250                 255
Leu Asp Thr Gln Pro Ile Leu Ser Pro Ser Ile Leu Asp His Leu Ile
            260                 265                 270
Asn Asn Asp Arg Lys Leu Pro Pro Glu Tyr Asn Leu Pro His Thr Tyr
        275                 280                 285
Val Glu Met Gln Ser Leu Gln Ile Ala Ala Phe Leu Phe Thr Val Cys
    290                 295                 300
His Val Val Ile Val Val Gln Asp Trp Phe Thr Asp Leu Ser Leu Tyr
305                 310                 315                 320
Arg Leu Trp Asp Leu Gly Cys Lys Cys Lys Ser Asn Ser His Ser Pro
                325                 330                 335
Gln Thr Pro Arg Phe Leu Gln Thr Ala Glu Met Val Lys Pro Ser Thr
            340                 345                 350
Pro Ser Pro Ser His Glu Ser Ser Ser Ser Ser Gly Ser Asp Glu Gly
        355                 360                 365
Thr Glu Tyr Tyr Pro His Leu Val Phe Leu Gln Asn Lys Ala Arg Arg
    370                 375                 380
Glu Asp Phe Cys Pro Arg Lys Leu Arg Gln Met His Leu Met Ile Asp
385                 390                 395                 400
Gln Leu Met Ala His Ser His Leu Arg Tyr Lys Gly Thr Leu Ser Met
                405                 410                 415
Leu Gln Cys Asn Val Phe Pro Gly Leu Pro Pro Asp Phe Leu Asp Ser
            420                 425                 430
Glu Val Asn Leu Phe Leu Val Pro Phe Met Asp Ser Glu Ala Glu Ser
        435                 440                 445
Glu Asn Pro Pro Arg Ala Gly Pro Gly Ser Ser Pro Leu Phe Ser Leu
    450                 455                 460
Leu Pro Gly Tyr Arg Gly His Pro Ser Phe Gln Ser Leu Val Ser Lys
465                 470                 475                 480
Leu Arg Ser Gln Val Met Ser Met Ala Arg Pro Gln Leu Ser His Thr
                485                 490                 495
Ile Leu Thr Glu Lys Asn Trp Phe His Tyr Ala Ala Arg Ile Trp Asp
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            500                 505                 510
Gly Val Arg Lys Ser Ser Ala Leu Ala Glu Tyr Ser Arg Leu Leu Ala
        515                 520                 525
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<210> 5419
<211> 989
<212> DNA
<213> Homo sapiens

<400> 5419
ttttcgtcca ggagtcggag gagcaagtcc aggtcccgtt cccgaaggcg ccaccagcgg
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aagtacaggc gctactcgcg gtcatactcg cggagccggt cgcgatcccg cagccgccgt
120
taccgagaga ggcgctacgg gttcaccagg agatactacc ggtctccttc gcggtaccgg
180
tcccggtccc gtagcaggtc gcgctctcgg ggaaggtcgt actgcggaag ggcgtacgcg
240
atcgcgcggg gacagcgcta ctacggcttt ggtcgcacag tgtacccgga ggagcacagc
300
agatggaggg acagatccag gacgaggtcg cggagcagaa ccccctttcg cttaagtgaa
360
aaagatcgaa tggagctgtt agaaatagca aaaaccaatg cagcgaaagc tctaggaaca
420
accaacattg acttgccagc tagtctcaga actgttcctt cagccaaaga aacaagccgt
480
ggaataggtg tatcaagtaa tggtgcaaag cctgaaaaat catgaatgtg gtctgcagac
540
attgatgaag aaaatctgtt gctgtcggaa aaggtaacag aagatggaac tcgaaatccc
600
aatgaaaaac ctacccagca aagaagcata gcttttagct ctaataattc tgtagcaaag
660
ccaatacaaa aatcagctaa agctgccaca gaagaggcat cttcaagatc accaaaaata
720
gatcagaaaa aaagtccata tggactgtgg atacctatct aaaagaagaa aactgatggc
780
taagtttgca tgaaaactgc actttattgc aagttagtgt ttctagcatt atcccatccc
840
tttgagccat tcaggggtac ttgtgcattt aaaaaccaac acaaaaagat gtaaatactt
900
aacactcaaa tattaacatt ttaggtttct cttgcagata tgagagatag cacagatgga
960
ccaaaggtta tgcacaggtg ggagtcttt
989

<210> 5420
<211> 174
<212> PRT
<213> Homo sapiens

<400> 5420
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Phe Ser Ser Arg Ser Arg Arg Ser Lys Ser Arg Ser Arg Ser Arg Arg
 1               5                  10                  15
Arg His Gln Arg Lys Tyr Arg Arg Tyr Ser Arg Ser Tyr Ser Arg Ser
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            20                  25                  30
Arg Ser Arg Ser Arg Ser Arg Arg Tyr Arg Glu Arg Arg Tyr Gly Phe
        35                  40                  45
Thr Arg Arg Tyr Tyr Arg Ser Pro Ser Arg Tyr Arg Ser Arg Ser Arg
    50                  55                  60
Ser Arg Ser Arg Ser Arg Gly Arg Ser Tyr Cys Gly Arg Ala Tyr Ala
65                  70                  75                  80
Ile Ala Arg Gly Gln Arg Tyr Tyr Gly Phe Gly Arg Thr Val Tyr Pro
                85                  90                  95
Glu Glu His Ser Arg Trp Arg Asp Arg Ser Arg Thr Arg Ser Arg Ser
            100                 105                 110
Arg Thr Pro Phe Arg Leu Ser Glu Lys Asp Arg Met Glu Leu Leu Glu
        115                 120                 125
Ile Ala Lys Thr Asn Ala Ala Lys Ala Leu Gly Thr Thr Asn Ile Asp
    130                 135                 140
Leu Pro Ala Ser Leu Arg Thr Val Pro Ser Ala Lys Glu Thr Ser Arg
145                 150                 155                 160
Gly Ile Gly Val Ser Ser Asn Gly Ala Lys Pro Glu Lys Ser
                165                 170
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<210> 5421
<211> 1239
<212> DNA
<213> Homo sapiens

<400> 5421
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ttacagcctg ttccaagtgt ggcttaatcc gtctccacca ccagatcttt ctccgtggat
120
tcctctgcta agaccgctgc catgccagtg acggtaaccc gcaccaccat cacaaccacc
180
acgacgtcat cttcgggcct ggggtccccc atgatcgtgg ggtcccctcg ggccctgaca
240
cagcccctgg gtctccttcg cctgctgcag ctggtgtcta cctgcgtggc cttctcgctg
300
gtggctagcg tgggcgcctg gacggggtcc atgggcaact ggtccatgtt cacctggtgc
360
ttctgcttct ccgtgaccct gatcatcctc atcgtggagc tgtgcgggct ccaggcccgc
420
ttccccctgt cttggcgcaa cttccccatc accttcgcct gctatgcggc cctcttctgc
480
ctctcggcct ccatcatcta ccccaccacc tatgtccagt tcctgtccca cggccgttcg
540
cgggaccacg ccatcgccgc caccttcttc tcctgcatcg cgtgtgtggc ttacgccacc
600
gaagtggcct ggacccgggc ccggcccggc gagatcactg gctatatggc caccgtaccc
660
gggctgctga aggtgctgga gaccttcgtt gcctgcatca tcttcgcgtt catcagcgac
720
cccaacctgt accagcacca gccggccctg gagtggtgcg tggcggtgta cgccatctgc
780
ttcatcctag cggccatcgc catcctgctg aacctggggg agtgcaccaa cgtgctaccc
840

atcccctcc ccagcttcct gtcggggctg gccttgtgtc tgtcctcctc tatgccaccg
900
cccttgttct ctggcccctc taccagttcg atgagaagta tggcggccag cctcggcgct
960
cgagagatgt aagctgcagc cgcagccatg cctactacgt gtgtgcctgg gaccgccgac
1020
tggctgtggc catcctgacg gccatcaacc tactggcgta tgtggctgac ctggtgcact
1080
ctgcccacct ggtttttgtc aaggtttaag actctcccaa gaggctcccg ttccctctcc
1140
aacctctttg ttcttgttgc ccgagttttc tttatggagt acttctttcc cccgcctttc
1200
gtctgttttc cttttcctgt ctcccctccc ttcacgcgt
1239

<210> 5422
<211> 276
<212> PRT
<213> Homo sapiens

<400> 5422
Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr Ser
1 5 10 15
Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg Ala Leu
20 25 30
Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr Cys
35 40 45
Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser Met
50 55 60
Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr Leu
65 70 75 80
Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu
85 90 95
Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Ala Leu Phe
100 105 110
Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu
115 120 125
Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe Ser
130 135 140
Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala
145 150 155 160
Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu
165 170 175
Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser
180 185 190
Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala
195 200 205
Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn
210 215 220
Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
225 230 235 240
Ser Gly Leu Ala Leu Cys Leu Ser Ser Ser Met Pro Pro Pro Leu Phe
245 250 255
Ser Gly Pro Ser Thr Ser Ser Met Arg Ser Met Ala Ala Ser Leu Gly

260 265 270
Ala Arg Glu Met
275

<210> 5423
<211> 2427
<212> DNA
<213> Homo sapiens

<400> 5423
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gggctgcact ccaacgtgcg gctcctcagc agcttgttac ttacaatgag taataacaac
120
cctgagttat tctccccacc tcagaagtac cagcttttgg tgtatcatgc agattctctc
180
tttcatgata aggaatatcg gaatgctgtg agtaagtata ccatggcttt acagcagaag
240
aaagcgctaa gtaaaacttc aaaagtgaga ccttcaactg gaaattctgc atctactcca
300
caaagtcagt gtcttccatc tgaaattgaa gtgaaataca aaatggctga atgttataca
360
atgctaaaac aagataaaga tgccattgct atacttgatg ggatcccttc aagacaaaga
420
actcccaaaa taaacatgat gctggcaaac ctgtacaaga aggctggtca ggagcgccct
480
tcagtcacca gctataagga ggtgctgagg cagtgcccat tagcccttga tgccattcta
540
ggcttgttgt ccctttctgt aaaaggggca gaggtggcat ccatgacaat gaatgtgatc
600
caaaccgtgc ctaacttgga ctggctctct gtgtggatca aagcgtatgc ttttgtgcac
660
actggtgaca actcaagagc aatcagtacc atctgttcac tagagaaaaa atccttattg
720
cgagataacg tggacctatt gggaagcttg gcagatctgt acttcagagc tggagacaat
780
aaaaactctg tcctcaagtt tgaacaggca cagatgttgg atccttatct gataaaagga
840
atggatgtat atggctacct actggcacga gaagggcggc tagaggatgt tgagaacctt
900
ggatgccgcc ttttcaatat ctctgatcag catgcagaac cgtgggtggt ttctggctgt
960
cacagcttct atagcaaacg ctactcccgg gccctctatt taggagccaa ggccattcag
1020
ctgaacagta atagtgttca agctctgcta cttaagggag cagcacttag gaacatgggc
1080
agagtccaag aagcaataat ccactttcgg gaggccatac ggctcgcacc ttgtcgctta
1140
gattgttatg aaggtcttat cgaatgttac ttagcctcca acagtattcg agaagcaatg
1200
gtaatggcta acaacgttta caaaactctg ggagcaaatg cacagaccct tacccttta
1260
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1320

gccctgaccc aaaggccaga ttacattaag gctgtggtga aaaaagcaga actacttagc
1380
agagaacaga aatatgaaga tggaattgct ttgctgagga acgcactggc taatcagagt
1440
gactgtgtcc tgcatcggat cctaggagat ttccttgtag ctgtcaatga gtatcaggag
1500
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1560
gggatgcaga agatggagaa ggaggagagt cccacggatg ccactcagga ggaggatgtg
1620
gacgacatgg aagggagtgg ggaagaaggg gacctggagg gcagcgacag tgaggcggcc
1680
cagtgggctg accaggagca gtggttcggc atgagtgagg gggcggcagc tccatggccg
1740
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1800
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1860
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1920
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1980
cttctgggcc aagagtactt tttatataac taatttctaa atccaaaagc tcaaggaata
2040
gacagtgttc tgtgacatgg attggtttga aggagttacc caccatccca gcacgataat
2100
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2160
gtcattgtcc tgggctatcc agatgtccct agtaaatctt gcttccttct gcaatgttag
2220
taatgcctta agctgacagt tgctattttg cagaacagtt ttcctctttg cttagctagt
2280
aacttgcctc tgagcctggg ctgatctgag aaacaggtgt gacaagagca tgaaccagag
2340
gtgcacctgg ggcagttccc taataaaact ggtttgtaca gtcatggtgt tggggtgatc
2400
agaatggaag ccctttttcaa aataaaa
2427

<210> 5424
<211> 570
<212> PRT
<213> Homo sapiens

<400> 5424
Met Ala Ala Ala Gly Leu His Ser Asn Val Arg Leu Leu Ser Ser Leu
1 5 10 15
Leu Leu Thr Met Ser Asn Asn Asn Pro Glu Leu Phe Ser Pro Pro Gln
20 25 30
Lys Tyr Gln Leu Leu Val Tyr His Ala Asp Ser Leu Phe His Asp Lys
35 40 45
Glu Tyr Arg Asn Ala Val Ser Lys Tyr Thr Met Ala Leu Gln Gln Lys
50 55 60
Lys Ala Leu Ser Lys Thr Ser Lys Val Arg Pro Ser Thr Gly Asn Ser

```
65                  70                  75                  80
Ala Ser Thr Pro Gln Ser Gln Cys Leu Pro Ser Glu Ile Glu Val Lys
                85                  90                  95
Tyr Lys Met Ala Glu Cys Tyr Thr Met Leu Lys Gln Asp Lys Asp Ala
            100                 105                 110
Ile Ala Ile Leu Asp Gly Ile Pro Ser Arg Gln Arg Thr Pro Lys Ile
        115                 120                 125
Asn Met Met Leu Ala Asn Leu Tyr Lys Lys Ala Gly Gln Glu Arg Pro
    130                 135                 140
Ser Val Thr Ser Tyr Lys Glu Val Leu Arg Gln Cys Pro Leu Ala Leu
145                 150                 155                 160
Asp Ala Ile Leu Gly Leu Leu Ser Leu Ser Val Lys Gly Ala Glu Val
                165                 170                 175
Ala Ser Met Thr Met Asn Val Ile Gln Thr Val Pro Asn Leu Asp Trp
            180                 185                 190
Leu Ser Val Trp Ile Lys Ala Tyr Ala Phe Val His Thr Gly Asp Asn
        195                 200                 205
Ser Arg Ala Ile Ser Thr Ile Cys Ser Leu Glu Lys Lys Ser Leu Leu
    210                 215                 220
Arg Asp Asn Val Asp Leu Leu Gly Ser Leu Ala Asp Leu Tyr Phe Arg
225                 230                 235                 240
Ala Gly Asp Asn Lys Asn Ser Val Leu Lys Phe Glu Gln Ala Gln Met
                245                 250                 255
Leu Asp Pro Tyr Leu Ile Lys Gly Met Asp Val Tyr Gly Tyr Leu Leu
            260                 265                 270
Ala Arg Glu Gly Arg Leu Glu Asp Val Glu Asn Leu Gly Cys Arg Leu
        275                 280                 285
Phe Asn Ile Ser Asp Gln His Ala Glu Pro Trp Val Val Ser Gly Cys
    290                 295                 300
His Ser Phe Tyr Ser Lys Arg Tyr Ser Arg Ala Leu Tyr Leu Gly Ala
305                 310                 315                 320
Lys Ala Ile Gln Leu Asn Ser Asn Ser Val Gln Ala Leu Leu Leu Lys
                325                 330                 335
Gly Ala Ala Leu Arg Asn Met Gly Arg Val Gln Glu Ala Ile Ile His
            340                 345                 350
Phe Arg Glu Ala Ile Arg Leu Ala Pro Cys Arg Leu Asp Cys Tyr Glu
        355                 360                 365
Gly Leu Ile Glu Cys Tyr Leu Ala Ser Asn Ser Ile Arg Glu Ala Met
    370                 375                 380
Val Met Ala Asn Asn Val Tyr Lys Thr Leu Gly Ala Asn Ala Gln Thr
385                 390                 395                 400
Leu Thr Leu Leu Ala Thr Val Cys Leu Glu Asp Pro Val Thr Gln Glu
                405                 410                 415
Lys Ala Lys Thr Leu Leu Asp Lys Ala Leu Thr Gln Arg Pro Asp Tyr
            420                 425                 430
Ile Lys Ala Val Val Lys Lys Ala Glu Leu Leu Ser Arg Glu Gln Lys
        435                 440                 445
Tyr Glu Asp Gly Ile Ala Leu Leu Arg Asn Ala Leu Ala Asn Gln Ser
    450                 455                 460
Asp Cys Val Leu His Arg Ile Leu Gly Asp Phe Leu Val Ala Val Asn
465                 470                 475                 480
Glu Tyr Gln Glu Ala Met Asp Gln Tyr Ser Ile Ala Leu Ser Leu Asp
                485                 490                 495
Pro Asn Asp Gln Lys Ser Leu Glu Gly Met Gln Lys Met Glu Lys Glu
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```
            500                 505                 510
Glu Ser Pro Thr Asp Ala Thr Gln Glu Glu Asp Val Asp Asp Met Glu
        515                 520                 525
Gly Ser Gly Glu Glu Gly Asp Leu Glu Gly Ser Asp Ser Glu Ala Ala
    530                 535                 540
Gln Trp Ala Asp Gln Glu Gln Trp Phe Gly Met Ser Glu Gly Ala Ala
545                 550                 555                 560
Ala Pro Trp Pro Gln Trp Pro Ala Leu Leu
                565                 570
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<210> 5425
<211> 639
<212> DNA
<213> Homo sapiens

<400> 5425
cggccgccca tgtgatcaaa cggtatacag cccaggcgcc agatgagctg tcctttgagg
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tgaggctgtg gggaagcaga ttccagctgg gctccccaca ccccctgctc cttctgaccc
120
ttctcttccc acccgccctc tcccaggtgg gagacattgt ctcggtgatc gacatgccac
180
ccacagagga tcggagctgg tggcggggca agcgaggctt ccaggtcggg ttcttcccca
240
gtgagtgtgt ggaactcttc acagagcggc caggtccggg cctgaaggcg gatgccgatg
300
gccccccatg tggcatcccg gctccccagg gtatctcgtc tctgacctca gctgtgccac
360
ggcctcgtgg gaagctggcc ggcctgctcc gcaccttcat gcgctcccgc ccttctcggc
420
agcggctgcg gcagcgggga atcctgcgac agagggtgtt tggctgcgat cttggcgagc
480
acctcagcaa ctcaggccag gatgtgccca gtgctgcgct gctgctccga gttcattgag
540
gccnacgggg tggtggatgg gatctaccgg ctctcaggcg tgtcttccaa catccagagg
600
cttcggcacg agtttgacag tgagaggata ccggagctg
639

<210> 5426
<211> 98
<212> PRT
<213> Homo sapiens

<400> 5426
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Pro Gln Leu Cys His Gly Leu Val Gly Ser Trp Pro Ala Cys Ser Ala
 1               5                  10                  15
Pro Ser Cys Ala Pro Ala Leu Leu Gly Ser Gly Cys Gly Ser Gly Glu
            20                  25                  30
Ser Cys Asp Arg Gly Cys Leu Ala Ala Ile Leu Ala Ser Thr Ser Ala
        35                  40                  45
Thr Gln Ala Arg Met Cys Pro Val Leu Arg Cys Cys Ser Glu Phe Ile
    50                  55                  60
Glu Ala Xaa Gly Val Val Asp Gly Ile Tyr Arg Leu Ser Gly Val Ser
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Glu Leu

<210> 5427
<211> 366
<212> DNA
<213> Homo sapiens

<400> 5427
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240
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<210> 5428
<211> 101
<212> PRT
<213> Homo sapiens

<400> 5428
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Phe Gly His Ser Val Glu Asp Pro Ile Pro Ala Arg Met His Val Phe
35 40 45
Ser Glu Tyr Leu Tyr Pro Phe Cys Pro Leu Met Tyr Pro Gln His Leu
50 55 60
Glu Glu His Leu Ala Cys Ser Arg Tyr Ser Thr Arg Ile Phe Asp Leu
65 70 75 80
Phe Val Gly Leu Phe Met Thr Glu Ser Cys Ser Val Ala Gln Thr Gly
85 90 95
Val Gln Tyr Ser Asp
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<210> 5429
<211> 612
<212> DNA
<213> Homo sapiens

<400> 5429

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<210> 5430
<211> 94
<212> PRT
<213> Homo sapiens

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20 25 30
His Glu Glu Glu Val Arg Val Pro Ala Leu Ser Trp Gly Arg Pro Arg
35 40 45
Ala Pro Ala Pro Ala Ser Lys Pro Arg Pro Arg Leu Asp Leu Asn Cys
50 55 60
Leu Trp Leu Arg Pro Gln Pro Ile Phe Leu Trp Lys Leu Arg Pro Arg
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Pro Val Pro Ala Ala Thr Pro Leu Thr Gly Pro Leu Pro Leu
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<210> 5431
<211> 3005
<212> DNA
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<210> 5432
<211> 863
<212> PRT
<213> Homo sapiens

<400> 5432
Xaa His Asp Val Ile Gln Gln Leu Pro Pro Pro His Tyr Arg Thr Leu
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Glu Tyr Leu Leu Arg His Leu Ala Arg Met Ala Arg His Ser Ala Asn
20 25 30
Thr Ser Met His Ala Arg Asn Leu Ala Ile Val Trp Ala Pro Asn Leu

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        35                  40                  45
Leu Arg Ser Met Glu Leu Glu Ser Val Gly Met Gly Gly Ala Ala Ala
    50                  55                  60
Phe Arg Glu Val Arg Val Gln Ser Val Val Val Glu Phe Leu Leu Thr
65                  70                  75                  80
His Val Asp Val Leu Phe Ser Asp Thr Phe Thr Ser Ala Gly Leu Asp
                85                  90                  95
Pro Ala Gly Arg Cys Leu Leu Pro Arg Pro Lys Ser Leu Ala Gly Ser
            100                 105                 110
Cys Pro Ser Thr Arg Leu Leu Thr Leu Glu Glu Ala Gln Ala Arg Thr
        115                 120                 125
Gln Gly Arg Leu Gly Thr Pro Thr Glu Pro Thr Thr Pro Lys Ala Pro
    130                 135                 140
Ala Ser Pro Ala Glu Arg Arg Lys Gly Glu Arg Gly Glu Lys Gln Arg
145                 150                 155                 160
Lys Pro Gly Gly Ser Ser Trp Lys Thr Phe Phe Ala Leu Gly Arg Gly
                165                 170                 175
Pro Ser Val Pro Arg Lys Lys Pro Leu Pro Trp Leu Gly Gly Thr Arg
            180                 185                 190
Ala Pro Pro Gln Pro Ser Gly Ser Arg Pro Asp Thr Val Thr Leu Arg
        195                 200                 205
Ser Ala Lys Ser Glu Glu Ser Leu Ser Ser Gln Ala Ser Gly Ala Gly
    210                 215                 220
Leu Gln Arg Leu His Arg Leu Arg Arg Pro His Ser Ser Ser Asp Ala
225                 230                 235                 240
Phe Pro Val Gly Pro Ala Pro Ala Gly Ser Cys Glu Ser Leu Ser Ser
                245                 250                 255
Ser Ser Ser Ser Glu Ser Ser Ser Ser Glu Ser Ser Ser Ser Ser Ser
            260                 265                 270
Glu Ser Ser Ala Ala Gly Leu Gly Ala Leu Ser Gly Ser Pro Ser His
        275                 280                 285
Arg Thr Ser Ala Trp Leu Asp Asp Gly Asp Glu Leu Asp Phe Ser Pro
    290                 295                 300
Pro Arg Cys Leu Glu Gly Leu Arg Gly Leu Asp Phe Asp Pro Leu Thr
305                 310                 315                 320
Phe Arg Cys Ser Ser Pro Thr Pro Gly Asp Pro Ala Pro Pro Ala Ser
                325                 330                 335
Pro Ala Pro Pro Ala Pro Ala Ser Ala Phe Pro Pro Arg Val Thr Pro
            340                 345                 350
Gln Ala Ile Ser Pro Arg Gly Pro Thr Ser Pro Ala Ser Pro Ala Ala
        355                 360                 365
Leu Asp Ile Ser Glu Pro Leu Ala Val Ser Val Pro Pro Ala Val Leu
    370                 375                 380
Glu Leu Leu Gly Ala Gly Gly Ala Pro Ala Ser Ala Thr Pro Thr Pro
385                 390                 395                 400
Ala Leu Ser Pro Gly Arg Ser Leu Arg Pro His Leu Ile Pro Leu Leu
                405                 410                 415
Leu Arg Gly Ala Glu Ala Pro Leu Thr Asp Ala Cys Gln Gln Glu Met
            420                 425                 430
Cys Ser Lys Leu Arg Gly Ala Gln Gly Pro Leu Gly Pro Asp Met Glu
        435                 440                 445
Ser Pro Leu Pro Pro Pro Pro Leu Ser Leu Leu Arg Pro Gly Gly Ala
    450                 455                 460
Pro Pro Pro Pro Pro Lys Asn Pro Ala Arg Leu Met Ala Leu Ala Leu
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465                 470                 475                 480
Ala Glu Arg Ala Gln Gln Val Ala Glu Gln Gln Ser Gln Gln Glu Cys
                485                 490                 495
Gly Gly Thr Pro Pro Ala Ser Gln Ser Pro Phe His Arg Ser Leu Ser
            500                 505                 510
Leu Glu Val Gly Gly Glu Pro Leu Gly Thr Ser Gly Ser Gly Pro Pro
        515                 520                 525
Pro Asn Ser Leu Ala His Pro Gly Ala Trp Val Pro Gly Pro Pro Pro
    530                 535                 540
Tyr Leu Pro Arg Gln Gln Ser Asp Gly Ser Leu Leu Arg Ser Gln Arg
545                 550                 555                 560
Pro Met Gly Thr Ser Arg Arg Gly Leu Arg Gly Pro Ala Gln Val Ser
                565                 570                 575
Ala Gln Leu Arg Ala Gly Gly Gly Gly Arg Asp Ala Pro Glu Ala Ala
            580                 585                 590
Ala Gln Ser Pro Cys Ser Val Pro Ser Gln Val Pro Thr Pro Gly Phe
        595                 600                 605
Phe Ser Pro Ala Pro Arg Glu Cys Leu Pro Pro Phe Leu Gly Val Pro
    610                 615                 620
Lys Pro Gly Leu Tyr Pro Leu Gly Pro Pro Ser Phe Gln Pro Ser Ser
625                 630                 635                 640
Pro Ala Pro Val Trp Arg Ser Ser Leu Gly Pro Pro Ala Pro Leu Asp
                645                 650                 655
Arg Gly Glu Asn Leu Tyr Tyr Glu Ile Gly Ala Ser Glu Gly Ser Pro
            660                 665                 670
Tyr Ser Gly Pro Thr Arg Ser Trp Ser Pro Phe Arg Ser Met Pro Pro
        675                 680                 685
Asp Arg Leu Asn Ala Ser Tyr Gly Met Leu Gly Gln Ser Pro Pro Leu
    690                 695                 700
His Arg Ser Pro Asp Phe Leu Leu Ser Tyr Pro Pro Ala Pro Ser Cys
705                 710                 715                 720
Phe Pro Pro Asp His Leu Gly Tyr Ser Ala Pro Gln His Pro Ala Arg
                725                 730                 735
Arg Pro Thr Pro Pro Glu Pro Leu Tyr Val Asn Leu Ala Leu Gly Pro
            740                 745                 750
Arg Gly Pro Ser Pro Ala Ser Ser Ser Ser Ser Ser Pro Pro Ala His
        755                 760                 765
Pro Arg Ser Arg Ser Asp Pro Gly Pro Pro Val Pro Arg Leu Pro Gln
    770                 775                 780
Lys Gln Arg Ala Pro Trp Gly Pro Arg Thr Pro His Arg Val Pro Gly
785                 790                 795                 800
Pro Trp Gly Pro Pro Glu Pro Leu Leu Leu Tyr Arg Ala Ala Pro Pro
                805                 810                 815
Ala Tyr Gly Arg Gly Gly Glu Leu His Arg Gly Ser Leu Tyr Arg Asn
            820                 825                 830
Gly Gly Gln Arg Gly Glu Gly Ala Gly Pro Pro Pro Pro Tyr Pro Thr
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Pro Ser Trp Ser Leu His Ser Glu Gly Gln Thr Arg Ser Tyr Cys
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<210> 5433
<211> 385
<212> DNA
<213> Homo sapiens

<400> 5433
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120
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180
acgctcaata agactgtgct ttcctcttcc ttaaataacc acccacagac atctgttccc
240
aacgcatctg ctcttcaccc ttcgctccgt ctgttttccc ttagcaaccc atctctttcc
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<210> 5434
<211> 128
<212> PRT
<213> Homo sapiens

<400> 5434
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Thr Thr Asp His His Phe Gly Ser Met Ser Val Gly Asn Ser Val Asn
20 25 30
Asn Ile Pro Ala Ala Met Thr His Leu Gly Ile Arg Ser Ser Ser Gly
35 40 45
Leu Gln Ser Ser Arg Ser Asn Pro Ser Ile Gln Ala Thr Leu Asn Lys
50 55 60
Thr Val Leu Ser Ser Ser Leu Asn Asn His Pro Gln Thr Ser Val Pro
65 70 75 80
Asn Ala Ser Ala Leu His Pro Ser Leu Arg Leu Phe Ser Leu Ser Asn
85 90 95
Pro Ser Leu Ser Thr Thr Asn Leu Ser Gly Pro Ser Arg Arg Arg Gln
100 105 110
Pro Pro Val Ser Pro Leu Thr Leu Ser Pro Gly Pro Glu Ala His Gln
115 120 125

<210> 5435
<211> 617
<212> DNA
<213> Homo sapiens

<400> 5435
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120
ccttgtataa gtatactttg tataacttct ggcaaaccat aattatgaac tcacattact
180
atagtactat aatactgcag aaagggatct tgcgtttcag aaatgtcact catccagttt
240

tcctcccctt tctctaaccc catctccctc ccaggctcat ggtttctgtt gcaatcctct
300
ttctccttac acaaggcaag aagttttctt accaatagat cagacctgtg aaggactgcc
360
cgacatgatc tgatatggtt gttcttcatt ttgggctgta gtattttaaa gtagaggttt
420
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480
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600
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617

<210> 5436
<211> 119
<212> PRT
<213> Homo sapiens

<400> 5436
Met Asn Phe Pro Leu Gly Ser Lys Ala Trp Gly Thr Asn Leu Lys Gln
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His Pro Leu Ile Ala Arg Ala Lys Gly Lys Thr Met Ala Ser Ser Asp
20 25 30
Gly Thr Ile Arg Ala Asn Leu Tyr Phe Lys Ile Leu Gln Pro Lys Met
35 40 45
Lys Asn Asn His Ile Arg Ser Cys Arg Ala Val Leu His Arg Ser Asp
50 55 60
Leu Leu Val Arg Lys Leu Leu Ala Leu Cys Lys Glu Lys Glu Asp Cys
65 70 75 80
Asn Arg Asn His Glu Pro Gly Arg Glu Met Gly Leu Glu Lys Gly Glu
85 90 95
Glu Asn Trp Met Ser Asp Ile Ser Glu Thr Gln Asp Pro Phe Leu Gln
100 105 110
Tyr Tyr Ser Thr Ile Val Met
115

<210> 5437
<211> 1422
<212> DNA
<213> Homo sapiens

<400> 5437
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240
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300

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780
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1260
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1380
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1422

<210> 5438
<211> 245
<212> PRT
<213> Homo sapiens

<400> 5438
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Leu Gln Val Val Arg Glu Gly Lys Phe Ser Gly Phe Leu Thr Ser Cys
35 40 45
Ser Leu Leu Leu Pro Arg Ala Ala Gln Ile Leu Ala Ala Glu Ala Gly
50 55 60
Leu Pro Ser Ser Arg Ser Phe Met Gly Phe Ala Ala Pro Phe Thr Asn

65 70 75 80
Lys Arg Lys Ala Tyr Ser Glu Arg Arg Ile Met Gly Tyr Ser Met Gln
85 90 95
Glu Met Tyr Glu Val Val Ser Asn Val Gln Glu Tyr Arg Glu Phe Val
100 105 110
Pro Trp Cys Lys Lys Ser Leu Val Val Ser Ser Arg Lys Gly His Leu
115 120 125
Lys Ala Gln Leu Glu Val Gly Phe Pro Pro Val Met Glu Arg Tyr Thr
130 135 140
Ser Ala Val Ser Met Val Lys Pro His Met Val Lys Ala Val Cys Thr
145 150 155 160
Asp Gly Lys Leu Phe Asn His Leu Glu Thr Ile Trp Arg Phe Ser Pro
165 170 175
Gly Ile Pro Ala Tyr Pro Arg Thr Cys Thr Val Asp Phe Ser Ile Ser
180 185 190
Phe Glu Phe Arg Ser Leu Leu His Ser Gln Leu Ala Thr Met Phe Phe
195 200 205
Asp Glu Val Val Lys Gln Asn Val Ala Ala Phe Glu Arg Arg Ala Ala
210 215 220
Thr Lys Phe Gly Pro Glu Thr Ala Ile Pro Arg Glu Leu Met Phe His
225 230 235 240
Glu Val His Gln Thr
245

<210> 5439
<211> 4234
<212> DNA
<213> Homo sapiens

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120
atcaaagttg tgggaaaatg gaaggaagtg aagattgacc caaatatgtt tgcagatgga
180
cagatggatg acttggtgtg ctttgaggaa ttgacagatt accagttggt ctcccctgcc
240
aagaatccct ccagtctctt ctcaaaggaa gcacccaaga gaaaggcaca agctgtttca
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gaagaagagg aggaggagga gggaaagtct agctcaccaa agaaaaagat caagttgaag
360
aaaagtaaaa atgtagcaac tgaaggaacc agtacccaga aagaatttga agtgaaagat
420
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480
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720

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840
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2340

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2460
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4080
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4234

<210> 5440
<211> 461
<212> PRT
<213> Homo sapiens

<400> 5440
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Gln Arg Met Leu Asn Arg Arg Pro Glu Ile Val Val Ala Thr Pro Gly
35 40 45
Arg Leu Trp Glu Leu Ile Lys Glu Lys His Tyr His Leu Arg Asn Leu
50 55 60
Arg Gln Leu Arg Cys Leu Val Val Asp Glu Ala Asp Arg Met Val Glu
65 70 75 80
Lys Gly His Phe Ala Glu Leu Ser Gln Leu Leu Glu Met Leu Asn Asp
85 90 95
Ser Gln Tyr Asn Pro Lys Arg Gln Thr Leu Val Phe Ser Ala Thr Leu
100 105 110
Thr Leu Val His Gln Ala Pro Ala Arg Ile Leu His Lys Lys His Thr
115 120 125
Lys Lys Met Asp Lys Thr Ala Lys Leu Asp Leu Leu Met Gln Lys Ile
130 135 140
Gly Met Arg Gly Lys Pro Lys Val Ile Asp Leu Thr Arg Asn Glu Ala
145 150 155 160
Thr Val Glu Thr Leu Thr Glu Thr Lys Ile His Cys Glu Thr Asp Glu
165 170 175
Lys Asp Phe Tyr Leu Tyr Tyr Phe Leu Met Gln Tyr Pro Gly Arg Ser
180 185 190
Leu Val Phe Ala Asn Ser Ile Ser Cys Ile Lys Arg Leu Ser Gly Leu
195 200 205
Leu Lys Val Leu Asp Ile Met Pro Leu Thr Leu His Ala Cys Met His
210 215 220
Gln Lys Gln Arg Leu Arg Asn Leu Glu Gln Phe Ala Arg Leu Glu Asp
225 230 235 240
Cys Val Leu Leu Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Ile Pro
245 250 255
Lys Val Gln His Val Ile His Tyr Gln Val Pro Arg Thr Ser Glu Ile
260 265 270
Tyr Val His Arg Ser Gly Arg Thr Ala Arg Ala Thr Asn Glu Gly Leu
275 280 285
Ser Leu Met Leu Ile Gly Pro Glu Asp Val Ile Asn Phe Lys Lys Ile

290 295 300
Tyr Lys Thr Leu Lys Lys Asp Glu Asp Ile Pro Leu Phe Pro Val Gln
305 310 315 320
Thr Lys Tyr Met Asp Val Val Lys Glu Arg Ile Arg Leu Ala Arg Gln
325 330 335
Ile Glu Lys Ser Glu Tyr Arg Asn Phe Gln Ala Cys Leu His Asn Ser
340 345 350
Trp Ile Glu Gln Ala Ala Ala Ala Leu Glu Ile Glu Leu Glu Glu Asp
355 360 365
Met Tyr Lys Gly Gly Lys Ala Asp Gln Gln Glu Glu Arg Arg Arg Gln
370 375 380
Lys Gln Met Lys Val Leu Lys Lys Glu Leu Arg His Leu Leu Ser Gln
385 390 395 400
Pro Leu Phe Thr Glu Ser Gln Lys Thr Lys Tyr Pro Thr Gln Ser Gly
405 410 415
Lys Pro Pro Leu Leu Val Ser Ala Pro Ser Lys Ser Glu Ser Ala Leu
420 425 430
Ser Cys Leu Ser Lys Gln Lys Lys Lys Lys Thr Lys Lys Pro Lys Glu
435 440 445
Pro Gln Pro Glu Gln Pro Gln Pro Ser Thr Ser Ala Asn
450 455 460

<210> 5441
<211> 1635
<212> DNA
<213> Homo sapiens

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120
cggcgcgggt cagccctggt tcgccggctt ctgggtcttt gaacagccgc gatgtcgatc
180
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240
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300
gaaaaagacc tcgatgaagt tctgcagacc cactcagtgt ttgtaaatgt ttctaaaggt
360
caggttgcca aaaaggaaga tctcatcagt gcgtttggaa cagatgacca aactgaaatc
420
tgtaagcaga ttttgactaa aggagaagtt caagtatcag ataaagaaag acacacacaa
480
ctggagcaga tgtttaggga cattgcaact attgtggcag acaaatgtgt gaatcctgaa
540
acaaagagac catacaccgt gatccttatt gagagagcca tgaaggacat ccactattcg
600
gtgaaaacca acaagagtac aaaacagcag gctttggaag tgataaagca gttaaaagag
660
aaaatgaaga tagaacgtgc tcacatgagg cttcggttca tccttccagt gaatgaaggc
720
aagaagctga aagaaaagct caagccactg atcaaggtca tagaaagtga agattatggc
780

caacagttag aaatcgtatg tctgattgac ccgggctgct tccgagaaat tgatgagcta
840
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900
gaaggagatg agaaatttga atgacaccca tcaatctctt cacctctaaa acactaaagt
960
gtttccgttt ccgacggcac tgtttcatgt ctgtggtctg ccaaatactt gcttaaacta
1020
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1080
aataatgtgg gaatgatttg gttttaatta taaactgggg tctaaatcct aaagcaaaat
1140
tgaaactcca agatgcaaag tccagagtgg cattttgcta ctctgtctca tgccttgata
1200
gctttccaaa atgaaagtta cttgaggcag ctcttgtggg tgaaaagtta tttgtacagt
1260
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1320
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1380
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1440
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1500
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1635

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<211> 250
<212> PRT
<213> Homo sapiens

<400> 5442
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Val Val Arg Met Lys Arg Ala Gly Lys Arg Phe Glu Ile Ala Cys Tyr
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Lys Asn Lys Val Val Gly Trp Arg Ser Gly Val Glu Lys Asp Leu Asp
        35   40   45
Glu Val Leu Gln Thr His Ser Val Phe Val Asn Val Ser Lys Gly Gln
    50   55   60
Val Ala Lys Lys Glu Asp Leu Ile Ser Ala Phe Gly Thr Asp Asp Gln
65   70   75   80
Thr Glu Ile Cys Lys Gln Ile Leu Thr Lys Gly Glu Val Gln Val Ser
                85   90   95
Asp Lys Glu Arg His Thr Gln Leu Glu Gln Met Phe Arg Asp Ile Ala
            100   105   110
Thr Ile Val Ala Asp Lys Cys Val Asn Pro Glu Thr Lys Arg Pro Tyr
        115   120   125
Thr Val Ile Leu Ile Glu Arg Ala Met Lys Asp Ile His Tyr Ser Val

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    130                 135                 140
Lys Thr Asn Lys Ser Thr Lys Gln Gln Ala Leu Glu Val Ile Lys Gln
145                 150                 155                 160
Leu Lys Glu Lys Met Lys Ile Glu Arg Ala His Met Arg Leu Arg Phe
                165                 170                 175
Ile Leu Pro Val Asn Glu Gly Lys Lys Leu Lys Glu Lys Leu Lys Pro
            180                 185                 190
Leu Ile Lys Val Ile Glu Ser Glu Asp Tyr Gly Gln Gln Leu Glu Ile
        195                 200                 205
Val Cys Leu Ile Asp Pro Gly Cys Phe Arg Glu Ile Asp Glu Leu Ile
    210                 215                 220
Lys Lys Glu Thr Lys Gly Lys Gly Ser Leu Glu Val Leu Asn Leu Lys
225                 230                 235                 240
Asp Val Glu Glu Gly Asp Glu Lys Phe Glu
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<211> 2021
<212> DNA
<213> Homo sapiens

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120
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180
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240
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660
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720
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780
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960

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1020
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1080
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1140
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2021

<210> 5444
<211> 438
<212> PRT
<213> Homo sapiens

<400> 5444
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Lys Ile Arg Leu Arg Cys Gln Lys Gly Ile Pro Pro Ser Leu Arg Gly
35 40 45
Arg Ala Trp Gln Tyr Leu Ser Gly Gly Lys Val Lys Leu Gln Gln Asn
50 55 60
Pro Gly Lys Phe Asp Glu Leu Asp Met Ser Pro Gly Asp Pro Lys Trp
65 70 75 80
Leu Asp Val Ile Glu Arg Asp Leu His Arg Gln Phe Pro Phe His Glu

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                85                  90                  95
Met Phe Val Ser Arg Gly Gly His Gly Gln Gln Asp Leu Phe Arg Val
            100                 105                 110
Leu Lys Ala Tyr Thr Leu Tyr Arg Pro Glu Glu Gly Tyr Cys Gln Ala
        115                 120                 125
Gln Ala Pro Ile Ala Ala Val Leu Leu Met His Met Pro Ala Glu Gln
    130                 135                 140
Ala Phe Trp Cys Leu Val Gln Ile Cys Glu Lys Tyr Leu Pro Gly Tyr
145                 150                 155                 160
Tyr Ser Glu Lys Leu Glu Ala Ile Gln Leu Asp Gly Glu Ile Leu Phe
                165                 170                 175
Ser Leu Leu Gln Lys Val Ser Pro Val Ala His Lys His Leu Ser Arg
            180                 185                 190
Gln Lys Ile Asp Pro Leu Leu Tyr Met Thr Glu Trp Phe Met Cys Ala
        195                 200                 205
Phe Ser Arg Thr Leu Pro Trp Ser Ser Val Leu Arg Val Trp Asp Met
    210                 215                 220
Phe Phe Cys Glu Gly Val Lys Ile Ile Phe Arg Val Gly Leu Val Leu
225                 230                 235                 240
Leu Lys His Ala Leu Gly Ser Pro Glu Lys Val Lys Ala Cys Gln Gly
                245                 250                 255
Gln Tyr Glu Thr Ile Glu Arg Leu Arg Ser Leu Ser Pro Lys Ile Met
            260                 265                 270
Gln Glu Ala Phe Leu Val Gln Glu Val Val Glu Leu Pro Val Thr Glu
        275                 280                 285
Arg Gln Ile Glu Arg Glu His Leu Ile Gln Leu Arg Arg Trp Gln Glu
    290                 295                 300
Thr Arg Gly Glu Leu Gln Cys Arg Ser Pro Pro Arg Leu His Gly Ala
305                 310                 315                 320
Lys Ala Ile Leu Asp Ala Glu Pro Gly Pro Arg Pro Ala Leu Gln Pro
                325                 330                 335
Ser Pro Ser Ile Arg Leu Pro Leu Asp Ala Pro Leu Pro Gly Ser Lys
            340                 345                 350
Ala Lys Pro Lys Pro Pro Lys Gln Ala Gln Lys Glu Gln Arg Lys Gln
        355                 360                 365
Met Lys Gly Arg Gly Gln Leu Glu Lys Pro Pro Ala Pro Asn Gln Ala
    370                 375                 380
Met Val Val Ala Ala Ala Gly Asp Ala Cys Pro Pro Gln His Val Pro
385                 390                 395                 400
Pro Lys Asp Ser Ala Pro Lys Asp Ser Ala Pro Gln Asp Leu Ala Pro
                405                 410                 415
Gln Val Ser Ala His His Arg Ser Gln Glu Ser Leu Thr Ser Gln Glu
            420                 425                 430
Ser Glu Asp Thr Tyr Leu
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<210> 5445
<211> 1187
<212> DNA
<213> Homo sapiens

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120
gttccatctc cctttccact gtgcctaacc ttacatctat tacctacatc cagcaagaca
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cgattttcca cgatgagttg attcgtaatt ccatttatgt gctagttttt agaattttcc
240
tgtgggtttt tttttactta cttatgattt taattttgtt tgctttaaaa aaaacacatg
300
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360
aaaaattcat tgaggggggg gctcgcgttg tacaaagaaa atcagaccca ccgggatggc
420
tgtgatcaaa gagacagtaa caagggtagg gaggtggaga tgcgaatcca aacacacaac
480
ttgtgcaaag gtcaagtggc cacagccgcc acggaaaaca ggctggcggt tcctccgacg
540
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600
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780
acgcctggac cctggcccca caccacagca tccacaatgt ggtgccaacc aacaggccac
840
gcacacagag gccatgggcc agacgcttcc actgacacga aatgcccaag agaggcacag
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1080
ggtgaattgt acggtgcttg tattatacct caataaagct atttttaaag aaacaaaatt
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1187

<210> 5446
<211> 107
<212> PRT
<213> Homo sapiens

<400> 5446
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20 25 30
Arg Lys Thr Gly Trp Arg Phe Leu Arg Arg Ser Thr His Ser Arg His
35 40 45
Gly Thr Gln Trp Phe His Pro Gln Val Cys Ser Asn Arg His His Ser
50 55 60
Pro Arg Pro His Ala Asp Ser Asp Thr Arg Ala His Ser Pro Arg Ser

65 70 75 80
His Ala Asp Ser Asp Met Arg Ala His Ser Leu Ser His Asp Ser Gln
85 90 95
Thr Val Glu Thr Arg Gln Val Gly Leu Gly Cys
100 105

<210> 5447
<211> 1444
<212> DNA
<213> Homo sapiens

<400> 5447
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120
gatgatctca tagttgtact ttgcagtaag aagacttttc agatcaccaa acaaggagat
180
ggcgttgact ttctgtcttg gtttctgaat gctctgcact cagctctggg gggcacaaag
240
aagaaaaaga agactattgt gactgatgtt ttccaggggt ccatgaggat cttcactaaa
300
aagcttcccc atcctgatct gccagcagaa gaaaaagagc agttgctcca taatgacgag
360
taccaggaga caatggtgga gtccactttt atgtacctga cgctggacct tcctactgcc
420
cccctctaca aggacgagaa ggagcagctc atcattcccc aagtgccact cttcaacatc
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540
aagcgcttcc agcttaccaa gttgcctcca tatctaatct tttgtatcaa gagattcact
600
aagaacaact tctttgttga gaagaatcca actnattgtc aatttcccta ttacaaatgt
660
ggatctgaga gaatacttgt ctgaagaagt acaagcagta cacaagaata ccacctatga
720
cctcattgcc aacatcgtgc atgacggcaa gccctccgag ggctcctacc ggatccacgt
780
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960
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1020
tcctaggcca gcccagcttg tatgggttct ggctacacca gagcaccaag agcccacttg
1080
cctgggatgg ccccacactg tcactcagct gttctttgat catttttttc tagattgatg
1140
ctcctttctc ccatgcattg agctcccatc tagcttcagc agggcagaac ccttctccag
1200
atgtgtgtaa cttatgtctt gagtatctgg gagtagttga agaacagata attccttcca
1260

aacatcaagc cttgggattc ttggagcaag cagaaagcca gtaacttcgc tctgttagag
1320
gtggaggatt ttcctatggt tccccccatt tcctgatttg tatttttaga tggattaaat
1380
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1440
aaaa
1444

<210> 5448
<211> 189
<212> PRT
<213> Homo sapiens

<400> 5448
Gly Ile Asp Asp Leu Ile Val Val Leu Cys Ser Lys Lys Thr Phe Gln
1 5 10 15
Ile Thr Lys Gln Gly Asp Gly Val Asp Phe Leu Ser Trp Phe Leu Asn
20 25 30
Ala Leu His Ser Ala Leu Gly Gly Thr Lys Lys Lys Lys Lys Thr Ile
35 40 45
Val Thr Asp Val Phe Gln Gly Ser Met Arg Ile Phe Thr Lys Lys Leu
50 55 60
Pro His Pro Asp Leu Pro Ala Glu Glu Lys Glu Gln Leu Leu His Asn
65 70 75 80
Asp Glu Tyr Gln Glu Thr Met Val Glu Ser Thr Phe Met Tyr Leu Thr
85 90 95
Leu Asp Leu Pro Thr Ala Pro Leu Tyr Lys Asp Glu Lys Glu Gln Leu
100 105 110
Ile Ile Pro Gln Val Pro Leu Phe Asn Ile Leu Ala Lys Phe Asn Gly
115 120 125
Ile Thr Glu Lys Glu Tyr Lys Thr Tyr Lys Glu Asn Phe Leu Lys Arg
130 135 140
Phe Gln Leu Thr Lys Leu Pro Pro Tyr Leu Ile Phe Cys Ile Lys Arg
145 150 155 160
Phe Thr Lys Asn Asn Phe Phe Val Glu Lys Asn Pro Thr Xaa Cys Gln
165 170 175
Phe Pro Tyr Tyr Lys Cys Gly Ser Glu Arg Ile Leu Val
180 185

<210> 5449
<211> 1359
<212> DNA
<213> Homo sapiens

<400> 5449
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cgaggggggca accagaccag tggcatcgac ttctttatta cccaagaacg gattgttttc
120
ctggacacac agcccatcct gagcccttct atcctagacc atctcatcaa taatgaccgc
180
aaactgcctc cagagtacaa ccttccccac acttacgttg aaatgcagtc actccagatt
240

gctgccttcc ttttcacggt ctgccatgtg gggattnntg tccaggactg gttcacagac
300
ctcagtctct acaggttcct gcagacagca gagatggtga agccctccac cccatccccc
360
agccacgagt ccagcagctc atcgggctcc gatgaaggca ccgagtacta cccccaccta
420
gtcttcttcc agaacaaagc tcgccgagag gacttctgtc ctcggaagct gcggcagatg
480
cacctgatga ttgaccagct catggcccac tcccacctgc gttacaaggg aactctgtcc
540
atgttacaat gcaatgtctt cccggggctt ccacctgact tcctggactc tgaggtcaac
600
ttattcctgg tacccttcat ggacagtgaa gcagagagtg aaaacccacc aagagcagga
660
cctggttcca gcccactctt ctccctgctg cctgggtatc gtggccaccc cagtttccag
720
tccttggtga gcaagctccg gagccaagtg atgtccatgg cccggccaca gctgtcacac
780
acgatcctca ccgagaagaa ctggttccac tacgctgccc ggatctggga tggggtgaga
840
aagtcctctg ctctggcaga gtacagccgc ctgctggcct gaggccaagg agaggaatgt
900
catgcagggg acctcctggg tccgcagtgt actgcgaggg agcacagatg tccatccccc
960
gctggggtgg agagcggcag caggcctgat ggatgaggga tcgtggcttc ccggcccaga
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gacatgaggt gtccagggcc aggcccccca ccctcagttg gggctgttcc gggggtgact
1080
gtgagcgatc ccaccccaaa cctgagatgg ggcagcccgt cctgtgtcct ccacagggac
1140
aagcagtggg aggagtctga atggtcacca ggaagcccgg gctccatctt gacctccttt
1200
ttcagggaca ggagcaacag gcccctcttc cctgactcta agcccttccc tgtaaggtga
1260
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1320
gcaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa
1359

<210> 5450
<211> 293
<212> PRT
<213> Homo sapiens

<400> 5450
Ser Pro Glu Glu Asp Gln Arg Thr Tyr Val Phe Arg Ala Gln Ser Ala
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Glu Met Lys Glu Arg Gly Gly Asn Gln Thr Ser Gly Ile Asp Phe Phe
            20   25   30
Ile Thr Gln Glu Arg Ile Val Phe Leu Asp Thr Gln Pro Ile Leu Ser
        35   40   45
Pro Ser Ile Leu Asp His Leu Ile Asn Asn Asp Arg Lys Leu Pro Pro
    50   55   60
Glu Tyr Asn Leu Pro His Thr Tyr Val Glu Met Gln Ser Leu Gln Ile

65 70 75 80
Ala Ala Phe Leu Phe Thr Val Cys His Val Gly Ile Xaa Val Gln Asp
85 90 95
Trp Phe Thr Asp Leu Ser Leu Tyr Arg Phe Leu Gln Thr Ala Glu Met
100 105 110
Val Lys Pro Ser Thr Pro Ser Pro Ser His Glu Ser Ser Ser Ser Ser
115 120 125
Gly Ser Asp Glu Gly Thr Glu Tyr Tyr Pro His Leu Val Phe Phe Gln
130 135 140
Asn Lys Ala Arg Arg Glu Asp Phe Cys Pro Arg Lys Leu Arg Gln Met
145 150 155 160
His Leu Met Ile Asp Gln Leu Met Ala His Ser His Leu Arg Tyr Lys
165 170 175
Gly Thr Leu Ser Met Leu Gln Cys Asn Val Phe Pro Gly Leu Pro Pro
180 185 190
Asp Phe Leu Asp Ser Glu Val Asn Leu Phe Leu Val Pro Phe Met Asp
195 200 205
Ser Glu Ala Glu Ser Glu Asn Pro Pro Arg Ala Gly Pro Gly Ser Ser
210 215 220
Pro Leu Phe Ser Leu Leu Pro Gly Tyr Arg Gly His Pro Ser Phe Gln
225 230 235 240
Ser Leu Val Ser Lys Leu Arg Ser Gln Val Met Ser Met Ala Arg Pro
245 250 255
Gln Leu Ser His Thr Ile Leu Thr Glu Lys Asn Trp Phe His Tyr Ala
260 265 270
Ala Arg Ile Trp Asp Gly Val Arg Lys Ser Ser Ala Leu Ala Glu Tyr
275 280 285
Ser Arg Leu Leu Ala
290

<210> 5451
<211> 1184
<212> DNA
<213> Homo sapiens

<400> 5451
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120
acagatgtga gccatcatgc ccggctaatt tttttgtatt ttagtagaga cagggtttca
180
ccgtgttagc caggatggtc ttgatctcct gaccttgtga tccaccagcc tcagcctccc
240
aaagtgctgg gattacaggc gtgagccact gtgcccggcc aagaattttt ttatcgataa
300
catagtgagc tctctgcctc ttcggaacga tgtccacttt gcttatgatc aacccaagca
360
ggactcttct ctccctggac gcctctcccc tggtctggaa tcttccagtt ctgccagaat
420
tggcctttcc cagatgctgc aaacttccag ttgaacccct ttttctgtgt ggcccctggg
480
gctgcgagac caaaatccat gagttctgtg taccctagac ctttggaagg tgagagcagg
540

gccctgagaa aaggcagcca cctcctctcc ctggctgaac ccctgccacc ctactcctca
600
ccagaattgt cagtggcctt tcaccacagt ggtccttcct gcctgagccc tgcactgtcc
660
cagaccacac agaagtctgg tcacctctgg gcgcctggga tggtcaccga agagaagcac
720
gctgtccccg tctctcctgg cttctgccag aaaatcgaac aagtgcaatt aacacactgt
780
tactgccgaa gcctgaaact cccaggactt gtccttgatc cttccagaaa ccaccaggtc
840
cggcacttgg agccccccgg agagggacct cccagccgag ccctcaaaga actccatgaa
900
atcaggaact gcttgatgaa atgtatctcc ttgtacctgg aagatgaagc ccaaacaccc
960
acacctctgt ctcccccagg gctcgggatg tctccagcag cccggccacg cagcttccca
1020
ggtgggctcg gggaggtggg agcagggacc atctctgtcc cctccaccct cactccatcc
1080
acctcggaga ccaccctccc ccagccagat acggaataaa actacagacg cagacgtcgg
1140
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa
1184

<210> 5452
<211> 206
<212> PRT
<213> Homo sapiens

<400> 5452
Met Ser Ser Val Tyr Pro Arg Pro Leu Glu Gly Glu Ser Arg Ala Leu
1 5 10 15
Arg Lys Gly Ser His Leu Leu Ser Leu Ala Glu Pro Leu Pro Pro Tyr
20 25 30
Ser Ser Pro Glu Leu Ser Val Ala Phe His His Ser Gly Pro Ser Cys
35 40 45
Leu Ser Pro Ala Leu Ser Gln Thr Thr Gln Lys Ser Gly His Leu Trp
50 55 60
Ala Pro Gly Met Val Thr Glu Glu Lys His Ala Val Pro Val Ser Pro
65 70 75 80
Gly Phe Cys Gln Lys Ile Glu Gln Val Gln Leu Thr His Cys Tyr Cys
85 90 95
Arg Ser Leu Lys Leu Pro Gly Leu Val Leu Asp Pro Ser Arg Asn His
100 105 110
Gln Val Arg His Leu Glu Pro Pro Gly Glu Gly Pro Pro Ser Arg Ala
115 120 125
Leu Lys Glu Leu His Glu Ile Arg Asn Cys Leu Met Lys Cys Ile Ser
130 135 140
Leu Tyr Leu Glu Asp Glu Ala Gln Thr Pro Thr Pro Leu Ser Pro Pro
145 150 155 160
Gly Leu Gly Met Ser Pro Ala Ala Arg Pro Arg Ser Phe Pro Gly Gly
165 170 175
Leu Gly Glu Val Gly Ala Gly Thr Ile Ser Val Pro Ser Thr Leu Thr
180 185 190
Pro Ser Thr Ser Glu Thr Thr Leu Pro Gln Pro Asp Thr Glu

195 200 205

<210> 5453
<211> 1974
<212> DNA
<213> Homo sapiens

<400> 5453
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cgcgacttcc tggtggtcaa caagcactgg gacgttcgca ttgacagcaa ggcgtggcgg
120
gagactctga ccctgcagaa gcagctgcgg taccgctttc ccgagctggc cgaccctgac
180
acctgctacg ggttcaggtt ctgccaccag ctggatttct ccaccagcgg ggcgctgtgc
240
gtggccctaa acaaggcagc cgccggcagc gcgtacaggt gcttcaagga gcggcgcgtg
300
accaaggctt acctggcatt gctgcggggg cacatccagg agagccgggt aaccatcagc
360
catgccattg gcaggaacag cacggagggc cgggcccaca ccatgtgcat cgagggctcg
420
cagggtgtgg caggttgtga gaacccaaag ccaagcctca cagatctcgt ggttctggaa
480
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540
acacaccagc tgcgcgtgca ctgcagtgcc ctgggccacc ccgtggtggg cgacctgacc
600
tacggagaag tctcgggccg ggaggaccgg ccgttcagaa tgatgctgca cgctttctac
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720
tccctggatg cctgctggag cccccacaca ctgctgcagt cgctggacca gctcgtgcag
780
gccttacggg ccacccccga ccctgacccc gaggataggg gccccaggcc aggcagcccc
840
tccgcactcc tgcctgggcc cggccggcct cctccacccc caaccaagcc ccctgagact
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gaggcacagc ggggcccctg cctgcagtgg ctgtcggagt ggacgctgga accggacagc
960
tgagagccgt ggggctgggg caggggtgt cagctgcaca gcgggactct agggagatgg
1020
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1080
ctgggttgcc ccggccaggc ctgcgaggaa gggctgaggt ggggccggca gggggcgcca
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1260
ttccggctct caagcgtcac cccaggggcg tcagttttac ggactcaagg tcacctcagg
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aagaggcagg gccaggtttt gggataggct ttgcctccag gatgggctgc tcctgggcct
1380

ggtgagctac tgcccccaac ctaccctcta gaggggctgg gaagggccgt tctgggctca
1440
cctggcctgg gagacccatc tggtccctgc gtcctctgcc cctcactgct ctgtgcagat
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1560
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1620
tgagctcagt gtggtgtttg gtgcacaggg gttggtcagg ggccatggcc aaggccctgc
1680
cacgcacgcc catccctcag atccactgtg agcaccaacc tgctgcagtc tcttgggccc
1740
ctgctggcag ctctgccacg tcaccgcctg cctggctccc acacagccat gcattgtcac
1800
tctgcctccg ggaccccagc ttgggagctg tgggtctgcc aggtcccacc tcctctgtcc
1860
cccatgccac aacctgggct cctggctaca gcagggctcc agggactcca aataaatgtt
1920
cagtgactgg caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa
1974

<210> 5454
<211> 320
<212> PRT
<213> Homo sapiens

<400> 5454
Xaa Gly Arg Pro Ala Met Glu Pro Gly Ser Val Glu Asn Leu Ser Ile
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Val Tyr Arg Ser Arg Asp Phe Leu Val Val Asn Lys His Trp Asp Val
20 25 30
Arg Ile Asp Ser Lys Ala Trp Arg Glu Thr Leu Thr Leu Gln Lys Gln
35 40 45
Leu Arg Tyr Arg Phe Pro Glu Leu Ala Asp Pro Asp Thr Cys Tyr Gly
50 55 60
Phe Arg Phe Cys His Gln Leu Asp Phe Ser Thr Ser Gly Ala Leu Cys
65 70 75 80
Val Ala Leu Asn Lys Ala Ala Ala Gly Ser Ala Tyr Arg Cys Phe Lys
85 90 95
Glu Arg Arg Val Thr Lys Ala Tyr Leu Ala Leu Leu Arg Gly His Ile
100 105 110
Gln Glu Ser Arg Val Thr Ile Ser His Ala Ile Gly Arg Asn Ser Thr
115 120 125
Glu Gly Arg Ala His Thr Met Cys Ile Glu Gly Ser Gln Gly Val Ala
130 135 140
Gly Cys Glu Asn Pro Lys Pro Ser Leu Thr Asp Leu Val Val Leu Glu
145 150 155 160
His Gly Leu Tyr Ala Gly Asp Pro Val Ser Lys Val Leu Leu Lys Pro
165 170 175
Leu Thr Gly Arg Thr His Gln Leu Arg Val His Cys Ser Ala Leu Gly
180 185 190
His Pro Val Val Gly Asp Leu Thr Tyr Gly Glu Val Ser Gly Arg Glu
195 200 205
Asp Arg Pro Phe Arg Met Met Leu His Ala Phe Tyr Leu Arg Ile Pro

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    210                 215                 220
Thr Asp Thr Glu Cys Val Glu Val Cys Thr Pro Asp Pro Phe Leu Pro
225                 230                 235                 240
Ser Leu Asp Ala Cys Trp Ser Pro His Thr Leu Leu Gln Ser Leu Asp
                245                 250                 255
Gln Leu Val Gln Ala Leu Arg Ala Thr Pro Asp Pro Asp Pro Glu Asp
            260                 265                 270
Arg Gly Pro Arg Pro Gly Ser Pro Ser Ala Leu Leu Pro Gly Pro Gly
        275                 280                 285
Arg Pro Pro Pro Pro Pro Thr Lys Pro Pro Glu Thr Glu Ala Gln Arg
    290                 295                 300
Gly Pro Cys Leu Gln Trp Leu Ser Glu Trp Thr Leu Glu Pro Asp Ser
305                 310                 315                 320
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<210> 5455
<211> 975
<212> DNA
<213> Homo sapiens

<400> 5455

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120
tgagcctaag gtaccacagt tagtctcatt tgcctcttgt cctgtgaact ccacttagaa
180
tgtcattgaa cttgggcaga cataattcta gtgtctgttc caaacgcact gtgtcacaga
240
agctagaatt accattagag gcacaaaccc ctgagaatac acaaggggc acgcttccag
300
tagatgtgtt ggggaaggag gagggcagag gggacagggg acaggattca gctttgtggt
360
gggtcctgag ggttcctacc aggggtagcc aggatctggg aaacagatca gcgactctag
420
tctgaagtgg ctgcctggtt cgggggctgc cttcagcaag attcaggcag gagagacgga
480
aatagccacc ttccaggcgt gagtcctgga gataaaaatg gattttaacc taggactgcc
540
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600
ccggtgtcta actggcttgt ttctctttat ggcttggctt cattccgacc tggggtgggg
660
ccacatccaa cccactgccc actggctgtc cgtctggcct gccccgcggt tccaaccaca
720
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780
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840
accatgaaca tccccttcca gtccatccac ttcatcacct atgagttcct gcaggagcag
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960
gccctcgccg cggcg
975
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<210> 5456
<211> 149
<212> PRT
<213> Homo sapiens

<400> 5456
Pro Arg Thr Ala Gly Ser Trp Pro Ser Ala Ala Ala Gln Thr Arg Ala
1 5 10 15
Val Cys Ala Gly Ser Arg Leu Phe Pro Val Ser Asn Trp Leu Val Ser
20 25 30
Leu Tyr Gly Leu Ala Ser Phe Arg Pro Gly Val Gly Pro His Pro Thr
35 40 45
His Cys Pro Leu Ala Val Arg Leu Ala Cys Pro Ala Val Pro Thr Thr
50 55 60
Val Val Lys Gln Arg Leu Gln Met Tyr Asn Ser Gln His Arg Ser Ala
65 70 75 80
Ile Ser Cys Ile Arg Thr Val Trp Arg Thr Glu Gly Leu Gly Ala Phe
85 90 95
Tyr Arg Ser Tyr Thr Thr Gln Leu Thr Met Asn Ile Pro Phe Gln Ser
100 105 110
Ile His Phe Ile Thr Tyr Glu Phe Leu Gln Glu Gln Val Asn Pro His
115 120 125
Arg Thr Tyr Asn Pro Gln Ser His Ile Ile Ser Gly Gly Leu Ala Gly
130 135 140
Ala Leu Ala Ala Ala
145

<210> 5457
<211> 448
<212> DNA
<213> Homo sapiens

<400> 5457
cgcagcggga gcgtgggcag ccaggcggtg gcgcggagga tggatgggga cagccgagat
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ggcggcggcg gcaaggacgc caccgggtcg gaggactacg agaacctgcc gactagcgcc
120
tccgtgtcca cccacatgac agcaggagcg atggccggga tcctggagca ctcggtcatg
180
tacccggtgg actcggtgaa ggtaatgtgg actgtggagc tctgtgctgg tcactttcaa
240
ccctgaacct gatgctactt attttgcagt tctaagtgca aagtcggcct ggtggatgct
300
tcccattata atattaaatt tgcttcttcg tgaggtcaca cctcacatcc ccagtgtcac
360
tttaataact agtgtttttt acatggtggg ccatgaccca ttagtggact ctgcatttaa
420
aaataaataa ataaataaaa gaaaaaaa
448

<210> 5458
<211> 81
<212> PRT

<213> Homo sapiens

<400> 5458

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Arg Ser Gly Ser Val Gly Ser Gln Ala Val Ala Arg Arg Met Asp Gly
 1               5                  10                  15
Asp Ser Arg Asp Gly Gly Gly Gly Lys Asp Ala Thr Gly Ser Glu Asp
            20                  25                  30
Tyr Glu Asn Leu Pro Thr Ser Ala Ser Val Ser Thr His Met Thr Ala
        35                  40                  45
Gly Ala Met Ala Gly Ile Leu Glu His Ser Val Met Tyr Pro Val Asp
    50                  55                  60
Ser Val Lys Val Met Trp Thr Val Glu Leu Cys Ala Gly His Phe Gln
65                  70                  75                  80
Pro
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<210> 5459
<211> 1468
<212> DNA
<213> Homo sapiens

<400> 5459

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ttttgcgccc ctccccctcc ctgcccacct cctgcagcct cctgcgcccc gccgagctgg
120
cggatggagc tgcgcagcgg gagcgtgggc agccaggcgg tggcgcggag gatggatggg
180
gacagccgag atggcggcgg cggcaaggac gccaccgggt cggaggacta cgagaacctg
240
ccgactagcg cctccgtgtc cacccacatg acagcaggag cgatggccgg gatcctggag
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600
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660
cccgcttgct cacgaataaa gaactcagag ttgtgtgtgc aatgcacacc cagacacacg
720
cacgcacaca cacgcgcgcg cacacacatg ctttttttctg ttcccctccg ctttctgaag
780
cctggggaga aatcagtgac agaggtgttt tggttttatt gttatgtggg ttttcttttg
840
tatttttttt gtttgttttg tttttaaaca ttcaaaagca attaatgatc agacatagga
900
gaaaccctga atagaaacaa aacttttgaa tgctggattc aaaaaaaaaa aaaagttatc
960
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tggacagctt ctttgagact atttaaaaac tggtacaaca ggtctctaca acgccaagat
1020
ctaactaagc tttaaaaggt caagaagttt tatggctgac aaaggactcg cgcaacgcag
1080
aaggcctttc ccaccttaag cttccgggga tctgggaatt ttacccccat tctcttctgt
1140
ttgtctgagt ctcatctctc tgcaagcaag ggctgaaatc attttgtttg ggatagctgg
1200
gagtatggcc accctgctcc acgatgcggt aatgaatcca gcagaaggta atgtttcatg
1260
gtcccaggga ggggcagtag gggatgtgca aaggggcaca aaaaaatggt tgtgggagag
1320
tggagaggac tgaaggtggg cagacggctc ctagtctcca gtcagagcag acaggagaat
1380
tgaatttttt actacgttat caaaggcctc aagaaaggac gtgaacataa gagtttttgg
1440
tattcctgtg ctcggagcta cttcaaag
1468

<210> 5460
<211> 155
<212> PRT
<213> Homo sapiens

<400> 5460
Met Glu Leu Arg Ser Gly Ser Val Gly Ser Gln Ala Val Ala Arg Arg
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Met Asp Gly Asp Ser Arg Asp Gly Gly Gly Gly Lys Asp Ala Thr Gly
            20   25   30
Ser Glu Asp Tyr Glu Asn Leu Pro Thr Ser Ala Ser Val Ser Thr His
        35   40   45
Met Thr Ala Gly Ala Met Ala Gly Ile Leu Glu His Ser Val Met Tyr
    50   55   60
Pro Val Asp Ser Val Lys Thr Arg Met Gln Ser Leu Ser Pro Asp Pro
65   70   75   80
Lys Ala Gln Tyr Thr Ser Ile Tyr Gly Ala Leu Lys Lys Ile Met Gln
                85   90   95
Thr Glu Gly Phe Trp Arg Pro Leu Arg Gly Val Asn Val Met Ile Met
            100   105   110
Gly Ala Gly Pro Ala His Ala Met Tyr Phe Ala Cys Tyr Glu Asn Met
        115   120   125
Lys Arg Thr Leu Asn Asp Val Phe His His Gln Gly Asn Ser His Leu
    130   135   140
Ala Asn Gly Ile Leu Lys Ala Phe Val Trp Ser
145   150   155

<210> 5461
<211> 1725
<212> DNA
<213> Homo sapiens

<400> 5461
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60

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120
ccgggaggca gcaacgcaag gagccaaaat agtttctttg ccggaatgct ttaattctcc
180
atatggagcg aaatattttc ctgaatatgc agagaaaatt cctggtgaat ccacacagaa
240
gctttctgaa gtagcaaagg aatgcagcat atatctcatt ggaggtaact tcctacccac
300
aaggctctat ccctgaagag gatgctggga aattatataa cacctgtgct gtgtttgggc
360
ctgatggaac tttactagca aagtatagaa agatccatct gtttgacatt gatgttcctg
420
gaaaaattac atttcaagaa tctaaaacat tgagtccggg tgatagtttc tccacatttg
480
atactcgtat gtaccagata agtttgcctc tttagcaatc tcagtagaag acaatcaggt
540
atttatttct tttttgtctc tctccgattt cttcacataa cctaactgaa agaccataag
600
tgagaaaggc agagaatcat cacagatctg gaaagttcgg gcttatttga gaactaagga
660
tttgacacga ttttgccctt tgatttgatt gtagcttcct gttacggctt ccagagtata
720
cctattaggc tacagttgag tacctcccat ctagataata agcattcaat tagaatgaat
780
ttctcatctt tactccgctg atgtaaatga tgtctttatg agatgaagtc caagtaggaa
840
tgagcttgta aattatctct gtcctcaggt cctgtgttaa tttatccctg tcagtgtttt
900
gtgatcatta tgtcatggag gatttcccct gccacaccat gctgtaggga gttaactttt
960
catttgtgca ttttctgttt ggaaacagct tactgcagag tgggtctggg catctgctac
1020
gacatgcggt ttgcagagct tgcacaaatc tacgcacaga gaggctgcca gctgttggta
1080
tatccaggag cttttaatct gaccactgga ccagcccatt gggagttact tcagcgaagc
1140
cgggctgttg ataatcaggt gtatgtggcc acagcctctc ctgcccggga tgacaaagcc
1200
tcctatgttg cctggggaca cagcaccgtg gtgaaccctt ggggggaggt tctagccaaa
1260
gctggcacag aagaagcaat cgtgtattca gacatagacc tgaagaagct ggctgaaata
1320
cgccagcaaa tccccgtttt tagacagaag cgatcagacc tctatgctgt ggagatgaaa
1380
aagccctaaa gtttatgttt ctaatgtgtc acagaatagg acgatatgat tctacaacat
1440
aatcaactcc ctattaaatt ctttaatgaa gatttttttt ttaattcggc cttgtccttc
1500
ctaggttctc tattgagatg agaaagcctc attatgctga cattttccac gccacattaa
1560
atagttaaaa aggatgcagc ctggagccag agagcagaaa gctgggctgg ttctgaagct
1620
tcttccatac ttaagttgcc tccaagcagt ttgtgaaagt atcagatcct ggtatcctgg
1680

tgattgattc acctaatata aatatatttg tgccatgaac ctctt
1725

<210> 5462
<211> 159
<212> PRT
<213> Homo sapiens

<400> 5462
Met Ser Trp Arg Ile Ser Pro Ala Thr Pro Cys Cys Arg Glu Leu Thr
1 5 10 15
Phe His Leu Cys Ile Phe Cys Leu Glu Thr Ala Tyr Cys Arg Val Gly
20 25 30
Leu Gly Ile Cys Tyr Asp Met Arg Phe Ala Glu Leu Ala Gln Ile Tyr
35 40 45
Ala Gln Arg Gly Cys Gln Leu Leu Val Tyr Pro Gly Ala Phe Asn Leu
50 55 60
Thr Thr Gly Pro Ala His Trp Glu Leu Leu Gln Arg Ser Arg Ala Val
65 70 75 80
Asp Asn Gln Val Tyr Val Ala Thr Ala Ser Pro Ala Arg Asp Asp Lys
85 90 95
Ala Ser Tyr Val Ala Trp Gly His Ser Thr Val Val Asn Pro Trp Gly
100 105 110
Glu Val Leu Ala Lys Ala Gly Thr Glu Glu Ala Ile Val Tyr Ser Asp
115 120 125
Ile Asp Leu Lys Lys Leu Ala Glu Ile Arg Gln Gln Ile Pro Val Phe
130 135 140
Arg Gln Lys Arg Ser Asp Leu Tyr Ala Val Glu Met Lys Lys Pro
145 150 155

<210> 5463
<211> 792
<212> DNA
<213> Homo sapiens

<400> 5463
nntttttttt ttttttaaag cctggattgt aaccagattt tctttttttcc cccttctcag
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ctgtagatat gatatctcct ttcagggccc cagcttaagg gcaaagtgag ttaatgtgta
120
gacaaaggcg agggacaaga gagagttaac atctagacag tggaaaaagc catggtgtgt
180
ggtttctggg aaccaccaac acttgcaggt ttagcttttt cccagggttg actacaagaa
240
agaaaaccat gtttttgcaa gattaaaatg tggttgagtg tgcctaaatt aaccatcccc
300
atttttatca tatttccacc atcacttcag ggttttaaga gtcagtgctc acctgggcgg
360
agctggtagt acattttgct tcttagaaag ctaagtcctg ggttccgtct gattttaggt
420
tccaggaact tcctgagaac acccgatcgc agagggtaat tttctggagt ttgttttgca
480
gggatagctg ggagtatggc caccctgctc cacgatgcgg taatgaatcc agcagaagtg
540

gtgaagcagc gcttgcagat gtacaactcg cagcaccggt cagcaatcag ctgcatccgg
600
acggtgtgga ggaccgaggg gttgggggcc ttctaccgga gctacaccac gcagctgacc
660
atgaacatcc ccttccagtc catccacttc atcacctatg agttcctgca ggagcaggtc
720
aacccccacc ggacctacaa cccgcagtcc cacatcatct caggcgggct ggccggggcc
780
ctcgccgcgg cc
792

<210> 5464
<211> 111
<212> PRT
<213> Homo sapiens

<400> 5464
Phe Ser Gly Val Cys Phe Ala Gly Ile Ala Gly Ser Met Ala Thr Leu
1 5 10 15
Leu His Asp Ala Val Met Asn Pro Ala Glu Val Val Lys Gln Arg Leu
20 25 30
Gln Met Tyr Asn Ser Gln His Arg Ser Ala Ile Ser Cys Ile Arg Thr
35 40 45
Val Trp Arg Thr Glu Gly Leu Gly Ala Phe Tyr Arg Ser Tyr Thr Thr
50 55 60
Gln Leu Thr Met Asn Ile Pro Phe Gln Ser Ile His Phe Ile Thr Tyr
65 70 75 80
Glu Phe Leu Gln Glu Gln Val Asn Pro His Arg Thr Tyr Asn Pro Gln
85 90 95
Ser His Ile Ile Ser Gly Gly Leu Ala Gly Ala Leu Ala Ala Ala
100 105 110

<210> 5465
<211> 497
<212> DNA
<213> Homo sapiens

<400> 5465
tttgacggtc ttcaggttta tttcttaaat caattaggaa ataaaaccac agtgcccagg
60
aaagttcaca tgagacgcca cggtgtctct tgccatggcc ccaccactcc aggggccagg
120
gggtgctgct ggagggagga cagacggaca ggcggcctgg gtggccggcc ccagaaaggc
180
tggcgtggat gttcgagatg agccaccagc gaagccagta gggatgtctg ggccgtcctg
240
gtgggattgt ctgggacatc gccaccaaca cggtgtcaga gccatcagtg gggacatcgg
300
aggggccacc accaggtggg gtatattcaa caggctagaa cccctgaggc ttgagaggcc
360
aacccccggc aggagacctc ccctgacccc tctgctgcct ctcctgtggg accctccagt
420
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480

gcagccacgc agtgcac
497

<210> 5466
<211> 134
<212> PRT
<213> Homo sapiens

<400> 5466
Met Ala Pro Pro Leu Gln Gly Pro Gly Gly Ala Ala Gly Gly Arg Thr
1 5 10 15
Asp Gly Gln Ala Ala Trp Val Ala Gly Pro Arg Lys Ala Gly Val Asp
20 25 30
Val Arg Asp Glu Pro Pro Ala Lys Pro Val Gly Met Ser Gly Pro Ser
35 40 45
Trp Trp Asp Cys Leu Gly His Arg His Gln His Gly Val Arg Ala Ile
50 55 60
Ser Gly Asp Ile Gly Gly Ala Thr Thr Arg Trp Gly Ile Phe Asn Arg
65 70 75 80
Leu Glu Pro Leu Arg Leu Glu Arg Pro Thr Pro Gly Arg Arg Pro Pro
85 90 95
Leu Thr Pro Leu Leu Pro Leu Leu Trp Asp Pro Pro Val Asp Thr Pro
100 105 110
Asp Glu Asp Thr Gln Glu Ala Ser Ser Gln Asp Arg Arg Gln Leu Pro
115 120 125
Gly Gln Pro Arg Ser Ala
130

<210> 5467
<211> 1329
<212> DNA
<213> Homo sapiens

<400> 5467
gtcgaatatc catgcagccg cgccgccgcc ctggagtgag ggaagcccag tggaaggggg
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tcccgggagc cggctgcgat ggacgccgtc ttggaaccct tcccggccga caggctgttc
120
cccggatcca gcttcctgga cttgggggat ctgaacgagt cggacttcct caacaatgcg
180
cactttcctg agcacctgga ccactttacg gagaacatgg aggacttctc caatgacctg
240
ttcagcagct tctttgatga ccctgtgctg gatgagaaga gccctctatt ggacatggaa
300
ctggactccc ctacgccagg catccaggcg gagcacagct actccctgag cggcgactca
360
gcgccccaga gccccccttgt gcccatcaag atggaggaca ccacccaaga tgcagagcat
420
ggagcatggg cgctgggaca caaactgtgc tccatcatgg tgaagcagga gcagagcccg
480
gagctgcccg tggaccctct ggctgccccc tcggccatgg ctgccgcggc cgccatggcc
540
accaccccgc tgctgggcct cagccccttg tccaggctgc ccatccccca ccaggccccg
600

ggagagatga ctcagctgcc agtgatcaaa gcagagcctc tggaggtgaa ccagttcctc
660
aaagtgacac cggaggacct ggtgcagatg cctccgacgc cccccagcag ccatggcagt
720
gacagcgacg gctcccagag tccccgctct ctgccccccc ccagccctgt caggcccatg
780
gcgcgctcct ccacggccat ctccagctcc ccactcctca cggctcctca taaattacag
840
gggacatcag gccctctggt cctgacagag gaggagaaga ggaccctgat tgctgagggc
900
tatcccatcc ccaccaaact ccccctcacc aaatcagagg agaaggcctt gaagaaaatt
960
cggaggaaga tcaagaataa gatttctgct caggaaagta ggagaaagaa gaaagaatac
1020
atggacagcc tggagaaaaa agtggagtct tgttcaactg agaacttgga gcttcggaag
1080
aaggtagaga ccctggagaa tgccaacagc ttctccagcg ggatccagcc actcctctgt
1140
tccctgattg gcctggagaa tcccacctga ccccccaccc cacccctctg tctctggctg
1200
gggttccttt ctggcccaaa gtaggtccaa gcccttgtag ttatttcgcc acctgctgta
1260
cattgtggga actgcaaccc ctacgtgccc gtttgggtgg agagagatta aacatttgcc
1320
caccaaaaa
1329

<210> 5468
<211> 363
<212> PRT
<213> Homo sapiens

<400> 5468
Met Asp Ala Val Leu Glu Pro Phe Pro Ala Asp Arg Leu Phe Pro Gly
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Ser Ser Phe Leu Asp Leu Gly Asp Leu Asn Glu Ser Asp Phe Leu Asn
            20   25   30
Asn Ala His Phe Pro Glu His Leu Asp His Phe Thr Glu Asn Met Glu
        35   40   45
Asp Phe Ser Asn Asp Leu Phe Ser Ser Phe Phe Asp Asp Pro Val Leu
    50   55   60
Asp Glu Lys Ser Pro Leu Leu Asp Met Glu Leu Asp Ser Pro Thr Pro
65   70   75   80
Gly Ile Gln Ala Glu His Ser Tyr Ser Leu Ser Gly Asp Ser Ala Pro
                85   90   95
Gln Ser Pro Leu Val Pro Ile Lys Met Glu Asp Thr Thr Gln Asp Ala
            100   105   110
Glu His Gly Ala Trp Ala Leu Gly His Lys Leu Cys Ser Ile Met Val
        115   120   125
Lys Gln Glu Gln Ser Pro Glu Leu Pro Val Asp Pro Leu Ala Ala Pro
    130   135   140
Ser Ala Met Ala Ala Ala Ala Ala Met Ala Thr Thr Pro Leu Leu Gly
145   150   155   160
Leu Ser Pro Leu Ser Arg Leu Pro Ile Pro His Gln Ala Pro Gly Glu

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                165                 170                 175
Met Thr Gln Leu Pro Val Ile Lys Ala Glu Pro Leu Glu Val Asn Gln
            180                 185                 190
Phe Leu Lys Val Thr Pro Glu Asp Leu Val Gln Met Pro Pro Thr Pro
        195                 200                 205
Pro Ser Ser His Gly Ser Asp Ser Asp Gly Ser Gln Ser Pro Arg Ser
    210                 215                 220
Leu Pro Pro Ser Ser Pro Val Arg Pro Met Ala Arg Ser Ser Thr Ala
225                 230                 235                 240
Ile Ser Ser Ser Pro Leu Leu Thr Ala Pro His Lys Leu Gln Gly Thr
                245                 250                 255
Ser Gly Pro Leu Val Leu Thr Glu Glu Glu Lys Arg Thr Leu Ile Ala
            260                 265                 270
Glu Gly Tyr Pro Ile Pro Thr Lys Leu Pro Leu Thr Lys Ser Glu Glu
        275                 280                 285
Lys Ala Leu Lys Lys Ile Arg Arg Lys Ile Lys Asn Lys Ile Ser Ala
    290                 295                 300
Gln Glu Ser Arg Arg Lys Lys Lys Glu Tyr Met Asp Ser Leu Glu Lys
305                 310                 315                 320
Lys Val Glu Ser Cys Ser Thr Glu Asn Leu Glu Leu Arg Lys Lys Val
                325                 330                 335
Glu Thr Leu Glu Asn Ala Asn Ser Phe Ser Ser Gly Ile Gln Pro Leu
            340                 345                 350
Leu Cys Ser Leu Ile Gly Leu Glu Asn Pro Thr
        355                 360
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<210> 5469
<211> 1292
<212> DNA
<213> Homo sapiens

<400> 5469
nncgcggccg cgtcgacgga aggggaggac gtgggatggt ggcggagctg gctgcagcag
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agctaccaag cagtcaaaga gaagtcctct gaagccttgg agtttatgaa gcgggacctg
120
acggagttta cccaggtggt gcagcatgac acggcctgta ccatcgcagc cacggccagc
180
gtggtcaagg agaagctggc tacggaaggc tcctcaggag caacagagaa gatgaagaaa
240
gggttatctg acttcctagg ggtgatctca gacacctttg ccccttcgcc agacaaaacc
300
atcgactgcg atgtcatcac cctgatgggc acaccgtctg gcacagctga gccctatgat
360
ggcaccaagg ctcgcctcta tagcctgcag tcggacccag caacctactg taatgaacca
420
gatgggcccc cggaattgtt tgacgcctgg ctttcccagt tctgcttgga ggagaagaag
480
ggggagatct cagagctcct tgtaggcagc ccctccatcc gggccctcta caccaagatg
540
gttccagcag ctgtttccca ttcagaattc tggcatcggt atttctataa agtccatcag
600
ttagagcagg agcaggcccg gagggacgcc ctgaagcagc gggcggaaca gagcatctct
660

gaagagcccg gctgggagga ggaggaagag gagctcatgg gcatttcacc catatctcca
720
aaagaggcaa aggttcctgt ggccaaaatt tctacattcc ctgaaggaga acctggcccc
780
cagagcccct gtgaagagaa tctggtgact tcagttgagc ccccagcaga ggtgactcca
840
tcagagagca gtgagagcat ctccctcgtg acacagatcg ccaacccggc cactgcacct
900
gaggcacgag tgctacccaa ggacctgtcc caaaagctgc tagaggcatc cttggaggaa
960
cagggcctgg ctgtggatgt gggtgagact ggaccctcac cccctattca ctccaagccc
1020
ctaacgcctg ctggccacac cggcggccca gagcccaggc ctccagccag agtagagact
1080
ctgagggagg aggcgcccac agacttacgg gtgtttgagc tgaactcgga tagtgggaag
1140
tctacaccct ccaacaatgg aaagaaaggc tcaagcacgg acatcagtga ggactgggag
1200
aaagactttg acttggacat gactgaagag gaggtgcaga tggcactttc caaagtggat
1260
gcctccgggg agctgaagat gtagaggggg aa
1292

<210> 5470
<211> 427
<212> PRT
<213> Homo sapiens

<400> 5470
Xaa Ala Ala Ala Ser Thr Glu Gly Glu Asp Val Gly Trp Trp Arg Ser
1 5 10 15
Trp Leu Gln Gln Ser Tyr Gln Ala Val Lys Glu Lys Ser Ser Glu Ala
20 25 30
Leu Glu Phe Met Lys Arg Asp Leu Thr Glu Phe Thr Gln Val Val Gln
35 40 45
His Asp Thr Ala Cys Thr Ile Ala Ala Thr Ala Ser Val Val Lys Glu
50 55 60
Lys Leu Ala Thr Glu Gly Ser Ser Gly Ala Thr Glu Lys Met Lys Lys
65 70 75 80
Gly Leu Ser Asp Phe Leu Gly Val Ile Ser Asp Thr Phe Ala Pro Ser
85 90 95
Pro Asp Lys Thr Ile Asp Cys Asp Val Ile Thr Leu Met Gly Thr Pro
100 105 110
Ser Gly Thr Ala Glu Pro Tyr Asp Gly Thr Lys Ala Arg Leu Tyr Ser
115 120 125
Leu Gln Ser Asp Pro Ala Thr Tyr Cys Asn Glu Pro Asp Gly Pro Pro
130 135 140
Glu Leu Phe Asp Ala Trp Leu Ser Gln Phe Cys Leu Glu Glu Lys Lys
145 150 155 160
Gly Glu Ile Ser Glu Leu Leu Val Gly Ser Pro Ser Ile Arg Ala Leu
165 170 175
Tyr Thr Lys Met Val Pro Ala Ala Val Ser His Ser Glu Phe Trp His
180 185 190
Arg Tyr Phe Tyr Lys Val His Gln Leu Glu Gln Glu Gln Ala Arg Arg

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       195                 200                 205
Asp Ala Leu Lys Gln Arg Ala Glu Gln Ser Ile Ser Glu Glu Pro Gly
    210                 215                 220
Trp Glu Glu Glu Glu Glu Glu Leu Met Gly Ile Ser Pro Ile Ser Pro
225                 230                 235                 240
Lys Glu Ala Lys Val Pro Val Ala Lys Ile Ser Thr Phe Pro Glu Gly
                245                 250                 255
Glu Pro Gly Pro Gln Ser Pro Cys Glu Glu Asn Leu Val Thr Ser Val
            260                 265                 270
Glu Pro Pro Ala Glu Val Thr Pro Ser Glu Ser Ser Glu Ser Ile Ser
        275                 280                 285
Leu Val Thr Gln Ile Ala Asn Pro Ala Thr Ala Pro Glu Ala Arg Val
    290                 295                 300
Leu Pro Lys Asp Leu Ser Gln Lys Leu Leu Glu Ala Ser Leu Glu Glu
305                 310                 315                 320
Gln Gly Leu Ala Val Asp Val Gly Glu Thr Gly Pro Ser Pro Pro Ile
                325                 330                 335
His Ser Lys Pro Leu Thr Pro Ala Gly His Thr Gly Gly Pro Glu Pro
            340                 345                 350
Arg Pro Pro Ala Arg Val Glu Thr Leu Arg Glu Glu Ala Pro Thr Asp
        355                 360                 365
Leu Arg Val Phe Glu Leu Asn Ser Asp Ser Gly Lys Ser Thr Pro Ser
    370                 375                 380
Asn Asn Gly Lys Lys Gly Ser Ser Thr Asp Ile Ser Glu Asp Trp Glu
385                 390                 395                 400
Lys Asp Phe Asp Leu Asp Met Thr Glu Glu Glu Val Gln Met Ala Leu
                405                 410                 415
Ser Lys Val Asp Ala Ser Gly Glu Leu Lys Met
            420                 425
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<210> 5471
<211> 534
<212> DNA
<213> Homo sapiens

<400> 5471
cggccgcccc gcgggggcgc agaaatagga ccgtcctggc agaggctgca gccgacccag
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ctggccccac tacgcggggc ccagagccag ggtgggggat gcagagaccg ggcgtgcggg
120
ttgccaggtg tggcgcacat gtgtgcccgt gggcagagta cagagacaca agcttgtgtg
180
gacacgaatg tgtagctatg tgcgagtgca cacggagtgg tgagtgcagg gaccccaggc
240
cggcctgcgt cggtgcgcag ggcatatagg ggcgtgcacg cagtcttgga ggtgtgtgca
300
cagagccccc ggcacccgcg tgtgtgcaaa gacacaggaa cccgtctgcg tggcgctgtg
360
tgtgcaaccc aaggaggtgg gcgcttggac tccaaagtgt gcgcttatcc ggatgtggat
420
gtgggggcag ccggggacag ggctgggtgt gcgtgactcg ggtgtgccgg gacccacaga
480
gcatatgtgt ccatgcctgg tgctgtgact catgtccctg gggtgggcac gcgt
534

<210> 5472
<211> 161
<212> PRT
<213> Homo sapiens

<400> 5472
Met Leu Cys Gly Ser Arg His Thr Arg Val Thr His Thr Gln Pro Cys
1 5 10 15
Pro Arg Leu Pro Pro His Pro His Pro Asp Lys Arg Thr Leu Trp Ser
20 25 30
Pro Ser Ala His Leu Leu Gly Leu His Thr Gln Arg His Ala Asp Gly
35 40 45
Phe Leu Cys Leu Cys Thr His Ala Gly Ala Gly Gly Ser Val His Thr
50 55 60
Pro Pro Arg Leu Arg Ala Arg Pro Tyr Met Pro Cys Ala Pro Thr Gln
65 70 75 80
Ala Gly Leu Gly Ser Leu His Ser Pro Leu Arg Val His Ser His Ile
85 90 95
Ala Thr His Ser Cys Pro His Lys Leu Val Ser Leu Tyr Ser Ala His
100 105 110
Gly His Thr Cys Ala Pro His Leu Ala Thr Arg Thr Pro Gly Leu Cys
115 120 125
Ile Pro His Pro Gly Ser Gly Pro Arg Val Val Gly Pro Ala Gly Ser
130 135 140
Ala Ala Ala Ser Ala Arg Thr Val Leu Phe Leu Arg Pro Arg Gly Ala
145 150 155 160
Ala

<210> 5473
<211> 691
<212> DNA
<213> Homo sapiens

<400> 5473
gcgaccagca gcgctggtgg ccatgctctt ggacactacg gcctggcggg cagccctcgc
60
cgctgccgcg ccccgcgccc ccaggaggcc gcaccctgcg ccagggcccg gagacagcaa
120
catcttctgg ggcctgcagg agacctgaca gatgccaaaa caaaggaaca gttgggatcc
180
aggcagcatg aggtagaatg gcaaacctac cagggtattc tgaagaagac aagagtcatg
240
gaaaaaacca agtggctgga tatcaaagga aatcatgaaa aagatggagg agctcttatt
300
actggccaag gaaagcagtc ggagcaacca tacaatttgg tttggacact ttacaacatc
360
cactattctt tctccatcac caggaatccg gtcaataatg agttcggcta tagcttattt
420
gtgtggacat ctccatacac ttggtggact gatgcctgtt ttgcacactc gtcacttcca
480
gggcactttg gaacttgagg tgggagactg gaaggataat aggaggtacc ggatttttgc
540

ttttgatcac gacctcttta gctttgcaga tttgatcttt gggaagtggc ctgtggttct
600
tatcaccaat cctaaatcac tcctttatag ttgtggtgaa catgaaccac tagaaagact
660
tcttcactca acccacatta gattggtaac a
691

<210> 5474
<211> 139
<212> PRT
<213> Homo sapiens

<400> 5474
Met Lys Lys Met Glu Glu Leu Leu Leu Leu Ala Lys Glu Ser Ser Arg
1 5 10 15
Ser Asn His Thr Ile Trp Phe Gly His Phe Thr Thr Ser Thr Ile Leu
20 25 30
Ser Pro Ser Pro Gly Ile Arg Ser Ile Met Ser Ser Ala Ile Ala Tyr
35 40 45
Leu Cys Gly His Leu His Thr Leu Gly Gly Leu Met Pro Val Leu His
50 55 60
Thr Arg His Phe Gln Gly Thr Leu Glu Leu Glu Val Gly Asp Trp Lys
65 70 75 80
Asp Asn Arg Arg Tyr Arg Ile Phe Ala Phe Asp His Asp Leu Phe Ser
85 90 95
Phe Ala Asp Leu Ile Phe Gly Lys Trp Pro Val Val Leu Ile Thr Asn
100 105 110
Pro Lys Ser Leu Leu Tyr Ser Cys Gly Glu His Glu Pro Leu Glu Arg
115 120 125
Leu Leu His Ser Thr His Ile Arg Leu Val Thr
130 135

<210> 5475
<211> 628
<212> DNA
<213> Homo sapiens

<400> 5475
ggcacacacg aaacagcctt cctgggaccc aaggacctgt tcccctacga caaatgtaaa
60
gacaagtacg ggaagcccaa caagaggaaa ggcttcaatg aagggctgtg ggagatccag
120
aacaaccccc acgccagcta cagcgccccc ccgccagtga gctcctccga cagcgaggcc
180
cccgaggcca accccgccga cggcagtgac gctgacgagg acgatgagga ccgggggggtc
240
atggccgtca cagcggtaac cgccacagct gccagcgaca ggatggagag cgactcagac
300
tcagacaaga gtagcgacaa cagtggcctg aagaggaaga cgcctgcgct aaagatgtcg
360
gtctcgaaac gagcccgaaa ggcctccagc gacctggatc aggccagcgt gtccccatcc
420
gaagaggaga actcggaaag ctcatctgag tcggagaaga ccagcgacca ggacttcaca
480

cctgagaaga aagcagcggt ccgggcgcca cggaggggcc ctctgggggg acggaaaaaa
540
aagaaggcgc cgtcagcctc cgactccgac tccaaggccg attcggacgg ggccaagcct
600
gagccggtgg ccatggcgcg gtcggcgt
628

<210> 5476
<211> 209
<212> PRT
<213> Homo sapiens

<400> 5476
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro Tyr
1 5 10 15
Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys Gly Phe
20 25 30
Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala Ser Tyr Ser
35 40 45
Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala Pro Glu Ala Asn
50 55 60
Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp Glu Asp Arg Gly Val
65 70 75 80
Met Ala Val Thr Ala Val Thr Ala Thr Ala Ala Ser Asp Arg Met Glu
85 90 95
Ser Asp Ser Asp Ser Asp Lys Ser Ser Asp Asn Ser Gly Leu Lys Arg
100 105 110
Lys Thr Pro Ala Leu Lys Met Ser Val Ser Lys Arg Ala Arg Lys Ala
115 120 125
Ser Ser Asp Leu Asp Gln Ala Ser Val Ser Pro Ser Glu Glu Glu Asn
130 135 140
Ser Glu Ser Ser Ser Glu Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr
145 150 155 160
Pro Glu Lys Lys Ala Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly
165 170 175
Gly Arg Lys Lys Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys
180 185 190
Ala Asp Ser Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser
195 200 205
Ala

<210> 5477
<211> 727
<212> DNA
<213> Homo sapiens

<400> 5477
ttttttgtta gtgtttcctt tattataaag cactgaaata agttaaataa acaggtggga
60
ggctgggcag tcccccagcc ggtttgtcca cagcccctgg gggcagtgga ggtgaataca
120
gggcccttct cactgagctc gtgaagtgcc tcagtcaagg caaggtcccc tggtccatat
180

gggccccccc gcccatgggg ttgggctggt ccttatagtg cctacgttag tctgtgtgga
240
gcccctggcc agcgggggag aaaaaggtgg cttctggtcc gtctgtataa aacatggccc
300
ctcacctgtc ggcccccccac acagctggca ggctgggctg gcctctcacc cctggcctcc
360
cctggacccc tggctggctc ctcaacttca ctctccgcac ttagtgcccg gccgccccca
420
gactcatcgt cgctcagccc atagggaagc ccaggcctgg cccccagaga gtctccttcc
480
gagtctctct cgaagcccat gagctggtca ctgttgccgt cgccttcctc ctcttcctct
540
tcctcctcaa actccagatc ctggcctagt agcaaatcac tctccaatac cagggccccg
600
ggtccttcgt cgagggagtc ttcagtatcc actttgaccc cctcgcattt cacgggctgc
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720
gcggccg
727

<210> 5478
<211> 99
<212> PRT
<213> Homo sapiens

<400> 5478
Ser Ala Ser Val Lys Ala Arg Ser Pro Gly Pro Tyr Gly Pro Pro Arg
1 5 10 15
Pro Trp Gly Trp Ala Gly Pro Tyr Ser Ala Tyr Val Ser Leu Cys Gly
20 25 30
Ala Pro Gly Gln Arg Gly Arg Lys Arg Trp Leu Leu Val Arg Leu Tyr
35 40 45
Lys Thr Trp Pro Leu Thr Cys Arg Pro Pro Thr Gln Leu Ala Gly Trp
50 55 60
Ala Gly Leu Ser Pro Leu Ala Ser Pro Gly Pro Leu Ala Gly Ser Ser
65 70 75 80
Thr Ser Leu Ser Ala Leu Ser Ala Arg Pro Pro Pro Asp Ser Ser Ser
85 90 95
Leu Ser Pro

<210> 5479
<211> 1386
<212> DNA
<213> Homo sapiens

<400> 5479
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cgggagcagc gggagcgcga ggagcaggag cggaggctgc aggcagaaag ggacaagcga
120
atgcgagagg agcagctggc acgggaggcc gaggcccggg cggagcggga ggcggaggcc
180

cggaggcggg aggagcagga ggcacgagag aaggcgcagg ccgagcagga ggagcaggag
240
cggctgcaga agcagaaaga ggaggccgaa gctcggtcgc gggaagaggc ggagcggcag
300
cgtctggagc gggaaaagca cttccagcag caggagcaag agcggcaaga gcgcagaaag
360
cgtctggagg agatcatgaa gaggactcgg aagtcagaag tttctgaaac caagcagaag
420
caggacagca aggaggccaa cgccaacggt tccagcccag agcctgtgaa agctgtggag
480
gctcggtccc cagggctgca gaaggaggct gtgcagaaag aggagcccat cccacaggag
540
cctcagtgga gtctcccaag caaggagttg ccagcgtccc tggtgaatgg cctgcagcct
600
ctcccagcac accaggagaa tggcttctcc accaacggac cctctgggga caagagtctg
660
agccgaacac cagagacact cctgcccttt gcagaggcag aagccttcct caagaaagct
720
gtggtgcagt ccccgcaggt cacagaagtc ctttaagagg gtttgccttg gatccgggca
780
cagttgtgag ggctcctctg catcacctac caggatgtct ggaggagaaa aagacagaac
840
aaagatggaa gtggcctggg cccctggggg tgggtcctct ctgttgtttt taatctgcac
900
cttatagact gatgtctctt tggccggagc cagatctgcc cctcagtgca ttcgtgtgct
960
cgcacgcgca gacatccctt ctcccccata cacacatata cactcacagc ctctctggcc
1020
tcttcccttg gggaggggcc acctgtagta tttgccttga tttggtgggg tacagtggat
1080
gtgaatactg taaatagctt gtgctcagac tcctctgcgt ggagagggtg ggtgcaggag
1140
gcagaccctc cccccaaagc cccctgggga gatcttcctc tctctattta actgtaactg
1200
agggggatcc caggtctggg gatgggggac accttgggcc acaggatact ggttgcttca
1260
ggggtaccca tgcccccctgc cctcgcctgg aatcagtgtt actgcatctg attaaatgtc
1320
tccagaaata aagaataatt ctgccaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
1380
aaaaaa
1386

<210> 5480
<211> 251
<212> PRT
<213> Homo sapiens

<400> 5480
Ala Gly Thr Thr Asp Arg Glu Glu Ala Thr Arg Leu Leu Ala Glu Lys
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Arg Arg Gln Ala Arg Glu Gln Arg Glu Arg Glu Glu Gln Glu Arg Arg
20 25 30
Leu Gln Ala Glu Arg Asp Lys Arg Met Arg Glu Glu Gln Leu Ala Arg

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        35                  40                  45
Glu Ala Glu Ala Arg Ala Glu Arg Glu Ala Glu Ala Arg Arg Arg Glu
    50                  55                  60
Glu Gln Glu Ala Arg Glu Lys Ala Gln Ala Glu Gln Glu Glu Gln Glu
65                  70                  75                  80
Arg Leu Gln Lys Gln Lys Glu Glu Ala Glu Ala Arg Ser Arg Glu Glu
                85                  90                  95
Ala Glu Arg Gln Arg Leu Glu Arg Glu Lys His Phe Gln Gln Gln Glu
            100                 105                 110
Gln Glu Arg Gln Glu Arg Arg Lys Arg Leu Glu Glu Ile Met Lys Arg
        115                 120                 125
Thr Arg Lys Ser Glu Val Ser Glu Thr Lys Gln Lys Gln Asp Ser Lys
    130                 135                 140
Glu Ala Asn Ala Asn Gly Ser Ser Pro Glu Pro Val Lys Ala Val Glu
145                 150                 155                 160
Ala Arg Ser Pro Gly Leu Gln Lys Glu Ala Val Gln Lys Glu Glu Pro
                165                 170                 175
Ile Pro Gln Glu Pro Gln Trp Ser Leu Pro Ser Lys Glu Leu Pro Ala
            180                 185                 190
Ser Leu Val Asn Gly Leu Gln Pro Leu Pro Ala His Gln Glu Asn Gly
        195                 200                 205
Phe Ser Thr Asn Gly Pro Ser Gly Asp Lys Ser Leu Ser Arg Thr Pro
    210                 215                 220
Glu Thr Leu Leu Pro Phe Ala Glu Ala Glu Ala Phe Leu Lys Lys Ala
225                 230                 235                 240
Val Val Gln Ser Pro Gln Val Thr Glu Val Leu
                245                 250
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<210> 5481
<211> 1513
<212> DNA
<213> Homo sapiens

<400> 5481
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aaggcggagg gaaggccgtg gggatggcca atcaaagggg gcgactcagg tcggtgggga
120
ccggcagcca atcaggagag cgctcgctcc tgactcgacc ggcccacgct tcccgccagt
180
cccctaaccc tgaggctgcc gcgcggcggt cactgcgccg gggtagtggg ccccagtgtt
240
gcgctctctg gccgttcctt acactttgct tcaggctcca gtgcaggggc gtagtgggat
300
atggccaact cgggctgcaa ggacgtcacg ggtccagatg aggagagttt tctgtacttt
360
gcctacggca gcaacctgct gacagagagg atccacctcc gaaacccctc ggcggcgttc
420
ttctgtgtgg cccgcctgca ggattttaag cttgactttg gcaattccca aggcaaaaca
480
agtcaaactt ggcatggagg gatagccacc atttttcaga gtcctggcga tgaattgtgg
540
ggagtagtat ggaaaatgaa caaaagcaat ttaaattctc tggatgagca agaaggggtt
600

aaaagtggaa tgtatgttgt aatagaagtt aaagttgcaa ctcaagaagg aaaagaaata
660
acctgtcgaa gttatctgat gacaaattac gaaagtgctc ccccatcccc acagtataaa
720
aagattattt gcatgggtgc aaaagaaaat ggtttgccgc tggagtatca agagaagtta
780
aaagcaatag aaccaaatga ctatacagga aaggtctcag aagaaattga agacatcatc
840
aaaaaggggg aaacacaaac tctttagaac ataacagaat atatctaagg gtattctatg
900
tgctaatata aaatattttt aacacttgag aacagggatc tgggggatct ccacgtttga
960
tccattttca gcagtgctct gaaggagtat cttacttggg tgattccttg tttttagact
1020
ataaaaagaa actgggatag gagttagaca atttaaaagg ggtgtatgag ggcctgaaat
1080
atgtgacaaa tgaatgtgag tacccccttct gtgaacactg aaagctattc tcttgaattg
1140
atcttaagtg tctccttgct ctggtaaaag atagatttgt agctcacttg atgatggtgc
1200
tggtgaattg ctctgctctg tctgagattt ttaaaaatca gcttaatgag agtaatctgc
1260
agacaattga taataacatt ttgaaaattg gaaagatggt atactgtttt tagaggaata
1320
aacgtatttg tggtttaaaa aaaaaagagc aacttccttt gcactgtata ccctttttgta
1380
ttattaggat tttatactat gtttatatgt tgcctattta ataaatcgct taaagttata
1440
tatcttgaat atctttccat aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
1500
aaaaaaaaaa aaa
1513

<210> 5482
<211> 188
<212> PRT
<213> Homo sapiens

<400> 5482
Met Ala Asn Ser Gly Cys Lys Asp Val Thr Gly Pro Asp Glu Glu Ser
1 5 10 15
Phe Leu Tyr Phe Ala Tyr Gly Ser Asn Leu Leu Thr Glu Arg Ile His
20 25 30
Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val Ala Arg Leu Gln Asp
35 40 45
Phe Lys Leu Asp Phe Gly Asn Ser Gln Gly Lys Thr Ser Gln Thr Trp
50 55 60
His Gly Gly Ile Ala Thr Ile Phe Gln Ser Pro Gly Asp Glu Leu Trp
65 70 75 80
Gly Val Val Trp Lys Met Asn Lys Ser Asn Leu Asn Ser Leu Asp Glu
85 90 95
Gln Glu Gly Val Lys Ser Gly Met Tyr Val Val Ile Glu Val Lys Val
100 105 110
Ala Thr Gln Glu Gly Lys Glu Ile Thr Cys Arg Ser Tyr Leu Met Thr

```
        115                 120                 125
Asn Tyr Glu Ser Ala Pro Pro Ser Pro Gln Tyr Lys Lys Ile Ile Cys
    130                 135                 140
Met Gly Ala Lys Glu Asn Gly Leu Pro Leu Glu Tyr Gln Glu Lys Leu
145                 150                 155                 160
Lys Ala Ile Glu Pro Asn Asp Tyr Thr Gly Lys Val Ser Glu Glu Ile
                165                 170                 175
Glu Asp Ile Ile Lys Lys Gly Glu Thr Gln Thr Leu
            180                 185
```

<210> 5483
<211> 1552
<212> DNA
<213> Homo sapiens

<400> 5483
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gtcaaagagg actacacgcg ggtggtgtgc cctgtgatcg atatcattaa cctggacacc
120
ttcacctaca tcgagtctgc ctcggagctc agaggggggt ttgactggag cctccacttc
180
cagtgggagc agctctcccc agagcagaag gctcggcgcc tggaccccac ggagcccatc
240
aggactccta tcatagctgg agggctcttc gtgatcgaca aagcttggtt tgattacctg
300
gggaaatatg atatggacat ggacatctgg ggtggggaga actttgaaat ctccttccga
360
gtgtggatgt gcgggggcag cctagagatc gtcccctgca gccgagtggg gcacgtcttc
420
cggaagaagc acccctacgt tttccctgat ggaaatgcca acacgtatat aaagaacacc
480
aagcggacag ctgaagtgtg gatggatgaa tacaagcaat actattacgc tgcccggcca
540
ttcgccctgg agaggccctt cgggaatgtt gagagcagat tggacctgag gaagaatctg
600
cgctgccaga gcttcaagtg gtacctggag aatatctacc ctgaactcag catccccaag
660
gagttctcca tccagaaggg caatatccga cagagacaga agtgcctgga atctcaaagg
720
cagaacaacc aagaaacccc aaacctaaag ttgagcccct gtgccaaggt caaaggcgaa
780
gatgcaaagt cccaggtatg ggccttcaca tacacccaga agatcctcca ggaggagctg
840
tgcctgtcag tcatcacctt gttccctggc gccccagtgg ttcttgtcct ttgcaagaat
900
ggagatgacc gacagcaatg gaccaaaact ggttcccaca tcgagcacat agcatcccac
960
ctctgcctcg atacagatat gttcggtgat ggcaccgaga acggcaagga aatcgtcgtc
1020
aacccatgtg agtcctcact catgagccag cactgggaca tggtgagctc ttgaggaccc
1080
ctgccagaag cagcaagggc catggggtgg tgcttccctg gaccagaaca gactggaaac
1140

tgggcagcaa gcagcctgca accacctcag acatcctgga ctgggaggtg gaggcagagc
1200
cccccaggac aggagcaact gtctcaggga ggacagagga aaacatcaca agccaatggg
1260
gctcaaagac aaatcccaca tgttctcaag gccgttaagt tccagtcctg gccagtcatt
1320
ccctgattgg tatctggaga cagaaaccta atgggaagtg tttattgttc cttttcctac
1380
aaaggaagca gtctctggag gccagaaaga aaagccttct ttttcactag gccaggacta
1440
cattgagaga tgaagaatgg aggttgtttc caaaagaaat aaagagaaac ttagaagttg
1500
tctctggaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa
1552

<210> 5484
<211> 357
<212> PRT
<213> Homo sapiens

<400> 5484
Thr Phe Leu Asp Ser His Cys Glu Val Asn Arg Asp Trp Leu Gln Pro
1 5 10 15
Leu Xaa Asp Arg Val Lys Glu Asp Tyr Thr Arg Val Val Cys Pro Val
20 25 30
Ile Asp Ile Ile Asn Leu Asp Thr Phe Thr Tyr Ile Glu Ser Ala Ser
35 40 45
Glu Leu Arg Gly Gly Phe Asp Trp Ser Leu His Phe Gln Trp Glu Gln
50 55 60
Leu Ser Pro Glu Gln Lys Ala Arg Arg Leu Asp Pro Thr Glu Pro Ile
65 70 75 80
Arg Thr Pro Ile Ile Ala Gly Gly Leu Phe Val Ile Asp Lys Ala Trp
85 90 95
Phe Asp Tyr Leu Gly Lys Tyr Asp Met Asp Met Asp Ile Trp Gly Gly
100 105 110
Glu Asn Phe Glu Ile Ser Phe Arg Val Trp Met Cys Gly Gly Ser Leu
115 120 125
Glu Ile Val Pro Cys Ser Arg Val Gly His Val Phe Arg Lys Lys His
130 135 140
Pro Tyr Val Phe Pro Asp Gly Asn Ala Asn Thr Tyr Ile Lys Asn Thr
145 150 155 160
Lys Arg Thr Ala Glu Val Trp Met Asp Glu Tyr Lys Gln Tyr Tyr Tyr
165 170 175
Ala Ala Arg Pro Phe Ala Leu Glu Arg Pro Phe Gly Asn Val Glu Ser
180 185 190
Arg Leu Asp Leu Arg Lys Asn Leu Arg Cys Gln Ser Phe Lys Trp Tyr
195 200 205
Leu Glu Asn Ile Tyr Pro Glu Leu Ser Ile Pro Lys Glu Phe Ser Ile
210 215 220
Gln Lys Gly Asn Ile Arg Gln Arg Gln Lys Cys Leu Glu Ser Gln Arg
225 230 235 240
Gln Asn Asn Gln Glu Thr Pro Asn Leu Lys Leu Ser Pro Cys Ala Lys
245 250 255
Val Lys Gly Glu Asp Ala Lys Ser Gln Val Trp Ala Phe Thr Tyr Thr

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            260                 265                 270
Gln Lys Ile Leu Gln Glu Glu Leu Cys Leu Ser Val Ile Thr Leu Phe
        275                 280                 285
Pro Gly Ala Pro Val Val Leu Val Leu Cys Lys Asn Gly Asp Asp Arg
    290                 295                 300
Gln Gln Trp Thr Lys Thr Gly Ser His Ile Glu His Ile Ala Ser His
305                 310                 315                 320
Leu Cys Leu Asp Thr Asp Met Phe Gly Asp Gly Thr Glu Asn Gly Lys
                325                 330                 335
Glu Ile Val Val Asn Pro Cys Glu Ser Ser Leu Met Ser Gln His Trp
            340                 345                 350
Asp Met Val Ser Ser
        355
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<210> 5485
<211> 1549
<212> DNA
<213> Homo sapiens

<400> 5485
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gtgtacccgg aggagcacag cagatggagg gacagctcca ggacgaggtt gtggaattcg
120
ccgttcgaaa gcagggacta aaagccccac ttcgtcttac gttccgaaag gaaggcgtct
180
gttgagcctt tctctcagtc gtgagggagg cgtcgacggc gtgcggaagt cctgagttga
240
ggcttgcggg atcctttccg gagaaagcgc aggctaaagc cgcaggtgaa gatgtccaac
300
tacgtgaacg acatgtggcc gggctcgccg caggagaagg attcgccctc gacctcgcgg
360
tcgggcgggt ccagccggct gtcgtcgcgg tctaggagcc gctcttttttc cagaagctct
420
cggtcccatt cccgcgtctc gagccggttt tcgtccagga gtcggaggag caagtccagg
480
tcccgttccc gaaggcgcca ccagcggaag tacaggcgct actcgcggtc atactcgcgg
540
agccggtcgc gatcccgcag ccgccgttac cgagagaggc gctacgggtt caccaggaga
600
tactaccggt ctccttcgcg gtaccggtcc cggtcccgta gcaggtcgcg ctctcgggga
660
aggtcgtact gcggaagggc gtacgcgatc gcgcggggac agcgctacta cggctttggt
720
cgcacagtgt acccggagga gcacagcaga tggagggaca gatccaggac gaggtcgcgg
780
agcagaaccc cctttcgctt aagtgaaaaa gatcgaatgg agctgttaga aatagcaaaa
840
accaatgcag cgaaagctct aggaacaacc aacattgact tgccagctag tctcagaact
900
gttccttcag ccaaagaaac aagccgtgga ataggtgtat caagtaatgg tgcaaagcct
960
gaactgtcgg aaaaggtaac agaagatgga actcgaaatc ccaatgaaaa acctacccag
1020

caaagaagca tagcttttag ctctaataat tctgtagcaa agccaataca aaaatcagct
1080
aaagctgcca cagaagaggc atcttcaaga tcaccaaaaa tagatcagaa aaaaagtcca
1140
tatggactgt ggatacctat ctaaaagaag aaaactgatg gctaagtttg catgaaaact
1200
gcactttatt gcaagttagt gtttctagca ttatcccatc cctttgagcc attcaggggt
1260
acttgtgcat ttaaaaacca acacaaaaag atgtaaatac ttaacactca aatattaaca
1320
ttttaggttt ctcttgcaga tatgagagat agcacagatg gaccaaaggt tatgcacagg
1380
tgggagtctt ttgtatatag ttgtaaatat tgtcttggtt atgtaaaaat gaaatttttt
1440
agacacagta attgaactgt attcctgttt tgtatattta ataaatttct tgttttcatt
1500
cttaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaga
1549

<210> 5486
<211> 290
<212> PRT
<213> Homo sapiens

<400> 5486
Met Ser Asn Tyr Val Asn Asp Met Trp Pro Gly Ser Pro Gln Glu Lys
1 5 10 15
Asp Ser Pro Ser Thr Ser Arg Ser Gly Gly Ser Ser Arg Leu Ser Ser
20 25 30
Arg Ser Arg Ser Arg Ser Phe Ser Arg Ser Ser Arg Ser His Ser Arg
35 40 45
Val Ser Ser Arg Phe Ser Ser Arg Ser Arg Arg Ser Lys Ser Arg Ser
50 55 60
Arg Ser Arg Arg Arg His Gln Arg Lys Tyr Arg Arg Tyr Ser Arg Ser
65 70 75 80
Tyr Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Arg Tyr Arg Glu Arg
85 90 95
Arg Tyr Gly Phe Thr Arg Arg Tyr Tyr Arg Ser Pro Ser Arg Tyr Arg
100 105 110
Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Gly Arg Ser Tyr Cys Gly
115 120 125
Arg Ala Tyr Ala Ile Ala Arg Gly Gln Arg Tyr Tyr Gly Phe Gly Arg
130 135 140
Thr Val Tyr Pro Glu Glu His Ser Arg Trp Arg Asp Arg Ser Arg Thr
145 150 155 160
Arg Ser Arg Ser Arg Thr Pro Phe Arg Leu Ser Glu Lys Asp Arg Met
165 170 175
Glu Leu Leu Glu Ile Ala Lys Thr Asn Ala Ala Lys Ala Leu Gly Thr
180 185 190
Thr Asn Ile Asp Leu Pro Ala Ser Leu Arg Thr Val Pro Ser Ala Lys
195 200 205
Glu Thr Ser Arg Gly Ile Gly Val Ser Ser Asn Gly Ala Lys Pro Glu
210 215 220
Leu Ser Glu Lys Val Thr Glu Asp Gly Thr Arg Asn Pro Asn Glu Lys

225 230 235 240
Pro Thr Gln Gln Arg Ser Ile Ala Phe Ser Ser Asn Asn Ser Val Ala
245 250 255
Lys Pro Ile Gln Lys Ser Ala Lys Ala Ala Thr Glu Glu Ala Ser Ser
260 265 270
Arg Ser Pro Lys Ile Asp Gln Lys Lys Ser Pro Tyr Gly Leu Trp Ile
275 280 285
Pro Ile
290

<210> 5487
<211> 1716
<212> DNA
<213> Homo sapiens

<400> 5487
acgccaccgg gtcggaggac tacgagaacc tgccgactag cgcctccgtg tccacccaca
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tgacagcagg agcgatggcc gggatcctgg agcactcggt catgtacccg gtggactcgg
120
tgaagagaca gggtcttgcc ttgtcgccta ggctggagtg cagtgttgag atcatagttt
180
actgcagcct cgaactcctg ggtacaagga atcctccctc ctcagcctcc tgagtagctg
240
ggattacaga cacgaatgca gagtttgagt ccagatccca aagcccagta cacaagtatc
300
tacggagccc tcaagaaaat catgcggacc gaaggcttct ggaggccctt gcgaggcgtc
360
aacgtcatga tcatgggtgc agggccagcc catgccatgt attttgcctg ctatgaaaac
420
atgaaaagga ctttaaatga cgttttccac caccaaggaa acagccacct agccaacggg
480
atagctggga gtatggccac cctgctccac gatgcggtaa tgaatccagc agaagtggtg
540
aagcagcgct tgcagatgta caactcgcag caccggtcag caatcagctg catccggacg
600
gtgtggagga ccgaggggtt gggggccttc taccggagct acaccacgca gctgaccatg
660
aacatcccct tccagtccat ccacttcatc acctatgagt tcctgcagga gcaggtcaac
720
ccccaccgga cctacaaccc gcagtcccac atcatctcag gcgggctggc cggggccctc
780
gccgcggccg ccacgacccc cctggacgtc tgtaagaccc ttctgaacac tcaggagaac
840
gtggccctct cgctggccaa catcagcggc cggctgtcgg gtatggccaa tgccttccgg
900
acggtgtacc agctcaacgg cctggccggc tacttcaaag gcatccaggc gcgtgtcatc
960
taccagatgc cctccaccgc catttcttgg tctgtctatg agttcttcaa gtactttctc
1020
accaagcgcc agctggaaaa tcgagctcca tactaaagga agggatcata gaatcttttc
1080
ttaaagtcat tctctgcctg catccagccc cttgccctct cctcacacgt agatcatttt
1140

tttttttttgc agggtgctgc ctatgggccc tctgctcccc aatgccttag agagaggagg
1200
ggacgggacg gcacggccgc tcaccggaag gctgtgtgcg gggacatccg aggtggtggt
1260
ggacaggaag gacttgggaa ggggagcgag aaattgcttt ttctcttcct ccctgggcag
1320
aatgtagctt ttctgcttca ctgtggcagc ctcctccctg gatccttaga tcccagagga
1380
gggaagaaaa tttgcagtga ctgaaaacag taaaaaaaaa aaaatttatg tatataaaag
1440
ttgcattaca cagtacaaaa tagatggata atgtttatcc tttatttttc tatgtagaag
1500
tttttgaatt tgtgtgtgtg cttgtgcgtg tctacaccta gtattacggc tgggactctc
1560
cagctgtttt tgttgttgtt atgtttttaa gagggttgaa ttcttccatc aggtgaacga
1620
aaaaggcaac aaagtaataa atcagtgaat gtggccggca gctgtgttta gcccctccag
1680
atggaagttt cacttgaatg taaaataata aagttt
1716

<210> 5488
<211> 272
<212> PRT
<213> Homo sapiens

<400> 5488
Leu Gly Leu Gln Thr Arg Met Gln Ser Leu Ser Pro Asp Pro Lys Ala
1 5 10 15
Gln Tyr Thr Ser Ile Tyr Gly Ala Leu Lys Lys Ile Met Arg Thr Glu
20 25 30
Gly Phe Trp Arg Pro Leu Arg Gly Val Asn Val Met Ile Met Gly Ala
35 40 45
Gly Pro Ala His Ala Met Tyr Phe Ala Cys Tyr Glu Asn Met Lys Arg
50 55 60
Thr Leu Asn Asp Val Phe His His Gln Gly Asn Ser His Leu Ala Asn
65 70 75 80
Gly Ile Ala Gly Ser Met Ala Thr Leu Leu His Asp Ala Val Met Asn
85 90 95
Pro Ala Glu Val Val Lys Gln Arg Leu Gln Met Tyr Asn Ser Gln His
100 105 110
Arg Ser Ala Ile Ser Cys Ile Arg Thr Val Trp Arg Thr Glu Gly Leu
115 120 125
Gly Ala Phe Tyr Arg Ser Tyr Thr Thr Gln Leu Thr Met Asn Ile Pro
130 135 140
Phe Gln Ser Ile His Phe Ile Thr Tyr Glu Phe Leu Gln Glu Gln Val
145 150 155 160
Asn Pro His Arg Thr Tyr Asn Pro Gln Ser His Ile Ile Ser Gly Gly
165 170 175
Leu Ala Gly Ala Leu Ala Ala Ala Ala Thr Thr Pro Leu Asp Val Cys
180 185 190
Lys Thr Leu Leu Asn Thr Gln Glu Asn Val Ala Leu Ser Leu Ala Asn
195 200 205
Ile Ser Gly Arg Leu Ser Gly Met Ala Asn Ala Phe Arg Thr Val Tyr

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    210                 215                 220
Gln Leu Asn Gly Leu Ala Gly Tyr Phe Lys Gly Ile Gln Ala Arg Val
225                 230                 235                 240
Ile Tyr Gln Met Pro Ser Thr Ala Ile Ser Trp Ser Val Tyr Glu Phe
                245                 250                 255
Phe Lys Tyr Phe Leu Thr Lys Arg Gln Leu Glu Asn Arg Ala Pro Tyr
            260                 265                 270
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<210> 5489
<211> 1600
<212> DNA
<213> Homo sapiens

<400> 5489
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<213> Homo sapiens

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Gly Ile Ile Phe Thr Arg Thr Arg Gln Ser Ala His Ser Leu Leu Leu
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Trp Leu Gln Gln Gln Gln Gly Leu Gln Thr Val Asp Ile Arg Ala Gln
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Leu Leu Ile Gly Ala Gly Asn Ser Ser Gln Ser Thr His Met Thr Gln
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Arg Asp Gln Gln Glu Val Ile Gln Lys Phe Gln Asp Gly Thr Leu Asn
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Leu Leu Val Ala Thr Ser Val Ala Glu Glu Gly Leu Asp Ile Pro His
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Cys Asn Val Val Val Arg Tyr Gly Leu Leu Thr Asn Glu Ile Ser Met
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Val Gln Ala Arg Gly Arg Ala Arg Ala Asp Gln Ser Val Tyr Ala Phe
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Leu Thr Lys Arg Ala Ala Gln Ala Ala Gln Arg Glu Asn Gln Arg Gln
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Gln Phe Pro Val Glu His Val Gln Leu Leu Cys Ile Asn Cys Met Val
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<213> Homo sapiens

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Arg Glu Leu Phe Leu Ser Arg Gln Tyr Glu Ser Leu Pro Ala Thr His
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Ile Arg Gly Lys Cys Ser Val Ala Leu Leu Asn Glu Thr Glu Ser Val
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Leu Ser Tyr Leu Asp Lys Glu Asp Thr Phe Phe Tyr Ser Leu Val Tyr
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Asp Pro Ser Leu Lys Thr Leu Leu Ala Asp Lys Gly Glu Ile Arg Val
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Gly Pro Arg Tyr Gln Ala Asp Ile Pro Glu Met Leu Leu Glu Gly Glu
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Ser Asp Glu Arg Glu Gln Ser Lys Leu Glu Val Lys Val Trp Asp Pro
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Arg Ala Val Gly Thr Phe Ala Arg Ala Leu Asp Cys Ser Ser Ser Val
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<212> PRT
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Ile Ala Tyr Gly Asp Lys Arg Tyr Asn Cys Glu Tyr Ser Gly Pro Pro
        35   40   45
Lys Pro Leu Pro Lys Asp Gly Tyr Asp Leu Val Gln Glu Leu Cys Pro
    50   55   60
Gly Phe Phe Phe Gly Asn Val Ser Leu Cys Cys Asp Val Arg Gln Leu
65   70   75   80
Gln Thr Leu Lys Asp Asn Leu Gln Leu Pro Leu Gln Phe Leu Ser Arg
                85   90   95
Cys Pro Ser Cys Phe Tyr Asn Leu Leu Asn Leu Phe Cys Glu Leu Thr
            100   105   110
Cys Ser Pro Arg Gln Ser Gln Phe Leu Asn Val Thr Ala Thr Glu Asp
        115   120   125
Tyr Val Asp Pro Val Thr Asn Gln Thr Lys Thr Asn Val Lys Glu Leu
    130   135   140
Gln Tyr Tyr Val Gly Gln Ser Phe Ala Asn Ala Met Tyr Asn Ala Cys

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Arg Asp Val Glu Ala Pro Ser Ser Asn Asp Lys Ala Leu Gly Leu Leu
                165                 170                 175
Cys Gly Lys Asp Ala Asp Ala Cys Asn Ala Thr Asn Trp Ile Glu Tyr
            180                 185                 190
Met Phe Asn Lys Asp Asn Gly Gln Ala Pro Phe Thr Ile Thr Pro Val
        195                 200                 205
Phe Ser Asp Phe Pro Val His Gly Met Glu Pro Met Asn Asn Ala Thr
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Lys Gly Cys Asp Glu Ser Val Asp Glu Val Thr Ala Pro Cys Ser Cys
225                 230                 235                 240
Gln Asp Cys Ser Ile Val Cys Gly Pro Lys Pro Gln Pro Pro Pro Pro
                245                 250                 255
Pro Ala Pro Trp Thr Ile Leu Gly Leu Asp Ala Met Tyr Val Ile Met
            260                 265                 270
Trp Ile Thr Tyr Met Ala Phe Leu Leu Val Phe Phe Gly Ala Phe Phe
        275                 280                 285
Ala Val Trp Cys Tyr Arg Lys Arg Tyr Phe Val Ser Glu Tyr Thr Pro
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Ile Asp Ser Asn Ile Ala Phe Ser Val Asn Ala Ser Asp Lys Gly Glu
305                 310                 315                 320
Ala Ser Cys Cys Asp Pro Val Ser Ala Ala Phe Glu Gly Cys Leu Arg
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Arg Leu Phe Thr Arg Trp Gly Ser Phe Cys Val Arg Asn Pro Gly Cys
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Val Ile Phe Phe Ser Leu Val Phe Ile Thr Ala Cys Ser Ser Gly Leu
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Val Phe Val Arg Val Thr Thr Asn Pro Val Asp Leu Trp Ser Ala Pro
    370                 375                 380
Ser Ser Gln Ala Arg Leu Glu Lys Glu Tyr Phe Asp Gln His Phe Gly
385                 390                 395                 400
Pro Phe Phe Arg Thr Glu Gln Leu Ile Ile Arg Ala Pro Leu Thr Asp
                405                 410                 415
Lys His Ile Tyr Gln Pro Tyr Pro Ser Gly Ala Asp Val Pro Phe Gly
            420                 425                 430
Pro Pro Leu Asp Ile Gln Ile Leu His Gln Val Leu Asp Leu Gln Ile
        435                 440                 445
Ala Ile Glu Asn Ile Thr Ala Ser Tyr Asp Asn Glu Thr Val Thr Leu
    450                 455                 460
Gln Asp Ile Cys Leu Ala Pro Leu Ser Pro Tyr Asn Thr Asn Cys Thr
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His Lys Lys Gly Asp Asp Phe Phe Val Tyr Ala Asp Tyr His Thr His
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Phe Leu Tyr Cys Val Arg Ala Pro Ala Ser Leu Asn Asp Thr Ser Leu
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Val Ile Ser Tyr Ala Ile Met Phe Leu Tyr Ile Ser Leu Ala Leu Gly
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Gly Ile Ala Gly Ile Leu Ile Val Leu Ser Ser Val Ala Cys Ser Leu
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Gly Val Phe Ser Tyr Ile Gly Leu Pro Leu Thr Leu Ile Val Ile Glu
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Leu Val Gln Ala Tyr Gln Arg Asp Glu Arg Leu Gln Gly Glu Thr Leu
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Leu Ser Ser Phe Ser Glu Thr Val Ala Phe Phe Leu Gly Ala Leu Ser
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Ser Ile Ala Val Leu Asn Lys Val Asp Ile Gly Leu Asp Gln Ser Leu
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Ser Met Pro Asp Asp Ser Tyr Met Val Asp Tyr Phe Lys Ser Ile Ser
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Gln Tyr Leu His Ala Gly Pro Pro Val Tyr Phe Val Leu Glu Glu Gly
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Leu Asp Asn Tyr Thr Arg Ile Gly Phe Ala Pro Ser Ser Trp Ile Asp
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Val Arg Cys Arg Pro Leu Thr Pro Gly Gly Lys Gln Arg Pro Gln Gly
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Gly Asp Phe Met Arg Phe Leu Pro Met Phe Leu Ser Asp Asn Pro Asn
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Pro Lys Cys Gly Lys Gly Gly His Ala Ala Tyr Ser Ser Ala Val Asn
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Lys Ala Arg Leu Ile Ala Ser Asn Val Thr Glu Thr Met Gly Ile Asn
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Gly Ser Ala Tyr Arg Val Phe Pro Tyr Ser Val Phe Tyr Val Phe Tyr
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Glu Gln Tyr Leu Thr Ile Ile Asp Asp Thr Ile Phe Asn Leu Gly Val
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Ser His Ile Thr Arg Ala Phe Thr Val Ser Met Lys Gly Ser Arg Val
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Glu Arg Ala Glu Glu Ala Leu Ala His Met Gly Ser Ser Val Phe Ser
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Gly Ile Thr Leu Thr Lys Phe Gly Gly Ile Val Val Leu Ala Phe Ala
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Lys Ser Gln Ile Phe Gln Ile Phe Tyr Phe Arg Met Tyr Leu Ala Met
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Val Leu Leu Gly Ala Thr His Gly Leu Ile Phe Leu Pro Val Leu Leu
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Ser Tyr Ile Gly Pro Ser Val Asn Lys Ala Lys Ser Cys Ala Thr Glu
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Lys Tyr Cys Leu Pro Leu Thr Phe Cys Ile His Thr Gly Leu Ser Gln
65 70 75 80
Tyr Ile Ala Val Glu Ala Ala Glu Gly Arg Asn Lys Asn Glu Val Phe
85 90 95
Tyr Gln Cys Pro Asp Gln Met Ala Arg Asn Pro Ala Ala Ile Asp Met
100 105 110
Phe Ile Ile Gly Ala Thr Phe Thr Asp Trp Phe Thr Ser Tyr Val Lys
115 120 125
Asn Val Val Ser Gly Gly Phe Pro Ile Ile Arg Asp Gln Ile Phe Arg
130 135 140
Tyr Val His Asp Pro Glu Cys Val Ala Thr Thr Gly Asp Ile Thr Val
145 150 155 160
Ser Val Ser Thr Ser Phe Leu Pro Glu Leu Ser Ser Val His Pro Pro
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180 185 190
Leu Pro Glu Lys Ala Cys Gln Leu Asp Ser Arg Tyr Trp Arg Ile Thr
195 200 205
Asn Ala Lys Gly Asp Val Glu Glu Val Gln Gly Pro Gly Val Val Gly
210 215 220
Glu Phe Pro Ile Ile Ser Pro Gly Arg Val Tyr Glu Tyr Thr Ser Cys
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Thr Thr Phe Ser Thr Thr Ser Gly Tyr Met Glu Gly Tyr Tyr Thr Phe
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His Phe Leu Tyr Phe Lys Asp Lys Ile Phe Asn Val Ala Ile Pro Arg

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His Pro Pro Ala Phe Ala Pro Arg Thr Leu Arg Met Ala Gln Leu Val
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Ala Gln Leu Trp Trp Ser Ser Pro Phe Ile His Ser Pro Gly Glu Thr
35 40 45
Asn Ile Pro His Thr Leu Thr Glu Pro His Ser Val Pro Gly Trp Cys
50 55 60
Trp Asp Thr Leu Arg Arg His Gly Ala Gly Gln Gly His Pro Gly Met
65 70 75 80
Ala Arg Ser Gly Thr Gly Glu Gly Gln Arg Glu Gly Asp Ile Glu Arg
85 90 95
Glu Glu Asp Glu Glu Glu Gly Asn Arg Ser Arg Lys Ser Arg Asp Ser
100 105 110
Arg Ser Gln Val Lys Gly Leu Pro Leu His Ser Arg Glu Gln Arg Asp
115 120 125
Pro Ser Ala Gly Ala Ser Glu Lys Ser Arg Asn Pro Ser Arg Met Gly
130 135 140
Thr Trp Gly Val Asn Phe
145 150

<210> 5499
<211> 1918
<212> DNA
<213> Homo sapiens

<400> 5499
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120
tgcctctgcc cttcgtagat tctctgctgg gcctttggaa ctaacacagc aacttccagg
180
gtctcatgtt gaagacttta tggagcatcc tggccagaac aagccaagga gccaagacga
240
gagggacaca cggacaaaca acagacagaa gacgtactgg ccgctggact ccgctgcctc
300
ccccatctcc ccgccatctg cgcccggagg atgagcccag ccttcagggc catggatgtg
360
gagccccgcg ccaaaggcgt ccttctggag ccctttgtcc accaggtcgg ggggcactca
420
tgcgtgctcc gcttcaatga gacaaccctg tgcaagcccc tggtcccaag ggaacatcag
480
ttctacgaga ccctccctgc tgagatgcgc aaattcactc cccagtacaa aggtgtggta
540
tctgtgcgct ttgaagaaga tgaagacagg aacttgtgtc taatagcata tccattgaaa
600

ggggaccatg gaattgtgga cattgcacat aattcagact gtgaaccaaa aagtaagctc
660
ctaaggtgga caacaaacaa aaaacatcat gtcttagaaa cagaaaagac ccctaaggac
720
tgggtgcgtc agcaccgtaa agaggagaaa atgaagagcc ataagttaga agaagaattt
780
gagtggctaa agaaatctga agtcttgtac tacactgtag agaagaaggg gaatataagt
840
tcccagctta aacactataa cccttggagc atgaaatgtc accagcaaca gttacagaga
900
atgaaggaga atgcaaagca tcggaaccag tacaaattta tcttactgga aaacctgact
960
tcccgctatg aggtgccttg tgtccttgac ctcaagatgg gcacacgaca acatggtgat
1020
gatgcttcag aggagaaggc agccaaccag atccgaaaat gtcagcagag cacatctgca
1080
gtcattggtg tgnctgtgtg tggcatgcag gtgtaccaag caggcagtgg gcagctcatg
1140
ttcatgaaca agtaccatgg acggaagcta tcggtgcagg gcttcaagga ggcacttttc
1200
cagttcttcc acaatgggcg gtacctgcgc cgtgaactcc tgggccctgt gctcaagaag
1260
ctgactgagc tcaaggcagt gttggagcga caggagtcct accgcttcta ctcaagctcc
1320
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1380
gatttggagg acctgtcaga ggaatcagct gatgagtctg ctggtgccta tgcctacaaa
1440
cccatcggcg ccagctctgt agatgtgcgc atgatcgact ttgcacacac cacctgcagg
1500
ctgtatggcg aggacaccgt ggtgcatgag ggccaggatg ctggctatat cttcgggctc
1560
cagagcctga tagacattgt cacagagata agtgaggaga gtggggagtg agcttgctag
1620
ctgctccagt acttgagagc gactctgtgt cccaggcaca gctgtgctgc gtcagggagg
1680
aagccagtat ggccaggtgg tggctcctgc agcctggagc tgatgtgcag tggcctctgt
1740
gagccccagc ctgagccagt cccagctgtg cttggagtct ttatttattt taactatttc
1800
ttcaacattc cacatttgat gatgatacct ctttcttccc tgagtgtata tgttctaata
1860
caaatctttt tgtttattgt aaaaaaaaaa aaaaaaaaaa aaagaaaaac tcgaaaag
1918

<210> 5500
<211> 426
<212> PRT
<213> Homo sapiens

<400> 5500
Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
1 5 10 15
Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val

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            20                  25                  30
Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu
        35                  40                  45
His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro
    50                  55                  60
Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg
65                  70                  75                  80
Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val
                85                  90                  95
Asp Ile Ala His Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg
            100                 105                 110
Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro
        115                 120                 125
Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His
    130                 135                 140
Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr
145                 150                 155                 160
Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr
                165                 170                 175
Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys
            180                 185                 190
Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn
        195                 200                 205
Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly
    210                 215                 220
Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln
225                 230                 235                 240
Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Xaa Val
                245                 250                 255
Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met
            260                 265                 270
Asn Lys Tyr His Gly Arg Lys Leu Ser Val Gln Gly Phe Lys Glu Ala
        275                 280                 285
Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu
    290                 295                 300
Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg
305                 310                 315                 320
Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp
                325                 330                 335
Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu
            340                 345                 350
Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala
        355                 360                 365
Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe
    370                 375                 380
Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu
385                 390                 395                 400
Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile
                405                 410                 415
Val Thr Glu Ile Ser Glu Glu Ser Gly Glu
            420                 425
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<210> 5501
<211> 568

<212> DNA
<213> Homo sapiens

<400> 5501
attcggcacg aggtgagtcg gtggcaggaa cgtgggctct agactgtgca ttcaggctct
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cctacttggc agaatgatct tggggaaacg acttcatctg aacttcagat atttcacatg
120
tgaagcgggg acaaaaccat gcagctcaga ggtccctgtg ggggctgggg gagctgccct
180
gcaggtcttg gcacatgcac agcaggctcc ccatagcttt gtcaccacaa agggcactgt
240
tctattcaca gcacctcctg cttctgcctg gcaactgtgt ctccctgtgc tatatttaat
300
tccaccagca aagctggcga ggcagggccc agccctgaag gagatctcct tgcctgaccc
360
ctggacctgg aaatggaggc ttcatgtgcc cgccttggcg gcttaagcct gctgctttgg
420
cagtgccatg ggtgagccga gcagctgtga ggtgggtggg gcagggctgt agcccacgcc
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540
acctggcatg ctgcagccct ctgccggc
568

<210> 5502
<211> 110
<212> PRT
<213> Homo sapiens

<400> 5502
Met Ile Leu Gly Lys Arg Leu His Leu Asn Phe Arg Tyr Phe Thr Cys
 1   5   10   15
Glu Ala Gly Thr Lys Pro Cys Ser Ser Glu Val Pro Val Gly Ala Gly
            20   25   30
Gly Ala Ala Leu Gln Val Leu Ala His Ala Gln Gln Ala Pro His Ser
        35   40   45
Phe Val Thr Thr Lys Gly Thr Val Leu Phe Thr Ala Pro Pro Ala Ser
    50   55   60
Ala Trp Gln Leu Cys Leu Pro Val Leu Tyr Leu Ile Pro Pro Ala Lys
65   70   75   80
Leu Ala Arg Gln Gly Pro Ala Leu Lys Glu Ile Ser Leu Pro Asp Pro
                85   90   95
Trp Thr Trp Lys Trp Arg Leu His Val Pro Ala Leu Ala Ala
            100   105   110

<210> 5503
<211> 1679
<212> DNA
<213> Homo sapiens

<400> 5503
tgtctgggaa aagggaactc acaaggggtg agtaccccca aattaggaga taccatgagc
60

taacgccgtc tcagaattgc ataaatttgt ctacattttt caaagaagtt gggttatctg
120
atttaatcct cacaatagtc aagctaggaa ggtaagtgtg gaattattac cccatttgat
180
aggtagacaa attaaagctt aagatcaaac cgtttgcaaa gcaggaagca gcacttcctc
240
ttggtccagt tcttccttct ccctggtgct aaggtcagtg gatgttggct ccccacaggc
300
cagaaagctg gagagaagcc cctggctgca ggacccgggg aggaggaact gctccggggc
360
tcagcccctc atgctcagga cactcagagt gaggaactgc caccctcctg caccatctca
420
ggagagaaga agccgccagc agtctctgga gaagccaccg gggctgatgc tgggagactg
480
tgcccgcccc cccgctccag ggctccccac aaagacagaa ctctagcccg ctccaggccc
540
cagactcagg gggaagattg ttccctccca gtgggagagg tgaagatagg aaagaggtcc
600
tattctccag cccccgggaa gcagaaaaag cctaatgcca tgggtctggc cccaacatca
660
tctccgggtg cccctaactc agcccgtgcc acacacaacc cagtgccctg tgggtcaggc
720
cgggggccct gccacctggc caatctcctc agtacattgg cgcagagcaa ccaaaacaga
780
gaccacaagc aggggccccc ggaagtgacc tgccaaatta ggaaaaagac acgaacccta
840
taccgctcag atcagctgga ggagctagag aagatattcc aagaagacca ctatcctgac
900
agtgataaac gccgagagat tgcccagacg gtgggggtga ccccccagcg catcatggta
960
aaggggggccg gctcactggt ggcagggtgg agtggcggag ggcccaccat tgaaacactc
1020
gaattgcaga gtgagcgctc agcggtagcc tgggtgtggt tccagaatcg ccgggccaag
1080
tggcgaaaaa tggagaaact gaatgggaaa gaaagcaagg acaatcctgc agcccctggc
1140
cctgccagca gtcaatgcag ctctgcagct gagatcctac ctgctgtgcc catggagcca
1200
aagcctgacc ctttccctca ggagtcccct ctggatacct ttccagagcc ccccatgctg
1260
ctgacttctg accagacttt ggcccccacc caacccagtg agggtgctca gagggtggtg
1320
acccccccac tcttcagccc cccacctgtg cgaagggccg atcttccttt ccccccttggc
1380
cctgtccaca ccccccaact gatgccactg ctgatggatg ttgctggcag tgacagcagc
1440
cacaaggacg gcccctgtgg gtcctggggg acaaggtaag gaacctacgg gggtaggtca
1500
ctctagttat ctgggtgggg gtaggggggt gtagatggag agaagataga cacagagagg
1560
agagggttaa ctgagaggag cacagagtgg tacaggagat ggggatgaaa gggataaggg
1620
gatctgggga atgacctagg ggatcacagc aatagagcag aaacaagggt aagatgcta
1679

<210> 5504
<211> 392
<212> PRT
<213> Homo sapiens

<400> 5504
Gln Lys Ala Gly Glu Lys Pro Leu Ala Ala Gly Pro Gly Glu Glu Glu
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Leu Leu Arg Gly Ser Ala Pro His Ala Gln Asp Thr Gln Ser Glu Glu
20 25 30
Leu Pro Pro Ser Cys Thr Ile Ser Gly Glu Lys Lys Pro Pro Ala Val
35 40 45
Ser Gly Glu Ala Thr Gly Ala Asp Ala Gly Arg Leu Cys Pro Pro Pro
50 55 60
Arg Ser Arg Ala Pro His Lys Asp Arg Thr Leu Ala Arg Ser Arg Pro
65 70 75 80
Gln Thr Gln Gly Glu Asp Cys Ser Leu Pro Val Gly Glu Val Lys Ile
85 90 95
Gly Lys Arg Ser Tyr Ser Pro Ala Pro Gly Lys Gln Lys Lys Pro Asn
100 105 110
Ala Met Gly Leu Ala Pro Thr Ser Ser Pro Gly Ala Pro Asn Ser Ala
115 120 125
Arg Ala Thr His Asn Pro Val Pro Cys Gly Ser Gly Arg Gly Pro Cys
130 135 140
His Leu Ala Asn Leu Leu Ser Thr Leu Ala Gln Ser Asn Gln Asn Arg
145 150 155 160
Asp His Lys Gln Gly Pro Pro Glu Val Thr Cys Gln Ile Arg Lys Lys
165 170 175
Thr Arg Thr Leu Tyr Arg Ser Asp Gln Leu Glu Glu Leu Glu Lys Ile
180 185 190
Phe Gln Glu Asp His Tyr Pro Asp Ser Asp Lys Arg Arg Glu Ile Ala
195 200 205
Gln Thr Val Gly Val Thr Pro Gln Arg Ile Met Val Lys Gly Ala Gly
210 215 220
Ser Leu Val Ala Gly Trp Ser Gly Gly Gly Pro Thr Ile Glu Thr Leu
225 230 235 240
Glu Leu Gln Ser Glu Arg Ser Ala Val Ala Trp Val Trp Phe Gln Asn
245 250 255
Arg Arg Ala Lys Trp Arg Lys Met Glu Lys Leu Asn Gly Lys Glu Ser
260 265 270
Lys Asp Asn Pro Ala Ala Pro Gly Pro Ala Ser Ser Gln Cys Ser Ser
275 280 285
Ala Ala Glu Ile Leu Pro Ala Val Pro Met Glu Pro Lys Pro Asp Pro
290 295 300
Phe Pro Gln Glu Ser Pro Leu Asp Thr Phe Pro Glu Pro Pro Met Leu
305 310 315 320
Leu Thr Ser Asp Gln Thr Leu Ala Pro Thr Gln Pro Ser Glu Gly Ala
325 330 335
Gln Arg Val Val Thr Pro Pro Leu Phe Ser Pro Pro Pro Val Arg Arg
340 345 350
Ala Asp Leu Pro Phe Pro Leu Gly Pro Val His Thr Pro Gln Leu Met
355 360 365
Pro Leu Leu Met Asp Val Ala Gly Ser Asp Ser Ser His Lys Asp Gly

370 375 380
Pro Cys Gly Ser Trp Gly Thr Arg
385 390

<210> 5505
<211> 1099
<212> DNA
<213> Homo sapiens

<400> 5505
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cagaagccac aagccatggc tgtggggaac atcaacgagc tgcccgagaa catcctgctg
120
gagctgttca cgcacgtgcc cgcccgccag ctgctgctga actgccgcct ggtctgcagc
180
ctctggcggg acctcatcga cctcgtgacc ctctggaaac gcaagtgcct gcgagagggc
240
ttcatcactg aggactggga ccagcccgtg gccgactgga agatcttcta cttcttacgg
300
agcctgcaca ggaacctcct gcacaacccg tgcgctgaag aggggttcga gttctggagc
360
ctggatgtga atggaggcga tgagtggaag gtggaggatc tctctcgaga ccagaggaag
420
gaattcccca atgaccaggt caagaaatac ttcgttactt catattacac ctgcctcaag
480
tcccaggtgg tggacctcaa ggccgaaggg tattgggagg agctactaga cacattccgg
540
ccggacatcg tggttaagga ctggtttgct gccagagccg actgtggctg cacctaccaa
600
ctcaaagtgc agctcctgtc ggctgactac ttcgtgttgg cctccttcga gccagacccg
660
gcgaccatcc agcagaagag cgatgccaag tggagggagg tctcccacac attctccaac
720
tacccgcccg gcgtccgcta catctggttt cagcacggcg gcgtggacac tcattactgg
780
gccggctggt acggcccgag ggtcaccaac agcagcatca ccatcgggcc cccgctgccc
840
tgacaccccc tgagccccca tctgctgaac cctgactggt aaacaactgc tgtcagaaaa
900
gggctgggct tgggaagggg aggtggaggc caggtgtccc cagacctcta acccttgccc
960
ctagcagcct cttctttgtg gagcctctca gtgtgggcag ccctcgcatg ctggggtcgg
1020
gccagctctc cccgaaaggt cttgacctga atgatggccg gggaagcctg cgtgtgcccc
1080
tttcagagac ggagcacct
1099

<210> 5506
<211> 280
<212> PRT
<213> Homo sapiens

<400> 5506
Lys Leu Gly Arg Pro Ser Gly Ser Cys Arg Gly Gly Arg Ala Gln Leu
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Gln Glu Gly Val Gln Lys Pro Gln Ala Met Ala Val Gly Asn Ile Asn
20 25 30
Glu Leu Pro Glu Asn Ile Leu Leu Glu Leu Phe Thr His Val Pro Ala
35 40 45
Arg Gln Leu Leu Leu Asn Cys Arg Leu Val Cys Ser Leu Trp Arg Asp
50 55 60
Leu Ile Asp Leu Val Thr Leu Trp Lys Arg Lys Cys Leu Arg Glu Gly
65 70 75 80
Phe Ile Thr Glu Asp Trp Asp Gln Pro Val Ala Asp Trp Lys Ile Phe
85 90 95
Tyr Phe Leu Arg Ser Leu His Arg Asn Leu Leu His Asn Pro Cys Ala
100 105 110
Glu Glu Gly Phe Glu Phe Trp Ser Leu Asp Val Asn Gly Gly Asp Glu
115 120 125
Trp Lys Val Glu Asp Leu Ser Arg Asp Gln Arg Lys Glu Phe Pro Asn
130 135 140
Asp Gln Val Lys Lys Tyr Phe Val Thr Ser Tyr Tyr Thr Cys Leu Lys
145 150 155 160
Ser Gln Val Val Asp Leu Lys Ala Glu Gly Tyr Trp Glu Glu Leu Leu
165 170 175
Asp Thr Phe Arg Pro Asp Ile Val Val Lys Asp Trp Phe Ala Ala Arg
180 185 190
Ala Asp Cys Gly Cys Thr Tyr Gln Leu Lys Val Gln Leu Leu Ser Ala
195 200 205
Asp Tyr Phe Val Leu Ala Ser Phe Glu Pro Asp Pro Ala Thr Ile Gln
210 215 220
Gln Lys Ser Asp Ala Lys Trp Arg Glu Val Ser His Thr Phe Ser Asn
225 230 235 240
Tyr Pro Pro Gly Val Arg Tyr Ile Trp Phe Gln His Gly Gly Val Asp
245 250 255
Thr His Tyr Trp Ala Gly Trp Tyr Gly Pro Arg Val Thr Asn Ser Ser
260 265 270
Ile Thr Ile Gly Pro Pro Leu Pro
275 280

<210> 5507
<211> 1658
<212> DNA
<213> Homo sapiens

<400> 5507
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actgaactcc gaaaacagcc tcttcgtaag tatgtcaccc catcagactt tgatcaactc
120
aagcaatttc tcacctttga caaacaggtc cttcgattct atgcaatctg ggatgataca
180
gacagcatgt atggtgaatg tcggacctac atcattcatt actatcttat ggatgatacg
240
gtggaaattc gagaggtcca cgaacggaat gatgggagag atcctttccc actcctaatg
300

aaccgccagc gtgtgcccaa agttttggtg gaaaatgcaa agaacttccc tcagtgtgtg
360
ctagaaatct ctgaccaaga agtgttggaa tggtatactg ctaaagactt cattgttggg
420
aagtcactca ctatccttgg gagaactttc ttcatttatg attgtgatcc atttactcga
480
cggtattaca aagagaagtt tggaatcact gatttaccac gtattgatgt gagcaagcgg
540
gaaccacctc cagtaaaaca ggagttgcct ccttataacg gttttggact agtggaagat
600
tctgctcaga attgttttgc tctcattcca aaagctccaa aaaaagacgt tattaaaatg
660
ctggtgaatg ataacaaggt gcttcgttat ttggctgtac tggaatcccc catcccagaa
720
gacaaagacc gcagatttgt cttctcttac tttctagcta ccgacatgat cagtatcttt
780
gagcctcctg ttcgcaattc tggtatcatt gggggcaagt accttggcag gactaaagtt
840
gttaaaccat actctacagt ggacaaccct gtctactatg gccccagtga cttcttcatt
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960
ttgaaataca tggagagcaa cgctgcccag tattcaccag aagcactcgc gtcaattcag
1020
aaccatgtcc gaaagcgaga agcgcctgct ccagaagcag aaagcaagca aactgaaaag
1080
gatccaggcg tgcaggaatt ggaagcatta atagacacaa ttcagaagca actgaaagat
1140
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1200
tatgtggaca gagacatgtt ctttaaaatc tgtgaatcgc ttaacgtccc agtggatgac
1260
tccttggtta aggagttaat caggatgtgc tctcatggag aaggcaaaat taactactat
1320
aactttgttc gtgctttctc aaactgacct gctgatgaga aaatgcaaga caatttttga
1380
tactggaact atgctttgaa atacacctta cactcttcat agaggcattt acagggttcc
1440
tgaagtttta tttctgtttt ggttcttatt tcactcctac tgaagtcgaa actaaattgg
1500
atctaatagg atctaagatt ggtgccttat ttagggtgat aggggtatag caatgtctaa
1560
ttttgtgtgt caaattgact tggccacagg gggcccaaat atttcctttc tttcttttta
1620
aaaaaataaa ttttttttgga gatgggaaaa aaaaaaaa
1658

<210> 5508
<211> 448
<212> PRT
<213> Homo sapiens

<400> 5508
Xaa Leu Glu Ser Gln Gly Ile Glu Leu Asn Pro Pro Glu Lys Met Ala

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Leu Asp Pro Tyr Thr Glu Leu Arg Lys Gln Pro Leu Arg Lys Tyr Val
            20                  25                  30
Thr Pro Ser Asp Phe Asp Gln Leu Lys Gln Phe Leu Thr Phe Asp Lys
        35                  40                  45
Gln Val Leu Arg Phe Tyr Ala Ile Trp Asp Asp Thr Asp Ser Met Tyr
    50                  55                  60
Gly Glu Cys Arg Thr Tyr Ile Ile His Tyr Tyr Leu Met Asp Asp Thr
65                  70                  75                  80
Val Glu Ile Arg Glu Val His Glu Arg Asn Asp Gly Arg Asp Pro Phe
                85                  90                  95
Pro Leu Leu Met Asn Arg Gln Arg Val Pro Lys Val Leu Val Glu Asn
            100                 105                 110
Ala Lys Asn Phe Pro Gln Cys Val Leu Glu Ile Ser Asp Gln Glu Val
        115                 120                 125
Leu Glu Trp Tyr Thr Ala Lys Asp Phe Ile Val Gly Lys Ser Leu Thr
    130                 135                 140
Ile Leu Gly Arg Thr Phe Phe Ile Tyr Asp Cys Asp Pro Phe Thr Arg
145                 150                 155                 160
Arg Tyr Tyr Lys Glu Lys Phe Gly Ile Thr Asp Leu Pro Arg Ile Asp
                165                 170                 175
Val Ser Lys Arg Glu Pro Pro Pro Val Lys Gln Glu Leu Pro Pro Tyr
            180                 185                 190
Asn Gly Phe Gly Leu Val Glu Asp Ser Ala Gln Asn Cys Phe Ala Leu
        195                 200                 205
Ile Pro Lys Ala Pro Lys Lys Asp Val Ile Lys Met Leu Val Asn Asp
    210                 215                 220
Asn Lys Val Leu Arg Tyr Leu Ala Val Leu Glu Ser Pro Ile Pro Glu
225                 230                 235                 240
Asp Lys Asp Arg Arg Phe Val Phe Ser Tyr Phe Leu Ala Thr Asp Met
                245                 250                 255
Ile Ser Ile Phe Glu Pro Pro Val Arg Asn Ser Gly Ile Ile Gly Gly
            260                 265                 270
Lys Tyr Leu Gly Arg Thr Lys Val Val Lys Pro Tyr Ser Thr Val Asp
        275                 280                 285
Asn Pro Val Tyr Tyr Gly Pro Ser Asp Phe Phe Ile Gly Ala Val Ile
    290                 295                 300
Glu Val Phe Gly His Arg Phe Ile Ile Leu Asp Thr Asp Glu Tyr Val
305                 310                 315                 320
Leu Lys Tyr Met Glu Ser Asn Ala Ala Gln Tyr Ser Pro Glu Ala Leu
                325                 330                 335
Ala Ser Ile Gln Asn His Val Arg Lys Arg Glu Ala Pro Ala Pro Glu
            340                 345                 350
Ala Glu Ser Lys Gln Thr Glu Lys Asp Pro Gly Val Gln Glu Leu Glu
        355                 360                 365
Ala Leu Ile Asp Thr Ile Gln Lys Gln Leu Lys Asp His Ser Cys Lys
    370                 375                 380
Asp Asn Ile Arg Glu Ala Phe Gln Ile Tyr Asp Lys Glu Ala Ser Gly
385                 390                 395                 400
Tyr Val Asp Arg Asp Met Phe Phe Lys Ile Cys Glu Ser Leu Asn Val
                405                 410                 415
Pro Val Asp Asp Ser Leu Val Lys Glu Leu Ile Arg Met Cys Ser His
            420                 425                 430
Gly Glu Gly Lys Ile Asn Tyr Tyr Asn Phe Val Arg Ala Phe Ser Asn
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435 440 445

<210> 5509
<211> 818
<212> DNA
<213> Homo sapiens

<400> 5509
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aaggagagct gtatttgtgt ttcatggttg ctttaccaaa taattctagc atcggaattg
120
ctatgtgaga ggaagtaagt atacacagcg taagaggtgt gataaccaag tcatagaaga
180
aatgtttgga gaacatggaa tcatgtgaac ttattatgtg gtaagtacag atacccaggg
240
ctgtcagtct caccatcctt ttctacacat gtggatgctt caggactcca gcctttgagg
300
atgtggcttt caacttcacc ctacaggaaa ggtagtcaat gtggagaagc cttcagccag
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420
gtgtgtggag aggtcggcgt gggctatcca tccactgaaa ggcacatcag agatcgcctt
480
ggacgcaaac cctgtgaata tcaggaatgt agacagaagg catatacatg taagccatgt
540
gggaatgcct ttcgttttca ccactccttt cacatacacg aaaggcctca cagtggagaa
600
aacctctatg aatgttagga atttcagaaa acattcactt ccccccccaaa ccttcaaaga
660
tgtgaaaatg catagtggag atggacctta caaatgcaag gtgggtagga aaacctttga
720
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780
taggcactgt gggagcacct acaatcattt cagttttg
818

<210> 5510
<211> 105
<212> PRT
<213> Homo sapiens

<400> 5510
Met Trp Leu Ser Thr Ser Pro Tyr Arg Lys Gly Ser Gln Cys Gly Glu
1 5 10 15
Ala Phe Ser Gln Ile Pro Gly His Asn Leu Asn Lys Lys Thr Pro Pro
20 25 30
Gly Val Lys Pro Pro Glu Ser His Val Cys Gly Glu Val Gly Val Gly
35 40 45
Tyr Pro Ser Thr Glu Arg His Ile Arg Asp Arg Leu Gly Arg Lys Pro
50 55 60
Cys Glu Tyr Gln Glu Cys Arg Gln Lys Ala Tyr Thr Cys Lys Pro Cys
65 70 75 80
Gly Asn Ala Phe Arg Phe His His Ser Phe His Ile His Glu Arg Pro

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                85                  90                  95
His Ser Gly Glu Asn Leu Tyr Glu Cys
            100                 105

<210> 5511
<211> 379
<212> DNA
<213> Homo sapiens

<400> 5511
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ccttccttgg gaaaagaggg catcgtctca atcgcatagt cacacacatc ccttaactca
120
ctctgctgag ttgctgagag tctgtgttcc tctctccact tataggatgg gtcctcatct
180
tcttgagctt caagccccaa ggcagagacc tggctgctcc tcatgggagc ctcagggata
240
atgctgaatt cctctatggc agagatggga ggagaggctc cacgctgggc ctcctcagcc
300
tccatcaggg ctgaatcctg gtcggtgtca catgctgctt cggccccagc gtcccctcca
360
ggtcccggcg ccggccgcn
379

<210> 5512
<211> 101
<212> PRT
<213> Homo sapiens

<400> 5512
Met Glu Ala Glu Glu Ala Gln Arg Gly Ala Ser Pro Pro Ile Ser Ala
 1               5                  10                  15
Ile Glu Glu Phe Ser Ile Ile Pro Glu Ala Pro Met Arg Ser Ser Gln
            20                  25                  30
Val Ser Ala Leu Gly Leu Glu Ala Gln Glu Asp Glu Asp Pro Ser Tyr
        35                  40                  45
Lys Trp Arg Glu Glu His Arg Leu Ser Ala Thr Gln Gln Ser Glu Leu
    50                  55                  60
Arg Asp Val Cys Asp Tyr Ala Ile Glu Thr Met Pro Ser Phe Pro Lys
65                  70                  75                  80
Glu Gly Ser Ala Asp Val Glu Pro Asn Gln Glu Ser Leu Val Ala Glu
                85                  90                  95
Ala Cys Asp Thr Pro
            100

<210> 5513
<211> 837
<212> DNA
<213> Homo sapiens

<400> 5513
nnaagcttga gttcctctgt ccaaggccag ggacctgtga ccatggaagc agagagaagc
60
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aaggccacag ccgcggccct gggcagtttc ccggcaggtg gcccggccga gctgtcgctg
120
agactcgggg agccattgac catcgtctct gaggatggag actggtggac ggtgctgtct
180
gaagtctcag gcagagagta taacatcccc agcgtccacg tggccaaagt ctcccatggg
240
tggctgtatg agggcctgag cagggagaaa gcagaggacc tgctgttgtt acctgggaac
300
cctggagggg ccttcctcat ccgggagagc cagaccagga gaggctctta ctctctgtca
360
gtccgcctca gccgccctgc atcctgggac cggatcagac actacaggat ccactgcctt
420
gacaatggct ggctgtacat ctcaccgcgc ctcaccttcc cctcactcca ggccctggtg
480
gaccattact ctgagctggc ggatgacatc tgctgcctac tcaaggagcc ctgtgtcctg
540
cagagggctg gcccgctccc tggcaaggat ataccctac ctgtgactgt gcagaggaca
600
ccactcaact ggaaagagct ggacagctcc ctcctgtttt ctgaagctgc cacaggggag
660
gagtctcttc tcagtgaggg tctccgggag tccctcagct tctacatcag cctgaatgac
720
gaggctgtct ctttggatga tgcctaggcc caaaggagag gccaaaaggg aaaccaaggc
780
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837

<210> 5514
<211> 248
<212> PRT
<213> Homo sapiens

<400> 5514
Xaa Ser Leu Ser Ser Ser Val Gln Gly Gln Gly Pro Val Thr Met Glu
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Ala Glu Arg Ser Lys Ala Thr Ala Ala Ala Leu Gly Ser Phe Pro Ala
20 25 30
Gly Gly Pro Ala Glu Leu Ser Leu Arg Leu Gly Glu Pro Leu Thr Ile
35 40 45
Val Ser Glu Asp Gly Asp Trp Trp Thr Val Leu Ser Glu Val Ser Gly
50 55 60
Arg Glu Tyr Asn Ile Pro Ser Val His Val Ala Lys Val Ser His Gly
65 70 75 80
Trp Leu Tyr Glu Gly Leu Ser Arg Glu Lys Ala Glu Asp Leu Leu Leu
85 90 95
Leu Pro Gly Asn Pro Gly Gly Ala Phe Leu Ile Arg Glu Ser Gln Thr
100 105 110
Arg Arg Gly Ser Tyr Ser Leu Ser Val Arg Leu Ser Arg Pro Ala Ser
115 120 125
Trp Asp Arg Ile Arg His Tyr Arg Ile His Cys Leu Asp Asn Gly Trp
130 135 140
Leu Tyr Ile Ser Pro Arg Leu Thr Phe Pro Ser Leu Gln Ala Leu Val
145 150 155 160
Asp His Tyr Ser Glu Leu Ala Asp Asp Ile Cys Cys Leu Leu Lys Glu

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                165                 170                 175
Pro Cys Val Leu Gln Arg Ala Gly Pro Leu Pro Gly Lys Asp Ile Pro
            180                 185                 190
Leu Pro Val Thr Val Gln Arg Thr Pro Leu Asn Trp Lys Glu Leu Asp
        195                 200                 205
Ser Ser Leu Leu Phe Ser Glu Ala Ala Thr Gly Glu Glu Ser Leu Leu
    210                 215                 220
Ser Glu Gly Leu Arg Glu Ser Leu Ser Phe Tyr Ile Ser Leu Asn Asp
225                 230                 235                 240
Glu Ala Val Ser Leu Asp Asp Ala
                245
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<210> 5515
<211> 420
<212> DNA
<213> Homo sapiens

<400> 5515
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gaaaggatgt ccgcacagct ggctgctgct gagagcagac aaaagaagct ggaaatggag
120
aagcttcagc tacaagccct tgagcaagag cacaagaagc tggctgcccg ccttgaggaa
180
gagcgtggca agaacaagca ggtggtcctg atgctggtca aagagtgcaa gcagctctca
240
agcaaagtca tagaggaggc ccagaagctc gaagacgtaa tggccaaact ggcttcttct
300
ctttgtcacc agcacctgct tcatagtctc tctggagtgc caggaacggg tcatatagat
360
taaatctccc ataccgttcc tggataaata cctccttcct gcgagcccgc agggcctcga
420

<210> 5516
<211> 120
<212> PRT
<213> Homo sapiens

<400> 5516
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Val Cys Thr Asn Pro Leu Ser Ile Leu Glu Ala Val Met Ala His Cys
 1               5                  10                  15
Lys Lys Met Gln Glu Arg Met Ser Ala Gln Leu Ala Ala Ala Glu Ser
            20                  25                  30
Arg Gln Lys Lys Leu Glu Met Glu Lys Leu Gln Leu Gln Ala Leu Glu
        35                  40                  45
Gln Glu His Lys Lys Leu Ala Ala Arg Leu Glu Glu Glu Arg Gly Lys
    50                  55                  60
Asn Lys Gln Val Val Leu Met Leu Val Lys Glu Cys Lys Gln Leu Ser
65                  70                  75                  80
Ser Lys Val Ile Glu Glu Ala Gln Lys Leu Glu Asp Val Met Ala Lys
                85                  90                  95
Leu Ala Ser Ser Leu Cys His Gln His Leu Leu His Ser Leu Ser Gly
            100                 105                 110
Val Pro Gly Thr Gly His Ile Asp
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115 120

<210> 5517
<211> 804
<212> DNA
<213> Homo sapiens

<400> 5517
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gtactgtact gttgtgatct actgattggc attggcatag tagtagggtc aagtgacaga
120
atccgtgcca gcagtctcca ggttcagaag caattcaaga ccctgatgat agctctccag
180
caaccaacac atggtgacat ggtgattgtg ccaacttgtt gctcagttat atgcagggcc
240
agtgattggt ttaagtgaag accatggttg agatcatttg tctttggtct aatagaattt
300
gagctagtag aatttgagtc tccagggaaa gagctacttg accaaattaa actagtagca
360
ggtagagcat gaatgacagc atattatacc atcaagatgt tcttagagca gtgtatggat
420
ggatcgattg tactgccatc agttgtgact gacgttgtat tcaaggagaa agagaaactt
480
gtttagaaag cactttgaaa gttttttgag tacgggggtg ccctgtatca ccccgttatg
540
gttgaacttt ctccttcaaa attaccagac ttggcagcag tggcaaatta ttgggctaaa
600
agacttaatc agacatattc tgggttcaag gctcctaata taatacctgg tgcaaacatt
660
atacttccac tcattcagat ggttgcatcc tgccaggcat ccagtgggac tgggaatatg
720
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780
tcagttctct atattaaaaa aaaa
804

<210> 5518
<211> 85
<212> PRT
<213> Homo sapiens

<400> 5518
Xaa Val Trp Pro Lys His Lys Gly Lys Asp Pro Gln Phe Thr Phe Leu
1 5 10 15
Glu Leu Ser Ser Val Leu Tyr Cys Cys Asp Leu Leu Ile Gly Ile Gly
20 25 30
Ile Val Val Gly Ser Ser Asp Arg Ile Arg Ala Ser Ser Leu Gln Val
35 40 45
Gln Lys Gln Phe Lys Thr Leu Met Ile Ala Leu Gln Gln Pro Thr His
50 55 60
Gly Asp Met Val Ile Val Pro Thr Cys Cys Ser Val Ile Cys Arg Ala
65 70 75 80
Ser Asp Trp Phe Lys

85

<210> 5519
<211> 401
<212> DNA
<213> Homo sapiens

<400> 5519
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tccttcgcat aacttgtaca ggggtaggta gcataaaaga cagccggtct caagaagcaa
120
ccatgcgcct cactacttac catgttcctg cgggcattcc cctcccgaag ggagtctctg
180
aaaacaaaca cacacagaag ttggcgctgg gcaccacatt ctcctcttga cctaaccatc
240
aggaatttgc tgtgccatct gttcataaaa cttagccagg cccagaaagc ttgtcccaac
300
cacatgctaa gagccaagca gatggaacag aagctccccc aagctgctgg ctcccactat
360
ggctgggatg aagcaagaac ctgggcccac acaggctgca a
401

<210> 5520
<211> 101
<212> PRT
<213> Homo sapiens

<400> 5520
Met Trp Leu Gly Gln Ala Phe Trp Ala Trp Leu Ser Phe Met Asn Arg
1 5 10 15
Trp His Ser Lys Phe Leu Met Val Arg Ser Arg Gly Glu Cys Gly Ala
20 25 30
Gln Arg Gln Leu Leu Cys Val Phe Val Phe Arg Asp Ser Leu Arg Glu
35 40 45
Gly Asn Ala Arg Arg Asn Met Val Ser Ser Glu Ala His Gly Cys Phe
50 55 60
Leu Arg Pro Ala Val Phe Tyr Ala Thr Tyr Pro Cys Thr Ser Tyr Ala
65 70 75 80
Lys Glu Thr Lys Pro Ser Ala Cys Leu Phe Pro Leu Leu Ile Ile Gly
85 90 95
Lys Trp Met Leu Trp
100

<210> 5521
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 5521
nggggggagct cgcccgctgt ccgccagccc gcgggaggga ggagagaagc gaagcgtttc
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cgcggttggc tactcagtgt cttggtctca agttgcctca ttgcggctgg cgttcccaat
120

acagacgcat cgtttctttt ttaatactcc ctaagaaagg gaataacctt caagctggcg
180
ggagcaatgg ttcacataaa gaaaggcgag ctgacccagg aggagaagga gctactggaa
240
gtcatcggga aaggtactgt ccaagaagct ggaacattat tatccagcaa gaatgttcgt
300
gtcaactgtt tggacgagaa tggaatgact cctctaatgc atgcagcata taaaggaaaa
360
ctcgatatgt gcaaattact actgcgacat ggagccgatg taaattgtca tcagcatgaa
420
catggataca cagccctcat gtttgctgca ctttctggta ataaagacat cacatgggta
480
atgttagagg ctggtgctga gacagatgtt gtcaactctg tgggaagaac agcagctcag
540
atggcagcct ttgtgggtca acatgattgt gtgaccataa tcaacaattt ctttcctcga
600
gagagactgg attattacac taagccccag ggactggata aagagccaaa actgccccca
660
aagttggcag gcccgctgca caaaattatc accacaacga atcttcatcc tgtcaagatc
720
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780
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900
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960
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1260
aatctgaagg acatttacga aaagcaacag ttggaggctg ccaaagaaaa gagacaagag
1320
gaaaaccacg gcaaacttga tgtcaattct aactgtgtta atgaagagca accagaggct
1380
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1440
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1740

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1800
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1860
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2160
aaggcatatt gacggttctc tcagcgtatg cattaaaaaa ggtacttcct gaaacttttg
2220
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2280
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2340
gaaactgatt tgtaactcat ttagagaatg tcctggcgtc ggtttttagc atatgtggta
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2520
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2524

<210> 5522
<211> 441
<212> PRT
<213> Homo sapiens

<400> 5522
Met Val His Ile Lys Lys Gly Glu Leu Thr Gln Glu Glu Lys Glu Leu
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Leu Glu Val Ile Gly Lys Gly Thr Val Gln Glu Ala Gly Thr Leu Leu
            20   25   30
Ser Ser Lys Asn Val Arg Val Asn Cys Leu Asp Glu Asn Gly Met Thr
        35   40   45
Pro Leu Met His Ala Ala Tyr Lys Gly Lys Leu Asp Met Cys Lys Leu
    50   55   60
Leu Leu Arg His Gly Ala Asp Val Asn Cys His Gln His Glu His Gly
65   70   75   80
Tyr Thr Ala Leu Met Phe Ala Ala Leu Ser Gly Asn Lys Asp Ile Thr
                85   90   95
Trp Val Met Leu Glu Ala Gly Ala Glu Thr Asp Val Val Asn Ser Val
            100   105   110
Gly Arg Thr Ala Ala Gln Met Ala Ala Phe Val Gly Gln His Asp Cys
        115   120   125
Val Thr Ile Ile Asn Asn Phe Phe Pro Arg Glu Arg Leu Asp Tyr Tyr
    130   135   140
Thr Lys Pro Gln Gly Leu Asp Lys Glu Pro Lys Leu Pro Pro Lys Leu

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145                 150                 155                 160
Ala Gly Pro Leu His Lys Ile Ile Thr Thr Thr Asn Leu His Pro Val
                165                 170                 175
Lys Ile Val Met Leu Val Asn Glu Asn Pro Leu Leu Thr Glu Glu Ala
            180                 185                 190
Ala Leu Asn Lys Cys Tyr Arg Val Met Asp Leu Ile Cys Glu Lys Cys
        195                 200                 205
Met Lys Gln Arg Asp Met Asn Glu Val Leu Ala Met Lys Met His Tyr
    210                 215                 220
Ile Ser Cys Ile Phe Gln Lys Cys Ile Asn Phe Leu Lys Asp Gly Glu
225                 230                 235                 240
Asn Lys Leu Asp Thr Leu Ile Lys Ser Leu Leu Lys Gly Arg Ala Ser
                245                 250                 255
Asp Gly Phe Pro Val Tyr Gln Glu Lys Ile Ile Arg Glu Ser Ile Arg
            260                 265                 270
Lys Phe Pro Tyr Cys Glu Ala Thr Leu Leu Gln Gln Leu Val Arg Ser
        275                 280                 285
Ile Ala Pro Val Glu Ile Gly Ser Asp Pro Thr Ala Phe Ser Val Leu
    290                 295                 300
Thr Gln Ala Ile Thr Gly Gln Val Gly Phe Val Asp Val Glu Phe Cys
305                 310                 315                 320
Thr Thr Cys Gly Glu Lys Gly Ala Ser Lys Arg Cys Ser Val Cys Lys
                325                 330                 335
Met Val Ile Tyr Cys Asp Gln Thr Cys Gln Lys Thr His Trp Phe Thr
            340                 345                 350
His Lys Lys Ile Cys Lys Asn Leu Lys Asp Ile Tyr Glu Lys Gln Gln
        355                 360                 365
Leu Glu Ala Ala Lys Glu Lys Arg Gln Glu Glu Asn His Gly Lys Leu
    370                 375                 380
Asp Val Asn Ser Asn Cys Val Asn Glu Glu Gln Pro Glu Ala Glu Val
385                 390                 395                 400
Gly Ile Ser Gln Arg Asp Ser Asn Pro Glu Asp Ser Gly Glu Gly Lys
                405                 410                 415
Lys Glu Ser Leu Glu Ser Glu Ala Glu Leu Glu Gly Leu Gln Asp Ala
            420                 425                 430
Pro Ala Gly Pro Gln Val Ser Glu Glu
        435                 440
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<210> 5523
<211> 6190
<212> DNA
<213> Homo sapiens

<400> 5523
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120
gaagcaggct gcgggccgtc ccagcacgac gtggagcccc gcggagacct cgagatgccc
180
cgcggggaag ctcctggccc cgggagacgg ggggctaagg acgaggccct gggcgaagaa
240
tcgggggagc ggtggagccc cgagttccat ctgcagagga aattggcgga cagcagccac
300

agtgaacagc aagatcgaaa cagagtttct gaagaactta tcatggttgt ccaagaaatg
360
aaaaaatact tcccctcgga gagacgcaat aaaccaagca ctctagatgc cctcaactat
420
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480
aatggagcac ctcaggcaga tgtgagcatg tacagtcttg aggagctggc cactatcgct
540
tcagaacaca cttccaaaaa cacagatacc tttgtggcag tattttcatt tctgtctgga
600
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720
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840
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900
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960
gaagctcctc ggatcccagt gaataaaaga atcttcacca ccacacacac cccagggtgt
1020
gtttttcttg aagtagatga aaaagcagtg cctttgctgg gttacctacc tcaggacctg
1080
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1380
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1560
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1620
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1680
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1860
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1920

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1980
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2040
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2280
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2520
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2580
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2640
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2700
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2760
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<212> PRT
<213> Homo sapiens

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35 40 45
Asn Arg Val Ser Glu Glu Leu Ile Met Val Val Gln Glu Met Lys Lys
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Tyr Phe Pro Ser Glu Arg Arg Asn Lys Pro Ser Thr Leu Asp Ala Leu
65 70 75 80
Asn Tyr Ala Leu Arg Cys Val His Ser Val Gln Ala Asn Ser Glu Phe

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Asn Thr Asp Thr Phe Val Ala Val Phe Ser Phe Leu Ser Gly Arg Leu
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Val His Ile Ser Glu Gln Ala Ala Leu Ile Leu Asn Arg Lys Lys Asp
145                 150                 155                 160
Val Leu Ala Ser Ser His Phe Val Asp Leu Leu Ala Pro Gln Asp Met
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Arg Val Phe Tyr Ala His Thr Ala Arg Ala Gln Leu Pro Phe Trp Asn
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Asn Trp Thr Gln Arg Ala Ala Arg Tyr Glu Cys Ala Pro Val Lys Pro
        195                 200                 205
Phe Phe Cys Arg Ile Arg Gly Gly Glu Asp Arg Lys Gln Glu Lys Cys
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His Ser Pro Phe Arg Ile Ile Pro Tyr Leu Ile His Val His His Pro
225                 230                 235                 240
Ala Gln Pro Glu Leu Glu Ser Glu Pro Cys Cys Leu Thr Val Val Glu
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Lys Ile His Ser Gly Tyr Glu Ala Pro Arg Ile Pro Val Asn Lys Arg
            260                 265                 270
Ile Phe Thr Thr Thr His Thr Pro Gly Cys Val Phe Leu Glu Val Asp
        275                 280                 285
Glu Lys Ala Val Pro Leu Leu Gly Tyr Leu Pro Gln Asp Leu Ile Gly
    290                 295                 300
Thr Ser Ile Leu Ser Tyr Leu His Pro Glu Asp Arg Ser Leu Met Val
305                 310                 315                 320
Ala Ile His Gln Lys Gly His Pro Pro Phe Glu His Ser Pro Ile Arg
                325                 330                 335
Phe Cys Thr Gln Asn Gly Asp Tyr Ile Ile Leu Asp Ser Ser Trp Ser
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Ser Phe Val Asn Pro Trp Ser Arg Lys Ile Ser Phe Ile Ile Gly Arg
        355                 360                 365
His Lys Val Arg Thr Ser Pro Leu Asn Glu Asp Val Phe Ala Thr Lys
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385                 390                 395                 400
Gln Ile Tyr Lys Leu Leu Leu Gln Pro Val His Val Ser Val Ser Ser
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Gly Tyr Gly Ser Leu Gly Ser Ser Gly Ser Gln Glu Gln Leu Val Ser
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Ile Ala Ser Ser Ser Glu Ala Ser Gly His Arg Val Glu Glu Thr Lys
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Ala Glu Gln Met Thr Leu Gln Gln Val Tyr Ala Ser Val Asn Lys Ile
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Lys Asn Leu Gly Gln Gln Leu Tyr Ile Glu Ser Met Thr Lys Ser Ser
465                 470                 475                 480
Phe Lys Pro Val Thr Gly Thr Arg Thr Glu Pro Asn Gly Gly Gly Glu
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Cys Lys Thr Phe Thr Ser Phe His Gln Thr Leu Lys Asn Asn Ser Val
            500                 505                 510
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Thr Ser Ser Ser Ser Glu Glu Asp Lys Gln Asn His Lys Ala Asp Asp
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Val Gln Ala Leu Gln Gly Asn Lys Asn Ala Pro Gln Lys Met Pro Thr
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Asn Gly Arg Ser Ile Asp Thr Gly Gly Gly Ala Pro Gln Ile Leu Ser
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Thr Ala Met Leu Ser Leu Gly Ser Gly Ile Ser Gln Cys Gly Tyr Ser
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Ser Thr Ile Val His Val Pro Pro Pro Glu Thr Ala Arg Asp Ala Thr
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Leu Phe Cys Glu Pro Trp Thr Leu Asn Met Gln Pro Ala Pro Leu Thr
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Ser Glu Glu Phe Lys His Val Gly Leu Thr Ala Ala Val Leu Ser Ala
            660                 665                 670
His Thr Gln Lys Glu Glu Gln Asn Tyr Val Asp Lys Phe Arg Glu Lys
        675                 680                 685
Ile Leu Ser Ser Pro Tyr Ser Ser Tyr Leu Gln Gln Glu Ser Arg Ser
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Lys Ala Lys Tyr Ser Tyr Phe Gln Gly Asp Ser Thr Ser Lys Gln Thr
705                 710                 715                 720
Arg Ser Ala Gly Cys Arg Lys Gly Lys His Lys Arg Lys Lys Leu Pro
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Glu Pro Pro Asp Ser Ser Ser Ser Asn Thr Gly Ser Gly Pro Arg Arg
            740                 745                 750
Gly Ala His Gln Asn Ala Gln Pro Cys Cys Pro Ser Ala Ala Ser Ser
        755                 760                 765
Pro His Thr Ser Ser Pro Thr Phe Pro Pro Ala Ala Met Val Pro Ser
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Gln Ala Pro Tyr Leu Val Pro Ala Phe Pro Leu Pro Ala Ala Thr Ser
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Pro Gly Arg Glu Tyr Ala Ala Pro Gly Thr Ala Pro Glu Gly Leu His
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Gly Pro Pro Leu Ser Glu Gly Leu Gln Pro Tyr Pro Ala Phe Pro Phe
            820                 825                 830
Pro Tyr Leu Asp Thr Phe Met Thr Val Phe Leu Pro Asp Pro Pro Val
        835                 840                 845
Cys Pro Leu Leu Ser Pro Ser Phe Leu Pro Cys Pro Phe Leu Gly Ala
    850                 855                 860
Thr Ala Ser Ser Ala Ile Ser Pro Ser Met Ser Ser Ala Met Ser Pro
865                 870                 875                 880
Thr Leu Asp Pro Pro Pro Ser Val Thr Ser Gln Arg Arg Glu Glu Glu
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Lys Trp Glu Ala Gln Ser Glu Gly His Pro Phe Ile Thr Ser Arg Ser
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Ser Ser Pro Leu Gln Leu Asn Leu Leu Gln Glu Glu Met Pro Arg Pro
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Ser Glu Ser Pro Asp Gln Met Arg Arg Asn Thr Cys Pro Gln Thr Glu
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980 985 990
Ser His Pro Thr Ala Ser Ala Leu Ser Thr Gly Ser Pro Pro Met Lys
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Pro Pro Ser Glu Ser Pro Ser Arg Thr Gly Ser Ala Ala Ser Gly Ser
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1105 1110 1115 1120
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1125 1130 1135
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1140 1145 1150
Trp Ile Gln Ser Gln Thr Val Thr Gln Glu Ile Asp Ile Gln Ala Cys
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<213> Homo sapiens

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<213> Homo sapiens

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35 40 45
Glu Ile Thr Gln Leu Glu Ser Trp Glu Glu Pro Phe Met Pro Ala Trp
50 55 60
Glu Val Val Thr Ser Ala Ile Pro Arg Glu Thr Leu Arg Met Ala Phe
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Met Arg Glu Leu Ala Ile Glu His His Ser Ser Lys Tyr Ala His Trp
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Arg Gln Asp Glu Asn Ser
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<210> 5527
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<212> DNA
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<212> PRT
<213> Homo sapiens

<400> 5528
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35 40 45
Tyr Leu Ala Thr Val Gln Ala Ile Ala Leu Gly Thr Arg Phe Ile Ile
50 55 60
Glu Ala Met Glu Ala Ala Gly His Ser Ile Ser Thr Leu Phe Leu Cys
65 70 75 80
Gly Gly Leu Ser Lys Asn Pro Leu Phe Val Gln Met His Ala Asp Ile
85 90 95
Thr Gly Met Pro Val Val Leu Ser Gln Glu Val Glu Ser Val Leu Val
100 105 110
Gly Ala Ala Val Leu Gly Ala Cys Ala Ser Gly Asp Phe Ala Ser Val
115 120 125
Gln Glu Ala Met Ala Lys Met Ser Lys Val Gly Lys Val Val Phe Pro
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Arg Leu Gln Asp Lys Lys Tyr Tyr Asp Lys Lys Tyr Gln Val Phe Leu
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<212> DNA
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<211> 603
<212> PRT
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Leu Asn Leu Cys Ala Arg Arg Arg Thr Arg Val Gln Arg Pro Ile Val
35 40 45
Arg Leu Leu Ser Cys Pro Gly Thr Val Ala Lys Asp Leu Arg Arg Asp
50 55 60
Glu Gln Pro Ser Gly Ser Val Glu Thr Gly Phe Glu Asp Lys Ile Pro
65 70 75 80
Lys Arg Arg Phe Ser Glu Met Gln Asn Glu Arg Arg Glu Gln Ala Gln
85 90 95
Arg Thr Val Leu Ile His Cys Pro Glu Lys Ile Ser Glu Asn Lys Phe
100 105 110
Leu Lys Tyr Leu Ser Gln Phe Gly Pro Ile Asn Asn His Phe Phe Tyr
115 120 125
Glu Ser Phe Gly Leu Tyr Ala Val Val Glu Phe Cys Gln Lys Glu Ser
130 135 140
Ile Gly Ser Leu Gln Asn Gly Thr His Thr Pro Ser Thr Ala Met Glu

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Thr Ala Ile Pro Phe Arg Ser Arg Phe Phe Asn Leu Lys Leu Lys Asn
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Gln Thr Ser Glu Arg Ser Arg Val Arg Ser Ser Asn Gln Leu Pro Arg
            180                 185                 190
Ser Asn Lys Gln Leu Phe Glu Leu Leu Cys Tyr Ala Glu Ser Ile Asp
        195                 200                 205
Asp Gln Leu Asn Thr Leu Leu Lys Glu Phe Gln Leu Thr Glu Glu Asn
    210                 215                 220
Thr Lys Leu Arg Tyr Leu Thr Cys Ser Leu Ile Glu Asp Met Ala Ala
225                 230                 235                 240
Ala Tyr Phe Pro Asp Cys Ile Val Arg Pro Phe Gly Ser Ser Val Asn
                245                 250                 255
Thr Phe Gly Lys Leu Gly Cys Asp Leu Asp Met Phe Leu Asp Leu Asp
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Glu Thr Arg Asn Leu Ser Ala His Lys Ile Ser Gly Asn Phe Leu Met
        275                 280                 285
Glu Phe Gln Val Lys Asn Val Pro Ser Glu Arg Ile Ala Thr Gln Lys
    290                 295                 300
Ile Leu Ser Val Leu Gly Glu Cys Leu Asp His Phe Gly Pro Gly Cys
305                 310                 315                 320
Val Gly Val Gln Lys Ile Leu Asn Ala Arg Cys Pro Leu Val Arg Phe
                325                 330                 335
Ser His Gln Ala Ser Gly Phe Gln Cys Asp Leu Thr Thr Asn Asn Arg
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Ile Ala Leu Thr Ser Ser Glu Leu Leu Tyr Ile Tyr Gly Ala Leu Asp
        355                 360                 365
Ser Arg Val Arg Ala Leu Val Phe Ser Val Arg Cys Trp Ala Arg Ala
    370                 375                 380
His Ser Leu Thr Ser Ser Ile Pro Gly Ala Trp Ile Thr Asn Phe Ser
385                 390                 395                 400
Leu Thr Met Met Val Ile Phe Phe Leu Gln Arg Arg Ser Pro Pro Ile
                405                 410                 415
Leu Pro Thr Leu Asp Ser Leu Lys Thr Leu Ala Asp Ala Glu Asp Lys
            420                 425                 430
Cys Val Ile Glu Gly Asn Asn Cys Thr Phe Val Arg Asp Leu Ser Arg
        435                 440                 445
Ile Lys Pro Ser Gln Asn Thr Glu Thr Leu Glu Leu Leu Leu Lys Glu
    450                 455                 460
Phe Phe Glu Tyr Phe Gly Asn Phe Ala Phe Asp Lys Asn Ser Ile Asn
465                 470                 475                 480
Ile Arg Gln Gly Arg Glu Gln Asn Lys Pro Asp Ser Ser Pro Leu Tyr
                485                 490                 495
Ile Gln Asn Pro Phe Glu Thr Ser Leu Asn Ile Ser Lys Asn Val Ser
            500                 505                 510
Gln Ser Gln Leu Gln Lys Phe Val Asp Leu Ala Arg Glu Ser Ala Trp
        515                 520                 525
Ile Leu Gln Gln Glu Asp Thr Asp Arg Pro Ser Ile Ser Ser Asn Arg
    530                 535                 540
Pro Trp Gly Leu Val Ser Leu Leu Leu Pro Ser Ala Pro Asn Arg Lys
545                 550                 555                 560
Ser Phe Thr Lys Lys Lys Ser Asn Lys Phe Ala Ile Glu Thr Val Lys
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<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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35 40 45
Glu Asn Gly Gln Arg Lys Tyr Gly Gly Pro Pro Pro Gly Trp Glu Gly
50 55 60
Pro His Pro Gln Arg Gly Cys Glu Val Phe Val Gly Lys Ile Pro Arg
65 70 75 80
Asp Val Tyr Glu Asp Glu Leu Val Pro Val Phe Glu Ala Val Gly Arg
85 90 95
Ile Tyr Glu Leu Arg Leu Met Met Asp Phe Asp Gly Lys Asn Arg Gly
100 105 110
Tyr Ala Phe Val Met Tyr Cys His Lys His Glu Ala Lys Arg Ala Val
115 120 125
Arg Glu Leu Asn Asn Tyr Glu Ile Arg Pro Gly Arg Leu Leu Gly Val
130 135 140
Cys Cys Ser Val Asp Asn Cys Arg Leu Phe Ile Gly Gly Ile Pro Lys
145 150 155 160
Met Lys Lys Arg Glu Glu Ile Leu Glu Glu Ile Ala Lys Val Thr Glu
165 170 175
Gly Val Leu Asp Val Ile Val Tyr Ala Ser Ala Ala Asp Lys Met Lys
180 185 190
Asn Arg Gly Phe Ala Phe Val Glu Tyr Glu Ser His Arg Ala Ala Ala
195 200 205
Met Ala Arg Arg Lys Leu Met Pro Gly Arg Ile Gln Leu Trp Gly His
210 215 220
Gln Ile Ala Val Asp Trp Ala Glu Pro Glu Ile Asp Val Asp Glu Asp
225 230 235 240
Val Met Glu Thr Val Lys Ile Leu Tyr Val Arg Asn Leu Met Ile Glu
245 250 255
Thr Thr Glu Asp Thr Ile Lys Lys Ser Phe Gly Gln Phe Asn Pro Gly
260 265 270
Cys Val Glu Arg Val Lys Lys Ile Arg Asp Tyr Ala Phe Val His Phe
275 280 285
Thr Ser Arg Glu Asp Ala Val His Ala Met Asn Asn Leu Asn Gly Thr
290 295 300
Glu Leu Glu Gly Ser Cys Leu Glu Val Thr Leu Ala Lys Pro Val Asp
305 310 315 320
Lys Glu Gln Tyr Ser Arg Tyr Gln Lys Ala Ala Arg Gly Gly Gly Ala
325 330 335
Ala Glu Ala Ala Gln Gln Pro Ser Tyr Val Tyr Ser Cys Asp Pro Tyr

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            340                 345                 350
Thr Leu Ala Tyr Tyr Gly Tyr Pro Tyr Asn Ala Leu Ile Gly Pro Asn
        355                 360                 365
Arg Asp Tyr Phe Val Lys Ala Gly Ser Ile Arg Gly Arg Gly Arg Gly
    370                 375                 380
Ala Ala Gly Asn Arg Ala Pro Gly Pro Arg Gly Ser Tyr Leu Gly Gly
385                 390                 395                 400
Tyr Ser Ala Gly Arg Gly Ile Tyr Ser Arg Tyr His Glu Gly Lys Gly
                405                 410                 415
Lys Gln Gln Glu Lys Gly Tyr Glu Leu Val Pro Asn Leu Glu Ile Pro
            420                 425                 430
Thr Val Asn Pro Val Ala Ile Lys Pro Gly Thr Val Ala Ile Pro Ala
        435                 440                 445
Ile Gly Ala Gln Tyr Ser Met Phe Pro Ala Ala Pro Ala Pro Lys Met
    450                 455                 460
Ile Glu Asp Gly Lys Ile His Thr Val Glu His Met Ile Ser Pro Ile
465                 470                 475                 480
Ala Val Gln Pro Asp Pro Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala
                485                 490                 495
Ala Ala Ala Ala Ala Ala Val Ile Pro Thr Val Ser Thr Pro Pro Pro
            500                 505                 510
Phe Gln Gly Arg Pro Ile Thr Pro Val Tyr Thr Val Ala Pro Asn Val
        515                 520                 525
Gln Arg Ile Pro Thr Ala Gly Ile Tyr Gly Ala Ser Tyr Val Pro Phe
    530                 535                 540
Ala Ala Pro Ala Thr Ala Thr Ile Ala Thr Leu Gln Lys Asn Ala Ala
545                 550                 555                 560
Ala Ala Ala Ala Val Tyr Gly Gly Tyr Ala Gly Tyr Ile Pro Gln Ala
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Phe Pro Ala Ala Ala Ile Gln Val Pro Ile Pro Asp Val Tyr Gln Thr
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<211> 505
<212> DNA
<213> Homo sapiens

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240
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300
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<211> 168
<212> PRT
<213> Homo sapiens

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Tyr Arg Arg Gly Leu Ser Lys Tyr Glu Ser Ile Asp Glu Asp Glu Leu
        35   40   45
Leu Ala Ser Leu Ser Ala Glu Glu Leu Lys Glu Leu Glu Arg Glu Leu
    50   55   60
Glu Asp Ile Glu Pro Asp Arg Asn Leu Pro Val Gly Leu Arg Gln Lys
65   70   75   80
Ser Leu Thr Glu Lys Thr Pro Thr Gly Thr Phe Ser Arg Glu Ala Leu
                85   90   95
Met Ala Tyr Trp Glu Lys Glu Ser Gln Lys Leu Leu Glu Lys Glu Arg
            100   105   110
Leu Gly Glu Cys Gly Lys Val Ala Glu Asp Lys Glu Glu Ser Glu Glu
        115   120   125
Glu Leu Ile Phe Thr Glu Ser Asn Ser Glu Val Ser Glu Glu Val Tyr
    130   135   140
Thr Glu Glu Glu Glu Glu Glu Ser Gln Glu Glu Glu Glu Glu Glu Asp
145   150   155   160
Ser Asp Glu Glu Glu Arg Thr Ile
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<210> 5535
<211> 1887
<212> DNA
<213> Homo sapiens

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1887

<210> 5536
<211> 306
<212> PRT

<213> Homo sapiens

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35 40 45
Arg Glu Glu Asp Asp Glu Leu Leu Gly Asn Asp Asp Ser Asp Lys Thr
50 55 60
Glu Leu Leu Ala Gly Gln Lys Lys Ser Ser Pro Phe Trp Thr Phe Glu
65 70 75 80
Tyr Tyr Gln Thr Phe Phe Asp Val Asp Thr Tyr Gln Val Phe Asp Arg
85 90 95
Ile Lys Gly Ser Leu Leu Pro Ile Pro Gly Lys Asn Phe Val Arg Leu
100 105 110
Tyr Ile Arg Ser Asn Pro Asp Leu Tyr Gly Pro Phe Trp Ile Cys Ala
115 120 125
Thr Leu Val Phe Ala Ile Ala Ile Ser Gly Asn Leu Ser Asn Phe Leu
130 135 140
Ile His Leu Gly Glu Lys Thr Tyr His Tyr Val Pro Glu Phe Arg Lys
145 150 155 160
Val Ser Ile Ala Ala Thr Ile Ile Tyr Ala Tyr Ala Trp Leu Val Pro
165 170 175
Leu Ala Leu Trp Gly Phe Leu Met Trp Arg Asn Ser Lys Val Met Asn
180 185 190
Ile Val Ser Tyr Ser Phe Leu Glu Ile Val Cys Val Tyr Gly Tyr Ser
195 200 205
Leu Phe Ile Tyr Ile Pro Thr Ala Ile Leu Trp Ile Ile Pro Gln Lys
210 215 220
Ala Val Arg Trp Ile Leu Val Met Ile Ala Leu Gly Ile Ser Gly Ser
225 230 235 240
Leu Leu Ala Met Thr Phe Trp Pro Ala Val Arg Glu Asp Asn Arg Arg
245 250 255
Val Ala Leu Ala Thr Ile Val Thr Ile Val Leu Leu His Met Leu Leu
260 265 270
Ser Val Gly Cys Leu Ala Tyr Phe Phe Asp Ala Pro Glu Met Asp His
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Ser Ser
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<211> 2881
<212> DNA
<213> Homo sapiens

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120

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2881

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<212> PRT
<213> Homo sapiens

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Ala Glu Leu Arg His Leu Asp Thr Gln Val Gln Arg Cys Glu Asp Ile
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Leu Gln Gln Leu Gln Ala Val Val Pro Gln Ile Asp Met Glu Gly Asp

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Arg Asn Ile Trp Ile Val Lys Pro Gly Ala Lys Ser Arg Gly Arg Gly
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Ile Met Cys Met Asp His Leu Glu Glu Met Leu Lys Leu Val Asn Gly
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Asn Pro Val Val Met Lys Asp Gly Lys Trp Val Val Gln Lys Tyr Ile
            100                 105                 110
Glu Arg Pro Leu Leu Ile Phe Gly Thr Lys Phe Asp Leu Arg Gln Trp
        115                 120                 125
Phe Leu Val Thr Asp Trp Asn Pro Leu Thr Val Trp Phe Tyr Arg Asp
    130                 135                 140
Ser Tyr Ile Arg Phe Ser Thr Gln Pro Phe Ser Leu Lys Asn Leu Asp
145                 150                 155                 160
Asn Ser Val His Leu Cys Asn Asn Ser Ile Gln Lys His Leu Glu Asn
                165                 170                 175
Ser Cys His Arg His Pro Leu Leu Pro Pro Asp Asn Met Trp Ser Ser
            180                 185                 190
Gln Arg Phe Gln Ala His Leu Gln Glu Met Gly Ala Pro Asn Ala Trp
        195                 200                 205
Ser Thr Ile Ile Val Pro Gly Met Lys Asp Ala Val Ile His Ala Leu
    210                 215                 220
Gln Thr Ser Gln Asp Thr Val Gln Cys Arg Lys Ala Ser Phe Glu Leu
225                 230                 235                 240
Tyr Gly Ala Asp Phe Val Phe Gly Glu Asp Phe Gln Pro Trp Leu Ile
                245                 250                 255
Glu Ile Asn Ala Ser Pro Thr Met Ala Pro Ser Thr Ala Val Thr Ala
            260                 265                 270
Arg Leu Cys Ala Gly Val Gln Ala Asp Thr Leu Arg Val Val Ile Asp
        275                 280                 285
Arg Arg Leu Asp Arg Asn Cys Asp Thr Gly Ala Phe Glu Leu Ile Tyr
    290                 295                 300
Lys Gln Pro Val Thr Thr Ser Pro Ala Ser Thr Pro Arg Pro Ser Cys
305                 310                 315                 320
Leu Leu Pro Met Tyr Ser Asp Thr Arg Ala Arg Ser Ser Asp Asp Ser
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Thr Ala Ser Trp Trp Ala Leu Arg Pro Cys Arg Pro Gln Ala Arg Pro
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<210> 5539
<211> 1887
<212> DNA
<213> Homo sapiens

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600
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720
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780
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1887

<210> 5540
<211> 378
<212> PRT
<213> Homo sapiens

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35 40 45
Ala Pro Trp Cys Ser Val Ser Ser Gly Pro Ser Arg Tyr Val Leu Gly
50 55 60
Met Gln Glu Leu Phe Arg Gly His Ser Lys Thr Arg Glu Phe Leu Ala
65 70 75 80
His Ser Ala Lys Val His Ser Val Ala Trp Ser Cys Asp Gly Arg Arg
85 90 95
Leu Ala Ser Gly Ser Phe Asp Lys Thr Ala Ser Val Phe Leu Leu Glu
100 105 110
Arg Thr Gly Trp Ser Lys Lys Thr Ile Ile Gly Asp Met Gly Ile Xaa
115 120 125
Val Asp Gln Leu Cys Trp His Pro Ser Asn Pro Asp Leu Phe Val Thr
130 135 140
Ala Ser Gly Asp Lys Thr Ile Arg Ile Trp Asp Val Arg Thr Thr Lys
145 150 155 160
Cys Ile Ala Thr Val Asn Thr Lys Gly Glu Asn Ile Asn Ile Cys Trp
165 170 175
Ser Pro Asp Gly Gln Thr Ile Ala Val Gly Asn Lys Asp Asp Val Val
180 185 190
Thr Phe Ile Asp Ala Lys Thr His Arg Ser Lys Ala Glu Glu Gln Phe
195 200 205
Lys Phe Glu Val Asn Glu Ile Ser Trp Asn Asn Asp Asn Asn Met Phe
210 215 220
Phe Leu Thr Asn Gly Asn Gly Cys Ile Asn Ile Leu Ser Tyr Pro Glu
225 230 235 240
Leu Lys Pro Val Gln Ser Ile Asn Ala His Pro Ser Asn Cys Ile Cys
245 250 255
Ile Lys Phe Asp Pro Met Gly Lys Tyr Phe Ala Thr Gly Ser Ala Asp
260 265 270
Ala Leu Val Ser Leu Trp Asp Val Asp Glu Leu Val Cys Val Arg Cys
275 280 285
Phe Ser Arg Leu Asp Trp Pro Val Arg Thr Leu Ser Phe Ser His Asp
290 295 300
Gly Lys Met Leu Ala Ser Ala Ser Glu Asp His Phe Ile Asp Ile Ala
305 310 315 320
Glu Val Glu Thr Gly Asp Lys Leu Trp Glu Val Gln Cys Glu Ser Pro
325 330 335
Thr Phe Thr Val Ala Trp His Pro Lys Arg Pro Leu Leu Ala Phe Ala
340 345 350
Cys Asp Asp Lys Asp Gly Lys Tyr Asp Ser Ser Arg Glu Ala Gly Thr
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Val Lys Leu Phe Gly Leu Pro Asn Asp Ser

370 375

<210> 5541
<211> 1854
<212> DNA
<213> Homo sapiens

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180
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240
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300
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420
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480
agtgataatg aaaccagcag gaagaatgaa gaagtaatga cccattcggg gctgtggagg
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600
gatgctgact acgaacagga cacagccgaa tatctcctgc gagctgtgag ggcctccagt
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1740
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1854

<210> 5542
<211> 315
<212> PRT
<213> Homo sapiens

<400> 5542
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Trp Leu Tyr Ser Arg Gly Val Cys Arg Thr Lys Ser Thr Ser Asp Asn
35 40 45
Glu Thr Ser Arg Lys Asn Glu Glu Val Met Thr His Ser Gly Leu Trp
50 55 60
Arg Thr Cys Cys Leu Glu Gly Ala Phe Arg Gly Val Cys Lys Lys Ile
65 70 75 80
Asp His Phe Pro Glu Asp Ala Asp Tyr Glu Gln Asp Thr Ala Glu Tyr
85 90 95
Leu Leu Arg Ala Val Arg Ala Ser Ser Val Phe Pro Ile Leu Ser Val
100 105 110
Thr Leu Leu Phe Phe Gly Gly Leu Cys Val Ala Ala Ser Glu Phe His
115 120 125
Arg Ser Arg His Asn Val Ile Leu Ser Ala Gly Ile Phe Phe Val Ser
130 135 140
Ala Gly Leu Ser Asn Ile Ile Gly Ile Ile Val Tyr Ile Ser Ala Asn
145 150 155 160
Ala Gly Asp Pro Gly Gln Arg Asp Ser Lys Lys Ser Tyr Ser Tyr Gly
165 170 175
Trp Ser Phe Tyr Phe Gly Ala Phe Ser Phe Ile Ile Ala Glu Ile Val
180 185 190
Gly Val Val Ala Val His Ile Tyr Ile Glu Lys His Gln Gln Leu Arg
195 200 205
Ala Lys Ser His Ser Glu Phe Leu Lys Lys Ser Thr Phe Ala Arg Leu
210 215 220
Pro Pro Tyr Arg Tyr Arg Phe Arg Arg Arg Ser Ser Ser Arg Ser Thr
225 230 235 240
Glu Pro Arg Ser Arg Asp Leu Ser Pro Ile Ser Lys Gly Phe His Thr

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                245                 250                 255
Ile Pro Ser Thr Asp Ile Ser Met Phe Thr Leu Ser Arg Asp Pro Ser
            260                 265                 270
Lys Ile Thr Met Gly Thr Leu Leu Asn Ser Asp Arg Asp His Ala Phe
        275                 280                 285
Leu Gln Phe His Asn Ser Thr Pro Lys Glu Phe Lys Glu Ser Leu His
    290                 295                 300
Asn Asn Pro Ala Asn Arg Arg Thr Thr Pro Val
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<210> 5543
<211> 4021
<212> DNA
<213> Homo sapiens

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240
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1140
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4021

<210> 5544
<211> 1141
<212> PRT
<213> Homo sapiens

<400> 5544
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Ile Tyr Glu Thr Glu Ser Cys Phe Ser Ala Asp Gly Met Ser Gly Arg

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        35                  40                  45
Val Thr Val Glu Val Lys Pro Val Leu Pro Arg Ala Met Pro Ser Ser
    50                  55                  60
Met Gly Gly Gly Gly Gly Gly Ser Pro Ser Pro Val Glu Leu Arg Gly
65                  70                  75                  80
Ala Leu Val Gly Ser Val Asp Pro Thr Leu Arg Glu Gln Gln Leu Gln
                85                  90                  95
Gln Glu Leu Leu Ala Leu Lys Gln Gln Gln Gln Leu Gln Lys Gln Leu
            100                 105                 110
Leu Phe Ala Glu Phe Gln Lys Gln His Asp His Leu Thr Arg Gln His
        115                 120                 125
Glu Val Gln Leu Gln Lys His Leu Lys Gln Gln Gln Glu Met Leu Ala
    130                 135                 140
Ala Lys Gln Gln Gln Glu Met Leu Ala Ala Lys Arg Gln Gln Glu Leu
145                 150                 155                 160
Glu Gln Gln Arg Gln Arg Glu Gln Gln Arg Gln Glu Glu Leu Glu Lys
                165                 170                 175
Gln Arg Leu Glu Gln Gln Leu Leu Ile Leu Arg Asn Lys Glu Lys Ser
            180                 185                 190
Lys Glu Ser Ala Ile Ala Ser Thr Glu Val Lys Leu Arg Leu Gln Glu
        195                 200                 205
Phe Leu Leu Ser Lys Ser Lys Glu Pro Thr Pro Gly Gly Leu Asn His
    210                 215                 220
Ser Leu Pro Gln His Pro Lys Cys Trp Gly Ala His His Ala Ser Leu
225                 230                 235                 240
Asp Gln Ser Ser Pro Pro Gln Ser Gly Pro Pro Gly Thr Pro Pro Ser
                245                 250                 255
Tyr Lys Leu Pro Leu Pro Gly Pro Tyr Asp Ser Arg Asp Asp Phe Pro
            260                 265                 270
Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Val Arg Ser Arg Leu
        275                 280                 285
Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys
    290                 295                 300
Asp Gly Thr Val Ile Ser Thr Phe Lys Lys Arg Ala Val Glu Ile Thr
305                 310                 315                 320
Gly Ala Gly Pro Gly Ala Ser Ser Val Cys Asn Ser Ala Pro Gly Ser
                325                 330                 335
Gly Pro Ser Ser Pro Asn Ser Ser His Ser Thr Ile Ala Glu Asn Gly
            340                 345                 350
Phe Thr Gly Ser Val Pro Asn Ile Pro Thr Glu Met Leu Pro Gln His
        355                 360                 365
Arg Ala Leu Pro Leu Asp Ser Ser Pro Asn Gln Phe Ser Leu Tyr Thr
    370                 375                 380
Ser Pro Ser Leu Pro Asn Ile Ser Leu Gly Leu Gln Ala Thr Val Thr
385                 390                 395                 400
Val Thr Asn Ser His Leu Thr Ala Ser Pro Lys Leu Ser Thr Gln Gln
                405                 410                 415
Glu Ala Glu Arg Gln Ala Leu Gln Ser Leu Arg Gln Gly Gly Thr Leu
            420                 425                 430
Thr Gly Lys Phe Met Ser Thr Ser Ser Ile Pro Gly Cys Leu Leu Gly
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Val Ala Leu Glu Gly Asp Gly Ser Pro His Gly His Ala Ser Leu Leu
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Ala Val Pro Leu His Gly Gln Ser Pro Leu Val Thr Gly Glu Arg Val
                485                 490                 495
Ala Thr Ser Met Arg Thr Val Gly Lys Leu Pro Arg His Arg Pro Leu
            500                 505                 510
Ser Arg Thr Gln Ser Ser Pro Leu Pro Gln Ser Pro Gln Ala Leu Gln
        515                 520                 525
Gln Leu Val Met Gln Gln Gln His Gln Gln Phe Leu Glu Lys Gln Lys
    530                 535                 540
Gln Gln Gln Leu Gln Leu Gly Lys Ile Leu Thr Lys Thr Gly Glu Leu
545                 550                 555                 560
Pro Arg Gln Pro Thr Thr His Pro Glu Glu Thr Glu Glu Glu Leu Thr
                565                 570                 575
Glu Gln Gln Glu Val Leu Leu Gly Glu Gly Ala Leu Thr Met Pro Arg
            580                 585                 590
Glu Gly Ser Thr Glu Ser Glu Ser Thr Gln Glu Asp Leu Glu Glu Glu
        595                 600                 605
Asp Glu Glu Glu Asp Gly Glu Glu Glu Glu Asp Cys Ile Gln Val Lys
    610                 615                 620
Asp Glu Glu Gly Glu Ser Gly Ala Glu Glu Gly Pro Asp Leu Glu Glu
625                 630                 635                 640
Pro Gly Ala Gly Tyr Lys Lys Leu Phe Ser Asp Ala Gln Pro Leu Gln
                645                 650                 655
Pro Leu Gln Val Tyr Gln Ala Pro Leu Ser Leu Ala Thr Val Pro His
            660                 665                 670
Gln Ala Leu Gly Arg Thr Gln Ser Ser Pro Ala Ala Pro Gly Gly Met
        675                 680                 685
Lys Ser Pro Pro Asp Gln Pro Val Lys His Leu Phe Thr Thr Gly Val
    690                 695                 700
Val Tyr Asp Thr Phe Met Leu Lys His Gln Cys Met Cys Gly Asn Thr
705                 710                 715                 720
His Val His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg
                725                 730                 735
Leu Gln Glu Thr Gly Leu Leu Ser Lys Cys Glu Arg Ile Arg Gly Arg
            740                 745                 750
Lys Ala Thr Leu Asp Glu Ile Gln Thr Val His Ser Glu Tyr His Thr
        755                 760                 765
Leu Leu Tyr Gly Thr Ser Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys
    770                 775                 780
Lys Leu Leu Gly Pro Ile Ser Gln Lys Met Tyr Ala Val Leu Pro Cys
785                 790                 795                 800
Gly Gly Ile Gly Val Asp Ser Asp Thr Val Trp Asn Glu Met His Ser
                805                 810                 815
Ser Ser Ala Val Arg Met Ala Val Gly Cys Leu Leu Glu Leu Ala Phe
            820                 825                 830
Lys Val Ala Ala Gly Glu Leu Lys Asn Gly Phe Ala Ile Ile Arg Pro
        835                 840                 845
Pro Gly His His Ala Glu Glu Ser Thr Ala Met Gly Phe Cys Phe Phe
    850                 855                 860
Asn Ser Val Ala Ile Thr Ala Lys Leu Leu Gln Gln Lys Leu Asn Val
865                 870                 875                 880
Gly Lys Val Leu Ile Val Asp Trp Asp Ile His His Gly Asn Gly Thr
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                885                 890                 895
Gln Gln Ala Phe Tyr Asn Asp Pro Ser Val Leu Tyr Ile Ser Leu His
            900                 905                 910
Arg Tyr Asp Asn Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Glu Glu
        915                 920                 925
Val Gly Gly Gly Pro Gly Val Gly Tyr Asn Val Asn Val Ala Trp Thr
    930                 935                 940
Gly Gly Val Asp Pro Pro Ile Gly Asp Val Glu Tyr Leu Thr Ala Phe
945                 950                 955                 960
Arg Thr Val Val Met Pro Ile Ala His Glu Phe Ser Pro Asp Val Val
                965                 970                 975
Leu Val Ser Ala Gly Phe Asp Ala Val Glu Gly His Leu Ser Pro Leu
            980                 985                 990
Gly Gly Tyr Ser Val Thr Ala Arg Cys Phe Gly His Leu Thr Arg Gln
        995                 1000                1005
Leu Met Thr Leu Ala Gly Gly Arg Val Val Leu Ala Leu Glu Gly Gly
    1010                1015                1020
His Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala
1025                1030                1035                1040
Leu Leu Ser Val Glu Leu Gln Pro Leu Asp Glu Ala Val Leu Gln Gln
                1045                1050                1055
Lys Pro Asn Ile Asn Ala Val Ala Thr Leu Glu Lys Val Ile Glu Ile
            1060                1065                1070
Gln Ser Lys His Trp Ser Cys Val Gln Lys Phe Ala Ala Gly Leu Gly
        1075                1080                1085
Arg Ser Leu Arg Glu Ala Gln Ala Gly Glu Thr Glu Glu Ala Glu Thr
    1090                1095                1100
Val Ser Ala Met Ala Leu Leu Ser Val Gly Ala Glu Gln Ala Gln Ala
1105                1110                1115                1120
Ala Ala Ala Arg Glu His Ser Pro Arg Pro Ala Glu Glu Pro Met Glu
                1125                1130                1135
Gln Glu Pro Ala Leu
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<210> 5545
<211> 1932
<212> DNA
<213> Homo sapiens

<400> 5545

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caggagtgaa actctgtatc aaaaagaaat aaaaaaacga ggtcaagtag taagagaagc
180
ggtaagagtg acgggaacag gagtcattga cctcttggga gaggagacat tggaggtggt
240
gatgatttgc tgaagcagcc acacacgttc agcttgtgag gacagcagtt gttaggcagg
300
ggatgaggga ggaagctggc agatctgtgc aggtgagagg tacctgtggc cttgggctca
360
tggaagtggg aggtgatggg attctaatgt gcttgggtac agtttacaaa tacaacctct
420
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cttagtttgc ccaatacctc caaattcctg gggtggcaca cctgaggttc aggtggcatg
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540
cacatggcgg tcccggcctg gcctcttggt cccacctcac ctggtgacta gtgcagacca
600
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gcctcgaggg tcttctgcgg ccgcatcctg agcatggtga acacagatga tgtcaacgcc
720
atcatcctgg cccagaagaa catgctggac cgctttgaga agaccaatga gatgctgctc
780
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840
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1020
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1080
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1140
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1260
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1380
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1800
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1920
gtaaaaaaaa aa
1932

<210> 5546

<211> 183
<212> PRT
<213> Homo sapiens

<400> 5546
Ala Ala Glu Glu Glu Lys Glu Met Asp Leu Pro Asp Ser Ala Ser Arg
1 5 10 15
Val Phe Cys Gly Arg Ile Leu Ser Met Val Asn Thr Asp Asp Val Asn
20 25 30
Ala Ile Ile Leu Ala Gln Lys Asn Met Leu Asp Arg Phe Glu Lys Thr
35 40 45
Asn Glu Met Leu Leu Asn Phe Asn Asn Leu Ser Ser Ala Arg Leu Gln
50 55 60
Gln Met Ser Glu Arg Phe Leu His His Thr Arg Thr Leu Val Glu Met
65 70 75 80
Lys Arg Asp Leu Asp Ser Ile Phe Arg Arg Ile Arg Thr Leu Lys Gly
85 90 95
Lys Leu Ala Arg Gln His Pro Glu Ala Phe Ser His Ile Pro Glu Ala
100 105 110
Ser Phe Leu Glu Glu Glu Asp Glu Asp Pro Ile Pro Pro Ser Thr Thr
115 120 125
Thr Thr Ile Ala Thr Ser Glu Gln Ser Thr Gly Ser Cys Asp Thr Ser
130 135 140
Pro Asp Thr Val Ser Pro Ser Leu Ser Pro Gly Phe Glu Asp Leu Ser
145 150 155 160
His Val Gln Pro Gly Ser Pro Ala Ile Asn Gly Arg Ser Gln Thr Asp
165 170 175
Asp Glu Glu Met Thr Gly Glu
180

<210> 5547
<211> 1391
<212> DNA
<213> Homo sapiens

<400> 5547
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cggaagcaag gcctctggaa aaccgcggcc cctgagttgc aaacaaatgt cagatcccag
120
atattaaggc taagacatac tgcatttgta ataccaaaga aaaacgttcc tacctcaaaa
180
cgtgaaactt acacagagga ttttattaaa aagcagattg aagagttcaa cataggaaag
240
agacatttag ccaacatgat gggagaagat ccagaaactt tcactcaaga agatattgac
300
agagctattg cttacctttt cccaagtggt ttgtttgaga aacgagccag gccagtaatg
360
aagcatcctg aacagatttt tccaagacaa agagcaatcc agtggggaga agatggcngt
420
ccatttcact atctcttcta tactggcaaa cagtcatact attcattaat gcatgatgta
480
nntatggaat gttactcaat ttagaaanaa catcaaagtc acttgcaagc caaaagtctg
540

cttccagaaa aaactgtaac cagagacgtg attggcagca gatggctgat taaggaggaa
600
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660
ctagaaaagt tattgacatc gcagtgtggt gctgctgagg aagaatttgt gcagaggttt
720
cgaagaagtg taactcttga atcaaaaaaa cagctgattg aacctgtaca gtatgatgag
780
caaggaatgg cctttagcaa aagcgaaggt aaaagaaaga ctgcaaaagc agaagcaatt
840
gtttataaac atggaagtgg aagaataaaa gtaaatggaa ttgattacca gctttacttc
900
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aagcacgacg tgacctgcac agtctcaggg ggcgggaggt cagcgcaggc tggagcaata
1020
cgactggcaa tggcaaaagc cttgtgcagc tttgtcaccg aggacgaggt cgagtggatg
1080
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1140
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1200
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1260
agcatgaggg cagtactgtc agaaatttct ttgagctgtg agatggattt atttttaaat
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1380
aaaaaaaaaa a
1391

<210> 5548
<211> 167
<212> PRT
<213> Homo sapiens

<400> 5548
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1 5 10 15
Gly Ser Leu Ala Arg Lys Gln Gly Leu Trp Lys Thr Ala Ala Pro Glu
20 25 30
Leu Gln Thr Asn Val Arg Ser Gln Ile Leu Arg Leu Arg His Thr Ala
35 40 45
Phe Val Ile Pro Lys Lys Asn Val Pro Thr Ser Lys Arg Glu Thr Tyr
50 55 60
Thr Glu Asp Phe Ile Lys Lys Gln Ile Glu Glu Phe Asn Ile Gly Lys
65 70 75 80
Arg His Leu Ala Asn Met Met Gly Glu Asp Pro Glu Thr Phe Thr Gln
85 90 95
Glu Asp Ile Asp Arg Ala Ile Ala Tyr Leu Phe Pro Ser Gly Leu Phe
100 105 110
Glu Lys Arg Ala Arg Pro Val Met Lys His Pro Glu Gln Ile Phe Pro
115 120 125
Arg Gln Arg Ala Ile Gln Trp Gly Glu Asp Gly Arg Pro Phe His Tyr

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    130                 135                 140
Leu Phe Tyr Thr Gly Lys Gln Ser Tyr Tyr Ser Leu Met His Asp Val
145                 150                 155                 160
Xaa Met Glu Cys Tyr Ser Ile
                165
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<210> 5549
<211> 1865
<212> DNA
<213> Homo sapiens

<400> 5549
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120
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180
agggcagtcc ttgtggggtc ctcgtggcca gccaagatgg ttgcccccgc agtgaaggtt
240
gcccgaggat ggtcgggcct ggcgttgggc gtgcggcggg ctgtcttgca gcttccaggg
300
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360
gaatattatc gcaagccagt ggaggagcta actgaggagg agaaatatgt tcgggagctc
420
aagaagactc agctcatcaa agctgctcca gcagggaaaa caagttctgt gtttgaagac
480
ccagtcatca gtaaattcac caacatgatg atgataggag gaaacaaagt actggccaga
540
tccctcatga ttcagactct ggaagctgtg aaaaggaagc agtttgagaa gtaccatgcc
600
gcttctgcag aggaacaggc aaccatcgaa cgcaacccct acaccatctt ccatcaagca
660
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720
caggtccctg tacccctacc cgaccggcgt cgccgcttcc tagccatgaa gtggatgatc
780
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840
ctgctggagg ctttccataa ccagggcccc gtgatcaaga ggaagcatga cttgcacaag
900
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1080
tattcactat ccgttaatcc ttctttcttt gaggctggaa cttgctctct ctgcccctat
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1200
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1260

gaaaagattt attagaaaat tctcacgctg aactggtgta gcatgtggtg cagcattcag
1320
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1380
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1440
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1560
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1620
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1680
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1740
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1860
gggcc
1865

<210> 5550
<211> 242
<212> PRT
<213> Homo sapiens

<400> 5550
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20 25 30
Arg Trp Ser Arg Tyr Ser Pro Glu Phe Lys Asp Pro Leu Ile Asp Lys
35 40 45
Glu Tyr Tyr Arg Lys Pro Val Glu Glu Leu Thr Glu Glu Glu Lys Tyr
50 55 60
Val Arg Glu Leu Lys Lys Thr Gln Leu Ile Lys Ala Ala Pro Ala Gly
65 70 75 80
Lys Thr Ser Ser Val Phe Glu Asp Pro Val Ile Ser Lys Phe Thr Asn
85 90 95
Met Met Met Ile Gly Gly Asn Lys Val Leu Ala Arg Ser Leu Met Ile
100 105 110
Gln Thr Leu Glu Ala Val Lys Arg Lys Gln Phe Glu Lys Tyr His Ala
115 120 125
Ala Ser Ala Glu Glu Gln Ala Thr Ile Glu Arg Asn Pro Tyr Thr Ile
130 135 140
Phe His Gln Ala Leu Lys Asn Cys Glu Pro Met Ile Gly Leu Val Pro
145 150 155 160
Ile Leu Lys Gly Gly Arg Phe Tyr Gln Val Pro Val Pro Leu Pro Asp
165 170 175
Arg Arg Arg Arg Phe Leu Ala Met Lys Trp Met Ile Thr Glu Cys Arg
180 185 190
Asp Lys Lys His Gln Arg Thr Leu Met Pro Glu Lys Leu Ser His Lys

195 200 205
Leu Leu Glu Ala Phe His Asn Gln Gly Pro Val Ile Lys Arg Lys His
210 215 220
Asp Leu His Lys Met Ala Glu Ala Asn Arg Ala Leu Ala His Tyr Arg
225 230 235 240
Trp Trp

<210> 5551
<211> 1689
<212> DNA
<213> Homo sapiens

<400> 5551
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ctgaagagtt tctccacgga gggaccaaga attccagacg ctggtaacac tgtcagtaac
180
ctacacaact ttcaatacaa aaaaatttac caaatatcct gtttaatgta aacaaggcag
240
gaggcaaaac agagtattac agtaacacta ttttacaggg cccagaaaat gtgattatct
300
accatgtttt aacacataaa gtgtcacaat gacatgcata tttgatttac tacataaccc
360
aaaatataat taccatatag tgtggtttta gcacttcact gtaacgtctt ctgtcaatac
420
tgatggactt cataattaaa tggcaattgt atgttaatgc aataatttat gaaaacatta
480
ccatgaattt atgaagtaat tccataattt gtgccctgta aaattaagtg taacaatgtt
540
tacactagca acagtgtaag cgagctaaga attttggtcc ttatatatat acatatatac
600
atatatacac acacaataat gtacaattaa accaaaaagc tatgaatcca ctcacagctt
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720
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780
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840
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900
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1140
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1380
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1440
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1560
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1680
tccagatct
1689

<210> 5552
<211> 104
<212> PRT
<213> Homo sapiens

<400> 5552
Met Gly Arg Ile Leu Asp Gln Pro Tyr Asp Val Asn Leu Gln Val Thr
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Ser Val Leu Ser Arg Leu Ser Leu Phe Pro His Pro His Ile His Glu
            20   25   30
Tyr Leu Leu Asp Pro Tyr Val Asn Leu Ala Pro Gly Cys Arg Ser Leu
        35   40   45
Phe Ser Val Ile Val Arg Val Val Gly Asp Leu Met Leu Arg Ile Gln
    50   55   60
Arg Ile Gln Asp Phe Thr Pro Lys Leu Leu Leu Val Arg Lys Arg Leu
65   70   75   80
Leu Gly Leu Glu Pro Glu Gly Pro Ile Ser Asp Leu Glu Pro Val Glu
                85   90   95
Ala Leu Thr Val Ser Ser Ile Cys
            100

<210> 5553
<211> 274
<212> DNA
<213> Homo sapiens

<400> 5553
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120
caccagaccc taaagtcaga ataaccggcc cagctacagc ccctgcggtc gtgcttagcc
180
actacagagg ctgctatttc cccagccagt gtccctggca gccttggaaa ccaatgaagc
240

aggctctgac acaggaatcc ctctgcatct ttat
274

<210> 5554
<211> 90
<212> PRT
<213> Homo sapiens

<400> 5554
Met Asp Gly Gly Gln Gly Thr Ser Gly Pro Leu Lys Thr Ala Lys Gln
1 5 10 15
Phe Leu Ala Ile Ser Glu Glu Val Ala Phe Val Pro Glu Lys Arg Thr
20 25 30
Pro Gln Pro His Pro Thr Ala Ser Pro Asp Pro Lys Val Arg Ile Thr
35 40 45
Gly Pro Ala Thr Ala Pro Ala Val Val Leu Ser His Tyr Arg Gly Cys
50 55 60
Tyr Phe Pro Ser Gln Cys Pro Trp Gln Pro Trp Lys Pro Met Lys Gln
65 70 75 80
Ala Leu Thr Gln Glu Ser Leu Cys Ile Phe
85 90

<210> 5555
<211> 414
<212> DNA
<213> Homo sapiens

<400> 5555
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120
cacagggctg tgattctaga agggacagct gtgaggggcc gggacaggct aagctggagg
180
actcaccaga cttgcggggg tcaacacgct ccagatgtct cctagacctc tcacactcag
240
cacatccaaa cctgaaccca gcacctggcc ccacacctgt cccctggcta gagacggggg
300
cctcagccca gctgttcccc ttctcccaca gcctctcagc tgcgtgtcgg gtccattctg
360
catcttgaac atctctccca gtggattccc ttctgctgtc ctggtccagg atcc
414

<210> 5556
<211> 115
<212> PRT
<213> Homo sapiens

<400> 5556
Met Gly Phe Gln Gly Phe Gln Ser Arg Gly Arg Arg His Ser Pro Ser
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Gly Gln Arg Ser Asp Val Gly Phe Arg Lys Gln Gly Pro Gly Gly Asp
20 25 30
Glu Ser Gln Gly Cys Asp Ser Arg Arg Asp Ser Cys Glu Gly Pro Gly

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        35                  40                  45
Gln Ala Lys Leu Glu Asp Ser Pro Asp Leu Arg Gly Ser Thr Arg Ser
    50                  55                  60
Arg Cys Leu Leu Asp Leu Ser His Ser Ala His Pro Asn Leu Asn Pro
65                  70                  75                  80
Ala Pro Gly Pro Thr Pro Val Pro Trp Leu Glu Thr Gly Ala Ser Ala
                85                  90                  95
Gln Leu Phe Pro Phe Ser His Ser Leu Ser Ala Ala Cys Arg Val His
            100                 105                 110
Ser Ala Ser
        115
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<210> 5557
<211> 1970
<212> DNA
<213> Homo sapiens

<400> 5557
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120
aaaacgtcta atccaatggt taaaagctgt tcagagggat aactggactc ccactaagta
180
ttcatttctc tgtagtgagc atttcaccaa agacagcttc tccaagaggc tggaggacca
240
gcatcgcctg ctgaagccca cggccgtgcc atccatcttc cacctgaccg agaagaagag
300
gggggctgga ggccatggcc gcacccggag aaaagatgcc agcaagggca caggggggtgt
360
gaggggacac tcgagtgccg ccaccgcgag aggagctgca ggttggtcac cgtcctcgag
420
tggaaacccg atggccaagc cagagtcccg caggttgaag caagctgctc tgcaaggtga
480
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Gln Ser Pro Pro Ser Ser Ser Leu Thr Ala Thr Arg Gln Lys Pro Ser
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Val Glu Val Glu Glu Gly Glu Val Asn Gly Gln Glu Leu Cys Ile Ala
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<400> 5559

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<212> PRT
<213> Homo sapiens

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Gln Leu Ala Ala Ile Lys Val Met Asp Val Thr Glu Asp Glu Glu Glu
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Glu Ile Lys Leu Glu Ile Asn Met Leu Lys Lys Tyr Ser His His Arg
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Ile Thr Asp Leu Val Lys Asn Thr Lys Gly Asn Thr Leu Lys Glu Asp
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His Ile His His Val Ile His Arg Asp Ile Lys Gly Gln Asn Val Leu
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Leu Thr Glu Asn Ala Glu Val Lys Leu Val Asp Phe Gly Val Ser Ala
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Gln Leu Asp Arg Thr Val Gly Arg Arg Asn Thr Phe Ile Gly Thr Pro
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Glu Met Ala Glu Gly Ala Pro Pro Leu Cys Asp Met His Pro Met Arg
225 230 235 240
Ala Leu Phe Leu Ile Pro Arg Asn Pro Pro Pro Arg Leu Lys Ser Lys
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Lys Trp Ser Lys Lys Phe Ile Asp Phe Ile Asp Thr Cys Leu Ile Lys
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Gly Glu Pro Ser Ser Ile Met Asn Val Pro Gly Glu Ser Thr Leu Arg

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Glu Ala Arg Arg Gln Gln Glu Arg Glu Gln Arg Arg Arg Glu Gln Glu
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        435                 440                 445
Glu Arg Arg Arg Ala Glu Glu Glu Lys Arg Arg Val Glu Arg Glu Gln
    450                 455                 460
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Asp Asp Val Glu Ser Glu Pro Ala Met Thr Pro Ser Lys Glu Gly Thr
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Gly Ser Val Val Asn Val Asn Pro Thr Asn Thr Arg Pro Gln Ser Asp
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Thr Pro Glu Ile Arg Lys Tyr Lys Lys Arg Phe Asn Ser Glu Ile Leu
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Lys Gln Gly Trp Thr Thr Val Gly Asp Leu Glu Gly Cys Val His Tyr
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Ile Tyr Leu Pro Thr His Val Arg Lys Asn Pro His Ser Met Ile Gln
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1105 1110 1115 1120
Phe Met His Lys Arg Ala Gln Arg Leu Lys Phe Leu Cys Glu Arg Asn
1125 1130 1135
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<212> DNA
<213> Homo sapiens

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Leu Tyr Phe Pro Gln Ser Leu Asp Phe Ser Gln Ile Leu Pro Met Lys
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Arg Glu Ser Cys Asp Ala Glu Glu Gln Ser Gly Gly Gln Tyr Glu Leu
    290                 295                 300
Phe Ala Val Ile Ala His Val Gly Met Ala Asp Ser Gly His Tyr Cys
305                 310                 315                 320
Val Tyr Ile Arg Asn Ala Val Asp Gly Lys Trp Phe Cys Phe Asn Asp
                325                 330                 335
Ser Asn Ile Cys Leu Val Ser Trp Glu Asp Ile Gln Cys Thr Tyr Gly
            340                 345                 350
Asn Pro Asn Tyr His Trp Gln Glu Thr Ala Tyr Leu Leu Val Tyr Met
        355                 360                 365
Lys Met Glu Cys
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<210> 5563
<211> 2878
<212> DNA
<213> Homo sapiens

<400> 5563

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2878

<210> 5564
<211> 683
<212> PRT
<213> Homo sapiens

<400> 5564
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Ser Ala Glu Arg Ala Leu Glu Glu Ala Val Ala Thr Gly Thr Leu Asn
35 40 45
Leu Ser Asn Arg Arg Leu Lys His Phe Pro Arg Gly Ala Ala Arg Ser
50 55 60
Tyr Asp Leu Ser Asp Ile Thr Gln Ala Asp Leu Ser Arg Asn Arg Phe
65 70 75 80
Pro Glu Val Pro Glu Ala Ala Cys Gln Leu Val Ser Leu Glu Gly Leu
85 90 95
Ser Leu Tyr His Asn Cys Leu Arg Cys Leu Asn Pro Ala Leu Gly Asn
100 105 110
Leu Thr Ala Leu Thr Tyr Leu Asn Leu Ser Arg Asn Gln Leu Ser Leu
115 120 125
Leu Pro Pro Tyr Ile Cys Gln Leu Pro Leu Arg Val Leu Ile Val Ser
130 135 140
Asn Asn Lys Leu Gly Ala Leu Pro Pro Asp Ile Gly Thr Leu Gly Ser
145 150 155 160
Leu Arg Gln Leu Asp Val Ser Ser Asn Glu Leu Gln Ser Leu Pro Ser
165 170 175
Glu Leu Cys Gly Leu Ser Ser Leu Arg Asp Leu Asn Val Arg Arg Asn
180 185 190
Gln Leu Ser Thr Leu Pro Glu Glu Leu Gly Asp Leu Pro Leu Val Arg
195 200 205
Leu Asp Phe Ser Cys Asn Arg Val Ser Arg Ile Pro Val Ser Phe Cys
210 215 220
Arg Leu Arg His Leu Gln Val Ile Leu Leu Asp Ser Asn Pro Leu Gln
225 230 235 240
Ser Pro Pro Ala Gln Val Cys Leu Lys Gly Lys Leu His Ile Phe Lys
245 250 255
Tyr Leu Ser Thr Glu Ala Gly Gln Arg Gly Ser Ala Leu Gly Asp Leu

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            260                 265                 270
Ala Pro Ser Arg Pro Pro Ser Phe Ser Pro Cys Pro Ala Glu Asp Leu
        275                 280                 285
Phe Pro Gly His Arg Tyr Asp Gly Gly Leu Asp Ser Gly Phe His Ser
    290                 295                 300
Val Asp Ser Gly Ser Lys Arg Trp Ser Gly Asn Glu Ser Thr Asp Glu
305                 310                 315                 320
Phe Ser Glu Leu Ser Phe Arg Ile Ser Glu Leu Ala Arg Glu Pro Arg
                325                 330                 335
Gly Pro Arg Glu Arg Lys Glu Asp Gly Ser Ala Asp Gly Asp Pro Val
            340                 345                 350
Gln Ile Asp Phe Ile Asp Ser His Val Pro Gly Glu Asp Glu Glu Arg
        355                 360                 365
Gly Thr Val Glu Glu Gln Arg Pro Pro Glu Leu Ser Pro Gly Ala Gly
    370                 375                 380
Asp Arg Glu Arg Ala Pro Ser Ser Arg Arg Glu Glu Pro Ala Gly Glu
385                 390                 395                 400
Glu Arg Arg Arg Pro Asp Thr Leu Gln Leu Trp Gln Glu Arg Glu Arg
                405                 410                 415
Arg Gln Gln Gln Gln Ser Gly Ala Trp Gly Ala Pro Arg Lys Asp Ser
            420                 425                 430
Leu Leu Lys Pro Gly Leu Arg Ala Val Val Gly Gly Ala Ala Ala Val
        435                 440                 445
Ser Thr Gln Ala Met His Asn Gly Ser Pro Lys Ser Ser Ala Ser Gln
    450                 455                 460
Ala Gly Gly Cys Ser Gly Ala Gly Ser Pro Ala Pro Ala Pro Ala Ser
465                 470                 475                 480
Gln Glu Pro Leu Pro Ile Ala Gly Pro Ala Thr Ala Pro Ala Pro Arg
                485                 490                 495
Pro Leu Gly Ser Ile Gln Arg Pro Asn Ser Phe Leu Phe Arg Ser Ser
            500                 505                 510
Ser Gln Ser Gly Ser Gly Pro Ser Ser Pro Asp Ser Val Leu Arg Pro
        515                 520                 525
Arg Arg Tyr Pro Gln Val Pro Asp Glu Lys Asp Leu Met Thr Gln Leu
    530                 535                 540
Arg Gln Val Leu Glu Ser Arg Leu Gln Arg Pro Leu Pro Glu Asp Leu
545                 550                 555                 560
Ala Glu Ala Leu Ala Ser Gly Val Ile Leu Cys Gln Leu Ala Asn Gln
                565                 570                 575
Leu Arg Pro Arg Ser Val Pro Phe Ile His Val Pro Ser Pro Ala Val
            580                 585                 590
Pro Lys Leu Ser Ala Leu Lys Ala Arg Lys Asn Val Glu Ser Phe Leu
        595                 600                 605
Glu Ala Cys Arg Lys Met Gly Val Pro Glu Ala Asp Leu Cys Ser Pro
    610                 615                 620
Ser Asp Leu Leu Gln Gly Thr Ala Arg Gly Leu Arg Thr Ala Leu Glu
625                 630                 635                 640
Ala Val Lys Arg Val Gly Gly Lys Ala Leu Pro Pro Leu Trp Pro Pro
                645                 650                 655
Ser Gly Leu Gly Gly Phe Val Val Phe Tyr Val Val Leu Met Leu Leu
            660                 665                 670
Leu Tyr Val Thr Tyr Thr Arg Leu Leu Gly Ser
        675                 680
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<210> 5565
<211> 472
<212> DNA
<213> Homo sapiens

<400> 5565
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tcacgcggta catgggctac agttccttgt ccgagggctt ccgggagctg gagccgcaca
120
gaatgaaggg gctcactggt agtggttccc aacttcgttg catattaaac cccccggaga
180
acttaaactc cagtgcccag tcctatgcaa tcagatcctg ggtctccact gtgcagcgcc
240
cgtggagagc cagcgatgtg gagggtcgag atcacccagt tctttgggga cagggtctca
300
ctgcccccaa ggctggagtc cggtggtgca atcacggctc acagcagtct cgacctccag
360
ggctcaagcg atcctccagc ctcagcctcc cgagcagctg ggagcacagg cgcataccac
420
gcgtggcttt tttgagacga gggcttgcca tgtttcccag gctggtctcg aa
472

<210> 5566
<211> 76
<212> PRT
<213> Homo sapiens

<400> 5566
Met Gln Ser Asp Pro Gly Ser Pro Leu Cys Ser Ala Arg Gly Glu Pro
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Ala Met Trp Arg Val Glu Ile Thr Gln Phe Phe Gly Asp Arg Val Ser
            20   25   30
Leu Pro Pro Arg Leu Glu Ser Gly Gly Ala Ile Thr Ala His Ser Ser
        35   40   45
Leu Asp Leu Gln Gly Ser Ser Asp Pro Pro Ala Ser Ala Ser Arg Ala
    50   55   60
Ala Gly Ser Thr Gly Ala Tyr His Ala Trp Leu Phe
65   70   75

<210> 5567
<211> 968
<212> DNA
<213> Homo sapiens

<400> 5567
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120
taaaaaccat ttttagctca caagctgtac aaaaacagac ggtgagtaaa ttggcccaca
180
gaccggtttg ctagcccctg ggcttaagag atctgtccac ttactcctca acatgcagag
240

tgtgaactgt gtgaactgca taggccacag caatcttact gcatccattc ccgctgcatc
300
attatttttg atttgtattc attcagtcca ccgaagcatt cacttggcac ctctccaaat
360
ctgggtactg tgcaagatcc ttccttggga cactgaagga aaatcagaca cggcccttct
420
ctcaagttcg cagactctcc ggtatccaga tactacggct ctcatagtat cagaaaacac
480
agccacaagc gcaggtaagt atcagaggtg ttttacgaga tacatgtatc agattcttaa
540
ggctgctgta ccaaaatacc acaaactgca tggcttaaaa caacagaaat ttattccctc
600
acaatcctgg aggccagatg tctgaaatca agatattggt agggttggtt ccttctcgag
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720
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780
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840
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960
cctattac
968

<210> 5568
<211> 130
<212> PRT
<213> Homo sapiens

<400> 5568
Met Gln Ser Val Asn Cys Val Asn Cys Ile Gly His Ser Asn Leu Thr
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Ala Ser Ile Pro Ala Ala Ser Leu Phe Leu Ile Cys Ile His Ser Val
20 25 30
His Arg Ser Ile His Leu Ala Pro Leu Gln Ile Trp Val Leu Cys Lys
35 40 45
Ile Leu Pro Trp Asp Thr Glu Gly Lys Ser Asp Thr Ala Leu Leu Ser
50 55 60
Ser Ser Gln Thr Leu Arg Tyr Pro Asp Thr Thr Ala Leu Ile Val Ser
65 70 75 80
Glu Asn Thr Ala Thr Ser Ala Gly Lys Tyr Gln Arg Cys Phe Thr Arg
85 90 95
Tyr Met Tyr Gln Ile Leu Lys Ala Ala Val Pro Lys Tyr His Lys Leu
100 105 110
His Gly Leu Lys Gln Gln Lys Phe Ile Pro Ser Gln Ser Trp Arg Pro
115 120 125
Asp Val
130

<210> 5569
<211> 876

<212> DNA
<213> Homo sapiens

<400> 5569
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ttaagtaaaa tgaagaacat tttacttatt tttatgtcca gtacagtcaa agcagccaca
120
ttgcataacc ccgggggacc cccttcctct ttgtgatgcc ccagaacaat attgatttga
180
ttatagaaag ccaccggcag cctacatgcg caacggtgag ttgttggtta tatacactgt
240
ggaccataca gtggaatatt acagtcaata aaaggtattt ttagagagaa aaaaaaacat
300
tggaacacgc ttatgatata atgttaggca aaatcgctgt tatgaacagc tcgtttgggg
360
cagagcaaat cctgggaagt aacgctgagg ctgttggtgc aggcggtgga gtacaacatc
420
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480
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720
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780
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gtttgtgacg gatgaaagca ccgacagccc acgcgt
876

<210> 5570
<211> 169
<212> PRT
<213> Homo sapiens

<400> 5570
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Leu Val Gln Ala Val Glu Tyr Asn Ile Phe Glu Gly Met Glu Cys His
            20   25   30
Gly Ser Pro Leu Val Val Ile Ser Gln Gly Lys Ile Val Phe Glu Asp
        35   40   45
Gly Asn Ile Asn Val Asn Lys Gly Met Gly Arg Phe Ile Pro Arg Lys
    50   55   60
Ala Phe Pro Glu His Ser Ser Thr Trp Leu Glu Leu His Asn His Gly
65   70   75   80
Arg Arg His Val Cys Glu Ala Ser Trp Gly Cys Thr Ala Asp Pro Leu
                85   90   95
Leu Ser Pro Leu Ala Leu Ser Ala Ala Phe Met Trp Leu Ser Pro Ser

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            100                 105                 110
Val Leu Gln Ala Phe Ile Ser Phe Arg Ala Ala Pro Ser Leu Cys Pro
        115                 120                 125
Gly Thr Leu Ala Lys Met Gln Cys Leu Pro Asn Ser His Ile Ser Phe
    130                 135                 140
Asn Gln Gly Ala Ile Pro Ala Trp Lys Ser Pro Ser Cys Ser Cys Trp
145                 150                 155                 160
Gln Val Gln Val Pro Val Cys Asp Gly
                165
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<210> 5571
<211> 405
<212> DNA
<213> Homo sapiens

<400> 5571
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atggtcacgg cttcagaaag gatctttgtt ctcaaccaac tcagagatcc cacttcgcct
120
aagtttccag aagactttga cgatggagag catgcaaagc agaaatcagt catctcctgg
180
ctgttgaacc acgatccagc aaaacggccc acagccacag aactgctcaa gagtgagctg
240
ctgcccccac cccagatgga ggagtcagag ctgcatgaag tgctgcacca cacgctgacc
300
aacgtggatg ggaaggccta ccgcaccatg atggcccaga tcttctcgca gcgcctcgct
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405

<210> 5572
<211> 135
<212> PRT
<213> Homo sapiens

<400> 5572
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Ser Tyr His Pro Met Val Thr Ala Ser Glu Arg Ile Phe Val Leu Asn
            20                  25                  30
Gln Leu Arg Asp Pro Thr Ser Pro Lys Phe Pro Glu Asp Phe Asp Asp
        35                  40                  45
Gly Glu His Ala Lys Gln Lys Ser Val Ile Ser Trp Leu Leu Asn His
    50                  55                  60
Asp Pro Ala Lys Arg Pro Thr Ala Thr Glu Leu Leu Lys Ser Glu Leu
65                  70                  75                  80
Leu Pro Pro Pro Gln Met Glu Glu Ser Glu Leu His Glu Val Leu His
                85                  90                  95
His Thr Leu Thr Asn Val Asp Gly Lys Ala Tyr Arg Thr Met Met Ala
            100                 105                 110
Gln Ile Phe Ser Gln Arg Leu Ala Gly Ala Gly Gly Gly Gly Tyr Arg
        115                 120                 125
Ser Arg Leu Gly Val Pro Arg
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130 135

<210> 5573
<211> 1279
<212> DNA
<213> Homo sapiens

<400> 5573
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120
tccgtcagag cctaggggag cctgccctcc cgcgcctcgt cggggcccgg ccaggcacct
180
tggccgccgg cgcacggacg cgggcacgag cactagatca cggctgctgg acctcggcac
240
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300
ggtctggcat atttagaact taagtctatt atttcgggca ccatgacttt gaggctttta
360
gaagactggt gcaggggat ggacatgaac cctcggaaag cgctattgat tgccggcatc
420
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480
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540
gtagggctta ctgcggagac tagtcacgcc ctggtcccta aggagatacc gggaaaaggg
600
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660
aatgaatttt tagcgggaga gggcatgaca gtgggtgagt tgagcagagc tcttggacat
720
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900
catactactc agatgataaa ggcgtggcag gtgccagatg tagagaagag aaggcgattg
960
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1140
gcttatgtac taaggctgga gcctttgtta cagaagctgg tacagagagg agcaattgag
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1260
attcgcagag agcttaata
1279

<210> 5574

<211> 312
<212> PRT
<213> Homo sapiens

<400> 5574
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Pro Arg Lys Ala Leu Leu Ile Ala Gly Ile Ser Gln Ser Cys Ser Val
20 25 30
Ala Glu Ile Glu Glu Ala Leu Gln Ala Gly Leu Ala Pro Leu Gly Glu
35 40 45
Tyr Arg Leu Leu Gly Arg Met Phe Arg Arg Asp Glu Asn Arg Lys Val
50 55 60
Ala Leu Val Gly Leu Thr Ala Glu Thr Ser His Ala Leu Val Pro Lys
65 70 75 80
Glu Ile Pro Gly Lys Gly Gly Ile Trp Arg Val Ile Phe Lys Pro Pro
85 90 95
Asp Pro Asp Asn Thr Phe Leu Ser Arg Leu Asn Glu Phe Leu Ala Gly
100 105 110
Glu Gly Met Thr Val Gly Glu Leu Ser Arg Ala Leu Gly His Glu Asn
115 120 125
Gly Ser Leu Asp Pro Glu Gln Gly Met Ile Pro Glu Met Trp Ala Pro
130 135 140
Met Leu Ala Gln Ala Leu Glu Ala Leu Gln Pro Ala Leu Gln Cys Leu
145 150 155 160
Lys Tyr Lys Lys Leu Arg Val Phe Ser Gly Arg Glu Ser Pro Glu Pro
165 170 175
Gly Glu Glu Glu Phe Gly Arg Trp Met Phe His Thr Thr Gln Met Ile
180 185 190
Lys Ala Trp Gln Val Pro Asp Val Glu Lys Arg Arg Arg Leu Leu Glu
195 200 205
Ser Leu Arg Gly Pro Ala Leu Asp Val Ile Arg Val Leu Lys Ile Asn
210 215 220
Asn Pro Leu Ile Thr Val Asp Glu Cys Leu Gln Ala Leu Glu Glu Val
225 230 235 240
Phe Gly Val Thr Asp Asn Pro Arg Glu Leu Gln Val Lys Tyr Leu Thr
245 250 255
Thr Tyr Gln Lys Asp Glu Glu Lys Leu Ser Ala Tyr Val Leu Arg Leu
260 265 270
Glu Pro Leu Leu Gln Lys Leu Val Gln Arg Gly Ala Ile Glu Arg Asp
275 280 285
Ala Val Asn Gln Ala Arg Leu Asp Gln Val Ile Ala Gly Ala Val His
290 295 300
Lys Thr Ile Arg Arg Glu Leu Asn
305 310

<210> 5575
<211> 2405
<212> DNA
<213> Homo sapiens

<400> 5575
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120
ttagcatata cagtagagtt tctaatgttg tcagcattcc ctagtgggcg gttacaagtt
180
aggttgggat tctaatcata ttttatgata tctcacagat taaattgcac tttgtctctg
240
cccagtcttg attccctttt ggccagcagt ttttaggtct gtcagtactg cactgcaaga
300
atggcagatt ttgggatctc tgctggccag tttgtggcag tggtctggga taagtcatcc
360
ccagtggagg ctctgaaagg tctggtggat aagcttcaag cgttaaccgg caatgagggc
420
cgcgtgtctg tggaaaacat caagcagctg ttgcaatgtt tagtcccagg aagcaccact
480
ctgcacagtg ctgagatttt ggctgaaatc gcccggatcc ttcggcctgg tggatgtctt
540
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600
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720
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780
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1140
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1200
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1260
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1320
gccagctgcc cctaccttgg gatgccagcc ttcaaacctg gggaaaaggt gcttctgagt
1380
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1440
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1560
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1680

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1800
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1980
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2040
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2100
agtttggacc attggaggaa cttagtgtca cgcacaaatg gggctattcc tacgcttaga
2160
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2220
ggcagaactc tgaacgacaa tacgtctctc tgagcagaga ccccctttgtt cttgttatcc
2280
acccatatgg acttggaatc aatcttgcca aatatttgga gagattgtgt ggatttaaga
2340
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2400
cttga
2405

<210> 5576
<211> 367
<212> PRT
<213> Homo sapiens

<400> 5576
Met Ala Asp Phe Gly Ile Ser Ala Gly Gln Phe Val Ala Val Val Trp
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Asp Lys Ser Ser Pro Val Glu Ala Leu Lys Gly Leu Val Asp Lys Leu
            20   25   30
Gln Ala Leu Thr Gly Asn Glu Gly Arg Val Ser Val Glu Asn Ile Lys
        35   40   45
Gln Leu Leu Gln Cys Leu Val Pro Gly Ser Thr Thr Leu His Ser Ala
    50   55   60
Glu Ile Leu Ala Glu Ile Ala Arg Ile Leu Arg Pro Gly Gly Cys Leu
65   70   75   80
Phe Leu Lys Glu Pro Val Glu Thr Ala Val Asp Asn Asn Ser Lys Val
                85   90   95
Lys Thr Ala Ser Lys Leu Cys Ser Ala Leu Thr Leu Ser Gly Leu Val
            100   105   110
Glu Val Lys Glu Leu Gln Arg Glu Pro Leu Thr Pro Glu Glu Val Gln
        115   120   125
Ser Val Arg Glu His Leu Gly His Glu Ser Asp Asn Leu Leu Phe Val
    130   135   140
Gln Ile Thr Gly Lys Lys Pro Asn Phe Glu Val Gly Ser Ser Arg Gln
145   150   155   160
Leu Lys Leu Ser Ile Thr Lys Lys Ser Ser Pro Ser Val Lys Pro Ala

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                165                 170                 175
Val Asp Pro Ala Ala Ala Lys Leu Trp Thr Leu Ser Ala Asn Asp Met
            180                 185                 190
Glu Asp Asp Ser Met Cys Ile Phe Cys Gly Cys Ser Leu Thr His Arg
        195                 200                 205
Trp Pro Leu Glu His Val Val Arg Leu Asn Met Met Ile Asn Gln Lys
    210                 215                 220
Glu Asp Arg Val Asp Thr Phe Phe Thr Leu Asp Ser Lys Phe Pro Leu
225                 230                 235                 240
Glu Ala Cys Ser His Phe Ser Phe Ser Leu Ala Glu Thr Thr Thr Val
                245                 250                 255
Ser Leu Ile Ala Leu Asn Thr Leu Gln Asp Leu Ile Asp Ser Asp Glu
            260                 265                 270
Leu Leu Asp Pro Glu Asp Leu Lys Lys Pro Asp Pro Ala Ser Leu Arg
        275                 280                 285
Ala Ala Ser Cys Gly Glu Gly Lys Lys Arg Lys Ala Cys Lys Asn Cys
    290                 295                 300
Thr Cys Gly Leu Ala Glu Glu Leu Glu Lys Glu Lys Ser Arg Glu Gln
305                 310                 315                 320
Met Ser Ser Gln Pro Lys Ser Ala Cys Gly Asn Cys Tyr Leu Gly Asp
                325                 330                 335
Ala Phe Arg Cys Ala Ser Cys Pro Tyr Leu Gly Met Pro Ala Phe Lys
            340                 345                 350
Pro Gly Glu Lys Val Leu Leu Ser Asp Ser Asn Leu His Asp Ala
        355                 360                 365
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<210> 5577
<211> 659
<212> DNA
<213> Homo sapiens

<400> 5577
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120
cctgtggccg acatgagggc actcctgaca ggcaaggact gcccccatgt ccgggagaag
180
ggctccggga agcagaacaa ggacctctat gagttggcct tctcaatcag ctatgaccgt
240
ggggaggagg aagcgtacct caacttcatt gccccctcca agcgggagtt ctacctgtgg
300
acagatgggc tcagtgcctt gctgggcagt cccatgggca gcgagcagac acggctggac
360
ctggagcagc tgctgaccat ggagaccaag ctgcgtctgc tggagctgga gaacgtgccc
420
atccccgagc ggccaccccc tgtgccccca ccccccacca acttcaactt ctgctatgac
480
tgcagcatcg ctgaaccttg acagtgtggc tggccatggg ccacagctgc ggccactgca
540
gcagccatga agggcagtgg gtagaggagt gcaggcaccc tgaccagcag agattgctgc
600
agaaataaag tctgcttggc tcttgggaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa
659

<210> 5578
<211> 166
<212> PRT
<213> Homo sapiens

<400> 5578
Leu His Ala Asp Lys Leu Trp Phe Cys Cys Leu Ser Pro Asn His Lys
1 5 10 15
Leu Leu Gln Tyr Gly Asp Met Glu Glu Gly Xaa Gln Pro Ala Tyr Pro
20 25 30
Xaa Glu Ser Leu Pro Glu Gln Leu Pro Val Ala Asp Met Arg Ala Leu
35 40 45
Leu Thr Gly Lys Asp Cys Pro His Val Arg Glu Lys Gly Ser Gly Lys
50 55 60
Gln Asn Lys Asp Leu Tyr Glu Leu Ala Phe Ser Ile Ser Tyr Asp Arg
65 70 75 80
Gly Glu Glu Glu Ala Tyr Leu Asn Phe Ile Ala Pro Ser Lys Arg Glu
85 90 95
Phe Tyr Leu Trp Thr Asp Gly Leu Ser Ala Leu Leu Gly Ser Pro Met
100 105 110
Gly Ser Glu Gln Thr Arg Leu Asp Leu Glu Gln Leu Leu Thr Met Glu
115 120 125
Thr Lys Leu Arg Leu Leu Glu Leu Glu Asn Val Pro Ile Pro Glu Arg
130 135 140
Pro Pro Pro Val Pro Pro Pro Pro Thr Asn Phe Asn Phe Cys Tyr Asp
145 150 155 160
Cys Ser Ile Ala Glu Pro
165

<210> 5579
<211> 1312
<212> DNA
<213> Homo sapiens

<400> 5579
actcctgtat caaccatgag ttcttctcag cctgtgtcac gaccattgca acccatacaa
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ccagcaccgc ctcttcaacc atctggggtg ccaacaagtg gaccatctca gaccaccata
120
cacttactac ctacagctcc aactaccgtg aatgtaacac atcgtccagt aactcaggtg
180
accacaagac tccctgtacc aagagctcct gcaaaccacc aggtggttta tacaactctt
240
cctgcaccac cagctcaggc tcccttgcga ggaactgtta tgcaggctcc tgctgttcgg
300
caggtcaatc cccaaaatag tgttacagtt cgagtgcctc aaacaaccac atatgttgta
360
aacaatggac taaccctggg atcaacagga cctcagctca cagtgcatca ccgaccacca
420
caagtgcata ctgagccccc acgccccgtg cacccagcac ccttaccaga agctccacaa
480
ccacagcgtc tgcccccaga agctgccagc acatctctgc ctcagaagcc acacttgaag
540

ttagcacgcg ttcagagtca aaatggcata gtactgtcat ggagtgtcct ggaggtggat
600
cgaagctgtg ccactgttga tagctaccat ctctatgctt accatgagga acccagtgcc
660
actgtgccct cacaatggaa aaagattggg gaagtcaagg cacttccctt gcccatggca
720
tgtactctca cccagtttgt atctggtagc aaatactact ttgcagtacg agccaaggat
780
atttatggac gttttgggcc tttctgtgat cctcagtcaa cagatgtgat ctcttctacc
840
cagagcagtt aaaccttgga gcctttatat tttcctcttt taaaatttcc acctttggt
900
cttgtttta atcttgtgca tgatacccca tgtaaaatcc accttgtgca agatttcttg
960
gacagatgtg tgtatacact acatttgttt ataaccagaa gcaaaataaa ctcagcccac
1020
aaagctagaa tcttttcctg gacagtttag gctttggggt ttggaaatgt aaatgtgtac
1080
cttgctttag ttttgaggct ggggaatatg tgtgggtgtt tatgtgtgtt tttccttatg
1140
taggtgttat tgcattggag tctcccattt tcattctcaa atttacctct taaagtacga
1200
agtaagtaga tcaaaggatt tgagatgtgt aactggcatg attctgcttt tgaaggatct
1260
atagtatcat tttagttaag tgggtcaaac agaatcaaaa caaaacccaa ag
1312

<210> 5580
<211> 283
<212> PRT
<213> Homo sapiens

<400> 5580
Thr Pro Val Ser Thr Met Ser Ser Ser Gln Pro Val Ser Arg Pro Leu
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Gln Pro Ile Gln Pro Ala Pro Pro Leu Gln Pro Ser Gly Val Pro Thr
20 25 30
Ser Gly Pro Ser Gln Thr Thr Ile His Leu Leu Pro Thr Ala Pro Thr
35 40 45
Thr Val Asn Val Thr His Arg Pro Val Thr Gln Val Thr Thr Arg Leu
50 55 60
Pro Val Pro Arg Ala Pro Ala Asn His Gln Val Val Tyr Thr Thr Leu
65 70 75 80
Pro Ala Pro Pro Ala Gln Ala Pro Leu Arg Gly Thr Val Met Gln Ala
85 90 95
Pro Ala Val Arg Gln Val Asn Pro Gln Asn Ser Val Thr Val Arg Val
100 105 110
Pro Gln Thr Thr Thr Tyr Val Val Asn Asn Gly Leu Thr Leu Gly Ser
115 120 125
Thr Gly Pro Gln Leu Thr Val His His Arg Pro Pro Gln Val His Thr
130 135 140
Glu Pro Pro Arg Pro Val His Pro Ala Pro Leu Pro Glu Ala Pro Gln
145 150 155 160
Pro Gln Arg Leu Pro Pro Glu Ala Ala Ser Thr Ser Leu Pro Gln Lys

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                165                 170                 175
Pro His Leu Lys Leu Ala Arg Val Gln Ser Gln Asn Gly Ile Val Leu
            180                 185                 190
Ser Trp Ser Val Leu Glu Val Asp Arg Ser Cys Ala Thr Val Asp Ser
        195                 200                 205
Tyr His Leu Tyr Ala Tyr His Glu Glu Pro Ser Ala Thr Val Pro Ser
    210                 215                 220
Gln Trp Lys Lys Ile Gly Glu Val Lys Ala Leu Pro Leu Pro Met Ala
225                 230                 235                 240
Cys Thr Leu Thr Gln Phe Val Ser Gly Ser Lys Tyr Tyr Phe Ala Val
                245                 250                 255
Arg Ala Lys Asp Ile Tyr Gly Arg Phe Gly Pro Phe Cys Asp Pro Gln
            260                 265                 270
Ser Thr Asp Val Ile Ser Ser Thr Gln Ser Ser
        275                 280
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<210> 5581
<211> 720
<212> DNA
<213> Homo sapiens

<400> 5581
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aagcccagct gctctacaga ctcgtcgttc acccggacgc cggtgcccac cgtgtctctc
120
gcgtcccgcg agctgcctgt ctcgtcgtgg caggtcaccg agccgtcaag caagaatctg
180
tgggagcaga tctgcaagga gtatgaagct gagcagcctc cctttccaga aggatataaa
240
gtcaaacagg agcctgtgat tacggttgcg ccagtagagg aaatgctttt tcatggcttc
300
agtgcagagc actattttcc ggtttcccat ttcaccatga tctcacgtac accctgtcct
360
caagataaat cggaaacaat caacccaaaa acatgttctc ccaaagaata tttggaaact
420
ttcatctttc ctgttctgct tcccggaatg gctagcctgc ttcaccaagc gaagaaagaa
480
aaatgttttg aggtcagttg tttggcagga tttctttatt ttgagattct caatcattca
540
ttattatcag atgatagctc attatcttgg taccatcagg ttgttctcca gatgacccct
600
tcgggaggga aagcctgtgt ttggggtcac ttacccagtt ccagccacac catctagttg
660
tgcacataca tgcgctgcca tctgtctgnc cacttggact ccggagagct tttccgcctt
720

<210> 5582
<211> 212
<212> PRT
<213> Homo sapiens

<400> 5582
Met Ala Ala Pro Arg Gln Ile Pro Ser His Ile Val Arg Leu Lys Pro

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 1               5                  10                  15
Ser Cys Ser Thr Asp Ser Ser Phe Thr Arg Thr Pro Val Pro Thr Val
            20                  25                  30
Ser Leu Ala Ser Arg Glu Leu Pro Val Ser Ser Trp Gln Val Thr Glu
        35                  40                  45
Pro Ser Ser Lys Asn Leu Trp Glu Gln Ile Cys Lys Glu Tyr Glu Ala
    50                  55                  60
Glu Gln Pro Pro Phe Pro Glu Gly Tyr Lys Val Lys Gln Glu Pro Val
65                  70                  75                  80
Ile Thr Val Ala Pro Val Glu Glu Met Leu Phe His Gly Phe Ser Ala
                85                  90                  95
Glu His Tyr Phe Pro Val Ser His Phe Thr Met Ile Ser Arg Thr Pro
            100                 105                 110
Cys Pro Gln Asp Lys Ser Glu Thr Ile Asn Pro Lys Thr Cys Ser Pro
        115                 120                 125
Lys Glu Tyr Leu Glu Thr Phe Ile Phe Pro Val Leu Leu Pro Gly Met
    130                 135                 140
Ala Ser Leu Leu His Gln Ala Lys Lys Glu Lys Cys Phe Glu Val Ser
145                 150                 155                 160
Cys Leu Ala Gly Phe Leu Tyr Phe Glu Ile Leu Asn His Ser Leu Leu
                165                 170                 175
Ser Asp Asp Ser Ser Leu Ser Trp Tyr His Gln Val Val Leu Gln Met
            180                 185                 190
Thr Pro Ser Gly Gly Lys Ala Cys Val Trp Gly His Leu Pro Ser Ser
        195                 200                 205
Ser His Thr Ile
    210
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<210> 5583
<211> 2101
<212> DNA
<213> Homo sapiens

<400> 5583
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gtctacctgc agcgcatcca gctcaacaac cccacggagc gcgtggccgc gctgcagact
120
gtggggccca ctgccggccc agcccccaat gccttcacca gtaccctgga gaaggtcgga
180
gaccatcagt tcctcctcta ctcaggccgg tccccgccta cgcccactgg gttggtgcac
240
ctggtggtgg tggccgccaa gaagctggtg aaccgcctcc aagtggctcc caagacgcag
300
ctggatgaga cggtgctgtg ggtggtgcac gtctctggcc ccattaaccc ccaggtgctc
360
aaaagcaaag cagccaagga gctcaaggcg ctgcaggact tggcacggaa ggaaatgctg
420
gagctcttgg acatgccagc ggcggagctg cttcaagacc accagctcct ctgggctcag
480
ctcttcagcc caggagtgga aatgaagaag atcactgaca cccacacgcc gtctggcctc
540
accgtgaacc tgacgctcta ttacatgctc tcctgctcgc cagccccact gctcagcccc
600

tccctgagcc acagggagcg agaccagatg gagtcgacgc tcaactatga agatcactgc
660
ttcagcgggc acgccaccat gcacgccgag aacctgtggc cggggcggct gtcctccgtc
720
cagcagatcc tgcagctctc tgacctgtgg aggctgaccc tccagaagcg tggctgcaag
780
gggctggtga aggtgggtgc cccaggcatc ctgcagggga tggtgctcag ctttgggggg
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900
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960
ccgagggcaa gccctaccta cacgtgtccg tggagtcccg tggccagcct gtcanagatc
1020
tatgcctgca aggcaggctg cctggacgag ccagtggagc tgacctcggc gcccacgggc
1080
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1200
gagcacatgg cccagcagga ccccgggctg cccttcctct tctggttcag cgtggcctcc
1260
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1320
ggagccaagc ccctcttcag gagtaaggaa gatcccagtg tctgagtgaa ctaacagtcc
1380
tgctttcagc caccatttgc acaagacacc cagcactgaa agtcccgctg ccaggagcaa
1440
gggatccttt ggaagcaccc gccctttgtg ccttgttggg ggaaaccggt gacgcagaag
1500
tgagtgtgga tacaccagag tttgcattgg aaggaatgag tgtcacgtgg ggagggaagg
1560
ggccagtgga ccttttgtaa gctttccact caataaaatg aacctgtatg gcaaatactt
1620
gaaatggaac tcactccttc cactttcccc ctttcttctg tcccaggaaa tagatcatct
1680
tttgaaaaga ctcttgtcta ggaaaagttg tgtccttttc ctaatttaac gtgttctttc
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1800
agatggtgag tgttggcggt gatgtccgtc tcggcgttcg gaggccccac ggtcccgagg
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1920
gtcatcctcg ggtttgcacg ccctttttta ggagcctgtg gacatctgtg gttttgtact
1980
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2100
a
2101

<210> 5584

<211> 454
<212> PRT
<213> Homo sapiens

<400> 5584
Xaa Gly Arg Asp Cys Val Leu Leu Gln Glu Asp Phe Leu Ala His Arg
1 5 10 15
Gly Arg Pro His Val Tyr Leu Gln Arg Ile Gln Leu Asn Asn Pro Thr
20 25 30
Glu Arg Val Ala Ala Leu Gln Thr Val Gly Pro Thr Ala Gly Pro Ala
35 40 45
Pro Asn Ala Phe Thr Ser Thr Leu Glu Lys Val Gly Asp His Gln Phe
50 55 60
Leu Leu Tyr Ser Gly Arg Ser Pro Pro Thr Pro Thr Gly Leu Val His
65 70 75 80
Leu Val Val Val Ala Ala Lys Lys Leu Val Asn Arg Leu Gln Val Ala
85 90 95
Pro Lys Thr Gln Leu Asp Glu Thr Val Leu Trp Val Val His Val Ser
100 105 110
Gly Pro Ile Asn Pro Gln Val Leu Lys Ser Lys Ala Ala Lys Glu Leu
115 120 125
Lys Ala Leu Gln Asp Leu Ala Arg Lys Glu Met Leu Glu Leu Leu Asp
130 135 140
Met Pro Ala Ala Glu Leu Leu Gln Asp His Gln Leu Leu Trp Ala Gln
145 150 155 160
Leu Phe Ser Pro Gly Val Glu Met Lys Lys Ile Thr Asp Thr His Thr
165 170 175
Pro Ser Gly Leu Thr Val Asn Leu Thr Leu Tyr Tyr Met Leu Ser Cys
180 185 190
Ser Pro Ala Pro Leu Leu Ser Pro Ser Leu Ser His Arg Glu Arg Asp
195 200 205
Gln Met Glu Ser Thr Leu Asn Tyr Glu Asp His Cys Phe Ser Gly His
210 215 220
Ala Thr Met His Ala Glu Asn Leu Trp Pro Gly Arg Leu Ser Ser Val
225 230 235 240
Gln Gln Ile Leu Gln Leu Ser Asp Leu Trp Arg Leu Thr Leu Gln Lys
245 250 255
Arg Gly Cys Lys Gly Leu Val Lys Val Gly Ala Pro Gly Ile Leu Gln
260 265 270
Gly Met Val Leu Ser Phe Gly Gly Leu Gln Phe Thr Glu Asn His Leu
275 280 285
Gln Phe Gln Ala Asp Pro Asp Val Leu His Asn Ser Tyr Ala Leu His
290 295 300
Gly Ile Arg Tyr Lys Asn Asp His Ile Asn Leu Ala Val Leu Arg Met
305 310 315 320
Pro Arg Ala Ser Pro Thr Tyr Thr Cys Pro Trp Ser Pro Val Ala Ser
325 330 335
Leu Ser Xaa Ile Tyr Ala Cys Lys Ala Gly Cys Leu Asp Glu Pro Val
340 345 350
Glu Leu Thr Ser Ala Pro Thr Gly His Thr Phe Ser Val Met Val Thr
355 360 365
Gln Pro Ile Thr Pro Leu Leu Tyr Ile Ser Thr Asp Leu Thr His Leu
370 375 380
Gln Asp Leu Arg His Thr Leu His Leu Lys Ala Ile Leu Ala His Asp

385 390 395 400
Glu His Met Ala Gln Gln Asp Pro Gly Leu Pro Phe Leu Phe Trp Phe
405 410 415
Ser Val Ala Ser Leu Ile Thr Leu Phe His Leu Phe Leu Phe Lys Leu
420 425 430
Ile Tyr Asn Glu Tyr Cys Gly Pro Gly Ala Lys Pro Leu Phe Arg Ser
435 440 445
Lys Glu Asp Pro Ser Val
450

<210> 5585
<211> 740
<212> DNA
<213> Homo sapiens

<400> 5585
ttttttttt gctttttttt ttttttttta ctttgaacat tagcattaag ttggttaccg
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tacacatcca aaggcccagc atctcagaaa aatcattagg cggcacacct gtaccagagt
120
ctcacaagaa taaaatatac aatgctacat tgagtggtta aaaatacaca aaaaagtagt
180
tttaacaatc tataaatttt ttatacttaa aatcatgatt gagttgaaat aaaaaagtgc
240
atttcaattg ctaaaaaaat aatatcggta tagttaacac aaggggggaaa tcagtacatt
300
gagggatctg acaggatgct ggaaaaaatg actcagggaa gccgggcagc atgggctcct
360
ttggagattc aggagcggag ctcagttcca cctcactgca gttccctggg gccaagcagc
420
cctcctctcc ccagtatctt tcccatctta agagatcctg tcctacctac ctgtcacctc
480
cccaacccaa agactcctct aaacttcttt gcagcatgac agctgcctgc cctacactga
540
gtctacttga ccttcaattg cgtctccgca gagaggtagg agagggacac tgccccattc
600
tggacttgac ataagtaccc cagccacatg gccttcatcc ttatgaccta gcaggcagaa
660
cagggaccaa gcagcttcta ttttgtcaaa ctcctttgga caaatattca acattcaaca
720
acaagctttg taaacctaac
740

<210> 5586
<211> 87
<212> PRT
<213> Homo sapiens

<400> 5586
Met Gly Ser Phe Gly Asp Ser Gly Ala Glu Leu Ser Ser Thr Ser Leu
1 5 10 15
Gln Phe Pro Gly Ala Lys Gln Pro Ser Ser Pro Gln Tyr Leu Ser His
20 25 30
Leu Lys Arg Ser Cys Pro Thr Tyr Leu Ser Pro Pro Gln Pro Lys Asp

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        35                  40                  45
Ser Ser Lys Leu Leu Cys Ser Met Thr Ala Ala Cys Pro Thr Leu Ser
    50                  55                  60
Leu Leu Asp Leu Gln Leu Arg Leu Arg Arg Glu Val Gly Glu Gly His
65                  70                  75                  80
Cys Pro Ile Leu Asp Leu Thr
                85
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<210> 5587
<211> 853
<212> DNA
<213> Homo sapiens

<400> 5587
ttttttagag attagtattt ccttgttcac aagacaccta attgacttgc aacaagacaa
60
aatattcagt gcatctggtt ggggccaaca tggatgatga cgtgtttctc ataagccctt
120
ttcattgttt tctcaatttg cttcagaaaa acttgcggga ttcgtccaca taaagtgtgc
180
acagtctcca aaaacttcag ctgaaggggg taatacatgg attgaaagag attgtcttga
240
aagggaaaat cccgtattgc ttcatagagt gctctgaacg ttggttgctt atcgtcatgg
300
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360
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<211> 204
<212> PRT
<213> Homo sapiens

<400> 5588
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    50                  55                  60
Lys Tyr Lys Asn Ala Ile Thr Trp Gly Asp Gln Asp Leu Leu Asn Ile
65                  70                  75                  80
Ile Phe Tyr Phe Asn Pro Glu Cys Leu Tyr Val Phe Pro Cys Gln Trp
                85                  90                  95
Asn Tyr Arg Pro Asp His Cys Met Tyr Gly Ser Asn Cys Arg Glu Ala
            100                 105                 110
Glu His Glu Gly Val Ser Val Leu His Gly Asn Arg Gly Val Tyr His
        115                 120                 125
Asp Asp Lys Gln Pro Thr Phe Arg Ala Leu Tyr Glu Ala Ile Arg Asp
    130                 135                 140
Phe Pro Phe Gln Asp Asn Leu Phe Gln Ser Met Tyr Tyr Pro Leu Gln
145                 150                 155                 160
Leu Lys Phe Leu Glu Thr Val His Thr Leu Cys Gly Arg Ile Pro Gln
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Val Phe Leu Lys Gln Ile Glu Lys Thr Met Lys Arg Ala Tyr Glu Lys
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His Val Ile Ile His Val Gly Pro Asn Gln Met His
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<211> 1327
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420
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480
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720
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<212> PRT
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<400> 5590
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35 40 45
Thr Lys Leu Ser Ser Lys Thr Thr Ala Lys Leu Ser Thr Ser Ala Lys
50 55 60
Arg Ile Gln Lys Glu Leu Ala Glu Ile Thr Leu Asp Pro Pro Pro Asn
65 70 75 80
Cys Ser Ala Gly Pro Lys Gly Asp Asn Ile Tyr Glu Trp Arg Ser Thr
85 90 95
Ile Leu Gly Pro Pro Gly Ser Val Tyr Glu Gly Gly Val Phe Phe Leu
100 105 110
Asp Ile Thr Phe Ser Ser Asp Tyr Pro Phe Lys Pro Pro Lys Val Thr
115 120 125
Phe Arg Thr Arg Ile Tyr His Cys Asn Ile Asn Ser Gln Gly Val Ile
130 135 140
Cys Leu Asp Ile Leu Lys Asp Asn Trp Ser Pro Ala Leu Thr Ile Ser
145 150 155 160
Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp Cys Asn Pro Ala
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Asp Pro Leu Val Gly Ser Ile Ala Thr Gln Tyr Leu Thr Asn Arg Ala
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Glu His Asp Arg Ile Ala Arg Gln Trp Thr Lys Arg Tyr Ala Thr

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<210> 5591
<211> 2194
<212> DNA
<213> Homo sapiens

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<211> 580
<212> PRT
<213> Homo sapiens

<400> 5592
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35 40 45
Arg Trp Asp Ser Asp Leu Gln Arg Glu Gly Val Ser His Tyr Arg Leu
50 55 60
Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser Lys Tyr Ser Leu Arg Glu
65 70 75 80
Leu His Leu Ser Phe Thr Gln Gly Phe Trp Arg Thr Arg Tyr Trp Gly
85 90 95Pro Phe Leu
Gln Ala Pro Ser Gly Ala Glu Leu Trp Val Trp Phe
100 105 110
Gln Asp Thr Val Thr Asp Val Asp Lys Ser Trp Arg Glu Leu Ser Asn
115 120 125
Val Leu Ser Gly Ile Phe Cys Ala Ser Leu Asn Phe Ile Asp Ser Thr
130 135 140
Asn Thr Val Thr Pro Thr Ala Ser Phe Lys Pro Leu Gly Leu Ala Asn

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Val Cys Thr Glu Asn Leu Thr Pro Trp Lys Lys Leu Leu Pro Cys Ser
            180                 185                 190
Ser Lys Ala Gly Leu Ser Val Leu Leu Lys Ala Asp Arg Leu Phe His
        195                 200                 205
Thr Ser Tyr His Ser Gln Ala Val His Ile Arg Pro Val Cys Arg Asn
    210                 215                 220
Ala Arg Cys Thr Ser Ile Ser Trp Glu Leu Arg Gln Thr Leu Ser Val
225                 230                 235                 240
Val Phe Asp Ala Phe Ile Thr Gly Gln Gly Lys Lys Asp Trp Ser Leu
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Phe Arg Met Phe Ser Arg Thr Leu Thr Glu Pro Cys Pro Leu Ala Ser
            260                 265                 270
Glu Ser Arg Val Tyr Val Asp Ile Thr Thr Tyr Asn Gln Pro Cys Leu
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Cys Val Gln Asp Asn Glu Thr Leu Glu Val His Pro Pro Pro Thr Thr
    290                 295                 300
Thr Tyr Gln Asp Val Ile Leu Gly Thr Arg Lys Thr Tyr Ala Ile Tyr
305                 310                 315                 320
Asp Leu Leu Asp Thr Ala Met Ile Asn Asn Ser Arg Asn Leu Asn Ile
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Gln Leu Lys Trp Lys Arg Pro Pro Glu Asn Glu Ala Pro Pro Val Pro
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Phe Leu His Ala Gln Arg Tyr Val Ser Gly Tyr Gly Leu Gln Lys Gly
        355                 360                 365
Glu Leu Ser Thr Leu Leu Tyr Asn Thr His Pro Tyr Arg Ala Phe Pro
    370                 375                 380
Val Leu Leu Leu Asp Thr Val Pro Trp Tyr Leu Arg Leu Tyr Val His
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Thr Leu Thr Ile Thr Ser Lys Gly Lys Glu Asn Lys Pro Ser Tyr Ile
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His Tyr Gln Pro Ala Gln Asp Arg Leu Gln Pro His Leu Leu Glu Met
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Leu Ile Gln Leu Pro Ala Asn Ser Val Thr Lys Val Ser Ile Gln Phe
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Glu Arg Ala Leu Leu Lys Trp Thr Glu Tyr Thr Pro Asp Pro Asn His
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Gly Phe Tyr Val Ser Pro Ser Val Leu Ser Ala Leu Val Pro Ser Met
465                 470                 475                 480
Val Ala Ala Lys Pro Val Asp Trp Glu Glu Ser Pro Leu Phe Asn Ser
                485                 490                 495
Leu Phe Pro Val Ser Asp Gly Ser Asn Tyr Phe Val Arg Leu Tyr Thr
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Glu Pro Leu Leu Val Asn Leu Pro Thr Pro Asp Phe Ser Met Pro Tyr
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Asn Val Ile Cys Leu Thr Cys Thr Val Val Ala Val Cys Tyr Gly Ser
    530                 535                 540
Phe Tyr Asn Leu Leu Thr Arg Thr Phe His Ile Glu Glu Pro Arg Thr
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<211> 3078
<212> DNA
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<210> 5594
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<212> PRT
<213> Homo sapiens

<400> 5594
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Gly Gly Asp Pro Asn His Val Thr Asp Asp Phe Ala Ala His Leu Thr
35 40 45
Leu Glu His Arg Ala Pro Arg Asp Leu Asp Glu Ser Ser Gly Val Arg
50 55 60
His Val Arg Arg Met Phe His Pro Gly Arg Gly Leu Gly Gly Pro Arg
65 70 75 80
Ala Arg Arg Ser Asn Met His Phe Thr Ser Ser Ser Thr Gly Gly Leu
85 90 95
Ser Ser Ser Gln Ser Ser Tyr Ser Pro Ser Asn Arg Glu Ala Met Asp
100 105 110
Pro Ile Ala Glu Leu Leu Ser Gln Leu Ser Gly Val Arg Arg Ser Ala
115 120 125
Gly Gly Gln Leu Asn Ser Ser Gly Pro Ser Ala Ser Gln Leu Gln Gln
130 135 140
Leu Gln Met Gln Leu Gln Leu Glu Arg Gln His Ala Gln Ala Ala Arg
145 150 155 160
Gln Gln Leu Glu Thr Ala Arg Asn Ala Thr Arg Arg Thr Asn Thr Ser
165 170 175
Ser Val Thr Thr Thr Ile Thr Gln Ser Thr Ala Thr Thr Asn Ile Ala
180 185 190
Asn Thr Glu Ser Ser Gln Gln Thr Leu Gln Asn Ser Gln Phe Leu Leu
195 200 205
Thr Arg Leu Asn Asp Pro Lys Met Ser Glu Thr Glu Arg Gln Ser Met
210 215 220
Glu Ser Glu Arg Ala Asp Arg Ser Leu Phe Val Gln Glu Leu Leu Leu
225 230 235 240
Ser Thr Leu Val Arg Glu Glu Ser Ser Ser Ser Asp Glu Asp Asp Arg
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Gly Glu Met Ala Asp Phe Gly Ala Met Gly Cys Val Asp Ile Met Pro
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<210> 5595
<211> 1515
<212> DNA
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<210> 5596
<211> 299
<212> PRT
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<400> 5596
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Asn Leu Gly Lys Lys Ile Ser Val Pro Arg Asp Val Met Leu Glu Glu
35 40 45
Leu Ser Leu Leu Thr Asn Arg Gly Ser Lys Met Phe Lys Leu Arg Gln
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Gln Leu Gly Thr Ala Gly Gln Gly Phe Ser Tyr Ser Lys Ser Asn Gly
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Arg Gly Gly Ser Gln Ala Gly Gly Ser Gly Ser Ala Gly Gln Tyr Gly
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Ser Asp Gln Gln His His Leu Gly Ser Gly Ser Gly Ala Gly Gly Thr
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Gly Gly Pro Ala Gly Gln Ala Gly Arg Gly Gly Ala Ala Gly Thr Ala
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Gly Val Gly Glu Thr Gly Ser Gly Asp Gln Ala Gly Gly Glu Gly Lys
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His Ile Thr Val Phe Lys Thr Tyr Ile Ser Pro Trp Glu Arg Ala Met
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Gly Val Asp Pro Gln Gln Lys Met Glu Leu Gly Ile Asp Leu Leu Ala
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Tyr Gly Ala Lys Ala Glu Leu Pro Lys Tyr Lys Ser Phe Asn Arg Thr
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Ala Met Pro Tyr Gly Gly Tyr Glu Lys Ala Ser Lys Arg Met Thr Phe
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Gln Met Pro Lys Phe Asp Leu Gly Pro Leu Leu Ser Glu Pro Leu Val
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<210> 5597
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<400> 5598
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Gln Leu Leu Gln Ser Ala His Lys Glu Ser Ser Phe Asp Ile Ile Leu
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Ser Gly Leu Val Pro Gly Ser Thr Thr Leu His Ser Ala Glu Ile Leu
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Glu Pro Val Glu Thr Ala Val Asp Asn Asn Ser Lys Val Lys Thr Ala
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Ser Lys Leu Cys Ser Ala Leu Thr Leu Ser Gly Leu Val Glu Val Lys
115 120 125
Glu Leu Gln Arg Glu Pro Leu Thr Pro Glu Glu Val Gln Ser Val Arg
130 135 140
Glu His Leu Gly His Glu Ser Asp Asn Leu Leu Phe Val Gln Ile Thr
145 150 155 160
Gly Lys Lys Pro Asn Phe Glu Val Gly Ser Ser Arg Gln Leu Lys Leu
165 170 175
Ser Ile Thr Lys Lys Ser Ser Pro Ser Val Lys Pro Ala Val Asp Pro
180 185 190
Ala Ala Ala Lys Leu Trp Thr Leu Ser Ala Asn Asp Met Glu Asp Asp
195 200 205
Ser Met Asp Leu Ile Asp Ser Asp Glu Leu Leu Asp Pro Glu Asp Leu

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Ala Cys Gly Asn Cys Tyr Leu Gly Asp Ala Phe Arg Cys Ala Ser Cys
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<212> DNA
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Tyr Phe Pro Phe Met Asp Leu Lys Leu Arg Ala Ala Ser Pro Ile Ile
50 55 60
Thr Leu Val Ala Leu Asp Glu Ala Leu Asp Asn Tyr Thr Ile Thr Phe
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Leu Ile Arg Gly Val Ala Ile Gly Gln Thr Ser Leu Thr Ala Ser Val
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Thr Asn Lys Ala Gly Gln Arg Ile Asn Ser Ala Pro Gln Gln Ile Glu
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145 150 155 160
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165 170 175
Leu Val Gln Ala Val Asp Ala Glu Thr Gly Lys Val Val Ile Ile Ser
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Gln Asp Leu Val Gln Val Glu Val Leu Leu Leu Arg Ala Val Arg Ile
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Arg Ala Pro Ile Met Arg Met Arg Thr Gly Thr Gln Met Pro Ile Tyr
210 215 220
Val Thr Gly Ile Thr Asn His Gln Asn Pro Phe Ser Phe Gly Asn Ala
225 230 235 240
Val Pro Gly Leu Thr Phe His Trp Ser Val Thr Lys Arg Asp Val Leu
245 250 255
Asp Leu Arg Gly Arg His His Glu Ala Ser Ile Arg Leu Pro Ser Gln
260 265 270
Tyr Asn Phe Ala Met Asn Val Leu Gly Arg Val Lys Gly Arg Thr Gly
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Leu Arg Val Val Val Lys Ala Val Asp Pro Thr Ser Gly Gln Leu Tyr
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385                 390                 395                 400
Ile Ile Val Ala Val Lys Val Ser Pro Val Ser Tyr Leu Arg Val Ser
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Pro Leu Gly Met Thr Val Thr Phe Thr Val His Phe His Asp Asn Ser
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Gly Asp Val Phe His Ala His Ser Ser Val Leu Asn Phe Ala Thr Asn
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Val Val Arg Thr Val Ser Val Gly Leu Thr Leu Leu Arg Val Trp Asp
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Ala Glu His Pro Gly Leu Ser Asp Phe Met Pro Leu Pro Val Leu Gln
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Ala Ile Ser Pro Glu Leu Ser Gly Ala Met Val Val Gly Asp Val Leu
        515                 520                 525
Cys Leu Ala Thr Val Leu Thr Ser Leu Glu Gly Leu Ser Gly Thr Trp
    530                 535                 540
Ser Ser Ser Ala Asn Ser Ile Leu His Ile Asp Pro Lys Thr Gly Val
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Ala Val Ala Arg Ala Val Gly Ser Val Thr Val Tyr Tyr Glu Val Ala
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Gly His Leu Arg Thr Tyr Lys Glu Val Val Val Ser Val Pro Gln Arg
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Ile Met Ala Arg His Leu His Pro Ile Gln Thr Ser Phe Gln Glu Ala
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Thr Ala Ser Lys Val Ile Val Ala Val Gly Asp Arg Ser Ser Asn Leu
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Arg Gly Glu Cys Thr Pro Thr Gln Arg Glu Val Ile Gln Ala Leu His
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Pro Glu Thr Leu Ile Ser Cys Gln Ser Gln Phe Lys Pro Ala Val Phe
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Asp Phe Pro Ser Gln Asp Val Phe Thr Val Glu Pro Gln Phe Asp Thr
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Lys Gln Arg Lys His Leu Ser Met Lys Lys Thr Ala Leu Val Val Ser
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Ala Ser Leu Ser Ser Ser His Phe Ser Thr Glu Gln Val Gly Ala Glu
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Val Gly Val Ser Asp Pro Ala Ala Gly Ser Gln Gly Pro Leu Ser Thr
785                 790                 795                 800
Thr Leu Thr Phe Ser Ser Pro Val Thr Asn Gln Ala Ile Ala Ile Pro
                805                 810                 815
Val Thr Val Ala Phe Val Met Asp Arg Arg Gly Pro Gly Pro Tyr Gly
            820                 825                 830
Ala Ser Leu Phe Gln His Phe Leu Asp Ser Tyr Gln Val Met Phe Phe
        835                 840                 845
Thr Leu Phe Ala Leu Leu Ala Gly Thr Ala Val Met Ile Ile Ala Tyr
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Pro Arg Ala Ser Pro Gly His Ser Pro His Tyr Phe Ala Ala Ser Ser
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<212> DNA
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<400> 5601

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Gln Glu Pro Glu Cys Arg Arg Asn Leu Val Gln Cys Leu Leu Glu Lys
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130 135 140
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145 150 155 160
Lys Arg Ser Ser Tyr Leu Gln Lys Leu Gly Leu Gly Glu Gly Lys Leu
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<212> DNA
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1920
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1980

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2070

<210> 5604
<211> 560
<212> PRT
<213> Homo sapiens

<400> 5604
Arg Phe Gln Arg Val Leu Tyr Phe Ile Cys Ala Phe Gln Asn Ile Ser
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Cys Gly Ile His Tyr Leu Ala Ser Val Phe Met Gly Val Thr Pro His
20 25 30
His Val Cys Arg Pro Pro Gly Asn Val Ser Gln Val Val Phe His Asn
35 40 45
His Ser Asn Trp Ser Leu Glu Asp Thr Gly Ala Leu Leu Ser Ser Gly
50 55 60
Gln Lys Asp Tyr Val Thr Val Gln Leu Gln Asn Gly Glu Ile Trp Glu
65 70 75 80
Leu Ser Arg Cys Ser Arg Asn Lys Arg Glu Asn Thr Ser Ser Leu Gly
85 90 95
Tyr Glu Tyr Thr Gly Ser Lys Lys Glu Phe Pro Cys Val Asp Gly Tyr
100 105 110
Ile Tyr Asp Gln Asn Thr Trp Lys Ser Thr Ala Val Thr Gln Trp Asn
115 120 125
Leu Val Cys Asp Arg Lys Trp Leu Ala Met Leu Ile Gln Pro Leu Phe
130 135 140
Met Phe Gly Val Leu Leu Gly Ser Val Thr Phe Gly Tyr Phe Ser Asp
145 150 155 160
Arg Leu Gly Arg Arg Val Val Leu Trp Ala Thr Ser Ser Ser Met Phe
165 170 175
Leu Phe Gly Ile Ala Ala Ala Phe Ala Val Asp Tyr Tyr Thr Phe Met
180 185 190
Ala Ala Arg Phe Phe Leu Ala Met Val Ala Ser Gly Tyr Leu Val Val
195 200 205
Gly Phe Val Tyr Val Met Glu Phe Ile Gly Met Lys Ser Arg Thr Trp
210 215 220
Ala Ser Val His Leu His Ser Phe Phe Ala Val Gly Thr Leu Leu Val
225 230 235 240
Ala Leu Thr Gly Tyr Leu Val Arg Thr Trp Trp Leu Tyr Gln Met Ile
245 250 255
Leu Ser Thr Val Thr Val Pro Phe Ile Leu Cys Cys Trp Val Leu Pro
260 265 270
Glu Thr Pro Phe Trp Leu Leu Ser Glu Gly Arg Tyr Glu Glu Ala Gln
275 280 285
Lys Ile Val Asp Ile Met Ala Lys Trp Asn Arg Ala Ser Ser Cys Lys
290 295 300
Leu Ser Glu Leu Leu Ser Leu Asp Leu Gln Gly Pro Val Ser Asn Ser
305 310 315 320
Pro Thr Glu Val Gln Lys His Asn Leu Ser Tyr Leu Phe Tyr Asn Trp
325 330 335
Ser Ile Thr Lys Arg Thr Leu Thr Val Trp Leu Ile Trp Phe Thr Gly

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            340                 345                 350
Ser Leu Gly Phe Tyr Ser Phe Ser Leu Asn Ser Val Asn Leu Gly Gly
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Asn Glu Tyr Leu Asn Leu Phe Leu Leu Gly Val Val Glu Ile Pro Ala
    370                 375                 380
Tyr Thr Phe Val Cys Ile Ala Met Asp Lys Val Gly Arg Arg Thr Val
385                 390                 395                 400
Leu Ala Tyr Ser Leu Phe Cys Ser Ala Leu Ala Cys Gly Val Val Met
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Val Ile Pro Gln Lys His Tyr Ile Leu Gly Val Val Thr Ala Met Val
            420                 425                 430
Gly Lys Phe Ala Ile Gly Ala Ala Phe Gly Leu Ile Tyr Leu Tyr Thr
        435                 440                 445
Ala Glu Leu Tyr Pro Thr Ile Val Arg Ser Leu Ala Val Gly Ser Gly
    450                 455                 460
Ser Met Val Cys Arg Leu Ala Ser Ile Leu Ala Pro Phe Ser Val Asp
465                 470                 475                 480
Leu Ser Ser Ile Trp Ile Phe Ile Pro Gln Leu Phe Val Gly Thr Met
                485                 490                 495
Ala Leu Leu Ser Gly Val Leu Thr Leu Lys Leu Pro Glu Thr Leu Gly
            500                 505                 510
Lys Arg Leu Ala Thr Thr Trp Glu Glu Ala Ala Lys Leu Glu Ser Glu
        515                 520                 525
Asn Glu Ser Lys Ser Ser Lys Leu Leu Leu Thr Thr Asn Asn Ser Gly
    530                 535                 540
Leu Glu Lys Thr Glu Ala Ile Thr Pro Arg Asp Ser Gly Leu Gly Glu
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<210> 5605
<211> 376
<212> DNA
<213> Homo sapiens

<400> 5605
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catccaggga ggcctctcca gggaggatga cggaacatca gaggaaagaa gcaaggagaa
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240
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360
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376

<210> 5606
<211> 101
<212> PRT
<213> Homo sapiens

<400> 5606
Met Thr Arg Ala Leu Leu Thr Ser Leu Val Leu Leu Pro Ala Arg Gln
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Ala His Pro Cys Arg Ala Leu Ala Leu Thr Ala Pro Ile Phe Leu Leu
20 25 30
Leu Phe Pro Ser Ser Glu Cys Gly Trp Phe Ser Leu Leu Leu Ser Ser
35 40 45
Asp Val Pro Ser Ser Ser Leu Glu Arg Pro Pro Trp Met Thr Glu Glu
50 55 60
Val Thr Thr Thr Ser Ser Arg Ser Thr Pro Arg Pro Ser Val Ser Pro
65 70 75 80
Ser Gln Cys Leu Ala Pro Ser Asn Ile Ala Phe Cys Val Tyr His Gln
85 90 95
Phe Pro Phe Thr Arg
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<210> 5607
<211> 320
<212> DNA
<213> Homo sapiens

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ggtttgggcc gacacgcgga aggccgggtg gagcccatcc atgctgtggt gttgcctcga
120
gggaagtcgc tggaccagtg tgtggagacc ctgcagaagc agaccagggt tggcaaggct
180
ggcaccaaca agccccccag gtgccgggga agaggggcca ggcctggggg ccgcccagct
240
cctcggaatg tgtttgactt cctcaatgaa aagctgcaag gtcaggctcc tggggcccta
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caagccgggc ggcctcagca
320

<210> 5608
<211> 106
<212> PRT
<213> Homo sapiens

<400> 5608
Val His Thr Arg Gly Ile Gly Ser Arg Leu Leu Thr Lys Met Gly Tyr
1 5 10 15
Glu Phe Gly Lys Gly Leu Gly Arg His Ala Glu Gly Arg Val Glu Pro
20 25 30
Ile His Ala Val Val Leu Pro Arg Gly Lys Ser Leu Asp Gln Cys Val
35 40 45
Glu Thr Leu Gln Lys Gln Thr Arg Val Gly Lys Ala Gly Thr Asn Lys
50 55 60
Pro Pro Arg Cys Arg Gly Arg Gly Ala Arg Pro Gly Gly Arg Pro Ala
65 70 75 80
Pro Arg Asn Val Phe Asp Phe Leu Asn Glu Lys Leu Gln Gly Gln Ala
85 90 95
Pro Gly Ala Leu Gln Ala Gly Arg Pro Gln

100 105

<210> 5609
<211> 1843
<212> DNA
<213> Homo sapiens

<400> 5609
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120
tttaacattt cagtccattc actttttta aaataaaaat aggacaaatt attcaattac
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240
taaaaataga cccgtattga tcatacaaat ctatcatgag aagttaccca gtgagagtga
300
gttattgtaa ttctgaatgt actcatcgtg tttctcactt ctacagaagc atcctcagtg
360
agttgtattg tgcgagaaaa tgacaccctt gcccacatca ctctccattc catagaggga
420
cacaacccta tctagccaaa cccagaagaa cgcaggcgct tacacaactt ttctcggaca
480
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acgagatggt catcataata aggacattgt tgtttgagcg gggggtgtgc aatcagtata
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660
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720
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900
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1380

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1740
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1843

<210> 5610
<211> 153
<212> PRT
<213> Homo sapiens

<400> 5610
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20 25 30
Phe Thr Gly Gly Arg Gln Asp His Thr Ser Leu Pro His Trp Ala Cys
35 40 45
Leu Leu Val Asp Ser Cys Met Gln Glu Ala Val Met Gly Ser Leu Arg
50 55 60
Ile Pro Gln Cys Gly Asn Gly Pro Leu Arg Leu Val Leu Arg Val Pro
65 70 75 80
Gly Ala Gln Ser Trp Val Gly Gly Cys Trp Trp Glu Val Arg Asn Lys
85 90 95
Phe Trp Leu Pro Ser Gly Gln Leu Pro Thr Ala Leu Thr Trp Glu Val
100 105 110
Asp Ala His Arg Gln Asp Ala Leu Gly Tyr Cys Cys Thr Val Leu His
115 120 125
Glu Ile Phe Ile Gln Pro Thr Arg Phe Asn Arg Ser Leu Gly Ser Ser
130 135 140
Ser Arg Leu Leu Cys Leu Phe Lys His
145 150

<210> 5611
<211> 1152
<212> DNA
<213> Homo sapiens

<400> 5611
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120

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240
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gcagttctga acaaactgaa aactgcaatt ggagcagtgg agaaagacgt gggcctgtcg
540
gatgaagaga aactgtttca ggtgcacacg tttgaaattt tccagaaaga gctgaatgaa
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660
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720
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1020
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1152

<210> 5612
<211> 289
<212> PRT
<213> Homo sapiens

<400> 5612
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1 5 10 15
Pro Trp Ala Val Gln Ala Val Glu His Glu Glu Val Ala Gln Arg Val
20 25 30
Ile Lys Leu His Arg Gly Arg Gly Val Ala Ala Met Gln Ser Arg Gln
35 40 45
Trp Val Arg Asp Ser Cys Arg Lys Leu Ser Gly Leu Leu Arg Gln Lys
50 55 60
Asn Ala Val Leu Asn Lys Leu Lys Thr Ala Ile Gly Ala Val Glu Lys
65 70 75 80
Asp Val Gly Leu Ser Asp Glu Glu Lys Leu Phe Gln Val His Thr Phe

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                85                  90                  95
Glu Ile Phe Gln Lys Glu Leu Asn Glu Ser Glu Asn Ser Val Phe Gln
            100                 105                 110
Ala Val Tyr Gly Leu Gln Arg Ala Leu Gln Gly Asp Tyr Lys Asp Val
        115                 120                 125
Val Asn Met Lys Glu Ser Ser Arg Gln Arg Leu Glu Ala Leu Arg Glu
    130                 135                 140
Ala Ala Ile Lys Glu Glu Thr Glu Tyr Met Glu Leu Leu Ala Ala Glu
145                 150                 155                 160
Lys His Gln Val Glu Ala Leu Lys Asn Met Gln His Gln Asn Gln Ser
                165                 170                 175
Leu Ser Met Leu Asp Glu Ile Leu Glu Asp Val Arg Lys Ala Ala Asp
            180                 185                 190
Arg Leu Glu Glu Glu Ile Glu Glu His Ala Phe Asp Asp Asn Lys Ser
        195                 200                 205
Val Lys Gly Val Asn Phe Glu Ala Val Leu Arg Val Glu Glu Glu Glu
    210                 215                 220
Ala Asn Ser Lys Gln Asn Ile Thr Lys Arg Glu Val Glu Asp Asp Leu
225                 230                 235                 240
Val Leu Ser Met Leu Ile Asp Ser Gln Asn Asn Gln Tyr Ile Leu Thr
                245                 250                 255
Lys Pro Arg Asp Ser Thr Ile Pro Arg Ala Asp His His Phe Ile Lys
            260                 265                 270
Asp Ile Val Thr Ile Gly Met Leu Ser Leu Pro Cys Gly Trp Arg Cys
        275                 280                 285
Thr
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<210> 5613
<211> 1679
<212> DNA
<213> Homo sapiens

<400> 5613

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ctcagaccct gtggggtcaa gtcggcggtg gaggccctag gctcagcctg tggggaccgg
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540
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600
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tcagattatg ctgctgccca gttacgccag tatcatcggt tgaccaagca gatcaaacct
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<210> 5614
<211> 242
<212> PRT
<213> Homo sapiens

<400> 5614
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Ser Leu Ala Ala Ala Ala Glu Leu Ala Ala Gln Lys Arg Glu Gln Arg
20 25 30
Leu Arg Lys Phe Arg Glu Leu His Leu Met Arg Asn Glu Ala Arg Lys
35 40 45
Leu Asn His Gln Glu Val Val Glu Glu Asp Lys Arg Leu Lys Leu Pro
50 55 60
Ala Asn Trp Glu Ala Lys Lys Ala Arg Leu Glu Trp Glu Leu Lys Glu
65 70 75 80
Glu Glu Lys Lys Lys Glu Cys Ala Ala Arg Gly Glu Asp Tyr Glu Lys

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                85                  90                  95
Val Lys Leu Leu Glu Ile Ser Ala Glu Asp Ala Glu Arg Trp Glu Arg
            100                 105                 110
Lys Lys Lys Arg Lys Asn Pro Asp Leu Gly Phe Ser Asp Tyr Ala Ala
        115                 120                 125
Ala Gln Leu Arg Gln Tyr His Arg Leu Thr Lys Gln Ile Lys Pro Asp
    130                 135                 140
Met Glu Thr Tyr Glu Arg Leu Arg Glu Lys His Gly Glu Glu Phe Phe
145                 150                 155                 160
Pro Thr Ser Asn Ser Leu Leu His Gly Thr His Val Pro Ser Thr Glu
                165                 170                 175
Glu Ile Asp Arg Met Val Ile Asp Leu Glu Lys Gln Ile Glu Lys Arg
            180                 185                 190
Asp Lys Tyr Ser Arg Arg Arg Pro Tyr Asn Asp Asp Ala Asp Ile Asp
        195                 200                 205
Tyr Ile Asn Glu Arg Asn Ala Lys Phe Asn Lys Lys Ala Glu Arg Phe
    210                 215                 220
Tyr Gly Lys Tyr Thr Ala Glu Ile Lys Gln Asn Leu Glu Arg Gly Thr
225                 230                 235                 240
Ala Val
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<210> 5615
<211> 1522
<212> DNA
<213> Homo sapiens

<400> 5615
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ccacagactg ttccttcaca accgtccagt agtactgtcc ctcctccacc acacagacct
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240
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420
gcaatttccc tttctgagcc tcgtatgctg tgggggtcag atccctatcc tcatgctgag
480
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720
gaagcacctg atcaaaagac cttatccact cctcaagagg agcggatttc agctgtagaa
780

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840
gagcagagaa gtgaaccatc tgcaggcatt cctaaagtaa ccagcagatg cattgattca
900
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1020
ccaagctcta acagaaggga agaagttaat gatagacctg tgagaagatc aggtcccatt
1080
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1140
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1200
gatcttcctc ctcccccacc accacctcag ccaccagcac caattcagcc acagtcagtt
1260
ccaccaccaa ttcaaccaga agcagagaaa tttccttcaa cagaaactgc aactttggct
1320
caaaaaccat ctcaggatac tgagaagcct ctggaacctg tgagtactgt tcaggtagag
1380
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1500
gaaaaagaac tacaaaaaaa aa
1522

<210> 5616
<211> 507
<212> PRT
<213> Homo sapiens

<400> 5616
Pro Ala Val Leu Ser Gly Tyr Phe Lys Gln Phe Gln Lys Ser Leu Pro
1 5 10 15
Pro Arg Phe Gln Arg Gln Gln Glu Gln Met Lys Gln Gln Gln Trp Gln
20 25 30
Gln Gln Gln Gln Gln Gly Val Leu Pro Gln Thr Val Pro Ser Gln Pro
35 40 45
Ser Ser Ser Thr Val Pro Pro Pro Pro His Arg Pro Leu Tyr Gln Pro
50 55 60
Met Gln Pro His Pro Gln His Leu Ala Ser Met Gly Phe Asp Pro Arg
65 70 75 80
Trp Leu Met Met Gln Ser Tyr Met Asp Pro Arg Met Met Ser Gly Arg
85 90 95
Pro Ala Met Asp Ile Pro Pro Ile His Pro Gly Met Ile Pro Pro Lys
100 105 110
Pro Leu Met Arg Arg Asp Gln Met Glu Gly Ser Pro Asn Ser Ser Glu
115 120 125
Ser Phe Glu His Ile Ala Arg Ser Ala Arg Asp His Ala Ile Ser Leu
130 135 140
Ser Glu Pro Arg Met Leu Trp Gly Ser Asp Pro Tyr Pro His Ala Glu
145 150 155 160
Pro Gln Gln Ala Thr Thr Pro Lys Ala Thr Glu Glu Pro Glu Asp Val

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                165                 170                 175
Arg Ser Glu Ala Ala Leu Asp Gln Glu Gln Ile Thr Ala Ala Tyr Ser
            180                 185                 190
Val Glu His Asn Gln Leu Glu Ala His Pro Lys Ala Asp Phe Ile Arg
        195                 200                 205
Glu Ser Ser Glu Ala Gln Val Gln Lys Phe Leu Ser Arg Ser Val Glu
    210                 215                 220
Asp Val Arg Pro His His Thr Asp Ala Asn Asn Gln Ser Ala Cys Phe
225                 230                 235                 240
Glu Ala Pro Asp Gln Lys Thr Leu Ser Thr Pro Gln Glu Glu Arg Ile
                245                 250                 255
Ser Ala Val Glu Ser Gln Pro Ser Arg Lys Arg Ser Val Ser His Gly
            260                 265                 270
Ser Asn His Thr Gln Lys Pro Asp Glu Gln Arg Ser Glu Pro Ser Ala
        275                 280                 285
Gly Ile Pro Lys Val Thr Ser Arg Cys Ile Asp Ser Lys Glu Pro Ile
    290                 295                 300
Glu Arg Pro Glu Glu Lys Pro Lys Lys Glu Gly Phe Ile Arg Ser Ser
305                 310                 315                 320
Glu Gly Pro Lys Pro Glu Lys Val Tyr Lys Ser Lys Ser Glu Thr Arg
                325                 330                 335
Trp Gly Pro Arg Pro Ser Ser Asn Arg Arg Glu Glu Val Asn Asp Arg
            340                 345                 350
Pro Val Arg Arg Ser Gly Pro Ile Lys Lys Pro Val Leu Arg Asp Met
        355                 360                 365
Lys Glu Glu Arg Glu Gln Arg Lys Glu Lys Glu Gly Glu Lys Ala Glu
    370                 375                 380
Lys Val Thr Glu Lys Val Val Val Lys Pro Glu Lys Thr Glu Lys Lys
385                 390                 395                 400
Asp Leu Pro Pro Pro Pro Pro Pro Pro Gln Pro Pro Ala Pro Ile Gln
                405                 410                 415
Pro Gln Ser Val Pro Pro Pro Ile Gln Pro Glu Ala Glu Lys Phe Pro
            420                 425                 430
Ser Thr Glu Thr Ala Thr Leu Ala Gln Lys Pro Ser Gln Asp Thr Glu
        435                 440                 445
Lys Pro Leu Glu Pro Val Ser Thr Val Gln Val Glu Pro Ala Val Lys
    450                 455                 460
Thr Val Asn Gln Gln Thr Met Ala Ala Pro Val Val Lys Glu Lys Glu
465                 470                 475                 480
Leu Gln Lys Lys Glu Arg Lys Gln Glu Lys Glu Lys Glu Leu Glu Arg
                485                 490                 495
Gln Lys Glu Lys Glu Lys Glu Leu Gln Lys Lys
            500                 505
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<210> 5617
<211> 3480
<212> DNA
<213> Homo sapiens

<400> 5617
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aataagtttt cgtaggttat actatcattt ttttttctga cttttagaaa aaaaatgatc
120

atttacttga ttttttttaa gttgtatttt taatttgaga ggatttcaca tgaactgtaa
180
tgtttgtgtt ttcagccagt gcacaaagac tctattagcc ttttcatggc acatgttcac
240
accactgtaa atgaaatgag taccagatat taccagaatg agagaagaca caactatacc
300
accccaaaga gttttctaga acaaatatca ctgtttaaga acctgttgaa gaagaagcaa
360
aatgaggtat ccgagaaaaa agaacgcctg gtgaacggca tccaaaagct aaaaaccaca
420
gcctctcagg tgggagatct aaaagccaga cttgcctctc aagaagccga gctgcaactg
480
agaaatcatg atgccgaagc tctgatcaca aagatcggcc ttcagacgga gaaagtgagc
540
cgggaaaaga ccatcgctga tgctgaggag cgaaaggtga cagccattca gactgaagtg
600
ttccagaaac agagagaatg tgaagctgac ttactcaagg ctgagcctgc actggtggct
660
gctacagctg cactcaatac actcaacagg gtcaacctca gtgagctgaa agcctttccc
720
aaccctccca tcgcagttac caatgttact gcagccgtga tggtccttct ggctcctcgg
780
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840
gatttttgc aagcattaat taactatgac aaagagcaca ttccagagaa ctgtctaaaa
900
gtggtgaatg aacactattt gaaagaccca gagtttaatc caaacctgat tcgaaccaaa
960
tcttttgcag cagctggcct gtgtgcctgg gtcatcaaca tcattaaatt ctatgaggtc
1020
tactgtgatg tggagccaaa acgccaagca ttagcccaag caaacttaga actggctgca
1080
gctactgaaa aactagaggc tatcaggaaa aagcttgtgg tgagtgcaaa ctatgacatt
1140
gaaaagtcag agaagattcg ctggggtcaa tccattaagt cctttgaagc tcaagagaag
1200
acactctgtg gagatgttct tctcacggcg gcatttgtgt cttacgtcgg acccttcaca
1260
aggcagtatc gccaggagct ggtgcactgc aagtgggttc cctttcttca acagaaggtt
1320
tccattccac taaccgaagg cctggacttg atatccatgt tgacggatga tgctacaatt
1380
gccgcctgga ataacgaagg actgcccagt gacagaatgt ccaccgaaaa tgccgctatc
1440
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1500
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1560
aatgccattg aaactgcttt ggcctttggt gatgtcatct taattgaaaa tctcgaggaa
1620
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1680
atcaggattg gagataaaga atgtgaattt aacaagaact ttcgccttat ccttcacaca
1740

aaattggcaa atcctcacta taagccggaa ttacaagctc agacaactct cctcaatttc
1800
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1860
ccagatttgg agaaacttaa gttggtattg acaaagcacc aaaatgattt taaaattgag
1920
ctcaagtatc tggaagacga tctccttttg cgcctttctg cggcagaggg aagctttctg
1980
gatgacacca aactggtaga gagattggag gcaacaaaga ccaccgtggc agagatagag
2040
cacaaggtga ttgaagccaa agaaaatgaa agaaaaatca acgaggcccg agaatgttac
2100
agaccagtgg cagcaagagc atctcttctt tattttgtta ttaatgacct ccaaaaaatc
2160
aacccctct accaattctc tttgaaggct tttaacgtgc tgttccacag agcgatcgag
2220
caggctgaca aggtggaaga catgcaggga cgcatctcta tcctgatgga gagcatcacc
2280
catgctgtct tcctctacac cagccaggcg ctgtttgaga aggacaagct caccttcctg
2340
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2400
ttcctgcttc gattcacagt tgaacacact catctgagtc ccgttgactt cctaacttct
2460
cagtcatgga gtgctatcaa ggcaattgcc gtcatggaag aatttcgagg catagaccga
2520
gatgtggaag gatctgccaa gcagtggagg aagtgggtag aatccgagtg tccagaaaaa
2580
gaaaaattac ctcaagaatg gaagaagaaa agtttaatac agaagctgat tcttctgaga
2640
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2700
gcgaagtatg tggagaggac cagattggac ttagttaaag cattcgaaga aagcagccca
2760
gccacccca tattcttcat cctgtctccg ggggtagatg cccttaaaga cctggagatt
2820
cttggcaaaa gacttggctt tacaattgac tctggaaaat tccacaatgt gtctttagga
2880
caaggtcagg agacggtggc agaagtggcc ctggagaaag cttccaaagg aggacactgg
2940
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3000
gaaagattca gccaaggaag ccacagagat tacagggttt tcatgagtgc tgagtctgca
3060
cctacaccag atgagcatat catccctcaa ggactcctgg aaaattccat taagatcact
3120
aatgaacccc caacagggat gctggccaat ttgcatgccg ccctgtacaa ctttgatcag
3180
gtaagaaagc gaagcaggct aggcagacaa tgaagtcaga gtcatctcac aagactgtgg
3240
ggcccagaat caacccaggc atgtcattga gagggatgaa gcaagttctt aatgttcgca
3300
tgtggaaggg taggggtggg cgtgttttaa tctcttgaaa gaattgcccc tgtcatttcc
3360

gattctaatg accagtaaat atatttcagt ctcaccctaa cattaagaaa acttcagcta
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3480

<210> 5618
<211> 1003
<212> PRT
<213> Homo sapiens

<400> 5618
His Lys Asp Ser Ile Ser Leu Phe Met Ala His Val His Thr Thr Val
1 5 10 15
Asn Glu Met Ser Thr Arg Tyr Tyr Gln Asn Glu Arg Arg His Asn Tyr
20 25 30
Thr Thr Pro Lys Ser Phe Leu Glu Gln Ile Ser Leu Phe Lys Asn Leu
35 40 45
Leu Lys Lys Lys Gln Asn Glu Val Ser Glu Lys Lys Glu Arg Leu Val
50 55 60
Asn Gly Ile Gln Lys Leu Lys Thr Thr Ala Ser Gln Val Gly Asp Leu
65 70 75 80
Lys Ala Arg Leu Ala Ser Gln Glu Ala Glu Leu Gln Leu Arg Asn His
85 90 95
Asp Ala Glu Ala Leu Ile Thr Lys Ile Gly Leu Gln Thr Glu Lys Val
100 105 110
Ser Arg Glu Lys Thr Ile Ala Asp Ala Glu Glu Arg Lys Val Thr Ala
115 120 125
Ile Gln Thr Glu Val Phe Gln Lys Gln Arg Glu Cys Glu Ala Asp Leu
130 135 140
Leu Lys Ala Glu Pro Ala Leu Val Ala Ala Thr Ala Ala Leu Asn Thr
145 150 155 160
Leu Asn Arg Val Asn Leu Ser Glu Leu Lys Ala Phe Pro Asn Pro Pro
165 170 175
Ile Ala Val Thr Asn Val Thr Ala Ala Val Met Val Leu Leu Ala Pro
180 185 190
Arg Gly Arg Val Pro Lys Asp Arg Ser Trp Lys Ala Ala Lys Val Phe
195 200 205
Met Gly Lys Val Asp Asp Phe Leu Gln Ala Leu Ile Asn Tyr Asp Lys
210 215 220
Glu His Ile Pro Glu Asn Cys Leu Lys Val Val Asn Glu His Tyr Leu
225 230 235 240
Lys Asp Pro Glu Phe Asn Pro Asn Leu Ile Arg Thr Lys Ser Phe Ala
245 250 255
Ala Ala Gly Leu Cys Ala Trp Val Ile Asn Ile Ile Lys Phe Tyr Glu
260 265 270
Val Tyr Cys Asp Val Glu Pro Lys Arg Gln Ala Leu Ala Gln Ala Asn
275 280 285
Leu Glu Leu Ala Ala Ala Thr Glu Lys Leu Glu Ala Ile Arg Lys Lys
290 295 300
Leu Val Val Ser Ala Asn Tyr Asp Ile Glu Lys Ser Glu Lys Ile Arg
305 310 315 320
Trp Gly Gln Ser Ile Lys Ser Phe Glu Ala Gln Glu Lys Thr Leu Cys
325 330 335
Gly Asp Val Leu Leu Thr Ala Ala Phe Val Ser Tyr Val Gly Pro Phe

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                340                 345                 350
Thr Arg Gln Tyr Arg Gln Glu Leu Val His Cys Lys Trp Val Pro Phe
        355                 360                 365
Leu Gln Gln Lys Val Ser Ile Pro Leu Thr Glu Gly Leu Asp Leu Ile
    370                 375                 380
Ser Met Leu Thr Asp Asp Ala Thr Ile Ala Ala Trp Asn Asn Glu Gly
385                 390                 395                 400
Leu Pro Ser Asp Arg Met Ser Thr Glu Asn Ala Ala Ile Leu Thr His
                405                 410                 415
Cys Glu Arg Trp Pro Leu Val Ile Asp Pro Gln Gln Gln Gly Ile Lys
            420                 425                 430
Trp Ile Lys Asn Lys Tyr Gly Met Asp Leu Lys Val Thr His Leu Gly
        435                 440                 445
Gln Lys Gly Phe Leu Asn Ala Ile Glu Thr Ala Leu Ala Phe Gly Asp
    450                 455                 460
Val Ile Leu Ile Glu Asn Leu Glu Glu Thr Ile Asp Pro Val Leu Asp
465                 470                 475                 480
Pro Leu Leu Gly Arg Asn Thr Ile Lys Lys Gly Lys Tyr Ile Arg Ile
                485                 490                 495
Gly Asp Lys Glu Cys Glu Phe Asn Lys Asn Phe Arg Leu Ile Leu His
            500                 505                 510
Thr Lys Leu Ala Asn Pro His Tyr Lys Pro Glu Leu Gln Ala Gln Thr
        515                 520                 525
Thr Leu Leu Asn Phe Thr Val Thr Glu Asp Gly Leu Glu Ala Gln Leu
    530                 535                 540
Leu Ala Glu Val Val Ser Ile Glu Arg Pro Asp Leu Glu Lys Leu Lys
545                 550                 555                 560
Leu Val Leu Thr Lys His Gln Asn Asp Phe Lys Ile Glu Leu Lys Tyr
                565                 570                 575
Leu Glu Asp Asp Leu Leu Leu Arg Leu Ser Ala Ala Glu Gly Ser Phe
            580                 585                 590
Leu Asp Asp Thr Lys Leu Val Glu Arg Leu Glu Ala Thr Lys Thr Thr
        595                 600                 605
Val Ala Glu Ile Glu His Lys Val Ile Glu Ala Lys Glu Asn Glu Arg
    610                 615                 620
Lys Ile Asn Glu Ala Arg Glu Cys Tyr Arg Pro Val Ala Ala Arg Ala
625                 630                 635                 640
Ser Leu Leu Tyr Phe Val Ile Asn Asp Leu Gln Lys Ile Asn Pro Leu
                645                 650                 655
Tyr Gln Phe Ser Leu Lys Ala Phe Asn Val Leu Phe His Arg Ala Ile
            660                 665                 670
Glu Gln Ala Asp Lys Val Glu Asp Met Gln Gly Arg Ile Ser Ile Leu
        675                 680                 685
Met Glu Ser Ile Thr His Ala Val Phe Leu Tyr Thr Ser Gln Ala Leu
    690                 695                 700
Phe Glu Lys Asp Lys Leu Thr Phe Leu Ser Gln Met Ala Phe Gln Ile
705                 710                 715                 720
Leu Leu Arg Lys Lys Glu Ile Asp Pro Leu Glu Leu Asp Phe Leu Leu
                725                 730                 735
Arg Phe Thr Val Glu His Thr His Leu Ser Pro Val Asp Phe Leu Thr
            740                 745                 750
Ser Gln Ser Trp Ser Ala Ile Lys Ala Ile Ala Val Met Glu Glu Phe
        755                 760                 765
Arg Gly Ile Asp Arg Asp Val Glu Gly Ser Ala Lys Gln Trp Arg Lys
```

```
    770                 775                 780
Trp Val Glu Ser Glu Cys Pro Glu Lys Glu Lys Leu Pro Gln Glu Trp
785                 790                 795                 800
Lys Lys Lys Ser Leu Ile Gln Lys Leu Ile Leu Leu Arg Ala Met Arg
                805                 810                 815
Pro Asp Arg Met Thr Tyr Ala Leu Arg Asn Phe Val Glu Glu Lys Leu
            820                 825                 830
Gly Ala Lys Tyr Val Glu Arg Thr Arg Leu Asp Leu Val Lys Ala Phe
        835                 840                 845
Glu Glu Ser Ser Pro Ala Thr Pro Ile Phe Phe Ile Leu Ser Pro Gly
    850                 855                 860
Val Asp Ala Leu Lys Asp Leu Glu Ile Leu Gly Lys Arg Leu Gly Phe
865                 870                 875                 880
Thr Ile Asp Ser Gly Lys Phe His Asn Val Ser Leu Gly Gln Gly Gln
                885                 890                 895
Glu Thr Val Ala Glu Val Ala Leu Glu Lys Ala Ser Lys Gly Gly His
            900                 905                 910
Trp Val Ile Leu Gln Asn Val His Leu Val Ala Lys Trp Leu Gly Thr
        915                 920                 925
Leu Glu Lys Leu Leu Glu Arg Phe Ser Gln Gly Ser His Arg Asp Tyr
    930                 935                 940
Arg Val Phe Met Ser Ala Glu Ser Ala Pro Thr Pro Asp Glu His Ile
945                 950                 955                 960
Ile Pro Gln Gly Leu Leu Glu Asn Ser Ile Lys Ile Thr Asn Glu Pro
                965                 970                 975
Pro Thr Gly Met Leu Ala Asn Leu His Ala Ala Leu Tyr Asn Phe Asp
            980                 985                 990
Gln Val Arg Lys Arg Ser Arg Leu Gly Arg Gln
        995                 1000
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<210> 5619
<211> 1219
<212> DNA
<213> Homo sapiens

<400> 5619
aagccggaga gctggagctt tgaagccacc ccggtcaaag gatgctgagt ccggagcgcc
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tagccctacc ggactacgag tatctggctc agcgacatgt cctcacctac atggaggatg
120
cagtgtgcca gctgctagaa aacagggaag atattagcca atatggaatt gccaggttct
180
tcactgaata ttttaacagt gtatgccagg gaacacacat tctctttcga gaattcagct
240
tcgtccaagc caccccccac aatagggtat cattttacg ggccttctgg agatgcttcc
300
gaactgtggg caaaaatggc gatttgctga ccatgaaaga atatcactgt ttgctgcaat
360
tactgtgtcc tgatttcccg ctggagctca ctcagaaagc agccaggatt gtgctcatgg
420
acgatgccat ggactgcttg atgtcttttt cagatttcct ctttgccttc cagatccagt
480
tttactactc agaattcctg gacagtgtgg ctgccatcta tgaggacctg ctgtcaggca
540

agaaccccaa cacagtgatt gtgccgacgt cgtccagtgg gcagcaccgc caacgacctg
600
ccttgggcgg ggccggcacg ctggagggcg tggaggcgtc gctgttctac cagtgtctgg
660
aaaacctgtg tgatcggcac aagtacagct gcccaccccc agcacttgtc aaagaggccc
720
tcagcaatgt tcagagactg accttctatg gattcctcat ggctctctca aagcaccgtg
780
gaatcaacca agccctcggt aagtcagagc taagcagccg tcagcctctc ctgccgcaca
840
acacagggag cagctggcct ctgttagcaa cacggctcca gaggggaagg ggcatcacca
900
tctctgcctt gacttcccag ggccggactc aatcccaggg agcaggaata tggcgacaaa
960
acatggctct tacacattcc catggtaggg gacagccctc cctgcctgca gccctgcccc
1020
aacatgaaac cacctcccca tagcagaagc gcccagcccc tcctcagaga accccagctc
1080
tgctttgggg agcagcctgc aggtcgggca gacacaggac tatttactca gtgacgctag
1140
agattatata tcagagagac ctgaatccca tttataaaca aggcaaaggt gtgtctgcgg
1200
agacctttt tccaagctg
1219

<210> 5620
<211> 333
<212> PRT
<213> Homo sapiens

<400> 5620
Met Leu Ser Pro Glu Arg Leu Ala Leu Pro Asp Tyr Glu Tyr Leu Ala
1 5 10 15
Gln Arg His Val Leu Thr Tyr Met Glu Asp Ala Val Cys Gln Leu Leu
20 25 30
Glu Asn Arg Glu Asp Ile Ser Gln Tyr Gly Ile Ala Arg Phe Phe Thr
35 40 45
Glu Tyr Phe Asn Ser Val Cys Gln Gly Thr His Ile Leu Phe Arg Glu
50 55 60
Phe Ser Phe Val Gln Ala Thr Pro His Asn Arg Val Ser Phe Leu Arg
65 70 75 80
Ala Phe Trp Arg Cys Phe Arg Thr Val Gly Lys Asn Gly Asp Leu Leu
85 90 95
Thr Met Lys Glu Tyr His Cys Leu Leu Gln Leu Leu Cys Pro Asp Phe
100 105 110
Pro Leu Glu Leu Thr Gln Lys Ala Ala Arg Ile Val Leu Met Asp Asp
115 120 125
Ala Met Asp Cys Leu Met Ser Phe Ser Asp Phe Leu Phe Ala Phe Gln
130 135 140
Ile Gln Phe Tyr Tyr Ser Glu Phe Leu Asp Ser Val Ala Ala Ile Tyr
145 150 155 160
Glu Asp Leu Leu Ser Gly Lys Asn Pro Asn Thr Val Ile Val Pro Thr
165 170 175
Ser Ser Ser Gly Gln His Arg Gln Arg Pro Ala Leu Gly Gly Ala Gly

```
            180                 185                 190
Thr Leu Glu Gly Val Glu Ala Ser Leu Phe Tyr Gln Cys Leu Glu Asn
        195                 200                 205
Leu Cys Asp Arg His Lys Tyr Ser Cys Pro Pro Pro Ala Leu Val Lys
    210                 215                 220
Glu Ala Leu Ser Asn Val Gln Arg Leu Thr Phe Tyr Gly Phe Leu Met
225                 230                 235                 240
Ala Leu Ser Lys His Arg Gly Ile Asn Gln Ala Leu Gly Lys Ser Glu
                245                 250                 255
Leu Ser Ser Arg Gln Pro Leu Leu Pro His Asn Thr Gly Ser Ser Trp
            260                 265                 270
Pro Leu Leu Ala Thr Arg Leu Gln Arg Gly Arg Gly Ile Thr Ile Ser
        275                 280                 285
Ala Leu Thr Ser Gln Gly Arg Thr Gln Ser Gln Gly Ala Gly Ile Trp
    290                 295                 300
Arg Gln Asn Met Ala Leu Thr His Ser His Gly Arg Gly Gln Pro Ser
305                 310                 315                 320
Leu Pro Ala Ala Leu Pro Gln His Glu Thr Thr Ser Pro
                325                 330
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<210> 5621
<211> 456
<212> DNA
<213> Homo sapiens

<400> 5621
ttttttgtgaa atagaattta ttgtggctct gattatgtac acgtgagatg gcctggctgg
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gccggccggg ctcacatggt ttgtacaata aatacatctg tggggcgggc tctccgcagc
120
cgggaagggc caccgccacg gttcagtcca gcttccgggc tcccagcttc atggggccct
180
tggccacctt cctctcggcg cgtttggcct ccatctcccg ccgccgctcc tcgcgcttct
240
tccgggccag ctcagccttg acctgtcctg ggtgctggga cgtgcagaca gggtagcgaa
300
ggggtcgccc ttgtcgctgg actctgggcc accccagtta tactcgctgg ccagccgtgt
360
accgtcagga ggtggctcct gggagcttgg ctgaacccgt ggcggtggcc cttcccggct
420
gcggagagcc cgccccacag atgtatttat tgtaca
456

<210> 5622
<211> 82
<212> PRT
<213> Homo sapiens

<400> 5622
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Met Ala Trp Leu Gly Arg Pro Gly Ser His Gly Leu Tyr Asn Lys Tyr
 1               5                  10                  15
Ile Cys Gly Ala Gly Ser Pro Gln Pro Gly Arg Ala Thr Ala Thr Val
            20                  25                  30
Gln Ser Ser Phe Arg Ala Pro Ser Phe Met Gly Pro Leu Ala Thr Phe
```

```
        35                  40                  45
Leu Ser Ala Arg Leu Ala Ser Ile Ser Arg Arg Arg Ser Ser Arg Phe
    50                  55                  60
Phe Arg Ala Ser Ser Ala Leu Thr Cys Pro Gly Cys Trp Asp Val Gln
65                  70                  75                  80
Thr Gly
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<210> 5623
<211> 357
<212> DNA
<213> Homo sapiens

<400> 5623
nctggaagaa ctcgtcatgc tctttgtagc gtggtgcttc tgttgctcac aggacaactt
60
gcctttgatg attttcaaga gagttgtgct atgatgtggc aaaagtatgc aggaagcagg
120
cggtcaatgc ctctgggagc aaggatcctt ttccacggtg tgttctatgc cgggggcttt
180
gccattgtgt attacctcat tcaaaagttt cattccaggg ctttatatta caagttggca
240
gtggagcagc tgcagagcca tcccgaggca caggaagctc tgggccctcc tctcaacatc
300
cattatctca agctcatcga cagggaaaac ttcgtggaca ttgttgatgc caagttg
357

<210> 5624
<211> 88
<212> PRT
<213> Homo sapiens

<400> 5624
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Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg Ser Met Pro Leu Gly Ala
 1               5                  10                  15
Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly Gly Phe Ala Ile Val
            20                  25                  30
Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Ala Leu Tyr Tyr Lys Leu
        35                  40                  45
Ala Val Glu Gln Leu Gln Ser His Pro Glu Ala Gln Glu Ala Leu Gly
    50                  55                  60
Pro Pro Leu Asn Ile His Tyr Leu Lys Leu Ile Asp Arg Glu Asn Phe
65                  70                  75                  80
Val Asp Ile Val Asp Ala Lys Leu
                85
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<210> 5625
<211> 1017
<212> DNA
<213> Homo sapiens

<400> 5625
gccgactcgt ggtacctggc gcttctgggc ttcgctgagc acttccgcac ttccagcccg
60

cccaaaatcc gcctgtgcgt gcactgcctg caggccgtgt tccccttcaa gccgccgcag
120
cgcatcgagg cccgtacaca cctgcagctg ggctccgttc tctatcacca caccaagaac
180
agcgagcagg cgcgcagcca cctggagaag gcgtggttga tatcacagca aatcccacag
240
ttcgaagatg ttaaatttga agcagcaagt ctgttgtctg aattgtactg tcaagagaat
300
tccgttgatg cagcaaagcc gctgctgcgg aaggcgatcc agatctcaca gcagacccca
360
tattggcact gccgcctgct cttccagctc gctcaactgc acacgcttga gaaggacctg
420
gtgtcggcct gtgacctcct gggtgtaggg gccgagtacg cccgggtggt gggatctgaa
480
tacacacggg cgctgttcct cctcagcaag gggatgctgc tgctgatgga gcgaaagctg
540
caggaggtgc acccgctgct gaccctctgc gggcagatcg tggagaactg gcaggggaac
600
cccatccaga aggagtcgct gcgtgtcttc ttcctggtgc tccaggtcac ccactatctg
660
gatgccgggc aggtgaagag cgtgaagccg tgtctgaagc agctgcagca gtgcatccag
720
accatctcca cactgcacga tgatgagatc ctgcccagca accccgctga cctcttccac
780
tggctgccca aggagcacat gtgtgtgctt gtctacctgg tgactgtgat gcactccatg
840
caggccggct acctggagaa ggcgcagaag tacacggaca aggccctcat gcagctggag
900
aagctcaaga tgctggactg cagccccatc ctgtcatcct tccaagtgat cctgctggag
960
cacatcatca tgtgccgcct tgtcacgggt cacaaggcca cggcgctgca ggagatc
1017

<210> 5626
<211> 339
<212> PRT
<213> Homo sapiens

<400> 5626
Ala Asp Ser Trp Tyr Leu Ala Leu Leu Gly Phe Ala Glu His Phe Arg
1 5 10 15
Thr Ser Ser Pro Pro Lys Ile Arg Leu Cys Val His Cys Leu Gln Ala
20 25 30
Val Phe Pro Phe Lys Pro Pro Gln Arg Ile Glu Ala Arg Thr His Leu
35 40 45
Gln Leu Gly Ser Val Leu Tyr His His Thr Lys Asn Ser Glu Gln Ala
50 55 60
Arg Ser His Leu Glu Lys Ala Trp Leu Ile Ser Gln Gln Ile Pro Gln
65 70 75 80
Phe Glu Asp Val Lys Phe Glu Ala Ala Ser Leu Leu Ser Glu Leu Tyr
85 90 95
Cys Gln Glu Asn Ser Val Asp Ala Ala Lys Pro Leu Leu Arg Lys Ala
100 105 110
Ile Gln Ile Ser Gln Gln Thr Pro Tyr Trp His Cys Arg Leu Leu Phe

```
        115                 120                 125
Gln Leu Ala Gln Leu His Thr Leu Glu Lys Asp Leu Val Ser Ala Cys
    130                 135                 140
Asp Leu Leu Gly Val Gly Ala Glu Tyr Ala Arg Val Val Gly Ser Glu
145                 150                 155                 160
Tyr Thr Arg Ala Leu Phe Leu Leu Ser Lys Gly Met Leu Leu Leu Met
                165                 170                 175
Glu Arg Lys Leu Gln Glu Val His Pro Leu Leu Thr Leu Cys Gly Gln
            180                 185                 190
Ile Val Glu Asn Trp Gln Gly Asn Pro Ile Gln Lys Glu Ser Leu Arg
        195                 200                 205
Val Phe Phe Leu Val Leu Gln Val Thr His Tyr Leu Asp Ala Gly Gln
    210                 215                 220
Val Lys Ser Val Lys Pro Cys Leu Lys Gln Leu Gln Gln Cys Ile Gln
225                 230                 235                 240
Thr Ile Ser Thr Leu His Asp Asp Glu Ile Leu Pro Ser Asn Pro Ala
                245                 250                 255
Asp Leu Phe His Trp Leu Pro Lys Glu His Met Cys Val Leu Val Tyr
            260                 265                 270
Leu Val Thr Val Met His Ser Met Gln Ala Gly Tyr Leu Glu Lys Ala
        275                 280                 285
Gln Lys Tyr Thr Asp Lys Ala Leu Met Gln Leu Glu Lys Leu Lys Met
    290                 295                 300
Leu Asp Cys Ser Pro Ile Leu Ser Ser Phe Gln Val Ile Leu Leu Glu
305                 310                 315                 320
His Ile Ile Met Cys Arg Leu Val Thr Gly His Lys Ala Thr Ala Leu
                325                 330                 335
Gln Glu Ile
```

<210> 5627
<211> 1401
<212> DNA
<213> Homo sapiens

<400> 5627
nctctcacac tgtggaattc tctctatcag cctcaaagtc cagatttgga aagggagtct
60
cagcgagggg cagcagctgg cccaacccgg aggcagagcg gcaactgaac tctagccgga
120
aagagccagg gttatgtgca catgggaggt ggggaggaca ggggctgtat gtgaccctca
180
catctgttcc tcgcgcccca gatggcttct gctgcctgct ccatggaccc catcgacagc
240
tttgagctcc tggatctcct gtttgaccgg caggacggca tcctgagaca cgtggagctg
300
ggcgagggct ggggtcacgt caaggaccag gtcctgccaa accccgactc tgacgacttc
360
ctcagctcca tcctgggctc tggagactca ctgcccagct ccccactctg gtcccccgaa
420
ggcagtgata gtggcatctc cgaagacctc ccctccgacc cccaggacac ccctccacgc
480
agcggaccag ccacctcccc cgccggctgc catcctgccc agcctggcaa ggggccctgc
540

ctctcctatc atcctggcaa ctcttgctcc accacaaccc cagggccagt gatccaacaa
600
cagcatcacc tgggggcctc ctacctcctg cgacctgggg ctgggcactg tcaggagctg
660
gtgctcaccg aggatgagaa gaagctgctg gctaaagaag gcatcaccct gcccactcag
720
ctgcccctca ctaagtacga ggagcgagtg ctgaaaaaaa tccgccggaa aatccggaac
780
aagcagtcgg cgcaagaaag caggaagaag aagaaggaat atatcgatgg cctggagact
840
cggtcctgtt gctgtccttt gccctcatca tcctcccctc catcagccct tttggcccca
900
acaaaaccga gagccctggg gactttgcgc ctgtacgagt gttctccaga actttgcaca
960
acgatgctgc ctcccgcgtg gctgctgatg ctgtgccagg ctccgaggcc ccaggacccc
1020
gacccgaggc tgacacaacc cgagaagagt ctccaggaag ccccggggca gactggggct
1080
tccaggacac cgcgaacctg accaattcga cggaggagct ggacaacgcc accctggtcc
1140
tgaggaatgc aacagagggg ctgggccagg tcgccctgct ggactgggtg gcgcctgggc
1200
cgagcactgg ctcaggacgt gcagggctgg aggcggcggg agacgagctg tgagccccac
1260
caggactatg ctcccaggcc cctctgccca ggggtgcctt ggggatgctg cactgggcag
1320
ctacccacct ggggatggga cgtgaggcca agaccccagc agagatgcca gaatgggggа
1380
ggcacagctc atagccacac a
1401

<210> 5628
<211> 299
<212> PRT
<213> Homo sapiens

<400> 5628
Met Ala Ser Ala Ala Cys Ser Met Asp Pro Ile Asp Ser Phe Glu Leu
 1   5   10   15
Leu Asp Leu Leu Phe Asp Arg Gln Asp Gly Ile Leu Arg His Val Glu
            20   25   30
Leu Gly Glu Gly Trp Gly His Val Lys Asp Gln Val Leu Pro Asn Pro
        35   40   45
Asp Ser Asp Asp Phe Leu Ser Ser Ile Leu Gly Ser Gly Asp Ser Leu
    50   55   60
Pro Ser Ser Pro Leu Trp Ser Pro Glu Gly Ser Asp Ser Gly Ile Ser
65   70   75   80
Glu Asp Leu Pro Ser Asp Pro Gln Asp Thr Pro Pro Arg Ser Gly Pro
                85   90   95
Ala Thr Ser Pro Ala Gly Cys His Pro Ala Gln Pro Gly Lys Gly Pro
            100   105   110
Cys Leu Ser Tyr His Pro Gly Asn Ser Cys Ser Thr Thr Thr Pro Gly
        115   120   125
Pro Val Ile Gln Gln Gln His His Leu Gly Ala Ser Tyr Leu Leu Arg

```
    130                 135                 140
Pro Gly Ala Gly His Cys Gln Glu Leu Val Leu Thr Glu Asp Glu Lys
145                 150                 155                 160
Lys Leu Leu Ala Lys Glu Gly Ile Thr Leu Pro Thr Gln Leu Pro Leu
                165                 170                 175
Thr Lys Tyr Glu Glu Arg Val Leu Lys Lys Ile Arg Arg Lys Ile Arg
            180                 185                 190
Asn Lys Gln Ser Ala Gln Glu Ser Arg Lys Lys Lys Lys Glu Tyr Ile
        195                 200                 205
Asp Gly Leu Glu Thr Arg Ser Cys Cys Cys Pro Leu Pro Ser Ser Ser
    210                 215                 220
Ser Pro Pro Ser Ala Leu Leu Ala Pro Thr Lys Pro Arg Ala Leu Gly
225                 230                 235                 240
Thr Leu Arg Leu Tyr Glu Cys Ser Pro Glu Leu Cys Thr Thr Met Leu
                245                 250                 255
Pro Pro Ala Trp Leu Leu Met Leu Cys Gln Ala Pro Arg Pro Gln Asp
            260                 265                 270
Pro Asp Pro Arg Leu Thr Gln Pro Glu Lys Ser Leu Gln Glu Ala Pro
        275                 280                 285
Gly Gln Thr Gly Ala Ser Arg Thr Pro Arg Thr
    290                 295
```

<210> 5629
<211> 428
<212> DNA
<213> Homo sapiens

<400> 5629
gtgcacgacc ccactgaatc atcccacaac catggatggg agacacactc agtctccttt
60
aacagaagat aaagctgggg cttacagaga atgtacaact tggcccaggg cacaccagtt
120
agccatcagg ggcagngctg ctattcaggt ctgggactgt gggactccag agcccatgtt
180
ttttacgagg atgccatact gccacaatgg atggtgtctt tatctcctga tatatgattg
240
tgtgttggga ggcgtggggt ggcagctgga agaatggaga ggcatatttg tggaggatct
300
tcccccattc tctgctaccc tctcttggag ctcccagttc catctgagaa attatctact
360
ctgagaaatc gtcacaacac agcatggttg tgagtgcagt ggcagaagcc tgtgcctggt
420
tgtatggg
428

<210> 5630
<211> 110
<212> PRT
<213> Homo sapiens

<400> 5630
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Met Asp Gly Arg His Thr Gln Ser Pro Leu Thr Glu Asp Lys Ala Gly
 1               5                  10                  15
Ala Tyr Arg Glu Cys Thr Thr Trp Pro Arg Ala His Gln Leu Ala Ile
```

```
            20                  25                  30
Arg Gly Xaa Ala Ala Ile Gln Val Trp Asp Cys Gly Thr Pro Glu Pro
        35                  40                  45
Met Phe Phe Thr Arg Met Pro Tyr Cys His Asn Gly Trp Cys Leu Tyr
    50                  55                  60
Leu Leu Ile Tyr Asp Cys Val Leu Gly Gly Val Gly Trp Gln Leu Glu
65                  70                  75                  80
Glu Trp Arg Gly Ile Phe Val Glu Asp Leu Pro Pro Phe Ser Ala Thr
                85                  90                  95
Leu Ser Trp Ser Ser Gln Phe His Leu Arg Asn Tyr Leu Leu
            100                 105                 110
```

<210> 5631
<211> 783
<212> DNA
<213> Homo sapiens

<400> 5631
acgcgtgccc agcacatgtg tgcacacgca gatgcaggag agaacacaca ccaccgtctc
60
tttgcacacg tgtgcccctg tccggcccgg ggggctcatc tctccttcac ggagagaatt
120
ctttttatta cgagtgaaca gatgaactaa ggtaagcggg tctcagcctt ccgctggtgc
180
agcatctcca cgcagggcct cagccccgtc ctggccttgc ctgaggactg caccatgggt
240
gttccttggg catggaggag gcagcaggaa ggggtgacag gagcaggagc aggtgcaggg
300
cacctcacac cacaggcctc ccccacctct gagctgccaa cagccaagac tcctggcgag
360
gccgggagag gaggggtgag agggaaggag ggtctctgtg aaagcaagcc ccacccccag
420
agcagagcag agacccaggt ctgcaaatca caccctcccc ccacgagttc ctcctttgag
480
gccagcagca cccgagggag ggcaggggct gcacagagac cagagaaagg aaaaccccac
540
agaagaaaac tcaaagcatc agtcccatgc gtgtctgctg aacgagtgaa tgggcccaaa
600
ggctcttctc tacaaacggc acgcatccat ccgacagggg gccacaggac acggccgggg
660
ccgtctgcgt ctgtgcctgt gcagcccaca ccagtgcagc ccggggccct ctcagacctc
720
accacacgcg tgcccagcac atgtgtgcac acgcagatgc aggagagaac acacaccacc
780
gtc
783

<210> 5632
<211> 183
<212> PRT
<213> Homo sapiens

<400> 5632
Met Gly Val Pro Trp Ala Trp Arg Arg Gln Gln Glu Gly Val Thr Gly

```
 1               5                  10                  15
Ala Gly Ala Gly Ala Gly His Leu Thr Pro Gln Ala Ser Pro Thr Ser
            20                  25                  30
Glu Leu Pro Thr Ala Lys Thr Pro Gly Glu Ala Gly Arg Gly Gly Val
        35                  40                  45
Arg Gly Lys Glu Gly Leu Cys Glu Ser Lys Pro His Pro Gln Ser Arg
    50                  55                  60
Ala Glu Thr Gln Val Cys Lys Ser His Pro Pro Pro Thr Ser Ser Ser
65                  70                  75                  80
Phe Glu Ala Ser Ser Thr Arg Gly Arg Ala Gly Ala Ala Gln Arg Pro
                85                  90                  95
Glu Lys Gly Lys Pro His Arg Arg Lys Leu Lys Ala Ser Val Pro Cys
            100                 105                 110
Val Ser Ala Glu Arg Val Asn Gly Pro Lys Gly Ser Ser Leu Gln Thr
        115                 120                 125
Ala Arg Ile His Pro Thr Gly Gly His Arg Thr Arg Pro Gly Pro Ser
    130                 135                 140
Ala Ser Val Pro Val Gln Pro Thr Pro Val Gln Pro Gly Ala Leu Ser
145                 150                 155                 160
Asp Leu Thr Thr Arg Val Pro Ser Thr Cys Val His Thr Gln Met Gln
                165                 170                 175
Glu Arg Thr His Thr Thr Val
            180
```

<210> 5633
<211> 2181
<212> DNA
<213> Homo sapiens

<400> 5633
gccaatgtcc ctgtggccac tcagctgaga ccgagggcga cctgggcagc tgcgggtgtc
60
tgtcacctcc gtgtcccaca tagatgccag gctctgcttc tgtggttctg gaggtcatta
120
gtcaattgta tgtggtgctg tctgtcctcc tgattgcaga ggaggaagga acccttaaa
180
tgagcgggtt ctgagtgctg gggccgctgg tctgctctgc ctggtgggat tctccagtgc
240
tggcttcatc tgtgccccag ccccactctc accaacaagg agggcgtgaa aatgacaagg
300
aatccatccc tagagttcac aggagatcta gggcagagtt tccaagctgc agctgctctg
360
gccctgtgtg agctgctgct ctgaggaagc cccaggctga ggtagctacc aggcggaggc
420
tgggtttgga ggcctccaca tcagggaatt gagcggtagg ggtttcagcc ttcacgttgg
480
tcgccgcact gtatgggaag tggggtctgg ggtctgcttg cccagtctca ccgtcctctt
540
cctccccaaa gccgcctgga taaggggctg gccgcactgg tgcgggagcg tggcgcggat
600
ctggtggtca tcgagggcat gggccgtgct gtccacacaa actaccacgc agccctgcgc
660
tgcgagagcc tcaagctggc cgtcatcaag aacgcgtggc tggccgagcg gctgggcggc
720

cggctcttca gcgccatctt caagtacgag gtcccagccg agtgaggcgc tgcagctgcc
780
ggactcttct gcttgtcact tgtccgagtg gcttcagaga ttaaaggggc cccctcataa
840
atgtgcctta attttcgcag ataacagggg gaatagacat cattttggga gtcttccct
900
ttgtcaggga gctactcctt agagggacag aggtcatcct ggcgtgcaac tcaggccccg
960
ccctgaacga cgtgacccac agcgagtccc tcatcgtggc agagcgtatt gcgggcatgg
1020
accctgaccg tgcgcagcct gctggacacc agggagcact gtctgaacga gttcaacttc
1080
ccggatccct actccaaagt gaagcagcgg gagaatggcg tggcgctgag gtgcttcccc
1140
ggggtcgtgc gctccctgga cgcgctgggc tgggaggaac ggcagctggc gctggtgaaa
1200
ggcctcctgg cggggaatgt cttcgactgg ggggccaaag ccgtgtctgc tgtccttgaa
1260
tccgaccccc actttgggtt tgaagaagca aagaggaagt tacaagaaag accctggctc
1320
gtggattcct acagcgagtg gcttcagaga ttaaaggggc cccctcataa atgtgcctta
1380
attttcgcag ataacagtgg aatagacatc attttgggag tcttcccctt tgtcagggag
1440
ctactcctta gagggacaga ggtcatcctg gcgtgcaact caggccccgc cctgaacgac
1500
gtgacccaca gcgagtccct catcgtggca gagcgtattg cgggcatgga ccctgtcgtg
1560
cactctgcgc tccaggaaga gaggctgctg ctggtgcaga cgggctccag ctccccgtgc
1620
ctcgacctca gccgcctgga taaggggctg gccgcactgg tgcgggagcg tggcgcggat
1680
ctggtggtca tcgagggcat gggccgtgct gtccacacaa actaccacgc agccctgcgc
1740
tgcgagagcc tcaagctggc cgtcatcaag aacgcgtggc tggccgagcg gctgggcggc
1800
cggctcttca gcgtcatctt caagtacgag gtcccagccg agtgaggcgc tgcagctgcc
1860
ggactcttct gcttgtcact tgtcaggaat gtgtttttac caccacaggg aaactgcgtt
1920
caaatcaacg tatttatatg gtactgctgt gacgcggcac atacacccca gccgcacaga
1980
tgcgtgtgac ccagaggcga gacgcagctt tgtcctggga gacgttcata ttggaatcta
2040
tttaactgct aaagaacctt ttatatatat atatatatat aaatagagag atctatacag
2100
gtatgtctga cgggacgcag caccgtgggc acgcaccaaa tagagttttt aaaagaggaa
2160
aaaaaactct atttggtgcg t
2181

<210> 5634
<211> 289
<212> PRT

<213> Homo sapiens

<400> 5634
Pro Thr Ala Ser Pro Ser Ser Trp Gln Ser Val Leu Arg Ala Trp Thr
1 5 10 15
Leu Thr Val Arg Ser Leu Leu Asp Thr Arg Glu His Cys Leu Asn Glu
20 25 30
Phe Asn Phe Pro Asp Pro Tyr Ser Lys Val Lys Gln Arg Glu Asn Gly
35 40 45
Val Ala Leu Arg Cys Phe Pro Gly Val Val Arg Ser Leu Asp Ala Leu
50 55 60
Gly Trp Glu Glu Arg Gln Leu Ala Leu Val Lys Gly Leu Leu Ala Gly
65 70 75 80
Asn Val Phe Asp Trp Gly Ala Lys Ala Val Ser Ala Val Leu Glu Ser
85 90 95
Asp Pro Tyr Phe Gly Phe Glu Glu Ala Lys Arg Lys Leu Gln Glu Arg
100 105 110
Pro Trp Leu Val Asp Ser Tyr Ser Glu Trp Leu Gln Arg Leu Lys Gly
115 120 125
Pro Pro His Lys Cys Ala Leu Ile Phe Ala Asp Asn Ser Gly Ile Asp
130 135 140
Ile Ile Leu Gly Val Phe Pro Phe Val Arg Glu Leu Leu Leu Arg Gly
145 150 155 160
Thr Glu Val Ile Leu Ala Cys Asn Ser Gly Pro Ala Leu Asn Asp Val
165 170 175
Thr His Ser Glu Ser Leu Ile Val Ala Glu Arg Ile Ala Gly Met Asp
180 185 190
Pro Val Val His Ser Ala Leu Gln Glu Glu Arg Leu Leu Leu Val Gln
195 200 205
Thr Gly Ser Ser Ser Pro Cys Leu Asp Leu Ser Arg Leu Asp Lys Gly
210 215 220
Leu Ala Ala Leu Val Arg Glu Arg Gly Ala Asp Leu Val Val Ile Glu
225 230 235 240
Gly Met Gly Arg Ala Val His Thr Asn Tyr His Ala Ala Leu Arg Cys
245 250 255
Glu Ser Leu Lys Leu Ala Val Ile Lys Asn Ala Trp Leu Ala Glu Arg
260 265 270
Leu Gly Gly Arg Leu Phe Ser Val Ile Phe Lys Tyr Glu Val Pro Ala
275 280 285
Glu

<210> 5635
<211> 614
<212> DNA
<213> Homo sapiens

<400> 5635
nntgtgaaag atgttgcaga agtgttccag aagtggctga agatagaagg aaaaaagtgc
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cactgcctat cagaaaaaac aaaacaaaac atgggaaata caaccaccaa attccgtaaa
120
gcactcatca atggtgatga aaacctggcc tgccaaatat atgaaaacaa tcctcagcta
180

aaagaatctc ttgatccaaa tacatcttat ggggagccct accagcacaa tactccatta
240
cattatgctg ctagacatgg aatgaataaa atattaggag atgatttcag aagagcagat
300
tgtctgcaga tgatcttaaa atggaaagga gcaaaacttg accagggtga atatgagaga
360
gcagctattg atgctgttga taacaaaaaa aacacaccct tgcactatgc tgctgcctca
420
gggatgaaag cctgtgtaga aaaacatgga ggagacttgt ttgctgagaa tgaaaataaa
480
gatactcctt gtgattgtgc tgaaaagcaa caccacaaag atttggccct caatctggaa
540
tctcaaatgg tattctcacg ggatcccgag gctgaagaaa tagaagctga atatgctgca
600
ttagacaaac gaga
614

<210> 5636
<211> 204
<212> PRT
<213> Homo sapiens

<400> 5636
Xaa Val Lys Asp Val Ala Glu Val Phe Gln Lys Trp Leu Lys Ile Glu
 1   5   10   15
Gly Lys Lys Cys His Cys Leu Ser Glu Lys Thr Lys Gln Asn Met Gly
            20   25   30
Asn Thr Thr Thr Lys Phe Arg Lys Ala Leu Ile Asn Gly Asp Glu Asn
        35   40   45
Leu Ala Cys Gln Ile Tyr Glu Asn Asn Pro Gln Leu Lys Glu Ser Leu
    50   55   60
Asp Pro Asn Thr Ser Tyr Gly Glu Pro Tyr Gln His Asn Thr Pro Leu
65   70   75   80
His Tyr Ala Ala Arg His Gly Met Asn Lys Ile Leu Gly Asp Asp Phe
                85   90   95
Arg Arg Ala Asp Cys Leu Gln Met Ile Leu Lys Trp Lys Gly Ala Lys
            100   105   110
Leu Asp Gln Gly Glu Tyr Glu Arg Ala Ala Ile Asp Ala Val Asp Asn
        115   120   125
Lys Lys Asn Thr Pro Leu His Tyr Ala Ala Ala Ser Gly Met Lys Ala
    130   135   140
Cys Val Glu Lys His Gly Gly Asp Leu Phe Ala Glu Asn Glu Asn Lys
145   150   155   160
Asp Thr Pro Cys Asp Cys Ala Glu Lys Gln His His Lys Asp Leu Ala
                165   170   175
Leu Asn Leu Glu Ser Gln Met Val Phe Ser Arg Asp Pro Glu Ala Glu
            180   185   190
Glu Ile Glu Ala Glu Tyr Ala Ala Leu Asp Lys Arg
        195   200

<210> 5637
<211> 825
<212> DNA
<213> Homo sapiens

<400> 5637
acgcgtccga ggctcctcaa acccagggcc ccacctggca cgtggaggaa gaagagaagg
60
gcaggaggca ggtgcccagg tgggagcccc ctctgtgccc cctgggagtg tccccccccgc
120
ccaggtactc agggccctgc cctcgtggcc ttgtccgctc gccgcgggtg gggctggcac
180
aaggcccgtt ttggaggaag tggaggctcc caggagaaag gcagtggctg tgatcgcaca
240
gcccaggctc tgccctgcac tgccctggac cacgaggctg cccaccccag acaggtggga
300
ccccttttccc gcatgcagac tctgagcagc agcttcctgt gacccccacc gcgtcctgct
360
cctcaggctc atgccctgcg ggaacagaag ccaagacccg gtagaaaatc caaggtgttt
420
aaatataaat aagagcgatt cccacagccc cacggtgctg gccagcctca caggtgcccg
480
ctggttctgt gacccatccc aggcacacgc tcccctggct gggcgcctgg ccagggctcc
540
cctgtggctg gcgtgtggag acacgtgggc ccttctccac gtgcccacga gggccgtagc
600
aggctccaag gaggcccagc cccggccagc ctgtgtggac cccgccggcc tgcgcgcccc
660
ggagctgctg actgtgtcag agcccggctg cccagcgccc cggcgccctc cctccagctg
720
cccagcctgg gatccgtccg ctgtctgtct cctgaaccag ggagtctgac ccactcacag
780
ctcccatggg gtccgtgcag ccaaggcccc gcagccacac tcact
825

<210> 5638
<211> 132
<212> PRT
<213> Homo sapiens

<400> 5638
Met Pro Cys Gly Asn Arg Ser Gln Asp Pro Val Glu Asn Pro Arg Cys
1 5 10 15
Leu Asn Ile Asn Lys Ser Asp Ser His Ser Pro Thr Val Leu Ala Ser
20 25 30
Leu Thr Gly Ala Arg Trp Phe Cys Asp Pro Ser Gln Ala His Ala Pro
35 40 45
Leu Ala Gly Arg Leu Ala Arg Ala Pro Leu Trp Leu Ala Cys Gly Asp
50 55 60
Thr Trp Ala Leu Leu His Val Pro Thr Arg Ala Val Ala Gly Ser Lys
65 70 75 80
Glu Ala Gln Pro Arg Pro Ala Cys Val Asp Pro Ala Gly Leu Arg Ala
85 90 95
Pro Glu Leu Leu Thr Val Ser Glu Pro Gly Cys Pro Ala Pro Arg Arg
100 105 110
Pro Pro Ser Ser Cys Pro Ala Trp Asp Pro Ser Ala Val Cys Leu Leu
115 120 125
Asn Gln Gly Val

130

<210> 5639
<211> 2433
<212> DNA
<213> Homo sapiens

<400> 5639
natagctaca aaataaaaaa aactaattca aacaaatgta cttatttaat ccaatatatc
60
ccaacaatta ttgcagcaca taatcaatat aaacattata tatatgaact atttgacact
120
atttgacatt tcttcttcca catccagtgt atctgacatt tagcgcacat ttgatttgca
180
ctcacccact ttgaggagct caattgccgc ttaagtccgt ggctagtggc tgccctaaag
240
ttcagcaccg ccacggagct ttgggtccac ccggactgta aaaaggaagc acttccgtta
300
gcatgacccg gcctgaagta gcggcggaac ggaagtcgct tgtgtatgaa cgcagcggcg
360
gacctgtgag gggatccgac ttgccggcag aacttacgct gcgggacccc gggcactgtt
420
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480
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660
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960
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1020
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1080
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1140
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1260
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1320
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1380

tcggaggtcc agttcaacag tgcagtgcct accaatctca gtcgtggctt taccaccaac
1440
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1620
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1740
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1860
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1920
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1980
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2160
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2280
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2340
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2400
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2433

<210> 5640
<211> 540
<212> PRT
<213> Homo sapiens

<400> 5640
Met Cys Pro Ser Pro Glu Arg Gln Glu Asp Gly Ala Arg Lys Asp Phe
1 5 10 15
Ser Ser Arg Leu Ala Ala Gly Pro Thr Phe Gln His Phe Leu Lys Ser
20 25 30
Ala Ser Ala Pro Gln Glu Lys Leu Ser Ser Glu Val Glu Asp Pro Pro
35 40 45
Pro Tyr Leu Met Met Asp Glu Leu Leu Gly Arg Gln Arg Lys Val Tyr
50 55 60
Leu Glu Thr Tyr Gly Cys Gln Met Asn Val Asn Asp Thr Glu Ile Ala
65 70 75 80
Trp Ser Ile Leu Gln Lys Ser Gly Tyr Leu Arg Pro Val Thr Ser Lys

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                85                  90                  95
Ala Asp Val Ile Leu Leu Val Thr Cys Ser Ile Arg Glu Lys Ala Glu
            100                 105                 110
Gln Thr Ile Trp Asn Arg Leu His Gln Leu Lys Ala Leu Lys Thr Arg
        115                 120                 125
Arg Pro Arg Ser Arg Val Pro Leu Arg Ile Gly Ile Leu Gly Cys Met
    130                 135                 140
Ala Glu Arg Leu Lys Glu Glu Ile Leu Asn Arg Glu Lys Met Val Asp
145                 150                 155                 160
Ile Leu Ala Gly Pro Asp Ala Tyr Arg Asp Leu Pro Arg Leu Leu Ala
                165                 170                 175
Val Ala Glu Ser Gly Gln Gln Ala Ala Asn Val Leu Leu Ser Leu Asp
            180                 185                 190
Glu Thr Tyr Ala Asp Val Met Pro Val Gln Thr Ser Ala Ser Ala Thr
        195                 200                 205
Ser Ala Phe Val Ser Ile Met Arg Gly Cys Asp Asn Met Cys Ser Tyr
    210                 215                 220
Cys Ile Val Pro Phe Thr Arg Gly Arg Glu Arg Ser Arg Pro Ile Ala
225                 230                 235                 240
Ser Ile Leu Glu Glu Val Lys Lys Leu Ser Glu Gln Gly Leu Lys Glu
                245                 250                 255
Val Thr Leu Leu Gly Gln Asn Val Asn Ser Phe Arg Asp Asn Ser Glu
            260                 265                 270
Val Gln Phe Asn Ser Ala Val Pro Thr Asn Leu Ser Arg Gly Phe Thr
        275                 280                 285
Thr Asn Tyr Lys Thr Lys Gln Gly Gly Leu Arg Phe Ala His Leu Leu
    290                 295                 300
Asp Gln Val Ser Arg Val Asp Pro Glu Met Arg Ile Arg Phe Thr Ser
305                 310                 315                 320
Pro His Pro Lys Asp Phe Pro Asp Glu Val Leu Gln Leu Ile His Glu
                325                 330                 335
Arg Asp Asn Ile Cys Lys Gln Ile His Leu Pro Ala Gln Ser Gly Ser
            340                 345                 350
Ser Arg Val Leu Glu Ala Met Arg Arg Gly Tyr Ser Arg Glu Ala Tyr
        355                 360                 365
Val Glu Leu Val His His Ile Arg Glu Ser Ile Pro Gly Val Ser Leu
    370                 375                 380
Ser Ser Asp Phe Ile Ala Gly Phe Cys Gly Glu Thr Glu Glu Asp His
385                 390                 395                 400
Val Gln Thr Val Ser Leu Leu Arg Glu Val Gln Tyr Asn Met Gly Phe
                405                 410                 415
Leu Phe Ala Tyr Ser Met Arg Gln Lys Thr Arg Ala Tyr His Arg Leu
            420                 425                 430
Lys Asp Asp Val Pro Glu Glu Val Lys Leu Arg Arg Leu Glu Glu Leu
        435                 440                 445
Ile Thr Ile Phe Arg Glu Glu Ala Thr Lys Ala Asn Gln Thr Ser Val
    450                 455                 460
Gly Cys Thr Gln Leu Val Leu Val Glu Gly Leu Ser Lys Arg Ser Ala
465                 470                 475                 480
Thr Asp Leu Cys Gly Arg Asn Asp Gly Asn Leu Lys Val Ile Phe Pro
                485                 490                 495
Asp Ala Glu Met Glu Asp Val Asn Asn Pro Gly Leu Arg Val Arg Ala
            500                 505                 510
Gln Pro Gly Asp Tyr Val Leu Val Lys Ile Thr Xaa Gln Pro Val Leu
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        515                 520                 525
Arg His Leu Gly Asp Met Phe Ser Ala Gly Pro Leu
    530                 535                 540

<210> 5641
<211> 293
<212> DNA
<213> Homo sapiens

<400> 5641
gcgtcgcata cagccaacct gtgcgtgctg ctgtaccgca gcggcgtcaa agtggtcacc
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ttctgtggcc acgcgtccaa aaccaatcag gtcaactcgg gcggtgtgct gctgaggttg
120
caggtgggcg aggaggtgtg gctggctggg gcacccctgg catcctgga gagccaggtg
180
aggagggcag atacaagcag aaattccagt cagtgttcac ggtcactcgg cagacccacc
240
agccccctgc acccaacagc ctgatcagat tcaacgcggg cctcaccaac ccg
293

<210> 5642
<211> 87
<212> PRT
<213> Homo sapiens

<400> 5642
Ala Ser His Thr Ala Asn Leu Cys Val Leu Leu Tyr Arg Ser Gly Val
 1               5                  10                  15
Lys Val Val Thr Phe Cys Gly His Ala Ser Lys Thr Asn Gln Val Asn
            20                  25                  30
Ser Gly Gly Val Leu Leu Arg Leu Gln Val Gly Glu Glu Val Trp Leu
        35                  40                  45
Ala Gly Ala Pro Leu Ala Ser Leu Glu Ser Gln Val Arg Arg Ala Asp
    50                  55                  60
Thr Ser Arg Asn Ser Ser Gln Cys Ser Arg Ser Leu Gly Arg Pro Thr
65                  70                  75                  80
Ser Pro Leu His Pro Thr Ala
                85

<210> 5643
<211> 1218
<212> DNA
<213> Homo sapiens

<400> 5643
nnacgcgtga ggagcctgag gcggcggcgg gggtggctcc gcgcgcggtg gtctcggggg
60
caaaataaca tggcagccag acgaattaca caggagactt ttgatgctgt attacaagaa
120
aaagccaaac gatatcacat ggatgccagt ggtgaggctg taagcgaaac tcttcagttt
180
aaagctcaag atctcttaag ggcagtccca agatccagag cagagatgta tgatgacgtc
240
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cacagcgatg gcagatactc cctcagtgga tctgtagctc actctagaga tgccggaaga
300
gaaggcctga gaagtgacgt atttccaggg ccttccttca gatcaagcaa cccttccatc
360
agtgatgaca gctactttcg caaagaatgt ggccgggatc tggaattttc tcactctgat
420
tctcgggacc aggtcattgg ccaccggaaa ttggggcatt tccgttctca ggactggaaa
480
tttgcgctcc gtggttcttg ggaacaagac tttggccatc cagtttctca agagtcctct
540
tggtcacagg agtatagttt tggtccctct gcagttttgg gggactttgg atcttccagg
600
ctgattgaga aagagtgttt ggagaaggag agtcgggatt atgacgtgga ccatcctggg
660
gaggctgact ctgtgcttag gggcagcagt caagtccagg ccagaggtcg agctctaaac
720
atcgttgacc aggaaggttc cctcctagga aaggggggaga ctcagggcct gctcacagct
780
aaggggggtg ttgggaaact tgtcacattg agaaatgtga gcacaaaaaa aatacccacc
840
gtgaatcgta ttactcccaa aactcagggc actaaccaaa tccagaaaaa cactccaagt
900
cctgatgtga ccctggggac aaacccaggg acagaagata tccagttccc cattcagaag
960
atccctctgg ggctggatct gaagaatctt cggctcccca gaagaaagat gagctttgac
1020
atcatagata agtctgatgt tttttcaaga tttgggatag aaataatcaa atgggcagga
1080
ttccacacca taaaattaga ttattaaatt tttcccaaac ttttccagac tctctttgaa
1140
cttgaaacag aaacctgtgc taaaatgctt gcctcattca aatgttcctt aaaaccagag
1200
cacagagatt tttgcttt
1218

<210> 5644
<211> 202
<212> PRT
<213> Homo sapiens

<400> 5644
Trp Glu Gln Asp Phe Gly His Pro Val Ser Gln Glu Ser Ser Trp Ser
1 5 10 15
Gln Glu Tyr Ser Phe Gly Pro Ser Ala Val Leu Gly Asp Phe Gly Ser
20 25 30
Ser Arg Leu Ile Glu Lys Glu Cys Leu Glu Lys Glu Ser Arg Asp Tyr
35 40 45
Asp Val Asp His Pro Gly Glu Ala Asp Ser Val Leu Arg Gly Ser Ser
50 55 60
Gln Val Gln Ala Arg Gly Arg Ala Leu Asn Ile Val Asp Gln Glu Gly
65 70 75 80
Ser Leu Leu Gly Lys Gly Glu Thr Gln Gly Leu Leu Thr Ala Lys Gly
85 90 95
Gly Val Gly Lys Leu Val Thr Leu Arg Asn Val Ser Thr Lys Lys Ile

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            100                 105                 110
Pro Thr Val Asn Arg Ile Thr Pro Lys Thr Gln Gly Thr Asn Gln Ile
        115                 120                 125
Gln Lys Asn Thr Pro Ser Pro Asp Val Thr Leu Gly Thr Asn Pro Gly
    130                 135                 140
Thr Glu Asp Ile Gln Phe Pro Ile Gln Lys Ile Pro Leu Gly Leu Asp
145                 150                 155                 160
Leu Lys Asn Leu Arg Leu Pro Arg Arg Lys Met Ser Phe Asp Ile Ile
                165                 170                 175
Asp Lys Ser Asp Val Phe Ser Arg Phe Gly Ile Glu Ile Ile Lys Trp
            180                 185                 190
Ala Gly Phe His Thr Ile Lys Leu Asp Tyr
        195                 200
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<210> 5645
<211> 156
<212> DNA
<213> Homo sapiens

<400> 5645
ccacgtccat cccgaagaag gaactgcagg tgggcggttt ttggcctggc acagagatgt
60
cctcagatca gcttcccctc tcccaggcaa gaggacacga gcactggcaa gttcacctgc
120
aaagtccccg gcctctacta ctttgtctac cacgcg
156

<210> 5646
<211> 52
<212> PRT
<213> Homo sapiens

<400> 5646

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Pro Arg Pro Ser Arg Arg Arg Asn Cys Arg Trp Ala Val Phe Gly Leu
 1               5                  10                  15
Ala Gln Arg Cys Pro Gln Ile Ser Phe Pro Ser Pro Arg Gln Glu Asp
            20                  25                  30
Thr Ser Thr Gly Lys Phe Thr Cys Lys Val Pro Gly Leu Tyr Tyr Phe
        35                  40                  45
Val Tyr His Ala
    50
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<210> 5647
<211> 150
<212> DNA
<213> Homo sapiens

<400> 5647
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aggcccaagg gggagccagg aatcccagcc attcccggga tccgaggacc caaagggcag
120
aagggagaac ccggcttacc cggccatccn
150

<210> 5648
<211> 50
<212> PRT
<213> Homo sapiens

<400> 5648
Pro Met Gly Pro Gly Thr Leu Ala Phe Pro Gly Gly Pro Met Gly Pro
1 5 10 15
Phe Phe Pro Gly Arg Pro Lys Gly Glu Pro Gly Ile Pro Ala Ile Pro
20 25 30
Gly Ile Arg Gly Pro Lys Gly Gln Lys Gly Glu Pro Gly Leu Pro Gly
35 40 45
His Pro
50

<210> 5649
<211> 345
<212> DNA
<213> Homo sapiens

<400> 5649
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aaccgcctgg tccctcggat cgcgcccagc ccagactcgg actcggacac agactcggag
120
gacccgagtc tccggcgcag cgcgggcggc ttgctccgct cgcaggtcat ccacagcggt
180
cacttcatgg tgtcgtcgcc gcacagcgac tcgctgcccc ggcggcgcga ccaggagggt
240
ccgtggggcc ctccgacttc gggccgcgca gtatcgaccc cacactcaca cgcctcttcg
300
agtgcttgag cctggcctac agtggcaagc tggggtctcc caagt
345

<210> 5650
<211> 100
<212> PRT
<213> Homo sapiens

<400> 5650
Met Ala Val Ala Ala Ala Thr Ala Trp Ser Leu Gly Ser Arg Pro Ala
1 5 10 15
Gln Thr Arg Thr Arg Thr Gln Thr Arg Arg Thr Arg Val Ser Gly Ala
20 25 30
Ala Arg Ala Ala Cys Ser Ala Arg Arg Ser Ser Thr Ala Val Thr Ser
35 40 45
Trp Cys Arg Arg Arg Thr Ala Thr Arg Cys Pro Gly Gly Ala Thr Arg
50 55 60
Arg Val Arg Gly Ala Leu Arg Leu Arg Ala Ala Gln Tyr Arg Pro His
65 70 75 80
Thr His Thr Pro Leu Arg Val Leu Glu Pro Gly Leu Gln Trp Gln Ala
85 90 95
Gly Val Ser Gln

100

<210> 5651
<211> 615
<212> DNA
<213> Homo sapiens

<400> 5651
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ggagaagtgg cgtcgagtcc ggccgggcag tagaggaaat tgcggtagtg accctcgggc
120
ctcgccatga agagccgctt tagcaccatt gacctccgcg ccgtactcgc ggagctgaat
180
gctagcttgc taggaatgag agtaaacaat gtttatgatg tggataataa gacatacctt
240
attcgtcttc aaaaaccgga ctttaaagct acacttttac ttgaatctgg catacaaatt
300
catacaacag aatttgagtg gcctaagaat atgatgccgt ctagttttgc catgaagtgc
360
cgaaaacatt tgaagagtcg gagattagtc agtgcaaaac agcttggtgt ggatagaatt
420
gtagattttc aatttggaag tgatgaagct gcttaccatt taatcattga gctctatgat
480
agggggaaca ttgttcttac agattatgag tacgtaattt taaatattct aaggtttcga
540
actgatgagg cagatgatgt taaatttgct gttcgtgaac gctatccact tgatcatgct
600
agagctgctg aacct
615

<210> 5652
<211> 163
<212> PRT
<213> Homo sapiens

<400> 5652
Met Lys Ser Arg Phe Ser Thr Ile Asp Leu Arg Ala Val Leu Ala Glu
1 5 10 15
Leu Asn Ala Ser Leu Leu Gly Met Arg Val Asn Asn Val Tyr Asp Val
20 25 30
Asp Asn Lys Thr Tyr Leu Ile Arg Leu Gln Lys Pro Asp Phe Lys Ala
35 40 45
Thr Leu Leu Leu Glu Ser Gly Ile Gln Ile His Thr Thr Glu Phe Glu
50 55 60
Trp Pro Lys Asn Met Met Pro Ser Ser Phe Ala Met Lys Cys Arg Lys
65 70 75 80
His Leu Lys Ser Arg Arg Leu Val Ser Ala Lys Gln Leu Gly Val Asp
85 90 95
Arg Ile Val Asp Phe Gln Phe Gly Ser Asp Glu Ala Ala Tyr His Leu
100 105 110
Ile Ile Glu Leu Tyr Asp Arg Gly Asn Ile Val Leu Thr Asp Tyr Glu
115 120 125
Tyr Val Ile Leu Asn Ile Leu Arg Phe Arg Thr Asp Glu Ala Asp Asp

130 135 140
Val Lys Phe Ala Val Arg Glu Arg Tyr Pro Leu Asp His Ala Arg Ala
145 150 155 160
Ala Glu Pro

<210> 5653
<211> 1439
<212> DNA
<213> Homo sapiens

<400> 5653
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caccttctgt ggccacacgt ccaaaaccaa tcaggtcaac tcgggcggtg tgctgctgag
120
gttgcaggtg aacttgccag tgctcgtgtc ataatctccc tgcgggttgg tgaggaccgc
180
gttgaatctg atcaggctgt tgggtgcagg gggctggtgg gtctgccgag tgaccactca
240
gacaccgtgt cctcttgcct gggagagggg aagcagatct gaggacatct ctgtgccagg
300
ccagaaaccg cccacctgca ggtgaggccc ggacccctgc ccagttcctt ctccgggatg
360
gacgtggggc ccagctccct gccccacctt gggctgaagc tgctgctgct cctgctgctg
420
ctgcccctca ggggccaagc caacacaggc tgctacggga tcccagggat gcccggcctg
480
cccggggcac cagggaagga tgggtacgac ggactgccgg ggcccaaggg ggagccagga
540
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840
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900
ctgtaccgca gcggcgtcaa agtggtcacc ttctgtggcc acacgtccaa aaccaatcag
960
gtcaactcgg gcggtgtgct gctgaggttg caggtgggcg aggaggtgtg gctggctgtc
1020
aatgactact acgacatggt gggcatccag ggctctgaca gcgtcttctc cggcttcctg
1080
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1140
gcttcctgca tggacccacc ttactggcca gtctgcatcc ttgcctagac cattctcccc
1200
accagatgga cttctcctcc agggagccca ccctgaccca cccccactgc acccccctccc
1260

catgggttct ctccttcctc tgaacttctt taggagtcac tgcttgtgtg gttcctggga
1320
cacttaacca atgccttctg gtactgccat tctttttttt ttttttcaag tattggaagg
1380
ggtggggaga tatataaata aatcatgaaa tcaataaaaa aaaaaaaaaa aaaaaaaaa
1439

<210> 5654
<211> 245
<212> PRT
<213> Homo sapiens

<400> 5654
Met Asp Val Gly Pro Ser Ser Leu Pro His Leu Gly Leu Lys Leu Leu
 1   5   10   15
Leu Leu Leu Leu Leu Leu Pro Leu Arg Gly Gln Ala Asn Thr Gly Cys
            20   25   30
Tyr Gly Ile Pro Gly Met Pro Gly Leu Pro Gly Ala Pro Gly Lys Asp
        35   40   45
Gly Tyr Asp Gly Leu Pro Gly Pro Lys Gly Glu Pro Gly Ile Pro Ala
    50   55   60
Ile Pro Gly Ile Arg Gly Pro Lys Gly Gln Lys Gly Glu Pro Gly Leu
65   70   75   80
Pro Gly His Pro Gly Lys Asn Gly Pro Met Gly Pro Pro Gly Met Pro
                85   90   95
Gly Val Pro Gly Pro Met Gly Ile Pro Gly Glu Pro Gly Glu Glu Gly
            100   105   110
Arg Tyr Lys Gln Lys Phe Gln Ser Val Phe Thr Val Thr Arg Gln Thr
        115   120   125
His Gln Pro Pro Ala Pro Asn Ser Leu Ile Arg Phe Asn Ala Val Leu
    130   135   140
Thr Asn Pro Gln Gly Asp Tyr Asp Thr Ser Thr Gly Lys Phe Thr Cys
145   150   155   160
Lys Val Pro Gly Leu Tyr Tyr Phe Val Tyr His Ala Ser His Thr Ala
                165   170   175
Asn Leu Cys Val Leu Leu Tyr Arg Ser Gly Val Lys Val Val Thr Phe
            180   185   190
Cys Gly His Thr Ser Lys Thr Asn Gln Val Asn Ser Gly Gly Val Leu
        195   200   205
Leu Arg Leu Gln Val Gly Glu Glu Val Trp Leu Ala Val Asn Asp Tyr
    210   215   220
Tyr Asp Met Val Gly Ile Gln Gly Ser Asp Ser Val Phe Ser Gly Phe
225   230   235   240
Leu Leu Phe Pro Asp
                245

<210> 5655
<211> 3810
<212> DNA
<213> Homo sapiens

<400> 5655
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gggnngccat ctccatcanc ctccaaggct gagctggcag aggtgaggcg agaatgggcc
120
aagtacatgg aagtccatga gaaggcctcc ttcaccaata gtgagctgca ccgtgccatg
180
aacctgcacg tcggcaacct gcgcctgctc agcgggccgc ttgaccaggt ccgggctgcc
240
ctgcccacac cggccctctc cccagaggac aaggccgtgc tgcaaaacct aaagcgcatc
300
ctggctaagg tgcaggagat gcgggaccag cgcgtgtccc tggagcagca gctgcgtgag
360
cttatccaga aagatgacat cactgcctcg ctggtcacca cagaccactc agagatgaag
420
aagttgttcg aggagcagct gaaaaagtat gaccagctga aggtgtacct ggagcagaac
480
ctggccgccc aggaccgtgt cctctgtgca ctgacagagg ccaacgtgca gtacgcagcc
540
gtgcggcggg tactcagcga cttggaccaa aagtggaact ccacgctgca gaccctggtg
600
gcctcgtatg aagcctatga ggacctgatg aagaagtcgc aggagggcag ggacttctac
660
gcagatctgg agagcaaggt ggctgctctg ctggagcgca cgcagtccac ctgccaggcc
720
cgcgaggctg cccgccagca gctcctggac agggagctga agaagaagcc gccgccacgg
780
cccacagccc caaagccgct gctgccccgc agggaggaga gtgaggcagt ggaagcagga
840
gacccccctg aggagctgcg cagcctcccc cctgacatgg tggctggccc acgactgcct
900
gacaccttcc tgggaagtgc caccccgctc cactttcctc ccagcccctt ccccagctcc
960
acaggcccag gaccccacta tctctcaggc cccttgcccc ctggtaccta ctcgggcccc
1020
acccagctga tacagcccag ggccccaggg ccccatgcaa tgcccgtagc acctgggcct
1080
gccctctacc cagcccctgc ctacacaccg gagctgggcc ttgtgccccg atcctcccca
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1200
ctcccctcgg ccccacctcc tcaattctca ggccccgagt tggccatggc ggttcggcca
1260
gccaccacca cagtagatag catccaggcg cccatcccca gccacacagc cccacggcca
1320
aaccccaccc ctgctcctcc cccgccctgc ttccctgtgc ccccaccgca gccactgccc
1380
acgccttaca cctaccctgc aggggctaag caacccatcc cagcacagca ccacttctct
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1500
cagccccatc cttcacaagc gtttgggcct cagcccccac agcagcccct tccactccag
1560
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2160
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2280
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2340
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2700
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3240
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3360
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3480
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3540
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3600
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3660
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3780
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3810

<210> 5656
<211> 987
<212> PRT
<213> Homo sapiens

<400> 5656
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1 5 10 15
Val Gly Gln Ala Gly Xaa Pro Ser Pro Ser Xaa Ser Lys Ala Glu Leu
20 25 30
Ala Glu Val Arg Arg Glu Trp Ala Lys Tyr Met Glu Val His Glu Lys
35 40 45
Ala Ser Phe Thr Asn Ser Glu Leu His Arg Ala Met Asn Leu His Val
50 55 60
Gly Asn Leu Arg Leu Leu Ser Gly Pro Leu Asp Gln Val Arg Ala Ala
65 70 75 80
Leu Pro Thr Pro Ala Leu Ser Pro Glu Asp Lys Ala Val Leu Gln Asn
85 90 95
Leu Lys Arg Ile Leu Ala Lys Val Gln Glu Met Arg Asp Gln Arg Val
100 105 110
Ser Leu Glu Gln Gln Leu Arg Glu Leu Ile Gln Lys Asp Asp Ile Thr
115 120 125
Ala Ser Leu Val Thr Thr Asp His Ser Glu Met Lys Lys Leu Phe Glu
130 135 140
Glu Gln Leu Lys Lys Tyr Asp Gln Leu Lys Val Tyr Leu Glu Gln Asn
145 150 155 160
Leu Ala Ala Gln Asp Arg Val Leu Cys Ala Leu Thr Glu Ala Asn Val
165 170 175
Gln Tyr Ala Ala Val Arg Arg Val Leu Ser Asp Leu Asp Gln Lys Trp
180 185 190
Asn Ser Thr Leu Gln Thr Leu Val Ala Ser Tyr Glu Ala Tyr Glu Asp
195 200 205
Leu Met Lys Lys Ser Gln Glu Gly Arg Asp Phe Tyr Ala Asp Leu Glu
210 215 220
Ser Lys Val Ala Ala Leu Leu Glu Arg Thr Gln Ser Thr Cys Gln Ala

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225                 230                 235                 240
Arg Glu Ala Ala Arg Gln Gln Leu Leu Asp Arg Glu Leu Lys Lys Lys
                245                 250                 255
Pro Pro Pro Arg Pro Thr Ala Pro Lys Pro Leu Leu Pro Arg Arg Glu
            260                 265                 270
Glu Ser Glu Ala Val Glu Ala Gly Asp Pro Pro Glu Glu Leu Arg Ser
        275                 280                 285
Leu Pro Pro Asp Met Val Ala Gly Pro Arg Leu Pro Asp Thr Phe Leu
    290                 295                 300
Gly Ser Ala Thr Pro Leu His Phe Pro Pro Ser Pro Phe Pro Ser Ser
305                 310                 315                 320
Thr Gly Pro Gly Pro His Tyr Leu Ser Gly Pro Leu Pro Pro Gly Thr
                325                 330                 335
Tyr Ser Gly Pro Thr Gln Leu Ile Gln Pro Arg Ala Pro Gly Pro His
            340                 345                 350
Ala Met Pro Val Ala Pro Gly Pro Ala Leu Tyr Pro Ala Pro Ala Tyr
        355                 360                 365
Thr Pro Glu Leu Gly Leu Val Pro Arg Ser Ser Pro Gln His Gly Val
    370                 375                 380
Val Ser Ser Pro Tyr Val Gly Val Gly Pro Ala Pro Pro Val Ala Gly
385                 390                 395                 400
Leu Pro Ser Ala Pro Pro Pro Gln Phe Ser Gly Pro Glu Leu Ala Met
                405                 410                 415
Ala Val Arg Pro Ala Thr Thr Thr Val Asp Ser Ile Gln Ala Pro Ile
            420                 425                 430
Pro Ser His Thr Ala Pro Arg Pro Asn Pro Thr Pro Ala Pro Pro Pro
        435                 440                 445
Pro Cys Phe Pro Val Pro Pro Pro Gln Pro Leu Pro Thr Pro Tyr Thr
    450                 455                 460
Tyr Pro Ala Gly Ala Lys Gln Pro Ile Pro Ala Gln His His Phe Ser
465                 470                 475                 480
Ser Gly Ile Pro Thr Gly Phe Pro Ala Pro Arg Ile Gly Pro Gln Pro
                485                 490                 495
Gln Pro His Pro Gln Pro His Pro Ser Gln Ala Phe Gly Pro Gln Pro
            500                 505                 510
Pro Gln Gln Pro Leu Pro Leu Gln His Pro His Leu Phe Pro Pro Gln
        515                 520                 525
Ala Pro Gly Leu Leu Pro Pro Gln Ser Pro Tyr Pro Tyr Ala Pro Gln
    530                 535                 540
Pro Gly Val Leu Gly Gln Pro Pro Pro Pro Leu His Thr Gln Leu Tyr
545                 550                 555                 560
Pro Gly Pro Ala Gln Asp Pro Leu Pro Ala His Ser Gly Ala Leu Pro
                565                 570                 575
Phe Pro Ser Pro Gly Pro Pro Gln Pro Pro His Pro Pro Leu Ala Tyr
            580                 585                 590
Gly Pro Ala Pro Ser Thr Arg Pro Met Gly Pro Gln Ala Ala Pro Leu
        595                 600                 605
Thr Ile Arg Gly Pro Ser Ser Ala Gly Gln Ser Thr Pro Ser Pro His
    610                 615                 620
Leu Val Pro Ser Pro Ala Pro Ser Pro Gly Pro Gly Pro Val Pro Pro
625                 630                 635                 640
Arg Pro Pro Ala Ala Glu Pro Pro Pro Cys Leu Arg Arg Gly Ala Ala
                645                 650                 655
Ala Ala Asp Leu Leu Ser Ser Ser Pro Glu Ser Gln His Gly Gly Thr
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            660                 665                 670
Gln Ser Pro Gly Gly Gly Gln Pro Leu Leu Gln Pro Thr Lys Val Asp
        675                 680                 685
Ala Ala Glu Gly Arg Arg Pro Gln Ala Leu Arg Leu Ile Glu Arg Asp
    690                 695                 700
Pro Tyr Glu His Pro Glu Arg Leu Arg Gln Leu Gln Gln Glu Leu Glu
705                 710                 715                 720
Ala Phe Arg Gly Gln Leu Gly Asp Val Gly Ala Leu Asp Thr Val Trp
                725                 730                 735
Arg Glu Leu Gln Asp Ala Gln Glu His Asp Ala Arg Gly Arg Ser Ile
            740                 745                 750
Ala Ile Ala Arg Cys Tyr Ser Leu Lys Asn Arg His Gln Asp Val Met
        755                 760                 765
Pro Tyr Asp Ser Asn Arg Val Val Leu Arg Ser Gly Lys Asp Asp Tyr
    770                 775                 780
Ile Asn Ala Ser Cys Val Glu Gly Leu Ser Pro Tyr Cys Pro Pro Leu
785                 790                 795                 800
Val Ala Thr Gln Ala Pro Leu Pro Gly Thr Ala Ala Asp Phe Trp Leu
                805                 810                 815
Met Val His Glu Gln Lys Val Ser Val Ile Val Met Leu Val Ser Glu
            820                 825                 830
Ala Glu Met Glu Lys Gln Lys Val Ala Arg Tyr Phe Pro Thr Glu Arg
        835                 840                 845
Gly Gln Pro Met Val His Gly Ala Leu Ser Leu Ala Leu Ser Ser Val
    850                 855                 860
Arg Ser Thr Glu Thr His Val Glu Arg Val Leu Ser Leu Gln Phe Arg
865                 870                 875                 880
Asp Gln Ser Leu Lys Arg Ser Leu Val His Leu His Phe Pro Thr Trp
                885                 890                 895
Pro Glu Leu Gly Leu Pro Asp Ser Pro Ser Asn Leu Leu Arg Phe Ile
            900                 905                 910
Gln Glu Val His Ala His Tyr Leu His Gln Arg Pro Leu His Thr Pro
        915                 920                 925
Ile Ile Val His Cys Ser Ser Gly Val Gly Arg Thr Gly Ala Phe Ala
    930                 935                 940
Leu Leu Tyr Ala Ala Val Gln Glu Val Glu Ala Gly Asn Gly Ile Pro
945                 950                 955                 960
Glu Leu Pro Gln Leu Val Arg Arg Met Arg Gln Gln Arg Lys His Met
                965                 970                 975
Leu Gln Glu Lys Leu His Leu Arg Xaa Leu Leu
            980                 985
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<210> 5657
<211> 1020
<212> DNA
<213> Homo sapiens

<400> 5657
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ggcaagaact gcaccgcagg cgccgtctac acctaccacg agaagaagaa ggacacagcg
120
gcctcgggct atgggaccca gaacattcga ctgagccggg atgccgtgaa ggacttcgac
180

tgctgttgtc tctccctgca gccttgccac gatcctgttg tcaccccaga tggctacctg
240
tatgagcgtg aggccatcct ggagtacatt ctgcaccaga agaaggagat tgcccggcag
300
atgaaggcct acgagaagca gcggggcacc cggcgcgagg agcagaagga gcttcagcgg
360
gcggcctcgc aggaccatgt gcggggcttc ctggagaagg agtcggctat cgtgagccgg
420
cccctcaacc ctttcacagc caaggccctc tcgggcacca gcccagatga tgtccaacct
480
gggcccagtg tgggtcctcc aagtaaggac aaggacaaag tgctgcccag cttctggatc
540
ccgtcgctga cgcccgaagc caaggccacc aagctggaga agccgtcccg cacggtgacc
600
tgccccatgt cagggaagcc cctgcgcatg tcggacctga cgcccgtgca cttcacaccg
660
ctagacagct ccgtggaccg cgtggggctc atcacccgca gcgagcgcta cgtgtgtgcc
720
gtgacccgcg acagcctgag caacgccacc ccctgcgctg tgctgcggcc ctctggggct
780
gtggtcaccc tcgaatgcgt ggagaagctg attcggaagg acatggtgga ccctgtgact
840
ggagacaaac tcacagaccg cgacatcatc gtgctgcagc ggggcggtac cggcttcgcg
900
ggctccggag tgaagctgca agcggagaaa tcacggccgg tgatgcaggc ctgagtgtgt
960
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1020

<210> 5658
<211> 301
<212> PRT
<213> Homo sapiens

<400> 5658
Met Thr Arg His Gly Lys Asn Cys Thr Ala Gly Ala Val Tyr Thr Tyr
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His Glu Lys Lys Lys Asp Thr Ala Ala Ser Gly Tyr Gly Thr Gln Asn
20 25 30
Ile Arg Leu Ser Arg Asp Ala Val Lys Asp Phe Asp Cys Cys Cys Leu
35 40 45
Ser Leu Gln Pro Cys His Asp Pro Val Val Thr Pro Asp Gly Tyr Leu
50 55 60
Tyr Glu Arg Glu Ala Ile Leu Glu Tyr Ile Leu His Gln Lys Lys Glu
65 70 75 80
Ile Ala Arg Gln Met Lys Ala Tyr Glu Lys Gln Arg Gly Thr Arg Arg
85 90 95
Glu Glu Gln Lys Glu Leu Gln Arg Ala Ala Ser Gln Asp His Val Arg
100 105 110
Gly Phe Leu Glu Lys Glu Ser Ala Ile Val Ser Arg Pro Leu Asn Pro
115 120 125
Phe Thr Ala Lys Ala Leu Ser Gly Thr Ser Pro Asp Asp Val Gln Pro
130 135 140
Gly Pro Ser Val Gly Pro Pro Ser Lys Asp Lys Asp Lys Val Leu Pro

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145                 150                 155                 160
Ser Phe Trp Ile Pro Ser Leu Thr Pro Glu Ala Lys Ala Thr Lys Leu
                165                 170                 175
Glu Lys Pro Ser Arg Thr Val Thr Cys Pro Met Ser Gly Lys Pro Leu
            180                 185                 190
Arg Met Ser Asp Leu Thr Pro Val His Phe Thr Pro Leu Asp Ser Ser
        195                 200                 205
Val Asp Arg Val Gly Leu Ile Thr Arg Ser Glu Arg Tyr Val Cys Ala
    210                 215                 220
Val Thr Arg Asp Ser Leu Ser Asn Ala Thr Pro Cys Ala Val Leu Arg
225                 230                 235                 240
Pro Ser Gly Ala Val Val Thr Leu Glu Cys Val Glu Lys Leu Ile Arg
                245                 250                 255
Lys Asp Met Val Asp Pro Val Thr Gly Asp Lys Leu Thr Asp Arg Asp
            260                 265                 270
Ile Ile Val Leu Gln Arg Gly Gly Thr Gly Phe Ala Gly Ser Gly Val
        275                 280                 285
Lys Leu Gln Ala Glu Lys Ser Arg Pro Val Met Gln Ala
    290                 295                 300
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<210> 5659
<211> 1263
<212> DNA
<213> Homo sapiens

<400> 5659

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120
tcagagaagg cttagatcta tgcattgggt gttattctca gatgcagaga tgtaaatgcc
180
atttttctct tctgttttca ggtcacatgt gccaatttaa cgaacggtgg aaagtcagaa
240
cttctgaaat caggaagcag caaatccaca ctaaagcaca tatggacaga aagcagcaaa
300
gacttgtcta tcagccgact cctgtcacag acttttcgtg gcaaagagaa tgatacagat
360
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420
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480
acgggcaagt ttaagaaaat gtttggatgg ggcgattttc attccaacat caaaacagtg
540
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600
tatttcaggc ataattcaac tggtcaaggg aatgtatctg tcagcttggt acccccctaca
660
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720
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780
tatgaccctt caaaaacctg ttaccaggag caaacccaaa gtcatgtatc ctggctctgc
840
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tccaagccct ttaaggtgat ctgtatttac atttcctttt atagtacaga ttataaactg
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960
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1020
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1080
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1260
att
1263

<210> 5660
<211> 253
<212> PRT
<213> Homo sapiens

<400> 5660
Val Thr Cys Ala Asn Leu Thr Asn Gly Gly Lys Ser Glu Leu Leu Lys
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Ser Gly Ser Ser Lys Ser Thr Leu Lys His Ile Trp Thr Glu Ser Ser
20 25 30
Lys Asp Leu Ser Ile Ser Arg Leu Leu Ser Gln Thr Phe Arg Gly Lys
35 40 45
Glu Asn Asp Thr Asp Leu Asp Leu Arg Tyr Asp Thr Pro Glu Pro Tyr
50 55 60
Ser Glu Gln Asp Leu Trp Asp Trp Leu Arg Asn Ser Thr Asp Leu Gln
65 70 75 80
Glu Pro Arg Pro Arg Ala Lys Arg Arg Pro Ile Val Lys Thr Gly Lys
85 90 95
Phe Lys Lys Met Phe Gly Trp Gly Asp Phe His Ser Asn Ile Lys Thr
100 105 110
Val Lys Leu Asn Leu Leu Ile Thr Gly Lys Ile Val Asp His Gly Asn
115 120 125
Gly Thr Phe Ser Val Tyr Phe Arg His Asn Ser Thr Gly Gln Gly Asn
130 135 140
Val Ser Val Ser Leu Val Pro Pro Thr Lys Ile Val Glu Phe Asp Leu
145 150 155 160
Ala Gln Gln Thr Val Ile Asp Ala Lys Asp Ser Lys Ser Phe Asn Cys
165 170 175
Arg Ile Glu Tyr Glu Lys Val Asp Lys Ala Thr Lys Asn Thr Leu Cys
180 185 190
Asn Tyr Asp Pro Ser Lys Thr Cys Tyr Gln Glu Gln Thr Gln Ser His
195 200 205
Val Ser Trp Leu Cys Ser Lys Pro Phe Lys Val Ile Cys Ile Tyr Ile
210 215 220
Ser Phe Tyr Ser Thr Asp Tyr Lys Leu Val Gln Lys Val Cys Pro Asp
225 230 235 240
Tyr Asn Tyr His Ser Asp Thr Pro Tyr Phe Pro Ser Gly

245 250

<210> 5661
<211> 578
<212> DNA
<213> Homo sapiens

<400> 5661
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actggatgcc ttggagcatg caagtccaga gcaccctggg agccctggtg catgggaccc
120
ataacccagt gcacggcaag gacccagcag gaagcaccag ccactggccc cgacctcccg
180
cacccaggac ctgacgggca cttagacaca cacagtggcc tgagctccaa ctccagcatg
240
accacgcggg agcttcagca gtactggcag aaccagaaat gccgctggaa gcacgtcaaa
300
ctgctctttg agatcgcttc agctcgcatc gaggagagaa aagtctctaa gtttgtgatg
360
gggaaatcaa ggcctggaga gatgacttat ccagggtcac gtggcgagac agggacagca
420
ccagaaccag acccgagatg tccacgtcaa agtgacatgc tctgagaggc agcacacaca
480
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540
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578

<210> 5662
<211> 148
<212> PRT
<213> Homo sapiens

<400> 5662
Met Thr Leu Leu Pro Asp Pro Trp Thr His Thr Ala Leu Gly Thr Gly
1 5 10 15
Cys Leu Gly Ala Cys Lys Ser Arg Ala Pro Trp Glu Pro Trp Cys Met
20 25 30
Gly Pro Ile Thr Gln Cys Thr Ala Arg Thr Gln Gln Glu Ala Pro Ala
35 40 45
Thr Gly Pro Asp Leu Pro His Pro Gly Pro Asp Gly His Leu Asp Thr
50 55 60
His Ser Gly Leu Ser Ser Asn Ser Ser Met Thr Thr Arg Glu Leu Gln
65 70 75 80
Gln Tyr Trp Gln Asn Gln Lys Cys Arg Trp Lys His Val Lys Leu Leu
85 90 95
Phe Glu Ile Ala Ser Ala Arg Ile Glu Glu Arg Lys Val Ser Lys Phe
100 105 110
Val Met Gly Lys Ser Arg Pro Gly Glu Met Thr Tyr Pro Gly Ser Arg
115 120 125
Gly Glu Thr Gly Thr Ala Pro Glu Pro Asp Pro Arg Cys Pro Arg Gln
130 135 140
Ser Asp Met Leu

145

<210> 5663
<211> 857
<212> DNA
<213> Homo sapiens

<400> 5663
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tgactcactg gctaggagtg ccccatgccc agttcttaga gacccttgat agctcctaga
120
agacaggagg ctgccgtggt caagaagggc caagccttga agtctcacgg caccccctgt
180
ggtggaggta taaggctcag gggccaacta ctgggtcttg cagtccccat cgttgctgtg
240
ggctgtcttc accttcttta gttccttctg tagctcagac tcggccacca caacctcctt
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tggcttctgg taagagatga tcagggtgca gttggcgtgg gcaaagctca gcaaggcgtc
360
atccagaggt agctggtgtc tatctagatc aggaatggag aacttcttgt agtacttctt
420
gttggttgtt ctgacaatga tgcagcgctc cttctggtcc acagagacac tatagacatc
480
cttaggatag gggaggtttc gaatccgcca ctggaaactc atcttggtgt ccttgcgcat
540
gaagatagga ttggcattgc tttccttgat gagttcaggc cccaggttcc ctgctcctag
600
gggcgctggg tctcctactt caagctgcca ctggcccatg gctcccaggg cacttttcac
660
acgccacttt ctcacaagta gttcactcgt cttctcgtca tattcttcag ccatttcctt
720
gccgtctggg aataaatagt gaaccttcct tctcccgtcc tgcagcagcg cagtcttctg
780
ggctgtccgc agactctcca accagcccgt caccgccatc tttcccctgc taagcagcac
840
gcccagccgc tgccatg
857

<210> 5664
<211> 203
<212> PRT
<213> Homo sapiens

<400> 5664
Met Ala Val Thr Gly Trp Leu Glu Ser Leu Arg Thr Ala Gln Lys Thr
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Ala Leu Leu Gln Asp Gly Arg Arg Lys Val His Tyr Leu Phe Pro Asp
20 25 30
Gly Lys Glu Met Ala Glu Glu Tyr Asp Glu Lys Thr Ser Glu Leu Leu
35 40 45
Val Arg Lys Trp Arg Val Lys Ser Ala Leu Gly Ala Met Gly Gln Trp
50 55 60
Gln Leu Glu Val Gly Asp Pro Ala Pro Leu Gly Ala Gly Asn Leu Gly

65 70 75 80
Pro Glu Leu Ile Lys Glu Ser Asn Ala Asn Pro Ile Phe Met Arg Lys
85 90 95
Asp Thr Lys Met Ser Phe Gln Trp Arg Ile Arg Asn Leu Pro Tyr Pro
100 105 110
Lys Asp Val Tyr Ser Val Ser Val Asp Gln Lys Glu Arg Cys Ile Ile
115 120 125
Val Arg Thr Thr Asn Lys Lys Tyr Tyr Lys Lys Phe Ser Ile Pro Asp
130 135 140
Leu Asp Arg His Gln Leu Pro Leu Asp Asp Ala Leu Leu Ser Phe Ala
145 150 155 160
His Ala Asn Cys Thr Leu Ile Ile Ser Tyr Gln Lys Pro Lys Glu Val
165 170 175
Val Val Ala Glu Ser Glu Leu Gln Lys Glu Leu Lys Lys Val Lys Thr
180 185 190
Ala His Ser Asn Asp Gly Asp Cys Lys Thr Gln
195 200

<210> 5665
<211> 531
<212> DNA
<213> Homo sapiens

<400> 5665
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gagtgggtgg ggtttgcccg cccgcagatc tccacgggag ggggaggggt caggcctccc
120
cagcggccct ctgaagtcac ttgcttcacg gaggtgttac tgtctgctgc tggacagagc
180
atgatggggg ctgcaagggc tccctcaaac cctggactcc tccaacagag ggctcctggt
240
tgccaggctc agctctgccc tgcgtcggcc ccagggcgta gggagggtgt ttaatcctgg
300
cccgggcctt ccccgcaggt ggagcgcgtg tcgcacccgc tgctgcagca gcagtatgag
360
ctgtaccggg agcgcctgct gcagcgatgc gagcggcgcc cggtggagca ggtgctgtac
420
cacggcacga cggcaccggc agtgcctgac atctgcgccc acggcttcaa ccgcagcttc
480
tgcggccgca acgccacggt ctacgggaag ggcgtgtatt tcgccaggcg c
531

<210> 5666
<211> 79
<212> PRT
<213> Homo sapiens

<400> 5666
Ser Trp Pro Gly Pro Ser Pro Gln Val Glu Arg Val Ser His Pro Leu
1 5 10 15
Leu Gln Gln Gln Tyr Glu Leu Tyr Arg Glu Arg Leu Leu Gln Arg Cys
20 25 30
Glu Arg Arg Pro Val Glu Gln Val Leu Tyr His Gly Thr Thr Ala Pro

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        35                  40                  45
Ala Val Pro Asp Ile Cys Ala His Gly Phe Asn Arg Ser Phe Cys Gly
    50                  55                  60
Arg Asn Ala Thr Val Tyr Gly Lys Gly Val Tyr Phe Ala Arg Arg
65                  70                  75
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<210> 5667
<211> 858
<212> DNA
<213> Homo sapiens

<400> 5667
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60
aagaaagata tgacatttct acatgaagga aatgactcca aagtagatgg tttagtaaac
120
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180
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240
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300
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360
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480
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540
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600
attcctgatg gctacactat ccaaaaaata gagggataag tagatcttta aaaagctttt
660
taattctttt aaaaactgga tcattataga ggaggctttc tgtttgagaa catttttata
720
ttcatcccta aagagtaaac ataagtggaa tttttacctc tttttatttc atggataata
780
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840
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858

<210> 5668
<211> 152
<212> PRT
<213> Homo sapiens

<400> 5668
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Xaa Ser Ala Arg Gly Ser Gln Ser Met Gln Pro Pro Ile Ile Pro Leu
 1               5                  10                  15
Phe Pro Val Val Lys Lys Asp Met Thr Phe Leu His Glu Gly Asn Asp
            20                  25                  30
Ser Lys Val Asp Gly Leu Val Asn Phe Glu Lys Leu Arg Met Ile Ser
```

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        35                  40                  45
Lys Glu Ile Arg Gln Val Val Arg Met Thr Ser Ala Asn Met Asp Pro
    50                  55                  60
Ala Met Met Phe Arg Gln Arg Ser Leu Ser Gln Gly Ser Thr Asn Ser
65                  70                  75                  80
Asn Met Leu Asp Val Gln Gly Gly Ala His Lys Lys Arg Ala Arg Arg
                85                  90                  95
Ser Ser Leu Leu Asn Ala Lys Lys Leu Tyr Glu Asp Ala Gln Met Ala
            100                 105                 110
Arg Lys Val Lys Gln Tyr Leu Ser Ser Leu Asp Val Glu Thr Asp Glu
        115                 120                 125
Glu Lys Phe Gln Met Met Ser Leu Gln Xaa Glu Pro Ala Tyr Gly Thr
    130                 135                 140
Cys Glu Tyr Lys Phe Ser Phe Met
145                 150
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<210> 5669
<211> 1842
<212> DNA
<213> Homo sapiens

<400> 5669
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120
gccatgatgc gcagctccat agagaggggc aaatgggtct tcttccagaa ctgccacctg
180
gcaccaagct ggatgccagc cctagaacgc ctcatcgagc acatcaaccc cgacaaggta
240
cacagggact tccgcctctg gctcaccagc ctgcccagca acaagttccc agtgtccatc
300
ctgcagaacg gctccaagat gaccattgag ccgccacgcg gtgtcagggc caacctgctg
360
aagtcctata gtagccttgg tgaagacttc ctcaactcct gccacaaggt gatggagttc
420
aagtctctgc tgctgtctct gtgcttgttc catgggaacg ccctggagcg ccgtaagttt
480
gggcccctgg gcttcaacat cccctatgag ttcacggatg gagatctgcg catctgcatc
540
agccagctca agatgttcct ggacgaatat gatgacatcc cctacaaggt cctcaagtac
600
acggcagggg agatcaatta cgggggccgt gtcactgatg actgggaccg gcgctgcatc
660
atgaacatct tggaggactt ctacaaccct gacgtgctct cccctgagca cagctacagc
720
gcctcgggca tctaccacca gatcccgcct acctacgacc tccacggcta cctctcctac
780
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840
atcacctttg cccagaacga gacgttcgcc ctcctgggca ccatcatcca gctgcaaccc
900
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960

attctgctca aggtgcctga gcctatcaac ttgcaatggg tgatggccaa gtacccagtg
1020
ctgtatgagg aatcaatgaa cacagtacta gtacaagagg tcattaggta caatcggctg
1080
ctgcaggtga tcacacagac actgcaagac ctactcaagg cactcaaggg gctggtagtg
1140
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1260
caacgcctgg actttctgca ggcctggatc caagatggca tcccagctgt cttctggatc
1320
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1380
tttgtcatct ccattgacac catctccttt gatttcaagg tgatgtttga ggcaccatca
1440
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1500
cgctgggatc cagaggcctt ccagctggct gagtctcagc ccaaggagct gtacacagag
1560
atggccgtta tctggctctt gccaacaccc aaccgcaagg cccaggacca ggacttttac
1620
ctgtgcccca tctacaagac actgactcgt gctggaacac tatcaaccac aggacactct
1680
accaactatg tcattgctgt ggagatcccc acccatcagc cccagcgaca ctggataaag
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1800
ttaaagctga attttctaag caaaaaaaaa aaaaaaaaaa aa
1842

<210> 5670
<211> 591
<212> PRT
<213> Homo sapiens

<400> 5670
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Ala Glu Glu Met Lys Phe Ser Lys Lys Leu Ser Ala Ile Ser Leu Gly
20 25 30
Gln Gly Gln Gly Pro Arg Ala Glu Ala Met Met Arg Ser Ser Ile Glu
35 40 45
Arg Gly Lys Trp Val Phe Phe Gln Asn Cys His Leu Ala Pro Ser Trp
50 55 60
Met Pro Ala Leu Glu Arg Leu Ile Glu His Ile Asn Pro Asp Lys Val
65 70 75 80
His Arg Asp Phe Arg Leu Trp Leu Thr Ser Leu Pro Ser Asn Lys Phe
85 90 95
Pro Val Ser Ile Leu Gln Asn Gly Ser Lys Met Thr Ile Glu Pro Pro
100 105 110
Arg Gly Val Arg Ala Asn Leu Leu Lys Ser Tyr Ser Ser Leu Gly Glu
115 120 125
Asp Phe Leu Asn Ser Cys His Lys Val Met Glu Phe Lys Ser Leu Leu

```
    130                 135                 140
Leu Ser Leu Cys Leu Phe His Gly Asn Ala Leu Glu Arg Arg Lys Phe
145                 150                 155                 160
Gly Pro Leu Gly Phe Asn Ile Pro Tyr Glu Phe Thr Asp Gly Asp Leu
                165                 170                 175
Arg Ile Cys Ile Ser Gln Leu Lys Met Phe Leu Asp Glu Tyr Asp Asp
            180                 185                 190
Ile Pro Tyr Lys Val Leu Lys Tyr Thr Ala Gly Glu Ile Asn Tyr Gly
        195                 200                 205
Gly Arg Val Thr Asp Asp Trp Asp Arg Arg Cys Ile Met Asn Ile Leu
    210                 215                 220
Glu Asp Phe Tyr Asn Pro Asp Val Leu Ser Pro Glu His Ser Tyr Ser
225                 230                 235                 240
Ala Ser Gly Ile Tyr His Gln Ile Pro Pro Thr Tyr Asp Leu His Gly
                245                 250                 255
Tyr Leu Ser Tyr Ile Lys Ser Leu Pro Leu Asn Asp Met Pro Glu Ile
            260                 265                 270
Phe Gly Leu His Asp Asn Ala Asn Ile Thr Phe Ala Gln Asn Glu Thr
        275                 280                 285
Phe Ala Leu Leu Gly Thr Ile Ile Gln Leu Gln Pro Lys Ser Ser Ser
    290                 295                 300
Ala Gly Ser Gln Gly Arg Glu Glu Ile Val Glu Asp Val Thr Gln Asn
305                 310                 315                 320
Ile Leu Leu Lys Val Pro Glu Pro Ile Asn Leu Gln Trp Val Met Ala
                325                 330                 335
Lys Tyr Pro Val Leu Tyr Glu Glu Ser Met Asn Thr Val Leu Val Gln
            340                 345                 350
Glu Val Ile Arg Tyr Asn Arg Leu Leu Gln Val Ile Thr Gln Thr Leu
        355                 360                 365
Gln Asp Leu Leu Lys Ala Leu Lys Gly Leu Val Val Met Ser Ser Gln
    370                 375                 380
Leu Glu Leu Met Ala Ala Ser Leu Tyr Asn Asn Thr Val Pro Glu Leu
385                 390                 395                 400
Trp Ser Ala Lys Ala Tyr Pro Ser Leu Lys Pro Leu Ser Ser Trp Val
                405                 410                 415
Met Asp Leu Leu Gln Arg Leu Asp Phe Leu Gln Ala Trp Ile Gln Asp
            420                 425                 430
Gly Ile Pro Ala Val Phe Trp Ile Ser Gly Phe Phe Phe Pro Gln Ala
        435                 440                 445
Phe Leu Thr Gly Thr Leu Gln Asn Phe Ala Arg Lys Phe Val Ile Ser
    450                 455                 460
Ile Asp Thr Ile Ser Phe Asp Phe Lys Val Met Phe Glu Ala Pro Ser
465                 470                 475                 480
Glu Leu Thr Gln Arg Pro Gln Val Gly Cys Tyr Ile His Gly Leu Phe
                485                 490                 495
Leu Glu Gly Ala Arg Trp Asp Pro Glu Ala Phe Gln Leu Ala Glu Ser
            500                 505                 510
Gln Pro Lys Glu Leu Tyr Thr Glu Met Ala Val Ile Trp Leu Leu Pro
        515                 520                 525
Thr Pro Asn Arg Lys Ala Gln Asp Gln Asp Phe Tyr Leu Cys Pro Ile
    530                 535                 540
Tyr Lys Thr Leu Thr Arg Ala Gly Thr Leu Ser Thr Thr Gly His Ser
545                 550                 555                 560
Thr Asn Tyr Val Ile Ala Val Glu Ile Pro Thr His Gln Pro Gln Arg
```

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                565                 570                 575
His Trp Ile Lys Arg Gly Val Ala Leu Ile Cys Ala Leu Asp Tyr
            580                 585                 590
```

<210> 5671
<211> 818
<212> DNA
<213> Homo sapiens
<400> 5671
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60
atggtcgtcg gattttgaag acttgaacta gactgggggt tctccttgca tttcttgcct
120
gttgcctatc tttgtcctct ctcttccggc ttcgagatga atgtgcagcc ctgttctagg
180
tgtgggtatg gggtttatcc tgccgagaag atcagctgta tagatcagat atggcataaa
240
gcctgttttc actgtgaagt ttgcaagatg atgctgtctg ttaataactt tgtgagtcac
300
cagaaaaagc cgtactgtca cgcccataac cctaagaaca acactttcac cagtgtctat
360
cacactccat taaatctaaa tgtgaggaca tttccagagg ccatcagtgg gatccatgac
420
caagaagatg gtgaacagtg taaatcagtt tttcattggg acatgaaatc caaggataag
480
gaaggtgcac ctaacaggca gccactggca aatgagagag cctattggac tggatatggg
540
gaagggaatg cttggtgccc aggagctctg ccagaccccg aaattgtaag gatggttgag
600
gctcgaaagt ctcttggtga ggaatataca gaagactatg agcaacccag gggcaagggg
660
agctttccag ccatgatcac acctgcttat caaagggcca agaaagccaa ccagctggcc
720
agccaagtgg agtataagag agggcatgat gaacgcatct ccaggttctc cacggtggcg
780
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818

<210> 5672
<211> 220
<212> PRT
<213> Homo sapiens

<400> 5672

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Met Asn Val Gln Pro Cys Ser Arg Cys Gly Tyr Gly Val Tyr Pro Ala
 1               5                  10                  15
Glu Lys Ile Ser Cys Ile Asp Gln Ile Trp His Lys Ala Cys Phe His
            20                  25                  30
Cys Glu Val Cys Lys Met Met Leu Ser Val Asn Asn Phe Val Ser His
        35                  40                  45
Gln Lys Lys Pro Tyr Cys His Ala His Asn Pro Lys Asn Asn Thr Phe
    50                  55                  60
Thr Ser Val Tyr His Thr Pro Leu Asn Leu Asn Val Arg Thr Phe Pro
65                  70                  75                  80
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Glu Ala Ile Ser Gly Ile His Asp Gln Glu Asp Gly Glu Gln Cys Lys
85 90 95
Ser Val Phe His Trp Asp Met Lys Ser Lys Asp Lys Glu Gly Ala Pro
100 105 110
Asn Arg Gln Pro Leu Ala Asn Glu Arg Ala Tyr Trp Thr Gly Tyr Gly
115 120 125
Glu Gly Asn Ala Trp Cys Pro Gly Ala Leu Pro Asp Pro Glu Ile Val
130 135 140
Arg Met Val Glu Ala Arg Lys Ser Leu Gly Glu Glu Tyr Thr Glu Asp
145 150 155 160
Tyr Glu Gln Pro Arg Gly Lys Gly Ser Phe Pro Ala Met Ile Thr Pro
165 170 175
Ala Tyr Gln Arg Ala Lys Lys Ala Asn Gln Leu Ala Ser Gln Val Glu
180 185 190
Tyr Lys Arg Gly His Asp Glu Arg Ile Ser Arg Phe Ser Thr Val Ala
195 200 205
Asp Thr Pro Glu Leu Leu Arg Ser Lys Ala Trp Gly
210 215 220

<210> 5673
<211> 1279
<212> DNA
<213> Homo sapiens

<400> 5673
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gcagaaatca atatttttgt ttgaaagatg cagtcatgct aatttcactt ttggctaaaa
120
ccgagacgat aaaagaacag ttgggtgttt ataggatgcc ctcaaagtga gctggctaag
180
tgagctgggc tctaacttca ctcacaaatt tatagtacag ctaagaaggc cagtctgtcc
240
atgaaaggga gccgagacaa gacgagggcg gcctcttcca ggcctgtgcc aagtgtcctt
300
ggggtcccgc catggtccac acttctgcag catccgcaga acatgtggcc gggtcctgcc
360
cagcagcagg gacagccaag tgggaggcag gcatggtgca cacctgggga ggcccctggt
420
gcagaagcag ccccacagta gcagccccat ccagaggaag accactccgg agggccacag
480
gcctctgcag ccctggcact gccgcccagc cctccatctc agcgggatgt gcagggtgag
540
acaggaatgc agggacgttc tgcccctagg tcagcctctt catccgcctg ttgtgcttcg
600
atggtcaagg ttgccctgtc cacagctgct gcaacgccat ccagggcttc gtcttgtctc
660
tccagctcac tctcggcctc cgggccagcc ccttcatcct cctcaggatc tgggttagtt
720
cctgggtatc tgcctcagaa agggctggca ggcttgtctg caggtgcagt gctgtgccct
780
cctggtctcc tgcgggtggc tcacggtgca gggtacggcc catcagccca gatgctgcat
840

gccagactga gcagctcttc tctgcggggg aagaggttct tgcgcttctg agcaccaatg
900
catcttctaa cagctccatc ttcttgctga actgcacttc taaaatgggg ataacctctg
960
gcatcttggc agatatcaaa cgataggcca tgtctggctt tccaataaac cgctggcgga
1020
tgctaatttc gtaaggtgag tggaccttga tgtcgtccac gtcttctctt tcaaacctgt
1080
gcatgagcaa agaactggag tcatgtattt ccaacccaga cacaaggacg gtgagcctcc
1140
ctggtttaac gtgagactct gttctgtggg aaataacagc aggaattttt atcagtatcc
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1260
gtggtgtctt ccaaagctt
1279

<210> 5674
<211> 81
<212> PRT
<213> Homo sapiens

<400> 5674
Leu His Ser Gln Ile Tyr Ser Thr Ala Lys Lys Ala Ser Leu Ser Met
1 5 10 15
Lys Gly Ser Arg Asp Lys Thr Arg Ala Ala Ser Ser Arg Pro Val Pro
20 25 30
Ser Val Leu Gly Val Pro Pro Trp Ser Thr Leu Leu Gln His Pro Gln
35 40 45
Asn Met Trp Pro Gly Pro Ala Gln Gln Gln Gly Gln Pro Ser Gly Arg
50 55 60
Gln Ala Trp Cys Thr Pro Gly Glu Ala Pro Gly Ala Glu Ala Ala Pro
65 70 75 80
Gln

<210> 5675
<211> 1074
<212> DNA
<213> Homo sapiens

<400> 5675
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ccctgagctc ccacccgagg cttaggccca aggggcctct tccaggctga gggcctgctg
120
gggctgggcc aggggctgag gctgaaagca gcagcctgcc tagtgggtga cgccaggggc
180
cggtgtaaca tggcaccgag gttggggcca cagcaatgtg tgggacggtg gggtgggctg
240
gggcccttgg ctccaagcat tagttctcca agctctggtc cgttctccta cctccttcaa
300
ggggcaccag ggctacaagg tggtagttga gtattggggc ccgactcctg gggcactgga
360

gtggtctcta ggcccgaggc cccaaggaga gggctgggtt tctgggagag tgctggtcct
420
tcctctctgg gcttggccat cttgacagct tcatcgtagg agggtggagg ctccggggtg
480
tacaggctgt aggcaggagg agccgtggag tccaggtcca gctccccaaa gggcaggggc
540
aaccgcatgc ccagtgggta ctgcacggag ctgtaggagg tcacagtgct gtgtacaggg
600
ctgtcactgt ccatagggat gactgccacg tcgcagggct gccgtgctgg tggcagatgt
660
ggctgggcct gtgcctgctt ccggaggcag cagaaccgga cacaaccagc tgtgacacca
720
cacagcagaa gcaggaggac cgccagcagg atgagcctag gagagcaagg ctctaccact
780
ggactgaccc tcggccaccg ggcacctgca ccctggggaa tgtcgtggca caaccaccga
840
agacaggtta acaggataaa aagcagacaa tgtctctcca tgtcggagac cgccgtggcc
900
agagcctggc ctcgggctgc tgggcctgcc ctggctatct ctcctgggct ggccaggggt
960
ggccttgggc tcactcccag gactcgctgt cctcagcgag tgccccactg ctgagcggga
1020
tcgtagggga ctcccgcgga ggccaggcgg gagagttggg agggaaggtc ctgg
1074

<210> 5676
<211> 145
<212> PRT
<213> Homo sapiens

<400> 5676
Glu Val Thr Val Leu Cys Thr Gly Leu Ser Leu Ser Ile Gly Met Thr
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Ala Thr Ser Gln Gly Cys Arg Ala Gly Gly Arg Cys Gly Trp Ala Cys
            20   25   30
Ala Cys Phe Arg Arg Gln Gln Asn Arg Thr Gln Pro Ala Val Thr Pro
        35   40   45
His Ser Arg Ser Arg Arg Thr Ala Ser Arg Met Ser Leu Gly Glu Gln
    50   55   60
Gly Ser Thr Thr Gly Leu Thr Leu Gly His Arg Ala Pro Ala Pro Trp
65   70   75   80
Gly Met Ser Trp His Asn His Arg Arg Gln Val Asn Arg Ile Lys Ser
                85   90   95
Arg Gln Cys Leu Ser Met Ser Glu Thr Ala Val Ala Arg Ala Trp Pro
            100   105   110
Arg Ala Ala Gly Pro Ala Leu Ala Ile Ser Pro Gly Leu Ala Arg Gly
        115   120   125
Gly Leu Gly Leu Thr Pro Arg Thr Arg Cys Pro Gln Arg Val Pro His
    130   135   140
Cys
145

<210> 5677
<211> 477

<212> DNA
<213> Homo sapiens

<400> 5677
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aaaaggacac tggtgaagta gcggtagcac tcctccacgt tgcccaaggg ggttgctggt
120
agggaaagca agatgcagca gtgaggccct ctctggtatc cattcattca cttcactcaa
180
cagctgttta tgaccatgag caatacaagc cttgtgaaga tcctggagca gggcacaagc
240
cgctgacgtc tgctccagtg agaagccctg ctgccttccc caattcgctt tctttccgca
300
gccgccgctg ccccgacccc ggatctgcat gtggaagtac ctggacgtcc attccatgca
360
ccagctggag aagaccacca atgctgagat gagggaggtg ctggctgagc tgctggagct
420
agggtgtcct gagcagagcc tgagcgacgc catcaccctg gacctcttct gccgcgg
477

<210> 5678
<211> 151
<212> PRT
<213> Homo sapiens

<400> 5678
Met Ala Ser Leu Arg Leu Cys Ser Gly His Pro Ser Ser Ser Ser Ser
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Ala Ser Thr Ser Leu Ile Ser Ala Leu Val Val Phe Ser Ser Trp Cys
            20   25   30
Met Glu Trp Thr Ser Arg Tyr Phe His Met Gln Ile Arg Gly Arg Gly
        35   40   45
Ser Gly Gly Cys Gly Lys Lys Ala Asn Trp Gly Arg Gln Gln Gly Phe
    50   55   60
Ser Leu Glu Gln Thr Ser Ala Ala Cys Ala Leu Leu Gln Asp Leu His
65   70   75   80
Lys Ala Cys Ile Ala His Gly His Lys Gln Leu Leu Ser Glu Val Asn
                85   90   95
Glu Trp Ile Pro Glu Arg Ala Ser Leu Leu His Leu Ala Phe Pro Thr
            100   105   110
Ser Asn Pro Leu Gly Gln Arg Gly Gly Val Leu Pro Leu Leu His Gln
        115   120   125
Cys Pro Phe Leu Pro Trp Ser Gln Ala Ala Ser Phe Gln His Arg Pro
    130   135   140
Leu Gln Arg Gly Thr Ala Ala
145   150

<210> 5679
<211> 665
<212> DNA
<213> Homo sapiens

<400> 5679

nngcccctcc aggagggagc cgggagatta cgcagctcca tgtaggtcta cgtttaggtt
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gggaggatct accatgaaga aggtcaagaa gaaaaggtca gaggccagac gccaccggac
120
tccacctccc agcatgctgg ctccaattcc acctctcagc agcctagccc tgaatccaca
180
ccacagcagc ctagtcctga atccacacca cagcagccta gccctgaatc cacaccacag
240
cattccagcc ttgaaaccac ctcccggcag ccagcattcc aagcccttcc agcacccgaa
300
atccgccgct cctcttgctg ccttttatct ccagatgcta acgtgaaggc agcccctcaa
360
tccaggaaag cagaaaatct tcaagaaaac cctccagtca tcgtaacgcg tgtcctccaa
420
gccctcggaa ctgtggctgt ggctctgggg gctctaggag ctgcctacta catcactgaa
480
tccttgtgaa caagccccta ggcccacagt ctggcagacc tccaccagcc ccaggagttg
540
ataggtgatg gcgctgggag aagatgttca gaatatctca aaagccaagt ccagaagatc
600
cagtttccat caaagggacc tctcttgtca ccaaaattta aaaaaagaaa aaaaaaacga
660
aaaaa
665

<210> 5680
<211> 143
<212> PRT
<213> Homo sapiens

<400> 5680
Val Gly Arg Ile Tyr His Glu Glu Gly Gln Glu Glu Lys Val Arg Gly
1 5 10 15
Gln Thr Pro Pro Asp Ser Thr Ser Gln His Ala Gly Ser Asn Ser Thr
20 25 30
Ser Gln Gln Pro Ser Pro Glu Ser Thr Pro Gln Gln Pro Ser Pro Glu
35 40 45
Ser Thr Pro Gln Gln Pro Ser Pro Glu Ser Thr Pro Gln His Ser Ser
50 55 60
Leu Glu Thr Thr Ser Arg Gln Pro Ala Phe Gln Ala Leu Pro Ala Pro
65 70 75 80
Glu Ile Arg Arg Ser Ser Cys Cys Leu Leu Ser Pro Asp Ala Asn Val
85 90 95
Lys Ala Ala Pro Gln Ser Arg Lys Ala Glu Asn Leu Gln Glu Asn Pro
100 105 110
Pro Val Ile Val Thr Arg Val Leu Gln Ala Leu Gly Thr Val Ala Val
115 120 125
Ala Leu Gly Ala Leu Gly Ala Ala Tyr Tyr Ile Thr Glu Ser Leu
130 135 140

<210> 5681
<211> 1402
<212> DNA
<213> Homo sapiens

<400> 5681
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gtcgggacct ggtttccggg catgagctga gagcaccacg ccgaggccac gagtatttca
120
tagacattga tggaagcaga aaccaaaact cttcccctgg agaatgcatc catcctttca
180
gagggctctc tgcaggaagg acaccgatta tggattggca acctggaccc caaaattacc
240
gaataccacc tcctcaagct cctccagaag tttggcaagg taaagcagtt tgacttcctc
300
ttccacaagt caggtgcttt ggagggacag cctcgaggct actgttttgt taactttgaa
360
actaagcagg aagcagagca agccatccag tgtctcaatg gcaagttggc cctgtccaag
420
aagctggtgg tgcgatgggc acatgctcaa gtaaagagat atgatcataa caagaatgat
480
aagattcttc caatcagtct cgagccatcc tcaagcactg agcctactca gtctaaccta
540
agtgtcactg caaagataaa agccattgaa gcaaaactga aaatgatggc ggaaaatcct
600
gatgcagagt atccagcagc gcctgtttat tcctacttta agccaccaga taaaaaaagg
660
actactccat attctagaac agcatggaaa tctcgaagat gatggttgtg aattactgta
720
gcagcaaaag caaattggtc tccacaccta aaatcgtctg cctgtgtact ttgtagatgt
780
gaatggtact attcaacgga gcacaatcac atgttagcat ttggtaacat aatgtttttg
840
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900
aatagcgttg tatcccaaat tgtgatttga accctgggat gctctaattg gctggttggt
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ttggatttgt aactccagaa acattctata gtgtgccaga gcaaaaggca aatacacaaa
1020
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1080
tacgctcgtg tgtcttttac aacataaaga aaaagtaaaa ggcagggagg gaagtgagag
1140
acagatttta aatcatgttc agaactgttg ttccagaatt tactacggca atccctccaa
1200
ctggactgaa aaagagaaag ttcttggcaa aaaggagctg attctttgaa caaatgttgt
1260
agtaatctgt ttaagaatta tgcttattgt ttcaaaatcc caactaggaa aacatggtgt
1320
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1380
cacaagttct atttgggata tt
1402

<210> 5682
<211> 190
<212> PRT

<213> Homo sapiens

<400> 5682
Met Glu Ala Glu Thr Lys Thr Leu Pro Leu Glu Asn Ala Ser Ile Leu
1 5 10 15
Ser Glu Gly Ser Leu Gln Glu Gly His Arg Leu Trp Ile Gly Asn Leu
20 25 30
Asp Pro Lys Ile Thr Glu Tyr His Leu Leu Lys Leu Leu Gln Lys Phe
35 40 45
Gly Lys Val Lys Gln Phe Asp Phe Leu Phe His Lys Ser Gly Ala Leu
50 55 60
Glu Gly Gln Pro Arg Gly Tyr Cys Phe Val Asn Phe Glu Thr Lys Gln
65 70 75 80
Glu Ala Glu Gln Ala Ile Gln Cys Leu Asn Gly Lys Leu Ala Leu Ser
85 90 95
Lys Lys Leu Val Val Arg Trp Ala His Ala Gln Val Lys Arg Tyr Asp
100 105 110
His Asn Lys Asn Asp Lys Ile Leu Pro Ile Ser Leu Glu Pro Ser Ser
115 120 125
Ser Thr Glu Pro Thr Gln Ser Asn Leu Ser Val Thr Ala Lys Ile Lys
130 135 140
Ala Ile Glu Ala Lys Leu Lys Met Met Ala Glu Asn Pro Asp Ala Glu
145 150 155 160
Tyr Pro Ala Ala Pro Val Tyr Ser Tyr Phe Lys Pro Pro Asp Lys Lys
165 170 175
Arg Thr Thr Pro Tyr Ser Arg Thr Ala Trp Lys Ser Arg Arg
180 185 190

<210> 5683
<211> 328
<212> DNA
<213> Homo sapiens

<400> 5683
ggatccatgc gttgccctag ggaggcctca gctgtcaagc actgaccatc tctgcagaca
60
cgcagggctg acctgtactg gtgagtaagc attagccatg ggacgcacac aatccagcca
120
atgctttcag aaggcaccac atgtgatgca cagcctctat ttacatgtga ataattacac
180
tgctgctttc tggttaaaag tagggaaata cagtgttcca gggcatagga atggtgctct
240
gggtagaaaa gtttattttg ctggtgggag gcaggttttg ttaataaagc tttgaaatac
300
acaaatttca ttctggatgc tgatgctg
328

<210> 5684
<211> 103
<212> PRT
<213> Homo sapiens

<400> 5684
Met Lys Phe Val Tyr Phe Lys Ala Leu Leu Thr Lys Pro Ala Ser His

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 1               5                  10                  15
Gln Gln Asn Lys Leu Phe Tyr Pro Glu His His Ser Tyr Ala Leu Glu
            20                  25                  30
His Cys Ile Ser Leu Leu Leu Thr Arg Lys Gln Gln Cys Asn Tyr Ser
        35                  40                  45
His Val Asn Arg Gly Cys Ala Ser His Val Val Pro Ser Glu Ser Ile
    50                  55                  60
Gly Trp Ile Val Cys Val Pro Trp Leu Met Leu Thr His Gln Tyr Arg
65                  70                  75                  80
Ser Ala Leu Arg Val Cys Arg Asp Gly Gln Cys Leu Thr Ala Glu Ala
                85                  90                  95
Ser Leu Gly Gln Arg Met Asp
            100
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<210> 5685
<211> 604
<212> DNA
<213> Homo sapiens

<400> 5685
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ctggcctacg agtctgacgg gatcgtggtt tccaacgaca cataccgtga cctccaaggc
120
gagcggcagg agtggaagcg cttcatcgag gagcggctgc tcatgtactc cttcgtcaat
180
gacaagtatg ttccctccca gaggccctga cagacttggg gtccacaggg gaagccagag
240
gtgcccttgg caagggtgga gctgggggct gggctctgcg gggccctgtg gccatgggag
300
gttgcgggtc ttggctccag gcagctttga gagtgagacg gatagctcac cacataggag
360
aaatcagacc gggaccaggc aggctgtggg gtggagagag tggctaattt gggagataga
420
gccgtagcac ttatgagggg atgtatgtgg ttgatggttc caggtggcct ctctacgaac
480
caacatggca tctctcgagc agaggccatg ggccagtggg tgcgggctgc catcccccga
540
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600
atcc
604

<210> 5686
<211> 69
<212> PRT
<213> Homo sapiens

<400> 5686
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Pro Cys Ser Arg Val Gly Gly Lys Arg Val Val Cys Tyr Asp Asp Arg
 1               5                  10                  15
Phe Ile Val Lys Leu Ala Tyr Glu Ser Asp Gly Ile Val Val Ser Asn
            20                  25                  30
Asp Thr Tyr Arg Asp Leu Gln Gly Glu Arg Gln Glu Trp Lys Arg Phe
```

```
        35                  40                  45
Ile Glu Glu Arg Leu Leu Met Tyr Ser Phe Val Asn Asp Lys Tyr Val
    50                  55                  60
Pro Ser Gln Arg Pro
65
```

<210> 5687
<211> 328
<212> DNA
<213> Homo sapiens

<400> 5687
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ccccggctct gcatgcacgc ctgcgtgaac accccgggct cttcccgttg cacctgcccc
120
ggtggatccg aaactctggc tgacgggaag agctgtgaga atgtggatga atgtgtgggc
180
ctgcagccgg tgtgccccca ggggaccaca tgcatcaaca ccggtggaag cttccagtgt
240
gtcagccctg agtgccccga gggcagcggc aatgtgagct acgtgaagac gtctccattc
300
cagtgtgagc ggaacccctg ccccatgg
328

<210> 5688
<211> 109
<212> PRT
<213> Homo sapiens

<400> 5688

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Thr Leu Ser Arg Pro Arg Gly Ala Gly Lys Gly Gly Gly Asp Gly Gly
 1               5                  10                  15
Gly Gly Glu Arg Pro Arg Leu Cys Met His Ala Cys Val Asn Thr Pro
            20                  25                  30
Gly Ser Ser Arg Cys Thr Cys Pro Gly Gly Ser Glu Thr Leu Ala Asp
        35                  40                  45
Gly Lys Ser Cys Glu Asn Val Asp Glu Cys Val Gly Leu Gln Pro Val
    50                  55                  60
Cys Pro Gln Gly Thr Thr Cys Ile Asn Thr Gly Gly Ser Phe Gln Cys
65                  70                  75                  80
Val Ser Pro Glu Cys Pro Glu Gly Ser Gly Asn Val Ser Tyr Val Lys
                85                  90                  95
Thr Ser Pro Phe Gln Cys Glu Arg Asn Pro Cys Pro Met
            100                 105
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<210> 5689
<211> 1897
<212> DNA
<213> Homo sapiens

<400> 5689
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tgaacaatca gaatcataga agagtgtgag cactggtcct ttgtcttcca ggtgggacag
120
tgtgtggtgg tcttcagcca ggctcctagt gggagagccc cactcagccc cagtttgaac
180
tctcgcccat cacctatcag tgccactncc tccagctctc gttcctgaaa cccgagagta
240
ccgctctcag tctccagtaa gaagcatgga tgaagctcct tgtgttaacg gccgctgggg
300
aacactgaga cccagggctc aaaggcagac tcctcaggtt cccgggaagg gagcctttcc
360
ccagccagag gagacggctc tcctatcctc aatggtggga gtttgtctcc aggaacggca
420
gctgtgggtg gctcttcttt ggacagtcct gtacaggcca tatctccaag tactccatct
480
gctgctgaag gatacgacct gaaaatagga ctttctttgg ccccccgacg aggatcaacc
540
agatcagaaa gatctgagat taggatccat agatctgaat tgggatctaa acccgcttcc
600
agtagtaatc ccatggatgg catggacaat aggacagttg ggggaagtat gagacaccct
660
cctgaacaga caaatggtgt gcatacccca cctcacgtgg ccagtgccct tgcaggggcc
720
gtctccccag gtgccctgcg tcggagtctg gaagccatca aagcgatgtc ctccaaaggc
780
ccctcggcct ctgcagcact aagtcctcct cttgggtctt ctccaggctc tcctgggagc
840
cagagtttga gcagtggaga aacagtgccc atccctcgcc cagggcctgc ccaaggagat
900
ggacattcct tacctcccat tgctcgccgc ctgggccacc accctccaca gtccctaaat
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gttggcaaac ccctatacca gagtatgaac tgcaagccca tgcagatgta cgtgctggac
1020
attaaagaca ccaaggagaa ggggcgggtc aaatggaaag tatttaatag cagttctgtg
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cagaagccaa aactctttaa ttcccaaccg aagtcactcc aggctgggat caaatctcca
1380
ttaagaaaaa aaattatata taaatatata tatatatatt atatagccaa ctctgttgac
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1560
catcagtaac ttcccaaaag aaactgaaga gccccctgta aatctttatg tggccttctt
1620
ggagttaaaa aatgaaaggg catatgtaag ttgcaaaggt ggagggtttt agactctcat
1680

gcttcaggtg ctgtcggggt aaaagtaact gtttttcccc ttctcttaaa accacagagg
1740
acctgtgaca gctctgcaga aatgccagtg cctggccccc tcttgccttt tatggctgag
1800
gaaagttacc caacaaagga ttttattcca catttgtgtg ccgggtcatt gtgaaataat
1860
gtttatgcag ccaacatctg aaaaaaaaaa aaaaaaa
1897

<210> 5690
<211> 54
<212> PRT
<213> Homo sapiens

<400> 5690
Thr Ile Arg Ile Ile Glu Glu Cys Glu His Trp Ser Phe Val Phe Gln
1 5 10 15
Val Gly Gln Cys Val Val Val Phe Ser Gln Ala Pro Ser Gly Arg Ala
20 25 30
Pro Leu Ser Pro Ser Leu Asn Ser Arg Pro Ser Pro Ile Ser Ala Thr
35 40 45
Xaa Ser Ser Ser Arg Ser
50

<210> 5691
<211> 1227
<212> DNA
<213> Homo sapiens

<400> 5691
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120
catcaaaacg aggacgaacc cattcgtgtt agctaccatc ggaatatcca ctataattca
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gtggtgaatc ctaacaaggc caccattggt gtggggctgg gctgccatca ttcaaaccag
240
ggtttgcaga gcagtctctg atgaagaatg ccataaaaac atcggaggag tcatggattg
300
aacagcagat gctagaagac aagaaacggg ccacagactg ggaggccaca aatgaagcca
360
tcgaggagca ggtggctcgg gaatcctacc tgcagtggtt gcgggatcag gagaaacagg
420
ctcgccaggt ccgaggcccc agccagcccc ggaaagccag cgccacatgc agttcggcca
480
cagcagcagc ctccagtggc ctggaggagt ggactagccg gtccccgcgg cagcggagtt
540
cagcctcgtc acctgagcac cctgagctgc atgctgaatt gggcatgaag ccccccttccc
600
caggcactgt tttagctctt gccaaacctc cttcgccctg tgcgccaggt acaagcagtc
660
agttctcggc aggggccgac cgggcaactt ccccccttgt gtccctctac cctgctttgg
720

agtgccgggc cctcattcag cagatgtccc cctctgcctt tggtctgaat gactgggatg
780
atgatgagat cctagcttcg gtgctggcag tgtcccaaca ggaataccta gacagtatga
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960
acagagacag accaactggc agccaggcag ccccagagga gagagacatt cagacagagg
1020
aaagtctccc tgcccctcat tccttccaag atgagaaaaa cttgccgcca ccccccgaca
1080
ctgatgccag ggaggtggga ggaagaagtg ggaaatttcc cttcccagta cccccaagaa
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1200
aactaatcaa aaatgaaaaa aaaaaaa
1227

<210> 5692
<211> 86
<212> PRT
<213> Homo sapiens

<400> 5692
Lys Arg Lys Asn Asn Cys His Gly Asn His Ile Glu Met Gln Ala Met
1 5 10 15
Ala Glu Met Tyr Asn Arg Pro Val Glu Val Tyr Gln Tyr Ser Thr Glu
20 25 30
Pro Ile Asn Thr Phe His Gly Ile His Gln Asn Glu Asp Glu Pro Ile
35 40 45
Arg Val Ser Tyr His Arg Asn Ile His Tyr Asn Ser Val Val Asn Pro
50 55 60
Asn Lys Ala Thr Ile Gly Val Gly Leu Gly Cys His His Ser Asn Gln
65 70 75 80
Gly Leu Gln Ser Ser Leu
85

<210> 5693
<211> 389
<212> DNA
<213> Homo sapiens

<400> 5693
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120
tccaaccccg cagggcccct cgtcgggcgg tcccaactta gtcgtcccct gacgcggcct
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cggaacatga tctacatgag ccgcttgggt atctggggcg agggcacacc cttccggaac
300

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atggacatga aggtcagcgg gcatgtaca
389

<210> 5694
<211> 60
<212> PRT
<213> Homo sapiens

<400> 5694
Arg Gln Leu Pro Pro Thr Gly Ala Ser Glu Pro Arg Asn Met Ile Tyr
 1   5   10   15
Met Ser Arg Leu Gly Ile Trp Gly Glu Gly Thr Pro Phe Arg Asn Phe
            20   25   30
Glu Glu Phe Leu His Ala Ile Glu Lys Arg Gly Val Gly Ala Met Glu
        35   40   45
Ile Val Ala Met Asp Met Lys Val Ser Gly His Val
    50   55   60

<210> 5695
<211> 1417
<212> DNA
<213> Homo sapiens

<400> 5695
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gatgtggagg agctggaccg ggcgctcagg gctgccttgg aggtccacgt ccaggaggag
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480
aacaacctgg agcgtctggc agagaacacc ggggagttcc aggaggtggt gcgggccttc
540
tacgacaccc tggacgctgc ccgcagcagc atccgcgtcg ttcgtgtgga gcgcgtgtcg
600
cacccgctgc tgcagcagca gtatgagctg taccgggagc gcctgctgca gcgatgcgag
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cggcgcccgg tggagcaggt gctgtaccac ggcacgacgg caccggcagt gcctgacatc
720
tgcgcccacg gcttcaaccg cagcttctgc ggccgcaacg ccacggtcta cgggaagggc
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840

gatggccata aggcggtgtt cgtggcacgg gtgctgactg gcgactacgg gcagggccgc
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960
gccgtggact gcatctgcca gcccagcatc ttcgtcatct tccacgacac ccaggcgctg
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1380
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1417

<210> 5696
<211> 368
<212> PRT
<213> Homo sapiens

<400> 5696
Val Ala Leu His Arg Ser Leu Lys Pro Gln Gly Gln Val Gly Glu Gln
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            20   25   30
Gln Pro Pro Leu Glu Ala Glu Glu Pro Pro Asp Arg Gly Thr Asp Gly
        35   40   45
Lys Ala Gln Leu Val Val His Ser Ala Phe Glu Gln Asp Val Glu Glu
    50   55   60
Leu Asp Arg Ala Leu Arg Ala Ala Leu Glu Val His Val Gln Glu Glu
65   70   75   80
Thr Val Gly Pro Trp Arg Arg Thr Leu Pro Ala Glu Leu Arg Ala Arg
                85   90   95
Leu Glu Arg Cys His Gly Val Ser Val Ala Leu Arg Gly Asp Cys Thr
            100   105   110
Ile Leu Arg Gly Phe Gly Ala His Pro Ala Arg Ala Ala Arg His Leu
        115   120   125
Val Ala Leu Leu Ala Gly Pro Trp Asp Gln Ser Leu Ala Phe Pro Leu
    130   135   140
Ala Ala Ser Gly Pro Thr Leu Ala Gly Gln Thr Leu Lys Gly Pro Trp
145   150   155   160
Asn Asn Leu Glu Arg Leu Ala Glu Asn Thr Gly Glu Phe Gln Glu Val
                165   170   175
Val Arg Ala Phe Tyr Asp Thr Leu Asp Ala Ala Arg Ser Ser Ile Arg
            180   185   190
Val Val Arg Val Glu Arg Val Ser His Pro Leu Leu Gln Gln Gln Tyr
        195   200   205
Glu Leu Tyr Arg Glu Arg Leu Leu Gln Arg Cys Glu Arg Arg Pro Val

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    210                 215                 220
Glu Gln Val Leu Tyr His Gly Thr Thr Ala Pro Ala Val Pro Asp Ile
225                 230                 235                 240
Cys Ala His Gly Phe Asn Arg Ser Phe Cys Gly Arg Asn Ala Thr Val
                245                 250                 255
Tyr Gly Lys Gly Val Tyr Phe Ala Arg Arg Ala Ser Leu Ser Val Gln
            260                 265                 270
Asp Arg Tyr Ser Pro Pro Asn Ala Asp Gly His Lys Ala Val Phe Val
        275                 280                 285
Ala Arg Val Leu Thr Gly Asp Tyr Gly Gln Gly Arg Arg Gly Leu Arg
    290                 295                 300
Ala Pro Pro Leu Arg Gly Pro Gly His Val Leu Leu Arg Tyr Asp Ser
305                 310                 315                 320
Ala Val Asp Cys Ile Cys Gln Pro Ser Ile Phe Val Ile Phe His Asp
                325                 330                 335
Thr Gln Ala Leu Pro Thr His Leu Ile Thr Cys Glu His Val Pro Arg
            340                 345                 350
Ala Ser Pro Asp Asp Pro Ser Gly Leu Pro Gly Arg Ser Pro Asp Thr
        355                 360                 365
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<210> 5697
<211> 3362
<212> DNA
<213> Homo sapiens

<400> 5697

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240
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3362

<210> 5698
<211> 403
<212> PRT
<213> Homo sapiens

<400> 5698
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Thr Ser Arg Gly Cys Gly Leu Asp Leu Leu Pro Gln Tyr Val Ser Leu
        35   40   45
Cys Asp Leu Asp Ala Ile Trp Gly Ile Val Val Glu Ala Val Ala Gly
    50   55   60
Ala Gly Ala Leu Ile Thr Leu Leu Leu Met Leu Ile Leu Leu Val Arg
65   70   75   80
Leu Pro Phe Ile Lys Glu Lys Glu Lys Lys Ser Pro Val Gly Leu His
                85   90   95
Phe Leu Phe Leu Leu Gly Thr Leu Gly Leu Phe Gly Leu Thr Phe Ala
            100   105   110
Phe Ile Ile Gln Glu Asp Glu Thr Ile Cys Ser Val Arg Arg Phe Leu
        115   120   125
Trp Gly Val Leu Phe Ala Leu Cys Phe Ser Cys Leu Leu Ser Gln Ala

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    130                 135                 140
Trp Arg Val Arg Arg Leu Val Arg His Gly Thr Gly Pro Ala Gly Trp
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Gln Leu Val Gly Leu Ala Leu Cys Leu Met Leu Val Gln Val Ile Ile
                165                 170                 175
Ala Val Glu Trp Leu Val Leu Thr Val Leu Arg Asp Thr Arg Pro Ala
            180                 185                 190
Cys Ala Tyr Glu Pro Met Asp Phe Val Met Ala Leu Ile Tyr Asp Met
        195                 200                 205
Val Leu Leu Val Val Thr Leu Gly Leu Ala Leu Phe Thr Leu Cys Gly
    210                 215                 220
Lys Phe Lys Arg Trp Lys Leu Asn Gly Ala Phe Leu Leu Ile Thr Ala
225                 230                 235                 240
Phe Leu Ser Val Leu Ile Trp Val Ala Trp Met Thr Met Tyr Leu Phe
                245                 250                 255
Gly Asn Val Lys Leu Gln Gln Gly Asp Ala Trp Asn Asp Pro Thr Leu
            260                 265                 270
Ala Ile Thr Leu Ala Ala Ser Gly Trp Val Phe Val Ile Phe His Ala
        275                 280                 285
Ile Pro Glu Ile His Cys Thr Leu Leu Pro Ala Leu Gln Glu Asn Thr
    290                 295                 300
Pro Asn Tyr Phe Asp Thr Ser Gln Pro Arg Met Arg Glu Thr Ala Phe
305                 310                 315                 320
Glu Glu Asp Val Gln Leu Pro Arg Ala Tyr Met Glu Asn Lys Ala Phe
                325                 330                 335
Ser Met Asp Glu His Asn Ala Ala Leu Arg Thr Ala Gly Phe Pro Asn
            340                 345                 350
Gly Ser Leu Gly Lys Arg Pro Ser Gly Ser Leu Gly Lys Arg Pro Ser
        355                 360                 365
Ala Pro Phe Arg Ser Asn Val Tyr Gln Pro Thr Glu Met Ala Val Val
    370                 375                 380
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His Leu Trp
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<210> 5699
<211> 1565
<212> DNA
<213> Homo sapiens

<400> 5699

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aatggttgct ctttaaaagt tagaatctca agagatacca aaagcactta agagttacca
180
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240
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300
cagttgagat ataaacgagg gaagaggtga agctttcagg aagccagaga gcccctgccg
360
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<210> 5700
<211> 197
<212> PRT
<213> Homo sapiens

<400> 5700
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Ser Gln Ala Asp Ser Lys Lys Lys Ser Asn Leu Met Met Ser Leu Phe
20 25 30
Glu Pro Gly Pro Glu Pro Leu Pro Trp Leu Gly Lys Met Ala Gln Leu

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        35                  40                  45
Gly Pro Ile Ser Asp Ala Lys Glu Asn Pro Tyr Gly Glu Asp Asp Asn
    50                  55                  60
Lys Ser Pro Phe Pro Leu Gln Pro Lys Asn Lys Arg Ser Tyr Ala Gln
65                  70                  75                  80
Asn Val Thr Val Trp Ile Lys Pro Ser Gly Leu Gln Thr Asp Val Gln
                85                  90                  95
Lys Ile Leu Arg Asn Ala Arg Lys Leu Pro Glu Lys Thr Gln Thr Phe
            100                 105                 110
Tyr Lys Glu Leu Asn Arg Leu Arg Lys Ala Ala Leu Ala Phe Gly Phe
        115                 120                 125
Leu Asp Leu Leu Lys Gly Val Ala Asp Met Leu Glu Arg Glu Cys Thr
    130                 135                 140
Leu Leu Pro Glu Thr Ala His Pro Asp Ala Ala Phe Gln Leu Thr His
145                 150                 155                 160
Ala Ala Gln Gln Leu Lys Leu Ala Ser Thr Gly Thr Ser Glu Tyr Ala
                165                 170                 175
Ala Tyr Asp Gln Asn Ile Thr Pro Leu His Thr Asp Phe Ser Gly Ser
            180                 185                 190
Ser Thr Glu Arg Ile
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<210> 5701
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 5701
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1885

<210> 5702
<211> 348
<212> PRT
<213> Homo sapiens

<400> 5702
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35 40 45
Leu Leu Leu Ile Pro Asn Val Leu Phe Leu Ile Phe Leu Leu Trp Lys
50 55 60
Leu Pro Ser Ala Arg Ala Lys Ile Arg Ile Thr Ser Ser Pro Ile Phe

65 70 75 80
Ile Thr Phe Tyr Ile Leu Val Phe Val Val Ala Leu Val Gly Ile Ala
85 90 95
Arg Ala Val Val Ser Met Thr Val Ser Thr Ser Asn Ala Ala Thr Val
100 105 110
Ala Asp Lys Ile Leu Trp Glu Ile Thr Arg Phe Phe Leu Leu Ala Ile
115 120 125
Glu Leu Ser Val Ile Ile Leu Gly Leu Ala Phe Gly His Leu Glu Ser
130 135 140
Lys Ser Ser Ile Lys Arg Val Leu Ala Ile Thr Thr Val Leu Ser Leu
145 150 155 160
Ala Tyr Ser Val Thr Gln Gly Thr Leu Glu Ile Leu Tyr Pro Asp Ala
165 170 175
His Leu Ser Ala Glu Asp Phe Asn Ile Tyr Gly His Gly Gly Arg Gln
180 185 190
Phe Trp Leu Val Ser Ser Cys Phe Phe Phe Leu Val Tyr Ser Leu Val
195 200 205
Val Ile Leu Pro Lys Thr Pro Leu Lys Glu Arg Ile Ser Leu Pro Ser
210 215 220
Arg Arg Ser Phe Tyr Val Tyr Ala Gly Ile Leu Ala Leu Leu Asn Leu
225 230 235 240
Leu Gln Gly Leu Gly Ser Val Leu Leu Cys Phe Asp Ile Ile Glu Gly
245 250 255
Leu Cys Cys Val Asp Ala Thr Thr Phe Leu Tyr Phe Ser Phe Phe Ala
260 265 270
Pro Leu Ile Tyr Val Ala Phe Leu Arg Gly Phe Phe Gly Ser Glu Pro
275 280 285
Lys Ile Leu Phe Xaa Leu Gln Met Pro Ser Gly Arg Asp Arg Gly Ala
290 295 300
Arg Cys Thr Pro Thr Pro Ala Leu Arg Cys Gly Pro Ala Gly Gly Pro
305 310 315 320
Gly Gly Cys Arg Gly Cys Trp Gly Leu Ser Cys Gln Leu Leu Glu His
325 330 335
Ala Val Arg Leu Cys Arg Arg Gly Gly Leu Pro Gly
340 345

<210> 5703
<211> 1496
<212> DNA
<213> Homo sapiens

<400> 5703
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1496

<210> 5704
<211> 269
<212> PRT
<213> Homo sapiens

<400> 5704
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20 25 30
Glu Gly Ser Val Leu Arg Arg Gly Phe Gln Thr Cys Glu His Trp Lys
35 40 45
Gln Ile Phe Met Glu Ile Val Gly Val Gln Ser Ala Leu Cys Gly Leu
50 55 60
Val Leu Ser Leu Leu Ile Cys Val Ala Ala Val Ala Val Phe Thr Thr

65 70 75 80
His Ile Leu Leu Leu Leu Pro Val Leu Leu Ser Ile Leu Gly Ile Val
85 90 95
Cys Leu Val Val Thr Ile Met Tyr Trp Ser Gly Trp Glu Met Gly Ala
100 105 110
Val Glu Ala Ile Ser Leu Ser Ile Leu Val Gly Ser Ser Val Asp Tyr
115 120 125
Cys Val His Leu Val Glu Gly Tyr Leu Leu Ala Gly Glu Asn Leu Pro
130 135 140
Pro His Gln Ala Glu Asp Ala Arg Thr Gln Arg Gln Trp Arg Thr Leu
145 150 155 160
Glu Ala Val Arg His Val Gly Val Ala Ile Val Ser Ser Ala Leu Thr
165 170 175
Thr Val Ile Ala Thr Val Pro Leu Phe Phe Cys Ile Ile Ala Pro Phe
180 185 190
Ala Lys Phe Gly Lys Ile Val Ala Leu Asn Thr Gly Val Ser Ile Leu
195 200 205
Tyr Thr Leu Thr Val Ser Thr Ala Leu Leu Gly Ile Met Ala Pro Ser
210 215 220
Ser Phe Thr Arg Thr Arg Thr Ser Phe Leu Lys Ala Leu Gly Ala Val
225 230 235 240
Leu Leu Ala Gly Ala Leu Gly Leu Gly Ala Cys Leu Val Leu Leu Gln
245 250 255
Ser Gly Tyr Lys Ile Pro Leu Pro Ala Gly Ala Ser Leu
260 265

<210> 5705
<211> 768
<212> DNA
<213> Homo sapiens

<400> 5705
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660

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768

<210> 5706
<211> 202
<212> PRT
<213> Homo sapiens

<400> 5706
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Gly Trp Glu Glu Ala Arg Asp Phe Asp Gly Lys Val Tyr Tyr Ile Asp
35 40 45
His Thr Asn Arg Thr Thr Ser Trp Ile Asp Pro Arg Asp Arg Tyr Thr
50 55 60
Lys Pro Leu Thr Phe Ala Asp Cys Ile Ser Asp Glu Leu Pro Leu Gly
65 70 75 80
Trp Glu Glu Ala Tyr Asp Pro Gln Val Gly Asp Tyr Phe Ile Asp His
85 90 95
Asn Thr Lys Thr Thr Gln Ile Glu Asp Pro Arg Val Gln Trp Arg Arg
100 105 110
Glu Gln Glu His Met Leu Lys Asp Tyr Leu Val Val Ala Gln Glu Ala
115 120 125
Leu Ser Ala Gln Lys Glu Ile Tyr Gln Val Lys Gln Gln Arg Leu Glu
130 135 140
Leu Ala Gln Gln Glu Tyr Gln Gln Leu His Ala Val Trp Glu His Lys
145 150 155 160
Leu Gly Ser Gln Val Ser Leu Val Ser Gly Ser Ser Ser Ser Ser Lys
165 170 175
Tyr Asp Pro Glu Ile Leu Lys Ala Glu Ile Ala Thr Ala Val Gln Arg
180 185 190
Ala Trp Leu Ser Asp Pro Glu Glu Asn Arg
195 200

<210> 5707
<211> 6988
<212> DNA
<213> Homo sapiens

<400> 5707
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<211> 506
<212> PRT
<213> Homo sapiens

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Leu Gln Leu Met Asp Val Arg Gln Asn Cys Cys Asp Phe Leu Gln Ser
50 55 60
Gln Leu His Pro Thr Asn Cys Leu Gly Ile Arg Ala Phe Ala Asp Val
65 70 75 80
His Thr Cys Thr Asp Leu Leu Gln Gln Ala Asn Ala Tyr Ala Glu Gln
85 90 95
His Phe Pro Glu Val Met Leu Gly Glu Glu Phe Leu Ser Leu Ser Leu
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Asp Gln Val Cys Ser Leu Ile Ser Ser Asp Lys Leu Thr Val Ser Ser
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Glu Glu Lys Val Phe Glu Ala Val Ile Ser Trp Ile Asn Tyr Glu Lys
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Glu Thr Arg Leu Glu His Met Ala Lys Leu Met Glu His Val Arg Leu
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Pro Leu Leu Pro Arg Asp Tyr Leu Val Gln Thr Val Glu Glu Glu Ala
165 170 175
Leu Ile Lys Asn Asn Asn Thr Cys Lys Asp Phe Leu Ile Glu Ala Met
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Lys Tyr His Leu Leu Pro Leu Asp Gln Arg Leu Leu Ile Lys Asn Pro
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Val Gly Gly Gln Ala Pro Lys Ala Ile Arg Ser Val Glu Cys Tyr Asp
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245 250 255
Cys Arg Ala Gly Val Val Phe Met Ala Gly His Val Tyr Ala Val Gly
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Gly Phe Asn Gly Ser Leu Arg Val Arg Thr Val Asp Val Tyr Asp Gly
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Val Lys Asp Gln Trp Thr Ser Ile Ala Ser Met Gln Glu Arg Arg Ser
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Val Gly Val Gly Val Val Glu Gly Lys Leu Tyr Ala Val Gly Gly Tyr
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Asp Gly Ala Ser Arg Gln Cys Leu Ser Thr Val Glu Gln Tyr Asn Pro
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Ala Thr Asn Glu Trp Ile Tyr Val Ala Asp Met Ser Thr Arg Arg Ser
385                 390                 395                 400
Gly Ala Gly Val Gly Val Leu Ser Gly Gln Leu Tyr Ala Thr Gly Gly
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His Asp Gly Pro Leu Val Arg Lys Ser Val Glu Val Tyr Asp Pro Gly
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Thr Asn Thr Trp Lys Gln Val Ala Asp Met Asn Met Cys Arg Arg Asn
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Ala Gly Val Cys Ala Val Asn Gly Leu Leu Tyr Val Val Gly Gly Asp
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Asp Gly Ser Cys Asn Leu Ala Ser Val Glu Tyr Tyr Asn Pro Val Thr
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<212> DNA
<213> Homo sapiens

<400> 5709

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<210> 5710
<211> 441
<212> PRT
<213> Homo sapiens

<400> 5710
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Ala Phe Asp Gly Leu Ala Ser Leu Val Glu Leu Asn Leu Ala His Asn

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Leu Trp Leu Ala Trp Trp Leu Arg Glu Tyr Ile Pro Thr Asn Ser Thr
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Cys Cys Gly Arg Cys His Ala Pro Met His Met Arg Gly Arg Tyr Leu
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Val Glu Val Asp Gln Ala Ser Phe Gln Cys Ser Ala Pro Phe Ile Met
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Asp Ala Pro Arg Asp Leu Asn Ile Ser Glu Gly Arg Met Ala Glu Leu
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Lys Cys Arg Thr Pro Pro Met Ser Ser Val Lys Trp Leu Leu Pro Asn
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Gly Thr Val Leu Ser His Ala Ser Arg His Pro Arg Ile Ser Val Leu
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Asn Asp Gly Thr Leu Asn Phe Ser His Val Leu Leu Ser Asp Thr Gly
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Val Tyr Thr Cys Met Val Thr Asn Val Ala Gly Asn Ser Asn Ala Ser
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Ala Tyr Leu Asn Val Ser Thr Ala Glu Leu Asn Thr Ser Asn Tyr Ser
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        275                 280                 285
Pro Lys Gln Val Ala Val Pro Ala Thr Asp Thr Thr Asp Lys Met Gln
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Thr Val Glu Ile Ile Gln Val Asp Glu Asp Ile Pro Ala Ala Thr Ser
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<211> 1142
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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Pro Pro Leu Asn Ile His Tyr Leu Lys Leu Ile Asp Arg Glu Asn Phe
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<210> 5713
<211> 1996
<212> DNA
<213> Homo sapiens

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aatacactag gttgtcgaaa taataattcc acagcctctt ctaacaatgc ctacaatgtg
720
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780
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840
cgaagaacat caagtttaaa agccagttat gaagcattta agaataatga ctttcagttg
900
ggaaaagaat tttcaatggc cagggaaaca gttggctatt catcatcttc ggcacttatg
960

acaacattaa cacagaatgc cagttcatca gcagccgact cacggagtgg tcgaaagagc
1020
aaaaacaaca acaagtcttc aagccagcag tcatcatctt cctcctcctc ttcttcctta
1080
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1140
ccagaatctg attcaaatag tcaggttgat tggacttacg acccaaatga acctcgatac
1200
tgcatttgta atcaggtatc ttatggtgag atggtgggat gtgataacca agattgccct
1260
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1320
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1380
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1620
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1680
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1740
gtatattctg ctgcatgtac tgtactccag agctgttatg taacactgta tataaatggt
1800
tgcaaaaaaa aaaaagtcag tgcttctaaa aagaatttaa gataatggtt tttaaaatgc
1860
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1920
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1980
ggttaaaagt attttg
1996

<210> 5714
<211> 408
<212> PRT
<213> Homo sapiens

<400> 5714
Ile Glu Gln Leu Pro Met Asp Leu Arg Asp Arg Phe Thr Glu Met Arg
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Glu Met Asp Leu Gln Val Gln Asn Ala Met Asp Gln Leu Glu Gln Arg
20 25 30
Val Ser Glu Phe Phe Met Asn Ala Lys Lys Asn Lys Pro Glu Trp Arg
35 40 45
Glu Glu Gln Met Ala Ser Ile Lys Lys Asp Tyr Tyr Lys Ala Leu Glu
50 55 60
Asp Ala Asp Glu Lys Val Gln Leu Ala Asn Gln Ile Tyr Asp Leu Val
65 70 75 80
Asp Arg His Leu Arg Lys Leu Asp Gln Glu Leu Ala Lys Phe Lys Met

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                85                  90                  95
Glu Leu Glu Ala Asp Asn Ala Gly Ile Thr Glu Ile Leu Glu Arg Arg
            100                 105                 110
Ser Leu Glu Leu Asp Thr Pro Ser Gln Pro Val Asn Asn His His Ala
        115                 120                 125
His Ser His Thr Pro Val Glu Lys Arg Lys Tyr Asn Pro Thr Ser His
    130                 135                 140
His Thr Thr Thr Asp His Ile Pro Glu Lys Lys Phe Lys Ser Glu Ala
145                 150                 155                 160
Leu Leu Ser Thr Leu Thr Ser Asp Ala Ser Lys Glu Asn Thr Leu Gly
                165                 170                 175
Cys Arg Asn Asn Asn Ser Thr Ala Ser Ser Asn Asn Ala Tyr Asn Val
            180                 185                 190
Asn Ser Ser Gln Pro Leu Gly Ser Tyr Asn Ile Gly Ser Leu Ser Ser
        195                 200                 205
Gly Thr Gly Ala Gly Ala Ile Thr Met Ala Ala Ala Gln Ala Val Gln
    210                 215                 220
Ala Thr Ala Gln Met Lys Glu Gly Arg Arg Thr Ser Ser Leu Lys Ala
225                 230                 235                 240
Ser Tyr Glu Ala Phe Lys Asn Asn Asp Phe Gln Leu Gly Lys Glu Phe
                245                 250                 255
Ser Met Ala Arg Glu Thr Val Gly Tyr Ser Ser Ser Ser Ala Leu Met
            260                 265                 270
Thr Thr Leu Thr Gln Asn Ala Ser Ser Ser Ala Ala Asp Ser Arg Ser
        275                 280                 285
Gly Arg Lys Ser Lys Asn Asn Asn Lys Ser Ser Ser Gln Gln Ser Ser
    290                 295                 300
Ser Ser Ser Ser Ser Ser Ser Leu Ser Ser Cys Ser Ser Ser Ser Thr
305                 310                 315                 320
Val Val Gln Glu Ile Ser Gln Gln Thr Thr Val Val Pro Glu Ser Asp
                325                 330                 335
Ser Asn Ser Gln Val Asp Trp Thr Tyr Asp Pro Asn Glu Pro Arg Tyr
            340                 345                 350
Cys Ile Cys Asn Gln Val Ser Tyr Gly Glu Met Val Gly Cys Asp Asn
        355                 360                 365
Gln Asp Cys Pro Ile Glu Trp Phe His Tyr Gly Cys Val Gly Leu Thr
    370                 375                 380
Glu Ala Pro Lys Gly Lys Trp Tyr Cys Pro Gln Cys Thr Ala Ala Met
385                 390                 395                 400
Lys Arg Arg Gly Ser Arg His Lys
                405
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<210> 5715
<211> 1458
<212> DNA
<213> Homo sapiens

<400> 5715
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ctgggcggag ggggagtgcc agcccccagg agctaatccc cggctgatgg cgcagggccg
120
ggggcttggc cgtctagtgt gatgaaggag gcgaccccca aggtgggaag gcgcacgggt
180

tggggtttga gggtggatga ttggtgacgg agggtgtatc ttcaggagga ggttcgagtg
240
aagatcaaag acttgaatga acacattgtt tgctgcctat gcgccggcta cttcgtggat
300
gccaccacca tcacagagtg tcttcatact ttctgcaaga gttgtattgt gaagtacctc
360
caaactagca agtactgccc catgtgcaac attaagatcc acgagacaca gccactgctc
420
aacctcaaac tggaccgggt catgcaggac atcgtgtata agctggtgcc tggcttgcaa
480
gacagtgaag agaaacggat tcgggaattc taccagtccc gaggtttgga ccgggtcacc
540
cagcccactg gggaagagcc agcactgagc aacctcggcc tccccttcag cagctttgac
600
cactctaaag cccactacta tcgctatgat gagcagttga acctgtgcct ggagcggctg
660
aggtgaggag aaggtcaggg gttgcaggag gtgacagtgc caatgaccca gagccaggga
720
gggtctaggg gagaggctga gcagtgagtg agtgcctatc cccttgaaga gagtatatca
780
tggctctggg tggggaagag gaggaaagat aggattccct aacctgtgtc tatttccccc
840
cagttctggc aaagacaaga ataaaagcgt cctgcaggtg agaagggctg aggggagggc
900
ctctctaagg agactcacct cccatggtcc ttccctcaca caccttgccc tcttccctcc
960
cctccctgct cccagaacaa gtatgtccga tgttctgtta gagctgaggt acgccatctc
1020
cggagggtcc tgtgtcaccg cttgatgcta aaccctcagc atgtgcagct ccttttttgac
1080
aatgaagttc tccctgatca catgacaatg aagcagatat gcctctcccg ctggttcggc
1140
aaggtaagcc aggccaccct ccctgggatc acacccccctt cagactcccc ccaaccatcc
1200
tacagtcctc aggggaaggg tgggctgagg ggccctttga ataatataag aacattcccc
1260
acgtactcca acttcctcat tctctcctta gccatcccct ttgcttttac aataaagtgt
1320
gaaagagaag aggaggtagg ggccaagccc ccaccccatc ccactcccct tccctcccca
1380
gatatttatg tgaaatgaac tgcagcttta ttttttgaaa taaaaacttt taaaaagcaa
1440
aaaaaaaaaa aaaaaaaa
1458

<210> 5716
<211> 148
<212> PRT
<213> Homo sapiens

<400> 5716
Leu Gln Glu Glu Val Arg Val Lys Ile Lys Asp Leu Asn Glu His Ile
 1   5   10   15
Val Cys Cys Leu Cys Ala Gly Tyr Phe Val Asp Ala Thr Thr Ile Thr

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            20                  25                  30
Glu Cys Leu His Thr Phe Cys Lys Ser Cys Ile Val Lys Tyr Leu Gln
        35                  40                  45
Thr Ser Lys Tyr Cys Pro Met Cys Asn Ile Lys Ile His Glu Thr Gln
    50                  55                  60
Pro Leu Leu Asn Leu Lys Leu Asp Arg Val Met Gln Asp Ile Val Tyr
65                  70                  75                  80
Lys Leu Val Pro Gly Leu Gln Asp Ser Glu Glu Lys Arg Ile Arg Glu
                85                  90                  95
Phe Tyr Gln Ser Arg Gly Leu Asp Arg Val Thr Gln Pro Thr Gly Glu
            100                 105                 110
Glu Pro Ala Leu Ser Asn Leu Gly Leu Pro Phe Ser Ser Phe Asp His
        115                 120                 125
Ser Lys Ala His Tyr Tyr Arg Tyr Asp Glu Gln Leu Asn Leu Cys Leu
    130                 135                 140
Glu Arg Leu Arg
145
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<210> 5717
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 5717

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120
tttcggttat tccctccatc tcgtcaacag ctgccgcgcg caggcttagc tcattcctct
180
gacctgccag gaagcagaga gacccacaga gcaggaggga ggcagaaagt ggagacggac
240
ctgagcccga ggaagaggca ggcagaggct gaggctgatt ccaccccagc ctgcctggac
300
aaccctcctt agccgcagcc ccttccagtt ccctaggggt tctgcccctc cccctctctg
360
gggcaccagc cccccagggt cctgcatccc accatgtcga tggctgtgga aacctttggc
420
ttcttcatgg caactgtggg gctgctgatg ctgggggtga ctctgccaaa cagctactgg
480
cgagtgtcca ctgtgcacgg gaacgtcatc accaccaaca ccatcttcga gaacctctgg
540
tttagctgtg ccaccgactc cctgggcgtc tacaactgct gggagttccc gtccatgctg
600
gccctctctg ggtatattca ggcctgccgg gcactcatga tcaccgccat cctcctgggc
660
ttcctcggcc tcttgctagg catagcgggc ctgcgctgca ccaacattgg gggcctggag
720
ctctccagga aagccaagct ggcggccacc gcaggggccc tccacattct ggccggtatc
780
tgcgggatgg tggccatctc ctggtacgcc ttcaacatca cccgggactt cttcgacccc
840
ttgtaccccg gaaccaagta cgagctgggc cccgccctct acctggggtg gagcgcctca
900
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ctgatctcca tcctgggtgg cctctgcctc tgctccgcct gctgctgcgg ctctgacgag
960
gacccagccg ccagcgcccg gcggccctac caggctcccg tgtccgtgat gcccgtcgcc
1020
acctcggacc aagaaggcga cagcagcttt ggcaaatacg gcagaaacgc ctacgtgtag
1080
cagctctggc ccgtgggccc cgctgtcttc ccactgcccc aaggagaggg gacctggccg
1140
gggcccattc ccctatagta acctcagggg ccggccacgc cccgctcccg tagccccgcc
1200
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1260
gaagtcgcat atctcccctc tgaggctgga tccctcatct tctgaccctg ggttctgggc
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1380
gcatattgtg accgttaaaa aaaaaaaaaa aaaaaaaaa
1419

<210> 5718
<211> 228
<212> PRT
<213> Homo sapiens

<400> 5718
Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly
 1   5   10   15
Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser
            20   25   30
Thr Val His Gly Asn Val Ile Thr Thr Asn Thr Ile Phe Glu Asn Leu
        35   40   45
Trp Phe Ser Cys Ala Thr Asp Ser Leu Gly Val Tyr Asn Cys Trp Glu
    50   55   60
Phe Pro Ser Met Leu Ala Leu Ser Gly Tyr Ile Gln Ala Cys Arg Ala
65   70   75   80
Leu Met Ile Thr Ala Ile Leu Leu Gly Phe Leu Gly Leu Leu Leu Gly
                85   90   95
Ile Ala Gly Leu Arg Cys Thr Asn Ile Gly Gly Leu Glu Leu Ser Arg
            100   105   110
Lys Ala Lys Leu Ala Ala Thr Ala Gly Ala Leu His Ile Leu Ala Gly
        115   120   125
Ile Cys Gly Met Val Ala Ile Ser Trp Tyr Ala Phe Asn Ile Thr Arg
    130   135   140
Asp Phe Phe Asp Pro Leu Tyr Pro Gly Thr Lys Tyr Glu Leu Gly Pro
145   150   155   160
Ala Leu Tyr Leu Gly Trp Ser Ala Ser Leu Ile Ser Ile Leu Gly Gly
                165   170   175
Leu Cys Leu Cys Ser Ala Cys Cys Cys Gly Ser Asp Glu Asp Pro Ala
            180   185   190
Ala Ser Ala Arg Arg Pro Tyr Gln Ala Pro Val Ser Val Met Pro Val
        195   200   205
Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe Gly Lys Tyr Gly Arg
    210   215   220
Asn Ala Tyr Val

225

<210> 5719
<211> 2267
<212> DNA
<213> Homo sapiens

<400> 5719
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ccgcctttga tgttaggtcc tggagaaggg gaagtggtgc gggacccaca ggtccagctg
120
ctccgtgcca tgcagtcggg aaagggaaac aggcactaat caaaggcaac tgctcactcg
180
tacctctttc ttctgaagca catgatgaag tctattctca gcagcgattt tctttacaaa
240
ctctttcgtt aatcccccca gagggaagat ggttctcctc agggcatcct gggaaacctg
300
gcatttctaa cttcaaaccg atttctgaaa agcccttcgg gcttcttaac gtgcttctgc
360
tcaaagactt cttcatcttc cagggaagtt cttgcatagt gacctgtggc aatggcatct
420
gcccctgaac acatcattcc aatactcctt tacgtaggac acttgatgga aagggatgtc
480
taagatctgg caaactctgt aagcatcttc acagtctttg tcggcagtac agaccccatg
540
ttcatccagt gagtcccagt tcttcataaa caccctgtc acctggtaac ctctccgcct
600
cagcagcagc gcggccacgg cgctgtccac gccgccggac agggcgcaca cgacgtgccg
660
caaggcctgc atccgccagt cgccccgtcc ggcggcgtgg acagcgccgt ggccgcgctg
720
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780
gatgaacatg gggtctgtac tgccgacaaa gactgtgaag atgcttacag agtttgccag
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900
agtgactttt tgaatgagta tgaaaaagga aggactccca atcctgacat agtttgcaac
960
aagcacatca aatttagttg ctttttttcat tatgctgtgg ataatcttgg ggcagatgcc
1020
attgccacag gtcactatgc aagaacttcc ctggaagatg aagaagtctt tgagcagaag
1080
cacgttaaga agcccgaagg gcttttcaga aatcggtttg aagttagaaa tgcggtaaaa
1140
ctcctccagg cagctgacag ctttaaagac cagaccttct ttctcagcca ggtttcccag
1200
gatgccctga ggagaaccat cttccctctg gggggattaa cgaaagagtt tgtaaagaaa
1260
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1320
ttcatcggga agaggaattt tgaacatttc cttcttcagt atctgcagcc tcgacctggt
1380

cactttattt ccatagaaga caataaggtt ctgggaacac ataaaggttg gttcctgtat
1440
accttgggcc agagagcaaa cataggtggc ctgagagagc cctggtacgt ggtggagaag
1500
gacagcgtca agggtgacgt gtttgtggcc ccccggacag accacccagc cctgtacagg
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gacctgctga ggaccagccg cgtgcactgg attgcggagg agcctcccgc agcactggtc
1620
cgggacaaga tgatggagtg ccacttccga ttccgccacc agatggcact agtgccctgt
1680
gtgctgaccc tcaatcaaga tggcaccgtg tgggtgacag ctgtgcaggc tgtgcgtgcc
1740
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gccactgaga gccccagtga cagcccagaa gatggtccag gcctgagtcc cttgctctga
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2100
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2160
gcccccaggg agggtttccc acctcagagt acaccgaggg gacctgcaga gggggctgtc
2220
gggacagcgt ggaataaaca ttatttcaag gaaaaaaaaa aaaaaaa
2267

<210> 5720
<211> 455
<212> PRT
<213> Homo sapiens

<400> 5720
Val Pro Val Leu His Lys His Pro Cys His Leu Val Thr Ser Pro Pro
1 5 10 15
Gln Gln Gln Arg Gly His Gly Ala Val His Ala Ala Gly Gln Gly Ala
20 25 30
His Asp Val Pro Gln Gly Leu His Pro Pro Val Ala Pro Ser Gly Gly
35 40 45
Val Asp Ser Ala Val Ala Ala Leu Leu Leu Arg Arg Arg Gly Tyr Gln
50 55 60
Val Thr Gly Val Phe Met Lys Asn Trp Asp Ser Leu Asp Glu His Gly
65 70 75 80
Val Cys Thr Ala Asp Lys Asp Cys Glu Asp Ala Tyr Arg Val Cys Gln
85 90 95
Ile Leu Asp Ile Pro Phe His Gln Val Ser Tyr Val Lys Glu Tyr Trp
100 105 110
Asn Asp Val Phe Ser Asp Phe Leu Asn Glu Tyr Glu Lys Gly Arg Thr
115 120 125
Pro Asn Pro Asp Ile Val Cys Asn Lys His Ile Lys Phe Ser Cys Phe

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    130                 135                 140
Phe His Tyr Ala Val Asp Asn Leu Gly Ala Asp Ala Ile Ala Thr Gly
145                 150                 155                 160
His Tyr Ala Arg Thr Ser Leu Glu Asp Glu Glu Val Phe Glu Gln Lys
                165                 170                 175
His Val Lys Lys Pro Glu Gly Leu Phe Arg Asn Arg Phe Glu Val Arg
            180                 185                 190
Asn Ala Val Lys Leu Leu Gln Ala Ala Asp Ser Phe Lys Asp Gln Thr
        195                 200                 205
Phe Phe Leu Ser Gln Val Ser Gln Asp Ala Leu Arg Arg Thr Ile Phe
    210                 215                 220
Pro Leu Gly Gly Leu Thr Lys Glu Phe Val Lys Lys Ile Ala Ala Glu
225                 230                 235                 240
Asn Arg Leu His His Val Leu Gln Lys Lys Glu Ser Met Gly Met Cys
                245                 250                 255
Phe Ile Gly Lys Arg Asn Phe Glu His Phe Leu Leu Gln Tyr Leu Gln
            260                 265                 270
Pro Arg Pro Gly His Phe Ile Ser Ile Glu Asp Asn Lys Val Leu Gly
        275                 280                 285
Thr His Lys Gly Trp Phe Leu Tyr Thr Leu Gly Gln Arg Ala Asn Ile
    290                 295                 300
Gly Gly Leu Arg Glu Pro Trp Tyr Val Val Glu Lys Asp Ser Val Lys
305                 310                 315                 320
Gly Asp Val Phe Val Ala Pro Arg Thr Asp His Pro Ala Leu Tyr Arg
                325                 330                 335
Asp Leu Leu Arg Thr Ser Arg Val His Trp Ile Ala Glu Glu Pro Pro
            340                 345                 350
Ala Ala Leu Val Arg Asp Lys Met Met Glu Cys His Phe Arg Phe Arg
        355                 360                 365
His Gln Met Ala Leu Val Pro Cys Val Leu Thr Leu Asn Gln Asp Gly
    370                 375                 380
Thr Val Trp Val Thr Ala Val Gln Ala Val Arg Ala Leu Ala Thr Gly
385                 390                 395                 400
Gln Phe Ala Val Phe Tyr Lys Gly Asp Glu Cys Leu Gly Ser Gly Lys
                405                 410                 415
Ile Leu Arg Leu Gly Pro Ser Ala Tyr Thr Leu Gln Lys Gly Gln Arg
            420                 425                 430
Arg Ala Gly Met Ala Thr Glu Ser Pro Ser Asp Ser Pro Glu Asp Gly
        435                 440                 445
Pro Gly Leu Ser Pro Leu Leu
    450                 455
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<210> 5721
<211> 400
<212> DNA
<213> Homo sapiens

<400> 5721
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cttatgttag ctatgggata tcatgagaag ggcagagctt tcctgaaaag aaaagaatat
120
ggaatagcct tgccatgtct gttggacgct gacaaatatt tctggtgggc gcttttgtac
180

ttggtgaaca ccagctttaa ggaagatggc ccagactata cagaacacct gccatgccct
240
tgagactgca gactttcatc tacaacagtg gttaatgtaa aagagtagtt atggtgtaaa
300
ctggtgaatt tcttcttccc tttgtatttc taattgacct ttcctccctg taaagaaaag
360
aattttcaag caggtaggat atgctctctt tttctgtaca
400

<210> 5722
<211> 80
<212> PRT
<213> Homo sapiens

<400> 5722
Leu Asp Ile Ala Asn Gln Thr Gly Arg Ser Ile Arg Ile Pro Pro Ser
1 5 10 15
Glu Arg Lys Ala Leu Met Leu Ala Met Gly Tyr His Glu Lys Gly Arg
20 25 30
Ala Phe Leu Lys Arg Lys Glu Tyr Gly Ile Ala Leu Pro Cys Leu Leu
35 40 45
Asp Ala Asp Lys Tyr Phe Trp Trp Ala Leu Leu Tyr Leu Val Asn Thr
50 55 60
Ser Phe Lys Glu Asp Gly Pro Asp Tyr Thr Glu His Leu Pro Cys Pro
65 70 75 80

<210> 5723
<211> 376
<212> DNA
<213> Homo sapiens

<400> 5723
nntaccacat tttcttcttt tcacccaccc cagccaaaac tcagtgccct caaggctcgg
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aagaatgtgg agagttttct agaagcctgt cgaaaaatgg gggtgcctga ggtatggggg
120
ctgctttcta aagagtggtg gcatgccgga ctcagcggag ccatgtggca tggatggtgg
180
gcttccattt gcagcggatg tctgctctca gatgaaggca caggctgccc ctgcctgccc
240
cagcatgccc cctgccctgc atgccccctg ccctgcatgt cacctgtcct acacatcccc
300
tgccctgcag gccccatctt gtcctgcatg tcacctgtcc tgcacatgcc ctgccctgca
360
ctcctcctgc acgcgt
376

<210> 5724
<211> 125
<212> PRT
<213> Homo sapiens

<400> 5724
Xaa Thr Thr Phe Ser Ser Phe His Pro Pro Gln Pro Lys Leu Ser Ala

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Leu Lys Ala Arg Lys Asn Val Glu Ser Phe Leu Glu Ala Cys Arg Lys
            20                  25                  30
Met Gly Val Pro Glu Val Trp Gly Leu Leu Ser Lys Glu Trp Trp His
        35                  40                  45
Ala Gly Leu Ser Gly Ala Met Trp His Gly Trp Trp Ala Ser Ile Cys
    50                  55                  60
Ser Gly Cys Leu Leu Ser Asp Glu Gly Thr Gly Cys Pro Cys Leu Pro
65                  70                  75                  80
Gln His Ala Pro Cys Pro Ala Cys Pro Leu Pro Cys Met Ser Pro Val
                85                  90                  95
Leu His Ile Pro Cys Pro Ala Gly Pro Ile Leu Ser Cys Met Ser Pro
            100                 105                 110
Val Leu His Met Pro Cys Pro Ala Leu Leu Leu His Ala
        115                 120                 125
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<210> 5725
<211> 1160
<212> DNA
<213> Homo sapiens

<400> 5725
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ccagccctcc ccctgctgct gagaagtggg ggagggtctc ggcctccagg ttcccgcccc
120
accgcgcacg ggcgagcatg gggggcaagc agagcacggc gacccgctcc cgggggcccc
180
ttcccggggg tctccaccga tgacagcgcc gtgccgccgc cgggaggggc gccccatttc
240
gggcactacc ggacgggcgg cggggccatg gggctgcgca gcgcatcggt cagctcggtg
300
gcaggcatgg gcatggaccc cagcacggcc gggggggtgc cctttggcct ctacaccccc
360
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420
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480
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600
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660
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960

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1160

<210> 5726
<211> 273
<212> PRT
<213> Homo sapiens

<400> 5726
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20 25 30
Ser Arg Pro Pro Gly Ser Arg Pro Thr Ala His Gly Arg Ala Trp Gly
35 40 45
Ala Ser Arg Ala Arg Arg Pro Ala Pro Gly Gly Pro Phe Pro Gly Val
50 55 60
Ser Thr Asp Asp Ser Ala Val Pro Pro Pro Gly Gly Ala Pro His Phe
65 70 75 80
Gly His Tyr Arg Thr Gly Gly Gly Ala Met Gly Leu Arg Ser Ala Ser
85 90 95
Val Ser Ser Val Ala Gly Met Gly Met Asp Pro Ser Thr Ala Gly Gly
100 105 110
Val Pro Phe Gly Leu Tyr Thr Pro Ala Ser Arg Gly Thr Gly Asp Ser
115 120 125
Glu Arg Ala Pro Gly Gly Gly Gly Ser Ala Ser Asp Ser Thr Tyr Ala
130 135 140
His Gly Asn Gly Tyr Gln Glu Thr Gly Gly Gly His His Arg Asp Gly
145 150 155 160
Met Leu Tyr Leu Gly Ser Arg Ala Ser Leu Ala Asp Ala Leu Pro Leu
165 170 175
His Ile Ala Pro Arg Trp Phe Ser Ser His Ser Gly Phe Lys Cys Pro
180 185 190
Ile Cys Ser Lys Ser Val Ala Ser Asp Glu Met Glu Met His Phe Ile
195 200 205
Met Cys Leu Ser Lys Pro Arg Leu Ser Tyr Asn Asp Asp Val Leu Thr
210 215 220
Lys Asp Ala Gly Glu Cys Val Ile Cys Leu Glu Glu Leu Leu Gln Gly
225 230 235 240
Asp Thr Ile Ala Arg Leu Pro Cys Leu Cys Ile Tyr His Lys Ser Cys
245 250 255
Ile Asp Ser Trp Phe Glu Val Asn Arg Ser Cys Pro Glu His Pro Ala
260 265 270
Asp

<210> 5727
<211> 1237

<212> DNA
<213> Homo sapiens

<400> 5727
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120
gagatcctaa ggaccttgag ccccgaggag ctagagcagc tggactgcga actacaggag
180
atggatcctg agaacatgct cctgccagct ggactaagac aacgtgacca gacaaagaag
240
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300
gaagtcaaag agcgtgatga cttggtgccc ttcacaggcg agaagaaggg gaaaccctat
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attcagccca agagggaaat cccagcagag gagcagatca ccctggagcc tgagctggag
420
gaggcactgg cacatgccac agatgctgaa atgtgtgaca ttgcagcaat tctggacatg
480
tacacactga tgagtaacaa gcaatactat gatgccctct gcagtggaga aatctgcaac
540
actgaaggca ttagcagtgt ggtacagcct gacaagtata agccagtgcc ggatgaaccc
600
ccaaatccca caaacattga ggagatacta aagagggtcc gaagcaatga caaggagctg
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720
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gaccccattg ccaatgcagt ggctgacatg ttgcgtgaga atcgtagcct ccagagccta
840
aacatcgaat ccaacttcat tagcagcaca ggactcatgg ctgtgctgaa ggcagttcgg
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1080
ctacgtcgcc agcaaaagaa gagataacac tgcatttccc tttaccaact agcgctggga
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1237

<210> 5728
<211> 368
<212> PRT
<213> Homo sapiens

<400> 5728
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Trp Glu Gly Val Gly Ala Thr Met Ser Ser Tyr Gln Lys Glu Leu Glu
            20                  25                  30
Lys Tyr Arg Asp Ile Asp Glu Asp Glu Ile Leu Arg Thr Leu Ser Pro
        35                  40                  45
Glu Glu Leu Glu Gln Leu Asp Cys Glu Leu Gln Glu Met Asp Pro Glu
    50                  55                  60
Asn Met Leu Leu Pro Ala Gly Leu Arg Gln Arg Asp Gln Thr Lys Lys
65                  70                  75                  80
Ser Pro Thr Gly Pro Leu Asp Arg Glu Ala Leu Leu Gln Tyr Leu Glu
                85                  90                  95
Gln Gln Ala Leu Glu Val Lys Glu Arg Asp Asp Leu Val Pro Phe Thr
            100                 105                 110
Gly Glu Lys Lys Gly Lys Pro Tyr Ile Gln Pro Lys Arg Glu Ile Pro
        115                 120                 125
Ala Glu Glu Gln Ile Thr Leu Glu Pro Glu Leu Glu Glu Ala Leu Ala
    130                 135                 140
His Ala Thr Asp Ala Glu Met Cys Asp Ile Ala Ala Ile Leu Asp Met
145                 150                 155                 160
Tyr Thr Leu Met Ser Asn Lys Gln Tyr Tyr Asp Ala Leu Cys Ser Gly
                165                 170                 175
Glu Ile Cys Asn Thr Glu Gly Ile Ser Ser Val Val Gln Pro Asp Lys
            180                 185                 190
Tyr Lys Pro Val Pro Asp Glu Pro Pro Asn Pro Thr Asn Ile Glu Glu
        195                 200                 205
Ile Leu Lys Arg Val Arg Ser Asn Asp Lys Glu Leu Glu Glu Val Asn
    210                 215                 220
Leu Asn Asn Ile Gln Asp Ile Pro Ile Pro Met Leu Ser Glu Leu Cys
225                 230                 235                 240
Glu Ala Met Lys Ala Asn Thr Tyr Val Arg Ser Phe Ser Leu Val Ala
                245                 250                 255
Thr Arg Ser Gly Asp Pro Ile Ala Asn Ala Val Ala Asp Met Leu Arg
            260                 265                 270
Glu Asn Arg Ser Leu Gln Ser Leu Asn Ile Glu Ser Asn Phe Ile Ser
        275                 280                 285
Ser Thr Gly Leu Met Ala Val Leu Lys Ala Val Arg Glu Asn Ala Thr
    290                 295                 300
Leu Thr Glu Leu Arg Val Asp Asn Gln Arg Gln Trp Pro Gly Asp Ala
305                 310                 315                 320
Val Glu Met Glu Met Ala Thr Val Leu Glu Gln Cys Pro Ser Ile Val
                325                 330                 335
Arg Phe Gly Tyr His Phe Thr Gln Gln Gly Pro Arg Ala Arg Ala Ala
            340                 345                 350
Gln Ala Met Thr Arg Asn Asn Glu Leu Arg Arg Gln Gln Lys Lys Arg
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<210> 5729
<211> 381
<212> DNA
<213> Homo sapiens

<400> 5729
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120
cagccagatg cgcctcaggt ctttctcgaa cttgatctgc aagacgcaga gagagggacc
180
gccaagtaat tcgtggcaaa gaaacgtgtt ctcagcactt tgccctccca gggccaagca
240
gggggccact cacctgcttg cgtctcaggc gtccctcctg gaccttcctc cgcaggaacc
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gcacgttttt gcactaaatt t
381

<210> 5730
<211> 64
<212> PRT
<213> Homo sapiens

<400> 5730
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Ala Gly Gly His Ser Pro Ala Cys Val Ser Gly Val Pro Pro Gly Pro
            20   25   30
Ser Ser Ala Gly Thr Ala Ser Ser Ser Pro Ala Ser Gly Thr Cys Gly
        35   40   45
Gly Ser Ser Ser Ala Gly Gly Ser Ser Ala Arg Phe Cys Thr Lys Phe
    50   55   60

<210> 5731
<211> 891
<212> DNA
<213> Homo sapiens

<400> 5731
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gcccagtact tgctcttcct gcggctctac ccggtgctca ccaaggcggc caccagtggc
120
attttgtcag cacttgggaa cttcctggcc cagatgattg agaagaagcg gaaaaaagaa
180
aactctagaa gtctggatgt cggtgggcct ctgagatatg ccgtttacgg gttcttcttc
240
acagggccgc tgagtcactt cttctacttc ttcatggaac attggatccc tcctgaggtc
300
cccctggcag ggctcaggag gcttctcctg gaccgcctcg tctttgcacc ggccttcctc
360
atgttgttct tcctcatcat gaactttctg gaggggaaag acgcctcagc cttcgccgcc
420
aagatgaggg ggggcttctg gccggcgctg aggatgaact ggcgggtgtg gacgccacta
480
cagttcatca acatcaacta cgtccctctg aagttccggg tgctcttcgc caacctggca
540
gctctgttct ggtatgccta cctggcctcc ttggggaagt gacgaccgct gggagaacat
600

caggtgcact gtggacgtgg gtctgggggt ctcacccgcc cagcgagagc agaaccaatc
660
cagtcaggat gtcactgact ctaaatcagg tgattcaaga tgcccaaaaa tgatggatag
720
agaaacagaa atctctgaat gtcagaaccc tgtcttttaa aaaggcagtc actgccttca
780
ggtggtgctg ccccagaaac ttaaaattta gtcgaggcag tttcaattgt tactgtggac
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891

<210> 5732
<211> 193
<212> PRT
<213> Homo sapiens

<400> 5732
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Leu Thr Lys Ala Ala Thr Ser Gly Ile Leu Ser Ala Leu Gly Asn Phe
        35   40   45
Leu Ala Gln Met Ile Glu Lys Lys Arg Lys Lys Glu Asn Ser Arg Ser
    50   55   60
Leu Asp Val Gly Gly Pro Leu Arg Tyr Ala Val Tyr Gly Phe Phe Phe
65   70   75   80
Thr Gly Pro Leu Ser His Phe Phe Tyr Phe Phe Met Glu His Trp Ile
                85   90   95
Pro Pro Glu Val Pro Leu Ala Gly Leu Arg Arg Leu Leu Leu Asp Arg
            100   105   110
Leu Val Phe Ala Pro Ala Phe Leu Met Leu Phe Phe Leu Ile Met Asn
        115   120   125
Phe Leu Glu Gly Lys Asp Ala Ser Ala Phe Ala Ala Lys Met Arg Gly
    130   135   140
Gly Phe Trp Pro Ala Leu Arg Met Asn Trp Arg Val Trp Thr Pro Leu
145   150   155   160
Gln Phe Ile Asn Ile Asn Tyr Val Pro Leu Lys Phe Arg Val Leu Phe
                165   170   175
Ala Asn Leu Ala Ala Leu Phe Trp Tyr Ala Tyr Leu Ala Ser Leu Gly
            180   185   190
Lys

<210> 5733
<211> 950
<212> DNA
<213> Homo sapiens

<400> 5733
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120

gtcagctata ctttcctctt ctggctgccc ctgtacatca cgaatgtgga tcaccttgat
180
gccaaaaagg cggggtgcac aggtagcccc gaccctctca ggcattccag ccacagaaca
240
tcaaagtgag cgagtactgc gctggctgtg gcttcagaga acctgtatgt gccacgtgga
300
aaaacaggac accagagccc accagacagt gccggccagc agagaagcag agagccagcg
360
ccacacaaca tcaagaaggc cgacaaccag gttggaaacc aagacggagc tcagacccac
420
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480
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540
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720
cacacaccac acctgggact gtttttaata catagcaaca gactgggtta tttatttaag
780
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840
caaactccaa ttgttctctg gctgtttttt tcagttgtgt ctagcaaaat acttatctgc
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950

<210> 5734
<211> 82
<212> PRT
<213> Homo sapiens

<400> 5734
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Ile Ser Phe Thr Gly Ala Leu Lys Ile Pro Gly Val Ile Glu Phe Ser
            20   25   30
Leu Cys Leu Leu Phe Ala Lys Leu Val Ser Tyr Thr Phe Leu Phe Trp
        35   40   45
Leu Pro Leu Tyr Ile Thr Asn Val Asp His Leu Asp Ala Lys Lys Ala
    50   55   60
Gly Cys Thr Gly Ser Pro Asp Pro Leu Arg His Ser Ser His Arg Thr
65   70   75   80
Ser Lys

<210> 5735
<211> 4241
<212> DNA
<213> Homo sapiens

<400> 5735

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120
ccccttctcg ggagtgcgcc aatgcctggg ccgacccaaa ccctgtcccc aaatggcgag
180
aacaacaacg acatcatcca ggataataac gggaccatca ttcctttccg gaagcacaca
240
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300
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360
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420
ctcttccctg gctgcattag tttgaagaaa gtaaaatttc aagcaaagct ggaacatgaa
480
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540
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720
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780
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1620

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4241

<210> 5736
<211> 327
<212> PRT
<213> Homo sapiens

<400> 5736
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Asp Ile Ile Gln Asp Asn Asn Gly Thr Ile Ile Pro Phe Arg Lys His
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Thr Val Arg Gly Glu Arg Ser Tyr Ser Trp Gly Met Ala Val Asn Val
35 40 45
Tyr Ser Thr Ser Ile Thr Gln Glu Thr Met Ser Arg His Asp Ile Ile
50 55 60
Ala Trp Val Asn Asp Ile Val Ser Leu Asn Tyr Thr Lys Val Glu Gln
65 70 75 80
Leu Cys Ser Gly Ala Ala Tyr Cys Gln Phe Met Asp Met Leu Phe Pro
85 90 95
Gly Cys Ile Ser Leu Lys Lys Val Lys Phe Gln Ala Lys Leu Glu His

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            100                 105                 110
Glu Tyr Ile His Asn Phe Lys Leu Leu Gln Ala Ser Phe Lys Arg Met
        115                 120                 125
Asn Val Asp Lys Val Ile Pro Val Glu Lys Leu Val Lys Gly Arg Phe
    130                 135                 140
Gln Asp Asn Leu Asp Phe Ile Gln Trp Phe Lys Lys Phe Tyr Asp Ala
145                 150                 155                 160
Asn Tyr Asp Gly Lys Glu Tyr Asp Pro Val Glu Ala Arg Gln Gly Gln
                165                 170                 175
Asp Ala Ile Pro Pro Pro Asp Pro Gly Glu Gln Ile Phe Asn Leu Pro
            180                 185                 190
Lys Lys Ser His His Ala Asn Ser Pro Thr Ala Gly Ala Ala Lys Ser
        195                 200                 205
Ser Pro Ala Ala Lys Pro Gly Ser Thr Pro Ser Arg Pro Ser Ser Ala
    210                 215                 220
Lys Arg Ala Ser Ser Ser Gly Ser Ala Ser Lys Ser Asp Lys Asp Leu
225                 230                 235                 240
Glu Thr Gln Val Ile Gln Leu Asn Glu Gln Val His Ser Leu Lys Leu
                245                 250                 255
Ala Leu Glu Gly Val Glu Lys Glu Arg Asp Phe Tyr Phe Gly Lys Leu
            260                 265                 270
Arg Glu Ile Glu Leu Leu Cys Gln Glu His Gly Gln Glu Asn Asp Asp
        275                 280                 285
Leu Val Gln Arg Leu Met Asp Ile Leu Tyr Ala Ser Glu Glu His Glu
    290                 295                 300
Gly His Thr Glu Glu Pro Glu Ala Glu Glu Gln Ala His Glu Gln Gln
305                 310                 315                 320
Pro Pro Gln Gln Glu Glu Tyr
                325
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<210> 5737
<211> 340
<212> DNA
<213> Homo sapiens

<400> 5737
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tgcgtggccc tgggacagct ggaccggcct ccagacctcg cccatgacgg gaggagtctg
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180
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240
aagatgttgc agtgccatcc tcacctggtg gcttgaaatc ggccaaggtg ggagcattta
300
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340

<210> 5738
<211> 99
<212> PRT
<213> Homo sapiens

<400> 5738
Met Leu Pro Pro Trp Pro Ile Ser Ser His Gln Val Arg Met Ala Leu
1 5 10 15
Gln His Leu Pro Leu Arg Leu Gln Leu Pro Ser Gln Val His Gln Glu
20 25 30
Thr Thr Gly His His Trp Gln Trp Arg Gly Asp Met Glu His Gly Leu
35 40 45
Gly Ser Arg Leu Leu Ala Pro Asp Val Gln Pro Gln Thr Pro Pro Val
50 55 60
Met Gly Glu Val Trp Arg Pro Val Gln Leu Ser Gln Gly His Ala His
65 70 75 80
Leu Ser Leu Gly Ser Val Gly Lys Ala Tyr Pro Lys Ser His Ile Gln
85 90 95
Gly Gly Xaa

<210> 5739
<211> 780
<212> DNA
<213> Homo sapiens

<400> 5739
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120
ttactcgtta attggaaaca cctctagcct gtactaaatt tccatattta tttggcccgt
180
ttcaaagtcc tctattctct gctcatctgt ccacatctaa gtgctttaac tattgtggct
240
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300
tccttgcaga caggtacttt aaataccatc tcacagcacc catcatgtcc tatcttcagg
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420
gagccagcac catggcccgt ccctgagcat gtccagcaaa ccctgccagg ctctgcagct
480
cctgagcacc ctgccttcgg gtctgccagt gtgtgggggc cagaagagaa aaacaaccca
540
gggggaatgc ctccttcccc cagcaggaaa gcagcttggt catcatctgt ctgaaagcag
600
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660
aaggccatgc cagagtccat cgttgcctcc accctacctg tgcaggaaac ctggacatca
720
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780

<210> 5740
<211> 120
<212> PRT
<213> Homo sapiens

<400> 5740
Met Ile Arg Lys Gln Ser Gln His His Gly Pro Ser Leu Ser Met Ser
1 5 10 15
Ser Lys Pro Cys Gln Ala Leu Gln Leu Leu Ser Thr Leu Pro Ser Gly
20 25 30
Leu Pro Val Cys Gly Gly Gln Lys Arg Lys Thr Thr Gln Gly Glu Cys
35 40 45
Leu Leu Pro Pro Ala Gly Lys Gln Leu Gly His His Leu Ser Glu Ser
50 55 60
Arg Cys Cys Ser Ser Trp Gln Gln Ser His Ser Glu Arg Ser Cys Val
65 70 75 80
His Cys Leu Ser Gly Arg Pro Cys Gln Ser Pro Ser Leu Pro Pro Pro
85 90 95
Tyr Leu Cys Arg Lys Pro Gly His His His Phe Lys Ala Leu Pro Ser
100 105 110
Phe Leu Gly Arg Ala Gln Pro Gln
115 120

<210> 5741
<211> 2444
<212> DNA
<213> Homo sapiens

<400> 5741
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gcggttggcg ggggcagtcc cgagcgtgag gaggtcggcg caggctacaa cagtgaggac
120
gagtatgagg cggctgcagc acgcatcgag gctatggacc ctgccactgt cgagcagcag
180
gagcattggt ttgaaaaggc cctacgagac aagaagggct tcatcatcaa gcagatgaag
240
gaggatggcg cctgtctctt ccgggctgta gctgaccagg tgtatggaga ccaggacatg
300
catgaggttg tgcgaaagca ttgcatggac tatctgatga agaatgccga ctacttctcc
360
aactatgtca cagaggactt taccacctac attaacagga agcggaaaaa caattgccat
420
ggcaaccaca ttgagatgca ggccatggca gagatgtaca accgtcctgt ggaggtgtac
480
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600
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660
atgaagaatg ccataaaaac atcggaggag tcatggattg aacagcagat gctagaagac
720
aagaaacggg ccacagactg ggaggccaca aatgaagcca tcgaggagca ggtggctcgg
780
gaatcctacc tgcagtggtt gcgggatcag gagaaacagg ctcgccaggt ccgaggcccc
840
agccagcccc ggaaagccag cgccacatgc agttcggcca cagcagcagc ctccagtggc
900

ctggaggagt ggactagccg gtccccgcgg cagcggagtt cagcctcgtc acctgagcac
960
cctgagctgc atgctgaatt gggcatgaag ccccccttccc caggcactgt tttagctctt
1020
gccaaacctc cttcgccctg tgcgccaggt acaagcagtc agttctcggc aggggccgac
1080
cgggcaactt ccccccttgt gtccctctac cctgctttgg agtgccgggc cctcattcag
1140
cagatgtccc cctctgcctt tggtctgaat gactgggatg atgatgagat cctagcttcg
1200
gtgctggcag tgtcccaaca ggaataccta gacagtatga agaaaaacaa agtgcacaga
1260
gacccgcccc cagacaagag ttgatggaga cccagggatt ggacaccatc tcccaacccc
1320
agtactcctg ctctccggtg ccacctcacc ttctttggct tcttccctct tgcctccttc
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1440
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gttgcccccc accccatccc gcacagaacc atccctgcat tccacagggg actcgggcaa
1560
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1620
agaggagaga gacattcaga cagaggaaag tctccctgcc cctcattcct tccaagatga
1680
gaaaaacttg ccgccacccc ccgacactga tgccagggag gtgggaggaa gaagtgggaa
1740
atttcccttc ccagtacccc caagaacgtc tgagccttca atgttgaatt ttttctttat
1800
taaaattact tttatcttat aaaatcaact aatcaaaaat gatatagacg acagcactgg
1860
ctctgtgaag gtggcatctt tctgggcagg caggccatgg ggcatggagg agggtgcaaa
1920
gatatgggtt gctgtcttct ggcctccagc tgcatggagg ccggcccagg gtctagggtg
1980
tgcactgggc aagggcaggg cggcaggtgt caggccggct tggacaatga aaccctgacc
2040
ttgctgcatt ccttttgctt ccaccaccac tagcttcttt ggaatcttgg ggtgggggtc
2100
atctttgggg attatggctg ccacccggga tttgagtgta gggagtgtgg gagcagcctt
2160
ggcagatggg gcacccgtgc cctgcaggtg ttgacaagat ccgccatctg taatgtcctt
2220
ggcacaataa aaccaaatgt cagtttccct gagcgactct gttctgtgtg gggcaggggt
2280
tgggcgggcc tctgggcaga ggatgcaatg gcacggacct tggcttgacc tcagaggtgt
2340
gaatgctctc cagcagggtc tgtctggggg cctggagttt gtatttgatt tgctgcttat
2400
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2444

<210> 5742

<211> 427
<212> PRT
<213> Homo sapiens

<400> 5742

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Pro Gly Val Gly Ala Val Gly Gly Gly Ser Pro Glu Arg Glu Glu Val
            20                  25                  30
Gly Ala Gly Tyr Asn Ser Glu Asp Glu Tyr Glu Ala Ala Ala Ala Arg
        35                  40                  45
Ile Glu Ala Met Asp Pro Ala Thr Val Glu Gln Gln Glu His Trp Phe
    50                  55                  60
Glu Lys Ala Leu Arg Asp Lys Lys Gly Phe Ile Ile Lys Gln Met Lys
65                  70                  75                  80
Glu Asp Gly Ala Cys Leu Phe Arg Ala Val Ala Asp Gln Val Tyr Gly
                85                  90                  95
Asp Gln Asp Met His Glu Val Val Arg Lys His Cys Met Asp Tyr Leu
            100                 105                 110
Met Lys Asn Ala Asp Tyr Phe Ser Asn Tyr Val Thr Glu Asp Phe Thr
        115                 120                 125
Thr Tyr Ile Asn Arg Lys Arg Lys Asn Asn Cys His Gly Asn His Ile
    130                 135                 140
Glu Met Gln Ala Met Ala Glu Met Tyr Asn Arg Pro Val Glu Val Tyr
145                 150                 155                 160
Gln Tyr Ser Thr Glu Pro Ile Asn Thr Phe His Gly Ile His Gln Asn
                165                 170                 175
Glu Asp Glu Pro Ile Arg Val Ser Tyr His Arg Asn Ile His Tyr Asn
            180                 185                 190
Ser Val Val Asn Pro Asn Lys Ala Thr Ile Gly Val Gly Leu Gly Leu
        195                 200                 205
Pro Ser Phe Lys Pro Gly Phe Ala Glu Gln Ser Leu Met Lys Asn Ala
    210                 215                 220
Ile Lys Thr Ser Glu Glu Ser Trp Ile Glu Gln Gln Met Leu Glu Asp
225                 230                 235                 240
Lys Lys Arg Ala Thr Asp Trp Glu Ala Thr Asn Glu Ala Ile Glu Glu
                245                 250                 255
Gln Val Ala Arg Glu Ser Tyr Leu Gln Trp Leu Arg Asp Gln Glu Lys
            260                 265                 270
Gln Ala Arg Gln Val Arg Gly Pro Ser Gln Pro Arg Lys Ala Ser Ala
        275                 280                 285
Thr Cys Ser Ser Ala Thr Ala Ala Ala Ser Ser Gly Leu Glu Glu Trp
    290                 295                 300
Thr Ser Arg Ser Pro Arg Gln Arg Ser Ser Ala Ser Ser Pro Glu His
305                 310                 315                 320
Pro Glu Leu His Ala Glu Leu Gly Met Lys Pro Pro Ser Pro Gly Thr
                325                 330                 335
Val Leu Ala Leu Ala Lys Pro Pro Ser Pro Cys Ala Pro Gly Thr Ser
            340                 345                 350
Ser Gln Phe Ser Ala Gly Ala Asp Arg Ala Thr Ser Pro Leu Val Ser
        355                 360                 365
Leu Tyr Pro Ala Leu Glu Cys Arg Ala Leu Ile Gln Gln Met Ser Pro
    370                 375                 380
Ser Ala Phe Gly Leu Asn Asp Trp Asp Asp Asp Glu Ile Leu Ala Ser
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385 390 395 400
Val Leu Ala Val Ser Gln Gln Glu Tyr Leu Asp Ser Met Lys Lys Asn
405 410 415
Lys Val His Arg Asp Pro Pro Pro Asp Lys Ser
420 425

<210> 5743
<211> 550
<212> DNA
<213> Homo sapiens

<400> 5743
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ttcctttagc cccgccttca gccagatgcg cctcaggtct ttctcgaact tgatctgctt
120
gcgtctcagg cgtccctcct ggaccttccc ctatctggct gggcggacac tggtaggatt
180
gcggtggagc cacatgtcct gcggtcccgg tatccagtct gggcaggaag cagcgggccg
240
tgagccagct ctccaggggg ctgacggaca tcttcctggg gaccagcatc tcctccagct
300
ccagctgggc ccccttgcga gggagagagg ccgccctacc tgggccggcc ggcgatgtgc
360
tgtaaagggg cccgcagacc cggctgccca actccagaga cgggccaagg cgggcggccg
420
ccgaaaggtc ccagaacggg gaggccggcc ccctccccgg gttcaccccc gcgcgaatcg
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540
ggcgccctca
550

<210> 5744
<211> 95
<212> PRT
<213> Homo sapiens

<400> 5744
Arg Thr Ser Ser Trp Gly Pro Ala Ser Pro Pro Ala Pro Ala Gly Pro
1 5 10 15
Pro Cys Glu Gly Glu Arg Pro Pro Tyr Leu Gly Arg Pro Ala Met Cys
20 25 30
Cys Lys Gly Ala Arg Arg Pro Gly Cys Pro Thr Pro Glu Thr Gly Gln
35 40 45
Gly Gly Arg Pro Pro Lys Gly Pro Arg Thr Gly Arg Pro Ala Pro Ser
50 55 60
Pro Gly Ser Pro Pro Arg Glu Ser Arg Cys Leu Ala Pro Xaa Asp Pro
65 70 75 80
Leu Gly Trp Thr Pro Gly Pro Pro Ala Ala Ala Pro Gly Ala Leu
85 90 95

<210> 5745
<211> 849

<212> DNA
<213> Homo sapiens

<400> 5745
aaagtttttt ttttttctg cttcaggcac acggggaacc acgcgtttta atcaacgtat
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cgataaaaaa caccagggca cggacactcc aggggaaatg cttattgagt aaagtatccg
120
aggaagtgat gcagggcagg taaacagctg gtgctcagca gcgagaggac gcgtcactct
180
gccgttctgc agggtgacgc cctccccgta cctcgctgag agccacctgc agacacagca
240
ggccacagca gaatgcacag gtcactgttg taggggaaca aatcgtaatg cccagagaaa
300
acctgatagt gaaatgtaaa cagacaggac agggtggttc caggtggcca ccaccgccag
360
gcccttcccg tgattgatct gagagcttca cagccggcgg cactgggacc catttccaga
420
aacactggaa caccaggtct ctcagatgcc cgcgggaggg gccccaggga ggcctttctc
480
agcatcagct tttgggtgac aaaccccata cagcaaaact gtacaaatac acacaacgga
540
cccccagctg acagtgagac caggacccta ggaaggtcag gtggtggtga agtcatcccc
600
tctccaaccg agcagagcct ggggttgggc tctgatgacc tcccgggcaa agtgtccagg
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tggaggaagc aaactcccaa atggggcaca aaggtaataa aaagcagctg agagattgcg
720
ggatggggtc ggggccactt ggccgacacc ttctgcctcg cctggccggg ccgggccagc
780
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840
gtcccatgg
849

<210> 5746
<211> 140
<212> PRT
<213> Homo sapiens

<400> 5746
Met Thr Ser Pro Pro Pro Asp Leu Pro Arg Val Leu Val Ser Leu Ser
 1   5   10   15
Ala Gly Gly Pro Leu Cys Val Phe Val Gln Phe Cys Cys Met Gly Phe
            20   25   30
Val Thr Gln Lys Leu Met Leu Arg Lys Ala Ser Leu Gly Pro Leu Pro
        35   40   45
Arg Ala Ser Glu Arg Pro Gly Val Pro Val Phe Leu Glu Met Gly Pro
    50   55   60
Ser Ala Ala Gly Cys Glu Ala Leu Arg Ser Ile Thr Gly Arg Ala Trp
65   70   75   80
Arg Trp Trp Pro Pro Gly Thr Thr Leu Ser Cys Leu Phe Thr Phe His
                85   90   95
Tyr Gln Val Phe Ser Gly His Tyr Asp Leu Phe Pro Tyr Asn Ser Asp

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            100                 105                 110
Leu Cys Ile Leu Leu Trp Pro Ala Val Ser Ala Gly Gly Ser Gln Arg
        115                 120                 125
Gly Thr Gly Arg Ala Ser Pro Cys Arg Thr Ala Glu
    130                 135                 140

<210> 5747
<211> 1999
<212> DNA
<213> Homo sapiens

<400> 5747
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gtcgccatcc aggaggccga ggacgtggac gagttggagg acgaggagga gggggcggag
120
actcggggcg ccggggaccc ggcccggtac ctcagccccg gctggggcag cgcgagcgag
180
gaggagccga gccgcgggca cagtggcacc actgcaagtg gaggtgagaa cgagcgtgag
240
gacctggagc aggagtggaa gcccccggat gaggagttga tcaagaaact ggtggatcag
300
atcgaattct acttttctga tgaaaacctg gagaaggacg ccttttttgct aaaacacgtg
360
aggaggaaca agctgggata tgtgagcgtt aagctactca catccttcaa aaaggtgaaa
420
catcttacac gggactggag aaccacagca catgctttga agtattcagt ggtccttgag
480
ttgaatgagg accaccggaa ggtgaggagg accacccccg tcccactgtt ccccaacgag
540
aacctcccca gcaagatgct cctggtctat gatctctact tgtctcctaa gctgtgggct
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ctggccaccc cccagaagaa tggaagggtg caagagaagg tgatggaaca cctgctcaag
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780
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840
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900
cctgccaaag acaaaaatca tgacgaggag cccactgcga gcatccacct gaacaagtcc
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ctgaacaaga gagtcgagga gcttcagtac atgggtgatg agtcttctgc caacagctcc
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1260
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tcctctgaca gcagcgtcac tccctctggc agcccctggg tccggaggcg tcgccaagcc
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1380
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1440
ggatttcatg gccatgagag gagcagggcc tgtgtataaa taccttctat ttttaataca
1500
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1560
ggaattcgtt ccccttgag agatttttta ttcatgtaga cctcttaatt tatctatctg
1620
taatatacat aaatcggtac gccatggttt gaagaccacc ttctagttca ggactcctgt
1680
tcttcccagc atggccacta ttttgatgat ggctgatgtg tgtgagtgtg atggccctga
1740
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1800
cttctttggt atggaatttt tcccttcagt gactgagctg tcctcgatag gccatgcaag
1860
ggcttcctga gagttcagga aagttctctt gtgcaacagc aagtagctaa gcctatagca
1920
tggtgtcttg taggaccaaa tcgatgttac ctgtcaagta aataaataat aaaacaccca
1980
aaaaaaaaaa aaaaaaaaa
1999

<210> 5748
<211> 492
<212> PRT
<213> Homo sapiens

<400> 5748
Xaa Met Ala Gln Ser Gly Gly Glu Ala Arg Pro Gly Pro Lys Thr Ala
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Val Gln Ile Arg Val Ala Ile Gln Glu Ala Glu Asp Val Asp Glu Leu
            20   25   30
Glu Asp Glu Glu Glu Gly Ala Glu Thr Arg Gly Ala Gly Asp Pro Ala
        35   40   45
Arg Tyr Leu Ser Pro Gly Trp Gly Ser Ala Ser Glu Glu Glu Pro Ser
    50   55   60
Arg Gly His Ser Gly Thr Thr Ala Ser Gly Gly Glu Asn Glu Arg Glu
65   70   75   80
Asp Leu Glu Gln Glu Trp Lys Pro Pro Asp Glu Glu Leu Ile Lys Lys
                85   90   95
Leu Val Asp Gln Ile Glu Phe Tyr Phe Ser Asp Glu Asn Leu Glu Lys
            100   105   110
Asp Ala Phe Leu Leu Lys His Val Arg Arg Asn Lys Leu Gly Tyr Val
        115   120   125
Ser Val Lys Leu Leu Thr Ser Phe Lys Lys Val Lys His Leu Thr Arg
    130   135   140
Asp Trp Arg Thr Thr Ala His Ala Leu Lys Tyr Ser Val Val Leu Glu
145   150   155   160
Leu Asn Glu Asp His Arg Lys Val Arg Arg Thr Thr Pro Val Pro Leu

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                165                 170                 175
Phe Pro Asn Glu Asn Leu Pro Ser Lys Met Leu Leu Val Tyr Asp Leu
            180                 185                 190
Tyr Leu Ser Pro Lys Leu Trp Ala Leu Ala Thr Pro Gln Lys Asn Gly
        195                 200                 205
Arg Val Gln Glu Lys Val Met Glu His Leu Leu Lys Leu Phe Gly Thr
    210                 215                 220
Phe Gly Val Ile Ser Ser Val Arg Ile Leu Lys Pro Gly Arg Glu Leu
225                 230                 235                 240
Pro Pro Asp Ile Arg Arg Ile Ser Ser Arg Tyr Ser Gln Val Gly Thr
                245                 250                 255
Gln Glu Cys Ala Ile Val Glu Phe Glu Glu Val Glu Ala Ala Ile Lys
            260                 265                 270
Ala His Glu Phe Met Ile Thr Glu Ser Gln Gly Lys Glu Asn Met Lys
        275                 280                 285
Ala Val Leu Ile Gly Met Lys Pro Pro Lys Lys Lys Pro Ala Lys Asp
    290                 295                 300
Lys Asn His Asp Glu Glu Pro Thr Ala Ser Ile His Leu Asn Lys Ser
305                 310                 315                 320
Leu Asn Lys Arg Val Glu Glu Leu Gln Tyr Met Gly Asp Glu Ser Ser
                325                 330                 335
Ala Asn Ser Ser Ser Asp Pro Glu Ser Asn Pro Thr Ser Pro Met Ala
            340                 345                 350
Gly Arg Arg His Ala Ala Thr Asn Lys Leu Ser Pro Ser Gly His Gln
        355                 360                 365
Asn Leu Phe Leu Ser Pro Asn Ala Ser Pro Cys Thr Ser Pro Trp Ser
    370                 375                 380
Ser Pro Leu Ala Gln Arg Lys Gly Val Ser Arg Lys Ser Pro Leu Ala
385                 390                 395                 400
Glu Glu Gly Arg Leu Asn Cys Ser Thr Ser Pro Glu Ile Phe Arg Lys
                405                 410                 415
Cys Met Asp Tyr Ser Ser Asp Ser Ser Val Thr Pro Ser Gly Ser Pro
            420                 425                 430
Trp Val Arg Arg Arg Arg Gln Ala Glu Met Gly Thr Gln Glu Lys Ser
        435                 440                 445
Pro Gly Thr Ser Pro Leu Leu Ser Arg Lys Met Gln Thr Ala Asp Gly
    450                 455                 460
Leu Pro Val Gly Val Leu Arg Leu Pro Arg Gly Pro Asp Asn Thr Arg
465                 470                 475                 480
Gly Phe His Gly His Glu Arg Ser Arg Ala Cys Val
                485                 490
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<210> 5749
<211> 2849
<212> DNA
<213> Homo sapiens

<400> 5749
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cccaggaaag aggaaaaaat acatttaaca gtgaagaggc aacacagagc tccctattgt
120
gaaataaaac ccatttcaaa agttattgga aagaaagtaa ggtatggctc ttatgggtta
180

actagtggta gtcagtttct gctttttact ccctctgaat tattaattgt ttgccaggtt
240
cactggtggg aggctgagcc ggtggaaaag acaccgggaa gagactcaga ggcgaccata
300
atgtcgttac gtgtacacac tctgcccacc ctgcttggag ccgtcgtcag accgggctgc
360
agggagctgc tgtgtttgct gatgatcaca gtgactgtgg gccctggtgc ctctggggtg
420
tgccccaccg cttgcatctg tgccactgac atcgtcagct gcaccaacaa aaacctgtcc
480
aaggtgcctg ggaacctttt cagactgatt aagagactgg acctgagtta taacagaatt
540
gggcttctgg attctgagtg gattccagta tcgtttgcaa agctgaacac cctaattctt
600
cgtcataaca acatcaccag catttccacg ggcagttttt ccacaactcc aaatttgaag
660
tgtcttgact tatcgtccaa taagctgaag acggtgaaaa atgctgtatt ccaagagttg
720
aaggttctgg aagtgcttct gctttacaac aatcacatat cctatctcga tccttcagcg
780
tttggagggc tctcccagtt gcagaaactc tacttaagtg gaaattttct cacacagttt
840
ccgatggatt tgtatgttgg aaggttcaag ctggcagaac tgatgttttt agatgtttct
900
tataaccgaa ttccttccat gccaatgcac cacataaatt tagtgccagg aaaacagctg
960
agaggcatct accttcatgg aaacccattt gtctgtgact gttccctgta ctccttgctg
1020
gtcttttggt atcgtaggca ctttagctca gtgatggatt ttaagaacga ttacacctgt
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1380
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1440
aatgtgagca atttcactgt aagcagatcc catgctcatg aggcatttaa cacagctttt
1500
accactcttg ctgcttgcgt ggccagtatc gttttggtac ttttgtacct ctatctgact
1560
ccatgcccct gcaagtgtaa aaccaagaga cagaaaaata tgctacacca aagcaatgcc
1620
cattcatcga ttctcagtcc tggccccgct agtgatgcct ccgctgatga acggaaggca
1680
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<212> PRT
<213> Homo sapiens

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Val Gly Pro Gly Ala Ser Gly Val Cys Pro Thr Ala Cys Ile Cys Ala
35 40 45
Thr Asp Ile Val Ser Cys Thr Asn Lys Asn Leu Ser Lys Val Pro Gly
50 55 60
Asn Leu Phe Arg Leu Ile Lys Arg Leu Asp Leu Ser Tyr Asn Arg Ile
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Gly Leu Leu Asp Ser Glu Trp Ile Pro Val Ser Phe Ala Lys Leu Asn

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Phe Ser Thr Thr Pro Asn Leu Lys Cys Leu Asp Leu Ser Ser Asn Lys
        115                 120                 125
Leu Lys Thr Val Lys Asn Ala Val Phe Gln Glu Leu Lys Val Leu Glu
    130                 135                 140
Val Leu Leu Leu Tyr Asn Asn His Ile Ser Tyr Leu Asp Pro Ser Ala
145                 150                 155                 160
Phe Gly Gly Leu Ser Gln Leu Gln Lys Leu Tyr Leu Ser Gly Asn Phe
                165                 170                 175
Leu Thr Gln Phe Pro Met Asp Leu Tyr Val Gly Arg Phe Lys Leu Ala
            180                 185                 190
Glu Leu Met Phe Leu Asp Val Ser Tyr Asn Arg Ile Pro Ser Met Pro
        195                 200                 205
Met His His Ile Asn Leu Val Pro Gly Lys Gln Leu Arg Gly Ile Tyr
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Leu His Gly Asn Pro Phe Val Cys Asp Cys Ser Leu Tyr Ser Leu Leu
225                 230                 235                 240
Val Phe Trp Tyr Arg Arg His Phe Ser Ser Val Met Asp Phe Lys Asn
                245                 250                 255
Asp Tyr Thr Cys Arg Leu Trp Ser Asp Ser Arg His Ser Arg Gln Val
            260                 265                 270
Leu Leu Leu Gln Asp Ser Phe Met Asn Cys Ser Asp Ser Ile Ile Asn
        275                 280                 285
Gly Ser Phe Arg Ala Leu Gly Phe Ile His Glu Ala Gln Val Gly Glu
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Arg Leu Met Val His Cys Asp Ser Lys Thr Gly Asn Ala Asn Thr Asp
305                 310                 315                 320
Phe Ile Trp Val Gly Pro Asp Asn Arg Leu Leu Glu Pro Asp Lys Glu
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Met Glu Asn Phe Tyr Val Phe His Asn Gly Ser Leu Val Ile Glu Ser
            340                 345                 350
Pro Arg Phe Glu Asp Ala Gly Val Tyr Ser Cys Ile Ala Met Asn Lys
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Gln Arg Leu Leu Asn Glu Thr Val Asp Val Thr Ile Asn Val Ser Asn
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Phe Thr Val Ser Arg Ser His Ala His Glu Ala Phe Asn Thr Ala Phe
385                 390                 395                 400
Thr Thr Leu Ala Ala Cys Val Ala Ser Ile Val Leu Val Leu Leu Tyr
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Leu Tyr Leu Thr Pro Cys Pro Cys Lys Cys Lys Thr Lys Arg Gln Lys
            420                 425                 430
Asn Met Leu His Gln Ser Asn Ala His Ser Ser Ile Leu Ser Pro Gly
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Pro Ala Ser Asp Ala Ser Ala Asp Glu Arg Lys Ala Gly Ala Gly Lys
    450                 455                 460
Arg Val Val Phe Leu Glu Pro Leu Lys Asp Thr Ala Ala Gly Gln Asn
465                 470                 475                 480
Gly Lys Val Arg Leu Phe Pro Ser Glu Ala Val Ile Ala Glu Gly Ile
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Leu Lys Ser Thr Arg Gly Lys Ser Asp Ser Asp Ser Val Asn Ser Val
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<210> 5751
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<212> DNA
<213> Homo sapiens

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<211> 129
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<213> Homo sapiens

<400> 5752
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Leu Glu Ile Arg Ser Val His Val Gly Val Val Val Ile Lys Ala Val
35 40 45
Ser Ser Gly Phe Tyr Val Ala Met Asn Arg Arg Gly Arg Leu Tyr Gly

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    50                  55                  60
Ser Arg Leu Tyr Thr Val Asp Cys Arg Phe Arg Glu Arg Ile Glu Glu
65                  70                  75                  80
Asn Gly His Asn Thr Tyr Ala Ser Gln Arg Trp Arg Arg Arg Gly Gln
                85                  90                  95
Pro Met Phe Leu Ala Leu Asp Arg Arg Gly Gly Pro Arg Pro Gly Gly
            100                 105                 110
Arg Thr Arg Arg Tyr His Leu Ser Ala His Phe Leu Pro Val Leu Val
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<210> 5753
<211> 5668
<212> DNA
<213> Homo sapiens

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<211> 221
<212> PRT
<213> Homo sapiens

<400> 5754
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Phe Pro Asn His Thr Asp Asn Leu Asn Ser Ser Gln Arg Leu Ser Pro
        35                  40                  45
Ser Ser Arg Met Arg Lys Leu Pro Gln Gly Arg Pro Val Pro Pro Leu
    50                  55                  60
Gly Pro Glu Thr Arg Val Ser Val Val Trp Val Glu Arg Tyr Asp Asp
65                  70                  75                  80
Ile Glu Asn Phe Pro Leu Ser Glu Leu Met Thr Glu Ile Ser Thr Gly
                85                  90                  95
Val Glu Thr Thr Ala Asn Ser Ser Thr Ser Leu Arg Ser Thr Thr Leu
            100                 105                 110
Glu Lys Glu Val Pro Val Ile Phe Ile His Pro Leu Asn Thr Gly Leu
        115                 120                 125
Phe Arg Ile Lys Ile Gln Gly Ala Thr Gly Lys Phe Asn Met Val Ile
    130                 135                 140
Pro Leu Val Asp Gly Met Ile Val Ser Arg Arg Ala Leu Gly Phe Leu
145                 150                 155                 160
Val Arg Gln Thr Val Ile Asn Ile Cys Arg Arg Lys Arg Leu Glu Ser
                165                 170                 175
Asp Ser Tyr Ser Pro Pro His Val Arg Arg Lys Gln Lys Ile Thr Asp
            180                 185                 190
Ile Val Asn Lys Tyr Arg Asn Lys Gln Leu Glu Pro Glu Phe Tyr Thr
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Ser Leu Phe Gln Glu Val Gly Leu Lys Asn Cys Ser Ser
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<212> DNA
<213> Homo sapiens

<400> 5755

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<211> 415
<212> PRT
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<400> 5756
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Ala Ala Leu Leu Ala Gln Asp Tyr Cys Asp Ala Ile Asp Leu Asn Leu
        35   40   45
Gly Cys Pro Gln Met Ile Ala Lys Arg Gly His Tyr Gly Ala Phe Leu
    50   55   60
Gln Asp Glu Trp Asp Leu Leu Gln Arg Met Ile Leu Leu Ala His Glu
65   70   75   80
Lys Leu Ser Val Pro Val Thr Cys Lys Ile Arg Val Phe Pro Glu Ile
                85   90   95
Asp Lys Thr Val Arg Tyr Ala Gln Met Leu Glu Lys Ala Gly Cys Gln
            100   105   110
Leu Leu Thr Val His Gly Arg Thr Lys Glu Gln Lys Gly Pro Leu Ser

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Gly Ala Ala Ser Trp Glu His Ile Lys Ala Val Arg Lys Ala Val Ala
    130                 135                 140
Ile Pro Val Phe Ala Asn Gly Asn Ile Gln Cys Leu Gln Asp Val Glu
145                 150                 155                 160
Arg Cys Leu Arg Asp Thr Gly Val Gln Gly Val Met Ser Ala Glu Gly
                165                 170                 175
Asn Leu His Asn Pro Ala Leu Phe Glu Gly Arg Ser Pro Ala Val Trp
            180                 185                 190
Glu Leu Ala Glu Glu Tyr Leu Asp Ile Val Arg Glu His Pro Cys Pro
        195                 200                 205
Leu Ser Tyr Val Arg Ala His Leu Phe Lys Leu Trp His His Thr Leu
    210                 215                 220
Gln Val His Gln Glu Leu Arg Glu Glu Leu Ala Lys Val Lys Thr Leu
225                 230                 235                 240
Glu Gly Ile Ala Ala Val Ser Gln Glu Leu Lys Leu Arg Cys Gln Glu
                245                 250                 255
Glu Ile Ser Arg Gln Glu Gly Ala Lys Pro Thr Gly Asp Leu Pro Phe
            260                 265                 270
His Trp Ile Cys Gln Pro Tyr Ile Arg Pro Gly Pro Arg Glu Gly Ser
        275                 280                 285
Lys Glu Lys Ala Gly Ala Arg Ser Lys Arg Ala Leu Glu Glu Glu Glu
    290                 295                 300
Gly Gly Thr Glu Val Leu Ser Lys Asn Lys Gln Lys Lys Gln Leu Arg
305                 310                 315                 320
Asn Pro His Lys Thr Phe Asp Pro Ser Leu Lys Pro Lys Tyr Ala Lys
                325                 330                 335
Cys Asp Gln Cys Gly Asn Pro Lys Gly Asn Arg Cys Val Phe Ser Leu
            340                 345                 350
Cys Arg Gly Cys Cys Lys Lys Arg Ala Ser Lys Glu Thr Ala Asp Cys
        355                 360                 365
Pro Gly His Gly Leu Leu Phe Lys Thr Lys Leu Glu Lys Ser Leu Ala
    370                 375                 380
Trp Lys Glu Ala Gln Pro Glu Leu Gln Glu Pro Gln Pro Ala Ala Pro
385                 390                 395                 400
Gly Thr Pro Gly Gly Phe Ser Glu Val Met Gly Ser Ala Leu Ala
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<210> 5757
<211> 2362
<212> DNA
<213> Homo sapiens

<400> 5757
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tggagcccgg tactggaggc cgacgggggt gacggggacg ctgaggacac agagcggagg
180
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240
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300

gagtcattca ctgccagcct gaagctgccc atgcgcatat tcgggctgga gcctctgagg
360
ccacacaaac gccggctggg gaggcgaagt gtggggctga gcaccagaac tccaggagcg
420
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480
gccgaggagg aacccagaag acgccagcga tggagctctg ccggggcgga atgtggccag
540
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600
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720
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1080
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1440
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1740
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1860
tccagcccca ccgagtcact cactgtggac cctgcctctg aataatcagg aacggtggct
1920

tcagagacgt ctcttgggcc ttccctctgg ccacgtctgc acccaccccc cctgggcacc
1980
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2040
cctgagttca aggctttctg cctgtagcct ggactcccgt ggacccccgt gggcaggtgg
2100
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2160
cggtcccacg accccacccc gagctcctga agccggggtc tgagcctgca tcacctctgg
2220
cctctcatcc cccactctcc tgagagcagt ggtcacagcg gccggccgct ctgctgagaa
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2362

<210> 5758
<211> 440
<212> PRT
<213> Homo sapiens

<400> 5758
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His Pro Glu Ala Ala Arg Ala Ile Leu Glu Tyr Arg Ile Arg Thr Leu
20 25 30
Asp Gly Ala Leu Glu Asn Ala Gln Asn Leu Gly Tyr Gln Gly Ala Lys
35 40 45
Phe Ala Trp Glu Ser Ala Asp Ser Gly Leu Glu Val Cys Pro Glu Asp
50 55 60
Ile Tyr Gly Val Gln Glu Val His Val Asn Gly Ala Val Val Leu Ala
65 70 75 80
Phe Glu Leu Tyr Tyr His Thr Thr Gln Asp Leu Gln Leu Phe Arg Glu
85 90 95
Gly Gly Gly Trp Glu Val Val Arg Ala Val Ala Lys Phe Trp Cys Ser
100 105 110
Arg Val Glu Trp Ser Pro Arg Glu Glu Lys Tyr His Leu Arg Gly Val
115 120 125
Met Ser Pro Asp Glu Tyr His Ser Gly Val Asn Asn Ser Val Tyr Thr
130 135 140
Asn Val Leu Val Gln Asn Ser Leu Arg Phe Ala Ala Ala Leu Ala Gln
145 150 155 160
Asp Leu Gly Leu Pro Ile Pro Ser Gln Trp Leu Ala Val Ala Asp Lys
165 170 175
Ile Lys Val Pro Phe Asp Val Glu Gln Asn Phe His Pro Glu Phe Asp
180 185 190
Gly Tyr Glu Pro Gly Glu Val Val Lys Gln Ala Asp Val Val Leu Leu
195 200 205
Gly Tyr Pro Val Pro Phe Ser Leu Ser Pro Asp Val Arg Arg Lys Asn
210 215 220
Leu Glu Ile Tyr Glu Ala Val Thr Ser Pro Gln Gly Pro Ala Met Thr
225 230 235 240
Trp Ser Met Phe Ala Val Gly Trp Met Glu Leu Lys Asp Ala Val Arg

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                245                 250                 255
Ala Arg Gly Leu Leu Asp Arg Ser Phe Ala Asn Met Ala Glu Pro Phe
            260                 265                 270
Lys Val Trp Thr Glu Asn Ala Asp Gly Ser Gly Ala Val Asn Phe Leu
        275                 280                 285
Thr Gly Met Gly Gly Phe Leu Gln Ala Val Val Phe Gly Cys Thr Gly
    290                 295                 300
Phe Arg Val Thr Arg Ala Gly Val Thr Phe Asp Pro Val Cys Leu Ser
305                 310                 315                 320
Gly Ile Ser Arg Val Ser Val Ser Gly Ile Phe Tyr Gln Gly Asn Lys
                325                 330                 335
Leu Asn Phe Ser Phe Ser Glu Asp Ser Val Thr Val Glu Val Thr Ala
            340                 345                 350
Arg Ala Gly Pro Trp Ala Pro His Leu Glu Ala Glu Leu Trp Pro Ser
        355                 360                 365
Gln Ser Arg Leu Ser Leu Leu Pro Gly His Lys Val Ser Phe Pro Arg
    370                 375                 380
Ser Ala Gly Arg Ile Gln Met Ser Pro Pro Lys Leu Pro Gly Ser Ser
385                 390                 395                 400
Ser Ser Glu Phe Pro Gly Arg Thr Phe Ser Asp Val Arg Asp Pro Leu
                405                 410                 415
Gln Ser Pro Leu Trp Val Thr Leu Gly Ser Ser Ser Pro Thr Glu Ser
            420                 425                 430
Leu Thr Val Asp Pro Ala Ser Glu
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<210> 5759
<211> 1333
<212> DNA
<213> Homo sapiens

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120
tcctctgagc gaaaacgagc gcggataccg tccgggaagg ccggagcagc aaatggattt
180
ctcatggaag tttgtgttga ttcagtggaa tcagctgtga atgcagaaag aggaggtgct
240
gatcggattg aattatgttc tggtttatca gaggggggaa ctacacccag catgggtgtc
300
cttcaagtag tgaagcagag tgttcagatc ccagtttttg tgatgattcg gccacgggga
360
ggtgattttt tgtattcaga tcgtgaaatt gaggtgatga aggctgacat tcgtcttgcc
420
aagctttatg gtgctgatgg tttggttttt ggggcattga ctgaagatgg acacattgac
480
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540
gcctttgaca tggttcatga tccaatggca gctctggaga ccctcttaac cttgggattt
600
gaacgcgtgt tgaccagtgg atgtgacagt tcagcattag aagggctacc cctaataaag
660

cgactcattg agcaggcaaa aggcaggatt gtggtaatgc caggaggtgg tataacagac
720
agaaatctac aaaggatcct tgagggttca ggtgctacag aattccactg ttctgctcgg
780
tctactagag actcgggaat gaagtttcga aattcatctg ttgccatggg agcctcactt
840
tcttgctcag aatattccct aaaggtaaca gatgtgacca aagtaaggac tttgaatgct
900
atcgcaaaga acatcctggt gtagccagac ctctctgaga gacatggata tcacaggatg
960
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1020
gacagtcgca atctttgttt taagtttcac atggccatgg agaatgtgcc caagaagaaa
1080
aagaatttga aacagagata cagtcacttc ctttgcttag tcttaccagt gattgtcatc
1140
atggttaaag ctggtctgtg cttcttccat agacagaagc ttagtctgtt ttcagtggaa
1200
ttaattgatg aactgggaaa attttaactg catggtatga attcagagtg tgacttaagg
1260
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1320
aaaaaaaaaa aaa
1333

<210> 5760
<211> 273
<212> PRT
<213> Homo sapiens

<400> 5760
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Ser Gly Lys Ala Gly Ala Ala Asn Gly Phe Leu Met Glu Val Cys Val
20 25 30
Asp Ser Val Glu Ser Ala Val Asn Ala Glu Arg Gly Gly Ala Asp Arg
35 40 45
Ile Glu Leu Cys Ser Gly Leu Ser Glu Gly Gly Thr Thr Pro Ser Met
50 55 60
Gly Val Leu Gln Val Val Lys Gln Ser Val Gln Ile Pro Val Phe Val
65 70 75 80
Met Ile Arg Pro Arg Gly Gly Asp Phe Leu Tyr Ser Asp Arg Glu Ile
85 90 95
Glu Val Met Lys Ala Asp Ile Arg Leu Ala Lys Leu Tyr Gly Ala Asp
100 105 110
Gly Leu Val Phe Gly Ala Leu Thr Glu Asp Gly His Ile Asp Lys Glu
115 120 125
Leu Cys Met Ser Leu Met Ala Ile Cys Arg Pro Leu Pro Val Thr Phe
130 135 140
His Arg Ala Phe Asp Met Val His Asp Pro Met Ala Ala Leu Glu Thr
145 150 155 160
Leu Leu Thr Leu Gly Phe Glu Arg Val Leu Thr Ser Gly Cys Asp Ser
165 170 175
Ser Ala Leu Glu Gly Leu Pro Leu Ile Lys Arg Leu Ile Glu Gln Ala

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            180                 185                 190
Lys Gly Arg Ile Val Val Met Pro Gly Gly Gly Ile Thr Asp Arg Asn
        195                 200                 205
Leu Gln Arg Ile Leu Glu Gly Ser Gly Ala Thr Glu Phe His Cys Ser
    210                 215                 220
Ala Arg Ser Thr Arg Asp Ser Gly Met Lys Phe Arg Asn Ser Ser Val
225                 230                 235                 240
Ala Met Gly Ala Ser Leu Ser Cys Ser Glu Tyr Ser Leu Lys Val Thr
                245                 250                 255
Asp Val Thr Lys Val Arg Thr Leu Asn Ala Ile Ala Lys Asn Ile Leu
            260                 265                 270
Val
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<210> 5761
<211> 1452
<212> DNA
<213> Homo sapiens

<400> 5761
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120
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180
cttaccaggg aaattgaaaa ctatccacac tttttcctgg attttgaaaa tgctcagcct
240
acagaaggag agagagaaat ctggaaccag atcagcgccg tccttcagga ttctgagagc
300
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360
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420
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480
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540
gcaaaggagt ttgccgaaat tttacatttt acccttcgat tcgatgagct gaagatgagg
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aacccggcta ttcagaatga cttcagctac tacagaagaa caatcagtcg caaccgcatc
660
aacaacatgc acctagacat tgagaatgaa gtcaataatg agatggccaa tcgaatgtcc
720
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780
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900
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960
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1020

aaggagcagg ccccagacag tgtggagggg ctgctaaatg ccctcaggtt cactacaaag
1080
cacttgaacg atgaatcaac ttccaaacag attcgagcaa tgcttcagta gagctctgct
1140
caaagaagag gatctatgtg ctgacctcag aagatgtata tgtttacata atttaataca
1200
gattgatgtt aatacttgtg tatttacata accgtttcct tcttgtcact gaaatatatg
1260
gaccttaatt tgtatcctga ctgactcaac ccagcagagc ataaattgac ttgagagcct
1320
tacctttgat gtctgaaatg aaacccccct ctccaaaggc aaaattcgga gactttgatc
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1440
tagtaaaaaa aa
1452

<210> 5762
<211> 333
<212> PRT
<213> Homo sapiens

<400> 5762
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Glu Asn Ala Gln Pro Thr Glu Gly Glu Arg Glu Ile Trp Asn Gln Ile
35 40 45
Ser Ala Val Leu Gln Asp Ser Glu Ser Ile Leu Ala Asp Leu Gln Ala
50 55 60
Tyr Lys Gly Ala Gly Pro Glu Ile Arg Asp Ala Ile Gln Asn Pro Asn
65 70 75 80
Asp Ile Gln Leu Gln Glu Lys Ala Trp Asn Ala Val Cys Pro Leu Val
85 90 95
Val Arg Leu Lys Arg Phe Tyr Glu Phe Ser Ile Arg Leu Glu Lys Ala
100 105 110
Leu Gln Ser Leu Leu Glu Ser Leu Thr Cys Pro Pro Tyr Thr Pro Thr
115 120 125
Gln His Leu Glu Arg Glu Gln Ala Leu Ala Lys Glu Phe Ala Glu Ile
130 135 140
Leu His Phe Thr Leu Arg Phe Asp Glu Leu Lys Met Arg Asn Pro Ala
145 150 155 160
Ile Gln Asn Asp Phe Ser Tyr Tyr Arg Arg Thr Ile Ser Arg Asn Arg
165 170 175
Ile Asn Asn Met His Leu Asp Ile Glu Asn Glu Val Asn Asn Glu Met
180 185 190
Ala Asn Arg Met Ser Leu Phe Tyr Ala Glu Ala Thr Pro Met Leu Lys
195 200 205
Thr Leu Ser Asn Ala Thr Met His Phe Val Ser Glu Asn Lys Thr Leu
210 215 220
Pro Ile Glu Asn Thr Thr Asp Cys Leu Ser Thr Met Thr Ser Val Cys
225 230 235 240
Lys Val Met Leu Glu Thr Pro Glu Tyr Arg Ser Arg Phe Thr Ser Glu

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                245                 250                 255
Glu Thr Leu Met Phe Cys Met Arg Val Met Val Gly Val Ile Ile Leu
            260                 265                 270
Tyr Asp His Val His Pro Val Gly Ala Phe Cys Lys Thr Ser Lys Ile
        275                 280                 285
Asp Met Lys Gly Cys Ile Lys Val Leu Lys Glu Gln Ala Pro Asp Ser
    290                 295                 300
Val Glu Gly Leu Leu Asn Ala Leu Arg Phe Thr Thr Lys His Leu Asn
305                 310                 315                 320
Asp Glu Ser Thr Ser Lys Gln Ile Arg Ala Met Leu Gln
                325                 330
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<210> 5763
<211> 3840
<212> DNA
<213> Homo sapiens

<400> 5763
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120
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180
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240
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300
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360
cgctggacgt ctagagatgt gggcatggca gacaaatctg tagctagtgg cggttggcag
420
gaacctgaaa atcctcacac acaacggatg aacaaattga ttgaatatta ccagcagctt
480
gctcagaaag agaaggttga gcgagatcgc aagaaactgg cacgacgtag aaactatatg
540
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600
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720
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900
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960
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1020
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1080

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1320
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1380
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1440
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1620
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1680
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1740
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1920
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1980
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2100
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2160
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2280
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2340
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2400
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2460
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2520
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2580
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2640
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2700

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2760
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2820
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2880
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2940
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3060
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3180
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3240
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3300
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3360
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3480
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<210> 5764
<211> 466
<212> PRT
<213> Homo sapiens

<400> 5764
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20 25 30
Leu Tyr Phe Cys Arg Tyr Cys Ser Glu Leu Arg Ser Leu Glu Cys Val
35 40 45
Ser His Glu Val Asp Ser His Tyr Cys Pro Ser Cys Leu Glu Asn Met
50 55 60
Pro Ser Ala Glu Ala Lys Leu Lys Lys Asn Arg Cys Ala Asn Cys Phe

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65                  70                  75                  80
Asp Cys Pro Gly Cys Met His Thr Leu Ser Thr Arg Ala Thr Ser Ile
                85                  90                  95
Ser Thr Gln Leu Pro Asp Asp Pro Ala Lys Thr Thr Met Lys Lys Ala
            100                 105                 110
Tyr Tyr Leu Ala Cys Gly Phe Cys Arg Trp Thr Ser Arg Asp Val Gly
        115                 120                 125
Met Ala Asp Lys Ser Val Ala Ser Gly Gly Trp Gln Glu Pro Glu Asn
    130                 135                 140
Pro His Thr Gln Arg Met Asn Lys Leu Ile Glu Tyr Tyr Gln Gln Leu
145                 150                 155                 160
Ala Gln Lys Glu Lys Val Glu Arg Asp Arg Lys Lys Leu Ala Arg Arg
                165                 170                 175
Arg Asn Tyr Met Pro Leu Ala Phe Ser Asp Lys Tyr Gly Leu Gly Thr
            180                 185                 190
Arg Leu Gln Arg Pro Arg Ala Gly Ala Ser Ile Ser Thr Leu Ala Gly
        195                 200                 205
Leu Ser Leu Lys Glu Gly Glu Asp Gln Lys Glu Val Lys Ile Glu Pro
    210                 215                 220
Ala Gln Ala Val Asp Glu Val Glu Pro Leu Pro Glu Asp Tyr Tyr Thr
225                 230                 235                 240
Arg Pro Val Asn Leu Thr Glu Val Thr Thr Leu Gln Gln Arg Leu Leu
                245                 250                 255
Gln Pro Asp Phe Gln Pro Val Cys Ala Ser Gln Leu Tyr Pro Arg His
            260                 265                 270
Lys His Leu Leu Ile Lys Arg Ser Leu Arg Cys Arg Lys Cys Glu His
        275                 280                 285
Asn Leu Ser Lys Pro Glu Phe Asn Pro Thr Ser Ile Lys Phe Lys Ile
    290                 295                 300
Gln Leu Val Ala Val Asn Tyr Ile Pro Glu Val Arg Ile Met Ser Ile
305                 310                 315                 320
Pro Asn Leu Arg Tyr Met Lys Glu Ser Gln Val Leu Leu Thr Leu Thr
                325                 330                 335
Asn Pro Val Glu Asn Leu Thr His Val Thr Leu Phe Glu Cys Glu Glu
            340                 345                 350
Gly Asp Pro Asp Asp Ile Asn Ser Thr Ala Lys Val Val Val Pro Pro
        355                 360                 365
Lys Glu Leu Val Leu Ala Gly Lys Asp Ala Ala Ala Glu Tyr Asp Glu
    370                 375                 380
Leu Ala Glu Pro Gln Asp Phe Gln Asp Asp Pro Asp Ile Ile Ala Phe
385                 390                 395                 400
Arg Lys Ala Asn Lys Val Gly Ile Phe Ile Lys Val Thr Pro Gln Arg
                405                 410                 415
Glu Glu Gly Glu Val Thr Val Cys Phe Lys Met Lys His Asp Phe Lys
            420                 425                 430
Asn Leu Ala Ala Pro Ile Arg Pro Ile Glu Glu Ser Asp Gln Gly Thr
        435                 440                 445
Glu Val Ile Trp Leu Thr Gln His Val Glu Leu Ser Leu Gly Pro Leu
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Leu Pro
465
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<210> 5765
<211> 3220

<212> DNA
<213> Homo sapiens

<400> 5765
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120
gagctggtga ctgccctcat gtgtgatttg cggcggccag cggcaggtgg gatgatggac
180
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240
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300
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360
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420
cggctcctgt cagcagatgc cgacgggcag atcaagtgct ggagcatggc ggaccacctg
480
gctaatagct gggagagctc agtgggcagc ctagtggagg gggaccccat tgtggccctg
540
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600
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720
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840
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900
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1080
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1260
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1380
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2340
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3220

<210> 5766
<211> 873
<212> PRT
<213> Homo sapiens

<400> 5766
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Tyr Val Cys Glu Trp Glu Lys Trp Ser Lys Ser Thr His Cys Pro Ser
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Val Pro Leu Ala Cys Ala Trp Ser Cys Arg Asn Leu Ile Ala Phe Thr
35 40 45
Met Asp Leu Arg Ser Asp Asp Gln Asp Leu Thr Arg Met Ile His Ile
50 55 60
Leu Asp Thr Glu His Pro Trp Asp Leu His Ser Ile Pro Ser Glu His
65 70 75 80
His Glu Ala Ile Thr Cys Leu Glu Trp Asp Gln Ser Gly Ser Arg Leu
85 90 95
Leu Ser Ala Asp Ala Asp Gly Gln Ile Lys Cys Trp Ser Met Ala Asp
100 105 110
His Leu Ala Asn Ser Trp Glu Ser Ser Val Gly Ser Leu Val Glu Gly
115 120 125
Asp Pro Ile Val Ala Leu Ser Trp Leu His Asn Gly Val Lys Leu Ala
130 135 140
Leu His Val Glu Lys Ser Gly Ala Ser Ser Phe Gly Glu Lys Phe Ser
145 150 155 160
Arg Val Lys Phe Ser Pro Ser Leu Thr Leu Phe Gly Gly Lys Pro Met
165 170 175
Glu Gly Trp Ile Ala Val Thr Val Ser Gly Leu Val Thr Val Ser Leu
180 185 190
Leu Lys Pro Ser Gly Gln Val Leu Thr Ser Thr Glu Ser Leu Cys Arg
195 200 205
Leu Arg Gly Arg Val Ala Leu Ala Asp Ile Ala Phe Thr Gly Gly Gly
210 215 220
Asn Ile Val Val Ala Thr Ala Asp Gly Ser Ser Ala Ser Pro Val Gln
225 230 235 240
Phe Tyr Lys Val Cys Val Ser Val Val Ser Glu Lys Cys Arg Ile Asp
245 250 255
Thr Glu Ile Leu Pro Ser Leu Phe Met Arg Cys Thr Thr Asp Leu Asn
260 265 270
Arg Lys Asp Lys Phe Pro Ala Ile Thr His Leu Lys Phe Leu Ala Arg
275 280 285
Asp Met Ser Glu Gln Val Leu Leu Cys Ala Ser Ser Gln Thr Ser Ser
290 295 300
Ile Val Glu Cys Trp Ser Leu Arg Lys Glu Gly Leu Pro Val Asn Asn
305 310 315 320
Ile Phe Gln Gln Ile Ser Pro Val Val Gly Asp Lys Gln Pro Thr Ile
325 330 335
Leu Lys Trp Arg Ile Leu Ser Ala Thr Asn Asp Leu Asp Arg Val Ser

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            340                 345                 350
Ala Val Ala Leu Pro Lys Leu Pro Ile Ser Leu Thr Asn Thr Asp Leu
        355                 360                 365
Lys Val Ala Ser Asp Thr Gln Phe Tyr Pro Gly Leu Gly Leu Ala Leu
    370                 375                 380
Ala Phe His Asp Gly Ser Val His Ile Val His Arg Leu Ser Leu Gln
385                 390                 395                 400
Thr Met Ala Val Phe Tyr Ser Ser Ala Ala Pro Arg Pro Val Asp Glu
                405                 410                 415
Pro Ala Met Lys Arg Pro Arg Thr Ala Gly Pro Ala Val His Leu Lys
            420                 425                 430
Ala Met Gln Leu Ser Trp Thr Ser Leu Ala Leu Val Gly Ile Asp Ser
        435                 440                 445
His Gly Lys Leu Ser Val Leu Arg Leu Ser Pro Ser Met Gly His Pro
    450                 455                 460
Leu Glu Val Gly Leu Ala Leu Arg His Leu Leu Phe Leu Leu Glu Tyr
465                 470                 475                 480
Cys Met Val Thr Gly Tyr Asp Trp Trp Asp Ile Leu Leu His Val Gln
                485                 490                 495
Pro Ser Met Val Gln Ser Leu Val Glu Lys Leu His Glu Glu Tyr Thr
            500                 505                 510
Arg Gln Thr Ala Ala Leu Gln Gln Val Leu Ser Thr Arg Ile Leu Ala
        515                 520                 525
Met Lys Ala Ser Leu Cys Lys Leu Ser Pro Cys Thr Val Thr Arg Val
    530                 535                 540
Cys Asp Tyr His Thr Lys Leu Phe Leu Ile Ala Ile Ser Ser Thr Leu
545                 550                 555                 560
Lys Ser Leu Leu Arg Pro His Phe Leu Asn Thr Pro Asp Lys Ser Pro
                565                 570                 575
Gly Asp Arg Leu Thr Glu Ile Cys Thr Lys Ile Thr Asp Val Asp Ile
            580                 585                 590
Asp Lys Val Met Ile Asn Leu Lys Thr Glu Glu Phe Val Leu Asp Met
        595                 600                 605
Thr His Cys Arg Arg Cys Ser Ser Ser Cys Ser Gly Trp Ala Thr Ser
    610                 615                 620
Cys Cys Thr Cys Trp Pro Ala Tyr Pro Thr Ser Pro Ala Pro Pro Arg
625                 630                 635                 640
Ser Pro Ala Pro Pro Arg Ser Pro Pro Pro Pro Arg Ser Pro Pro Pro
                645                 650                 655
Pro Arg Ser Pro Pro Leu His Glu Ala Ser Ala Gly Ser Leu Leu Arg
            660                 665                 670
Pro Gly His Ser Phe Leu Arg Asp Gly Thr Ser Leu Gly Met Leu Arg
        675                 680                 685
Glu Leu Met Val Val Ile Arg Ile Trp Gly Leu Leu Lys Pro Ser Cys
    690                 695                 700
Leu Pro Val Tyr Thr Ala Thr Ser Asp Thr Gln Asp Ser Met Ser Leu
705                 710                 715                 720
Leu Phe Arg Leu Leu Thr Lys Leu Trp Ile Cys Cys Arg Asp Glu Gly
                725                 730                 735
Pro Ala Ser Glu Pro Asp Glu Ala Leu Val Asp Glu Cys Cys Leu Leu
            740                 745                 750
Pro Ser Gln Leu Leu Ile Pro Ser Leu Asp Trp Leu Pro Ala Ser Asp
        755                 760                 765
Gly Leu Val Ser Arg Leu Gln Pro Lys Gln Pro Leu Arg Leu Gln Phe
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    770                 775                 780
Gly Arg Ala Pro Thr Leu Pro Gly Ser Ala Ala Thr Leu Gln Leu Asp
785                 790                 795                 800
Gly Leu Ala Arg Ala Pro Gly Gln Pro Lys Ile Asp His Leu Arg Arg
                805                 810                 815
Leu His Leu Gly Ala Cys Pro Thr Glu Glu Cys Lys Ala Cys Thr Arg
            820                 825                 830
Cys Gly Cys Val Thr Met Leu Lys Ser Pro Asn Arg Thr Thr Ala Val
        835                 840                 845
Lys Gln Trp Glu Gln Arg Trp Ile Lys Asn Cys Leu Cys Gly Gly Leu
    850                 855                 860
Trp Trp Arg Val Pro Leu Ser Tyr Pro
865                 870
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<210> 5767
<211> 1910
<212> DNA
<213> Homo sapiens

<400> 5767
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120
tcagtatcgt gggttttgct gctattctga agggatcccc catcacgctg gcagctgtgt
180
gccaggagag accctgaggg ctgcctcacc acagcaggaa cgcccttctc agtcccagcc
240
caatcctctc tcacactgcg gtgctctgtc cctatggaaa cagcctctgt atgtgtgtgt
300
gtgtgtgtgt gtgtgtgtgt gtgtgaataa tatatggaat aaagtttgag attccctgct
360
ttttcatgtt accttagcct caattttaaa cttacattgt ttgttaaaat tatcaaatgg
420
acaacctcat tgctatggaa caaaaaagac tgtgaggaaa aagaatcata acttggaaaa
480
aaataagtga aaaggcattg agagattgct aagatttgtt aagttaaaac aataatatat
540
ctagaaaaga ctgtgaaaat atatatctca aaagagaaca aggcatagtc agaaggctca
600
gtaaaacaat tactttaaaa gctgactaat aaaaagggta agtgaaagaa ctcttccatc
660
cttgaccctt cctcacttcc tccctccgac tctaccagtc tggatgcact aaagcagaat
720
aacctaaaag ccatgaaaaa gtgctggtat ttttcaggat ctcttcaaga caccttccgt
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cttggtaacc tgaattctct ctctgatcaa ggcagctgat ggactttcaa tgtatttgga
840
gatgccggtt caaaaacgtc atcatcatct tctgctcctt cttctatcgg tttcatcttg
900
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1020

aacatggaga tctgtgtgca gaggctgagc tgatgttcca gctttttggc tttcttatca
1080
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1140
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1200
cagcataaaa atctgcagtt atcatctgca ataatggtga cctggaattt ttcacctttg
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1320
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1380
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1620
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1680
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1800
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1910

<210> 5768
<211> 360
<212> PRT
<213> Homo sapiens

<400> 5768
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20 25 30
Thr Cys Glu Asn Trp Arg Glu Ile His His Leu Val Phe His Val Ala
35 40 45
Asn Ile Cys Phe Ala Val Gly Leu Val Ile Pro Thr Thr Leu His Leu
50 55 60
His Met Ile Phe Leu Arg Gly Met Leu Thr Leu Gly Cys Thr Leu Tyr
65 70 75 80
Ile Val Trp Ala Thr Leu Tyr Arg Cys Ala Leu Asp Ile Met Ile Trp
85 90 95
Asn Ser Val Phe Leu Gly Val Asn Ile Leu His Leu Ser Tyr Leu Leu
100 105 110
Tyr Lys Lys Arg Pro Val Lys Ile Glu Lys Glu Leu Ser Gly Met Tyr
115 120 125
Arg Arg Leu Phe Glu Pro Leu Arg Val Pro Pro Asp Leu Phe Arg Arg

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    130                 135                 140
Leu Thr Gly Gln Phe Cys Met Ile Gln Thr Leu Lys Lys Gly Gln Thr
145                 150                 155                 160
Tyr Ala Ala Glu Asp Lys Thr Ser Val Asp Asp Arg Leu Ser Ile Leu
                165                 170                 175
Leu Lys Gly Lys Met Lys Val Ser Tyr Arg Gly His Phe Leu His Asn
            180                 185                 190
Ile Tyr Pro Cys Ala Phe Ile Asp Ser Pro Glu Phe Arg Ser Thr Gln
        195                 200                 205
Met His Lys Gly Glu Lys Phe Gln Val Thr Ile Ile Ala Asp Asp Asn
    210                 215                 220
Cys Arg Phe Leu Cys Trp Ser Arg Glu Arg Leu Thr Tyr Phe Leu Glu
225                 230                 235                 240
Ser Glu Pro Phe Leu Tyr Glu Ile Phe Arg Tyr Leu Ile Gly Lys Asp
                245                 250                 255
Ile Thr Asn Lys Leu Tyr Ser Leu Asn Asp Pro Thr Leu Asn Asp Lys
            260                 265                 270
Lys Ala Lys Lys Leu Glu His Gln Leu Ser Leu Cys Thr Gln Ile Ser
        275                 280                 285
Met Leu Glu Met Arg Asn Ser Ile Ala Ser Ser Ser Asp Ser Asp Asp
    290                 295                 300
Gly Leu His Gln Phe Leu Arg Ser Thr Ser Ser Met Ser Ser Leu His
305                 310                 315                 320
Val Ser Ser Pro His Gln Arg Ala Ser Ala Lys Met Lys Pro Ile Glu
                325                 330                 335
Glu Gly Ala Glu Asp Asp Asp Asp Val Phe Glu Pro Ala Ser Pro Asn
            340                 345                 350
Thr Leu Lys Val His Gln Leu Pro
        355                 360
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<210> 5769
<211> 427
<212> DNA
<213> Homo sapiens

<400> 5769
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120
ctgcagacac agctgaagga agtattaaga gaaaatgatc tcttgcggaa ggatgtggaa
180
gtaaaggaga gcaaattgag ttcttcaatg aatagcatca agatcttctg gggcccagag
240
ctgaagaagg aacgagccct gagaaaggat gaagcttcca aaatccccat ttggaaggaa
300
cagtacagag ttgtacaaga ggaaaaccag gtaagttcta cgtgtgttta cctttattgg
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420
cacgcgt
427

<210> 5770

<211> 85
<212> PRT
<213> Homo sapiens

<400> 5770
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20 25 30
Ile Lys Ile Phe Trp Gly Pro Glu Leu Lys Lys Glu Arg Ala Leu Arg
35 40 45
Lys Asp Glu Ala Ser Lys Ile Pro Ile Trp Lys Glu Gln Tyr Arg Val
50 55 60
Val Gln Glu Glu Asn Gln Val Ser Ser Thr Cys Val Tyr Leu Tyr Trp
65 70 75 80
Leu Asn Ser Cys Ile
85

<210> 5771
<211> 2539
<212> DNA
<213> Homo sapiens

<400> 5771
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120
gtcagatgtg ccaccccgcc acaactggcc aatggggtga cggaaggcct ggactatggc
180
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240
cacctgtcag tcagaggcaa ctgggatgca gagattcctc tctgtaaacc agtcaactgt
300
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360
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420
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480
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540
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660
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720
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780
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840
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900

gaaggttata cgatggatac agatacagat acaatcacct gtcagaaaga tggtcgctgg
960
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1020
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1080
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1140
ccattctccg atgaatcttg cagtccagtt tcttgtggga aacctgaaag tccagaacat
1200
ggatttgtgg ttggcagtaa atacaccttt gaaagcacaa ttatttatca gtgtgagcct
1260
ggctatgaac tagaggggaa cagggaacgt gtctgccagg agaacagaca gtggagtgga
1320
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1380
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1440
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1500
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1560
tctgaaaagg agttttatgt tgatcagaat gtgtccatca aatgtaggga aggttttctg
1620
ctgcagggcc acggcatcat tacctgcaac cccgacgaga cgtggacaca gacaagcgcc
1680
aaatgtgaaa aaatctcatg tggtccacca gctcacgtag aaaatgcaat tgctcgaggc
1740
gtacattatc aatatggaga catgatcacc tactcatgtt acagtggata catgttggag
1800
ggtttcctga ggagtgtttg tttagaaaat ggaacatgga catcacctcc tatttgcaga
1860
gctgtctgtc gatttccatg tcagaatggg gggcatctgc caacgcccaa atgcttgttc
1920
ctgtccagag ggctggatgg ggcgcctctg tgaagaacca atctgcattc ttccctgtct
1980
gaacggaggt cgctgtgtgg ccccttacca gtgtgactgc ccgcctggct ggacggggtc
2040
tcgctgtcat acagctgttt gccagtctcc ctgcttaaat ggtggaaaat gtgtaagacc
2100
aaaccgatgt cactgtcttt cttcttggac gggacataac tgttccagga aaaggaggac
2160
tgggttttaa ccactgcacg accatctggc tctcccaaaa gcaggatcat ctctcctcgg
2220
tagtgcctgg gcatcctgga acttatgcaa agaaagtcca acatggtgct gggtcttgtt
2280
tagtaaactt gttacttggg gttacttttt ttattttgtg atatattttg ttattccttg
2340
tgacatactt tcttacatgt ttccattttt aaatatgcct gtattttcta tataaaaatt
2400
atattaaata gatgctgctc taccctcaca aaatgtacat attctgctgt ctattgggaa
2460
agttcctggt acacattttt attcagttac ttaaaatgat ttttccatta aagtatattt
2520

tgctactaaa taaaaaaaa
2539

<210> 5772
<211> 642
<212> PRT
<213> Homo sapiens

<400> 5772
Tyr Thr Cys Asn Glu Gly Phe Leu Leu Glu Gly Ala Arg Ser Arg Val
1 5 10 15
Cys Leu Ala Asn Gly Ser Trp Ser Gly Ala Thr Pro Asp Cys Val Pro
20 25 30
Val Arg Cys Ala Thr Pro Pro Gln Leu Ala Asn Gly Val Thr Glu Gly
35 40 45
Leu Asp Tyr Gly Phe Met Lys Glu Val Thr Phe His Cys His Gly Leu
50 55 60
His Leu Ala Arg Cys Ser Lys Thr His Leu Ser Val Arg Gly Asn Trp
65 70 75 80
Asp Ala Glu Ile Pro Leu Cys Lys Pro Val Asn Cys Gly Pro Pro Glu
85 90 95
Asp Leu Ala His Gly Phe Pro Asn Gly Phe Ser Phe Ile His Gly Gly
100 105 110
His Ile Gln Tyr Gln Cys Phe Pro Gly Tyr Lys Leu His Gly Asn Ser
115 120 125
Ser Arg Arg Cys Leu Ser Asn Gly Ser Trp Ser Gly Ser Ser Pro Ser
130 135 140
Cys Leu Pro Cys Arg Cys Ser Thr Pro Val Ile Glu Tyr Gly Thr Val
145 150 155 160
Asn Gly Thr Asp Phe Asp Cys Gly Lys Ala Ala Arg Ile Gln Cys Phe
165 170 175
Lys Gly Phe Lys Leu Leu Gly Leu Ser Glu Ile Thr Cys Glu Ala Asp
180 185 190
Gly Gln Trp Ser Ser Gly Phe Pro His Cys Glu His Thr Ser Cys Gly
195 200 205
Ser Leu Pro Met Ile Pro Asn Ala Phe Ile Ser Glu Thr Ser Ser Trp
210 215 220
Lys Glu Asn Val Ile Thr Tyr Ser Cys Arg Ser Gly Tyr Val Ile Gln
225 230 235 240
Gly Ser Ser Asp Leu Ile Cys Thr Glu Lys Gly Val Trp Asn Gln Pro
245 250 255
Tyr Pro Val Cys Glu Pro Leu Ser Cys Gly Ser Pro Pro Ser Val Ala
260 265 270
Asn Ala Val Ala Thr Gly Glu Ala His Thr Tyr Glu Ser Glu Val Lys
275 280 285
Leu Arg Cys Leu Glu Gly Tyr Thr Met Asp Thr Asp Thr Asp Thr Ile
290 295 300
Thr Cys Gln Lys Asp Gly Arg Trp Phe Pro Glu Arg Ile Ser Cys Ser
305 310 315 320
Pro Lys Lys Cys Pro Leu Pro Glu Asn Ile Thr His Ile Leu Val His
325 330 335
Gly Asp Asp Phe Ser Val Asn Arg Gln Val Ser Val Ser Cys Ala Glu
340 345 350
Gly Tyr Thr Phe Glu Gly Val Asn Ile Ser Val Cys Gln Leu Asp Gly

```
        355                 360                 365
Thr Trp Glu Pro Pro Phe Ser Asp Glu Ser Cys Ser Pro Val Ser Cys
    370                 375                 380
Gly Lys Pro Glu Ser Pro Glu His Gly Phe Val Val Gly Ser Lys Tyr
385                 390                 395                 400
Thr Phe Glu Ser Thr Ile Ile Tyr Gln Cys Glu Pro Gly Tyr Glu Leu
                405                 410                 415
Glu Gly Asn Arg Glu Arg Val Cys Gln Glu Asn Arg Gln Trp Ser Gly
            420                 425                 430
Gly Val Ala Ile Cys Lys Glu Thr Arg Cys Glu Thr Pro Leu Glu Phe
        435                 440                 445
Leu Asn Gly Lys Ala Asp Ile Glu Asn Arg Thr Thr Gly Pro Asn Val
    450                 455                 460
Val Tyr Ser Cys Asn Arg Gly Tyr Ser Leu Glu Gly Pro Ser Glu Ala
465                 470                 475                 480
His Cys Thr Glu Asn Gly Thr Trp Ser His Pro Val Pro Leu Cys Lys
                485                 490                 495
Pro Asn Pro Cys Pro Val Pro Phe Val Ile Pro Glu Asn Ala Leu Leu
            500                 505                 510
Ser Glu Lys Glu Phe Tyr Val Asp Gln Asn Val Ser Ile Lys Cys Arg
        515                 520                 525
Glu Gly Phe Leu Leu Gln Gly His Gly Ile Ile Thr Cys Asn Pro Asp
    530                 535                 540
Glu Thr Trp Thr Gln Thr Ser Ala Lys Cys Glu Lys Ile Ser Cys Gly
545                 550                 555                 560
Pro Pro Ala His Val Glu Asn Ala Ile Ala Arg Gly Val His Tyr Gln
                565                 570                 575
Tyr Gly Asp Met Ile Thr Tyr Ser Cys Tyr Ser Gly Tyr Met Leu Glu
            580                 585                 590
Gly Phe Leu Arg Ser Val Cys Leu Glu Asn Gly Thr Trp Thr Ser Pro
        595                 600                 605
Pro Ile Cys Arg Ala Val Cys Arg Phe Pro Cys Gln Asn Gly Gly His
    610                 615                 620
Leu Pro Thr Pro Lys Cys Leu Phe Leu Ser Arg Gly Leu Asp Gly Ala
625                 630                 635                 640
Pro Leu
```

<210> 5773
<211> 579
<212> DNA
<213> Homo sapiens

<400> 5773

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nnacgcgtga ggggcctgag gcgagcggtt agagcgtctc ccggaaggat gggccggtct
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cggagccgga gctcgtcccg ctccaagcac accaagagca gcaagcacaa caagaagcgc
120
agccggtccc ggtcgcgatc ccgggacaag gagcgcgtgc ggaagcgttc caaatctcgg
180
gaaagtaaac ggaaccggcg gcgggagtcg cggtcccgtt cgcgctccac caacacggcc
240
gtgtcccggc gcgagcggga ccgggagcgc cctcgtcccc gcccgaccgc atcgacatct
300
```

tcgggcgcac ggtgagcaag cgcagcagcc tggacgagaa gcagaagcga gaggaggagg
360
agaagaaagc ggagttcgag cggcagcgaa aaattcgaca gcaagaaata gaagaaaaac
420
tcatcgagga agaaacagca cgaagagtag aagaattggt agcaanaaag ggtggaggaa
480
gaactggaga aaaggaagga tgaaattgaa cgagaagttc tccgaagggt ggaggaagcc
540
aaacgcatca tggaaaagca gttgctcgaa gaactcgag
579

<210> 5774
<211> 104
<212> PRT
<213> Homo sapiens

<400> 5774
Xaa Arg Val Arg Gly Leu Arg Arg Ala Val Arg Ala Ser Pro Gly Arg
 1   5   10   15
Met Gly Arg Ser Arg Ser Arg Ser Ser Ser Arg Ser Lys His Thr Lys
            20   25   30
Ser Ser Lys His Asn Lys Lys Arg Ser Arg Ser Arg Ser Arg Ser Arg
        35   40   45
Asp Lys Glu Arg Val Arg Lys Arg Ser Lys Ser Arg Glu Ser Lys Arg
    50   55   60
Asn Arg Arg Arg Glu Ser Arg Ser Arg Ser Arg Ser Thr Asn Thr Ala
65   70   75   80
Val Ser Arg Arg Glu Arg Asp Arg Glu Arg Pro Arg Pro Arg Pro Thr
                85   90   95
Ala Ser Thr Ser Ser Gly Ala Arg
            100

<210> 5775
<211> 1441
<212> DNA
<213> Homo sapiens

<400> 5775
cgtcctcctc ccgctcggaa ggtcccaagg tgagacacct tcagcaggtc tcagggaaga
60
tggcagccct aggggacatt caggagtccc cttctgtccc gtcccctgtc agtctctcat
120
caccggggac acctggaacc cagcaccacg agcctcagct tcacctccat gggcatcaac
180
atgcctaagg tgctctccca gccgtccgac ctggatctcc aagacgtaga ggaagtggag
240
atcggcagag acaccttctg gcccgactcc gagcccaagc cggagcaggc tccacgctct
300
cctggctctc aggcccctga cgaggggggcg ggcggggcgc tgcgcacctc cgtgaggagc
360
cttccccgca gggcccggtg cagcgccggc ttcgggcctg aatccagcgc ggagcggccg
420
gcgggccagc cgcctggggc cgtcccttgc gcccagccgc ggggcgcctg gcgcgtgacg
480

ctcgtgcagc aagcagcggc cgggcccgag ggtgcgcccg agcgggctgc cgagctggga
540
gtcaacttcg gtcggagccg gcagggcagc gcgcggggga ccaagccgca caggtgcgag
600
gcctgcggca agagtttcaa gtataactcg ctgctcctga agcaccagcg catccacacg
660
ggcgagaagc cctacgcctg ccacgagtgc ggcaagtgtt tcgccgcagc ttcgcgcttc
720
atccagcacc agcgcatcca cagcggcgag aagccctacg cctgccccga gtgcagcaag
780
accttcacgc gcagctccaa cctcatcaag caccaggtca tccacagcgg cgagcggccc
840
ttcgcctgcg gcgactgcgg caaactgttc cgccgcagct tcgcgctcct ggagcacgcg
900
cgcgtgcaca gcggcgagaa gccctacgag tgctccgact gcggcaagtg cttccgcggc
960
cgctcgcact tcttccggca caaccgcaca cacacgggcg agaagcccta ccactgcctc
1020
gactgcggca agagcttcag ccacagctcg cacctcatca agcaccagcg cacccaccgt
1080
ggcgtgcggc cctacgcctg cccgttgtgt ggcaagagct tcagccggcg ctccaacctg
1140
caccggcacg agaagatcca caccaccggg cccaaggccc tggccatgct gatgctgggg
1200
gcggcggcgg cgggggctct ggccacaccc ccacccgctc ccacctagga ggccaggaaa
1260
gggggagcgg ggcgcccagg gccactggaa cagccccact ggagtcaagg ctccgaggga
1320
ggagagaggg gctcgggaag ggagctgggg cggtgagggc atggggtgag gcatggcgat
1380
gggggagggc gagggcgaga aagggcaggc actctgcgaa ttaaaggcct tggacttgaa
1440
a
1441

<210> 5776
<211> 359
<212> PRT
<213> Homo sapiens

<400> 5776
Met Gly Ile Asn Met Pro Lys Val Leu Ser Gln Pro Ser Asp Leu Asp
1 5 10 15
Leu Gln Asp Val Glu Glu Val Glu Ile Gly Arg Asp Thr Phe Trp Pro
20 25 30
Asp Ser Glu Pro Lys Pro Glu Gln Ala Pro Arg Ser Pro Gly Ser Gln
35 40 45
Ala Pro Asp Glu Gly Ala Gly Gly Ala Leu Arg Thr Ser Val Arg Ser
50 55 60
Leu Pro Arg Arg Ala Arg Cys Ser Ala Gly Phe Gly Pro Glu Ser Ser
65 70 75 80
Ala Glu Arg Pro Ala Gly Gln Pro Pro Gly Ala Val Pro Cys Ala Gln
85 90 95
Pro Arg Gly Ala Trp Arg Val Thr Leu Val Gln Gln Ala Ala Ala Gly

```
            100                 105                 110
Pro Glu Gly Ala Pro Glu Arg Ala Ala Glu Leu Gly Val Asn Phe Gly
        115                 120                 125
Arg Ser Arg Gln Gly Ser Ala Arg Gly Thr Lys Pro His Arg Cys Glu
    130                 135                 140
Ala Cys Gly Lys Ser Phe Lys Tyr Asn Ser Leu Leu Leu Lys His Gln
145                 150                 155                 160
Arg Ile His Thr Gly Glu Lys Pro Tyr Ala Cys His Glu Cys Gly Lys
                165                 170                 175
Cys Phe Ala Ala Ala Ser Arg Phe Ile Gln His Gln Arg Ile His Ser
            180                 185                 190
Gly Glu Lys Pro Tyr Ala Cys Pro Glu Cys Ser Lys Thr Phe Thr Arg
        195                 200                 205
Ser Ser Asn Leu Ile Lys His Gln Val Ile His Ser Gly Glu Arg Pro
    210                 215                 220
Phe Ala Cys Gly Asp Cys Gly Lys Leu Phe Arg Arg Ser Phe Ala Leu
225                 230                 235                 240
Leu Glu His Ala Arg Val His Ser Gly Glu Lys Pro Tyr Glu Cys Ser
                245                 250                 255
Asp Cys Gly Lys Cys Phe Arg Gly Arg Ser His Phe Phe Arg His Asn
            260                 265                 270
Arg Thr His Thr Gly Glu Lys Pro Tyr His Cys Leu Asp Cys Gly Lys
        275                 280                 285
Ser Phe Ser His Ser Ser His Leu Ile Lys His Gln Arg Thr His Arg
    290                 295                 300
Gly Val Arg Pro Tyr Ala Cys Pro Leu Cys Gly Lys Ser Phe Ser Arg
305                 310                 315                 320
Arg Ser Asn Leu His Arg His Glu Lys Ile His Thr Thr Gly Pro Lys
                325                 330                 335
Ala Leu Ala Met Leu Met Leu Gly Ala Ala Ala Ala Gly Ala Leu Ala
            340                 345                 350
Thr Pro Pro Pro Ala Pro Thr
        355
```

<210> 5777
<211> 1431
<212> DNA
<213> Homo sapiens

<400> 5777
ggaaggctcg cctgggagct catacctggc tggggccgag gattggctgt tccggggcta
60
gggagcgctt tctcccggga accgcggctg tgacccaagt ggcccggacc agtttggggc
120
tgcgtgcggc ctgcctcaag caaccaggta cgtaggtcgg cggcccagct cggcgctgcg
180
gtgggagccg gagggcgaca gtcagagccg gggtgccagc gggacgcgac cgccagatcc
240
acttaggacc ccgtcgttct gcgaagcggc cacgtctgag tcccggggcc tcctcgtgct
300
gcagatgtcg ccttaggacc tcggccagga taccctctgc catgctcttg tgctgcccgt
360
gatcaccgac tggcccttgt aagcaccttc gcagcaggaa gcccagagct gcgcctgccc
420

tttctgaagg ctgtggaaga ggttggagtg ggcgcatctt agcttgcccc atccccattt
480
gaggtctgtc ggagctgccc ttcagtgtga gcatccacaa tgggtacccc agcctcggtg
540
gtcagtgagc caccccctg gcaggccccg attgaggccc ggggccgcaa gcaggcctcg
600
gccaacatct tccaggacgc cgagctgctg cagatccaag ccctgtttca acgcagcggg
660
gaccagctgg ccgaggaacg ggcacagatc atctgggaat gtgcagggga ccaccgtgtg
720
gctgaggccc tcaagaggct gcgcaggaag aggcccccaa ggcagaaacc ccctgggcca
780
ctcgctacac cactgcagcc gcctcagaat cctggagccc cactctgcac tggccaaccc
840
acagagtgcc acagagacag cctccagtga gcagtatctg cactctagga agaaaagtgc
900
caggatccgc cggaactgga ggaagtcagg ccccacaagc tacctccacc agatcagaca
960
ctgatccagg gaaagagcca ggaatggcag tgtcttccct cttgccaaaa ggcctgggga
1020
ggtgaaggaa gagagacttt aggcaagcag cccaaagggg taaatgaaag caagaggctg
1080
ctgccactga cctgctccat tcagaacaag actggatgct tctgttgagc tctccattat
1140
gtgggaccca ttcctcacca aaatgaggag agacagtgac tgttcctgcc acagtccttc
1200
ccagtctaac actattcctg ggctgcatga tattcccctg ggagcaaagt gacaggcact
1260
tagatgcagc atttcaccac tcatgctact aatcatctac ctgctactac tgtaaaccat
1320
ggttccagca gcctgttcca cacccccaca ccatcaggat agcacaggga aactgtagtt
1380
taagtggcaa ataaaaacat ttgcatcaaa aaaaaaaaaa aaaaaaaaaa a
1431

<210> 5778
<211> 164
<212> PRT
<213> Homo sapiens

<400> 5778
Met Leu Thr Leu Lys Gly Ser Ser Asp Arg Pro Gln Met Gly Met Gly
1 5 10 15
Gln Ala Lys Met Arg Pro Leu Gln Pro Leu Pro Gln Pro Ser Glu Arg
20 25 30
Ala Gly Ala Ala Leu Gly Phe Leu Leu Arg Arg Cys Leu Gln Gly Pro
35 40 45
Val Gly Asp His Gly Gln His Lys Ser Met Ala Glu Gly Ile Leu Ala
50 55 60
Glu Val Leu Arg Arg His Leu Gln His Glu Glu Ala Pro Gly Leu Arg
65 70 75 80
Arg Gly Arg Phe Ala Glu Arg Arg Gly Pro Lys Trp Ile Trp Arg Ser
85 90 95
Arg Pro Ala Gly Thr Pro Ala Leu Thr Val Ala Leu Arg Leu Pro Pro

```
            100                 105                 110
Gln Arg Arg Ala Gly Pro Pro Thr Tyr Val Pro Gly Cys Leu Arg Gln
        115                 120                 125
Ala Ala Arg Ser Pro Lys Leu Val Arg Ala Thr Trp Val Thr Ala Ala
    130                 135                 140
Val Pro Gly Arg Lys Arg Ser Leu Ala Pro Glu Gln Pro Ile Leu Gly
145                 150                 155                 160
Pro Ser Gln Val
```

<210> 5779
<211> 371
<212> DNA
<213> Homo sapiens

<400> 5779
ctcttgagac gtgtggaggg aaggaaggga agaacccatg atctacccca gaggcatgga
60
cgggagagag gggtgatttc agccttgtct ggcatccctt gtgtctgcnt gagggtgtgt
120
gcacacggga atgtgtgcgg gtgtgtgtgc gtgcatgcag ctgtgtgtgg atgtgcantc
180
gtgtgtgggt gtgtaggtgt gtgtgggtgt gtgcaccagt gcaggtgtgc atgggtgtgt
240
acaggtgggt gtgtgtatgt gtgtgggggt gtgcccatct gtgcaggtgt gtgggtgtgc
300
agggtcncat gcctgtgtgt gggtgtgncc ccgtgtgtac ccctgtggag gtgtgtgggt
360
gtgtgcagtg t
371

<210> 5780
<211> 123
<212> PRT
<213> Homo sapiens

<400> 5780

```
Leu Leu Arg Arg Val Glu Gly Arg Lys Gly Arg Thr His Asp Leu Pro
 1               5                  10                  15
Gln Arg His Gly Arg Glu Arg Gly Val Ile Ser Ala Leu Ser Gly Ile
            20                  25                  30
Pro Cys Val Cys Xaa Arg Val Cys Ala His Gly Asn Val Cys Gly Cys
        35                  40                  45
Val Cys Val His Ala Ala Val Cys Gly Cys Ala Xaa Val Cys Gly Cys
    50                  55                  60
Val Gly Val Cys Gly Cys Val His Gln Cys Arg Cys Ala Trp Val Cys
65                  70                  75                  80
Thr Gly Gly Cys Val Tyr Val Cys Gly Gly Val Pro Ile Cys Ala Gly
                85                  90                  95
Val Trp Val Cys Arg Val Xaa Cys Leu Cys Val Gly Val Xaa Pro Cys
            100                 105                 110
Val Pro Leu Trp Arg Cys Val Gly Val Cys Ser
        115                 120
```

<210> 5781
<211> 845
<212> DNA
<213> Homo sapiens

<400> 5781
ggggttccgt gccccaaaat cgagggagcc gtgggcttgg ggtccggatc gcggccgcgg
60
ggcgctggcg tgcggtgtca tttctgcggt gtaaatgctc ccaccttggc cgatttcaag
120
ccaccaggtg aggatggcac tgcaacatct tccactgagg ctccagctgc cctctcaggt
180
acatcagggc ctggancgtc ctctcctcca ggagggccag gactcggccc cctgccagcc
240
cccgaagcat tgcagccagg agtgcagcgt gggggccctg caggccatgg ccaggcccca
300
gcgccaccag caccaggtca ggctggaagc cataggccag gggcagcacc aagcccaaga
360
tgcagctcag gaaaccaccg gtcatcactg gcagtggcgt ggagacatgg aacatggata
420
gggcagccgc ctccttgccc ctgatgttca gccacagact cctcccgtca tgggcgaggt
480
ctggaggccg gtccagctgt cccagggcca cgcacagcag cctggaagaa gagctggcct
540
caggacaggt gttcatgttg tccagagtcc attcccagaa ctctctgtgc ttggccagcc
600
aggatagggg tgcccacagg tcctgccgtc agaggctcag gatggccaag tgaggcttac
660
ctctgggctc cgtgggacag gcctctccga acagccacat ccagggtggc tgctgcagca
720
gaggctggag tggctgctat accactgttc acctgtggga tgaataaaca gtggagaatg
780
aggcaccaac caactcccaa gccaggtaaa cagatccaca gttcccttca ttcggtgtgt
840
ctctg
845

<210> 5782
<211> 147
<212> PRT
<213> Homo sapiens

<400> 5782
Gly Val Pro Cys Pro Lys Ile Glu Gly Ala Val Gly Leu Gly Ser Gly
1 5 10 15
Ser Arg Pro Arg Gly Ala Gly Val Arg Cys His Phe Cys Gly Val Asn
20 25 30
Ala Pro Thr Leu Ala Asp Phe Lys Pro Pro Gly Glu Asp Gly Thr Ala
35 40 45
Thr Ser Ser Thr Glu Ala Pro Ala Ala Leu Ser Gly Thr Ser Gly Pro
50 55 60
Gly Xaa Ser Ser Pro Pro Gly Gly Pro Gly Leu Gly Pro Leu Pro Ala
65 70 75 80
Pro Glu Ala Leu Gln Pro Gly Val Gln Arg Gly Gly Pro Ala Gly His

```
                85                  90                  95
Gly Gln Ala Pro Ala Pro Pro Ala Pro Gly Gln Ala Gly Ser His Arg
            100                 105                 110
Pro Gly Ala Ala Pro Ser Pro Arg Cys Ser Ser Gly Asn His Arg Ser
        115                 120                 125
Ser Leu Ala Val Ala Trp Arg His Gly Thr Trp Ile Gly Gln Pro Pro
    130                 135                 140
Pro Cys Pro
145
```

<210> 5783
<211> 1839
<212> DNA
<213> Homo sapiens

<400> 5783
gtgggagcgg ccatggaccg cttcgtttgg accagcggcc tcctggagat caacgagacc
60
ctggtgatcc agcagcgcgg ggtgcgaatc tacgatggcg aggagaagat aaaatttgat
120
gctgggactc tccttcttag tacacaccga ctgatttgga gagatcagaa aaatcatgag
180
tgttgcatgg ccattctcct ttcccaaatt gtgttcattg aagaacaggc ggctggaatt
240
gggaagagtg ccaaaatagt ggttcatctt cacccagctc ctcctaacaa agaacctggc
300
ccattccaga gtagtaagaa ctcctacatc aaactctcct tcaaagaaca tggccagatt
360
gagttttaca ggcgtttatc agaggaaatg acacaaagaa gatgggagaa tatgccagtt
420
tcccagtcat tacaaacaaa tagaggaccc cagccaggaa gaataagggc tgtaggaatt
480
gtaggtattg aaaggaaact ggaagaaaaa agaaaagaaa ctgacaaaaa catttctgag
540
gcctttgaag acctcagcaa actaatgatc aaggctaagg aaatggtgga attatcaaaa
600
tcaattgcta ataaaattaa agacaaacaa ggtgacatca cagaagatga gaccatcagg
660
tttaaatcct acttgctgag catgggaata gctaacccag ttaccagaga aacctacggc
720
tcaggcacac agtaccacat gcagctggcc aaacaactgg ctggaatatt gcaggtgcct
780
ttagaggaac gaggggaat aatgtcactc acggaggtgt actgcttagt aaaccgagct
840
cgaggaatgg aattgctctc accagaagat ttagtgaatg cgtgcaagat gctggaagca
900
ctgaaattac ctctcaggct ccgtgtgttt gacagtggcg tcatggtaat tgagcttcag
960
tctcacaagg aagaggaaat ggtggcctcg gccctggaga cagtttcaga aaagggatcc
1020
ctaacatcag aagagtttgc taagcttgtg ggaatgtctg tcctcctagc caaagaaagg
1080
ttgctgcttg cagagaagat gggccatctt tgccgtgatg actcagtgga aggcctgcgt
1140

ttttacccaa atttatttat gacacagagc taagggtttt gtatttaaaa tccttttttgt
1200
ccatatgctt gcgtcatgta gaggttgtat gacattgagc taagagataa accccgatca
1260
attgagaatt tattggaact tcacagtgca atgtaaatct cttttaattt ctccccaaat
1320
atggtccagg aaatttattt agtatacgca taggaaaatt cagaaaagtg aatgccaata
1380
tgaatttaaa atcatgctat agtgcagaac cctcagagtt taacttggaa tatagtggat
1440
tttaacttga tcctcaaatc taatcatttt ataaagaagg gaatttagtt ttgcagagaa
1500
taaaaagaga agttgcatgt tcagacaggt tagattatta ttttggtgta actgaaattc
1560
actgattgca catgacaatg ttgggacaaa atatactgca gcatgctata tgaggctcct
1620
ccccagggct tttagaagca gtcatagaca tgtcttcaac ataccaaata aaataccttt
1680
aaaaatgaaa taattttatt tgacacatta tttatatata ttctatctag gtttctcttt
1740
gtttttttta aagtgatgat ttcatggact gggcatttaa aagaaatggc aactgtggtc
1800
cattttggt ttttccaaat gctgtggaat ttttggaaa
1839

<210> 5784
<211> 386
<212> PRT
<213> Homo sapiens

<400> 5784
Met Asp Arg Phe Val Trp Thr Ser Gly Leu Leu Glu Ile Asn Glu Thr
1 5 10 15
Leu Val Ile Gln Gln Arg Gly Val Arg Ile Tyr Asp Gly Glu Glu Lys
20 25 30
Ile Lys Phe Asp Ala Gly Thr Leu Leu Leu Ser Thr His Arg Leu Ile
35 40 45
Trp Arg Asp Gln Lys Asn His Glu Cys Cys Met Ala Ile Leu Leu Ser
50 55 60
Gln Ile Val Phe Ile Glu Glu Gln Ala Ala Gly Ile Gly Lys Ser Ala
65 70 75 80
Lys Ile Val Val His Leu His Pro Ala Pro Pro Asn Lys Glu Pro Gly
85 90 95
Pro Phe Gln Ser Ser Lys Asn Ser Tyr Ile Lys Leu Ser Phe Lys Glu
100 105 110
His Gly Gln Ile Glu Phe Tyr Arg Arg Leu Ser Glu Glu Met Thr Gln
115 120 125
Arg Arg Trp Glu Asn Met Pro Val Ser Gln Ser Leu Gln Thr Asn Arg
130 135 140
Gly Pro Gln Pro Gly Arg Ile Arg Ala Val Gly Ile Val Gly Ile Glu
145 150 155 160
Arg Lys Leu Glu Glu Lys Arg Lys Glu Thr Asp Lys Asn Ile Ser Glu
165 170 175
Ala Phe Glu Asp Leu Ser Lys Leu Met Ile Lys Ala Lys Glu Met Val

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            180                 185                 190
Glu Leu Ser Lys Ser Ile Ala Asn Lys Ile Lys Asp Lys Gln Gly Asp
        195                 200                 205
Ile Thr Glu Asp Glu Thr Ile Arg Phe Lys Ser Tyr Leu Leu Ser Met
    210                 215                 220
Gly Ile Ala Asn Pro Val Thr Arg Glu Thr Tyr Gly Ser Gly Thr Gln
225                 230                 235                 240
Tyr His Met Gln Leu Ala Lys Gln Leu Ala Gly Ile Leu Gln Val Pro
                245                 250                 255
Leu Glu Glu Arg Gly Gly Ile Met Ser Leu Thr Glu Val Tyr Cys Leu
            260                 265                 270
Val Asn Arg Ala Arg Gly Met Glu Leu Leu Ser Pro Glu Asp Leu Val
        275                 280                 285
Asn Ala Cys Lys Met Leu Glu Ala Leu Lys Leu Pro Leu Arg Leu Arg
    290                 295                 300
Val Phe Asp Ser Gly Val Met Val Ile Glu Leu Gln Ser His Lys Glu
305                 310                 315                 320
Glu Glu Met Val Ala Ser Ala Leu Glu Thr Val Ser Glu Lys Gly Ser
                325                 330                 335
Leu Thr Ser Glu Glu Phe Ala Lys Leu Val Gly Met Ser Val Leu Leu
            340                 345                 350
Ala Lys Glu Arg Leu Leu Leu Ala Glu Lys Met Gly His Leu Cys Arg
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Asp Asp Ser Val Glu Gly Leu Arg Phe Tyr Pro Asn Leu Phe Met Thr
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Gln Ser
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<210> 5785
<211> 785
<212> DNA
<213> Homo sapiens

<400> 5785
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240
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420
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480
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600
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785

<210> 5786
<211> 159
<212> PRT
<213> Homo sapiens

<400> 5786
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Lys Pro Ala Ala Arg Ala Ala Asp Leu Ala Ala Pro Ala Gly Ala Ala
35 40 45
Leu Ala Gln Pro Leu Gly Pro Trp Pro Leu Ser Ser Ala Gly Pro Arg
50 55 60
Leu Val Phe Asn Arg Val Asn Arg Arg Arg Asp Pro Ser Lys Ser Pro
65 70 75 80
Ser Leu Gln Gly Thr Gln Glu Thr Tyr Thr Leu Ala His Lys Glu Asn
85 90 95
Val Arg Phe Val Ser Glu Ala Trp Gln Gln Val Gln Gln Gln Leu Asp
100 105 110
Gly Gly Pro Ala Gly Glu Gly Gly Pro Arg Pro Val Gln Tyr Val Glu
115 120 125
Arg Thr Pro Asn Pro Arg Leu Gln Asn Phe Val Pro Ile Asp Leu Asp
130 135 140
Glu Trp Trp Ala Gln Gln Phe Leu Ala Arg Ile Thr Ser Cys Ser
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<210> 5787
<211> 1683
<212> DNA
<213> Homo sapiens

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240
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300
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360

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420
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480
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720
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1020
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1140
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1683

<210> 5788
<211> 417
<212> PRT
<213> Homo sapiens

<400> 5788
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Ser Cys Glu Tyr Glu Thr Arg Leu Pro Gly Asn His Ser Thr Ser Gln
        35                  40                  45
Glu Ile Phe Arg Gln Arg Phe Arg His Leu Arg Tyr Gln Glu Thr Pro
    50                  55                  60
Gly Pro Arg Glu Ala Leu Ser Gln Leu Arg Val Leu Cys Cys Glu Trp
65                  70                  75                  80
Leu Arg Pro Glu Lys His Thr Lys Glu Gln Ile Leu Glu Phe Leu Val
                85                  90                  95
Leu Glu Gln Phe Leu Thr Ile Leu Pro Glu Glu Leu Gln Ser Trp Val
            100                 105                 110
Arg Gly His His Pro Lys Ser Gly Glu Glu Ala Val Thr Val Leu Glu
        115                 120                 125
Asp Leu Glu Lys Gly Leu Glu Pro Glu Pro Gln Val Pro Gly Pro Ala
    130                 135                 140
His Gly Pro Ala Gln Glu Glu Pro Trp Glu Lys Lys Glu Ser Leu Gly
145                 150                 155                 160
Ala Ala Gln Glu Ala Leu Ser Ile Gln Leu Gln Pro Lys Glu Thr Gln
                165                 170                 175
Pro Phe Pro Lys Ser Glu Gln Val Tyr Leu His Phe Leu Ser Val Val
            180                 185                 190
Thr Glu Asp Gly Pro Glu Pro Lys Asp Lys Gly Ser Leu Pro Gln Pro
        195                 200                 205
Pro Ile Thr Glu Val Glu Ser Gln Val Phe Ser Glu Lys Leu Ala Thr
    210                 215                 220
Asp Thr Ser Thr Phe Glu Ala Thr Ser Glu Gly Thr Leu Glu Leu Gln
225                 230                 235                 240
Gln Arg Asn Pro Lys Ala Glu Arg Leu Arg Trp Ser Pro Ala Gln Glu
                245                 250                 255
Glu Ser Phe Arg Gln Met Val Val Ile His Lys Glu Ile Pro Thr Gly
            260                 265                 270
Lys Lys Asp His Glu Cys Ser Glu Cys Gly Lys Thr Phe Ile Tyr Asn
        275                 280                 285
Ser His Leu Val Val His Gln Arg Val His Ser Gly Glu Lys Pro Tyr
    290                 295                 300
Lys Cys Ser Asp Cys Gly Lys Thr Phe Lys Gln Ser Ser Asn Leu Gly
305                 310                 315                 320
Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Phe Glu Cys Asn Glu
                325                 330                 335
Cys Gly Lys Ala Phe Arg Trp Gly Ala His Leu Val Gln His Gln Arg
            340                 345                 350
Ile His Ser Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala
        355                 360                 365
Phe Ser Gln Ser Ser Tyr Leu Ser Gln His Arg Arg Ile His Ser Gly
    370                 375                 380
Glu Lys Pro Phe Ile Cys Lys Glu Cys Gly Lys Ala Tyr Gly Trp Cys
385                 390                 395                 400
Ser Glu Leu Ile Arg His Arg Arg Val His Ala Arg Lys Glu Pro Ser
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<210> 5789
<211> 1201
<212> DNA
<213> Homo sapiens

<400> 5789
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420
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1080
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<210> 5790
<211> 400
<212> PRT
<213> Homo sapiens

<400> 5790
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35 40 45
Pro Gln Pro Gly Ala Gly His Asp Glu Gly Pro Gly Ser Gly Trp Ala
50 55 60
Ala Lys Gly Thr Val Arg Gly Trp Asn Arg Arg Ala Arg Glu Ser Pro
65 70 75 80
Gly His Val Ser Glu Pro Asp Arg Thr Gln Leu Ser Gln Asp Leu Gly
85 90 95
Gly Gly Thr Leu Ala Met Asp Thr Leu Pro Asp Asn Arg Thr Arg Val
100 105 110
Val Glu Asp Asn His Ser Tyr Tyr Val Ser Arg Leu Tyr Gly Pro Ser
115 120 125
Glu Pro His Ser Arg Glu Leu Trp Val Asp Val Ala Glu Ala Asn Arg
130 135 140
Ser Gln Val Lys Ile His Thr Ile Leu Ser Asn Thr His Arg Gln Ala
145 150 155 160
Ser Arg Val Val Leu Ser Phe Asp Phe Pro Phe Tyr Gly His Pro Leu
165 170 175
Arg Gln Ile Thr Ile Ala Thr Gly Gly Phe Ile Phe Met Gly Asp Val
180 185 190
Ile His Arg Met Leu Thr Ala Thr Gln Tyr Val Ala Pro Leu Met Ala
195 200 205
Asn Phe Asn Pro Gly Tyr Ser Asp Asn Ser Thr Val Val Tyr Phe Asp
210 215 220
Asn Gly Thr Val Phe Val Val Gln Trp Asp His Val Tyr Leu Gln Gly
225 230 235 240
Trp Glu Asp Lys Gly Ser Phe Thr Phe Gln Ala Ala Leu His His Asp
245 250 255
Gly Arg Ile Val Phe Ala Tyr Lys Glu Ile Pro Met Ser Val Pro Glu
260 265 270
Ile Ser Ser Ser Gln His Pro Val Lys Thr Gly Leu Ser Asp Ala Phe
275 280 285
Met Ile Leu Asn Pro Ser Pro Asp Val Pro Glu Ser Arg Arg Arg Ser
290 295 300
Ile Phe Glu Tyr His Arg Ile Glu Leu Asp Pro Ser Lys Val Thr Ser
305 310 315 320
Met Ser Ala Val Glu Phe Thr Pro Leu Pro Thr Cys Leu Gln His Arg
325 330 335
Ser Cys Asp Ala Cys Met Ser Ser Asp Leu Thr Phe Asn Cys Ser Trp
340 345 350
Cys His Val Leu Gln Arg Cys Ser Ser Gly Phe Asp Arg Tyr Arg Gln
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Glu Trp Met Asp Tyr Gly Cys Ala Gln Glu Ala Glu Gly Arg Met Cys
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Glu Asp Phe Gln Asp Glu Asp His Asp Ser Ala Ser Pro Asp Thr Phe
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<210> 5791
<211> 3285

<212> DNA
<213> Homo sapiens

<400> 5791
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720
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2340
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<210> 5792
<211> 479
<212> PRT
<213> Homo sapiens

<400> 5792
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35 40 45
Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr
50 55 60
Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr
65 70 75 80
Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu
85 90 95
Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln
100 105 110
Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile
115 120 125
Gly Glu Glu Glu Met Asp Ala Ser Thr Thr His His Lys Arg Lys Thr
130 135 140
Met Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly
145 150 155 160
Lys Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met
165 170 175
Lys Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His
180 185 190
Thr Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu
195 200 205
Thr Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val
210 215 220
Met Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu
225 230 235 240
Arg Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val
245 250 255
Ser Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu
260 265 270
Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr
275 280 285
Asp Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys
290 295 300
Thr Ser Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp
305 310 315 320
Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met

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Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu
            340                 345                 350
Lys Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr
        355                 360                 365
Leu Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp
    370                 375                 380
Pro Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met
385                 390                 395                 400
Arg His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys
                405                 410                 415
Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr
            420                 425                 430
Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro
        435                 440                 445
Pro Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg
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Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu
465                 470                 475
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<210> 5793
<211> 2767
<212> DNA
<213> Homo sapiens

<400> 5793
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240
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420
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<213> Homo sapiens

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Thr Ala Phe Ile Gly Ser Asn Ile Val Thr Ser Gln Thr Ile Trp Glu
        35   40   45
Gly Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
    50   55   60
Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
65   70   75   80
Arg Ala Leu Val Ile Ile Ser Ile Ile Val Ala Ala Leu Gly Val Leu
                85   90   95
Leu Ser Val Val Gly Gly Lys Cys Thr Asn Cys Leu Glu Asp Glu Ser
            100   105   110
Ala Lys Ala Lys Thr Met Ile Val Ala Gly Val Val Phe Leu Leu Ala
        115   120   125
Gly Leu Met Val Ile Val Pro Val Ser Trp Thr Ala His Asn Ile Ile
    130   135   140
Gln Asp Phe Tyr Asn Pro Leu Val Ala Ser Gly Gln Lys Arg Glu Met
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Gly Ala Ser Leu Tyr Val Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu
                165   170   175
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Tyr Ser Ala Lys Tyr Ser Ala Ala Arg Ser Ala Ala Ala Ser Asn Tyr
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<212> DNA
<213> Homo sapiens

<400> 5795

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<210> 5796
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<212> PRT
<213> Homo sapiens

<400> 5796

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            20                  25                  30
Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe
        35                  40                  45
Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg
    50                  55                  60
Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu
65                  70                  75                  80
Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val
                85                  90                  95
Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe
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            100                 105                 110
Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser
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Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val
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Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys
145                 150                 155                 160
Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met
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<213> Homo sapiens

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<210> 5798
<211> 109
<212> PRT
<213> Homo sapiens

<400> 5798
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Arg Arg Val Glu Gly Ser Arg Asp Gln Ala Trp Pro Leu Gln Thr Phe
        35                  40                  45
Ser Gln Arg Asn Tyr Arg Ser Leu Ser Leu Tyr Cys Trp Leu Ala Arg
    50                  55                  60
Glu Gly Arg Thr Ser Ser Tyr Gln Gly Asn Gln Gly Ser Leu Arg Pro
65                  70                  75                  80
Arg Pro Glu Pro Arg Gly Pro Glu Gly Ser Lys Arg Ser Gly Arg Pro
                85                  90                  95
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<210> 5800
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<212> PRT
<213> Homo sapiens

<400> 5800
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Ile Val Gly Asn Ile Ile Gly Ser Gly Ile Phe Val Ser Pro Lys Gly
    50                  55                  60
Val Leu Glu Asn Ala Gly Ser Val Gly Leu Ala Leu Ile Val Trp Ile
65                  70                  75                  80
Val Thr Gly Phe Ile Thr Val Val Gly Ala Leu Cys Tyr Ala Glu Leu
                85                  90                  95
Gly Val Thr Ile Pro Lys Ser Gly Gly Asp Tyr Ser Tyr Val Lys Asp
            100                 105                 110
Ile Phe Gly Gly Leu Ala Gly Phe Leu Arg Leu Trp Ile Ala Val Leu
        115                 120                 125
Val Ile Tyr Pro Thr Asn Gln Ala Val Ile Ala Leu Thr Phe Ser Asn
    130                 135                 140
Tyr Val Leu Gln Pro Leu Phe Pro Thr Cys Phe Pro Pro Glu Ser Gly
145                 150                 155                 160
Leu Arg Leu Leu Ala Ala Ile Cys Leu Leu Leu Leu Thr Trp Val Asn
                165                 170                 175
Cys Ser Ser Val Arg Trp Ala Thr Arg Val Gln Asp Ile Phe Thr Ala
            180                 185                 190
Gly Lys Leu Leu Ala Leu Ala Leu Ile Ile Ile Met Gly Ile Val Gln
        195                 200                 205
Ile Cys Lys Gly Glu Tyr Phe Trp Leu Glu Pro Lys Asn Ala Phe Glu
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225                 230                 235                 240
Gly Ser Phe Ala Tyr Gly Gly Trp Asn Phe Leu Asn Tyr Val Thr Glu
                245                 250                 255
Glu Leu Val Asp Pro Tyr Lys Asn Leu Pro Arg Ala Ile Phe Ile Ser
            260                 265                 270
Ile Pro Leu Val Thr Phe Val Tyr Val Phe Ala Asn Val Ala Tyr Val
        275                 280                 285
Thr Ala Met Ser Pro Gln Glu Leu Leu Ala Ser Asn Ala Val Ala Val
    290                 295                 300
Thr Phe Gly Glu Lys Leu Leu Gly Val Met Ala Trp Ile Met Pro Ile
305                 310                 315                 320
Ser Val Ala Leu Ser Thr Phe Gly Gly Val Asn Gly Ser Leu Phe Thr
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Ser Ser Arg Leu Phe Phe Ala Gly Ala Arg Glu Gly His Leu Pro Ser
            340                 345                 350
Val Leu Ala Met Ile His Val Lys Arg Cys Thr Pro Ile Pro Ala Leu
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Leu Phe Thr Cys Ile Ser Thr Leu Leu Met Leu Val Thr Ser Asp Met
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Tyr Thr Leu Ile Asn Tyr Val Gly Phe Ile Asn Tyr Leu Phe Tyr Gly
385                 390                 395                 400
Val Thr Val Ala Gly Gln Ile Val Leu Arg Trp Lys Lys Pro Asp Ile
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Pro Arg Pro Ile Lys Ile Asn Leu Leu Phe Pro Ile Ile Tyr Leu Leu
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Phe Trp Ala Phe Leu Leu Val Phe Ser Leu Trp Ser Glu Pro Val Val
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Cys Gly Ile Gly Leu Ala Ile Met Leu Thr Gly Val Pro Val Tyr Phe
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Glu Val Glu Arg Gly Ser Gly Thr Glu Glu Ala Asn Glu Asp Met Glu
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1560
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1920
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1980
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2040
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2100
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2160
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2280
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<211> 350
<212> PRT
<213> Homo sapiens

<400> 5802
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Phe Glu Lys Val Pro Leu Phe Met Ser Arg Ala Pro Ser Glu Ile Asp
        35                  40                  45
Pro Arg Glu Asn Pro Asp Leu Ala Cys Leu Gln Ser Ile Ile Phe Asp
    50                  55                  60
Glu Glu Arg Ser Pro Glu Glu Gln Ala Lys Thr Tyr Lys Asp Glu Gly
65                  70                  75                  80
Asn Asp Tyr Phe Lys Glu Lys Asp Tyr Lys Lys Ala Val Ile Ser Tyr
                85                  90                  95
Thr Glu Gly Leu Lys Lys Lys Cys Ala Asp Pro Asp Leu Asn Ala Val
            100                 105                 110
Leu Tyr Thr Asn Arg Ala Ala Ala Gln Tyr Tyr Leu Gly Asn Phe Arg
        115                 120                 125
Ser Ala Leu Asn Asp Val Thr Ala Ala Arg Lys Leu Lys Pro Cys His
    130                 135                 140
Leu Lys Ala Ile Ile Arg Gly Ala Leu Cys His Leu Glu Leu Lys His
145                 150                 155                 160
Phe Ala Glu Ala Val Asn Trp Cys Asp Glu Gly Leu Gln Ile Asp Ala
                165                 170                 175
Lys Glu Lys Lys Leu Leu Glu Met Arg Ala Lys Ala Asp Lys Leu Lys
            180                 185                 190
Arg Ile Glu Gln Arg Asp Val Arg Lys Ala Asn Leu Lys Glu Lys Lys
        195                 200                 205
Glu Arg Asn Gln Asn Glu Ala Leu Leu Gln Ala Ile Lys Ala Arg Asn
    210                 215                 220
Ile Arg Leu Ser Glu Ala Ala Cys Glu Asp Glu Asp Ser Ala Ser Glu
225                 230                 235                 240
Gly Leu Gly Glu Leu Phe Leu Asp Gly Leu Ser Thr Glu Asn Pro His
                245                 250                 255
Gly Ala Arg Leu Ser Leu Asp Gly Gln Gly Arg Leu Ser Trp Pro Val
            260                 265                 270
Leu Phe Leu Tyr Pro Glu Tyr Ala Gln Ser Asp Phe Ile Ser Ala Phe
        275                 280                 285
His Glu Asp Ser Arg Phe Ile Asp His Leu Met Val Met Phe Gly Glu
    290                 295                 300
Thr Pro Ser Trp Asp Leu Glu Gln Lys Tyr Cys Leu Ile Ile Trp Arg
305                 310                 315                 320
Ser Thr Leu Arg Met Arg Thr Gly Gln Asn Tyr Thr Gly Cys Leu Pro
                325                 330                 335
Arg Ala Pro Cys Tyr Arg Phe Tyr Ser Thr Arg Gly Thr Leu
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<211> 692
<212> DNA
<213> Homo sapiens

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120

ggagtgaatt tggaccaaac tgtaaaggaa tttatcgtat ttctaaagca agatgtccct
180
ttaaggacca acctgccacc accattcaga aattataaat atgatgcact aaagattatt
240
catcaagcac ataaatcaaa gacaaatgaa cttgtgttga gtttggaaga tgacgaaaga
300
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360
gcattcttct gtgaagaaga ttataggaac tacaaagcta atcccatttc atcctggtga
420
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480
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540
aatctggtta tttctttctc ttcaggtctt tctttccttc tctctttctt tttctttgtt
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attaaaaatt aaaaaaaaaa aaaaaaaaaa aa
692

<210> 5804
<211> 126
<212> PRT
<213> Homo sapiens

<400> 5804
Met Ala Pro Gly Glu Val Thr Ile Thr Val Arg Leu Ile Arg Ser Phe
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Glu His Arg Asn Phe Lys Pro Val Val Tyr His Gly Val Asn Leu Asp
20 25 30
Gln Thr Val Lys Glu Phe Ile Val Phe Leu Lys Gln Asp Val Pro Leu
35 40 45
Arg Thr Asn Leu Pro Pro Pro Phe Arg Asn Tyr Lys Tyr Asp Ala Leu
50 55 60
Lys Ile Ile His Gln Ala His Lys Ser Lys Thr Asn Glu Leu Val Leu
65 70 75 80
Ser Leu Glu Asp Asp Glu Arg Leu Leu Leu Lys Glu Asp Ser Thr Leu
85 90 95
Lys Ala Ala Gly Ile Ala Ser Glu Thr Glu Ile Ala Phe Phe Cys Glu
100 105 110
Glu Asp Tyr Arg Asn Tyr Lys Ala Asn Pro Ile Ser Ser Trp
115 120 125

<210> 5805
<211> 1112
<212> DNA
<213> Homo sapiens

<400> 5805
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acggtccttc agtttgcagc agcggtcaaa atctgacggg tctgggaaga tctggtagga
120

aaggccatcc ttgcgggggc tgaggccgat ctcctccatg ggctgagtgc tcagtggaga
180
gcggggagtt gtgtccacct tgccgacgtc gctagccgtg gggctgtcct gggaaggcgg
240
acggcgagcg cccggtgtcc gcactcggcc gcctgccgtg cccgtctgcg cccgtgtcat
300
cctcactcgg gacgcaggga ccgtttttaa atcacagggg cgtgtgtcag cctgccctag
360
gacttcatgt ctatatattt ccccattcac tgccccgact atctgagatc ggccaagatg
420
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780
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960
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1020
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1080
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1112

<210> 5806
<211> 105
<212> PRT
<213> Homo sapiens

<400> 5806
Met Ser Ile Tyr Phe Pro Ile His Cys Pro Asp Tyr Leu Arg Ser Ala
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Lys Met Thr Glu Val Met Met Asn Thr Gln Pro Met Glu Glu Ile Gly
20 25 30
Leu Ser Pro Arg Lys Asp Gly Leu Ser Tyr Gln Ile Phe Pro Asp Pro
35 40 45
Ser Asp Phe Asp Arg Cys Cys Lys Leu Lys Asp Arg Leu Pro Ser Ile
50 55 60
Val Val Glu Pro Thr Glu Gly Glu Val Glu Ser Gly Glu Leu Arg Trp
65 70 75 80
Pro Pro Glu Glu Phe Leu Val Gln Glu Asp Glu Gln Asp Asn Cys Glu
85 90 95
Glu Thr Ala Lys Glu Asn Lys Glu Gln

100 105

<210> 5807
<211> 1429
<212> DNA
<213> Homo sapiens

<400> 5807
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120
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240
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360
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acctgggtgc cgctcctctg ctttgtgctc catgtcatct cctggctcct catctttagc
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ctgcgccacc cagtgtgtgt ggagctgctg acagtgctgt gggtggtgcc taccctgggc
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780
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840
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960
gctccatacc ctaaattctg agtttcagcc actgaactcc aaggtccact tctcaccagc
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aaggaagagt ggggtatgga agtcatctgt cccttcactg tttagagcat gacactctcc
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1260
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1320
gtcaagggga ttctcctgct cttaactcga tgacttgggg ctccctgctc tcccgaggaa
1380

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1429

<210> 5808
<211> 261
<212> PRT
<213> Homo sapiens

<400> 5808
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            20   25   30
Leu Leu Gly Gly Ile Pro Glu Ser Gly Gly Pro Asp Ala Arg Gln Gly
        35   40   45
Trp Leu Ala Ala Leu Gln Asp Arg Ser Ile Leu Ala Pro Leu Ala Trp
    50   55   60
Asp Leu Gly Leu Leu Leu Leu Phe Val Gly Gln His Ser Leu Met Ala
65   70   75   80
Ala Glu Arg Val Lys Ala Trp Thr Ser Arg Tyr Phe Gly Val Leu Gln
                85   90   95
Arg Ser Leu Tyr Val Ala Cys Thr Ala Leu Ala Leu Gln Leu Val Met
            100   105   110
Arg Tyr Trp Glu Pro Ile Pro Lys Gly Pro Val Leu Trp Glu Ala Arg
        115   120   125
Ala Glu Pro Trp Ala Thr Trp Val Pro Leu Leu Cys Phe Val Leu His
    130   135   140
Val Ile Ser Trp Leu Leu Ile Phe Ser Ile Leu Leu Val Phe Asp Tyr
145   150   155   160
Ala Glu Leu Met Gly Leu Lys Gln Val Tyr Tyr His Val Leu Gly Leu
                165   170   175
Gly Glu Pro Leu Ala Leu Lys Ser Pro Arg Ala Leu Arg Leu Phe Ser
            180   185   190
His Leu Arg His Pro Val Cys Val Glu Leu Leu Thr Val Leu Trp Val
        195   200   205
Val Pro Thr Leu Gly Thr Asp Arg Leu Leu Leu Ala Phe Leu Leu Thr
    210   215   220
Leu Tyr Leu Gly Leu Ala His Gly Leu Asp Gln Gln Asp Leu Arg Tyr
225   230   235   240
Leu Arg Ala Gln Leu Gln Arg Lys Leu His Leu Leu Ser Arg Pro Gln
                245   250   255
Asp Gly Glu Ala Glu
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<210> 5809
<211> 2009
<212> DNA
<213> Homo sapiens

<400> 5809
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120

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240
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420
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480
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600
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660
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720
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780
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1740

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1860
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1980
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2009

<210> 5810
<211> 52
<212> PRT
<213> Homo sapiens

<400> 5810
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Gly Gly Gln Trp Arg Asp Leu Gly Ser Leu Gln Pro Pro Pro Pro Gly
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Phe Lys Gln Phe Ser Cys Leu Ser Leu Leu Ser Ser Trp His Tyr Lys
        35   40   45
His Pro Thr Pro
    50

<210> 5811
<211> 1607
<212> DNA
<213> Homo sapiens

<400> 5811
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tcctgagaaa agcatcacaa aaagagatgt ttgcccatcc tgtttgctgg ggtagtggga
120
agagaccggg ggtgatggtg gtgctggctg gacgtgggtg gtttcacagg acctgctgtg
180
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240
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1607

<210> 5812
<211> 463
<212> PRT
<213> Homo sapiens

<400> 5812
Trp Trp Cys Trp Leu Asp Val Gly Gly Phe Thr Gly Pro Ala Val Ser
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Glu Arg Ser His Ala Val Ile Arg Ser Leu Glu Ala Ala Asp Leu Pro
20 25 30
Thr Pro Gln Ala Ile Glu Pro Gln Ala Ile Val Gln Gln Val Pro Ala
35 40 45
Pro Ser Arg Met Gln Met Pro Gln Gly Asn Pro Leu Leu Leu Ser His
50 55 60
Thr Leu Gln Glu Leu Leu Ala Arg Asp Thr Val Gln Val Glu Leu Ile
65 70 75 80
Pro Glu Lys Lys Gly Leu Phe Leu Lys His Val Glu Tyr Glu Val Ser
85 90 95
Ser Gln Arg Phe Lys Ser Ser Val Tyr Arg Arg Tyr Asn Asp Phe Val
100 105 110
Val Phe Gln Glu Met Leu Leu His Lys Phe Pro Tyr Arg Met Val Pro

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        115                 120                 125
Ala Leu Pro Pro Lys Arg Met Leu Gly Ala Asp Arg Glu Phe Ile Glu
    130                 135                 140
Ala Arg Arg Arg Ala Leu Lys Arg Phe Val Asn Leu Val Ala Arg His
145                 150                 155                 160
Pro Leu Phe Ser Glu Asp Val Val Leu Lys Leu Phe Leu Ser Phe Ser
                165                 170                 175
Gly Ser Asp Val Gln Asn Lys Leu Lys Glu Ser Ala Gln Cys Val Gly
            180                 185                 190
Asp Glu Phe Leu Asn Cys Lys Leu Ala Thr Arg Ala Lys Asp Phe Leu
        195                 200                 205
Pro Ala Asp Ile Gln Ala Gln Phe Ala Ile Ser Arg Glu Leu Ile Arg
    210                 215                 220
Asn Ile Tyr Asn Ser Phe His Lys Leu Arg Asp Arg Ala Glu Arg Ile
225                 230                 235                 240
Ala Ser Arg Ala Ile Asp Asn Ala Ala Asp Leu Leu Ile Phe Gly Lys
                245                 250                 255
Glu Leu Ser Ala Ile Gly Ser Asp Thr Thr Pro Leu Pro Ser Trp Ala
            260                 265                 270
Ala Leu Asn Ser Ser Thr Trp Gly Ser Leu Lys Gln Ala Leu Lys Gly
        275                 280                 285
Leu Ser Val Glu Phe Ala Leu Leu Ala Asp Lys Ala Ala Gln Gln Gly
    290                 295                 300
Lys Gln Glu Glu Asn Asp Val Val Glu Lys Leu Asn Leu Phe Leu Asp
305                 310                 315                 320
Leu Leu Gln Ser Tyr Lys Asp Leu Cys Glu Arg His Glu Lys Gly Val
                325                 330                 335
Leu His Lys His Gln Arg Ala Leu His Lys Tyr Ser Leu Met Lys Arg
            340                 345                 350
Gln Met Met Ser Ala Thr Ala Gln Asn Arg Glu Pro Glu Ser Val Glu
        355                 360                 365
Gln Leu Glu Ser Arg Ile Val Glu Gln Glu Asn Ala Ile Gln Thr Met
    370                 375                 380
Glu Leu Arg Asn Tyr Phe Ser Leu Tyr Cys Leu His Gln Glu Thr Gln
385                 390                 395                 400
Leu Ile His Val Tyr Leu Pro Leu Thr Ser His Ile Leu Arg Ala Phe
                405                 410                 415
Val Asn Ser Gln Ile Gln Gly His Lys Glu Met Ser Lys Val Trp Asn
            420                 425                 430
Asp Leu Arg Pro Lys Leu Ser Cys Leu Phe Ala Gly Pro His Ser Thr
        435                 440                 445
Leu Thr Pro Pro Cys Ser Pro Pro Glu Asp Gly Leu Cys Pro His
    450                 455                 460
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<210> 5813
<211> 2991
<212> DNA
<213> Homo sapiens

<400> 5813
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120

ttcccatttc aaggctgatt ctgatgatga taatgtttaa gtagcattga ttgttctcta
180
attgaatttt tctttcttta ggcctcttct gaagagctga aagctgccta ccggaggctc
240
tgtatgctct accatccaga caagcacaga gacccagagc tcaagtcaca ggcggaacga
300
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420
agaacccctg ctgaaattcg agaggagttt gagcggctgc agagagagag agaagagagg
480
agattgcagc agcgaaccaa tcccaagctt tgtgacaaca aactgtgctc tgcagttttc
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cgtgggctac ctgcagtggc gatggggtat ccagtcagcc atgaacacta gcatcgtccg
660
agacactaaa accagccact tcactgtggc cctgcagctg ggaatccctc actcctttgc
720
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780
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840
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1380
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1560
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1620
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1680
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1740

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2160
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2280
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2700
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2760
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2820
tctgacggcc ccacggcccg agccgcggtg agcgtcgtgt tgcatgagcc tgggccccgg
2880
gcttcccgtg cgcctctgcc gcaggtgctt ctgggcaccc atcctctgcg tttcatttgc
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2991

<210> 5814
<211> 149
<212> PRT
<213> Homo sapiens

<400> 5814
Ala Ser Ser Glu Glu Leu Lys Ala Ala Tyr Arg Arg Leu Cys Met Leu
 1   5   10   15
Tyr His Pro Asp Lys His Arg Asp Pro Glu Leu Lys Ser Gln Ala Glu
            20   25   30
Arg Leu Phe Asn Leu Val His Gln Ala Tyr Glu Val Leu Ser Asp Pro

```
        35                  40                  45
Gln Thr Arg Ala Ile Tyr Asp Ile Tyr Gly Lys Arg Gly Leu Glu Met
    50                  55                  60
Glu Gly Trp Glu Val Val Glu Arg Arg Arg Thr Pro Ala Glu Ile Arg
65                  70                  75                  80
Glu Glu Phe Glu Arg Leu Gln Arg Glu Arg Glu Glu Arg Arg Leu Gln
                85                  90                  95
Gln Arg Thr Asn Pro Lys Leu Cys Asp Asn Lys Leu Cys Ser Ala Val
            100                 105                 110
Phe Ile Pro Trp Asn Pro Thr Arg Pro Asp His Cys Pro Ser Ser Glu
        115                 120                 125
Pro Arg Gln Glu His Arg Gly Leu Pro Ala Val Ala Met Gly Tyr Pro
    130                 135                 140
Val Ser His Glu His
145
```

<210> 5815
<211> 590
<212> DNA
<213> Homo sapiens

<400> 5815
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gttctagctg ttctaaagaa tgaaaagctg cgggacaagg aaaggcgaaa ggagattgac
120
ctgctgctgg gtcaaacaga tgataccaga taccatgtgc tagtgaacct gggcctcccg
180
agtctcttta gttttgggct tgtagatgat gcccaccatc tcatcaatgc cctccgacag
240
cagagtataa cccttcatct tgttgatgtc atgccggtcc tcatcacgct ttcttcgctt
300
ggctcttctt tcctcctgca tctgcggttt ggtccgttga gccttgtctc ccatacgggt
360
gccctccagc ttcccaacaa gggacagcac ctctcctgtg ggttcatccc ggcgggtccg
420
gtcaatgaga gaacggtcag cttggagcac aagattcgag ttcgccttgt actcgtattg
480
cagactacgg gcggttacat ccgccatggc cgcggctgct cggaggcttc agaccaccac
540
gcctccatac cgcaagctgc aaacggccgc agatctctgc tcctggcgcc
590

<210> 5816
<211> 196
<212> PRT
<213> Homo sapiens

<400> 5816
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Phe Ile Gln Ala Ala Leu Gly Asp Gln Pro Arg Asp Ile Leu Cys Gly
 1               5                  10                  15
Ala Ala Asp Glu Val Leu Ala Val Leu Lys Asn Glu Lys Leu Arg Asp
            20                  25                  30
Lys Glu Arg Arg Lys Glu Ile Asp Leu Leu Leu Gly Gln Thr Asp Asp
```

```
        35                  40                  45
Thr Arg Tyr His Val Leu Val Asn Leu Gly Leu Pro Ser Leu Phe Ser
    50                  55                  60
Phe Gly Leu Val Asp Asp Ala His His Leu Ile Asn Ala Leu Arg Gln
65                  70                  75                  80
Gln Ser Ile Thr Leu His Leu Val Asp Val Met Pro Val Leu Ile Thr
                85                  90                  95
Leu Ser Ser Leu Gly Ser Ser Phe Leu Leu His Leu Arg Phe Gly Pro
            100                 105                 110
Leu Ser Leu Val Ser His Thr Gly Ala Leu Gln Leu Pro Asn Lys Gly
        115                 120                 125
Gln His Leu Ser Cys Gly Phe Ile Pro Ala Gly Pro Val Asn Glu Arg
    130                 135                 140
Thr Val Ser Leu Glu His Lys Ile Arg Val Arg Leu Val Leu Val Leu
145                 150                 155                 160
Gln Thr Thr Gly Gly Tyr Ile Arg His Gly Arg Gly Cys Ser Glu Ala
                165                 170                 175
Ser Asp His His Ala Ser Ile Pro Gln Ala Ala Asn Gly Arg Arg Ser
            180                 185                 190
Leu Leu Leu Ala
        195
```

<210> 5817
<211> 648
<212> DNA
<213> Homo sapiens

<400> 5817

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cccaaagatg cagaactaca aagcaagccc caagatggag tgagcaacaa caatgaaatt
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cagaagaaag ccaccatggg gcagttacag aacaaggaga acaataacac caaggacagc
120
cctagtaggc agtgctcctg ggacaagtct gagtcacccc agagaagcag catgaacaat
180
ggatccccca cagctctatc aggcagcaaa accaacagcc caaagaacag tgttcacaag
240
ctagatgtgt ctagaagccc ccctctcatg gtcaaaaaga acccagcctt taataagggt
300
agtgggatag ttaccaatgg gtccttcagc agcagtaatg cagaaggtct tgagaaaacc
360
caaaccaccc ccaatgggag cctacaggcc agaaggagct cttcactgaa ggtatctggt
420
accaaaatgg gcacgcacag tgtacagaat ggaacggtgc gcatgggcat tttgaacagc
480
gacacactcg ggaaccccac aaatgttcga aacatgagct ggctgccaaa tggctatgtg
540
accctgaggg ataacaagca gaaagaacaa gctggagagt taggccagca caacagactg
600
tcacctatga taatgtccat cacagttctc catgatgaac ttgatgac
648
```

<210> 5818
<211> 191
<212> PRT

<213> Homo sapiens

<400> 5818

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Met Gly Gln Leu Gln Asn Lys Glu Asn Asn Asn Thr Lys Asp Ser Pro
 1               5                  10                  15
Ser Arg Gln Cys Ser Trp Asp Lys Ser Glu Ser Pro Gln Arg Ser Ser
            20                  25                  30
Met Asn Asn Gly Ser Pro Thr Ala Leu Ser Gly Ser Lys Thr Asn Ser
        35                  40                  45
Pro Lys Asn Ser Val His Lys Leu Asp Val Ser Arg Ser Pro Pro Leu
    50                  55                  60
Met Val Lys Lys Asn Pro Ala Phe Asn Lys Gly Ser Gly Ile Val Thr
65                  70                  75                  80
Asn Gly Ser Phe Ser Ser Ser Asn Ala Glu Gly Leu Glu Lys Thr Gln
                85                  90                  95
Thr Thr Pro Asn Gly Ser Leu Gln Ala Arg Arg Ser Ser Ser Leu Lys
            100                 105                 110
Val Ser Gly Thr Lys Met Gly Thr His Ser Val Gln Asn Gly Thr Val
        115                 120                 125
Arg Met Gly Ile Leu Asn Ser Asp Thr Leu Gly Asn Pro Thr Asn Val
    130                 135                 140
Arg Asn Met Ser Trp Leu Pro Asn Gly Tyr Val Thr Leu Arg Asp Asn
145                 150                 155                 160
Lys Gln Lys Glu Gln Ala Gly Glu Leu Gly Gln His Asn Arg Leu Ser
                165                 170                 175
Pro Met Ile Met Ser Ile Thr Val Leu His Asp Glu Leu Asp Asp
            180                 185                 190
```

<210> 5819
<211> 1652
<212> DNA
<213> Homo sapiens

<400> 5819

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tgggatctta gaagcagccg aagcagcgtg agggcggccg agggccagcc acgatttgaa
120
cgctctgcct tgcagctctt ctggaccgag gagcccaaag ccctaccctc accattcacc
180
aggtcctgtg ggaagagcag cgtggaggtg ggctgaggtt agaaggtgca gagcgtggaa
240
gaagattgtg agctgagtat tggacatctg ttcttgaata gtccctgggc ctgccatagg
300
aaaggaagtt ctccagggtt acagttctta tccgcgtgaa tacacatggc tctgttacga
360
aaaattaatc aggtgctgct gttccttctg atcgtgaccc tctgtgtgat tctgtataag
420
aaagttcata aggggactgt gcccaagaat gacgcagatg atgaatccga gactcctgaa
480
gaactggaag aagagattcc tgtggtgatt tgtgctgcag cagggaggat gggtgccact
540
atggctgcca tcaatagcat ctacagcaac cctgacgcca acatcttgtt ctatgtagtg
600
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ggactccgga atactctgac tcgaatacga aaatggattg aacattccaa actgagagaa
660
ataaacttta aaatcgtgga attcaacccg atggtcctca aagggaagat cagaccagac
720
tcatcgaggc ctgaattgct ccagcctctg aactttgttc gattttatct ccctctactt
780
atccaccaac acgagaaagt catctatttg gacgatgatg taattgtaca aggtgatatc
840
caagaactgt atgacaccac cttggccctg ggccacgcgg cggctttctc agatgactgc
900
gatttgccct ctgctcagga cataaacaga ctcgtgggac ttcagaacac atatatgggc
960
tatctggact accggaagaa ggccatcaag gaccttggca tcagccccag cacctgctct
1020
ttcaatcctg gtgtgattgt tgccaacatg acagaatgga agcaccagcg catcaccaag
1080
caattggaga aatggatgca aaagaatgtg gagtacgtga aggcttctct accatttttt
1140
ccatgcttgg aaacaaaatc attcaattaa ttttccacac atagttcaag ggttagaaat
1200
atttcacagt catctcaggt cagattttct tacagaggca atgttaagaa agaaaagggg
1260
gcagtcaatt aaaacctttc ctcaaaagat ataaatcaga ggaatcaaga tcctgtggag
1320
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1380
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1440
attaaggatt attatataaa gtcaattttg ctttttaagg tttatttta taatttataa
1500
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1560
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1620
ccttgaattt gcaagtaaag ttattctaaa ta
1652

<210> 5820
<211> 274
<212> PRT
<213> Homo sapiens

<400> 5820
Met Ala Leu Leu Arg Lys Ile Asn Gln Val Leu Leu Phe Leu Leu Ile
1 5 10 15
Val Thr Leu Cys Val Ile Leu Tyr Lys Lys Val His Lys Gly Thr Val
20 25 30
Pro Lys Asn Asp Ala Asp Asp Glu Ser Glu Thr Pro Glu Glu Leu Glu
35 40 45
Glu Glu Ile Pro Val Val Ile Cys Ala Ala Ala Gly Arg Met Gly Ala
50 55 60
Thr Met Ala Ala Ile Asn Ser Ile Tyr Ser Asn Pro Asp Ala Asn Ile
65 70 75 80
Leu Phe Tyr Val Val Gly Leu Arg Asn Thr Leu Thr Arg Ile Arg Lys

```
                85                  90                  95
Trp Ile Glu His Ser Lys Leu Arg Glu Ile Asn Phe Lys Ile Val Glu
            100                 105                 110
Phe Asn Pro Met Val Leu Lys Gly Lys Ile Arg Pro Asp Ser Ser Arg
        115                 120                 125
Pro Glu Leu Leu Gln Pro Leu Asn Phe Val Arg Phe Tyr Leu Pro Leu
    130                 135                 140
Leu Ile His Gln His Glu Lys Val Ile Tyr Leu Asp Asp Asp Val Ile
145                 150                 155                 160
Val Gln Gly Asp Ile Gln Glu Leu Tyr Asp Thr Thr Leu Ala Leu Gly
                165                 170                 175
His Ala Ala Ala Phe Ser Asp Asp Cys Asp Leu Pro Ser Ala Gln Asp
            180                 185                 190
Ile Asn Arg Leu Val Gly Leu Gln Asn Thr Tyr Met Gly Tyr Leu Asp
        195                 200                 205
Tyr Arg Lys Lys Ala Ile Lys Asp Leu Gly Ile Ser Pro Ser Thr Cys
    210                 215                 220
Ser Phe Asn Pro Gly Val Ile Val Ala Asn Met Thr Glu Trp Lys His
225                 230                 235                 240
Gln Arg Ile Thr Lys Gln Leu Glu Lys Trp Met Gln Lys Asn Val Glu
                245                 250                 255
Tyr Val Lys Ala Ser Leu Pro Phe Phe Pro Cys Leu Glu Thr Lys Ser
            260                 265                 270
Phe Asn
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<210> 5821
<211> 3292
<212> DNA
<213> Homo sapiens

<400> 5821
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120
taaaaaggaa aaaatataac ttagagcccc ctatgaaaaa ctaaattagc atcatgacag
180
gatacacttt ggggagtgaa atttcacagt acctttattt aattccaagc catagagcct
240
ggtaatattt ttctctttat cagctgtggc actaaaataa cagtggattt tttccctcta
300
gacattcttc ttttggccga tgaaaaattt gacttcgatc tttcattgtc ttcttcgagt
360
gcaaatgaag atgatgaagt cttcttcgga ccctttggac ataaagaaag atgtattgct
420
gccagcttgg aattaaataa tccggttccc gaacagcctc cgttgcccac atctgagagt
480
ccctttgcct ggagccctct ggccggggag aagttcgtgg aggtgtacaa agaagctcac
540
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600
gaagaccctc ggagccaggg cgtggaaaga ttcatacagg agtcaaaatt aaaaataaac
660

ctctttgaga aagaaaagga aatgaagaaa agccccacgt ctcttaaaag ggagacatac
720
tacctgtcag acagcccctt gctggggccc cctgtgggtg agcctcggct cttggcctcc
780
tccccggccc tgcccagctc tggtgcccag gcccgcctca cccgggcgcc ggggcctccg
840
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960
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1020
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1200
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1260
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1320
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1380
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1440
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1500
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1560
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1620
acaaatcaat ttaaaattcc taagttttct attggtgact ccccggacag ctcaacacca
1680
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1980
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2040
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2100
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2160
gatatcaaac tggaaccact cgcggtcact ccagatgctg caagccagcc cctcattgac
2220
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2280

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2400
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2460
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2520
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2580
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2820
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2880
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2940
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3060
taaatagtta gatattctag atttacatta aattgtaaaa taaatggact tattgaagca
3120
tatcttgatt tttaagctta tcttgatttt caaacatgca tagctatttt tatcactcta
3180
atcagtaagg ctactatcta gactcgaatg ctttcataca agtgattttc aaaaattagt
3240
caatataaat tgatgtcagt gcaggcccgg cccgccccca gatacactag tt
3292

<210> 5822
<211> 712
<212> PRT
<213> Homo sapiens

<400> 5822
Ile Leu Leu Leu Ala Asp Glu Lys Phe Asp Phe Asp Leu Ser Leu Ser
1 5 10 15
Ser Ser Ser Ala Asn Glu Asp Asp Glu Val Phe Phe Gly Pro Phe Gly
20 25 30
His Lys Glu Arg Cys Ile Ala Ala Ser Leu Glu Leu Asn Asn Pro Val
35 40 45
Pro Glu Gln Pro Pro Leu Pro Thr Ser Glu Ser Pro Phe Ala Trp Ser
50 55 60
Pro Leu Ala Gly Glu Lys Phe Val Glu Val Tyr Lys Glu Ala His Leu
65 70 75 80
Leu Ala Leu His Ile Glu Ser Ser Ser Arg Asn Gln Ala Ala Gln Ala
85 90 95
Ala Lys Pro Glu Asp Pro Arg Ser Gln Gly Val Glu Arg Phe Ile Gln

```
            100                 105                 110
Glu Ser Lys Leu Lys Ile Asn Leu Phe Glu Lys Glu Lys Glu Met Lys
        115                 120                 125
Lys Ser Pro Thr Ser Leu Lys Arg Glu Thr Tyr Tyr Leu Ser Asp Ser
    130                 135                 140
Pro Leu Leu Gly Pro Pro Val Gly Glu Pro Arg Leu Leu Ala Ser Ser
145                 150                 155                 160
Pro Ala Leu Pro Ser Ser Gly Ala Gln Ala Arg Leu Thr Arg Ala Pro
                165                 170                 175
Gly Pro Pro His Ser Ala His Ala Leu Pro Arg Glu Ser Cys Thr Ala
            180                 185                 190
His Ala Ala Ser Gln Ala Ala Thr Gln Arg Lys Pro Gly Thr Lys Leu
        195                 200                 205
Leu Leu Pro Arg Ala Ala Ser Val Arg Gly Arg Ser Ile Pro Gly Ala
    210                 215                 220
Ala Glu Lys Pro Lys Lys Glu Ile Pro Ala Ser Pro Ser Arg Thr Lys
225                 230                 235                 240
Ile Pro Ala Glu Lys Glu Ser His Arg Asp Val Leu Pro Asp Lys Pro
                245                 250                 255
Ala Pro Gly Ala Val Asn Val Pro Ala Ala Gly Ser His Leu Gly Gln
            260                 265                 270
Gly Lys Arg Ala Ile Pro Val Pro Asn Lys Leu Gly Leu Lys Lys Thr
        275                 280                 285
Leu Leu Lys Ala Pro Gly Ser Thr Ser Asn Leu Ala Arg Lys Ser Ser
    290                 295                 300
Ser Gly Pro Val Trp Ser Gly Ala Ser Ser Ala Cys Thr Ser Pro Ala
305                 310                 315                 320
Val Gly Lys Ala Lys Ser Ser Glu Phe Ala Ser Ile Pro Ala Asn Ser
                325                 330                 335
Ser Arg Pro Leu Ser Asn Ile Ser Lys Ser Gly Arg Met Gly Pro Ala
            340                 345                 350
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Gln Ala Lys Arg Val Asp Val Ser Glu Leu Ala Ala Glu Gln Leu Thr
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Thr Lys Val Met Pro Thr Pro Thr Asn Gln Phe Lys Ile Pro Lys Phe
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Ser Ile Gly Asp Ser Pro Asp Ser Ser Thr Pro Lys Leu Ser Arg Ala
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Gln Arg Pro Gln Ser Cys Thr Ser Val Gly Arg Val Thr Val His Ser
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Ala Trp Arg Val Ser Ala Leu Pro Thr Pro Ala Ser Arg Arg Cys Ser
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Gly Leu Pro Pro Met Thr Pro Lys Thr Met Pro Arg Ala Val Gly Ser
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Ser Lys Ser Thr Ala Thr Glu Val Ala Arg Glu Glu Ala Lys Pro Gly
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Gly Asp Ala Ala Pro Ser Glu Ala Leu Leu Val Asp Ile Lys Leu Glu
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Pro Leu Ala Val Thr Pro Asp Ala Ala Ser Gln Pro Leu Ile Asp Leu
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Pro Leu Ile Asp Phe Cys Asp Thr Pro Glu Ala His Val Ala Val Gly
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Ser Glu Ser Arg Pro Leu Ile Asp Leu Met Thr Asn Thr Pro Asp Met
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Asn Lys Asn Val Ala Lys Pro Ser Pro Val Val Gly Gln Leu Ile Asp
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<400> 5823

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Trp Glu Arg Pro Leu Phe Ile Lys Leu Gly Phe Phe Leu Ile Ser Leu
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Pro Asn Val Val Ser Gln Tyr Ser Ser Tyr Ser Ser Leu Gln Gly Val
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5700

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5747

<210> 5830
<211> 1479
<212> PRT
<213> Homo sapiens

<400> 5830
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20 25 30
Pro Gly Asp Ala Ala Leu Pro Glu Pro Asn Val Phe Leu Ile Phe Ser
35 40 45
His Gly Leu Gln Gly Cys Leu Glu Ala Gln Gly Gly Gln Val Arg Val
50 55 60
Thr Pro Ala Cys Asn Thr Ser Leu Pro Ala Gln Arg Trp Lys Trp Val
65 70 75 80
Ser Arg Asn Arg Leu Phe Asn Leu Gly Thr Met Gln Cys Leu Gly Thr
85 90 95
Gly Trp Pro Gly Thr Asn Thr Thr Ala Ser Leu Gly Met Tyr Glu Cys
100 105 110
Asp Arg Glu Ala Leu Asn Leu Arg Trp His Cys Arg Thr Leu Gly Asp
115 120 125
Gln Leu Ser Leu Leu Leu Gly Ala Arg Thr Ser Asn Ile Ser Lys Pro
130 135 140
Gly Thr Leu Glu Arg Gly Asp Gln Thr Arg Ser Gly Gln Trp Arg Ile
145 150 155 160
Tyr Gly Ser Glu Glu Asp Leu Cys Ala Leu Pro Tyr His Glu Val Tyr
165 170 175
Thr Ile Gln Gly Asn Ser His Gly Lys Pro Cys Thr Ile Pro Phe Lys
180 185 190
Tyr Asp Asn Gln Trp Phe His Gly Cys Thr Ser Thr Gly Arg Glu Asp
195 200 205
Gly His Leu Trp Cys Ala Thr Thr Gln Asp Tyr Gly Lys Asp Glu Arg
210 215 220
Trp Gly Phe Cys Pro Ile Lys Ser Asn Asp Cys Glu Thr Phe Trp Asp
225 230 235 240
Lys Asp Gln Leu Thr Asp Ser Cys Tyr Gln Phe Asn Phe Gln Ser Thr
245 250 255
Leu Ser Trp Arg Glu Ala Trp Ala Ser Cys Glu Gln Gln Gly Ala Asp
260 265 270
Leu Leu Ser Ile Thr Glu Ile His Glu Gln Thr Tyr Ile Asn Gly Leu
275 280 285
Leu Thr Gly Tyr Ser Ser Thr Leu Trp Ile Gly Leu Asn Asp Leu Asp
290 295 300
Thr Ser Gly Gly Trp Gln Trp Ser Asp Asn Ser Pro Leu Lys Tyr Leu
305 310 315 320
Asn Trp Glu Ser Asp Gln Pro Asp Asn Pro Ser Glu Glu Asn Cys Gly
325 330 335
Val Ile Arg Thr Glu Ser Ser Gly Gly Trp Gln Asn Arg Asp Cys Ser
340 345 350
Ile Ala Leu Pro Tyr Val Cys Lys Lys Lys Pro Asn Ala Thr Ala Glu

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        355                 360                 365
Pro Thr Pro Pro Asp Arg Trp Ala Asn Val Lys Val Glu Cys Glu Pro
    370                 375                 380
Ser Trp Gln Pro Phe Gln Gly His Cys Tyr Arg Leu Gln Ala Glu Lys
385                 390                 395                 400
Arg Ser Trp Gln Glu Ser Lys Lys Ala Cys Leu Arg Gly Gly Gly Asp
                405                 410                 415
Leu Val Ser Ile His Ser Met Ala Glu Leu Glu Phe Ile Thr Lys Gln
            420                 425                 430
Ile Lys Gln Glu Val Glu Glu Leu Trp Ile Gly Leu Asn Asp Leu Lys
        435                 440                 445
Leu Gln Met Asn Phe Glu Trp Ser Asp Gly Ser Leu Val Ser Phe Thr
    450                 455                 460
His Trp His Pro Phe Glu Pro Asn Asn Phe Arg Asp Ser Leu Glu Asp
465                 470                 475                 480
Cys Val Thr Ile Trp Gly Pro Glu Gly Arg Trp Asn Asp Ser Pro Cys
                485                 490                 495
Asn Gln Ser Leu Pro Ser Ile Cys Lys Lys Ala Gly Gln Leu Ser Gln
            500                 505                 510
Gly Ala Ala Glu Glu Asp His Gly Cys Arg Lys Gly Trp Thr Trp His
        515                 520                 525
Ser Pro Ser Cys Tyr Trp Leu Gly Glu Asp Gln Val Thr Tyr Ser Glu
    530                 535                 540
Ala Arg Arg Leu Cys Thr Asp His Gly Ser Gln Leu Val Thr Ile Thr
545                 550                 555                 560
Asn Arg Phe Glu Gln Ala Phe Val Ser Ser Leu Ile Tyr Asn Trp Glu
                565                 570                 575
Gly Glu Tyr Phe Trp Thr Ala Leu Gln Asp Leu Asn Ser Thr Gly Ser
            580                 585                 590
Phe Phe Trp Leu Ser Gly Asp Glu Val Met Tyr Thr His Trp Asn Arg
        595                 600                 605
Asp Gln Pro Gly Tyr Ser Arg Gly Gly Cys Val Ala Leu Ala Thr Gly
    610                 615                 620
Ser Ala Met Gly Leu Trp Glu Val Lys Asn Cys Thr Ser Phe Arg Ala
625                 630                 635                 640
Arg Tyr Ile Cys Arg Gln Ser Leu Gly Thr Pro Val Thr Pro Glu Leu
                645                 650                 655
Pro Gly Pro Asp Pro Thr Pro Ser Leu Thr Gly Ser Cys Pro Gln Gly
            660                 665                 670
Trp Ala Ser Asp Thr Lys Leu Arg Tyr Cys Tyr Lys Val Phe Ser Ser
        675                 680                 685
Glu Arg Leu Gln Asp Lys Lys Ser Trp Val Gln Ala Gln Gly Ala Cys
    690                 695                 700
Gln Glu Leu Gly Ala Gln Leu Leu Ser Leu Ala Ser Tyr Glu Glu Glu
705                 710                 715                 720
His Phe Val Ala Asn Met Leu Asn Lys Ile Phe Gly Glu Ser Glu Pro
                725                 730                 735
Glu Ile His Glu Gln His Trp Phe Trp Ile Gly Leu Asn Arg Arg Asp
            740                 745                 750
Pro Arg Gly Gly Gln Ser Trp Arg Trp Ser Asp Gly Val Gly Phe Ser
        755                 760                 765
Tyr His Asn Phe Asp Arg Ser Arg His Asp Asp Asp Asp Ile Arg Gly
    770                 775                 780
Cys Ala Val Leu Asp Leu Ala Ser Leu Gln Trp Val Ala Met Gln Cys
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785 790 795 800
Asp Thr Gln Leu Asp Trp Ile Cys Lys Ile Pro Arg Gly Thr Asp Val
805 810 815
Arg Glu Pro Asp Asp Ser Pro Gln Gly Arg Arg Glu Trp Leu Arg Phe
820 825 830
Gln Glu Ala Glu Tyr Lys Phe Phe Glu His His Ser Thr Trp Ala Gln
835 840 845
Ala Gln Arg Ile Cys Thr Trp Phe Gln Ala Glu Leu Thr Ser Val His
850 855 860
Ser Gln Ala Glu Leu Asp Phe Leu Ser His Asn Leu Gln Lys Phe Ser
865 870 875 880
Arg Ala Gln Glu Gln His Trp Trp Ile Gly Leu His Thr Ser Glu Ser
885 890 895
Asp Gly Arg Phe Arg Trp Thr Asp Gly Ser Ile Ile Asn Phe Ile Ser
900 905 910
Trp Ala Pro Gly Lys Pro Arg Pro Val Gly Lys Asp Lys Lys Cys Val
915 920 925
Tyr Met Thr Ala Ser Arg Glu Asp Trp Gly Asp Gln Arg Cys Leu Thr
930 935 940
Ala Leu Pro Tyr Ile Cys Lys Arg Ser Asn Val Thr Lys Glu Thr Gln
945 950 955 960
Pro Pro Asp Leu Pro Thr Thr Ala Leu Gly Gly Cys Pro Ser Asp Trp
965 970 975
Ile Gln Phe Leu Asn Lys Cys Phe Gln Val Gln Gly Gln Glu Pro Gln
980 985 990
Ser Arg Val Lys Trp Ser Glu Ala Gln Phe Ser Cys Glu Gln Gln Glu
995 1000 1005
Ala Gln Leu Val Thr Ile Thr Asn Pro Leu Glu Gln Ala Phe Ile Thr
1010 1015 1020
Ala Ser Leu Pro Asn Val Thr Phe Asp Leu Trp Ile Gly Leu His Ala
1025 1030 1035 1040
Ser Gln Arg Asp Phe Gln Trp Val Glu Gln Glu Pro Leu Met Tyr Ala
1045 1050 1055
Asn Trp Ala Pro Gly Glu Pro Ser Gly Pro Ser Pro Ala Pro Ser Gly
1060 1065 1070
Asn Lys Pro Thr Ser Cys Ala Val Val Leu His Ser Pro Ser Ala His
1075 1080 1085
Phe Thr Gly Arg Trp Asp Asp Arg Ser Cys Thr Glu Glu Thr His Gly
1090 1095 1100
Phe Ile Cys Gln Lys Gly Thr Asp Pro Ser Leu Ser Pro Ser Pro Ala
1105 1110 1115 1120
Ala Leu Pro Pro Ala Pro Gly Thr Glu Leu Ser Tyr Leu Asn Gly Thr
1125 1130 1135
Phe Arg Leu Leu Gln Lys Pro Leu Arg Trp His Asp Ala Leu Leu Leu
1140 1145 1150
Cys Glu Ser His Asn Ala Ser Leu Ala Tyr Val Pro Asp Pro Tyr Thr
1155 1160 1165
Gln Ala Phe Leu Thr Gln Ala Ala Arg Gly Leu Arg Thr Pro Leu Trp
1170 1175 1180
Ile Gly Leu Ala Gly Glu Glu Gly Ser Arg Arg Tyr Ser Trp Val Ser
1185 1190 1195 1200
Glu Glu Pro Leu Asn Tyr Val Gly Trp Gln Asp Gly Glu Pro Gln Gln
1205 1210 1215
Pro Gly Gly Cys Thr Tyr Val Asp Val Asp Gly Ala Trp Arg Thr Thr

1220 1225 1230
Ser Cys Asp Thr Lys Leu Gln Gly Ala Val Cys Gly Val Ser Ser Gly
1235 1240 1245
Pro Pro Pro Pro Arg Arg Ile Ser Tyr His Gly Ser Cys Pro Gln Gly
1250 1255 1260
Leu Ala Asp Ser Ala Trp Ile Pro Phe Arg Glu His Cys Tyr Ser Phe
1265 1270 1275 1280
His Met Glu Leu Leu Leu Gly His Lys Glu Ala Arg Gln Arg Cys Gln
1285 1290 1295
Arg Ala Gly Gly Ala Val Leu Ser Ile Leu Asp Glu Met Glu Asn Val
1300 1305 1310
Phe Val Trp Glu His Leu Gln Ser Tyr Glu Gly Gln Ser Arg Gly Ala
1315 1320 1325
Trp Leu Gly Met Asn Phe Asn Pro Lys Gly Gly Thr Leu Val Trp Gln
1330 1335 1340
Asp Asn Thr Ala Val Asn Tyr Ser Asn Trp Gly Pro Pro Gly Leu Gly
1345 1350 1355 1360
Pro Ser Met Leu Ser His Asn Ser Cys Tyr Trp Ile Gln Ser Asn Ser
1365 1370 1375
Gly Leu Trp Arg Pro Gly Ala Cys Thr Asn Ile Thr Met Gly Val Val
1380 1385 1390
Cys Lys Leu Pro Arg Ala Glu Gln Ser Ser Phe Ser Pro Ser Ala Leu
1395 1400 1405
Pro Glu Asn Pro Ala Ala Leu Val Val Val Leu Met Ala Val Leu Leu
1410 1415 1420
Leu Leu Ala Leu Leu Thr Ala Ala Leu Ile Leu Tyr Arg Arg Arg Gln
1425 1430 1435 1440
Ser Ile Glu Arg Gly Ala Phe Glu Gly Ala Arg Tyr Ser Arg Ser Ser
1445 1450 1455
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Glu Met Asn Glu Gln Gln Glu
1475

<210> 5831
<211> 2216
<212> DNA
<213> Homo sapiens

<400> 5831
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actcttaagt tctcagcact atgttatgca cttgacgggc attactttaa tcctccactg
180
tgagatactt gttattgcct cattttgtag acgagaaaac gggcatagag ggtgagacat
240
tggcccaggt tcattccgta agggttggag cctggaattc agatacagga ggaagttaac
300
atccctaata ggagggttct ggttactggt gccactgggc ttcttggcag agctgtacac
360
aaagaatttc agcagaataa ttggcatgca gttggctgtg gtttcagaag agcaagacca
420

aaatttgaac aggttaatct gttggattct aatgcagttc atcacatcat tcatgatttt
480
cagccccatg ttatagtaca ttgtgcagca gagagaagac cagatgttgt agaaaatcag
540
ccagatgctg cctctcaact taatgtggat gcttctggga atttagcaaa ggaagcagct
600
gctgttggag catttctcat ctacattagc tcagattatg tatttgatgg aacaaatcca
660
ccttacagag aggaagacat accagctccc ctaaatttgt atggcaaaac aaaattagat
720
ggagaaaagg ctgtcctgga gaacaatcta ggagctgctg ttttgaggat tcctattctg
780
tatggggaag ttgaaaagct cgaagaaagt gctgtgactg ttatgtttga taaagtgcag
840
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900
gatgtggcca ctgtgtgccg gcagctagca gagaagagaa tgctggatcc atcaattaag
960
ggaacctttc actggtctgg caatgaacag atgactaagt atgaaatggc atgtgcaatt
1020
gcagatgcct tcaacctccc cagcagtcac ttaagaccta ttactgacag ccctgtccta
1080
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1140
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aagagatgga gacaaacggt ctttcattag tttatttgtg ttgggttctt ttttttttt
1260
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1320
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1380
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1440
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1560
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1620
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1680
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1740
caacatgtta tgtatattgg aacttctaca gcttgatgcc tcctgctttt atagcagttt
1800
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1860
caaacgtgta ttttttaat ataaatatat aactgtcctt ttcatcccat gttgccgcta
1920
agtgatattt catatgtgtg gttatactca taataatggg ccttgtaagt cttttcacca
1980
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2040

ttctttttt aaatgtaagg accaaacttc taaactaatt gttcttttgt tgctttaatt
2100
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2216

<210> 5832
<211> 322
<212> PRT
<213> Homo sapiens

<400> 5832
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Arg Arg Val Leu Val Thr Gly Ala Thr Gly Leu Leu Gly Arg Ala Val
20 25 30
His Lys Glu Phe Gln Gln Asn Asn Trp His Ala Val Gly Cys Gly Phe
35 40 45
Arg Arg Ala Arg Pro Lys Phe Glu Gln Val Asn Leu Leu Asp Ser Asn
50 55 60
Ala Val His His Ile Ile His Asp Phe Gln Pro His Val Ile Val His
65 70 75 80
Cys Ala Ala Glu Arg Arg Pro Asp Val Val Glu Asn Gln Pro Asp Ala
85 90 95
Ala Ser Gln Leu Asn Val Asp Ala Ser Gly Asn Leu Ala Lys Glu Ala
100 105 110
Ala Ala Val Gly Ala Phe Leu Ile Tyr Ile Ser Ser Asp Tyr Val Phe
115 120 125
Asp Gly Thr Asn Pro Pro Tyr Arg Glu Glu Asp Ile Pro Ala Pro Leu
130 135 140
Asn Leu Tyr Gly Lys Thr Lys Leu Asp Gly Glu Lys Ala Val Leu Glu
145 150 155 160
Asn Asn Leu Gly Ala Ala Val Leu Arg Ile Pro Ile Leu Tyr Gly Glu
165 170 175
Val Glu Lys Leu Glu Glu Ser Ala Val Thr Val Met Phe Asp Lys Val
180 185 190
Gln Phe Ser Asn Lys Ser Ala Asn Met Asp His Trp Gln Gln Arg Phe
195 200 205
Pro Thr His Val Lys Asp Val Ala Thr Val Cys Arg Gln Leu Ala Glu
210 215 220
Lys Arg Met Leu Asp Pro Ser Ile Lys Gly Thr Phe His Trp Ser Gly
225 230 235 240
Asn Glu Gln Met Thr Lys Tyr Glu Met Ala Cys Ala Ile Ala Asp Ala
245 250 255
Phe Asn Leu Pro Ser Ser His Leu Arg Pro Ile Thr Asp Ser Pro Val
260 265 270
Leu Gly Ala Gln Arg Pro Arg Asn Ala Gln Leu Asp Cys Ser Lys Leu
275 280 285
Glu Thr Leu Gly Ile Gly Gln Arg Thr Pro Phe Arg Ile Gly Ile Lys
290 295 300
Glu Ser Leu Trp Pro Phe Leu Ile Asp Lys Arg Trp Arg Gln Thr Val
305 310 315 320
Phe His

<210> 5833
<211> 805
<212> DNA
<213> Homo sapiens

<400> 5833
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gaaacatgtc caaaaggaga cgagccaaga ggtgacgagc aacaggtgga aagtatgacc
120
cctaaacctg tgctccagga agaaaacaac caagagtctt ttattgcatt tgctcgggtg
180
ttcagtggtg tggctcgaag aggaaagaaa atttttgtct tggggcccaa atacagtcct
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cttgagtttt tacgaagggt accattaggc ttctcagctc caccagatgg cctcccccaa
300
gtcccccaca tggcatactg tgctctggaa aacctgtatc ttctgatggg aagggaactg
360
gaatatctag aggaggtacc tccaggaaat gtgctaggaa taggaggcct tcaagatttt
420
gtgctgaaat ctgcaacact gtgtagcctg ccatcctgcc caccatttat accactcaac
480
ttcgaagcca ctcctattgt gagagttgct gttgaaccaa aacatccaag tgaaatgcct
540
cagctcgtaa aaggaatgaa actgttaaac caggctgatc cctgtgtcca gattttaatt
600
caggaaacgg gagagcacgt tttagtcaca gcaggagaag tccaccttca gcgatgcctg
660
gatgacttaa aagaaaggtt tgcaaagatt catatcagtg tatctgaacc tattattcca
720
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780
cagcaaaaag ttgcagtcat acacc
805

<210> 5834
<211> 268
<212> PRT
<213> Homo sapiens

<400> 5834
Lys Leu Ala Ala Ala Gln Gly Gln Ala Pro Leu Glu Pro Thr Gln Asp
 1   5   10   15
Gly Ser Ala Ile Glu Thr Cys Pro Lys Gly Asp Glu Pro Arg Gly Asp
            20   25   30
Glu Gln Gln Val Glu Ser Met Thr Pro Lys Pro Val Leu Gln Glu Glu
        35   40   45
Asn Asn Gln Glu Ser Phe Ile Ala Phe Ala Arg Val Phe Ser Gly Val
    50   55   60
Ala Arg Arg Gly Lys Lys Ile Phe Val Leu Gly Pro Lys Tyr Ser Pro
65   70   75   80
Leu Glu Phe Leu Arg Arg Val Pro Leu Gly Phe Ser Ala Pro Pro Asp

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                85                  90                  95
Gly Leu Pro Gln Val Pro His Met Ala Tyr Cys Ala Leu Glu Asn Leu
            100                 105                 110
Tyr Leu Leu Met Gly Arg Glu Leu Glu Tyr Leu Glu Glu Val Pro Pro
        115                 120                 125
Gly Asn Val Leu Gly Ile Gly Gly Leu Gln Asp Phe Val Leu Lys Ser
    130                 135                 140
Ala Thr Leu Cys Ser Leu Pro Ser Cys Pro Pro Phe Ile Pro Leu Asn
145                 150                 155                 160
Phe Glu Ala Thr Pro Ile Val Arg Val Ala Val Glu Pro Lys His Pro
                165                 170                 175
Ser Glu Met Pro Gln Leu Val Lys Gly Met Lys Leu Leu Asn Gln Ala
            180                 185                 190
Asp Pro Cys Val Gln Ile Leu Ile Gln Glu Thr Gly Glu His Val Leu
        195                 200                 205
Val Thr Ala Gly Glu Val His Leu Gln Arg Cys Leu Asp Asp Leu Lys
    210                 215                 220
Glu Arg Phe Ala Lys Ile His Ile Ser Val Ser Glu Pro Ile Ile Pro
225                 230                 235                 240
Phe Arg Glu Thr Ile Thr Lys Pro Pro Lys Val Asp Met Val Asn Glu
                245                 250                 255
Glu Ile Gly Lys Gln Gln Lys Val Ala Val Ile His
            260                 265
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<210> 5835
<211> 420
<212> DNA
<213> Homo sapiens

<400> 5835
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120
gcactgcata agcaagttct tatgggccca tataatccag acacttgtcc tgaggttgga
180
ttctttgatg tgttggggaa tgacaggagg agagaatggg cagccctggg aaacatgtct
240
aaagaggatg ccatggtgga gtttgtcaag ctcttaaata ggtgttgcca tctcttttca
300
acatatgttg cgtcccacaa aatagagaag gaagagcaag acaaaaaaag gaaggaggaa
360
gaggagcgaa ggcggcgtga agaggaagaa agagaacgtc tgcaaaagga ggaagagaaa
420

<210> 5836
<211> 140
<212> PRT
<213> Homo sapiens

<400> 5836
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Xaa Leu Glu Gln Arg Trp Gly Phe Gly Leu Glu Glu Leu Tyr Gly Leu
 1               5                  10                  15
Ala Leu Arg Phe Phe Lys Glu Lys Asp Gly Lys Ala Phe His Pro Thr
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            20                  25                  30
Tyr Glu Glu Lys Leu Lys Leu Val Ala Leu His Lys Gln Val Leu Met
        35                  40                  45
Gly Pro Tyr Asn Pro Asp Thr Cys Pro Glu Val Gly Phe Phe Asp Val
    50                  55                  60
Leu Gly Asn Asp Arg Arg Arg Glu Trp Ala Ala Leu Gly Asn Met Ser
65                  70                  75                  80
Lys Glu Asp Ala Met Val Glu Phe Val Lys Leu Leu Asn Arg Cys Cys
                85                  90                  95
His Leu Phe Ser Thr Tyr Val Ala Ser His Lys Ile Glu Lys Glu Glu
            100                 105                 110
Gln Asp Lys Lys Arg Lys Glu Glu Glu Glu Arg Arg Arg Arg Glu Glu
        115                 120                 125
Glu Glu Arg Glu Arg Leu Gln Lys Glu Glu Glu Lys
    130                 135                 140
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<210> 5837
<211> 582
<212> DNA
<213> Homo sapiens

<400> 5837
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120
tgggccaagg gggacatcca gggggcaggg gccgcctccc gccgtgcctt cctgctgggg
180
gtcctcgccg tcgggctggg cgtgtgcacg tatgcggctg ccctggtgac cctggccgcc
240
taccttgcct cccgagaccc gccctagttg cccctacagc cctcactgtg aaccctgagg
300
ccggcagccc agcaaatctg tgggcagaga gtggagaatc ttggtggatg aggctgcggc
360
ggcggcagga gcatctagaa acgggagcga gctggactgg aacccttccc cttcctggcc
420
accgctcttc gggcggcagc aacctgagat taaacaccag acacccttgg cctgggctca
480
cgaggaaggg gctgcagttc tccaaggatt cccgcctgct cccagatccc cgggagtcgt
540
aggaacccgt tcctggacgc tgacgtcggc tttcagggat cc
582

<210> 5838
<211> 88
<212> PRT
<213> Homo sapiens

<400> 5838
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Xaa Arg Leu Ser Pro Phe Leu Pro His Asp His Leu Gly Leu Ala Val
 1               5                  10                  15
Phe Ser Met Leu Cys Cys Phe Trp Pro Val Gly Ile Ala Ala Phe Cys
            20                  25                  30
Leu Ala Gln Lys Thr Asn Lys Ala Trp Ala Lys Gly Asp Ile Gln Gly
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35 40 45
Ala Gly Ala Ala Ser Arg Arg Ala Phe Leu Leu Gly Val Leu Ala Val
50 55 60
Gly Leu Gly Val Cys Thr Tyr Ala Ala Ala Leu Val Thr Leu Ala Ala
65 70 75 80
Tyr Leu Ala Ser Arg Asp Pro Pro
85

<210> 5839
<211> 1895
<212> DNA
<213> Homo sapiens

<400> 5839
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aaatattaaa caataaataa aacagagcgg gggctgagga aagcaggatc ttgctgaagt
120
cattcgaatg catcccaacc agtgctcagc tgcgtaacga catggagaga ggcaggggggg
180
aatagaaagc aaatttaaaa acaccaacac ccaaacacac aagactgcac acaagaaaaa
240
gtgctcaaga aactttggct ttgaagggaa ttcagtgaag ggaagcgatt gtgcaggagg
300
aagggaagaa acccacgatc accctaaggg gcgggggggct ggagggcgag gccctgagac
360
aggctagggt taaagctgac gtcccacagc tcaggacgta caaccgatgg cagttttgta
420
ctaggaagaa gctgagtgat gaggctgggt gatgggatcg cttgacgggc tgggagggag
480
gacaggaggt gtaaaggtgg ctcaccttcc cctaggaaat tcagtgctct tttggtaaga
540
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600
gccttttctt ctaagttttc ctccttttct ttgcacaggt gtcaggtagc accccagggg
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tgcaggagct ggtgttttca tgacaaacaa aaatggggag gttgactcta tctcaaaact
720
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840
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900
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960
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1020
aatgttcttt gtggtttgaa tcctggcaga ggccagggtc acatccaagt gggactggcc
1080
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Ser Gly Phe Tyr Trp Asn Gly Val Ala Val Phe Pro Lys Pro Pro Pro
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Asp Gly Val Tyr Pro Asn Met Ser Glu Pro Val Thr Pro Ala Asn Ile
115 120 125
Asn Leu Tyr Ala Glu Ala Leu Val Ala Asn Val Lys Gln Arg Ala Ala
130 135 140
Trp Phe Arg Thr Pro His Val Leu Trp Pro Trp Gly Cys Asp Lys Gln
145 150 155 160
Phe Phe Asn Ala Ser Val Gln Phe Ala Asn Met Asp Pro Leu Leu Asp

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                165                 170                 175
His Ile Asn Ser His Ala Ala Glu Leu Gly Val Ser Val Gln Tyr Ala
            180                 185                 190
Thr Leu Gly Asp Tyr Phe Arg Ala Leu His Ala Leu Asn Val Thr Trp
        195                 200                 205
Arg Val Arg Asp His His Asp Phe Leu Pro Tyr Ser Thr Glu Pro Phe
    210                 215                 220
Gln Ala Trp Thr Gly Phe Tyr Thr Ser Arg Ser Ser Leu Lys Gly Leu
225                 230                 235                 240
Ala Arg Arg Ala Ser Ala Leu Leu Tyr Ala Gly Glu Ser Met Phe Thr
                245                 250                 255
Arg Tyr Leu Trp Pro Ala Pro Arg Gly His Leu Asp Pro Thr Trp Ala
            260                 265                 270
Leu Gln Gln Leu Gln Gln Leu Arg Trp Ala Val Ser Glu Val Gln His
        275                 280                 285
His Asp Ala Ile Thr Gly Thr Glu Ser Pro Lys Val Arg Asp Met Tyr
    290                 295                 300
Ala Thr His Leu Ala Ser Gly Met Leu Gly Val Arg Lys Leu Met Ala
305                 310                 315                 320
Ser Ile Val Leu Asp Glu Leu Gln Pro Gln Ala Pro Met Ala Ala Ser
                325                 330                 335
Ser Asp Ala Gly Pro Ala Gly His Phe Ala Ser Val Tyr Asn Pro Leu
            340                 345                 350
Ala Trp Thr Val Thr Thr Ile Val Thr Leu Thr Val Gly Phe Pro Gly
        355                 360                 365
Val Arg Val Thr Asp Glu Ala Gly His Pro Val Pro Ser Gln Ile Gln
    370                 375                 380
Asn Ser Thr Glu Thr Pro Ser Ala Tyr Asp Leu Leu Ile Leu Thr Thr
385                 390                 395                 400
Ile Pro Gly Leu Ser Tyr Arg His Tyr Ser Ile Arg Pro Thr Ala Gly
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Ala Gln Glu Gly Thr Gln Glu Pro Ala Ala Thr Val Ala Ser Thr Leu
            420                 425                 430
Gln Phe Gly Arg Arg Leu Arg Arg Arg Thr Ser His Ala Gly Arg Tyr
        435                 440                 445
Leu Val Pro Val Ala Asn Asp Cys Tyr Ile Val Leu Leu Asp Gln Asp
    450                 455                 460
Thr Asn Leu Met His Ser Ile Trp Glu Arg Gln Ser Asn Arg Thr Val
465                 470                 475                 480
Arg Val Thr Gln Glu Phe Leu Glu Tyr His Val Asn Arg Asp Val Lys
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Gln Gly Pro Ile Ser Asp Asn Tyr Leu Phe Thr Pro Gly Lys Ala Ala
            500                 505                 510
Val Pro Ala Trp Glu Ala Val Glu Met Glu Ile Val Ala Gly Gln Leu
        515                 520                 525
Val Thr Glu Ile Arg Gln Tyr Phe Tyr Arg Asn Met Thr Ala Gln Asn
    530                 535                 540
Tyr Thr Tyr Ala Ile Arg Ser Arg Leu Thr His Val Pro Gln Gly His
545                 550                 555                 560
Asp Gly Glu Leu Leu Cys His Arg Ile Glu Gln Glu Tyr Gln Ala Gly
                565                 570                 575
Pro Leu Glu Leu Asn Arg Glu Ala Val Leu Arg Thr Ser Thr Asn Leu
            580                 585                 590
Asn Ser Gln Gln Val Ile Tyr Ser Asp Asn Asn Gly Tyr Gln Met Gln
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Arg Arg Pro Tyr Val Ser Tyr Val Asn Asn Ser Ile Ala Arg Asn Tyr
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Tyr Pro Met Val Gln Ser Ala Phe Met Glu Asp Gly Lys Ser Arg Leu
625                 630                 635                 640
Val Leu Leu Ser Glu Arg Ala His Gly Ile Ser Ser Gln Gly Asn Gly
                645                 650                 655
Gln Val Glu Val Met Leu His Arg Arg Leu Trp Asn Asn Phe Asp Trp
            660                 665                 670
Asp Leu Gly Tyr Asn Leu Thr Leu Asn Asp Thr Ser Val Val His Pro
        675                 680                 685
Val Leu Trp Leu Leu Leu Gly Ser Trp Ser Leu Thr Thr Ala Leu Arg
    690                 695                 700
Gln Arg Ser Ala Leu Ala Leu Gln His Arg Pro Val Val Leu Phe Gly
705                 710                 715                 720
Asp Leu Ala Gly Thr Ala Pro Lys Leu Pro Gly Pro Gln Gln Gln Glu
                725                 730                 735
Ala Val Thr Leu Pro Pro Asn Leu His Leu Gln Ile Leu Ser Ile Pro
            740                 745                 750
Gly Trp Arg Tyr Ser Ser Asn His Thr Glu His Ser Gln Asn Leu Arg
        755                 760                 765
Lys Gly His Arg Gly Glu Ala Gln Ala Asp Leu Arg Arg Val Leu Leu
    770                 775                 780
Arg Leu Tyr His Leu Tyr Glu Val Gly Glu Asp Pro Val Leu Ser Gln
785                 790                 795                 800
Pro Val Thr Val Asn Leu Glu Val Asn Phe Pro Thr Pro Ile Gln Thr
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Ile Ser Gln Gly Ser Lys Pro
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<210> 5845
<211> 2762
<212> DNA
<213> Homo sapiens

<400> 5845

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2160
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2220

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2280
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2762

<210> 5846
<211> 257
<212> PRT
<213> Homo sapiens

<400> 5846
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Gln Gln Glu Lys Glu Trp Leu Leu Ala Glu Glu Thr Ala Ala Thr Ala
        35   40   45
Ser Ala Ile Glu Ala Met Lys Lys Ala Tyr Gln Glu Glu Leu Ser Arg
    50   55   60
Glu Leu Ser Lys Thr Arg Ser Leu Gln Gln Gly Pro Asp Gly Leu Arg
65   70   75   80
Lys Gln His Gln Ser Asp Val Glu Ala Leu Lys Arg Glu Leu Gln Val
                85   90   95
Leu Ser Glu Gln Tyr Ser Gln Lys Cys Leu Glu Ile Gly Ala Leu Met
            100   105   110
Arg Gln Ala Glu Glu Arg Glu His Thr Leu Arg Arg Cys Gln Gln Glu
        115   120   125
Gly Gln Glu Leu Leu Arg His Asn Gln Glu Leu His Gly Arg Leu Ser
    130   135   140
Glu Glu Ile Asp Gln Leu Arg Gly Phe Ile Ala Ser Gln Gly Met Gly
145   150   155   160
Asn Gly Cys Gly Arg Ser Asn Glu Arg Ser Ser Cys Glu Leu Glu Val
                165   170   175
Leu Leu Arg Val Lys Glu Asn Glu Leu Gln Tyr Leu Lys Lys Glu Val
            180   185   190
Gln Cys Leu Arg Asp Glu Leu Gln Met Met Gln Lys Asp Lys Arg Phe
        195   200   205
Thr Ser Gly Lys Tyr Gln Asp Val Tyr Val Glu Leu Ser His Ile Lys

210 215 220
Thr Arg Ser Glu Arg Glu Ile Glu Gln Leu Lys Glu His Leu Arg Leu
225 230 235 240
Ala Met Ala Ala Leu Gln Glu Lys Glu Ser Met Arg Asn Ser Leu Ala
245 250 255
Glu

<210> 5847
<211> 1021
<212> DNA
<213> Homo sapiens

<400> 5847
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120
cgagccctct ccacatttct atttggatcc attcgaggtg cagcccccgt ggctgtggaa
180
cccggggcag cagtgcgctc acttctctca cccggcctcc tgccccatct gctgcctgcg
240
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300
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<210> 5848
<211> 120
<212> PRT

<213> Homo sapiens

<400> 5848

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Asn Met Ala Asn Leu Phe Ile Arg Lys Met Val Asn Pro Leu Leu Tyr
            20                  25                  30
Leu Ser Arg His Thr Val Lys Pro Arg Ala Leu Ser Thr Phe Leu Phe
        35                  40                  45
Gly Ser Ile Arg Gly Ala Ala Pro Val Ala Val Glu Pro Gly Ala Ala
    50                  55                  60
Val Arg Ser Leu Leu Ser Pro Gly Leu Leu Pro His Leu Leu Pro Ala
65                  70                  75                  80
Leu Gly Phe Lys Asn Lys Thr Val Leu Lys Lys Arg Cys Lys Asp Cys
                85                  90                  95
Tyr Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr Cys Lys Thr His
            100                 105                 110
Pro Arg His Lys Gln Arg Gln Met
        115                 120
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<210> 5849
<211> 3174
<212> DNA
<213> Homo sapiens

<400> 5849

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aaaaatctca agaccacagg acagcgtgag ccccaccccc ctcccccaat gaccccagca
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tgcggtaatg ccaggcgggt ggcccctggg catgcggggg ggagtgatgc atggaaggaa
240
aagccaccgg ccatggaaat tagtacagaa ccccccccaca cacactcaga cacaggatac
300
agggtggacg acacctagcc ggggtgggaa ggatgggaat tgaaacccac acagcctgct
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420
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480
ctcttaccca gcctgggcag ggggctctgc cctgagggcg ggccaaggaa caatggggaa
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gtttatgtgg acaaaccagt tcccaagcta cttcccactt ctccctcctc caaccagaag
600
gggggaaaag ggagaggcca cagggcaaag agtgtattag ggcctgagct gcagctgcct
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720
gcatctggaa gcggctagag gcctgctgag atcctcctct ccctctggcc tcctctcgga
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840
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<210> 5850
<211> 154
<212> PRT
<213> Homo sapiens

<400> 5850
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His Ser Val Pro Ala Tyr Pro Trp Asp Trp Gly His Leu Ile Arg Phe
20 25 30
Cys Thr Gln Thr Gly His Ala Gln Pro Cys Pro Ser Ala Pro Ser Thr
35 40 45
Gly Pro Ile His Ile Ala Glu Gly Gly Arg Gly Arg Pro Pro Pro Gly
50 55 60
Ser Ala Ser Asn Pro Gln Pro Pro Gly Ser Pro His Cys Pro Ser Ala
65 70 75 80
Gly Leu Ser Pro Val Pro Gly Val Gly Gly Arg Gln Cys Pro Gly Thr
85 90 95
Val Pro Arg Val Arg Arg Pro Gly Leu Ala Gly His Pro Val Thr His
100 105 110
Arg Ile Asn Arg Lys Thr Ala Ser Pro Pro Asn Leu Cys Pro Arg His
115 120 125
Asn Met Ser Arg Ser Glu Ser Cys Thr Pro Arg Ser Arg Ala Pro Leu
130 135 140
Gln Arg Thr Leu Thr Pro Pro Arg Gly Ala
145 150

<210> 5851
<211> 488

<212> DNA
<213> Homo sapiens

<400> 5851
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cttggtttgg tctcaaaggc aaaaggaaag gacgaggaag gggccaggcc tcccgccagg
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240
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tgacgcgt
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<210> 5852
<211> 82
<212> PRT
<213> Homo sapiens

<400> 5852
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20 25 30
Leu Thr Lys Gly Thr Ser Ala Ala His Leu Asn Ser Met Glu Val Thr
35 40 45
Thr Glu Asp Thr Ser Arg Thr Asp Ala Tyr Glu Ser Tyr Lys Lys Lys
50 55 60
Asp Tyr Thr Gln Val Asp Tyr Leu Ile Asn Gly Met Tyr Ala Asp Ser
65 70 75 80
Glu Met

<210> 5853
<211> 487
<212> DNA
<213> Homo sapiens

<400> 5853
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120
tcaggcccag cagctccatg gaggacgccg gcgaggaccc caccacgttt gctgcccact
180

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300
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360
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480
ctttccg
487

<210> 5854
<211> 68
<212> PRT
<213> Homo sapiens

<400> 5854
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Tyr Arg Arg Ser Gln Glu Gly Gly Pro Ala Arg Pro Ala Ala Pro Asp
20 25 30
Thr Pro Ser Gly Arg Ser Gly Pro Ala Ala Pro Trp Arg Thr Pro Ala
35 40 45
Arg Thr Pro Pro Arg Leu Leu Pro Thr Leu Cys Pro Val Thr Pro Val
50 55 60
Ser Trp Pro Leu
65

<210> 5855
<211> 362
<212> DNA
<213> Homo sapiens

<400> 5855
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180
taacgaggtt gttgcagaag tcctcctggc ggcacacgaa ggtgtaggag atcagggaga
240
ggccggggcc catccggtgc tcagtgacgc ggggctcctg gtccttggcc tccgtgcagc
300
ccttggagag caccaggctc acttggggtc cgctctcaat gagcatcaac gtgtcctggc
360
an
362

<210> 5856
<211> 113
<212> PRT

<213> Homo sapiens

<400> 5856
Met Glu Pro Ala Arg Val Gly Ile Ala Ser Glu Gly Gly Arg Asp Ser
1 5 10 15
Val Thr Ala Pro Leu Cys Ser Ala Asp Pro Leu Leu Ala Val Pro Pro
20 25 30
Ser Pro Pro Asp Pro Pro Ala Gly Thr Cys Trp Gly Leu Trp Gly Pro
35 40 45
Lys Arg Glu Gly Val Asn Glu Val Val Ala Glu Val Leu Leu Ala Ala
50 55 60
His Glu Gly Val Gly Asp Gln Gly Glu Ala Gly Ala His Pro Val Leu
65 70 75 80
Ser Asp Ala Gly Leu Leu Val Leu Gly Leu Arg Ala Ala Leu Gly Glu
85 90 95
His Gln Ala His Leu Gly Ser Ala Leu Asn Glu His Gln Arg Val Leu
100 105 110
Ala

<210> 5857
<211> 1751
<212> DNA
<213> Homo sapiens

<400> 5857
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aggcgtggga ggaagatgga ctcggtggag aaggggccg ccacctccgt ctccaacccg
120
cgggggcgac cgtcccgggg ccggccgccg aagctgcagc gcaactctcg cggcggccag
180
ggccgaggtg gggagaagcc cccgcacctg gcagccctaa ttctggcccg gggaggcagc
240
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300
ctgcgtgcgg ccctggattc aggggccttc cagagtgtat gggtttcgac agaccatgat
360
gaaattgaga atgtggccaa acaatttggt gcacaagttc atcgaagaag ttctgaagtt
420
tcaaaagaca gctctacctc actagatgcc atcatagaat ttcttaatta tcataatgag
480
gttgacattg taggaaatat tcaagctact tctccatgtt tacatcctac tgatcttcaa
540
aaagttgcag aaatgattcg agaagaagca tatgattctg ttttctctgt tgtgagacgc
600
catcagtttc gatggagtga aattcagaaa ggagttcgtg aagtgaccga acctctgaat
660
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720
tcattttatt ttgctaaaag acatttgata gagatgggtt acttgcaggg tggaaaaatg
780
gcatactacg aaatgcgagc tgaacatagt gtggatatag atgtggatat tgattggcct
840

attgcagagc aaagagtatt aagatatggc tattttggca aagagaagct taaggaaata
900
aaacttttgg tttgcaatat tgatggatgt ctcaccaatg gccacattta tgtatcagga
960
gaccaaaaag aaataatatc ttatgatgta aaagatgcta ttgggataag tttattaaag
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aaaagtggta ttgaggtgag gctaatctca gaaagggcct gttcaaagca gacgctgtct
1080
tctttaaaac tggattgcaa aatggaagtc agtgtatcag acaagctagc agttgtagat
1140
gaatggagaa aagaaatggg cctgtgctgg aaagaagtgg catatcttgg aaatgaagtg
1200
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1260
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1320
gaatttgcag agcacatttg cctactaatg gaaaaggtta ataattcatg ccaaaaatag
1380
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1440
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1500
tatatattgt gctctacttt tctctttacg caagataatt atttagagac tgattacagt
1560
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1620
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1740
aaaaaaaaaa a
1751

<210> 5858
<211> 434
<212> PRT
<213> Homo sapiens

<400> 5858
Met Asp Ser Val Glu Lys Gly Ala Ala Thr Ser Val Ser Asn Pro Arg
 1   5   10   15
Gly Arg Pro Ser Arg Gly Arg Pro Pro Lys Leu Gln Arg Asn Ser Arg
            20   25   30
Gly Gly Gln Gly Arg Gly Gly Glu Lys Pro Pro His Leu Ala Ala Leu
        35   40   45
Ile Leu Ala Arg Gly Gly Ser Lys Gly Ile Pro Leu Lys Asn Ile Lys
    50   55   60
His Leu Ala Gly Val Pro Leu Ile Gly Trp Val Leu Arg Ala Ala Leu
65   70   75   80
Asp Ser Gly Ala Phe Gln Ser Val Trp Val Ser Thr Asp His Asp Glu
                85   90   95
Ile Glu Asn Val Ala Lys Gln Phe Gly Ala Gln Val His Arg Arg Ser
            100   105   110
Ser Glu Val Ser Lys Asp Ser Ser Thr Ser Leu Asp Ala Ile Ile Glu

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        115                 120                 125
Phe Leu Asn Tyr His Asn Glu Val Asp Ile Val Gly Asn Ile Gln Ala
    130                 135                 140
Thr Ser Pro Cys Leu His Pro Thr Asp Leu Gln Lys Val Ala Glu Met
145                 150                 155                 160
Ile Arg Glu Glu Gly Tyr Asp Ser Val Phe Ser Val Val Arg Arg His
                165                 170                 175
Gln Phe Arg Trp Ser Glu Ile Gln Lys Gly Val Arg Glu Val Thr Glu
            180                 185                 190
Pro Leu Asn Leu Asn Pro Ala Lys Arg Pro Arg Arg Gln Asp Trp Asp
        195                 200                 205
Gly Glu Leu Tyr Glu Asn Gly Ser Phe Tyr Phe Ala Lys Arg His Leu
    210                 215                 220
Ile Glu Met Gly Tyr Leu Gln Gly Gly Lys Met Ala Tyr Tyr Glu Met
225                 230                 235                 240
Arg Ala Glu His Ser Val Asp Ile Asp Val Asp Ile Asp Trp Pro Ile
                245                 250                 255
Ala Glu Gln Arg Val Leu Arg Tyr Gly Tyr Phe Gly Lys Glu Lys Leu
            260                 265                 270
Lys Glu Ile Lys Leu Leu Val Cys Asn Ile Asp Gly Cys Leu Thr Asn
        275                 280                 285
Gly His Ile Tyr Val Ser Gly Asp Gln Lys Glu Ile Ile Ser Tyr Asp
    290                 295                 300
Val Lys Asp Ala Ile Gly Ile Ser Leu Leu Lys Lys Ser Gly Ile Glu
305                 310                 315                 320
Val Arg Leu Ile Ser Glu Arg Ala Cys Ser Lys Gln Thr Leu Ser Ser
                325                 330                 335
Leu Lys Leu Asp Cys Lys Met Glu Val Ser Val Ser Asp Lys Leu Ala
            340                 345                 350
Val Val Asp Glu Trp Arg Lys Glu Met Gly Leu Cys Trp Lys Glu Val
        355                 360                 365
Ala Tyr Leu Gly Asn Glu Val Ser Asp Glu Glu Cys Leu Lys Arg Val
    370                 375                 380
Gly Leu Ser Gly Ala Pro Ala Asp Ala Cys Ser Thr Ala Gln Lys Ala
385                 390                 395                 400
Val Gly Tyr Ile Cys Lys Cys Asn Gly Gly Arg Gly Ala Ile Arg Glu
                405                 410                 415
Phe Ala Glu His Ile Cys Leu Leu Met Glu Lys Val Asn Asn Ser Cys
            420                 425                 430
Gln Lys
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<210> 5859
<211> 2267
<212> DNA
<213> Homo sapiens

<400> 5859
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aaatatatat ataaaaaaaa taataagaca attacagcac taaaccaggc accttcgacc
120
aaatcacaac ctcctctttg attccccttc acgctaagcc tctttcaaat tctttttcct
180

gagctggaag accagtcaga tgcccgcagg gtcagcgcca agcacattcc caaccgggca
240
actgtgtacc tttctctagg agtgcacgac acccttcccc cacaactcct tgttttaaag
300
gatttaaccc attaggaagc ccatgtttca atctaagcca gaaggagctg cgggacaagg
360
cagtcttcac tttgaaggtc cctttcctgc tccagtccct gggctagggt tctagaagag
420
gctggctgcc acgtttacat gaggccaccg aagatctaag tccagctaag cccagggagg
480
ctcctgcaaa ggctgggacc tcgggtgctg cgtcctcaac cctctcggtg accacggctc
540
aaaggagaga cctcaagggt gccaggagca caggtgcctg ggctgcattc caggaaagag
600
acctgtccag ggaaacggat caggctgtcg catggaagct tacgtcagag atggtggttt
660
tggggtgatt tggacaaatt aggttagttt agcaaagctc tgaagtagca gaagcttctc
720
ccctggacta ctgattgaac acagaacaag agatgcgcgt ggcgtcagac taagtcttag
780
agagatgcag gccagtctcc tcccacaggg ccttgggact ggcaggacag acactgctac
840
atgccctcca agggcaggag tcacggtaag gagcgactgg ggtggaaaat agggaaaaaa
900
gcaacaacaa ctacatcatt tttggcattt taacatggag acagtgacaa gtggtaacaa
960
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1020
cacacttaag ttctagtccc atctcccccа taagcaccac tgaactaaat atctatttta
1080
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1140
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1200
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1260
tgctgacatg tgaggaaggg gactctttgg taatcccaac tatttggtac tagagccaag
1320
caaacgtgac taaagggagc tgggtcagca gaacggtacc ccgagtctca gcaacaggat
1380
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1560
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1620
cccatggttc cacaatcacc tgattttcat ttggacctct ttaacagcta aagtagatat
1680
aaatggctaa acacagatcc ccaatccccc accaggggggg acacggccga ttctataatg
1740
tcgcagccag aaggctgtgg gcgtacaggc agccaagggg agaaacagaa ccgacaccgg
1800

cctaggccca tctgcaagaa aaagcggaga aggagtgacc cggatgcttc cgaagcacgc
1860
gagcgtgatt ttggatggag gcgggccggt gactgcctag ctgctgccgg ttcctgtaag
1920
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1980
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2040
aaacttaaaa aaaaaaaaaa aacctagatt gctcaaagtt tctgcctctt ttgtaggaat
2100
ggtaaatcaa ctatgagcaa gtattttaat tcaacattaa gggaaaaaaa aggactttgg
2160
aaagcataca gaaaaaaagg tagttaacgt tggatcatgt gtaaaacgga acctcaggga
2220
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2267

<210> 5860
<211> 96
<212> PRT
<213> Homo sapiens

<400> 5860
Met Glu Glu Glu Ser Pro Phe Thr Gln Lys Lys Cys Pro Leu Gln Glu
1 5 10 15
Pro Ala Ala Ala Arg Gln Ser Pro Ala Arg Leu His Pro Lys Ser Arg
20 25 30
Ser Arg Ala Ser Glu Ala Ser Gly Ser Leu Leu Leu Arg Phe Phe Leu
35 40 45
Gln Met Gly Leu Gly Arg Cys Arg Phe Cys Phe Ser Pro Trp Leu Pro
50 55 60
Val Arg Pro Gln Pro Ser Gly Cys Asp Ile Ile Glu Ser Ala Val Ser
65 70 75 80
Pro Leu Val Gly Asp Trp Gly Ser Val Phe Ser His Leu Tyr Leu Leu
85 90 95

<210> 5861
<211> 1951
<212> DNA
<213> Homo sapiens

<400> 5861
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120
cttgtgaggc ccaaggctgg ccagacactg cagcagaggg ttttccagat cctagacagt
180
aagctatttg agaaagtcaa agaagtttgt ccaaatgtgc atgagaagat cagagctatt
240
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300
tcctgtacaa acataatatt tcactgtgca gccactgtac gctttgacga cactctcaga
360

catgctgtgc aacttaacgt cactgccacc cggcagctct tgcttatggc tagtcagatg
420
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480
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540
gagtggttag acgatgctat tattgacgag attacaccca agctgatcag agattggccc
600
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720
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780
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840
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900
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1020
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1080
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1200
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1260
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1320
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1380
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1620
gaaagtaaca aggaatatgc ccaaactgtc aaatgtcacc tgttatgtat tcgtccctat
1680
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1740
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1800
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1860
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1920
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1951

<210> 5862
<211> 514
<212> PRT
<213> Homo sapiens

<400> 5862
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Thr Gly Phe Leu Gly Lys Val Leu Met Glu Lys Leu Phe Arg Thr Ser
20 25 30
Pro Asp Leu Lys Val Ile Tyr Ile Leu Val Arg Pro Lys Ala Gly Gln
35 40 45
Thr Leu Gln Gln Arg Val Phe Gln Ile Leu Asp Ser Lys Leu Phe Glu
50 55 60
Lys Val Lys Glu Val Cys Pro Asn Val His Glu Lys Ile Arg Ala Ile
65 70 75 80
Tyr Ala Asp Leu Asn Gln Asn Asp Phe Ala Ile Ser Lys Glu Asp Met
85 90 95
Gln Glu Leu Leu Ser Cys Thr Asn Ile Ile Phe His Cys Ala Ala Thr
100 105 110
Val Arg Phe Asp Asp Thr Leu Arg His Ala Val Gln Leu Asn Val Thr
115 120 125
Ala Thr Arg Gln Leu Leu Leu Met Ala Ser Gln Met Pro Lys Leu Glu
130 135 140
Ala Phe Ile His Ile Ser Thr Ala Tyr Ser Asn Cys Asn Leu Lys His
145 150 155 160
Ile Asp Glu Val Ile Tyr Pro Cys Pro Val Glu Pro Lys Lys Lys Ile
165 170 175
Ile Asp Ser Leu Glu Trp Leu Asp Asp Ala Ile Ile Asp Glu Ile Thr
180 185 190
Pro Lys Leu Ile Arg Asp Trp Pro Asn Ile Tyr Thr Tyr Thr Lys Ala
195 200 205
Leu Gly Glu Met Val Val Gln Gln Glu Ser Arg Asn Leu Asn Ile Ala
210 215 220
Ile Ile Arg Pro Ser Ile Val Gly Ala Thr Trp Gln Glu Pro Phe Pro
225 230 235 240
Gly Trp Val Asp Asn Ile Asn Gly Pro Asn Gly Ile Ile Ile Ala Thr
245 250 255
Gly Lys Gly Phe Leu Arg Ala Ile Lys Ala Thr Pro Met Ala Val Ala
260 265 270
Asp Val Ile Pro Val Asp Thr Val Val Asn Leu Met Leu Ala Val Gly
275 280 285
Trp Tyr Thr Ala Val His Arg Pro Lys Ser Thr Leu Val Tyr His Ile
290 295 300
Thr Ser Gly Asn Met Asn Pro Cys Asn Trp His Lys Met Gly Val Gln
305 310 315 320
Val Leu Ala Thr Phe Glu Lys Ile Pro Phe Glu Arg Pro Phe Arg Arg
325 330 335
Pro Asn Ala Asn Phe Thr Ser Asn Ser Phe Thr Ser Gln Tyr Trp Asn
340 345 350
Ala Val Ser His Arg Ala Pro Ala Ile Ile Tyr Asp Cys Tyr Leu Arg
355 360 365
Leu Thr Gly Arg Lys Pro Arg Met Thr Lys Leu Met Asn Arg Leu Leu

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    370                 375                 380
Arg Thr Val Ser Met Leu Glu Tyr Phe Ile Asn Arg Ser Trp Glu Trp
385                 390                 395                 400
Ser Thr Tyr Asn Thr Glu Met Leu Met Ser Glu Leu Ser Pro Glu Asp
                405                 410                 415
Gln Arg Val Phe Asn Phe Asp Val Arg Gln Leu Asn Trp Leu Glu Tyr
            420                 425                 430
Ile Glu Asn Tyr Val Leu Gly Val Lys Lys Tyr Leu Leu Lys Glu Asp
        435                 440                 445
Met Ala Gly Ile Pro Lys Ala Lys Gln Arg Leu Lys Arg Leu Arg Asn
    450                 455                 460
Ile His Tyr Leu Phe Asn Thr Ala Leu Phe Leu Ile Ala Trp Arg Leu
465                 470                 475                 480
Leu Ile Ala Arg Ser Gln Met Ala Arg Asn Val Trp Phe Phe Ile Val
                485                 490                 495
Ser Phe Cys Tyr Lys Phe Leu Ser Tyr Phe Arg Ala Ser Ser Thr Leu
            500                 505                 510
Lys Val
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<210> 5863
<211> 438
<212> DNA
<213> Homo sapiens

<400> 5863
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120
agaagtgcca gtcttaacat tcactgtttg tgactgattt atagaaaaag gggctggatt
180
ctggtagccg ggggagccca gggtgaacac tgaggttcta ccctgttcta gtggttgctt
240
tgattgatac tcagccatga aagggacata gctcagatac tgacaaaaca gctttgtatt
300
tgagtgtgtt tgtccaactg gcaaggaaca gtctggggac aaacagtgcc ttatttggag
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420
tgaatcagat tttgtaca
438

<210> 5864
<211> 104
<212> PRT
<213> Homo sapiens

<400> 5864
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Met Gly Glu Lys Asn Lys Gln Leu Gln Ile Arg His Cys Leu Ser Pro
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Asp Cys Ser Leu Pro Val Gly Gln Thr His Ser Asn Thr Lys Leu Phe
            20                  25                  30
Cys Gln Tyr Leu Ser Tyr Val Pro Phe Met Ala Glu Tyr Gln Ser Lys
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35 40 45
Gln Pro Leu Glu Gln Gly Arg Thr Ser Val Phe Thr Leu Gly Ser Pro
50 55 60
Gly Tyr Gln Asn Pro Ala Pro Phe Ser Ile Asn Gln Ser Gln Thr Val
65 70 75 80
Asn Val Lys Thr Gly Thr Ser Cys Leu Glu Thr Gln Ile Leu Phe Gln
85 90 95
Glu Glu Tyr Leu Arg Ile Phe Leu
100

<210> 5865
<211> 1229
<212> DNA
<213> Homo sapiens

<400> 5865
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120
aacaacccag gcatagtctt aacctttgtg cttcccacgg agcagttcca cttaggcaag
180
attgaggagc ttctcgtgga gagaacaggg gccccattct gctcccctac cagttccgga
240
tggaggagat cgagggcttc cgctatcgct gcaggtgtcc acccccagga tgccatgcgc
300
tcagtgacta agcaggccat tcgggaggca agattgaagg agatcaagga agagcttctg
360
cattctgaga agcttaagac atactttgaa gacaacccta gggacctcca gctgctgcgg
420
catgacctac ctttgcaccc cgcagtggtg aagccccacc tgggccatgt tcctgactac
480
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540
tcctcttgta ggaaggccaa gagagcaaag tcccagaacc cactgcgcag cttcaagcac
600
aaaggaaaga aattcagacc cacagccaag ccctcctgag gttgttgggc ctctctggag
660
ctgagcacat tgtggagcac aggcttacac ccttcgtgga caggcgaggc tctggtgctt
720
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780
cacttccaag ctggcatctt gcccccttgac aacagaataa aaattttagc tgccccagtt
840
tgtgcctcca gcatatgaaa aggactattt gaatccccaa aacatcagga gtcgggaaac
900
ttcggaagac agctgtgcct ggctctgtgg ctgcatgcag tgcttcactt ggccagcaga
960
ggtcagctgt gccgagctgc cccagccatg agaagagaag cctgcccttg ctggcaggtg
1020
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1140

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1229

<210> 5866
<211> 212
<212> PRT
<213> Homo sapiens

<400> 5866
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Ala Val Leu Asn Phe Asp Leu Pro Pro Thr Pro Glu Ala Tyr Ile His
20 25 30
Arg Ala Gly Arg Thr Ala Arg Ala Asn Asn Pro Gly Ile Val Leu Thr
35 40 45
Phe Val Leu Pro Thr Glu Gln Phe His Leu Gly Lys Ile Glu Glu Leu
50 55 60
Leu Val Glu Arg Thr Gly Ala Pro Phe Cys Ser Pro Thr Ser Ser Gly
65 70 75 80
Trp Arg Arg Ser Arg Ala Ser Ala Ile Ala Ala Gly Val His Pro Gln
85 90 95
Asp Ala Met Arg Ser Val Thr Lys Gln Ala Ile Arg Glu Ala Arg Leu
100 105 110
Lys Glu Ile Lys Glu Glu Leu Leu His Ser Glu Lys Leu Lys Thr Tyr
115 120 125
Phe Glu Asp Asn Pro Arg Asp Leu Gln Leu Leu Arg His Asp Leu Pro
130 135 140
Leu His Pro Ala Val Val Lys Pro His Leu Gly His Val Pro Asp Tyr
145 150 155 160
Leu Val Pro Pro Ala Leu Arg Gly Leu Val Arg Pro His Lys Lys Arg
165 170 175
Lys Lys Leu Ser Ser Ser Cys Arg Lys Ala Lys Arg Ala Lys Ser Gln
180 185 190
Asn Pro Leu Arg Ser Phe Lys His Lys Gly Lys Lys Phe Arg Pro Thr
195 200 205
Ala Lys Pro Ser
210

<210> 5867
<211> 1882
<212> DNA
<213> Homo sapiens

<400> 5867
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120
gcgtcccatt gccttcactg cccgttccag gaagctctgg atcaacttca agacaagcga
180
ggccaacagc gcccgtggct tccagattcc ctatgttacc tatgatgagg actatgagca
240

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Ile Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Glu Gln Leu Val Glu Asp
50 55 60
Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu Ile
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Leu Lys Asp Lys Lys Leu Ile Lys Ala Phe Phe Glu Val Leu Ala His
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Pro Gln Asn Tyr Phe Lys Tyr Thr Glu Lys His Lys Glu Met Leu Pro
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Pro Tyr Lys
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65 70 75 80
Val Phe Pro Asn Glu Gly Cys Leu Pro Tyr Ser Cys Gln Glu Pro Asn
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<212> DNA
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Phe Thr His Asp Asp Gly Tyr Met Ile Cys Cys Asp Lys Cys Ser Val
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Ala Phe Gln His Thr Pro Thr Ser Ile Thr Leu Thr Ala Ser Arg Val
195 200 205
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Tyr Ile Tyr Ser Ile His Ser Ile Pro Lys Gly Thr Glu Ile Thr Ile
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Ala Phe Asp Phe Asp Tyr Gly Asn Cys Lys Tyr Lys Val Asp Cys Ala
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Thr Lys Gln Arg Lys Leu Ser Pro Leu Arg Leu Ser Val Ser Asn Asn
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<212> DNA
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<400> 5873

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<212> PRT
<213> Homo sapiens

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<212> DNA
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Glu Val Ser Ala Asp Gly Val Asn Met Leu Pro Leu Ser Thr Pro Val
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Val Thr Ser Gly Leu Thr Tyr Ile Lys Ile Gln Leu Val Lys Ala Glu
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Val Ala Ser Ala Val Cys Leu Arg Leu His Arg Pro Arg Asp Ala Ser

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Gln Val Ser Lys Thr Ser Ile Gly Trp Leu Arg Leu Leu His His Cys
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Leu Thr His Ile Ser Asp Leu Glu Gly Met Met Ala Ser Ala Ala Ala
    130                 135                 140
Pro Thr Ala Asn Leu Leu Gln Thr Cys Ala Ala Leu Leu Met Ser Pro
145                 150                 155                 160
Tyr Cys Gly Met His Ser Pro Asn Ile Glu Val Val Leu Val Lys Ile
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Gly Leu Gln Ser Thr Arg Ile Gly Leu Lys Leu Ile Asp Ile Leu Leu
            180                 185                 190
Arg Asn Cys Ala Ala Ser Gly Ser Asp Pro Thr Asp Leu Asn Ser Pro
        195                 200                 205
Leu Leu Phe Gly Arg Leu Asn Gly Leu Ser Ser Asp Ser Thr Ile Asp
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Ile Leu Tyr Gln Leu Gly Thr Thr Gln Asp Pro Gly Thr Lys Asp Arg
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Ile Gln Ala Leu Leu Lys Trp Val Ser Asp Ser Ala Arg Val Ala Ala
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Met Lys Arg Ser Gly Arg Met Asn Tyr Met Cys Pro Asn Ser Ser Thr
            260                 265                 270
Val Glu Tyr Gly Leu Leu Met Pro Ser Pro Ser His Leu His Cys Val
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Ala Ala Ile Leu Trp His Ser Tyr Glu Leu Leu Val Glu Tyr Asp Leu
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Pro Ala Leu Leu Asp Gln Glu Leu Phe Glu Leu Leu Phe Asn Trp Ser
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Met Ser Leu Pro Cys Asn Met Val Leu Lys Lys Ala Val Asp Ser Leu
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Leu Cys Ser Met Cys His Val His Pro Asn Tyr Phe Ser Leu Leu Met
            340                 345                 350
Gly Trp Met Gly Ile Thr Pro Pro Pro Val Gln Cys His His Arg Leu
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Ser Met Thr Asp Asp Ser Lys Lys Gln Asp Leu Ser Ser Ser Leu Thr
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Asp Asp Ser Lys Asn Ala Gln Ala Pro Leu Ala Leu Thr Glu Ser His
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Leu Ala Thr Leu Ala Ser Ser Ser Gln Ser Pro Glu Ala Ile Lys Gln
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Leu Leu Asp Ser Gly Leu Pro Ser Leu Leu Val Arg Ser Leu Ala Ser
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Phe Cys Phe Ser His Ile Ser Ser Ser Glu Ser Ile Ala Gln Ser Ile
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Asp Ile Ser Gln Asp Lys Leu Arg Arg His His Val Pro Gln Gln Cys
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Asn Lys Met Pro Ile Thr Ala Asp Leu Val Ala Pro Ile Leu Arg Phe
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Cys Ile Ser Cys His Pro Asn Asn Gln Lys Leu Met Ala Gln Val Leu
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Cys Glu Leu Phe Gln Thr Ser Pro Gln Arg Gly Asn Leu Pro Thr Ser
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Gly Asn Ile Ser Gly Phe Ile Arg Arg Leu Phe Leu Gln Leu Met Leu
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Glu Asp Glu Lys Val Thr Met Phe Leu Gln Ser Pro Cys Pro Leu Tyr
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Lys Gly Arg Ile Asn Ala Thr Ser His Val Ile Gln His Pro Met Tyr
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Lys Leu Ile Ser Glu Gln Lys Asp Asp Lys Glu Lys Lys Asn His Glu
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Glu Lys Glu Lys Val Lys Ala Glu Asn Gly Phe Gln Asp Asn Tyr Ser
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Val Val Val Ala Ser Gly Leu Lys Ser Gln Ser Lys Arg Ala Val Ser
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Ala Thr Pro Pro Arg Pro Pro Ser Arg Arg Gly Arg Thr Ile Pro Asp
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Lys Ile Gly Ser Thr Ser Gly Ala Glu Ala Ala Asn Lys Ile Ile Thr
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Ser Arg Val Ile Thr Asp Pro Ser Leu Ser Lys Thr Asp Ser Tyr Lys
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Arg Leu His Pro Glu Lys Asp His Gly Asp Leu Leu Ala Ser Cys Pro
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Glu Asp Glu Ala Leu Thr Pro Gly Asp Glu Cys Met Asp Gly Ile Leu
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Asp Glu Ser Leu Leu Glu Thr Cys Pro Ile Gln Ser Pro Leu Gln Val
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Phe Ala Gly Met Gly Gly Leu Ala Leu Ile Ala Glu Arg Leu Pro Met
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Leu Tyr Pro Glu Val Ile Gln Gln Val Ser Ala Pro Val Val Thr Ser
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Thr Thr Gln Glu Lys Pro Lys Asp Ser Asp Gln Phe Glu Trp Val Thr
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Ile Glu Gln Ser Gly Glu Leu Val Tyr Glu Ala Pro Glu Thr Val Ala
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Ala Glu Pro Pro Pro Ile Lys Ser Ala Val Gln Thr Met Ser Pro Ile
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Tyr Ala Glu Val Leu Leu Lys Glu Arg Lys His Ala Gln Cys Leu Leu
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Arg Leu Val Leu Gly Val Thr Asp Asp Gly Glu Gly Ser His Ile Leu
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Gln Ser Pro Ser Ala Asn Val Leu Pro Thr Leu Pro Phe His Val Leu
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Arg Ser Leu Phe Ser Thr Thr Pro Leu Thr Thr Asp Asp Gly Val Leu
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Cys Leu Ser Ala Leu Ser His His Ser Pro Arg Val Pro Asn Ser Ser
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Gln Asp Tyr Pro Ser Ser Pro Pro Leu Val Asn Leu Glu Thr Thr Gly
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Gly His Ser Val Arg Phe Asn Pro Asn Leu Tyr Asn Asp Gly Lys Val
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Cys Leu Ser Ile Leu Asn Thr Trp His Gly Arg Pro Glu Glu Lys Trp
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Asn Pro Ser Pro Cys Phe Lys Glu Val Ile His Lys His Phe Tyr Leu
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Gln Ala Ile His Ser Arg Val Lys Pro Ile Gln Leu Lys Gly Glu His
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His Ser Asn Ile Phe Cys Leu Ala Phe Asn Ser Gly Asn Thr Lys Val
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1320
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1380
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<210> 5880
<211> 185
<212> PRT
<213> Homo sapiens

<400> 5880
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Gly Arg Ile Arg Gly Ile His Arg Leu Gly Ala Ala Val Ala Pro Glu
20 25 30
Gly Ser Gln Lys Lys Lys Arg Thr Ile Leu Gln Phe Leu Thr Asn Tyr
35 40 45
Phe Tyr Asp Val Glu Ala Leu Arg Asp Tyr Leu Leu Gln Arg Glu Met
50 55 60
Tyr Lys Val His Glu Lys Asn Arg Ser Tyr Thr Trp Leu Glu Lys Gln
65 70 75 80
His Gly Pro Tyr Gly Ala Gly Ala Phe Phe Ile Leu Lys Gln Gly Gly
85 90 95
Ala Val Lys Phe Arg Asp Lys Glu Trp Ile Arg Pro Asp Lys Tyr Gly
100 105 110
His Phe Ser Gln Glu Phe Trp Asn Phe Cys Glu Val Pro Val Glu Ala
115 120 125
Val Asp Ala Gly Asp Cys Asp Ile Asn Tyr Glu Gly Leu Asp Asn Leu
130 135 140
Arg Thr Ser Ala Gly Trp Thr Ser Arg Thr Ser Leu Pro Cys Pro Thr
145 150 155 160
Leu Ala Ser Leu Arg Tyr Trp Trp Arg Arg Cys Cys Pro Ile Ala Arg
165 170 175
Leu Trp Glu Ser Thr Gly Leu Arg Ala
180 185

<210> 5881
<211> 327
<212> DNA
<213> Homo sapiens

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accatccacg tgccgctgga cgcctcgcgc tccaagcagc tcatcagcga gtggaagcag
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327

<210> 5882
<211> 109
<212> PRT

<213> Homo sapiens

<400> 5882
Xaa Ala Pro Arg Pro Val Ala Arg Glu Lys Thr Ser Leu Gly Ser Leu
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Lys Arg Ala Ser Val Asp Val Asp Leu Leu Ala Pro Arg Ser Pro Met
20 25 30
Ala Lys Glu Asn Met Val Thr Phe Ser His Thr Leu Pro Arg Ala Ser
35 40 45
Ala Pro Ser Leu Asp Asp Pro Ala Arg Arg His Met Thr Ile His Val
50 55 60
Pro Leu Asp Ala Ser Arg Ser Lys Gln Leu Ile Ser Glu Trp Lys Gln
65 70 75 80
Lys Ser Leu Glu Gly Arg Gly Leu Gly Leu Pro Asp Asp Ala Ser Pro
85 90 95
Gly His Leu Arg Ala Pro Ala Glu Pro Met Pro Glu Xaa
100 105

<210> 5883
<211> 579
<212> DNA
<213> Homo sapiens

<400> 5883
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tgcctaacct tgagttggcc cccaatccct ctggctgcag aagtcccctt acccccaatg
120
agaggagggg caggaccaga tcttttgaga gctgagggtt gagggcattg agccaacaca
180
cagatttgtc gcctctgtcc ccgaagacac ctgcaccctc catgcggagc caagatgggg
240
aatggaactg aggaagatta taactttgtc ttcaaggtgg tgctgatcgg cgaatcaggt
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360
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420
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<210> 5884
<211> 71
<212> PRT
<213> Homo sapiens

<400> 5884
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Leu Ile Gly Glu Ser Gly Val Gly Lys Thr Asn Leu Leu Ser Arg Phe

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Thr Arg Asn Glu Phe Ser His Asp Ser Arg Thr Thr Ile Gly Val Glu
        35                  40                  45
Phe Ser Thr Arg Thr Val Met Leu Gly Thr Ala Ala Val Lys Ala Gln
    50                  55                  60
Ile Trp Asp Thr Ala Gly Val
65                  70

<210> 5885
<211> 1905
<212> DNA
<213> Homo sapiens

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240
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420
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1200
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1680
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<210> 5886
<211> 265
<212> PRT
<213> Homo sapiens

<400> 5886
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20 25 30
Gly Ala Gly Pro Leu Tyr Ser His His Leu Pro Thr Ser Pro Leu Gln
35 40 45
Lys Ala Leu Leu Ala Ala Gly Ser Ala Ala Met Ala Leu Tyr Asn Pro
50 55 60
Tyr Arg His Asp Met Val Ala Val Leu Gly Glu Thr Thr Gly His Arg
65 70 75 80
Thr Leu Lys Val Leu Arg Asp Gln Met Arg Arg Asp Pro Glu Gly Ala
85 90 95
Gln Ile Leu Gln Glu Arg Pro Arg Ile Ser Thr Ser Thr Leu Asp Leu
100 105 110
Gly Lys Leu Gln Ser Leu Pro Glu Gly Ser Leu Gly Arg Glu Tyr Leu
115 120 125
Arg Phe Leu Asp Val Asn Arg Val Ser Pro Asp Thr Arg Ala Pro Thr
130 135 140
Arg Phe Val Asp Asp Glu Glu Leu Ala Tyr Val Ile Gln Arg Tyr Arg
145 150 155 160
Glu Val His Asp Met Leu His Thr Leu Leu Gly Met Pro Thr Asn Ile
165 170 175
Leu Gly Glu Ile Val Val Lys Trp Phe Glu Ala Val Gln Thr Gly Leu

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            180                 185                 190
Pro Met Cys Ile Leu Gly Ala Phe Phe Gly Pro Ile Arg Leu Gly Ala
        195                 200                 205
Gln Ser Leu Gln Val Leu Val Ser Glu Leu Ile Pro Trp Ala Val Gln
    210                 215                 220
Asn Gly Arg Arg Ala Pro Cys Val Leu Asn Leu Tyr Tyr Glu Arg Arg
225                 230                 235                 240
Trp Glu Gln Ser Leu Arg Ala Leu Arg Glu Glu Leu Gly Ile Thr Ala
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Pro Pro Met His Val Gln Gly Leu Ala
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<210> 5887
<211> 3779
<212> DNA
<213> Homo sapiens

<400> 5887
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120
aaccaactgg gacttgattg gtcgaaaaga agtgcctaaa cagcaagctg cttaccgcaa
180
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240
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1080

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<210> 5888
<211> 166
<212> PRT
<213> Homo sapiens

<400> 5888
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Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
            20   25   30
Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe Thr
        35   40   45
Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys Gly Leu
    50   55   60
Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly Phe Thr Thr
65   70   75   80
Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val Tyr Asp Val Thr

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                85                  90                  95
Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu Leu Gly Ile Leu Tyr
            100                 105                 110
Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg Arg Phe Pro Leu Glu
        115                 120                 125
Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln Trp Leu His Lys Leu
    130                 135                 140
Tyr Gln Glu Lys Asp Ala Leu Gln Glu Val Lys Thr Leu Asp Gly Met
145                 150                 155                 160
Phe Pro Gly Glu Gln Phe
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<210> 5889
<211> 2198
<212> DNA
<213> Homo sapiens

<400> 5889
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2198

<210> 5890
<211> 118
<212> PRT
<213> Homo sapiens

<400> 5890
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Leu Pro Leu Val Ala Gly Arg Asp Ser Leu Ala Leu Phe Pro Arg Leu
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Glu Cys Ser Gly Thr Ile Thr Ala His Cys Ser Leu Asp Phe Pro Gly
35 40 45
Ser Ser His Ser Pro Thr Ser Ala Ser Gln Ala Val Gly Thr Thr Gly
50 55 60
Glu Glu Arg Gln Gln His Gly Glu Cys Pro Val Pro Thr Pro Trp Lys

65 70 75 80
Ala Val Pro Pro Gly Ser Pro Gly Val Gly Thr Gln Cys Leu Gly Gly
85 90 95
Ala Leu Gly Cys Pro Thr Leu Gly Ala Thr Ala Arg Arg Gly Arg Ser
100 105 110
Pro Ala Phe His His Leu
115

<210> 5891
<211> 1459
<212> DNA
<213> Homo sapiens

<400> 5891
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420
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480
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540
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720
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840
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900
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960
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1020
tccagctgtg cagctgactt ctgtgagact ggggccagcc acactactct ctaggcctca
1080
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caactgttct tatgtcacag agggctcctt gctggtgggc agtgggttgt aaatactttt
1200

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1260
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1320
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1440
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1459

<210> 5892
<211> 212
<212> PRT
<213> Homo sapiens

<400> 5892
Met Ala Ala Pro Pro Gln Leu Arg Ala Leu Leu Val Val Val Asn Ala
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Leu Leu Arg Lys Arg Arg Tyr His Ala Ala Leu Ala Val Leu Lys Gly
            20   25   30
Phe Arg Asn Gly Ala Val Tyr Gly Ala Lys Ile Arg Ala Pro His Ala
        35   40   45
Leu Val Met Thr Phe Leu Phe Arg Asn Gly Ser Leu Gln Glu Lys Leu
    50   55   60
Trp Ala Ile Leu Gln Ala Thr Tyr Ile His Ser Trp Asn Leu Ala Arg
65   70   75   80
Phe Val Phe Thr Tyr Lys Gly Leu Arg Ala Leu Gln Ser Tyr Ile Gln
                85   90   95
Gly Lys Thr Tyr Pro Ala His Ala Phe Leu Ala Ala Phe Leu Gly Gly
            100   105   110
Ile Leu Val Phe Gly Glu Asn Asn Asn Ile Asn Ser Gln Ile Asn Met
        115   120   125
Tyr Leu Leu Ser Arg Val Leu Phe Ala Leu Ser Arg Leu Ala Val Glu
    130   135   140
Lys Gly Tyr Ile Pro Glu Pro Arg Trp Asp Pro Phe Pro Leu Leu Thr
145   150   155   160
Ala Val Val Trp Gly Leu Val Leu Trp Leu Phe Glu Tyr His Arg Ser
                165   170   175
Thr Leu Gln Pro Ser Leu Gln Ser Ser Met Thr Tyr Leu Tyr Glu Asp
            180   185   190
Ser Asn Val Trp His Asp Ile Ser Asp Phe Leu Val Tyr Asn Lys Ser
        195   200   205
Arg Pro Ser Asn
    210

<210> 5893
<211> 1389
<212> DNA
<213> Homo sapiens

<400> 5893
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120
agctcccgaa gaagagccag aatgagaagt accggctgaa gtacctgcgg ctgcgcaaag
180
cggccaaggc cacggtgttt gaaaatgctg ctatttgtga tgaaattgct cgtcttgagg
240
aaaaatttct taaagcaaaa gaagaaagaa ggtacttgct aaagaagctc ctccagcttc
300
aggctctaac tgaaggggaa gtacaggctg cagctccttc ccacagttcc agtttgcccc
360
tgacttatgg tgtggccagc tctgtgggaa ctatacaggg agctgggcct atttcagggc
420
ccagcactgg ggctgaggaa ccatttggga agaaaactaa gaaggagaaa aaagaaaaag
480
gcaaagagaa caacaaactg gaagatcatc accgaccgac ctggctttca tgatgagagt
540
gccatctacc ccgtgggcta ttgcagtact cgaatatatg ccagcatgaa gtgcccagac
600
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660
gttcctgaag atgaccccca gaatgccatt gtcagctctt ctgcagatgc ttgtcatgca
720
gaactgctca ggactataag cactactatg gggaaactaa tgcctaacct gcttccagct
780
ggagctgact tttttggatt ttctcatcca gccatccaca acctgatcca gagctgtcca
840
ggagctcgaa aatgcatcaa ttaccagtgg gtgaaatttg atgtgtgcaa acctggagat
900
gggcagctac ctgaggggct gccggagaat gatgcagcta tgagctttga agcctttcag
960
agacagatct ttgatgaaga tcagaatgat ccccttctgc caggatcctt ggacctccca
1020
gagcttcagc ctgcagcctt tgtgtcttct taccagccca tgtacctgac acatgaaccc
1080
ttggtagata ctcacctgca gcacttgaag tctccatcac agggtagccc aattcagtct
1140
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1200
aactaaaatt ttgggtatat gaaagaaggc agcaattcag aagtaaagaa gatactaacg
1260
tatttcatca tggaaggtcc tgtggtgatg gttttccctg ggaaaacctt cagctgcttt
1320
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1380
aaaaaaaaa
1389

<210> 5894
<211> 260
<212> PRT
<213> Homo sapiens

<400> 5894
Met Val Trp Pro Ala Leu Trp Glu Leu Tyr Arg Glu Leu Gly Leu Phe

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            20                  25                  30
Arg Arg Lys Lys Lys Lys Ala Lys Arg Thr Thr Asn Trp Lys Ile Ile
        35                  40                  45
Thr Asp Arg Pro Gly Phe His Asp Glu Ser Ala Ile Tyr Pro Val Gly
    50                  55                  60
Tyr Cys Ser Thr Arg Ile Tyr Ala Ser Met Lys Cys Pro Asp Gln Lys
65                  70                  75                  80
Cys Leu Tyr Thr Cys Gln Ile Lys Asp Gly Gly Val Gln Pro Gln Phe
                85                  90                  95
Glu Ile Val Pro Glu Asp Asp Pro Gln Asn Ala Ile Val Ser Ser Ser
            100                 105                 110
Ala Asp Ala Cys His Ala Glu Leu Leu Arg Thr Ile Ser Thr Thr Met
        115                 120                 125
Gly Lys Leu Met Pro Asn Leu Leu Pro Ala Gly Ala Asp Phe Phe Gly
    130                 135                 140
Phe Ser His Pro Ala Ile His Asn Leu Ile Gln Ser Cys Pro Gly Ala
145                 150                 155                 160
Arg Lys Cys Ile Asn Tyr Gln Trp Val Lys Phe Asp Val Cys Lys Pro
                165                 170                 175
Gly Asp Gly Gln Leu Pro Glu Gly Leu Pro Glu Asn Asp Ala Ala Met
            180                 185                 190
Ser Phe Glu Ala Phe Gln Arg Gln Ile Phe Asp Glu Asp Gln Asn Asp
        195                 200                 205
Pro Leu Leu Pro Gly Ser Leu Asp Leu Pro Glu Leu Gln Pro Ala Ala
    210                 215                 220
Phe Val Ser Ser Tyr Gln Pro Met Tyr Leu Thr His Glu Pro Leu Val
225                 230                 235                 240
Asp Thr His Leu Gln His Leu Lys Ser Pro Ser Gln Gly Ser Pro Ile
                245                 250                 255
Gln Ser Ser Asp
            260
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<210> 5895
<211> 2748
<212> DNA
<213> Homo sapiens

<400> 5895
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agaatcagtc ggcctattgt caacctcttt gtttcccggg accttggtgg cagttctgca
120
gccacagagg cagtggcgat tttgacagcc acataccctg tgggtcacat gccatacggc
180
tggttgacgg aaatccgtgc tgtgtatcct gctttcgaca agaataaccc cagcaacaaa
240
ctggtgagca cgagcaacac agtcacggca gcccacatca agaagttcac cttcgtctgc
300
atggctctgt cactcacgct ctgtttcgtg atgttttgga cacccaacgt gtctgagaaa
360
atcttgatag acatcatcgg agtggacttt gcctttgcag aactctgtgt tgttcctttg
420

cggatcttct ccttcttccc agttccagtc acagtgaggg cgcatctcac cgggtggctg
480
atgacactga agaaaacctt cgtccttgcc cccagctctg tgctgcggat catcgtcctc
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600
tccctcctgg cgggctttgt gggagaatcc accatggtcg ccatcgctgc gtgctatgtc
660
taccggaagc agaaaaagaa gatggagaat gagtcggcca cggaggggga agactctgcc
720
atgacagaca tgcctccgac agaggaggtg acagacatcg tggaaatgag agaggagaat
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900
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960
tgacgggggg acctagtgaa tggtctttac tgttgctatg taaaaacaaa cgaaacaact
1020
gacttcatac ccctgcctca cgaaaaccca aaagacacag ctgcctcacg gttgacgttg
1080
tgtcctcctc ccctggacaa tctcctcttg gaaccaaagg actgcagctg tgccatcgcg
1140
cctcggtcac cctgcacagc aggccacaga ctctcctgtc ccccttcatc gctcttaaga
1200
atcaacaggt taaaactcgg cttcctttga tttgcttccc agtcacatgg ccgtacaaag
1260
agatggagcc ccggtggcct cttaaatttc ccttccgcca cggagttcga aaccatctac
1320
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1380
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1560
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1920
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1980
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2100
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2160
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2220
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2280
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2340
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2400
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2520
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2580
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2640
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2700
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2748

<210> 5896
<211> 261
<212> PRT
<213> Homo sapiens

<400> 5896
Ala Thr Ile Arg Lys Met Leu Ser Phe Trp Trp Pro Leu Xaa Leu Ile
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Leu Ala Thr Gln Arg Ile Ser Arg Pro Ile Val Asn Leu Phe Val Ser
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Arg Asp Leu Gly Gly Ser Ser Ala Ala Thr Glu Ala Val Ala Ile Leu
35 40 45
Thr Ala Thr Tyr Pro Val Gly His Met Pro Tyr Gly Trp Leu Thr Glu
50 55 60
Ile Arg Ala Val Tyr Pro Ala Phe Asp Lys Asn Asn Pro Ser Asn Lys
65 70 75 80
Leu Val Ser Thr Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe
85 90 95
Thr Phe Val Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe
100 105 110
Trp Thr Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val
115 120 125
Asp Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser
130 135 140
Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp Leu
145 150 155 160
Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val Leu Arg
165 170 175
Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr Leu Gly Val

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            180                 185                 190
His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala Gly Phe Val Gly
        195                 200                 205
Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr Val Tyr Arg Lys Gln
    210                 215                 220
Lys Lys Lys Met Glu Asn Glu Ser Ala Thr Glu Gly Glu Asp Ser Ala
225                 230                 235                 240
Met Thr Asp Met Pro Pro Thr Glu Glu Val Thr Asp Ile Val Glu Met
                245                 250                 255
Arg Glu Glu Asn Glu
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<210> 5897
<211> 1930
<212> DNA
<213> Homo sapiens

<400> 5897
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120
cgccgcctcg gagcattccg aaaagcccct gaccgccggc cacgagtcaa gctgccctac
180
ccggccacga gtcaagctgc cctacccgag gcactctcca aggggagaga aactcctagg
240
ccagcgactc accctgcccg cagccaggac gtgaagcccc taagctgccc gtttgatttt
300
ctcagggaca atgtggagtg gtcggaagag caagccgcgg cggcggagag aaaagtccag
360
gagaacagta tccagcgggt gtgccaggag aaacaagttg attatgagat caatgcccac
420
aaatactgga atgacttcta caaaatccac gaaaatgggt ttttcaagga tagacattgg
480
ctttttaccg aattccctga gctggcacct agccaaaatc aaaatcattt gaaggactgg
540
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720
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1020
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1080

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1620
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gaattgtaaa ccttaaacca ccaatttatt tccatgtgaa aaagtgttat atatgacaag
1800
tgtttttga ttgtaattgc gttaaatctt ttgagagtgt aaatgccggc aaagtttcgc
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<210> 5898
<211> 242
<212> PRT
<213> Homo sapiens

<400> 5898
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Gln Thr Pro Pro Val Glu Glu Asn Val Thr Gln Lys Ile Ser Asp Leu
20 25 30
Glu Ile Cys Ala Asp Glu Phe Pro Gly Ser Ser Ala Thr Tyr Arg Ile
35 40 45
Leu Glu Val Gly Cys Gly Val Gly Asn Thr Val Phe Pro Ile Leu Gln
50 55 60
Thr Asn Asn Asp Pro Gly Leu Phe Val Tyr Cys Cys Asp Phe Ser Ser
65 70 75 80
Thr Ala Ile Glu Leu Val Gln Thr Asn Ser Glu Tyr Asp Pro Ser Arg
85 90 95
Cys Phe Ala Phe Val His Asp Leu Cys Asp Glu Glu Lys Ser Tyr Pro
100 105 110
Val Pro Lys Gly Ser Leu Asp Ile Ile Ile Leu Ile Phe Val Leu Ser
115 120 125
Ala Ile Val Pro Asp Lys Met Gln Lys Ala Ile Asn Arg Leu Ser Arg

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    130                 135                 140
Leu Leu Lys Pro Gly Gly Met Val Leu Leu Arg Asp Tyr Gly Arg Tyr
145                 150                 155                 160
Asp Met Ala Gln Leu Arg Phe Lys Lys Gly Gln Cys Leu Ser Gly Asn
                165                 170                 175
Phe Tyr Val Arg Gly Asp Gly Thr Arg Val Tyr Phe Phe Thr Gln Glu
            180                 185                 190
Glu Leu Asp Thr Leu Phe Thr Thr Ala Gly Leu Glu Lys Val Gln Asn
        195                 200                 205
Leu Val Asp Arg Arg Leu Gln Val Asn Arg Gly Lys Gln Leu Thr Met
    210                 215                 220
Tyr Arg Val Trp Ile Gln Cys Lys Tyr Cys Lys Pro Leu Leu Ser Ser
225                 230                 235                 240
Thr Ser
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<210> 5899
<211> 1589
<212> DNA
<213> Homo sapiens

<400> 5899

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120
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480
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720
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960
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1140
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gcctcctgcc tgcctggtgc cctgtcccag ccccaggtcc tgtgcagggc acctgcgtgg
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1560
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1589

<210> 5900
<211> 345
<212> PRT
<213> Homo sapiens

<400> 5900
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Ile Pro Thr Ile Ile Arg Asp Glu Glu Leu Lys Thr Arg Gly Phe Gly
35 40 45
Gly Ile Tyr Gly Val Gly Lys Ala Ala Leu His Pro Pro Ala Leu Ala
50 55 60
Val Leu Ser His Thr Pro Asp Gly Ala Thr Gln Thr Ile Ala Trp Val
65 70 75 80
Gly Lys Gly Ile Val Tyr Asp Thr Gly Gly Leu Ser Ile Lys Gly Lys
85 90 95
Thr Thr Met Pro Gly Met Lys Arg Asp Cys Gly Gly Ala Ala Ala Val
100 105 110
Leu Gly Ala Phe Arg Ala Ala Ile Lys Gln Gly Phe Lys Asp Asn Leu
115 120 125
His Ala Val Phe Cys Leu Ala Glu Asn Ser Val Gly Pro Asn Ala Thr
130 135 140
Arg Pro Asp Asp Ile His Leu Leu Tyr Ser Gly Lys Thr Val Glu Ile
145 150 155 160
Asn Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala Asp Gly Val Ser
165 170 175
Tyr Ala Cys Lys Asp Leu Gly Ala Asp Ile Ile Leu Asp Met Ala Thr
180 185 190
Leu Thr Gly Ala Gln Gly Ile Ala Thr Gly Lys Tyr His Ala Ala Val

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        195                 200                 205
Leu Thr Asn Ser Ala Glu Trp Glu Ala Ala Cys Val Lys Ala Gly Arg
    210                 215                 220
Lys Cys Gly Asp Leu Val His Pro Leu Val Tyr Cys Pro Glu Leu His
225                 230                 235                 240
Phe Ser Glu Phe Thr Ser Ala Val Ala Asp Met Lys Asn Ser Val Ala
                245                 250                 255
Asp Arg Asp Asn Ser Pro Ser Ser Cys Ala Gly Leu Phe Ile Ala Ser
            260                 265                 270
His Ile Gly Phe Asp Trp Pro Gly Val Trp Val His Leu Asp Ile Ala
        275                 280                 285
Ala Pro Val His Ala Gly Glu Arg Ala Thr Gly Phe Gly Val Ala Leu
    290                 295                 300
Leu Leu Ala Leu Phe Gly Arg Ala Ser Glu Asp Pro Leu Leu Asn Leu
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<210> 5901
<211> 984
<212> DNA
<213> Homo sapiens

<400> 5901

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<212> PRT
<213> Homo sapiens

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Val Glu Ala Gly Lys Ala Tyr Val Ser Thr Ser Arg Leu Phe Val Ser
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Gly Val Arg Asp Leu Ser Gln Gln Cys Gln Gly Asp Thr Val Ile Ser
65 70 75 80
Glu Cys Leu Gln Arg Phe Ala Asp Ser Leu Gln Glu Val Val Asn Tyr
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115 120 125
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145 150 155 160
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Asp Ser Met Leu Ser Phe Met His Ala Gln Ser Ser Phe Phe Gln Gln
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Gly Tyr Ser Leu Leu His Gln Leu Asp Pro Tyr Met Lys Lys Leu Ala
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Ala Glu Leu Asp Gln Leu Val Ile Asp Ser Ala Val Glu Lys Arg Glu
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245 250 255
Ser Tyr Asp Glu Ser Lys Val Glu Phe Asp Val Asp Ala Pro Ser Gly
260 265 270
Val Val Met Glu Gly Tyr Leu Phe Lys Arg Ala Ser Asn Xaa Phe Lys
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Thr Trp Asn Arg Arg Trp Phe Ser Ile Gln Asn Ser Gln Leu Val Tyr
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<210> 5904
<211> 308
<212> PRT
<213> Homo sapiens

<400> 5904
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35 40 45
Leu Gln Lys Ser Glu Ala Met Leu Arg Lys His Val Glu Phe Arg Lys
50 55 60
Gln Lys Asp Ile Asp Asn Ile Ile Ser Trp Gln Pro Pro Glu Val Ile
65 70 75 80
Gln Gln Tyr Leu Ser Gly Gly Met Cys Gly Tyr Asp Leu Asp Gly Cys
85 90 95
Pro Val Trp Tyr Asp Ile Ile Gly Pro Leu Asp Ala Lys Gly Leu Leu
100 105 110
Leu Ser Ala Ser Lys Gln Asp Met Ile Arg Lys Gly Ile Lys Val Cys
115 120 125
Glu Leu Leu Leu His Glu Cys Glu Leu Gln Thr Gln Lys Leu Gly Arg
130 135 140
Lys Ile Glu Met Ala Leu Met Val Phe Asp Met Glu Gly Leu Ser Leu
145 150 155 160
Lys His Leu Trp Lys Pro Ala Val Glu Val Tyr Gln Gln Phe Phe Ser

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        195                 200                 205
Met Ser Glu Asp Thr Arg Lys Lys Ile Met Val Leu Gly Ala Asn Trp
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Lys Glu Val Leu Leu Lys His Ile Ser Pro Asp Gln Val Pro Val Glu
225                 230                 235                 240
Tyr Gly Gly Thr Met Thr Asp Pro Asp Gly Asn Pro Lys Cys Lys Ser
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Lys Ile Asn Tyr Gly Gly Asp Ile Pro Arg Lys Tyr Tyr Val Arg Asp
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Gln Val Lys Gln Gln Tyr Glu His Ser Val Gln Ile Ser Arg Gly Ser
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<212> DNA
<213> Homo sapiens

<400> 5905

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<210> 5906
<211> 215
<212> PRT
<213> Homo sapiens

<400> 5906
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35 40 45
Ser Ala Gly Val Thr Val Val Ile Val Arg Asp Asp Leu Leu Gly Phe
50 55 60
Ala Leu Arg Glu Cys Pro Ser Val Leu Glu Tyr Lys Val Gln Ala Gly
65 70 75 80
Asn Ser Ser Leu Tyr Asn Thr Pro Pro Cys Phe Ser Ile Tyr Val Met
85 90 95
Gly Leu Val Leu Glu Trp Ile Lys Asn Asn Gly Gly Ala Ala Ala Met
100 105 110
Glu Lys Leu Ser Ser Ile Lys Ser Leu Thr Ile Tyr Glu Ile Ile Asp
115 120 125
Asn Ser Gln Gly Phe Tyr Val Cys Pro Val Glu Pro Gln Asn Arg Ser
130 135 140
Lys Met Asn Ile Pro Phe Arg Ile Gly Asn Ala Lys Gly Asp Asp Ala
145 150 155 160
Leu Glu Lys Arg Phe Leu Asp Lys Ala Leu Glu Leu Asn Met Leu Ser
165 170 175
Leu Lys Gly His Arg Ser Val Gly Gly Ile Arg Ala Ser Leu Tyr Asn
180 185 190
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Phe Leu Glu Met His Gln Leu
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<210> 5907
<211> 1989
<212> DNA
<213> Homo sapiens

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<210> 5908
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<212> PRT

<213> Homo sapiens

<400> 5908

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Leu Phe Lys Val Leu Ser Val Gly Arg Gly Gly Ser Pro Arg Leu Gln
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Pro Asp Ser Arg Ala Leu His Tyr Met Lys Lys Leu Tyr Lys Thr Tyr
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Thr Val Arg Leu Phe Thr Pro Cys Thr Arg His Lys Gln Ala Pro Gly
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Asp Gln Val Thr Gly Ile Leu Pro Ser Val Glu Leu Leu Phe Asn Leu
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His Lys Trp Ile Gln Ile Asp Val Thr Ser Leu Leu Gln Pro Leu Val
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Ala Ser Asn Lys Arg Ser Ile His Met Ser Ile Asn Phe Thr Cys Met
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Lys Asp Gln Leu Glu His Pro Ser Ala Gln Asn Gly Leu Phe Asn Met
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            260                 265                 270
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        275                 280                 285
Gln Gly Pro Asp Gln Glu Arg Ser Leu Ser Ala Tyr Pro Val Gly Glu
    290                 295                 300
Glu Ala Ala Glu Asp Gly Arg Ser Ser His His Arg His Arg Arg Gly
305                 310                 315                 320
Gln Glu Thr Val Ser Ser Glu Leu Lys Lys Pro Leu Gly Pro Ala Ser
                325                 330                 335
Phe Asn Leu Ser Glu Tyr Phe Arg Gln Phe Leu Leu Pro Gln Asn Glu
            340                 345                 350
Cys Glu Leu His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp
        355                 360                 365
Asn Trp Ile Val Ala Pro His Arg Tyr Asn Pro Arg Tyr Cys Lys Gly
    370                 375                 380
Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Ser Pro Val His Thr
385                 390                 395                 400
Met Val Gln Asn Ile Ile Tyr Glu Lys Leu Asp Ser Ser Val Pro Arg
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                405                 410                 415
Pro Ser Cys Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Thr Ile
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Thr Lys Cys Thr Cys Arg
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<210> 5909
<211> 4343
<212> DNA
<213> Homo sapiens

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240
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360
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420
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480
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2820

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4343

<210> 5910

<211> 899
<212> PRT
<213> Homo sapiens

<400> 5910
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Lys Asp Asp Pro Glu Glu Leu Phe Ile Gly Leu His Glu Ile Gly His
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Gly Ser Phe Gly Ala Val Tyr Phe Ala Thr Asn Ala His Thr Ser Glu
35 40 45
Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys Gln Thr His Glu
50 55 60
Lys Trp Gln Asp Ile Leu Lys Glu Val Lys Phe Leu Arg Gln Leu Lys
65 70 75 80
His Pro Asn Thr Ile Glu Tyr Lys Gly Cys Tyr Leu Lys Glu His Thr
85 90 95
Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala Ser Asp Leu Leu
100 105 110
Glu Val His Lys Lys Pro Leu Gln Glu Val Glu Ile Ala Ala Ile Thr
115 120 125
His Gly Ala Leu His Gly Leu Ala Tyr Leu His Ser His Ala Leu Ile
130 135 140
His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Thr Glu Pro Gly Gln
145 150 155 160
Val Lys Leu Ala Asp Phe Gly Ser Ala Ser Met Ala Ser Pro Ala Asn
165 170 175
Ser Phe Val Gly Thr Pro Tyr Trp Met Ala Pro Glu Val Ile Leu Ala
180 185 190
Met Asp Glu Gly Gln Tyr Asp Gly Lys Val Asp Ile Trp Ser Leu Gly
195 200 205
Ile Thr Cys Ile Glu Leu Ala Glu Arg Lys Pro Pro Leu Phe Asn Met
210 215 220
Asn Ala Met Ser Ala Leu Tyr His Ile Ala Gln Asn Asp Ser Pro Thr
225 230 235 240
Leu Gln Ser Asn Glu Trp Thr Asp Ser Phe Arg Arg Phe Val Asp Tyr
245 250 255
Cys Leu Gln Lys Ile Pro Gln Glu Arg Pro Thr Ser Ala Glu Leu Leu
260 265 270
Arg His Asp Phe Val Arg Arg Asp Arg Pro Leu Arg Val Leu Ile Asp
275 280 285
Leu Ile Gln Arg Thr Lys Asp Ala Val Arg Glu Leu Asp Asn Leu Gln
290 295 300
Tyr Arg Lys Met Lys Lys Ile Leu Phe Gln Glu Thr Arg Asn Gly Pro
305 310 315 320
Leu Asn Glu Ser Gln Glu Asp Glu Glu Asp Ser Glu His Gly Thr Ser
325 330 335
Leu Asn Arg Glu Met Asp Ser Leu Gly Ser Asn His Ser Ile Pro Ser
340 345 350
Met Ser Val Ser Thr Gly Ser Gln Ser Ser Ser Val Asn Ser Met Gln
355 360 365
Glu Val Met Asp Glu Ser Ser Ser Glu Leu Val Met Met His Asp Asp
370 375 380
Glu Ser Thr Ile Asn Ser Ser Ser Ser Val Val His Lys Lys Asp His

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385                 390                 395                 400
Val Phe Ile Arg Asp Glu Ala Gly His Gly Asp Pro Arg Pro Glu Pro
                405                 410                 415
Arg Pro Thr Gln Ser Val Gln Ser Gln Ala Leu His Tyr Arg Asn Arg
            420                 425                 430
Glu Arg Phe Ala Thr Ile Lys Ser Ala Ser Leu Val Thr Arg Gln Ile
        435                 440                 445
His Glu His Glu Gln Glu Asn Glu Leu Arg Glu Gln Met Ser Gly Tyr
    450                 455                 460
Lys Arg Met Arg Arg Gln His Gln Lys Gln Leu Ile Ala Leu Glu Asn
465                 470                 475                 480
Lys Leu Lys Ala Glu Met Asp Glu His Arg Leu Lys Leu Gln Lys Glu
                485                 490                 495
Val Glu Thr His Ala Asn Asn Ser Ser Ile Glu Leu Glu Lys Leu Ala
            500                 505                 510
Lys Lys Gln Val Ala Ile Ile Glu Lys Glu Ala Lys Val Ala Ala Ala
        515                 520                 525
Asp Glu Lys Lys Phe Gln Gln Gln Ile Leu Ala Gln Gln Lys Lys Asp
    530                 535                 540
Leu Thr Thr Phe Leu Glu Ser Gln Lys Lys Gln Tyr Lys Ile Cys Lys
545                 550                 555                 560
Glu Lys Ile Lys Glu Glu Met Asn Glu Asp His Ser Thr Pro Lys Lys
                565                 570                 575
Glu Lys Gln Glu Arg Ile Phe Lys His Lys Glu Asn Leu Gln His Thr
            580                 585                 590
Gln Ala Glu Glu Glu Ala His Leu Leu Thr Ser Thr Gly Asp Trp Thr
        595                 600                 605
Thr Thr Lys Asn Cys Arg Phe Phe Lys Arg Lys Ile Met Ile Lys Arg
    610                 615                 620
His Glu Val Glu Gln Gln Asn Ile Arg Glu Glu Leu Asn Lys Lys Arg
625                 630                 635                 640
Thr Met Lys Glu Met Glu His Ala Met Leu Ile Arg His Asp Glu Ser
                645                 650                 655
Thr Arg Glu Leu Glu Tyr Arg Gln Leu His Thr Leu Gln Lys Leu Arg
            660                 665                 670
Met Asp Leu Ile Arg Leu Gln His Gln Thr Glu Leu Glu Asn Gln Leu
        675                 680                 685
Glu Tyr Asn Lys Arg Arg Glu Arg Glu Leu His Arg Lys His Val Met
    690                 695                 700
Glu Leu Arg Gln Gln Pro Lys Asn Leu Lys Ala Met Glu Met Gln Ile
705                 710                 715                 720
Lys Lys Gln Phe Gln Asp Thr Cys Lys Val Gln Thr Lys Gln Tyr Lys
                725                 730                 735
Ala Leu Lys Asn His Gln Leu Glu Val Thr Pro Lys Asn Glu His Lys
            740                 745                 750
Thr Ile Leu Lys Thr Leu Lys Asp Glu Gln Thr Arg Lys Leu Ala Ile
        755                 760                 765
Leu Ala Glu Gln Tyr Glu Gln Ser Ile Asn Glu Met Met Ala Ser Gln
    770                 775                 780
Ala Leu Arg Leu Asp Glu Ala Gln Glu Ala Glu Cys Gln Ala Leu Arg
785                 790                 795                 800
Leu Gln Leu Gln Gln Glu Met Glu Leu Leu Asn Ala Tyr Gln Ser Lys
                805                 810                 815
Ile Lys Met Gln Thr Glu Ala Gln His Glu Arg Glu Leu Gln Lys Leu
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            820                 825                 830
Glu Gln Arg Val Ser Leu Arg Arg Ala His Leu Glu Gln Lys Ile Glu
        835                 840                 845
Glu Glu Leu Ala Ala Leu Gln Lys Glu Arg Ser Glu Arg Ile Lys Asn
    850                 855                 860
Leu Leu Glu Arg Gln Glu Arg Glu Ile Glu Thr Phe Asp Met Glu Ser
865                 870                 875                 880
Leu Arg Met Gly Phe Gly Asn Leu Val Thr Leu Asp Phe Pro Lys Glu
                885                 890                 895
Asp Tyr Arg
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<210> 5911
<211> 645
<212> DNA
<213> Homo sapiens

<400> 5911
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cccgacggtg gtactccagc aggtacttca agtccagctt cttcatcttc ccttctcaac
180
agacttcagc ttgatgatga tattgatggt gagactagag atctcttcgt tatagtcgat
240
gatcccaaga agcatgtgtg tacaatggag acttacatca cctataggat caccaccaaa
300
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360
gactggttga ggagcaaact ggaagaatcc cagcccactc atctcattcc ccctcttccc
420
gagaagtttg tggtaaaagg tgttgtggat cgtttttcag aagagtttgt ggagaccaga
480
agaaaagctt tggataaatt tctaaaaaga attacggacc atcctgtgct gtctttcaat
540
gaacacttta atattttcct tactgctaag gacctgaacg cctacaagaa gcaagggata
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645

<210> 5912
<211> 211
<212> PRT
<213> Homo sapiens

<400> 5912
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Cys Arg Pro Glu Leu Phe Leu Phe Gly Asn Leu Gly Ser Ser Ala Glu
            20                  25                  30
Asp Leu Ile Leu Pro Asp Gly Gly Thr Pro Ala Gly Thr Ser Ser Pro
        35                  40                  45
Ala Ser Ser Ser Ser Leu Leu Asn Arg Leu Gln Leu Asp Asp Asp Ile
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    50                  55                  60
Asp Gly Glu Thr Arg Asp Leu Phe Val Ile Val Asp Asp Pro Lys Lys
65                  70                  75                  80
His Val Cys Thr Met Glu Thr Tyr Ile Thr Tyr Arg Ile Thr Thr Lys
                85                  90                  95
Ser Thr Arg Val Glu Phe Asp Leu Pro Glu Tyr Ser Val Arg Arg Arg
            100                 105                 110
Tyr Gln Asp Phe Asp Trp Leu Arg Ser Lys Leu Glu Glu Ser Gln Pro
        115                 120                 125
Thr His Leu Ile Pro Pro Leu Pro Glu Lys Phe Val Val Lys Gly Val
    130                 135                 140
Val Asp Arg Phe Ser Glu Glu Phe Val Glu Thr Arg Arg Lys Ala Leu
145                 150                 155                 160
Asp Lys Phe Leu Lys Arg Ile Thr Asp His Pro Val Leu Ser Phe Asn
                165                 170                 175
Glu His Phe Asn Ile Phe Leu Thr Ala Lys Asp Leu Asn Ala Tyr Lys
            180                 185                 190
Lys Gln Gly Ile Ala Leu Leu Thr Arg Met Gly Glu Ser Val Lys His
        195                 200                 205
Val Thr Arg
    210
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<210> 5913
<211> 2495
<212> DNA
<213> Homo sapiens

<400> 5913
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660
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780

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2280
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2340
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2400

tggctttgag ttgcagcgcg attttcccca tggtagccct ctccgcccgg tgctggctgc
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2495

<210> 5914
<211> 158
<212> PRT
<213> Homo sapiens

<400> 5914
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            20   25   30
Arg Ser Phe Ser Ile Leu Arg Leu Trp Phe Ser Ile Leu Phe Leu Thr
        35   40   45
Gly Gln Gly Phe Asp Arg His Leu Phe Ala Leu Arg His Leu Ala Ala
    50   55   60
Ala Xaa Gly Ile Ile Leu Pro Glu Leu Tyr Leu Asp Pro Ala Tyr Gly
65   70   75   80
Gln Ile Asn His Asn Val Leu Ser Thr Ser Thr Leu Ser Ser Pro Ala
                85   90   95
Val Asn Xaa Cys Arg Phe Ala Pro Val Val Ser Asp Ala Phe Gly Val
            100   105   110
Gly Tyr Ala Val His Asp Asn Trp Ile Gly Cys Asn Val Ser Ser Tyr
        115   120   125
Pro Gly Arg Asn Ala Arg Glu Phe Leu Gln Cys Val Glu Lys Ala Xaa
    130   135   140
Glu Asp Met Phe Asp Ala Leu Glu Gly Lys Ser Ile Lys Ser
145   150   155

<210> 5915
<211> 457
<212> DNA
<213> Homo sapiens

<400> 5915
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120
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180
gtgtacagaa agtggattct ccaggacaaa cctgtgttca tggaggagcc agatagaaaa
240
gatgttgccc aagaagatgc tgaaaaatta ggattttccg agactgatag caaggaggcc
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360
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457

<210> 5916
<211> 152
<212> PRT
<213> Homo sapiens

<400> 5916
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Arg Met Val Tyr Glu Met Val Gln Arg Ile Leu Leu Ser Thr Arg Gly
20 25 30
Tyr Val Asn Phe Val Asn Glu Val Phe His Gln Ala Phe Leu Leu Pro
35 40 45
Ser Cys Glu Ile Ala Val Thr Arg Lys Val Val Gln Val Tyr Arg Lys
50 55 60
Trp Ile Leu Gln Asp Lys Pro Val Phe Met Glu Glu Pro Asp Arg Lys
65 70 75 80
Asp Val Ala Gln Glu Asp Ala Glu Lys Leu Gly Phe Ser Glu Thr Asp
85 90 95
Ser Lys Glu Ala Ser Ser Glu Ser Ser Gly His Lys Arg Ser Ser Ser
100 105 110
Trp Gly Arg Thr Tyr Ser Phe Thr Ser Ala Met Ser Arg Gly Cys Val
115 120 125
Thr Glu Glu Glu Asn Thr Asn Val Lys Ala Gly Val Gln Ala Leu Leu
130 135 140
Gln Val Phe Leu Ala Asn Ser Ala
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<210> 5917
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Arg Thr Met Leu Phe Thr Ile Gly Gln Ser Glu Val Tyr Leu Ile Ser
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785 790 795 800
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Gln Lys Ser Val Ser Lys His Lys Ser Ser Ser Lys Ile Ile Cys Cys
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Ile Ile Ser Ile Arg Asn Lys Asn Gly Glu Glu Lys Val Lys Ile Glu
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Arg Pro Gly Gly Ser Leu Ser Pro Ile Trp Ser Ile Cys Trp Asn Pro
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Ser Ser Arg Trp Glu Ser Phe Trp Met Asn Arg Glu Asn Glu Asp Ala
145 150 155 160
Glu Asp Val Ile Val Asn Arg Tyr Ile Gln Glu Ile Pro Ser Thr Leu
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Lys Ser Ala Val Tyr Ser Ser Gln Gly Ser Glu Ala Glu Glu Glu Glu
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Pro Glu Glu Glu Asp Asp Ser Pro Arg Asp Asp Asn Leu Glu Glu Arg
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Asn Asp Ile Leu Ala Val Ala Asp Trp Gly Gln Lys Val Ser Phe Tyr

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Gln Leu Ser Gly Lys Gln Ile Gly Lys Asp Arg Ala Leu Asn Phe Asp
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Pro Cys Cys Ile Ser Tyr Phe Thr Lys Gly Glu Tyr Ile Leu Leu Gly
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Gly Ser Asp Lys Gln Val Ser Leu Phe Thr Lys Asp Gly Val Arg Leu
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Gly Thr Val Gly Glu Gln Asn Ser Trp Val Trp Thr Cys Gln Ala Lys
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Pro Asp Ser Asn Tyr Val Val Val Gly Cys Gln Asp Gly Thr Ile Ser
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Phe Tyr Gln Leu Ile Phe Ser Thr Val His Gly Leu Tyr Lys Asp Arg
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Tyr Ala Tyr Arg Asp Ser Met Thr Asp Val Ile Val Gln His Leu Ile
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Thr Glu Gln Lys Val Arg Ile Lys Cys Lys Glu Leu Val Lys Lys Ile
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Ala Ile Tyr Arg Asn Arg Leu Ala Ile Gln Leu Pro Glu Lys Ile Leu
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Ile Tyr Glu Leu Tyr Ser Glu Asp Leu Ser Asp Met His Tyr Arg Val
    370                 375                 380
Lys Glu Lys Ile Ile Lys Lys Phe Glu Cys Asn Leu Leu Val Val Cys
385                 390                 395                 400
Ala Asn His Ile Ile Leu Cys Gln Glu Lys Arg Leu Gln Cys Leu Ser
                405                 410                 415
Phe Ser Gly Val Lys Glu Arg Glu Trp Gln Met Glu Ser Leu Ile Arg
            420                 425                 430
Tyr Ile Lys Val Ile Gly Gly Pro Pro Gly Arg Glu Gly Leu Leu Val
        435                 440                 445
Gly Leu Lys Asn Gly Gln Ile Leu Lys Ile Phe Val Asp Asn Leu Phe
    450                 455                 460
Ala Ile Val Leu Leu Lys Gln Ala Thr Ala Val Arg Cys Leu Asp Met
465                 470                 475                 480
Ser Ala Ser Arg Lys Lys Leu Ala Val Val Asp Glu Asn Asp Thr Cys
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Leu Val Tyr Asp Ile Asp Thr Lys Glu Leu Leu Phe Gln Glu Pro Asn
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Ala Asn Ser Val Ala Trp Asn Thr Gln Cys Glu Asp Met Leu Cys Phe
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Ser Gly Gly Gly Tyr Leu Asn Ile Lys Ala Ser Thr Phe Pro Val His
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Arg Gln Lys Leu Gln Gly Phe Val Val Gly Tyr Asn Gly Ser Lys Ile
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Ala Pro Met Tyr Gln Tyr Leu Asp Arg Lys Leu Phe Lys Glu Ala Tyr
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Gln Ile Ala Cys Leu Gly Val Thr Asp Thr Asp Trp Arg Glu Leu Ala
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Met Glu Ala Leu Glu Gly Leu Asp Phe Glu Thr Ala Lys Lys Ala Phe
    610                 615                 620
Ile Arg Val Gln Asp Leu Arg Tyr Leu Glu Leu Ile Ser Ser Ile Glu
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Glu Arg Lys Lys Arg Gly Glu Thr Asn Asn Asp Leu Phe Leu Ala Asp
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Val Phe Ser Tyr Gln Gly Lys Phe His Glu Ala Ala Lys Leu Tyr Lys
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Arg Ser Gly His Glu Asn Leu Ala Leu Glu Met Tyr Thr Asp Leu Cys
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Met Phe Glu Tyr Ala Lys Asp Phe Leu Gly Ser Gly Asp Pro Lys Glu
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Thr Lys Met Leu Ile Thr Lys Gln Ala Asp Trp Ala Arg Asn Ile Lys
705                 710                 715                 720
Glu Pro Lys Ala Ala Val Glu Met Tyr Ile Ser Ala Gly Glu His Val
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Lys Ala Ile Glu Ile Cys Gly Asp His Gly Trp Val Asp Met Leu Ile
            740                 745                 750
Asp Ile Ala Arg Lys Leu Asp Lys Ala Glu Arg Glu Pro Leu Leu Leu
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Cys Ala Thr Tyr Leu Lys Lys Leu Asp Ser Pro Gly Tyr Ala Ala Glu
    770                 775                 780
Thr Tyr Leu Lys Met Gly Asp Leu Lys Ser Leu Val Gln Leu His Val
785                 790                 795                 800
Glu Thr Gln Arg Trp Asp Glu Ala Phe Ala Leu Gly Glu Lys His Pro
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Glu Phe Lys Asp Asp Ile Tyr Met Pro Tyr Ala Gln Trp Leu Ala Glu
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Asn Asp Arg Phe Glu Glu Ala Gln Lys Ala Phe His Lys Ala Gly Arg
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Gln Arg Glu Ala Val Gln Val Leu Glu Gln Leu Thr Asn Asn Ala Val
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Ala Glu Ser Arg Phe Asn Asp Ala Ala Tyr Tyr Tyr Trp Met Leu Ser
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Met Gln Cys Leu Asp Ile Ala Gln Ala Asp Pro Ala Gln Lys Asp Thr
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Met Leu Gly Lys Phe Tyr His Phe Gln Arg Leu Ala Glu Leu Tyr His
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Gly Tyr His Ala Ile His Arg His Thr Glu Asp Pro Phe Ser Val His
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Arg Pro Glu Thr Leu Phe Asn Ile Ser Arg Phe Leu Leu His Ser Leu
    930                 935                 940
Pro Lys Asp Thr Pro Ser Gly Ile Ser Lys Val Lys Ile Leu Phe Thr
945                 950                 955                 960
Leu Ala Lys Gln Ser Lys Ala Leu Gly Ala Tyr Arg Leu Ala Arg His
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Ala Tyr Asp Lys Leu Arg Gly Leu Tyr Ile Pro Ala Arg Phe Gln Lys
            980                 985                 990
Ser Ile Glu Leu Gly Thr Leu Thr Ile Arg Ala Lys Pro Phe His Asp
        995                 1000                1005
Ser Glu Glu Leu Val Pro Leu Cys Tyr Arg Cys Ser Thr Asn Asn Pro
    1010                1015                1020
Leu Leu Asn Asn Leu Gly Asn Val Cys Ile Asn Cys Arg Gln Pro Phe
1025                1030                1035                1040
Ile Phe Ser Ala Ser Ser Tyr Asp Val Leu His Leu Val Glu Phe Tyr
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Leu Glu Glu Gly Ile Thr Asp Glu Glu Ala Ile Ser Leu Ile Asp Leu
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Glu Val Leu Arg Pro Lys Arg Asp Asp Arg Gln Leu Glu Ile Ala Asn
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        1075                1080                1085
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Asp Glu Asp Pro Phe Thr Ala Lys Leu Ser Phe Glu Gln Gly Gly Ser
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Glu Phe Val Pro Val Val Val Ser Arg Leu Val Leu Arg Ser Met Ser
                1125                1130                1135
Arg Arg Asp Val Leu Ile Lys Arg Trp Pro Pro Pro Leu Arg Trp Gln
            1140                1145                1150
Tyr Phe Arg Ser Leu Leu Pro Asp Ala Ser Ile Thr Met Cys Pro Ser
        1155                1160                1165
Cys Phe Gln Val Gly Gly His Pro Gly Ser Ser His Val Leu Leu Leu
    1170                1175                1180
Ala Thr Phe Pro Leu Pro Lys Cys Pro Ser Gly Arg Arg Gly Pro Trp
1185                1190                1195                1200
Glu Gly Gly Ala His Pro Trp Leu Gln Val Gly Thr Glu Ala Cys Leu
                1205                1210                1215
Ser Ser Pro Leu Leu Ala Phe His Val His Leu Lys Trp Thr Ser Leu
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Ala Pro Ala Leu Ser Thr Ser Ser Pro Asn Pro Gly Gly Pro Ala Ser
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Val Met Cys Pro
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<210> 5923
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 5923

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180
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240
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300
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360
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420
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480
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600
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660
aatcgaaatg ttatttcacg gcaaagcttt agaggtctac actgctgcct accagaatat
720
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acaaaacatt gatgaagatg aagatttaga ggttttccga aattctctgt atgcaccaga
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<210> 5924
<211> 146
<212> PRT
<213> Homo sapiens

<400> 5924
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Lys Met Lys Asp Ile Lys Thr Ile Phe Ser Glu Phe Ile Thr Ile Glu
        35                  40                  45
Met Leu Phe His Gly Lys Ala Leu Glu Val Tyr Thr Ala Ala Tyr Gln
    50                  55                  60
Asn Ile Gln Asn Ile Asp Glu Asp Glu Asp Leu Glu Val Phe Arg Asn
65                  70                  75                  80
Ser Leu Tyr Ala Pro Asp Tyr Ser Ser Arg Leu Asp Ile Val Arg Ala
                85                  90                  95
Asn Ser Lys Ser Pro Leu Gln Arg Ser Leu Ser Ala Lys Cys Val Ser
            100                 105                 110
Gly Thr Gly Gln Val Ser Thr Cys Arg Leu Arg Lys Asp Gln Gln Ala
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Glu Asp Asp Glu Asp Asp Glu Leu Asp Val Thr Glu Glu Glu Asn Phe
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Leu Lys
145
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<210> 5925
<211> 4538
<212> DNA
<213> Homo sapiens

<400> 5925

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900
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4538

<210> 5926
<211> 526
<212> PRT
<213> Homo sapiens

<400> 5926
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35 40 45
Ala Pro Pro Pro Ile Ser Pro Val Leu Pro Leu Val Pro Pro Pro Ala
50 55 60
Thr Ala Leu Asn Pro Pro Ala Pro Pro Thr Phe His Gln Pro Gln Lys
65 70 75 80
Phe Ala Gly Val Asn Lys Ala Pro Ser Val Ile Thr His Thr Ala Ser
85 90 95
Ala Thr Leu Thr His Asp Ala Pro Ala Thr Thr Phe Ser Gln Ser Gln
100 105 110
Gly Leu Val Ile Thr Thr His His Pro Ala Pro Ser Ala Ala Pro Cys
115 120 125
Gly Leu Ala Leu Ser Pro Val Thr Arg Pro Pro Gln Pro Arg Leu Thr
130 135 140
Phe Val His Pro Lys Pro Val Ser Leu Thr Gly Gly Arg Pro Lys Gln
145 150 155 160
Pro His Lys Ile Val Pro Ala Pro Lys Pro Glu Pro Val Ser Leu Val
165 170 175
Leu Lys Asn Ala Arg Ile Ala Pro Ala Ala Phe Ser Gly Gln Pro Gln
180 185 190
Ala Val Ile Met Thr Ser Gly Pro Leu Lys Arg Glu Gly Met Leu Ala
195 200 205
Ser Thr Val Ser Gln Ser Asn Val Val Ile Ala Pro Ala Ala Ile Ala
210 215 220
Arg Ala Pro Gly Val Pro Glu Phe His Ser Ser Ile Leu Val Thr Asp
225 230 235 240
Leu Gly His Gly Thr Ser Ser Pro Pro Ala Pro Val Ser Arg Leu Phe
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Pro Ser Thr Ala Gln Asp Pro Leu Gly Lys Gly Glu Gln Val Pro Leu

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Pro Asn Ser Gly Gln Ala Ser Pro Cys Ala Ser Glu Gln Ser Pro Ser
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Pro Gln Ser Pro Gln Asn Asn Cys Ser Gly Lys Ser Asp Pro Lys Asn
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Val Ala Ala Leu Lys Asn Arg Gln Met Lys His Ile Ser Ala Glu Gln
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Lys Arg Arg Phe Asn Ile Lys Met Cys Phe Asp Met Leu Asn Ser Leu
            340                 345                 350
Ile Ser Asn Asn Ser Lys Leu Thr Ser His Ala Ile Thr Leu Gln Lys
        355                 360                 365
Thr Val Glu Tyr Ile Thr Lys Leu Gln Gln Glu Arg Gly Gln Met Gln
    370                 375                 380
Glu Glu Ala Arg Arg Leu Arg Glu Glu Ile Glu Glu Leu Asn Ala Thr
385                 390                 395                 400
Ile Ile Ser Cys Gln Gln Leu Leu Pro Ala Thr Gly Val Pro Val Thr
                405                 410                 415
Arg Arg Gln Phe Asp His Met Lys Asp Met Phe Asp Glu Tyr Val Lys
            420                 425                 430
Thr Arg Thr Leu Gln Asn Trp Lys Phe Trp Ile Phe Ser Ile Ile Ile
        435                 440                 445
Lys Pro Leu Phe Glu Ser Phe Lys Gly Met Val Ser Thr Ser Ser Leu
    450                 455                 460
Glu Glu Leu His Arg Thr Ala Leu Ser Trp Leu Asp Gln His Cys Ser
465                 470                 475                 480
Leu Pro Ile Leu Arg Pro Met Val Leu Ser Thr Leu Arg Gln Leu Ser
                485                 490                 495
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            500                 505                 510
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<212> DNA
<213> Homo sapiens

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1786

<210> 5928
<211> 202
<212> PRT
<213> Homo sapiens

<400> 5928
Met Leu Glu Leu Pro Thr Ile Tyr Arg Lys Val Tyr Asp Gln Pro Phe

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His Ser Ser Ala Leu Glu Lys Glu Glu Ala Leu Ser Asn Pro Gly Ala
            20                  25                  30
Leu Asp Leu Pro Ser Leu Thr Ser Leu Leu Ser Glu Lys Ala Lys Glu
        35                  40                  45
Phe Leu Met Glu Asn Arg Val Gln Ser Phe Tyr Gln Gln Glu Leu Glu
    50                  55                  60
Met Val Glu Ser Leu Leu Ser Leu Ala Asn Gln Pro Val Ile His Ser
65                  70                  75                  80
Ala Cys Ser Asp Gln Val Asn Phe Lys Lys Asp Thr Thr Ser Lys Ala
                85                  90                  95
Ile His Ser Ile Phe Lys Asn Ala Ile Gln Leu Leu Gln Glu Lys Gly
            100                 105                 110
Leu Val Phe Gln Lys Asp Asp Gly Phe Asp Asn Leu Tyr Tyr Val Thr
        115                 120                 125
Arg Glu Asp Lys Asp Leu His Arg Lys Ile His Arg Ile Ile Gln Gln
    130                 135                 140
Asp Cys Gln Lys Pro Asn His Met Glu Lys Gly Cys His Phe Leu His
145                 150                 155                 160
Ile Leu Ala Cys Ala Arg Leu Ser Ile Arg Pro Gly Leu Ser Glu Ala
                165                 170                 175
Val Leu Gln Gln Val Leu Glu Leu Leu Glu Asp Gln Ser Asp Ile Val
            180                 185                 190
Ser Thr Met Glu His Tyr Tyr Thr Ala Phe
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<210> 5929
<211> 606
<212> DNA
<213> Homo sapiens

<400> 5929

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480
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606
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<210> 5930
<211> 144
<212> PRT
<213> Homo sapiens

<400> 5930
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20 25 30
Lys Glu Pro Leu Gly Arg Ala Glu Arg Pro Gly Arg Pro Cys Thr Arg
35 40 45
Leu Gln Pro Ala Gly Ser Val Ser Ser Thr Pro Leu Ser Thr Pro Cys
50 55 60
Ser Ser Val Pro Ser Ser Pro Ser Phe Ser Pro Thr Glu Gln Lys Thr
65 70 75 80
His Leu Glu Asp Leu Tyr Trp Met Ala Ser Asn Tyr Gln Gln Met Asn
85 90 95
Pro Glu Ala Leu Asn Leu Thr Pro Glu Asp Ala Val Glu Ala Leu Ile
100 105 110
Gly Ser His Pro Val Pro Gln Pro Leu Gln Ser Phe Asp Ser Phe Arg
115 120 125
Gly Ala His His His His His His His His Pro His Pro His His Ala
130 135 140

<210> 5931
<211> 478
<212> DNA
<213> Homo sapiens

<400> 5931
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ccgccttgga aagaggcttt ccggcagaga tgcctggaga gaatgagaaa cagccgggac
120
aggctcctaa acaggtaccg ccaggctgga agcagtgggc cagggaattc tcagaacagc
180
tttctagttc aagaggtgat ggaagaagag tggaatgctt tgcagtcagt ggagaattgt
240
ccagaagact tggctcagct ggaggagctg atagacatgg ctgtgctgga ggaaattcaa
300
caggagctga tcaaccaagg tacaacctga gaatcacaag cggtgtggtg gtgtgtcagt
360
gtggcctgtc catcccatct cattcttctg agttgacaga gcagaagctt cgtgcctgtt
420
tagagggtag tataaatgag cacagtgcac attgtcccca cacacccccc tcacgcgt
478

<210> 5932
<211> 109
<212> PRT
<213> Homo sapiens

<400> 5932
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1 5 10 15
Leu Val Gly Ser Pro Pro Trp Lys Glu Ala Phe Arg Gln Arg Cys Leu
20 25 30
Glu Arg Met Arg Asn Ser Arg Asp Arg Leu Leu Asn Arg Tyr Arg Gln
35 40 45
Ala Gly Ser Ser Gly Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln
50 55 60
Glu Val Met Glu Glu Glu Trp Asn Ala Leu Gln Ser Val Glu Asn Cys
65 70 75 80
Pro Glu Asp Leu Ala Gln Leu Glu Glu Leu Ile Asp Met Ala Val Leu
85 90 95
Glu Glu Ile Gln Gln Glu Leu Ile Asn Gln Gly Thr Thr
100 105

<210> 5933
<211> 1953
<212> DNA
<213> Homo sapiens

<400> 5933
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120
caggagctgg aagagctgac ggccagcctg tttgaggaag ctcacaagat ggttcgagaa
180
gccaacatga agcaggcggc atcagaaaag cagctgaagg aggctcgggg caagatcgac
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300
cccaaccgcg agcttcaccc ccagctgctg agccccacca aggccgggcc ccgaaagggc
360
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420
cacaccctca ccccagacag agagggcaag gaggtggaca caatcctgtt tgcagagttc
480
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540
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600
gccgccgtgg aggacaacac gctcaccatt gagccggtgg cttcgcagac gctgcccaca
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gtgaaggtgg ccgaggttga ctgtagcagc accaacacat gtgccctgag cgggctgacc
720
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tcttcccggg ccaggatcac cgcagtgtgc aacttcttca cctacatccg ctacatccag
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caaggcctgg tgcggcagga cgcagagccc atgttctggg agatcatgag gttgcggaag
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960

tgaaggggag ctctgagaca gagcaaacac ccaccccaga acaagccgac acacagggag
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acgggggcct ggagccagcc ctgagccaga ggcagaatgg atggacagac aggccatgga
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1380
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1620
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1680
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1740
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1800
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1920
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1953

<210> 5934
<211> 314
<212> PRT
<213> Homo sapiens

<400> 5934
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Arg Ala Gln Lys Glu Leu Lys Leu Lys Asp Glu Glu Cys Glu Arg Leu
20 25 30
Ser Lys Val Arg Glu Gln Leu Glu Gln Glu Leu Glu Glu Leu Thr Ala
35 40 45
Ser Leu Phe Glu Glu Ala His Lys Met Val Arg Glu Ala Asn Met Lys
50 55 60
Gln Ala Ala Ser Glu Lys Gln Leu Lys Glu Ala Arg Gly Lys Ile Asp
65 70 75 80
Met Leu Gln Ala Glu Val Thr Ala Leu Lys Thr Leu Val Ile Thr Ser
85 90 95
Thr Pro Ala Ser Pro Asn Arg Glu Leu His Pro Gln Leu Leu Ser Pro

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            100                 105                 110
Thr Lys Ala Gly Pro Arg Lys Gly His Ser Arg His Lys Ser Thr Ser
        115                 120                 125
Ser Thr Leu Cys Pro Ala Val Cys Pro Ala Ala Gly His Thr Leu Thr
    130                 135                 140
Pro Asp Arg Glu Gly Lys Glu Val Asp Thr Ile Leu Phe Ala Glu Phe
145                 150                 155                 160
Gln Ala Trp Arg Glu Ser Pro Thr Leu Asp Lys Thr Cys Pro Phe Leu
                165                 170                 175
Glu Arg Val Tyr Arg Glu Asp Val Gly Pro Cys Leu Asp Phe Thr Met
            180                 185                 190
Gln Glu Leu Ser Val Leu Val Arg Ala Ala Val Glu Asp Asn Thr Leu
        195                 200                 205
Thr Ile Glu Pro Val Ala Ser Gln Thr Leu Pro Thr Val Lys Val Ala
    210                 215                 220
Glu Val Asp Cys Ser Ser Thr Asn Thr Cys Ala Leu Ser Gly Leu Thr
225                 230                 235                 240
Arg Thr Cys Arg His Arg Ile Arg Leu Gly Asp Ser Lys Ser His Tyr
                245                 250                 255
Tyr Ile Ser Pro Ser Ser Arg Ala Arg Ile Thr Ala Val Cys Asn Phe
            260                 265                 270
Phe Thr Tyr Ile Arg Tyr Ile Gln Gln Gly Leu Val Arg Gln Asp Ala
        275                 280                 285
Glu Pro Met Phe Trp Glu Ile Met Arg Leu Arg Lys Glu Met Ser Leu
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Ala Lys Leu Gly Phe Phe Pro Gln Glu Ala
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<210> 5935
<211> 2727
<212> DNA
<213> Homo sapiens

<400> 5935

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120
ctccggaata tggggaactg cctcaaatcc cccacctcgg atgacatctc cctgcttcac
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gagtctcagt ccgaccgggc tagctttggc gaggggacgg agccggatca ggagccgccg
240
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420
gagtgtgtga tctgtatgat ggactttgtt tatggggacc caattcgatt tctgccgtgc
480
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600
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2100
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2160
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2220

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2280
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2580
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2700
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2727

<210> 5936
<211> 154
<212> PRT
<213> Homo sapiens

<400> 5936
Met Gly Asn Cys Leu Lys Ser Pro Thr Ser Asp Asp Ile Ser Leu Leu
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His Glu Ser Gln Ser Asp Arg Ala Ser Phe Gly Glu Gly Thr Glu Pro
            20   25   30
Asp Gln Glu Pro Pro Pro Pro Tyr Gln Glu Gln Val Pro Val Pro Val
        35   40   45
Tyr His Pro Thr Pro Ser Gln Thr Arg Leu Ala Thr Gln Leu Thr Glu
    50   55   60
Glu Glu Gln Ile Arg Ile Ala Gln Arg Ile Gly Leu Ile Gln His Leu
65   70   75   80
Pro Lys Gly Val Tyr Asp Pro Gly Arg Asp Gly Ser Glu Lys Lys Ile
                85   90   95
Arg Glu Cys Val Ile Cys Met Met Asp Phe Val Tyr Gly Asp Pro Ile
            100   105   110
Arg Phe Leu Pro Cys Met His Ile Tyr His Leu Asp Cys Ile Asp Asp
        115   120   125
Trp Leu Met Arg Ser Phe Thr Cys Pro Ser Cys Met Glu Pro Val Asp
    130   135   140
Ala Ala Leu Leu Ser Ser Tyr Glu Thr Asn
145   150

<210> 5937
<211> 1536
<212> DNA
<213> Homo sapiens

<400> 5937
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tttgcatcag ttatctcaag gtctgagacc tgtggttgtc gaaccccagt ggactttagt
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660
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<210> 5938
<211> 406
<212> PRT

<213> Homo sapiens

<400> 5938

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            20                  25                  30
Gly Lys Ser Leu Ile Val Pro Phe Lys Gly Ser Arg Val Ile Asp Ser
        35                  40                  45
Thr Val Leu Pro Gly Ile Leu Ile Glu Met Ser Glu Val Gln Leu Met
    50                  55                  60
Arg Leu Leu Pro Ile Lys Lys Ser Thr Ala Leu Lys Val Ala Leu Phe
65                  70                  75                  80
Cys Thr Thr Leu Ser Gly Asp Thr Ser Asp Thr Gly Glu Gly Thr Val
                85                  90                  95
Val Val Ser Tyr Gly Val Ser Leu Glu Asn Ala Val Leu Asp Gln Leu
            100                 105                 110
Leu Asn Leu Gly Arg Gln Leu Ile Ser Asp His Val Asp Leu Val Leu
        115                 120                 125
Cys Gln Lys Val Ile His Pro Ser Leu Lys Gln Phe Leu Asn Met His
    130                 135                 140
Arg Ile Ile Ala Ile Asp Arg Ile Gly Val Thr Leu Met Glu Pro Leu
145                 150                 155                 160
Thr Lys Met Thr Gly Thr Gln Pro Ile Gly Ser Leu Gly Ser Ile Cys
                165                 170                 175
Pro Asn Ser Tyr Gly Ser Val Lys Asp Val Cys Thr Ala Lys Phe Gly
            180                 185                 190
Ser Lys His Phe Phe His Leu Ile Pro Asn Glu Ala Thr Ile Cys Ser
        195                 200                 205
Leu Leu Leu Cys Asn Arg Asn Asp Thr Ala Trp Asp Glu Leu Lys Leu
    210                 215                 220
Thr Cys Gln Thr Ala Leu His Val Leu Gln Leu Thr Leu Lys Glu Pro
225                 230                 235                 240
Trp Ala Leu Leu Gly Gly Gly Cys Thr Glu Thr His Leu Ala Ala Tyr
                245                 250                 255
Ile Arg His Lys Thr His Asn Asp Pro Glu Ser Ile Leu Lys Asp Asp
            260                 265                 270
Glu Cys Thr Gln Thr Glu Leu Gln Leu Ile Ala Glu Ala Phe Cys Ser
        275                 280                 285
Ala Leu Glu Ser Val Val Gly Ser Leu Glu His Asp Gly Gly Glu Ile
    290                 295                 300
Leu Thr Asp Met Lys Tyr Gly His Leu Trp Ser Val Gln Ala Asp Ser
305                 310                 315                 320
Pro Cys Val Ala Asn Trp Pro Asp Leu Leu Ser Gln Cys Gly Cys Gly
                325                 330                 335
Leu Tyr Asn Ser Gln Glu Glu Leu Asn Trp Ser Phe Leu Arg Ser Thr
            340                 345                 350
Arg Arg Pro Phe Val Pro Gln Ser Cys Leu Pro His Glu Ala Val Gly
        355                 360                 365
Ser Ala Ser Asn Leu Thr Leu Asp Cys Leu Thr Ala Lys Leu Ser Gly
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Leu Gln Val Ala Val Glu Thr Ala Asn Leu Ile Leu Asp Leu Ser Tyr
385                 390                 395                 400
Val Ile Glu Asp Lys Asn
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405

<210> 5939
<211> 795
<212> DNA
<213> Homo sapiens

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420
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<210> 5940
<211> 96
<212> PRT
<213> Homo sapiens

<400> 5940
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Ala Ile Phe Lys Glu Asn Lys Arg Pro Ser Lys Glu Met Gln Val Thr
35 40 45
Ile Ser Gln Gln Leu Gly Leu Glu Leu Asn Thr Val Ser Asn Phe Phe
50 55 60
Met Asn Ala Arg Arg Arg Cys Met Asn Arg Trp Ala Glu Glu Pro Ser
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Thr Ala Pro Gly Gly Pro Ala Gly Ala Thr Ala Thr Phe Ser Lys Ala

85 90 95

<210> 5941
<211> 2590
<212> DNA
<213> Homo sapiens

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<210> 5942
<211> 89
<212> PRT
<213> Homo sapiens

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Arg Gln Ser Leu Ala Leu Leu Xaa Gln Val Gly Val Gln Trp His Asp
            20   25   30
Pro Gly Ser Leu Gln Pro Pro Pro Pro Gly Phe Lys Gln Phe Ser Cys

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        35                  40                  45
Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Cys Leu Ser Ser Arg Leu
    50                  55                  60
Ala Thr Phe Cys Ile Phe Ser Arg Asp Arg Val Ser Pro Cys Trp Pro
65                  70                  75                  80
Gly Trp Ser Gln Thr Pro Asp Leu Lys
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<211> 781
<212> DNA
<213> Homo sapiens

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<210> 5944
<211> 174
<212> PRT
<213> Homo sapiens

<400> 5944
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            20                  25                  30
Gly Val Ser Ser Ile Thr Lys Leu Gln Arg Gln Pro Phe Gly Val Glu
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        35                  40                  45
Thr Lys Pro Gly Ile Leu Cys Cys Phe Gln Asn Glu Phe Glu Asn Pro
    50                  55                  60
Cys Phe Pro Lys Ser His Phe Ser Val Thr Gln Ala Gly Glu Gln Trp
65                  70                  75                  80
Arg Asp Leu Ser Ser Pro Gln Pro Pro Pro Pro Arg Phe Lys Gln Phe
                85                  90                  95
Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp His Arg His Pro Pro Pro
            100                 105                 110
Arg Pro Ala Asn Phe Cys Ile Phe Ser Arg Asp Glu Val Ser Pro Arg
        115                 120                 125
Ser Arg Ser Pro Asp Leu Met Xaa Ser Ala His Leu Gly Leu Pro Lys
    130                 135                 140
Cys Trp Asp Tyr Arg Arg Glu Pro Leu Arg Pro Ala Gln Ile Ser Leu
145                 150                 155                 160
Leu Phe Ser Lys Ser Pro Ser Gln Asp Ile Gln Ala Lys Ala
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<210> 5945
<211> 869
<212> DNA
<213> Homo sapiens

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180
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240
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300
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360
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420
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720
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869

<210> 5946
<211> 121
<212> PRT
<213> Homo sapiens

<400> 5946
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Arg Lys Gln Tyr Glu Lys Ser Ser Arg Phe Met Lys Val Gly Tyr Glu
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Arg Asp Phe Leu Arg Tyr Leu Gln Ser Leu Leu Ala Glu Val Glu Arg
35 40 45
Arg Ile Arg Arg Gly His Ala Arg Leu Ala Leu Ser Gln Asn Gln Gln
50 55 60
Ser Ser Gly Ala Ala Gly Pro Thr Gly Lys Asn Gly Glu Lys Ile Gln
65 70 75 80
Val Leu Thr Asp Lys Ile Asp Val Leu Leu Gln Gln Ile Glu Glu Leu
85 90 95
Gly Ser Glu Gly Lys Val Glu Glu Ala Gln Gly Met Met Lys Leu Val
100 105 110
Glu Gln Leu Lys Glu Glu Arg Glu Leu
115 120

<210> 5947
<211> 2283
<212> DNA
<213> Homo sapiens

<400> 5947
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gaagtatctg tttctcctag agcttcaaaa catcattatt caagatcacg atcaaggtca
180
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240
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300
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360
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420
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<210> 5948
<211> 76
<212> PRT
<213> Homo sapiens

<400> 5948
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20 25 30
Pro Arg Ala Ser Lys His His Tyr Ser Arg Ser Arg Ser Arg Ser Arg
35 40 45
Glu Arg Lys Arg Lys Ser Asp Asn Glu Gly Arg Lys His Arg Ser Arg
50 55 60
Ser Arg Ser Lys Glu Arg Ala Tyr Ala Arg Arg Asp
65 70 75

<210> 5949
<211> 4706
<212> DNA
<213> Homo sapiens

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3360
aaccaaacag ctgccctcat tagcggattc cgttccatta tcaaacccga gtggatccga
3420
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3540
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aagttcgtga ccagctgctc cagacccccg ctcctgggat tcgcctacct caagcctcca
3660
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3780
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4080
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4140

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4200
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4380
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4440
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4500
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4560
agctgccaga gagtcttccc ggacctattc ccgtcctatg cattcacatt ggcatcctgg
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4680
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4706

<210> 5950
<211> 397
<212> PRT
<213> Homo sapiens

<400> 5950
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Leu Thr Phe Phe Lys Asp Gly Tyr Glu Gln Leu Arg Gln Leu Ser Gln
20 25 30
His Ala Met Lys Gly Val Ile Arg Val Lys Phe Val Asn Asp Leu Gly
35 40 45
Val Asp Glu Ala Gly Ile Asp Gln Asp Gly Val Phe Lys Glu Phe Leu
50 55 60
Glu Glu Ile Ile Lys Arg Val Phe Asp Pro Ala Leu Asn Leu Phe Lys
65 70 75 80
Thr Thr Ser Gly Asp Glu Arg Leu Tyr Pro Ser Pro Thr Ser Tyr Ile
85 90 95
His Glu Asn Tyr Leu Gln Leu Phe Glu Phe Val Gly Lys Met Leu Gly
100 105 110
Lys Ala Val Tyr Glu Gly Ile Val Val Asp Val Pro Phe Ala Ser Phe
115 120 125
Phe Leu Ser Gln Leu Leu Gly His His His Ser Val Phe Tyr Ser Ser
130 135 140
Val Asp Glu Leu Pro Ser Leu Asp Ser Glu Phe Tyr Lys Asn Leu Thr
145 150 155 160
Ser Ile Lys Arg Tyr Asp Gly Asp Ile Thr Asp Leu Gly Leu Thr Leu
165 170 175
Ser Tyr Asp Glu Asp Val Met Gly Gln Leu Val Cys His Glu Leu Ile
180 185 190
Pro Gly Gly Lys Thr Ile Pro Val Thr Asn Glu Asn Lys Ile Ser Tyr
195 200 205
Ile His Leu Met Ala His Phe Arg Met His Thr Gln Ile Lys Asn Gln

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    210                 215                 220
Thr Ala Ala Leu Ile Ser Gly Phe Arg Ser Ile Ile Lys Pro Glu Trp
225                 230                 235                 240
Ile Arg Met Phe Ser Thr Pro Glu Leu Gln Arg Leu Ile Ser Gly Asp
                245                 250                 255
Asn Ala Glu Ile Asp Leu Glu Asp Leu Lys Lys His Thr Val Tyr Tyr
            260                 265                 270
Gly Gly Phe His Gly Ser His Arg Val Ile Ile Trp Leu Trp Asp Ile
        275                 280                 285
Leu Ala Ser Asp Phe Thr Pro Asp Glu Arg Ala Met Phe Leu Lys Phe
    290                 295                 300
Val Thr Ser Cys Ser Arg Pro Pro Leu Leu Gly Phe Ala Tyr Leu Lys
305                 310                 315                 320
Pro Pro Phe Ser Ile Arg Cys Val Glu Val Ser Asp Asp Gln Asp Thr
                325                 330                 335
Gly Asp Thr Leu Gly Ser Val Leu Arg Gly Phe Phe Thr Ile Arg Lys
            340                 345                 350
Arg Glu Pro Gly Gly Arg Leu Pro Thr Ser Ser Thr Cys Phe Asn Leu
        355                 360                 365
Leu Lys Leu Pro Asn Tyr Ser Lys Lys Ser Val Leu Arg Glu Lys Leu
    370                 375                 380
Arg Tyr Ala Ile Ser Met Asn Thr Gly Phe Glu Leu Ser
385                 390                 395
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<210> 5951
<211> 1724
<212> DNA
<213> Homo sapiens

<400> 5951
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120
agaggagggg tcgccaggtt cccgtctgct ttcggaggcg gatcgagcgg gtgacttttg
180
tgcattcgtt ttaatttttg gaaatctctc ttttttcctc cctcgctcgc tgccgggcat
240
gtcctgatct ggcggccgct cctaccaccc tgggcagccg agcagagtgg tccccagcgg
300
tctccctccc tgcctccctg actttgcaac accgcgttcc gggaggaccg gcctcggcga
360
gggaggaggc gggggagctg cgaacaccca gacccaaacc ctgacatgct ctggggcgga
420
gaggaggaag ccaggagctg agcgcgccgc gtgggctgct tcgccctccg gctccgagcg
480
ccgggctccg ggcgccctgc cctgcgcctg ggcagcagcc ttgctggtct tgggggcgcc
540
ccccgcttcc cgcccggggg gttcgcggcc ggcaggacca tgctgctgaa agagtaccgg
600
atctgcatgc cgctcaccgt agacgagtac aaaattggac agctgtacat gatcagcaaa
660
cacagccatg aacagagtga ccggggagaa ggggtggagg tcgtccagaa tgagcccttt
720

gaggaccctc accatggcaa tgggcagttc accgagaagc gggtgtatct caacagcaaa
780
ctgcctagtt gggctagagc tgttgtcccc aaaatatttt atgtgacaga gaaggcttgg
840
aactattatc cctacacaat tacagaatac acatgttcct ttctgccgaa attctccatt
900
catatagaaa ccaagtatga ggacaacaaa ggaagcaatg acaccatttt cgacaatgaa
960
gccaaagacg tggagagaga agtttgcttt attgatattg cctgcgatga aattccagag
1020
cgctactaca aagaatctga ggatcctaag cacttcaagt cagagaagac aggacgggga
1080
cagttgaggg aaggctggag agatagtcat cagcctatca tgtgctccta caagctggtg
1140
actgtgaagt ttgaggtctg ggggcttcag accagagtgg aacaatttgt acacaaggtg
1200
gtccgagaca ttctgctgat tggacataga caggcttttg catgggttga tgagtggtat
1260
gacatgacaa tggatgaagt ccgagaattt gaacgagcca ctcaggaagc caccaacaag
1320
aaaatcggca ttttcccacc tgcaatttct atctccagca tccccctgct gccttcttcc
1380
gtccgcagtg cgccttctag tgctccatcc acccctctct ccacagacgc acccgaattt
1440
ctgtccgttc ccaaagatcg gccccggaaa aagtctgccc cagaaactct cacacttcca
1500
gaccctgaga aaaaagccac cctgaattta cccggcatgc actcttcaga taagccatgt
1560
cggcccaaat ctgagtaact ttatataaat atctcatggg gttttatatt ttcatttgtt
1620
gttgttgttt ttttttaaga atcttctgat agagaaaaag actgctttgt cactcaaaca
1680
tgttccttcg accttaaaaa aaaaaaaaaa aaaaaaaaaa aaaa
1724

<210> 5952
<211> 378
<212> PRT
<213> Homo sapiens

<400> 5952
Ala Arg Arg Val Gly Cys Phe Ala Leu Arg Leu Arg Ala Pro Gly Ser
1 5 10 15
Gly Arg Pro Ala Leu Arg Leu Gly Ser Ser Leu Ala Gly Leu Gly Gly
20 25 30
Ala Pro Arg Phe Pro Pro Gly Gly Phe Ala Ala Gly Arg Thr Met Leu
35 40 45
Leu Lys Glu Tyr Arg Ile Cys Met Pro Leu Thr Val Asp Glu Tyr Lys
50 55 60
Ile Gly Gln Leu Tyr Met Ile Ser Lys His Ser His Glu Gln Ser Asp
65 70 75 80
Arg Gly Glu Gly Val Glu Val Val Gln Asn Glu Pro Phe Glu Asp Pro
85 90 95
His His Gly Asn Gly Gln Phe Thr Glu Lys Arg Val Tyr Leu Asn Ser

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            100                 105                 110
Lys Leu Pro Ser Trp Ala Arg Ala Val Val Pro Lys Ile Phe Tyr Val
        115                 120                 125
Thr Glu Lys Ala Trp Asn Tyr Tyr Pro Tyr Thr Ile Thr Glu Tyr Thr
    130                 135                 140
Cys Ser Phe Leu Pro Lys Phe Ser Ile His Ile Glu Thr Lys Tyr Glu
145                 150                 155                 160
Asp Asn Lys Gly Ser Asn Asp Thr Ile Phe Asp Asn Glu Ala Lys Asp
                165                 170                 175
Val Glu Arg Glu Val Cys Phe Ile Asp Ile Ala Cys Asp Glu Ile Pro
            180                 185                 190
Glu Arg Tyr Tyr Lys Glu Ser Glu Asp Pro Lys His Phe Lys Ser Glu
        195                 200                 205
Lys Thr Gly Arg Gly Gln Leu Arg Glu Gly Trp Arg Asp Ser His Gln
    210                 215                 220
Pro Ile Met Cys Ser Tyr Lys Leu Val Thr Val Lys Phe Glu Val Trp
225                 230                 235                 240
Gly Leu Gln Thr Arg Val Glu Gln Phe Val His Lys Val Val Arg Asp
                245                 250                 255
Ile Leu Leu Ile Gly His Arg Gln Ala Phe Ala Trp Val Asp Glu Trp
            260                 265                 270
Tyr Asp Met Thr Met Asp Glu Val Arg Glu Phe Glu Arg Ala Thr Gln
        275                 280                 285
Glu Ala Thr Asn Lys Lys Ile Gly Ile Phe Pro Pro Ala Ile Ser Ile
    290                 295                 300
Ser Ser Ile Pro Leu Leu Pro Ser Ser Val Arg Ser Ala Pro Ser Ser
305                 310                 315                 320
Ala Pro Ser Thr Pro Leu Ser Thr Asp Ala Pro Glu Phe Leu Ser Val
                325                 330                 335
Pro Lys Asp Arg Pro Arg Lys Lys Ser Ala Pro Glu Thr Leu Thr Leu
            340                 345                 350
Pro Asp Pro Glu Lys Lys Ala Thr Leu Asn Leu Pro Gly Met His Ser
        355                 360                 365
Ser Asp Lys Pro Cys Arg Pro Lys Ser Glu
    370                 375
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<210> 5953
<211> 777
<212> DNA
<213> Homo sapiens

<400> 5953

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120
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180
aacagctttc tagttcaaga ggtgatggaa gaagagtgga atgctttgca gtcagtggag
240
aattgtccag aagacttggc tcagctggag gagctgatag acatggctgt gctggaggaa
300
attcaacagg agctgatcaa ccaagagcag tccatcatca gcgagtatga gaagagcttg
360
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cagtttgatg aaaagtgtct cagcatcatg ctggctgagt gggaggcaaa cccactcatc
420
tgtcctgtat gtacaaagcc tgtgatactt gggctgtgat cctctagagc cagcttggac
480
tcacatcatt ctatggggtt gaagacaact cattccctct gaggagcctt gtacatacaa
540
gccttttatt tataacttat tttgtattga aacttttaaa caatactgaa gaaaaaaaaa
600
cttttccgac atctgttctt ggtctttttgt gacgcaggtt gaaggggggag gaatagaaaa
660
agacaaactg ccttggagga gataaaccaa ttttatgtct atcatgttat acaaaaatct
720
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777

<210> 5954
<211> 152
<212> PRT
<213> Homo sapiens

<400> 5954
Phe Arg His Glu Ala Arg Ser Arg Lys Arg Ser Pro Arg Arg Ser Leu
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Tyr Lys Leu Val Gly Ser Pro Pro Trp Lys Glu Ala Phe Arg Gln Arg
20 25 30
Cys Leu Glu Arg Met Arg Asn Ser Arg Asp Arg Leu Leu Asn Arg Tyr
35 40 45
Arg Gln Leu Xaa Ser Ser Gly Pro Gly Asn Ser Gln Asn Ser Phe Leu
50 55 60
Val Gln Glu Val Met Glu Glu Glu Trp Asn Ala Leu Gln Ser Val Glu
65 70 75 80
Asn Cys Pro Glu Asp Leu Ala Gln Leu Glu Glu Leu Ile Asp Met Ala
85 90 95
Val Leu Glu Glu Ile Gln Gln Glu Leu Ile Asn Gln Glu Gln Ser Ile
100 105 110
Ile Ser Glu Tyr Glu Lys Ser Leu Gln Phe Asp Glu Lys Cys Leu Ser
115 120 125
Ile Met Leu Ala Glu Trp Glu Ala Asn Pro Leu Ile Cys Pro Val Cys
130 135 140
Thr Lys Pro Val Ile Leu Gly Leu
145 150

<210> 5955
<211> 1459
<212> DNA
<213> Homo sapiens

<400> 5955
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agatatcctg gagggctcat gagtgaattt agtccaagat ttaaagccct gcccccaggt
120
gctcagcctg tgatctgtat ccactcagca tgcacttggg cagatgattt gtctgtgtgc
180

taccctccc cccatattac catacatatg cacggcggga ccagcagcga cggtagcagc
240
agcatggccg cgatctatgg gggtgtagag gggggaggca cacgatccga ggtcctttta
300
gtctcagagg atgggaagat cctggcagaa gcagatggac tgagcacaaa ccactggctg
360
atcgggacag acaagtgtgt ggagaggatc aatgagatgg tgaacagggc caaacggaaa
420
gcaggggtgg atcctctggt accgctgcga agcttgggcc tatctctgag cggtggggac
480
caggaggacg cggggaggat cctgatcgag gagctgaggg accgatttcc ctacctgagt
540
gaaagctact taatcaccac cgatgccgcc ggctccatcg ccacagctac accggatggt
600
ggagttgtgc tcatatctgg aacaggctcc aactgcaggc tcatcaaccc tgatggctcc
660
gagagtggct gcggcggctg gggccatatg atgggtgatg agggttcagc cctctctgct
720
ccctcagcct actggatcgc acaccaagca gtgaaaatag tgtttgactc cattgacaac
780
ctagaggcgg ctcctcatga tatcggctac gtcaaacagg ccatgttcca ctatttccag
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900
gctgggtttt gccggaaaat tgcagaaggt gctcagcagg gagacccccc ttcccgctat
960
atcttcagga aggctgggga gatgctgggc agacacatcg tagcagtgtt gcccgagatt
1020
gacccggtct tgttccaggg caagattgga ctccccatcc tgtgcgtggg ctctgtgtgg
1080
aagagctggg agctgctgaa ggaaggtttt cttttggcgc tgacccaggg cagagagatc
1140
caggctcaga acttcttctc cagcttcacc ctgatgaagc tgaggcactc ctccgctctg
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ggtggggcca gcctaggggc caggcacatc gggcacctcc tccccatgga ctatagcgcc
1260
aatgccattg ccttctattc ctacaccttt tcctaggggg ctggtcccgg ctccaccccc
1320
tccaagctca gtggacactg ggtctgaaag gaaggagtct tttgcttcct ttctcctttt
1380
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1440
aaaaaaaaaa aagtcgacg
1459

<210> 5956
<211> 431
<212> PRT
<213> Homo sapiens

<400> 5956
Xaa Asn Trp Thr Ala Leu Ser Asn Thr Cys Ala Met Tyr Ile Leu Ser
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Ala Pro Ala Ser Arg Tyr Pro Gly Gly Leu Met Ser Glu Phe Ser Pro

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            20                  25                  30
Arg Phe Lys Ala Leu Pro Pro Gly Ala Gln Pro Val Ile Cys Ile His
        35                  40                  45
Ser Ala Cys Thr Trp Ala Asp Asp Leu Ser Val Cys Tyr Pro Ser Pro
    50                  55                  60
His Ile Thr Ile His Met His Gly Gly Thr Ser Ser Asp Gly Ser Ser
65                  70                  75                  80
Ser Met Ala Ala Ile Tyr Gly Gly Val Glu Gly Gly Gly Thr Arg Ser
                85                  90                  95
Glu Val Leu Leu Val Ser Glu Asp Gly Lys Ile Leu Ala Glu Ala Asp
            100                 105                 110
Gly Leu Ser Thr Asn His Trp Leu Ile Gly Thr Asp Lys Cys Val Glu
        115                 120                 125
Arg Ile Asn Glu Met Val Asn Arg Ala Lys Arg Lys Ala Gly Val Asp
    130                 135                 140
Pro Leu Val Pro Leu Arg Ser Leu Gly Leu Ser Leu Ser Gly Gly Asp
145                 150                 155                 160
Gln Glu Asp Ala Gly Arg Ile Leu Ile Glu Glu Leu Arg Asp Arg Phe
                165                 170                 175
Pro Tyr Leu Ser Glu Ser Tyr Leu Ile Thr Thr Asp Ala Ala Gly Ser
            180                 185                 190
Ile Ala Thr Ala Thr Pro Asp Gly Gly Val Val Leu Ile Ser Gly Thr
        195                 200                 205
Gly Ser Asn Cys Arg Leu Ile Asn Pro Asp Gly Ser Glu Ser Gly Cys
    210                 215                 220
Gly Gly Trp Gly His Met Met Gly Asp Glu Gly Ser Ala Leu Ser Ala
225                 230                 235                 240
Pro Ser Ala Tyr Trp Ile Ala His Gln Ala Val Lys Ile Val Phe Asp
                245                 250                 255
Ser Ile Asp Asn Leu Glu Ala Ala Pro His Asp Ile Gly Tyr Val Lys
            260                 265                 270
Gln Ala Met Phe His Tyr Phe Gln Val Pro Asp Arg Leu Gly Ile Leu
        275                 280                 285
Thr His Leu Tyr Arg Asp Phe Asp Lys Cys Arg Phe Ala Gly Phe Cys
    290                 295                 300
Arg Lys Ile Ala Glu Gly Ala Gln Gln Gly Asp Pro Leu Ser Arg Tyr
305                 310                 315                 320
Ile Phe Arg Lys Ala Gly Glu Met Leu Gly Arg His Ile Val Ala Val
                325                 330                 335
Leu Pro Glu Ile Asp Pro Val Leu Phe Gln Gly Lys Ile Gly Leu Pro
            340                 345                 350
Ile Leu Cys Val Gly Ser Val Trp Lys Ser Trp Glu Leu Leu Lys Glu
        355                 360                 365
Gly Phe Leu Leu Ala Leu Thr Gln Gly Arg Glu Ile Gln Ala Gln Asn
    370                 375                 380
Phe Phe Ser Ser Phe Thr Leu Met Lys Leu Arg His Ser Ser Ala Leu
385                 390                 395                 400
Gly Gly Ala Ser Leu Gly Ala Arg His Ile Gly His Leu Leu Pro Met
                405                 410                 415
Asp Tyr Ser Ala Asn Ala Ile Ala Phe Tyr Ser Tyr Thr Phe Ser
            420                 425                 430
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<210> 5957
<211> 855

<212> DNA
<213> Homo sapiens

<400> 5957
atggcggagt cgttgaggtc tccgcgccgc tccctgtaca aactggtggg ctcgccgcct
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tggaaagagg ctttccggca gagatgcctg gagagaatga gaaacagccg ggacaggctc
120
ctaaacaggt accgccaggc tggaagcagt gggccaggga attctcagaa cagctttcta
180
gttcaagagg tgatggaaga agagtggaat gctttgcagt cagtggagaa ttgtccagaa
240
gacttggctc agctggagga gctgatagac atggctgtgc tggaggaaat tcaacaggag
300
ctgatcaacc aaggcctgtg atacttgggc tgtgatcctc tagagccagc ttggactcac
360
atcattctat ggggttgaag acaactcatt ccctctgagg agccttgtac atacaagcct
420
tttatttata acttattttg tattgaaact tttaaacaat actgaagaaa aaaaaacttt
480
tccgacatct gttcttggtc ttttgtgaca caggttgaag ggggaggaat agaaaaagac
540
aaactgcctt ggaggagata aaccaatttt atgtctatca tgttatacaa aaatctagaa
600
ataatagatt tgtacagaaa aaaatgataa taaatgagag cacaaaacat ataatttaaa
660
tctggtattt tttcccccat gatattagga tgataatcat ttcaaagcac atgtctagct
720
tcagagtagg atttgttcac tggccaaagc ctgccatgaa actatggctt tcagcatctg
780
tctgctctac tggctcttga caaaactctt gaggtcttca agaaaagtaa tgtactcctg
840
gtgctccagg gctgt
855

<210> 5958
<211> 106
<212> PRT
<213> Homo sapiens

<400> 5958
Met Ala Glu Ser Leu Arg Ser Pro Arg Arg Ser Leu Tyr Lys Leu Val
 1   5   10   15
Gly Ser Pro Pro Trp Lys Glu Ala Phe Arg Gln Arg Cys Leu Glu Arg
            20   25   30
Met Arg Asn Ser Arg Asp Arg Leu Leu Asn Arg Tyr Arg Gln Ala Gly
        35   40   45
Ser Ser Gly Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln Glu Val
    50   55   60
Met Glu Glu Glu Trp Asn Ala Leu Gln Ser Val Glu Asn Cys Pro Glu
65   70   75   80
Asp Leu Ala Gln Leu Glu Glu Leu Ile Asp Met Ala Val Leu Glu Glu
                85   90   95
Ile Gln Gln Glu Leu Ile Asn Gln Gly Leu

100 105

<210> 5959
<211> 830
<212> DNA
<213> Homo sapiens

<400> 5959
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ttttctcggg gccttatgat gctggttctt gagaagttag ccactgatat tccttgtctg
120
ctatatgatg acaatctctt ctgtcatttg gtggatgaag tactcttgtt tgaaagggag
180
ctacacagtg ttcatggcta tcctggcact tttgctaatt gtatgcatat tctatcagag
240
gaaacctgtt ttcaaagatg ggtgacgggg gagagaaaat ttgctcttca aaaaatggac
300
tcaatgcttt cctcagaagc tgcctgggta tcgcaatata aggatatcac tgacgtggat
360
gaaatgaaag ttccagattg tgcagaaact tttatgactc tactcttggt tataactgac
420
aggtataaaa atcttcccac agcttcccga aagcttcagt tcctggagtt acagaaggac
480
ttagtagatg attttaggat acgattaaca caagtgatga aagaagagac tagagcttcc
540
cttggctttc gatactgtgc aattcttaat gctgtgaact acatctcaac agtactagca
600
gattgggctg acaatgtttt ctttctacaa cttcaacagg ctgcactgga ggtgtttgca
660
gagaataata ctctgagtaa attgcagcta ggacagctag cctctatgga gagctctgtc
720
tttgatgaca tgattaacct cttagaacgt ttaaagcatg atatgttgac ccgtcaagta
780
gaccacgttt ttagagaagt taaagatgct gcaaaattgt ataaaaaaga
830

<210> 5960
<211> 251
<212> PRT
<213> Homo sapiens

<400> 5960
Met Met Leu Val Leu Glu Lys Leu Ala Thr Asp Ile Pro Cys Leu Leu
1 5 10 15
Tyr Asp Asp Asn Leu Phe Cys His Leu Val Asp Glu Val Leu Leu Phe
20 25 30
Glu Arg Glu Leu His Ser Val His Gly Tyr Pro Gly Thr Phe Ala Asn
35 40 45
Cys Met His Ile Leu Ser Glu Glu Thr Cys Phe Gln Arg Trp Val Thr
50 55 60
Gly Glu Arg Lys Phe Ala Leu Gln Lys Met Asp Ser Met Leu Ser Ser
65 70 75 80
Glu Ala Ala Trp Val Ser Gln Tyr Lys Asp Ile Thr Asp Val Asp Glu

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                85                  90                  95
Met Lys Val Pro Asp Cys Ala Glu Thr Phe Met Thr Leu Leu Leu Val
            100                 105                 110
Ile Thr Asp Arg Tyr Lys Asn Leu Pro Thr Ala Ser Arg Lys Leu Gln
        115                 120                 125
Phe Leu Glu Leu Gln Lys Asp Leu Val Asp Asp Phe Arg Ile Arg Leu
    130                 135                 140
Thr Gln Val Met Lys Glu Glu Thr Arg Ala Ser Leu Gly Phe Arg Tyr
145                 150                 155                 160
Cys Ala Ile Leu Asn Ala Val Asn Tyr Ile Ser Thr Val Leu Ala Asp
                165                 170                 175
Trp Ala Asp Asn Val Phe Phe Leu Gln Leu Gln Gln Ala Ala Leu Glu
            180                 185                 190
Val Phe Ala Glu Asn Asn Thr Leu Ser Lys Leu Gln Leu Gly Gln Leu
        195                 200                 205
Ala Ser Met Glu Ser Ser Val Phe Asp Asp Met Ile Asn Leu Leu Glu
    210                 215                 220
Arg Leu Lys His Asp Met Leu Thr Arg Gln Val Asp His Val Phe Arg
225                 230                 235                 240
Glu Val Lys Asp Ala Ala Lys Leu Tyr Lys Lys
                245                 250
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<210> 5961
<211> 585
<212> DNA
<213> Homo sapiens

<400> 5961
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60
aatgaagcga gaccccgtct ctaaaaaaaa aattgagggg tcaaagagga tgccaaactt
120
aattagagac tgagacaggg cagggtgccg aggtgtctgc atgcgtttca tgtggatgcc
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cgtgtctatt ctggcctgct cctgggcccc ctccccactc agccctggct gatgagaatg
240
ggacagggac tcccttctcg tgtccctgtg cagcgtcggc ccaggaggta gcagagcagt
300
atatgcacat ctgggtgtgc cctcctgcat gtccccacac atctgtcatt cctgtctttg
360
cacacctatg tgactcccgc atgtttgtgt ccttatgtgt cccatgcatg ctccccatct
420
gaccttgcgt gttctcgcgt gtctgtgtgc ggccagtcct gccttcactc tctcatgggt
480
ggccctggca gcatgtctgg ctccccagca ggtgagctca ggagataaga tggaagatgc
540
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585

<210> 5962
<211> 114
<212> PRT
<213> Homo sapiens

<400> 5962
Met Cys Gly Asp Met Gln Glu Gly Thr Pro Arg Cys Ala Tyr Thr Ala
1 5 10 15
Leu Leu Pro Pro Gly Pro Thr Leu His Arg Asp Thr Arg Arg Glu Ser
20 25 30
Leu Ser His Ser His Gln Pro Gly Leu Ser Gly Glu Gly Ala Gln Glu
35 40 45
Gln Ala Arg Ile Asp Thr Gly Ile His Met Lys Arg Met Gln Thr Pro
50 55 60
Arg His Pro Ala Leu Ser Gln Ser Leu Ile Lys Phe Gly Ile Leu Phe
65 70 75 80
Asp Pro Ser Ile Phe Phe Leu Glu Thr Gly Ser Arg Phe Ile Ala Gln
85 90 95
Ala Glu Cys Ser Gly Tyr Ser Gln Ala Pro Leu Glu Arg Thr Ala Ala
100 105 110
Pro Ser

<210> 5963
<211> 1288
<212> DNA
<213> Homo sapiens

<400> 5963
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ttgaagataa gaaaggaaat gagagttgtt gacaggcaaa taagggatat ccaaagagaa
120
gaagaaaaag tgaaacgatc tgtgaaagat gctgccaaga agggccagaa ggatgtctgc
180
atagttctgg ccaaggagat gatcaggtca aggaaggctg tgagcaagct gtatgcatcc
240
aaagcacaca tgaactcagt gctcatgggg atgaagaacc agctcgcggt cttgcgagtg
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360
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420
gaggagatgt tagaggacac ttttgaaagc atggacgatc aggaagaaat ggaggaagaa
480
gcagaaatgg aaattgacag aattctcttt gaaattacag caggggcctt gggcaaagca
540
cccagtaaag tgactgatgc ccttccagag ccagaacctc caggagcgat ggctgcctca
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gaggatgagg aggaggagga agaggctctg gaggccatgc agtcccggct ggccacactc
660
cgcagctagg ggctgcctac cccgctgggt gtgcacacac tcctctcaag agctgccatt
720
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780
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tggcataaat aaatgcatca tttttaggag tatagacaga tatatcttat tgtggggagg
900

ggaaagaaat ccatctgctc atgaagcact tctgaaaata taggtgattg cctgaatgtc
960
gaagactcta cttttgtcta taaaacacta tataaatgaa ttttaataaa ttttttgcttc
1020
agcacttggc cccattgtag attgccctgt gcagtaaact ttcaaggtgt cagctgcccc
1080
agattgcttc atttgctggg tgtggaaaga gttgctatgg ccaggcatat gggatttgga
1140
agctcagcag aagtgacttc tgctctgtgg ttgctgctcc ccggctttca cagacatggt
1200
atggcagcca ttctttttatc tatttaacca agaggatgct ggggaattgt gctgcttgtc
1260
ctgttggctg gtggctgcat tatgtccg
1288

<210> 5964
<211> 222
<212> PRT
<213> Homo sapiens

<400> 5964
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Asn Glu Trp Ser Leu Lys Ile Arg Lys Glu Met Arg Val Val Asp Arg
            20   25   30
Gln Ile Arg Asp Ile Gln Arg Glu Glu Glu Lys Val Lys Arg Ser Val
        35   40   45
Lys Asp Ala Ala Lys Lys Gly Gln Lys Asp Val Cys Ile Val Leu Ala
    50   55   60
Lys Glu Met Ile Arg Ser Arg Lys Ala Val Ser Lys Leu Tyr Ala Ser
65   70   75   80
Lys Ala His Met Asn Ser Val Leu Met Gly Met Lys Asn Gln Leu Ala
                85   90   95
Val Leu Arg Val Ala Gly Ser Leu Gln Lys Ser Thr Glu Val Met Lys
            100   105   110
Ala Met Gln Ser Leu Val Lys Ile Pro Glu Ile Gln Ala Thr Met Arg
        115   120   125
Glu Leu Ser Lys Glu Met Met Lys Ala Gly Ile Ile Glu Glu Met Leu
    130   135   140
Glu Asp Thr Phe Glu Ser Met Asp Asp Gln Glu Glu Met Glu Glu Glu
145   150   155   160
Ala Glu Met Glu Ile Asp Arg Ile Leu Phe Glu Ile Thr Ala Gly Ala
                165   170   175
Leu Gly Lys Ala Pro Ser Lys Val Thr Asp Ala Leu Pro Glu Pro Glu
            180   185   190
Pro Pro Gly Ala Met Ala Ala Ser Glu Asp Glu Glu Glu Glu Glu Glu
        195   200   205
Ala Leu Glu Ala Met Gln Ser Arg Leu Ala Thr Leu Arg Ser
    210   215   220

<210> 5965
<211> 1011
<212> DNA
<213> Homo sapiens

<400> 5965
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120
agatgcctgg agagaatgag aaacagccgg gacaggctcc taaacaggta ccgccaggct
180
ggaagcagtg ggccagggaa ttctcagaac agctttctag ttcaagaggt gatggaagaa
240
gagtggaatg ctttgcagnn tcagtggnag aattgtccag aagacttggc tcagttggag
300
gagctgatag acatggctgt gctggaggaa attcaacagg agctgatcaa ccaagagcag
360
tccatcatca gcgagtatga gaagagcttg cagtttgatg aaaagtgtct cagcatcatg
420
ctggctgagt gggaggcaaa cccactcatc tgtcctgtat gtacaaagta caacctgaga
480
atcacaagcg gtgtggtggt gtgtcagtgt ggcctgtcca tcccatctca ttcttctgag
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ttgacagagc agaagcttcg tgcctgttta gagggtagta taaatgagca cagtgcacat
600
tgtccccaca cacctgaatt ttcagtcact ggaggaacag aagaaaagtc cagtcttctc
660
atgagctgtc tggcctgtga tacttgggct gtgatcctct agagccagct tggactcaca
720
tcattctatg gggttgaaga caactcattc cctctgagga gccttgtaca tacaagcctt
780
ttatttataa cttattttgt attgaaactt ttaaacaata ctgaagaaaa aaaaactttt
840
ccgacatctg ttcttggtct tttgtgacgc aggttgaagg gggaggaata gaaaaagaca
900
aactgccttg gaggagataa accaatttta tgtctatcat gttatacaaa aatctagaaa
960
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1011

<210> 5966
<211> 233
<212> PRT
<213> Homo sapiens

<400> 5966
Gly Asn Gly Ser Cys Gly Phe Val Ser Arg Glu Glu Glu Met Ala Glu
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Ser Leu Arg Ser Pro Arg Arg Ser Leu Tyr Lys Leu Val Gly Ser Pro
20 25 30
Pro Trp Lys Glu Ala Phe Arg Gln Arg Cys Leu Glu Arg Met Arg Asn
35 40 45
Ser Arg Asp Arg Leu Leu Asn Arg Tyr Arg Gln Ala Gly Ser Ser Gly
50 55 60
Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln Glu Val Met Glu Glu
65 70 75 80
Glu Trp Asn Ala Leu Gln Xaa Gln Trp Xaa Asn Cys Pro Glu Asp Leu

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                85                  90                  95
Ala Gln Leu Glu Glu Leu Ile Asp Met Ala Val Leu Glu Glu Ile Gln
            100                 105                 110
Gln Glu Leu Ile Asn Gln Glu Gln Ser Ile Ile Ser Glu Tyr Glu Lys
        115                 120                 125
Ser Leu Gln Phe Asp Glu Lys Cys Leu Ser Ile Met Leu Ala Glu Trp
    130                 135                 140
Glu Ala Asn Pro Leu Ile Cys Pro Val Cys Thr Lys Tyr Asn Leu Arg
145                 150                 155                 160
Ile Thr Ser Gly Val Val Val Cys Gln Cys Gly Leu Ser Ile Pro Ser
                165                 170                 175
His Ser Ser Glu Leu Thr Glu Gln Lys Leu Arg Ala Cys Leu Glu Gly
            180                 185                 190
Ser Ile Asn Glu His Ser Ala His Cys Pro His Thr Pro Glu Phe Ser
        195                 200                 205
Val Thr Gly Gly Thr Glu Glu Lys Ser Ser Leu Leu Met Ser Cys Leu
    210                 215                 220
Ala Cys Asp Thr Trp Ala Val Ile Leu
225                 230
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<210> 5967
<211> 1806
<212> DNA
<213> Homo sapiens

<400> 5967

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120
tgtgcttttg ttgctaggca gtcaacagca gggctactaa agcacttcta atttagacaa
180
atcttttcct ctattttaga aatggatttc aatggtgttc agtttgtttg cagaaaccta
240
ctgaaagtga gcatgttttt gaacacatta acaccgaagt tctacgtggc cctaacaggc
300
acttcctcac taatatcagg gcttattttg atatttgaat ggtggtattt tcgcaaatac
360
ggaacttcat tcattgaaca agtctcagta agccacttgc gccccttct gggaggggtt
420
gacaacaact cttccaacaa ttctaattcc agtaacgggg actcagattc caataggcaa
480
agtgtctcag aatgcaaagt atggcgaaat ccactaaatt tatttagggg tgctgaatac
540
aatcggtata cttgggtgac aggacgagag cctcttactt actatgacat gaatctctct
600
gcccaagacc accagacatt ctttacttgt gactcggacc atctgcgtcc cgcagatgca
660
ataatgcaga aagcctggag agagagaaac ccccaagcta ggatttctgc agctcatgaa
720
gccttggaga taaatgagac gagacaccaa tgtcttggtg tacatcaaaa gaaggctagc
780
aatgtgtgcc agaagactcg ggaggaccag ggaagcaaag ccctttctgga actacaagca
840
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tatgctgatg ttcaggcagt cttagcaaag tatgatgata taagcttacc aaagtcagca
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acaatatgct acacagctgc tttgctcaaa gcaagagctg tctctgacaa attctctcct
960
gaggctgcat ctcggcgggg gctgagcaca gcagagatga atgcagtaga ggccattcat
1020
agagctgtgg aattcaatcc tcatgtgcca aaatacctac tagaaatgaa aagcttaatc
1080
ctacccccag aacatatcct gaagagagga gacagtgaag caatagcata tgcattcttt
1140
catcttgcac actggaagag agtggaaggg gctttgaatc ttttgcattg tacgtgggaa
1200
ggcacttttc ggatgatccc ttatcccttg gaaaaggggc acctatttta tccttaccca
1260
atctgtacag aaacagcaga ccgagagctg cttccatctt tccatgaagt ctcagtttac
1320
ccaaagaagg agcttccctt ctttattctc tttactgctg gattatgttc cttcacagcc
1380
atgctggccc tcctgacaca tcagttcccg gaacttatgg gggtcttcgc aaaagctgtg
1440
agtgtttgcc tagagggagg ccttggggaa tggatgggga aagccaaggg cataaaagca
1500
gcgtgagaga aatggggttg ccttacagaa atgggtacga gcctgcaaag atcattgctc
1560
accatttaat tttcatgatc gtcaatggaa tcaaagcatt aagggtcaaa tgagaaagtg
1620
caggttgtta ctgcatgcct tgcctcattt cacaacaaat tcttagcagt ttccaaaaaa
1680
tgcaggaggt ccaaaaggat ggaatgattt aggaaatcct agcaaatgaa aatgtgtggg
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1800
ctttcc
1806

<210> 5968
<211> 434
<212> PRT
<213> Homo sapiens

<400> 5968
Met Asp Phe Asn Gly Val Gln Phe Val Cys Arg Asn Leu Leu Lys Val
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Ser Met Phe Leu Asn Thr Leu Thr Pro Lys Phe Tyr Val Ala Leu Thr
20 25 30
Gly Thr Ser Ser Leu Ile Ser Gly Leu Ile Leu Ile Phe Glu Trp Trp
35 40 45
Tyr Phe Arg Lys Tyr Gly Thr Ser Phe Ile Glu Gln Val Ser Val Ser
50 55 60
His Leu Arg Pro Leu Leu Gly Gly Val Asp Asn Asn Ser Ser Asn Asn
65 70 75 80
Ser Asn Ser Ser Asn Gly Asp Ser Asp Ser Asn Arg Gln Ser Val Ser
85 90 95
Glu Cys Lys Val Trp Arg Asn Pro Leu Asn Leu Phe Arg Gly Ala Glu

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            100                 105                 110
Tyr Asn Arg Tyr Thr Trp Val Thr Gly Arg Glu Pro Leu Thr Tyr Tyr
        115                 120                 125
Asp Met Asn Leu Ser Ala Gln Asp His Gln Thr Phe Phe Thr Cys Asp
    130                 135                 140
Ser Asp His Leu Arg Pro Ala Asp Ala Ile Met Gln Lys Ala Trp Arg
145                 150                 155                 160
Glu Arg Asn Pro Gln Ala Arg Ile Ser Ala Ala His Glu Ala Leu Glu
                165                 170                 175
Ile Asn Glu Thr Arg His Gln Cys Leu Gly Val His Gln Lys Lys Ala
            180                 185                 190
Ser Asn Val Cys Gln Lys Thr Arg Glu Asp Gln Gly Ser Lys Ala Leu
        195                 200                 205
Leu Glu Leu Gln Ala Tyr Ala Asp Val Gln Ala Val Leu Ala Lys Tyr
    210                 215                 220
Asp Asp Ile Ser Leu Pro Lys Ser Ala Thr Ile Cys Tyr Thr Ala Ala
225                 230                 235                 240
Leu Leu Lys Ala Arg Ala Val Ser Asp Lys Phe Ser Pro Glu Ala Ala
                245                 250                 255
Ser Arg Arg Gly Leu Ser Thr Ala Glu Met Asn Ala Val Glu Ala Ile
            260                 265                 270
His Arg Ala Val Glu Phe Asn Pro His Val Pro Lys Tyr Leu Leu Glu
        275                 280                 285
Met Lys Ser Leu Ile Leu Pro Pro Glu His Ile Leu Lys Arg Gly Asp
    290                 295                 300
Ser Glu Ala Ile Ala Tyr Ala Phe Phe His Leu Ala His Trp Lys Arg
305                 310                 315                 320
Val Glu Gly Ala Leu Asn Leu Leu His Cys Thr Trp Glu Gly Thr Phe
                325                 330                 335
Arg Met Ile Pro Tyr Pro Leu Glu Lys Gly His Leu Phe Tyr Pro Tyr
            340                 345                 350
Pro Ile Cys Thr Glu Thr Ala Asp Arg Glu Leu Leu Pro Ser Phe His
        355                 360                 365
Glu Val Ser Val Tyr Pro Lys Lys Glu Leu Pro Phe Phe Ile Leu Phe
    370                 375                 380
Thr Ala Gly Leu Cys Ser Phe Thr Ala Met Leu Ala Leu Leu Thr His
385                 390                 395                 400
Gln Phe Pro Glu Leu Met Gly Val Phe Ala Lys Ala Val Ser Val Cys
                405                 410                 415
Leu Glu Gly Gly Leu Gly Glu Trp Met Gly Lys Ala Lys Gly Ile Lys
            420                 425                 430
Ala Ala
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<210> 5969
<211> 429
<212> DNA
<213> Homo sapiens

<400> 5969
cggccgcccg tgtgtgacgt cagggagctg caggcccagg aagccttgca gaacggccag
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ctgggcggcg gggaaggggt cccggatctg cagcctgggg tcttggccag ccaggccatg
120

attgagaaga tcctgagcga ggacccccgg tggcaagatg ccaacttcgt gctgggcagc
180
tacaagacgg agcagtgccc gaagccgcca cgcctgtgcc gccagggcta tgcgtgccca
240
cactaccaca atagccggga caggcggcgc aacccccggc ggttccagta caggtccacg
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ccctgcccca gcgtgaagca cggggatgag tgggggggaac cctcacgctg cgatggcggc
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gacggctgcc agtattgcca ctcccgcacg gagcagcagt tccatcccga gatctacaaa
420
tctacaaaa
429

<210> 5970
<211> 143
<212> PRT
<213> Homo sapiens

<400> 5970
Arg Pro Pro Val Cys Asp Val Arg Glu Leu Gln Ala Gln Glu Ala Leu
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Gln Asn Gly Gln Leu Gly Gly Gly Glu Gly Val Pro Asp Leu Gln Pro
            20   25   30
Gly Val Leu Ala Ser Gln Ala Met Ile Glu Lys Ile Leu Ser Glu Asp
        35   40   45
Pro Arg Trp Gln Asp Ala Asn Phe Val Leu Gly Ser Tyr Lys Thr Glu
    50   55   60
Gln Cys Pro Lys Pro Pro Arg Leu Cys Arg Gln Gly Tyr Ala Cys Pro
65   70   75   80
His Tyr His Asn Ser Arg Asp Arg Arg Arg Asn Pro Arg Arg Phe Gln
                85   90   95
Tyr Arg Ser Thr Pro Cys Pro Ser Val Lys His Gly Asp Glu Trp Gly
            100   105   110
Glu Pro Ser Arg Cys Asp Gly Gly Asp Gly Cys Gln Tyr Cys His Ser
        115   120   125
Arg Thr Glu Gln Gln Phe His Pro Glu Ile Tyr Lys Ser Thr Lys
    130   135   140

<210> 5971
<211> 565
<212> DNA
<213> Homo sapiens

<400> 5971
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tgtgaatagc acagtcttcc ctttcatgtg gcactgaagt taaaatgcat agagctcttt
120
catgtccctt aggtcagcta agcccacatc agtgtccaaa taggcaacat ccctatttta
180
tagatggtca tccccatttt agagatagct ccctttttata tccccatttt acaggtgaag
240
gaattgaggc acagaaggtt aggtcacttc tgcaagatga ccagctgaac caaaatttca
300

gggcttcaaa caccaaatgt gttcctttgt cttccgtttc ccacttgctt cccagaggct
360
cagcaagtag cctctggcca ctgagcatcc tcccgcccac tttgctccct gcctcctgat
420
cccaggactg tggccgtgga tgccagagcg aggatgtgaa tcctgttggg ttctgaagcc
480
cacacctacc ctcagccttg aagctgcagc aatggctgct tccagatgag cacaccctcg
540
gggtgcangc gtccagtgtc acgat
565

<210> 5972
<211> 104
<212> PRT
<213> Homo sapiens

<400> 5972
Met His Arg Ala Leu Ser Cys Pro Leu Gly Gln Leu Ser Pro His Gln
 1   5   10   15
Cys Pro Asn Arg Gln His Pro Tyr Phe Ile Asp Gly His Pro His Phe
            20   25   30
Arg Asp Ser Ser Leu Leu Tyr Pro His Phe Thr Gly Glu Gly Ile Glu
        35   40   45
Ala Gln Lys Val Arg Ser Leu Leu Gln Asp Asp Gln Leu Asn Gln Asn
    50   55   60
Phe Arg Ala Ser Asn Thr Lys Cys Val Pro Leu Ser Ser Val Ser His
65   70   75   80
Leu Leu Pro Arg Gly Ser Ala Ser Ser Leu Trp Pro Leu Ser Ile Leu
                85   90   95
Pro Pro Thr Leu Leu Pro Ala Ser
            100

<210> 5973
<211> 797
<212> DNA
<213> Homo sapiens

<400> 5973
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cgcccagtga gttagcatgg agggcagtgg gaccggaaaa agacgtggaa aagctgcgaa
120
aacgagcctt cgaatcatgg acgcgcgggc ccagctcctc ctccgagttc ctcatccggg
180
gccgtcactc acatccgggg ccctcactca catccgggac cctcatccgg ggctctcacc
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360
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cccctccccc cggtgagtac ccggaagccg ttttggggtc gcagcggggt ggcagcttgt
480

tttgccttca cgggagtaga aggaggcggc gtccgccgcg gccgacggta gttcgcttcc
540
ccgagagtgc gcggaggccc gggtgcgagg agggcctgtt tctcttcagc cctggttcat
600
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660
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780
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797

<210> 5974
<211> 107
<212> PRT
<213> Homo sapiens

<400> 5974
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Ser Leu Arg Ile Met Asp Ala Arg Ala Gln Leu Leu Leu Arg Val Pro
20 25 30
His Pro Gly Pro Ser Leu Thr Ser Gly Ala Leu Thr His Ile Arg Asp
35 40 45
Pro His Pro Gly Leu Ser Pro Thr Ser Gly Thr Leu Met Pro Gly Arg
50 55 60
Arg Arg Gly Gly Pro Ser Phe Gly Thr Pro Ala Leu Arg Arg Arg Lys
65 70 75 80
Cys His Arg Glu Ala Pro Ala Ser Gly Leu Ser Thr Ala Ala Arg Glu
85 90 95
Arg Leu Trp Trp Pro Arg Ala Arg Val Cys Arg
100 105

<210> 5975
<211> 2175
<212> DNA
<213> Homo sapiens

<400> 5975
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120
cagagggcca cgtacaagta tgagatgatt aacaagcaga atgagcagat gcatgcgctg
180
ctggccattg ccctcacgat gtaccccatg cgtatcgatg agagcattca cctccagctg
240
cgggagaaat atggggacaa gatgttgcgc atgtcttatc ccgctgatga ttatgagtct
300
gaggcggctt atgaccccta cgcttatccc agcgactatg atatgcacac aggagatcca
360
aagcaggacc ttgcttatga acgtcagtat gaacagcaaa cctatcaggt gatccctgag
420

gtgatcaaaa acttcatcca gtatttccac aaaactgtct cagatttgat tgaccagaaa
480
gtgtatgagc tacaggccag tcgtgtctcc agtgatgtca ttgaccagaa ggtgtatgag
540
atccaggaca tctatgagaa cagctggacc aagctgactg aaagattctt caagaataca
600
ccttggcccg aggctgaagc cattgctcca caggttggca atgatgctgt cttcctgatt
660
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780
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840
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900
gagattgact ttcttcgttc caatcccaaa atctggaatg ttcatagtgt cctcaatgtc
960
cttcattccc tggtagacaa atccaacatc aaccgacagt tggaggtata cacaagcgga
1020
ggtgaccctg agagtgtggc tggggagtat gggcggcact ccctctacaa aatgcttggt
1080
tacttcagcc tggtcgggct tctccgcctg cactccctgt taggagatta ctaccaggcc
1140
atcaaggtgc tggagaacat cgaactgaac aagaagagta tgtattcccg tgtgccagag
1200
tgccaggtca ccacatacta ttatgttggg tttgcatatt tgatgatgcg tcgttaccag
1260
gatgccatcc gggtcttcgc caacatcctc ctctacatcc agaggaccaa gagcatgttc
1320
cagaggacca cgtacaagta tgagatgatt aacaagcaga atgagcagat gcatgcgctg
1380
ctggccattg ccctcacgat gtaccccatg cgtatcgatg agagcattca cctccagctg
1440
cgggagaaat atggggacaa gatgttgcgc atgcagaaag gtgacccaca agtctatgaa
1500
gaacttttca gttactcctg ccccaagttc ctgtcgcctg tagtgcccaa ctatgataat
1560
gtgcacccca actaccacaa agagcccttc ctgcagcagc tgaaggtgtt ttctgatgaa
1620
gtacagcagc aggcccagct ttcaaccatc cgcagcttcc tgaagctcta caccaccatg
1680
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<210> 5976
<211> 564
<212> PRT
<213> Homo sapiens

<400> 5976
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35 40 45
Pro Glu Val Ile Lys Asn Phe Ile Gln Tyr Phe His Lys Thr Val Ser
50 55 60
Asp Leu Ile Asp Gln Lys Val Tyr Glu Leu Gln Ala Ser Arg Val Ser
65 70 75 80
Ser Asp Val Ile Asp Gln Lys Val Tyr Glu Ile Gln Asp Ile Tyr Glu
85 90 95
Asn Ser Trp Thr Lys Leu Thr Glu Arg Phe Phe Lys Asn Thr Pro Trp
100 105 110
Pro Glu Ala Glu Ala Ile Ala Pro Gln Val Gly Asn Asp Ala Val Phe
115 120 125
Leu Ile Leu Tyr Lys Glu Leu Tyr Tyr Arg His Ile Tyr Ala Lys Val
130 135 140
Ser Gly Gly Pro Ser Leu Glu Gln Arg Phe Glu Ser Tyr Tyr Asn Tyr
145 150 155 160
Cys Asn Leu Phe Asn Tyr Ile Leu Asn Ala Asp Gly Pro Ala Pro Leu
165 170 175
Glu Leu Pro Asn Gln Trp Leu Trp Asp Ile Ile Asp Glu Phe Ile Tyr
180 185 190
Gln Phe Gln Ser Phe Ser Gln Tyr Arg Cys Lys Thr Ala Lys Lys Ser
195 200 205
Glu Glu Glu Ile Asp Phe Leu Arg Ser Asn Pro Lys Ile Trp Asn Val
210 215 220
His Ser Val Leu Asn Val Leu His Ser Leu Val Asp Lys Ser Asn Ile
225 230 235 240
Asn Arg Gln Leu Glu Val Tyr Thr Ser Gly Gly Asp Pro Glu Ser Val
245 250 255
Ala Gly Glu Tyr Gly Arg His Ser Leu Tyr Lys Met Leu Gly Tyr Phe
260 265 270
Ser Leu Val Gly Leu Leu Arg Leu His Ser Leu Leu Gly Asp Tyr Tyr
275 280 285
Gln Ala Ile Lys Val Leu Glu Asn Ile Glu Leu Asn Lys Lys Ser Met
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Tyr Ser Arg Val Pro Glu Cys Gln Val Thr Thr Tyr Tyr Tyr Val Gly
305 310 315 320
Phe Ala Tyr Leu Met Met Arg Arg Tyr Gln Asp Ala Ile Arg Val Phe

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Thr Thr Tyr Lys Tyr Glu Met Ile Asn Lys Gln Asn Glu Gln Met His
        355                 360                 365
Ala Leu Leu Ala Ile Ala Leu Thr Met Tyr Pro Met Arg Ile Asp Glu
    370                 375                 380
Ser Ile His Leu Gln Leu Arg Glu Lys Tyr Gly Asp Lys Met Leu Arg
385                 390                 395                 400
Met Gln Lys Gly Asp Pro Gln Val Tyr Glu Glu Leu Phe Ser Tyr Ser
                405                 410                 415
Cys Pro Lys Phe Leu Ser Pro Val Val Pro Asn Tyr Asp Asn Val His
            420                 425                 430
Pro Asn Tyr His Lys Glu Pro Phe Leu Gln Gln Leu Lys Val Phe Ser
        435                 440                 445
Asp Glu Val Gln Gln Gln Ala Gln Leu Ser Thr Ile Arg Ser Phe Leu
    450                 455                 460
Lys Leu Tyr Thr Thr Met Pro Val Ala Lys Leu Ala Gly Phe Leu Asp
465                 470                 475                 480
Leu Thr Glu Gln Glu Phe Arg Ile Gln Leu Leu Val Phe Lys His Lys
                485                 490                 495
Met Lys Asn Leu Val Trp Thr Ser Gly Ile Ser Ala Leu Asp Gly Glu
            500                 505                 510
Phe Gln Ser Ala Ser Glu Val Asp Phe Tyr Ile Asp Lys Asp Met Ile
        515                 520                 525
His Ile Ala Asp Thr Lys Val Ala Arg Arg Tyr Gly Asp Phe Phe Ile
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Arg Gln Ile His Lys Phe Glu Glu Leu Asn Arg Thr Leu Lys Lys Met
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<210> 5977
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 5977

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1380
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<210> 5978
<211> 77
<212> PRT
<213> Homo sapiens

<400> 5978
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Ile Arg Leu Gly Ser Val Ala His Ala Cys Asp Pro Ser Thr Leu Gly
20 25 30
Gly Arg Gly Gly Gln Ile Ile Xaa Ala Arg Ser Ser Arg Pro Ala Trp
35 40 45
Thr Thr Trp Arg Xaa Val Phe Thr Lys Asn Thr Lys Ile Ser Trp Ala
50 55 60
Trp Trp Tyr Thr Pro Val Ile Pro Ala Thr Gln Glu Ala
65 70 75

<210> 5979
<211> 1095
<212> DNA
<213> Homo sapiens

<400> 5979
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aattgaggcc taaggcaggg tcacttgcct ggccccttcc ccttcacccg tcagagtcca
240
gacagggagg ggacgtcccc tgacccccgc tgctctgtgc tttcagggca agaagactat
300
gaccggctgc ggcccctgtc ctaccagaac acccacctcg tgctcatctg ctatgacgtc
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cggcagaaga agcgccggct ctgcctgctg ctctgaccca gggcagacag acctcacgac
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960
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aaaaaaaaaa aaaaa
1095

<210> 5980
<211> 169
<212> PRT
<213> Homo sapiens

<400> 5980
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Ser Pro Asp Arg Glu Gly Thr Ser Pro Asp Pro Arg Cys Ser Val Leu
20 25 30
Ser Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Gln Asn
35 40 45
Thr His Leu Val Leu Ile Cys Tyr Asp Val Met Asn Pro Thr Ser Tyr
50 55 60
Asp Asn Val Leu Ile Lys Trp Phe Pro Glu Val Thr His Phe Cys Arg
65 70 75 80
Gly Ile Pro Met Val Leu Ile Gly Cys Lys Thr Asp Leu Arg Lys Asp
85 90 95
Lys Glu Gln Leu Arg Lys Leu Arg Ala Ala Gln Leu Glu Pro Ile Thr
100 105 110
Tyr Met Gln Gly Leu Ser Ala Cys Glu Gln Ile Arg Ala Ala Leu Tyr
115 120 125
Leu Glu Cys Ser Ala Lys Phe Arg Glu Asn Val Glu Asp Val Phe Arg
130 135 140
Glu Ala Ala Lys Val Ala Leu Ser Ala Leu Lys Lys Ala Gln Arg Gln
145 150 155 160
Lys Lys Arg Arg Leu Cys Leu Leu Leu
165

<210> 5981
<211> 677
<212> DNA
<213> Homo sapiens

<400> 5981
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aaaacgcaag gggacactta ccctaggggt ggacgaacag ctagcttttt ggaatttggg
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ttggtcttca tttccaagtg cgaaatttgc ctgcaaaact ttttatttgc agtcatagat
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677

<210> 5982
<211> 98
<212> PRT
<213> Homo sapiens

<400> 5982
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Arg Ile Pro Lys Ser Asp Asp Gly Thr Arg Thr Gly Arg Asn Asp Ser
20 25 30
Pro Arg Ala Pro Leu Pro Arg Ser Ser Ala Arg Arg Pro Ser Lys Ala
35 40 45
Asn Leu His Thr Leu Gly Gln Leu Lys Leu Ser Arg Arg Cys Arg Glu
50 55 60
Pro Arg Leu Gly Arg Ala Gly Gln Gln Arg Leu His Pro Arg Thr Arg
65 70 75 80
Pro Arg Arg Gly Ser Gly Pro Leu Val Arg Ala Gly Arg Arg Gly Trp
85 90 95
Gly Lys

<210> 5983
<211> 790
<212> DNA
<213> Homo sapiens

<400> 5983
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tatagtcaag aggtaagaag ttaacttaaa aagggtgaat tggtagtttt tttcctatta
120

cattgttttc cttaaattac tggtaaattt tgaaataaac agtcccaaga tgtgattatt
180
tgtgtaattt ttttttttaa tttgtaaaca gggatatgac agatcttcaa ccatgttaac
240
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300
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360
acctgtgtca gaccttcagc taggactcga tgcagttgag ccaactgccc tacataaaac
420
cctggaaacg cctgcacatg acagggctga gcccaacagc caactggact cgactcactc
480
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790

<210> 5984
<211> 186
<212> PRT
<213> Homo sapiens

<400> 5984
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Leu Gln Glu Ile Lys Thr Ile Gly Tyr Thr Ser Pro Arg Ser Arg Thr
            20   25   30
Glu Val Asn Arg Gln Cys Pro Gly Glu Lys Glu Pro Val Ser Asp Leu
        35   40   45
Gln Leu Gly Leu Asp Ala Val Glu Pro Thr Ala Leu His Lys Thr Leu
    50   55   60
Glu Thr Pro Ala His Asp Arg Ala Glu Pro Asn Ser Gln Leu Asp Ser
65   70   75   80
Thr His Ser Gly Arg Gly Thr Met Tyr Ser Ser Trp Val Lys Ser Pro
                85   90   95
Asp Arg Thr Gly Val Asn Phe Ser Val Asn Ser Asn Leu Arg Asp Leu
            100   105   110
Thr Pro Ser His Gln Leu Glu Val Gly Gly Gly Phe Arg Ile Ser Glu
        115   120   125
Ser Lys Cys Leu Met Gln Asp Asp Thr Arg Gly Met Phe Met Glu Thr
    130   135   140
Thr Val Phe Cys Thr Ser Glu Asp Gly Leu Val Ser Gly Phe Gly Arg
145   150   155   160
Thr Val Asn Asp Asn Leu Ile Asp Gly Asn Cys Thr Pro Gln Asn Pro
                165   170   175
Pro Gln Lys Lys Lys Val Ser Leu Leu Glu

180 185

<210> 5985
<211> 737
<212> DNA
<213> Homo sapiens

<400> 5985
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120
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420
caacatggtt gaggtctgag attttacaca gagtcattca agagttgctt gtggactact
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540
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600
tacctccact gctggggctg gagaaagcgg accttctgga actcatgcca ctctcagagg
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aaaaaaaaaa aaaaaaa
737

<210> 5986
<211> 165
<212> PRT
<213> Homo sapiens

<400> 5986
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20 25 30
Asp Leu Leu Gln Asn Pro Tyr Phe Ser Lys Leu Leu Leu Asn Leu Ser
35 40 45
Gln His Val Asp Glu Ser Gly Leu Ser Leu Thr Leu Ala Lys Glu Gln
50 55 60
Ala Gln Ala Trp Lys Glu Val Arg Leu His Lys Thr Thr Trp Leu Arg
65 70 75 80
Ser Glu Ile Leu His Arg Val Ile Gln Glu Leu Leu Val Asp Tyr Tyr
85 90 95
Val Lys Ile Gln Asp Thr Asn Val Thr Ser Glu Asp Lys Lys Phe His

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            100                 105                 110
Glu Thr Leu Glu Gln Arg Leu Leu Val Thr Glu Leu Met Arg Leu Leu
        115                 120                 125
Gly Pro Ser Gln Glu Arg Glu Ile Pro Pro Leu Leu Gly Leu Glu Lys
    130                 135                 140
Ala Asp Leu Leu Glu Leu Met Pro Leu Ser Glu Val Gly Gly Glu Ile
145                 150                 155                 160
Leu Glu Pro Asn Lys
                165
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<210> 5987
<211> 1444
<212> DNA
<213> Homo sapiens

<400> 5987
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180
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240
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360
ccagatgccc ttatattgga atctccattc actaatatcc gcgaagaagc taagagccat
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caggggggagt ccgggcaggg gactcttggg gctcgggacc atgctgagct ttttggcacc
1140

acccacagag aacgtggggt ccaggttctt tctgcacctt cccagcacat gcagaatgac
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1444

<210> 5988
<211> 216
<212> PRT
<213> Homo sapiens

<400> 5988
Gly Gly Asp His Arg Val Glu Leu Tyr Lys Val Leu Ser Ser Leu Gly
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20 25 30
Thr Pro Ser Glu Arg Gly Met Thr Tyr Asp Ala Leu His Val Phe Asp
35 40 45
Trp Ile Lys Ala Arg Ser Gly Asp Asn Pro Val Tyr Ile Trp Gly His
50 55 60
Ser Leu Gly Thr Gly Val Ala Thr Ile Trp Cys Gly Ala Ser Val Ser
65 70 75 80
Glu Thr Pro Pro Asp Ala Leu Ile Leu Glu Ser Pro Phe Thr Asn Ile
85 90 95
Arg Glu Glu Ala Lys Ser His Pro Phe Ser Val Ile Tyr Arg Tyr Phe
100 105 110
Pro Gly Phe Asp Trp Phe Phe Leu Asp Pro Ile Thr Ser Ser Gly Ile
115 120 125
Lys Phe Ala Asn Asp Glu Asn Val Lys His Ile Ser Cys Pro Leu Leu
130 135 140
Ile Leu His Ala Glu Asp Asp Pro Val Val Pro Phe Gln Leu Gly Arg
145 150 155 160
Lys Leu Tyr Ser Ile Ala Ala Pro Ala Arg Ser Phe Arg Asp Phe Lys
165 170 175
Val Gln Phe Val Pro Phe His Ser Asp Leu Gly Tyr Arg His Lys Tyr
180 185 190
Ile Tyr Lys Ser Pro Glu Leu Pro Arg Ile Leu Arg Glu Phe Leu Gly
195 200 205
Lys Ser Glu Pro Glu His Gln His
210 215

<210> 5989
<211> 1583
<212> DNA
<213> Homo sapiens

<400> 5989

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120
tgagccttat accgatcaat ctaggcacac ctcctttcct gggggtgact gaatgcccag
180
ccagggacgc gacgtctctg gccagcagaa atacggcctc ctccccgccg actgggcaaa
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360
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<212> PRT
<213> Homo sapiens

<400> 5994
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Arg Ser Ser Ser Pro Thr Ala Gly Pro Ser Thr Glu Gly Ala Glu Gly
35 40 45
Pro Glu Glu Lys Lys Lys Val Lys Met Arg Arg Lys Arg Arg Leu Pro
50 55 60
Asn Lys Glu Leu Ser Arg Glu Leu Ser Lys Glu Leu Asn His Glu Ile
65 70 75 80
Gln Arg Thr Glu Asn Ser Leu Ala Asn Glu Asn Gln Gln Pro Ile Lys
85 90 95
Ser Glu Pro Glu Ser Glu Gly Glu Glu Pro Lys Arg Pro Pro Gly Ile
100 105 110
Cys Glu Arg Pro His Arg Phe Ser Lys Gly Leu Asn Gly Thr Pro Arg
115 120 125
Glu Leu Arg His Gln Leu Gly Pro Ser Leu Arg Ser Pro Pro Arg Val
130 135 140
Ile Ser Arg Pro Pro Pro Ser Val Ser Pro Pro Lys Cys Ile Gln Met
145 150 155 160
Glu Arg His Val Ile Arg Pro Pro Pro Ile Ser Pro Pro Pro Asp Ser
165 170 175
Leu Pro Leu Asp Asp Gly Ala Ala His Val Met His Arg Glu Val Trp
180 185 190
Met Ala Val Phe Ser Tyr Leu Ser His Gln Asp Leu Cys Val Cys Met
195 200 205
Arg Val Cys Arg Thr Trp Asn Arg Trp Cys Cys Asp Lys Arg Leu Trp
210 215 220
Thr Arg Ile Asp Leu Asn His Cys Lys Ser Ile Thr Pro Leu Met Leu
225 230 235 240
Ser Gly Ile Ile Arg Arg Gln Pro Val Ser Leu Asp Leu Ser Trp Thr
245 250 255
Asn Ile Ser Lys Lys Gln Leu Ser Trp Leu Ile Asn Arg Leu Pro Gly
260 265 270
Leu Arg Asp Leu Val Leu Ser Gly Cys Ser Trp Ile Ala Val Ser Ala
275 280 285
Leu Cys Ser Ser Ser Cys Pro Leu Leu Arg Thr Leu Asp Val Gln Trp

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    290                 295                 300
Val Glu Gly Leu Lys Asp Ala Gln Met Arg Asp Leu Leu Ser Pro Pro
305                 310                 315                 320
Thr Asp Asn Arg Pro Gly Glu Leu Pro Gly Trp Gly Phe Leu Trp Gly
                325                 330                 335
Trp Gly Glu Arg Ala Arg Leu Leu Asp Leu Leu Leu Pro Ser Asp Pro
            340                 345                 350
Ser Cys Ser Pro Lys Asp Ile Gly Met Ser Leu Cys Cys His Val Leu
        355                 360                 365
Ser Leu Leu Gln Ala Gln Arg Gly Ser Gly Arg Arg Gln Gly Leu Leu
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Cys Thr Arg Glu Thr Arg Ser Trp Gly Ser Ala Cys Val Ser Leu Leu
385                 390                 395                 400
Ser Cys
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<210> 5995
<211> 1528
<212> DNA
<213> Homo sapiens

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180
gcgtgccata gcaggcagtt tgtacctttg gcgtctggcc aagcacaggt ggttctctcg
240
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300
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360
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420
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480
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<210> 5996
<211> 140
<212> PRT
<213> Homo sapiens

<400> 5996
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Glu Arg Cys Pro Gly Ala Pro Ser Val Cys Asp Ile Gln Leu Asn Gln
20 25 30
Val Ser Pro Ala Asp Phe Thr Val Leu Ser Asp Val Leu Pro Met Phe
35 40 45
Ser Val Asp Phe Ser Lys Gln Val Ser Ser Ser Ala Ala Cys His Ser
50 55 60
Arg Gln Phe Val Pro Leu Ala Ser Gly Gln Ala Gln Val Val Leu Ser
65 70 75 80
Trp Trp Asp Ile Glu Met Asp Pro Glu Gly Lys Ile Lys Cys Thr Met
85 90 95
Ala Pro Phe Trp Ala His Ser Asp Pro Glu Glu Met Gln Trp Arg Asp
100 105 110
His Trp Xaa Ala Val Cys Val Leu Pro Ala Thr Arg Gly Ala Cys Gly
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<210> 5997
<211> 1759
<212> DNA
<213> Homo sapiens

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120
cagttctaga tggaagaccc agatggcact cctcccgggg aggggttcca gcccccaccc
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240
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300
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360
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420
gtaagataca caaaccacct ccacgacctc cgacctcccc cctccctccg gctgctctga
480
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720
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1759

<210> 5998
<211> 72
<212> PRT
<213> Homo sapiens

<400> 5998
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Gly Ser Ala Gly Arg Trp Ala Pro Gly Trp Gly Arg Val Pro Ala Gly
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Pro Arg Cys Gly Ser Ser Cys Pro Ala Pro Arg Arg Arg Pro Ala Ala
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Pro Pro Ala Gly Arg Thr Ala Arg Cys Arg Pro Gly Ala Val Val Leu
50 55 60
Cys Pro Pro Gly Leu Pro Thr Gly
65 70

<210> 5999
<211> 2759
<212> DNA
<213> Homo sapiens

<400> 5999
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<210> 6000
<211> 757
<212> PRT
<213> Homo sapiens

<400> 6000
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Gln Arg Pro Asp Gln Leu Asp Lys Val Glu Gln Tyr Arg Arg Arg Glu
35 40 45
Ala Arg Lys Lys Ala Ser Val Glu Ala Arg Leu Lys Ala Ala Ile Gln
50 55 60
Ser Gln Leu Asp Gly Val Arg Thr Gly Leu Ser Gln Leu His Asn Ala
65 70 75 80
Leu Asn Asp Val Lys Asp Ile Gln Gln Ser Leu Ala Asp Val Ser Lys
85 90 95
Asp Trp Arg Gln Ser Ile Asn Thr Ile Glu Ser Leu Lys Asp Val Lys
100 105 110
Asp Ala Val Val Gln His Ser Gln Leu Ala Ala Ala Val Glu Asn Leu
115 120 125
Lys Asn Ile Phe Ser Val Pro Glu Ile Val Arg Glu Thr Gln Asp Leu
130 135 140
Ile Glu Gln Gly Ala Leu Leu Gln Ala His Arg Lys Leu Met Asp Leu
145 150 155 160
Glu Cys Ser Arg Asp Gly Leu Met Tyr Glu Gln Tyr Arg Met Asp Ser
165 170 175
Gly Asn Thr Arg Asp Met Thr Leu Ile His Gly Tyr Phe Gly Ser Thr
180 185 190
Gln Gly Leu Ser Asp Glu Leu Ala Lys Gln Leu Trp Met Val Leu Gln
195 200 205
Arg Ser Leu Val Thr Val Arg Arg Asp Pro Thr Leu Leu Val Ser Val
210 215 220
Val Arg Ile Ile Glu Arg Glu Glu Lys Ile Asp Arg Arg Ile Leu Asp
225 230 235 240
Arg Lys Lys Gln Thr Gly Phe Val Pro Pro Gly Arg Pro Lys Asn Trp
245 250 255
Lys Glu Lys Met Phe Thr Ile Leu Glu Arg Thr Val Thr Thr Arg Ile
260 265 270
Glu Gly Thr Gln Ala Asp Thr Arg Glu Ser Asp Lys Met Trp Leu Val

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Arg His Leu Glu Ile Ile Arg Lys Tyr Val Leu Asp Asp Leu Ile Val
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Ala Lys Asn Leu Met Val Gln Cys Phe Pro Pro His Tyr Glu Ile Phe
305                 310                 315                 320
Lys Asn Leu Leu Asn Met Tyr His Gln Ala Leu Ser Thr Arg Met Gln
                325                 330                 335
Asp Leu Ala Ser Glu Asp Leu Glu Ala Asn Glu Ile Val Ser Leu Leu
            340                 345                 350
Thr Trp Val Leu Asn Thr Tyr Thr Ser Thr Glu Met Met Arg Asn Val
        355                 360                 365
Glu Leu Ala Pro Glu Val Asp Val Gly Thr Leu Glu Pro Leu Leu Ser
    370                 375                 380
Pro His Val Val Ser Glu Leu Leu Asp Thr Tyr Met Ser Thr Leu Thr
385                 390                 395                 400
Ser Asn Ile Ile Ala Trp Leu Arg Lys Ala Leu Glu Thr Asp Lys Lys
                405                 410                 415
Asp Trp Val Lys Glu Thr Glu Pro Glu Ala Asp Gln Asp Gly Tyr Tyr
            420                 425                 430
Gln Thr Thr Leu Pro Ala Ile Val Phe Gln Met Phe Glu Gln Asn Leu
        435                 440                 445
Gln Val Ala Ala Gln Ile Ser Glu Asp Leu Lys Thr Lys Val Leu Val
    450                 455                 460
Leu Cys Leu Gln Gln Met Asn Ser Phe Leu Ser Arg Tyr Lys Asp Glu
465                 470                 475                 480
Ala Gln Leu Tyr Lys Glu Glu His Leu Arg Asn Arg Gln His Pro His
                485                 490                 495
Cys Tyr Val Gln Tyr Met Ile Ala Ile Ile Asn Asn Cys Gln Thr Phe
            500                 505                 510
Lys Glu Ser Ile Val Ser Leu Lys Arg Lys Tyr Leu Lys Asn Glu Val
        515                 520                 525
Glu Glu Gly Val Ser Pro Ser Gln Pro Ser Met Asp Gly Ile Leu Asp
    530                 535                 540
Ala Ile Ala Lys Glu Gly Cys Ser Gly Leu Leu Glu Glu Val Phe Leu
545                 550                 555                 560
Asp Leu Glu Gln His Leu Asn Glu Leu Met Thr Lys Lys Trp Leu Leu
                565                 570                 575
Gly Ser Asn Ala Val Asp Ile Ile Cys Val Thr Val Glu Asp Tyr Phe
            580                 585                 590
Asn Asp Phe Ala Lys Ile Lys Lys Pro Tyr Lys Lys Arg Met Thr Ala
        595                 600                 605
Glu Ala His Arg Arg Val Val Val Glu Tyr Leu Arg Ala Val Met Gln
    610                 615                 620
Lys Arg Ile Ser Phe Arg Ser Pro Glu Glu Arg Lys Glu Gly Ala Glu
625                 630                 635                 640
Lys Met Val Arg Glu Ala Glu Gln Arg Arg Phe Leu Phe Arg Lys Leu
                645                 650                 655
Ala Ser Gly Phe Gly Glu Asp Val Asp Gly Tyr Cys Asp Thr Ile Val
            660                 665                 670
Ala Val Ala Glu Val Ile Lys Leu Thr Asp Pro Ser Leu Leu Tyr Leu
        675                 680                 685
Glu Val Ser Thr Leu Val Ser Lys Tyr Pro Asp Ile Arg Asp Asp His
    690                 695                 700
Ile Gly Ala Leu Leu Ala Val Arg Gly Asp Ala Ser Arg Asp Met Lys
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705 710 715 720
Gln Thr Ile Met Glu Thr Leu Glu Gln Gly Pro Ala Gln Ala Ser Pro
725 730 735
Ser Tyr Val Pro Leu Phe Lys Asp Ile Val Val Pro Ser Leu Asn Val
740 745 750
Ala Lys Leu Leu Lys
755

<210> 6001
<211> 2490
<212> DNA
<213> Homo sapiens

<400> 6001
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120
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<210> 6002
<211> 263
<212> PRT
<213> Homo sapiens

<400> 6002
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Tyr Arg Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu Asn
        35                  40                  45
Trp Leu Asp Ala Gln Ser Gly Leu Ala Ser Ala Pro Val Ser Gly Ala
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Gly Asn His Ser Tyr Cys Arg Asn Pro Asp Glu Asp Pro Ala Gly Pro
65                  70                  75                  80
Trp Cys Tyr Val Ser Gly Glu Ala Gly Val Pro Glu Lys Arg Pro Cys
                85                  90                  95
Glu Asp Leu Arg Cys Pro Glu Thr Thr Ser Gln Ala Leu Pro Ala Phe
            100                 105                 110
Thr Thr Glu Ile Gln Glu Ala Ser Glu Gly Pro Gly Ala Asp Glu Val
        115                 120                 125
Gln Val Phe Ala Pro Ala Asn Ala Leu Pro Ala Arg Ser Glu Ala Ala
    130                 135                 140
Ala Val Gln Pro Val Ile Gly Ile Ser Gln Arg Val Arg Met Asn Ser
145                 150                 155                 160
Lys Glu Lys Lys Asp Leu Gly Thr Leu Gly Tyr Val Leu Gly Ile Thr
                165                 170                 175
Met Met Val Ile Ile Ile Ala Ile Gly Ala Gly Ile Ile Leu Gly Tyr
            180                 185                 190
Ser Tyr Lys Arg Gly Lys Asp Leu Lys Glu Gln His Asp Gln Lys Val
        195                 200                 205
Cys Glu Arg Glu Met Gln Arg Ile Thr Leu Pro Leu Ser Ala Phe Thr
    210                 215                 220
Asn Pro Thr Cys Glu Ile Val Asp Glu Lys Thr Val Val Val His Thr
225                 230                 235                 240
Ser Gln Thr Pro Val Asp Pro Gln Glu Gly Thr Thr Pro Leu Met Gly
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Gln Ala Gly Thr Pro Gly Ala
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<210> 6003
<211> 3107
<212> DNA
<213> Homo sapiens

<400> 6003

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3107

<210> 6004
<211> 140
<212> PRT
<213> Homo sapiens

<400> 6004
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Pro Ala Val Pro Lys Val Ala Pro Gly Thr Met Pro Thr Arg Pro Glu
35 40 45
Gly Gly Thr Glu Thr Thr Ser Met Leu Xaa Val Pro Gly Val Thr Gln
50 55 60
Ser Pro Arg Gly Glu Arg Gly Ser Gly Pro His Ala Val Gln Gly Val
65 70 75 80
Ala Leu Pro Xaa Arg Gly Ser Pro Arg Gly Pro Gly Pro Arg Ala Pro
85 90 95
Gly Arg Gly Arg Asp Cys Gly Gly Asn Gly Pro Ala Glu Ala Pro Ala

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            100                 105                 110
Pro Leu Ser Ser Ala Phe Gln Pro Pro Ala Leu Gly Pro Ala Pro Lys
        115                 120                 125
Glu Gly Gly Pro Ser Ser Leu Asn Lys Arg Cys Thr
    130                 135                 140

<210> 6005
<211> 1735
<212> DNA
<213> Homo sapiens

<400> 6005
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1260
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<210> 6006
<211> 200
<212> PRT
<213> Homo sapiens

<400> 6006
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Lys Gly Gln Lys Gly Asp Pro Gly Glu Pro Gly Pro Ala Gly Leu Lys
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Gly Glu Ala Gly Glu Met Gly Leu Ser Gly Leu Pro Gly Ala Asp Gly
35 40 45
Leu Lys Gly Glu Lys Gly Glu Ser Ala Ser Gln Pro Thr Gly Glu Pro
50 55 60
Gly Ser Ala His Ser Glu Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro
65 70 75 80
Gly Pro Met Gly Leu Gln Gly Ile Gln Gly Pro Lys Gly Leu Asp Gly
85 90 95
Ala Lys Gly Glu Lys Gly Ala Ser Gly Glu Arg Gly Ser Ser Gly Leu
100 105 110
Pro Gly Pro Val Gly Pro Pro Gly Leu Ile Gly Leu Pro Gly Thr Lys
115 120 125
Gly Glu Lys Gly Arg Pro Gly Glu Pro Gly Leu Asp Gly Phe Pro Gly
130 135 140
Pro Arg Gly Glu Lys Gly Asp Arg Ser Glu Arg Gly Glu Lys Gly Glu
145 150 155 160
Arg Gly Val Pro Gly Arg Lys Gly Val Lys Gly Gln Lys Gly Glu Pro
165 170 175
Gly Pro Pro Gly Leu Asp Gln Pro Cys Pro Val Gly Pro Asp Gly Leu
180 185 190
Pro Val Pro Gly Cys Trp His Lys
195 200

<210> 6007
<211> 693
<212> DNA
<213> Homo sapiens

<400> 6007
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693

<210> 6008
<211> 214
<212> PRT
<213> Homo sapiens

<400> 6008
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Gly Lys Met Val Lys Lys Val Cys Pro Cys Asn Gln Leu Cys Arg Thr
        35   40   45
Ser Ser Thr Asn Thr Val Gly Ala Thr Val Asn Ser Gln Ala Ala Gln
    50   55   60
Ala Gln Pro Pro Ala Met Thr Ser Ser Arg Lys Gly Thr Phe Thr Asp
65   70   75   80
Asp Leu His Lys Leu Val Asp Asn Trp Ala Arg Asp Ala Met Asn Leu
                85   90   95
Ser Gly Arg Arg Gly Ser Lys Gly His Met Asn Tyr Glu Gly Pro Gly
            100   105   110
Met Ala Arg Lys Phe Ser Ala Pro Gly Gln Leu Cys Ile Ser Met Thr
        115   120   125
Ser Asn Leu Gly Gly Ser Ala Pro Ile Ser Ala Ala Ser Ala Thr Ser
    130   135   140
Leu Gly His Phe Thr Lys Ser Met Cys Pro Pro Gln Gln Tyr Gly Phe
145   150   155   160
Pro Ala Thr Pro Phe Gly Ala Gln Trp Ser Gly Thr Gly Gly Pro Ala

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                165                 170                 175
Pro Gln Pro Leu Gly Gln Phe Gln Pro Val Gly Thr Ala Ser Leu Gln
            180                 185                 190
Asn Phe Asn Ile Ser Asn Leu Gln Lys Ser Ile Ser Asn Pro Pro Gly
        195                 200                 205
Ser Asn Leu Arg Thr Thr
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<210> 6009
<211> 1570
<212> DNA
<213> Homo sapiens

<400> 6009
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<210> 6010
<211> 468
<212> PRT
<213> Homo sapiens

<400> 6010
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35 40 45
Ala Met Ala Cys Ala Leu Gly Tyr Asp Ile His Phe His Asp Lys Lys
50 55 60
Ile Leu Leu Leu Glu Ala Gly Pro Lys Lys Val Leu Glu Lys Leu Ser
65 70 75 80
Glu Thr Tyr Ser Asn Arg Val Ser Ser Ile Ser Pro Gly Ser Ala Thr
85 90 95
Leu Leu Ser Ser Phe Gly Ala Trp Asp His Ile Cys Asn Met Arg Tyr
100 105 110
Arg Ala Phe Arg Arg Met Gln Val Trp Asp Ala Cys Ser Glu Ala Leu
115 120 125
Ile Met Phe Asp Lys Asp Asn Leu Asp Asp Met Gly Tyr Ile Val Glu
130 135 140
Asn Asp Val Ile Met His Ala Leu Thr Lys Gln Leu Glu Ala Val Ser
145 150 155 160
Asp Arg Val Thr Val Leu Tyr Arg Ser Lys Ala Ile Arg Tyr Thr Trp
165 170 175
Pro Cys Pro Phe Pro Met Ala Asp Ser Ser Pro Trp Val His Ile Thr
180 185 190
Leu Gly Asp Gly Ser Thr Phe Gln Thr Lys Leu Leu Ile Gly Ala Asp
195 200 205
Gly His Asn Ser Gly Val Arg Gln Ala Val Gly Ile Gln Asn Val Ser
210 215 220
Trp Asn Tyr Asp Gln Ser Ala Val Val Ala Thr Leu His Leu Ser Glu
225 230 235 240
Ala Thr Glu Asn Asn Val Ala Trp Gln Arg Phe Leu Pro Ser Gly Pro
245 250 255
Ile Ala Leu Leu Pro Leu Ser Asp Thr Leu Ser Ser Leu Val Trp Ser

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            260                 265                 270
Thr Ser His Glu His Ala Ala Glu Leu Val Ser Met Asp Glu Glu Lys
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Phe Val Asp Ala Val Asn Ser Ala Phe Trp Ser Asp Ala Asp His Thr
    290                 295                 300
Asp Phe Ile Asp Thr Ala Gly Ala Met Leu Gln Tyr Pro Val Ser Leu
305                 310                 315                 320
Leu Lys Pro Thr Lys Val Ser Ala Arg Gln Leu Pro Pro Ser Val Pro
                325                 330                 335
Trp Val Asp Ala Lys Ser Arg Val Leu Phe Pro Leu Gly Leu Gly His
            340                 345                 350
Ala Ala Glu Tyr Val Arg Pro Arg Val Ala Leu Ile Gly Asp Ala Ala
        355                 360                 365
His Arg Val His Pro Leu Ala Gly Gln Gly Val Asn Met Gly Phe Gly
    370                 375                 380
Asp Ile Ser Ser Leu Ala His His Leu Ser Thr Ala Ala Phe Asn Gly
385                 390                 395                 400
Lys Asp Leu Gly Ser Val Ser His Leu Thr Gly Tyr Glu Thr Glu Arg
                405                 410                 415
Gln Arg His Asn Thr Ala Leu Leu Ala Ala Thr Asp Leu Leu Lys Arg
            420                 425                 430
Leu Tyr Ser Thr Ser Ala Ser Pro Leu Val Leu Leu Arg Thr Trp Gly
        435                 440                 445
Leu Gln Ala Thr Asn Ala Val Ser Pro Leu Lys Glu Gln Ile Met Ala
    450                 455                 460
Phe Ala Ser Lys
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<210> 6011
<211> 1331
<212> DNA
<213> Homo sapiens

<400> 6011

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600
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1320
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1331

<210> 6012
<211> 219
<212> PRT
<213> Homo sapiens

<400> 6012
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Val Phe Ser Lys Gly Val Arg Glu Val Glu Arg Val Leu Gln Leu Pro
20 25 30
Lys Glu Pro Gly Asp Ser Ala Gln Phe Thr Lys Ala Ile Ala Ile Ile
35 40 45
Phe Pro Phe Leu Tyr Leu Leu Glu Lys Val Glu Cys Thr Pro Ser Gln
50 55 60
Glu His Leu Lys His Gln Thr Val Tyr Arg Leu Leu Lys Cys Ala Pro
65 70 75 80
Arg Gly Lys Asn Gly Phe Thr Pro Leu His Met Ala Val Asp Lys Asp
85 90 95
Thr Thr Asn Val Gly Arg Tyr Pro Val Gly Arg Phe Pro Ser Leu His
100 105 110
Val Val Lys Val Leu Leu Asp Cys Gly Ala Asp Pro Asp Ser Arg Asp
115 120 125
Phe Asp Asn Asn Thr Pro Leu His Ile Ala Ala Gln Asn Asn Cys Pro
130 135 140
Ala Ile Met Asn Ala Leu Ile Glu Ala Gly Ala His Met Asp Ala Thr
145 150 155 160
Asn Ala Phe Lys Lys Thr Ala Tyr Glu Leu Leu Asp Glu Lys Leu Leu

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                165                 170                 175
Ala Arg Gly Thr Met Gln Pro Phe Asn Tyr Val Thr Leu Gln Cys Leu
            180                 185                 190
Ala Ala Arg Ala Leu Asp Lys Asn Lys Ile Pro Tyr Lys Gly Phe Ile
        195                 200                 205
Pro Glu Asp Leu Glu Ala Phe Ile Glu Leu His
    210                 215
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<210> 6013
<211> 2204
<212> DNA
<213> Homo sapiens

<400> 6013
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180
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300
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360
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420
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480
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540
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720
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780
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1200

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1260
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1320
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1380
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1440
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1860
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1920
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1980
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gtccttttt tccctctctc cacccctgtc ctctagccac agcatttttc tttttgtctt
2100
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2160
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2204

<210> 6014
<211> 182
<212> PRT
<213> Homo sapiens

<400> 6014
Arg Gln His Asn Lys Asp Lys Pro Phe Lys Cys His Asn Cys His Arg
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20 25 30
Val Lys His Ala Lys Val Tyr Thr Cys Thr Ile Cys Ser Arg Ala Tyr
35 40 45
Thr Ser Glu Thr Tyr Leu Met Lys His Met Arg Lys His Asn Pro Pro
50 55 60
Asp Leu Gln Gln Gln Val Gln Ala Ala Ala Ala Ala Ala Ala Val Ala
65 70 75 80
Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala
85 90 95
Gln Ala Gln Ala Gln Ala Ser Gln Ala Ser Gln Gln Gln Gln Gln Gln

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            100                 105                 110
Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro His Phe Gln Ser
        115                 120                 125
Pro Gly Ala Ala Pro Gln Gly Gly Gly Gly Gly Asp Ser Asn Pro Asn
    130                 135                 140
Pro Pro Pro Gln Cys Ser Phe Asp Leu Thr Pro Tyr Lys Thr Ala Glu
145                 150                 155                 160
His His Lys Asp Ile Cys Leu Thr Val Thr Thr Ser Thr Ile Gln Val
                165                 170                 175
Glu His Leu Ala Ser Ser
            180
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<210> 6015
<211> 612
<212> DNA
<213> Homo sapiens

<400> 6015
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120
tgagaatcct gattgaatgg aagtgaagag ccatgagaag ctcgcccagg agagtctaat
180
ttattctgat tacagctcat ggagagtgta gggcatgtga ggccactcca gctattgtta
240
ttcaacttgc atctgcccct gctgatcccc tgagaggctg gcagcctctc agggctcctt
300
gggcggtgag ccctcctccg cagcctgcaa gccttttttac ctctttccat cacctgagcc
360
tgaaagtgtg cctgcccgac cttgctcctg gccttatttc tcttcctatc ttatctccat
420
tccgcaggtg cctcagccat tgcctaccct tttgcacaaa attaaaaaga aaagaaaaaa
480
gccagtgaga gaacagtcac acgataaagg cacagcacag cagttggttg tctcttttta
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aacaggaagt agcagtcatt ctatatggat gttcagctag acccacgggg ctttaacctt
600
acctggcatg gc
612

<210> 6016
<211> 99
<212> PRT
<213> Homo sapiens

<400> 6016
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Met Glu Arg Gly Lys Lys Ala Cys Arg Leu Arg Arg Arg Ala His Arg
 1               5                  10                  15
Pro Arg Ser Pro Glu Arg Leu Pro Ala Ser Gln Gly Ile Ser Arg Gly
            20                  25                  30
Arg Cys Lys Leu Asn Asn Asn Ser Trp Ser Gly Leu Thr Cys Pro Thr
        35                  40                  45
Leu Ser Met Ser Cys Asn Gln Asn Lys Leu Asp Ser Pro Gly Arg Ala
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    50                  55                  60
Ser His Gly Ser Ser Leu Pro Phe Asn Gln Asp Ser Gln Lys Pro Ala
65                  70                  75                  80
Phe Tyr Asn Ile Phe Leu Lys Lys Ser His Ser Phe Gln Ser Leu Leu
                85                  90                  95
Gln Tyr Ile
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<210> 6017
<211> 2091
<212> DNA
<213> Homo sapiens

<400> 6017
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120
tggaatttca gagaactgag tgaaaacagc cagcaggcag ccaacgtcct ctcgggagcc
180
tgtggcctgc agcgtgggga tcgtgtggca gtgatgctgc cccgagtgcc tgagtggtgg
240
ctggtgatcc tgggctgcat tcgagcaggt ctcatcttta tgcctggaac catccagatg
300
aaatccactg acatactgta taggttgcag atgtctaagg ccaaggctat tgttgctggg
360
gatgaagtca tccaagaagt ggacacagtg gcatctgaat gtccttctct gagaattaag
420
ctactggtgt ctgagaaaag ctgcgatggg tggctgaact tcaagaaact actaaatgag
480
gcatccacca ctcatcactg tgtggagact ggaagccagg aagcatctgc catctacttc
540
actagtggga ccagtggtct tcccaagatg gcagaacatt cctactcgag cctgggcctc
600
aaggccaaga tggatgctgg ttggacaggc ctgcaagcct ctgatataat gtggaccata
660
tcagacacag gttggatact gaacatcttg ggctcacttt tggaatcttg gacattagga
720
gcatgcacat ttgttcatct cttgccaaag tttgacccac tggttattct aaagacactc
780
tccagttatc caatcaagag tatgatgggt gcccctattg tttaccggat gttgctacag
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1080
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1140
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1200

ttttggctcc ttggagaccg gggaatcaaa gatgaagatg ggtatttcca gtttatggga
1260
cgggcagatg atatcattaa ctccagcggg taccggattg gaccctcgga ggtagagaat
1320
gcactgatga agcaccctgc tgtggttgag acggctgtga tcagcagccc agaccccgtc
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1440
gaacagctca ccaaggagct gcagcagcat gtgaagtcag tgacagcccc atacaagtac
1500
ccaagaaaga tagagtttgt cttgaacctg cccaagactg tcacagggaa aattcaacga
1560
gccaagcttc gagacaagga gtggaagatg tccggaaaag cccgtgcgca gtgagacatc
1620
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1680
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1740
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1920
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1980
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2040
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2091

<210> 6018
<211> 537
<212> PRT
<213> Homo sapiens

<400> 6018
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Asn Gly Lys Gly Lys Glu Leu Met Trp Asn Phe Arg Glu Leu Ser Glu
35 40 45
Asn Ser Gln Gln Ala Ala Asn Val Leu Ser Gly Ala Cys Gly Leu Gln
50 55 60
Arg Gly Asp Arg Val Ala Val Met Leu Pro Arg Val Pro Glu Trp Trp
65 70 75 80
Leu Val Ile Leu Gly Cys Ile Arg Ala Gly Leu Ile Phe Met Pro Gly
85 90 95
Thr Ile Gln Met Lys Ser Thr Asp Ile Leu Tyr Arg Leu Gln Met Ser
100 105 110
Lys Ala Lys Ala Ile Val Ala Gly Asp Glu Val Ile Gln Glu Val Asp
115 120 125
Thr Val Ala Ser Glu Cys Pro Ser Leu Arg Ile Lys Leu Leu Val Ser

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    130                 135                 140
Glu Lys Ser Cys Asp Gly Trp Leu Asn Phe Lys Lys Leu Leu Asn Glu
145                 150                 155                 160
Ala Ser Thr Thr His His Cys Val Glu Thr Gly Ser Gln Glu Ala Ser
                165                 170                 175
Ala Ile Tyr Phe Thr Ser Gly Thr Ser Gly Leu Pro Lys Met Ala Glu
            180                 185                 190
His Ser Tyr Ser Ser Leu Gly Leu Lys Ala Lys Met Asp Ala Gly Trp
        195                 200                 205
Thr Gly Leu Gln Ala Ser Asp Ile Met Trp Thr Ile Ser Asp Thr Gly
    210                 215                 220
Trp Ile Leu Asn Ile Leu Gly Ser Leu Leu Glu Ser Trp Thr Leu Gly
225                 230                 235                 240
Ala Cys Thr Phe Val His Leu Leu Pro Lys Phe Asp Pro Leu Val Ile
                245                 250                 255
Leu Lys Thr Leu Ser Ser Tyr Pro Ile Lys Ser Met Met Gly Ala Pro
            260                 265                 270
Ile Val Tyr Arg Met Leu Leu Gln Gln Asp Leu Ser Ser Tyr Lys Phe
        275                 280                 285
Pro His Leu Gln Asn Cys Leu Ala Gly Gly Glu Ser Leu Leu Pro Glu
    290                 295                 300
Thr Leu Glu Asn Trp Arg Ala Gln Thr Gly Leu Asp Ile Arg Glu Phe
305                 310                 315                 320
Tyr Gly Gln Thr Glu Thr Gly Leu Thr Cys Met Val Ser Lys Thr Met
                325                 330                 335
Lys Ile Lys Pro Gly Tyr Met Gly Thr Ala Ala Ser Cys Tyr Asp Val
            340                 345                 350
Gln Val Ile Asp Asp Lys Gly Asn Val Leu Pro Pro Gly Thr Glu Gly
        355                 360                 365
Asp Ile Gly Ile Arg Val Lys Pro Ile Arg Pro Ile Gly Ile Phe Ser
    370                 375                 380
Gly Tyr Val Glu Asn Pro Asp Lys Thr Ala Ala Asn Ile Arg Gly Asp
385                 390                 395                 400
Phe Trp Leu Leu Gly Asp Arg Gly Ile Lys Asp Glu Asp Gly Tyr Phe
                405                 410                 415
Gln Phe Met Gly Arg Ala Asp Asp Ile Ile Asn Ser Ser Gly Tyr Arg
            420                 425                 430
Ile Gly Pro Ser Glu Val Glu Asn Ala Leu Met Lys His Pro Ala Val
        435                 440                 445
Val Glu Thr Ala Val Ile Ser Ser Pro Asp Pro Val Arg Gly Glu Val
    450                 455                 460
Val Lys Ala Phe Val Val Leu Ala Ser Gln Phe Leu Ser His Asp Pro
465                 470                 475                 480
Glu Gln Leu Thr Lys Glu Leu Gln Gln His Val Lys Ser Val Thr Ala
                485                 490                 495
Pro Tyr Lys Tyr Pro Arg Lys Ile Glu Phe Val Leu Asn Leu Pro Lys
            500                 505                 510
Thr Val Thr Gly Lys Ile Gln Arg Ala Lys Leu Arg Asp Lys Glu Trp
        515                 520                 525
Lys Met Ser Gly Lys Ala Arg Ala Gln
    530                 535
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<210> 6019
<211> 3002

<212> DNA
<213> Homo sapiens

<400> 6019
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420
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1620
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1680
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3002

<210> 6020

<211> 387
<212> PRT
<213> Homo sapiens

<400> 6020

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            20                  25                  30
Thr Gly Arg Asp Leu Ile Ala Tyr Glu Val Lys Ala Asn Gln Arg Asn
        35                  40                  45
Ile Glu Asp Ile Cys Ile Cys Cys Gly Ser Leu Gln Val His Thr Gln
    50                  55                  60
His Pro Leu Phe Glu Gly Gly Ile Cys Ala Pro Cys Lys Asp Lys Phe
65                  70                  75                  80
Leu Asp Ala Leu Phe Leu Tyr Asp Asp Asp Gly Tyr Gln Ser Tyr Cys
                85                  90                  95
Ser Ile Cys Cys Ser Gly Glu Thr Leu Leu Ile Cys Gly Asn Pro Asp
            100                 105                 110
Cys Thr Arg Cys Tyr Cys Phe Glu Cys Val Asp Ser Leu Val Gly Pro
        115                 120                 125
Gly Thr Ser Gly Lys Val His Ala Met Ser Asn Trp Val Cys Tyr Leu
    130                 135                 140
Cys Leu Pro Ser Ser Arg Ser Gly Leu Leu Gln Arg Arg Arg Lys Trp
145                 150                 155                 160
Arg Ser Gln Leu Lys Ala Phe Tyr Asp Arg Glu Ser Glu Asn Pro Leu
                165                 170                 175
Glu Met Phe Glu Thr Val Pro Val Trp Arg Arg Gln Pro Val Arg Val
            180                 185                 190
Leu Ser Leu Phe Glu Asp Ile Lys Lys Glu Leu Thr Ser Leu Gly Phe
        195                 200                 205
Leu Glu Ser Gly Ser Asp Pro Gly Gln Leu Lys His Val Val Asp Val
    210                 215                 220
Thr Asp Thr Val Arg Lys Asp Val Glu Glu Trp Gly Pro Phe Asp Leu
225                 230                 235                 240
Val Tyr Gly Ala Thr Ala Pro Leu Gly His Thr Cys Asp Arg Pro Pro
                245                 250                 255
Ser Trp Tyr Leu Phe Gln Phe His Arg Phe Leu Gln Tyr Ala Arg Pro
            260                 265                 270
Lys Pro Gly Ser Pro Arg Pro Phe Phe Trp Met Phe Val Asp Asn Leu
        275                 280                 285
Val Leu Asn Lys Glu Asp Leu Asp Val Ala Ser Arg Phe Leu Glu Met
    290                 295                 300
Glu Pro Val Thr Ile Pro Asp Val His Gly Gly Ser Leu Gln Asn Ala
305                 310                 315                 320
Val Arg Val Trp Ser Asn Ile Pro Ala Ile Arg Ser Ser Arg His Trp
                325                 330                 335
Ala Leu Val Ser Glu Glu Glu Leu Ser Leu Leu Ala Gln Asn Lys Gln
            340                 345                 350
Ser Ser Lys Leu Ala Ala Lys Trp Pro Thr Lys Leu Val Lys Asn Cys
        355                 360                 365
Phe Leu Pro Leu Arg Glu Tyr Phe Lys Tyr Phe Ser Thr Glu Leu Thr
    370                 375                 380
Ser Ser Leu
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385

<210> 6021
<211> 3145
<212> DNA
<213> Homo sapiens

<400> 6021
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Arg Val Thr Ala Ile Asp Phe Arg Asp Ile Met Val Thr Ile Arg Pro
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Tyr Lys Leu Ala Val Ala Thr Phe Ala Gly Ile Glu Asn Lys Phe Gly
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Pro Ile Lys Ile Ser Ser Thr Pro Pro Ser Gly Ser Arg Leu Asp Pro
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Gln Ile Ala Ser Ser Ala Phe Pro Gly Leu Gly Ser Leu Gly Gly Gln
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Thr Ser Asp Asn Gly Lys Asp Gly Leu Ala Tyr Ser Ala Leu Leu Lys
                85                  90                  95
Asn Glu Leu Leu Gly Ala Gly Ile Glu Lys Val Gln Asp Pro Gln Thr
            100                 105                 110
Glu Asp Arg Arg Leu Gln Pro Ser Thr Pro Glu Lys Lys Gly Leu Phe
        115                 120                 125
Thr Tyr Ser Leu Ser Thr Lys Arg Ser Ser Pro Asp Asp Gly Asn Asp
    130                 135                 140
Val Ser Pro Tyr Ser Leu Ser Pro Val Ser Asn Lys Ser Gln Lys Leu
145                 150                 155                 160
Leu Arg Ser Pro Arg Lys Pro Thr Arg Lys Ile Ser Lys Ile Pro Phe
                165                 170                 175
Lys Val Leu Asp Ala Pro Glu Leu Gln Asp Asp Phe Tyr Leu Asn Leu
            180                 185                 190
Val Asp Trp Ser Ser Leu Asn Val Leu Ser Val Gly Leu Gly Thr Cys
        195                 200                 205
Val Tyr Leu Trp Ser Ala Cys Thr Ser Gln Val Thr Arg Leu Cys Asp
    210                 215                 220
Leu Ser Val Glu Gly Asp Ser Val Thr Ser Val Gly Trp Ser Glu Arg
225                 230                 235                 240
Gly Asn Leu Val Ala Val Gly Thr His Lys Gly Phe Val Gln Ile Trp
                245                 250                 255
Asp Ala Ala Ala Gly Lys Lys Leu Ser Met Leu Glu Gly His Thr Ala
            260                 265                 270
Arg Val Gly Ala Leu Ala Trp Asn Ala Glu Gln Leu Ser Ser Gly Ser
        275                 280                 285
Arg Asp Arg Met Ile Leu Gln Arg Asp Ile Arg Thr Pro Pro Leu Gln
    290                 295                 300
Ser Glu Arg Arg Leu Gln Gly His Arg Gln Glu Val Cys Gly Leu Lys
305                 310                 315                 320
Trp Ser Thr Asp His Gln Leu Leu Ala Ser Gly Gly Asn Asp Asn Lys
                325                 330                 335
Leu Leu Val Trp Asn His Ser Ser Leu Ser Pro Val Gln Gln Tyr Thr
            340                 345                 350
Glu His Leu Ala Ala Val Lys Ala Ile Ala Trp Ser Pro His Gln His
        355                 360                 365
Gly Leu Leu Ala Ser Gly Gly Gly Thr Ala Asp Arg Cys Ile Arg Phe
    370                 375                 380
Trp Asn Thr Leu Thr Gly Gln Pro Leu Gln Cys Ile Asp Thr Gly Ser
385                 390                 395                 400
Gln Val Cys Asn Leu Ala Trp Ser Lys His Ala Asn Glu Leu Val Ser
                405                 410                 415
Thr His Gly Tyr Ser Gln Asn Gln Ile Leu Val Trp Lys Tyr Pro Ser
            420                 425                 430
Leu Thr Gln Val Ala Lys Leu Thr Gly His Ser Tyr Arg Val Leu Tyr
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        435                 440                 445
Leu Ala Met Ser Pro Asp Gly Glu Ala Ile Val Thr Gly Ala Gly Asp
    450                 455                 460
Glu Thr Leu Arg Phe Trp Asn Val Phe Ser Lys Thr Arg Ser Thr Lys
465                 470                 475                 480
Val Lys Trp Glu Ser Val Ser Val Leu Asn Leu Phe Thr Arg Ile Arg
                485                 490                 495
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<210> 6027
<211> 305
<212> DNA
<213> Homo sapiens

<400> 6027
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120
gcggccaccc aaatggagtc ggggcttggg gctgccggga agcccaactg cctggtcatc
180
gatgagatcg acggggcccc cgtggtgggc tccttgatgc ctgggtaggt gggtgggcgg
240
gcaggcaggc gggcagcagg gcctggactc accgtgtcct ctgacctccc ccaaggccgc
300
catca
305

<210> 6028
<211> 75
<212> PRT
<213> Homo sapiens

<400> 6028
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 1               5                  10                  15
Ala Gly Tyr Ser Val Val Glu Met Asn Ala Ser Asp Asp Arg Ser Pro
            20                  25                  30
Glu Val Phe Arg Thr Arg Ile Glu Ala Ala Thr Gln Met Glu Ser Gly
        35                  40                  45
Leu Gly Ala Ala Gly Lys Pro Asn Cys Leu Val Ile Asp Glu Ile Asp
    50                  55                  60
Gly Ala Pro Val Val Gly Ser Leu Met Pro Gly
65                  70                  75
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<210> 6029
<211> 1350
<212> DNA
<213> Homo sapiens

<400> 6029
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agaagcaggg gtgcccaggc tgtcacagcc ttgcagtgca tggtgggttc cgtggccaac
120

ttgccagggg acaggcctgt tgctggcact ccccccacaa ttacagggtg ggagtgaagg
180
acctcgcggc tgcggacagg tccttgttag taaggaggag gctctgcagt cccggtgggg
240
tcatcttgcc tctccggact gctccctctg actggtgaag ccacactctg tgaagctgtc
300
tgacagaagg ggacacgcct ttgctgccca ggatggacct gggccaccca ggatgccgct
360
ggcctcagcc agggcacgtg tgcccagcgc tggctcctgc tgacccctgg actggctccc
420
atctcgggaa tgacgcctgc cgtgggaatc gtggagaggg ggtttaattt aacttggaag
480
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540
gctggggatg gccacaccct ggcagcaggc ggccagagac caggaaggcc tacccagcac
600
ctgtccagaa aagattggtg tgggttgacc tggcctatgc ggggcagctc agtttgaagc
660
aggaacttcc ccaaacgtgc ccaggctcca agacagcagc attcactttg caccgtgctg
720
agcagagcgg ggcctcgcca ggtggaaagc cctaggaagg ctgcgtgctc tgcaaaccca
780
ggggtgctgt ggccgtacag caggggcgtc cgtgtccagg cagctttgtc atgtcttcca
840
aaggtcagga aggcgccacc gccctgcccc acgacagctg cgtctgcaag cgccagctct
900
gagcactgtt ctccgccgac atgaggacac catccaagaa ttcctcctgg gagacctcct
960
gaggagacgc gaagaccatc gatgctttgg aagaatgaaa agaagtttct gctaagccaa
1020
acctaggtgg atgggaagtg cctgtgtgga tgtgaagcca ccttgggtgg gcggctcgga
1080
gctcctctgc ccacatcgcc tcactgggac tcgccatcca gtctgacgtc tttgatgtcc
1140
ccataaatct gctggctttc aggagaacac gtcttgaagc acagctgaac ttgaatcttt
1200
tctgggtcct cctgctgggc cgtggtgggg agccgctccc gttgcctcaa ggcctccaag
1260
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atgcgcggct tcggcagccc agccgagcct
1350

<210> 6030
<211> 99
<212> PRT
<213> Homo sapiens

<400> 6030
Met Gly Thr Ser Lys Thr Ser Asp Trp Met Ala Ser Pro Ser Glu Ala
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Met Trp Ala Glu Glu Leu Arg Ala Ala His Pro Arg Trp Leu His Ile
20 25 30
His Thr Gly Thr Ser His Pro Pro Arg Phe Gly Leu Ala Glu Thr Ser

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        35                  40                  45
Phe His Ser Ser Lys Ala Ser Met Val Phe Ala Ser Pro Gln Glu Val
    50                  55                  60
Ser Gln Glu Glu Phe Leu Asp Gly Val Leu Met Ser Ala Glu Asn Ser
65                  70                  75                  80
Ala Gln Ser Trp Arg Leu Gln Thr Gln Leu Ser Trp Gly Arg Ala Val
                85                  90                  95
Ala Pro Ser
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<210> 6031
<211> 1316
<212> DNA
<213> Homo sapiens

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120
gttgccaagt ctacctgtgc catcaacaac accctcattg ctttcttcat tttgactacg
180
ataaaaggca gtgctttcct cagtgctatt tttcttgcct tagcgacata ccagtctctg
240
tacccactca ccttgtttgt cccaggactc ctctatctcc tccagcggca gtacatacct
300
gtgaaaatga agagcaaagc cttctggatc ttttcttggg agtatgccat gatgtatgtg
360
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420
cccgcagtct atggctttat actttctgtt ccagatctca ctccaaacat tggtcttttc
480
tggtacttct ttgcagagat gtttgagcac ttcagcctct tctttgtatg tgtgtttcag
540
atcaacgtct tcttctacac catcccctta gccataaagc taaaggagca ccccatcttc
600
ttcatgttta tccagatcgc tgtcatcgcc atctttaagt cctacccgac agtgggggac
660
gtggcgctct acatggcctt cttccccgtg tggaaccatc tctacagatt cctgagaaac
720
atctttgtcc tcacctgcat catcatcgtc tgttccctgc tcttccctgt cctgtggcac
780
ctctggattt atgcaggaag tgccaactct aatttctttt atgccatcac actgaccttc
840
aacgttgggc agatcctgct catctctgat tacttctatg ccttcctgcg gcgggagtac
900
tacctcacac atggcctcta cttgaccgcc aaggatggca cagaggccat gctcgtgctc
960
aagtaggcct ggctggcaca gggctgcatg gacctcaggg ggctgtgggg ccagaagctg
1020
ggccaagccc tccagccaga gttgccagca ggcgagtgct tgggcagaag aggttcgagt
1080
ccagggtcac aagtctctgg taccaaaagg gacccatggc tgactgacag caaggcctat
1140

ggggaagaac tgggagctcc ccaacttgga ccccccacctt gtggctctgc acaccaagga
1200
gccccctccc agacaggaag gagaagaggc aggtgagcag ggcttgttag attgtggcta
1260
cttaataaat gtttttttgtt atgaagtcta aaaaaaaaaa aaaaaaaaaa aaaaaa
1316

<210> 6032
<211> 321
<212> PRT
<213> Homo sapiens

<400> 6032
Xaa Leu Asp Gln Tyr Ala Pro Asp Val Ala Glu Leu Ile Arg Thr Pro
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Met Glu Met Arg Tyr Ile Pro Leu Lys Val Ala Leu Phe Tyr Leu Leu
20 25 30
Asn Pro Tyr Thr Ile Leu Ser Cys Val Ala Lys Ser Thr Cys Ala Ile
35 40 45
Asn Asn Thr Leu Ile Ala Phe Phe Ile Leu Thr Thr Ile Lys Gly Ser
50 55 60
Ala Phe Leu Ser Ala Ile Phe Leu Ala Leu Ala Thr Tyr Gln Ser Leu
65 70 75 80
Tyr Pro Leu Thr Leu Phe Val Pro Gly Leu Leu Tyr Leu Leu Gln Arg
85 90 95
Gln Tyr Ile Pro Val Lys Met Lys Ser Lys Ala Phe Trp Ile Phe Ser
100 105 110
Trp Glu Tyr Ala Met Met Tyr Val Gly Ser Leu Val Val Ile Ile Cys
115 120 125
Leu Ser Phe Phe Leu Leu Ser Ser Trp Asp Phe Ile Pro Ala Val Tyr
130 135 140
Gly Phe Ile Leu Ser Val Pro Asp Leu Thr Pro Asn Ile Gly Leu Phe
145 150 155 160
Trp Tyr Phe Phe Ala Glu Met Phe Glu His Phe Ser Leu Phe Phe Val
165 170 175
Cys Val Phe Gln Ile Asn Val Phe Phe Tyr Thr Ile Pro Leu Ala Ile
180 185 190
Lys Leu Lys Glu His Pro Ile Phe Phe Met Phe Ile Gln Ile Ala Val
195 200 205
Ile Ala Ile Phe Lys Ser Tyr Pro Thr Val Gly Asp Val Ala Leu Tyr
210 215 220
Met Ala Phe Phe Pro Val Trp Asn His Leu Tyr Arg Phe Leu Arg Asn
225 230 235 240
Ile Phe Val Leu Thr Cys Ile Ile Ile Val Cys Ser Leu Leu Phe Pro
245 250 255
Val Leu Trp His Leu Trp Ile Tyr Ala Gly Ser Ala Asn Ser Asn Phe
260 265 270
Phe Tyr Ala Ile Thr Leu Thr Phe Asn Val Gly Gln Ile Leu Leu Ile
275 280 285
Ser Asp Tyr Phe Tyr Ala Phe Leu Arg Arg Glu Tyr Tyr Leu Thr His
290 295 300
Gly Leu Tyr Leu Thr Ala Lys Asp Gly Thr Glu Ala Met Leu Val Leu
305 310 315 320
Lys

<210> 6033
<211> 5157
<212> DNA
<213> Homo sapiens

<400> 6033
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120
caggagcatg acttaaagtt aaacttgaag tttgaaatcg aggttctctg caagaacctt
180
gcattagaca tcaatgagct aaaacctgga aacctcctaa aggataaaga tcgcctgaag
240
aatttagatg agcaactctc tgctccaagg aaagatgtca agcagccaga agaactccct
300
cccatcacaa ccacaacaac ttctactaca ccagctacca acaccacttg tacagccacg
360
gttccaccac agccacagta cagctaccac gacatcaatg tctattccct tgcgggcttg
420
gcaccacaca ttactctaaa tccaacaatt cccttgtttc aggcccatcc acagttgaag
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540
cgatcaatta agattgccat gactacttgt gagcaaatag tcaggaagga ttttgccctg
600
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660
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720
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780
gcagctgctc aattagctca ggacaattgt gagttggctt gctgttttat tcagaagact
840
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900
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960
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1140
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5040
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<210> 6034
<211> 1096
<212> PRT
<213> Homo sapiens

<400> 6034
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20 25 30
Arg Lys Asp Val Lys Gln Pro Glu Glu Leu Pro Pro Ile Thr Thr Thr
35 40 45
Thr Thr Ser Thr Thr Pro Ala Thr Asn Thr Thr Cys Thr Ala Thr Val
50 55 60
Pro Pro Gln Pro Gln Tyr Ser Tyr His Asp Ile Asn Val Tyr Ser Leu
65 70 75 80
Ala Gly Leu Ala Pro His Ile Thr Leu Asn Pro Thr Ile Pro Leu Phe
85 90 95
Gln Ala His Pro Gln Leu Lys Gln Cys Val Arg Gln Ala Ile Glu Arg
100 105 110
Ala Val Gln Glu Leu Val His Pro Val Val Asp Arg Ser Ile Lys Ile
115 120 125
Ala Met Thr Thr Cys Glu Gln Ile Val Arg Lys Asp Phe Ala Leu Asp
130 135 140
Ser Glu Glu Ser Arg Met Arg Ile Ala Ala His His Met Met Arg Asn
145 150 155 160
Leu Thr Ala Gly Met Ala Met Ile Thr Cys Arg Glu Pro Leu Leu Met
165 170 175
Ser Ile Ser Thr Asn Leu Lys Asn Ser Phe Ala Ser Ala Leu Arg Thr
180 185 190
Ala Ser Pro Gln Gln Arg Glu Met Met Asp Gln Ala Ala Ala Gln Leu
195 200 205
Ala Gln Asp Asn Cys Glu Leu Ala Cys Cys Phe Ile Gln Lys Thr Ala
210 215 220
Val Glu Lys Ala Gly Pro Glu Met Asp Lys Arg Leu Ala Thr Glu Phe

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225                 230                 235                 240
Glu Leu Arg Lys His Ala Arg Gln Glu Gly Arg Arg Tyr Cys Asp Pro
                245                 250                 255
Val Val Leu Thr Tyr Gln Ala Glu Arg Met Pro Glu Gln Ile Arg Leu
            260                 265                 270
Lys Val Gly Gly Val Asp Pro Lys Gln Leu Ala Val Tyr Glu Glu Phe
        275                 280                 285
Ala Arg Asn Val Pro Gly Phe Leu Pro Thr Asn Asp Leu Ser Gln Pro
    290                 295                 300
Thr Gly Phe Leu Ala Gln Pro Met Lys Gln Ala Trp Ala Thr Asp Asp
305                 310                 315                 320
Val Ala Gln Ile Tyr Asp Lys Cys Ile Thr Glu Leu Glu Gln His Leu
                325                 330                 335
His Ala Ile Pro Pro Thr Leu Ala Met Asn Pro Gln Ala Gln Ala Leu
            340                 345                 350
Arg Ser Leu Leu Glu Val Val Val Leu Ser Arg Asn Ser Arg Asp Ala
        355                 360                 365
Ile Ala Ala Leu Gly Leu Leu Gln Lys Ala Val Glu Gly Leu Leu Asp
    370                 375                 380
Ala Thr Ser Gly Ala Asp Ala Asp Leu Leu Leu Arg Tyr Arg Glu Cys
385                 390                 395                 400
His Leu Leu Val Leu Lys Ala Leu Gln Asp Gly Arg Ala Tyr Gly Ser
                405                 410                 415
Pro Trp Cys Asn Lys Gln Ile Thr Arg Cys Leu Ile Glu Cys Arg Asp
            420                 425                 430
Glu Tyr Lys Tyr Asn Val Glu Ala Val Glu Leu Leu Ile Arg Asn His
        435                 440                 445
Leu Val Asn Met Gln Gln Tyr Asp Leu His Leu Ala Gln Ser Met Glu
    450                 455                 460
Asn Gly Leu Asn Tyr Met Ala Val Ala Phe Ala Met Gln Leu Val Lys
465                 470                 475                 480
Ile Leu Leu Val Asp Glu Arg Ser Val Ala His Val Thr Glu Ala Asp
                485                 490                 495
Leu Phe His Thr Ile Glu Thr Leu Met Arg Ile Asn Ala His Ser Arg
            500                 505                 510
Gly Asn Ala Pro Glu Gly Leu Pro Gln Leu Met Glu Val Val Arg Ser
        515                 520                 525
Asn Tyr Glu Ala Met Ile Asp Arg Ala His Gly Gly Pro Asn Phe Met
    530                 535                 540
Met His Ser Gly Ile Ser Gln Ala Ser Glu Tyr Asp Asp Pro Pro Gly
545                 550                 555                 560
Leu Arg Glu Lys Ala Glu Tyr Leu Leu Arg Glu Trp Val Asn Leu Tyr
                565                 570                 575
His Ser Ala Ala Ala Gly Arg Asp Ser Thr Lys Ala Phe Ser Ala Phe
            580                 585                 590
Val Gly Gln Val Glu Leu Leu Glu Arg Lys Met His Gln Gln Gly Ile
        595                 600                 605
Leu Lys Thr Asp Asp Leu Ile Thr Arg Phe Phe Arg Leu Cys Thr Glu
    610                 615                 620
Met Cys Val Glu Ile Ser Tyr Arg Ala Gln Ala Glu Gln Gln His Asn
625                 630                 635                 640
Pro Ala Ala Asn Pro Thr Met Ile Arg Ala Lys Cys Tyr His Asn Leu
                645                 650                 655
Asp Ala Phe Val Arg Leu Ile Ala Leu Leu Val Lys His Ser Gly Glu
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Ala Thr Asn Thr Val Thr Lys Ile Asn Leu Leu Asn Lys Val Leu Gly
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Ile Val Val Gly Val Leu Leu Gln Asp His Asp Val Arg Gln Ser Glu
    690                 695                 700
Phe Gln Gln Leu Pro Tyr His Arg Ile Phe Ile Met Leu Leu Leu Glu
705                 710                 715                 720
Leu Asn Ala Pro Glu His Val Leu Glu Thr Ile Asn Phe Gln Thr Leu
                725                 730                 735
Thr Ala Phe Cys Asn Thr Phe His Ile Leu Arg Pro Thr Lys Ala Pro
            740                 745                 750
Gly Phe Val Tyr Ala Trp Leu Glu Leu Ile Ser His Arg Ile Phe Ile
        755                 760                 765
Ala Arg Met Leu Ala His Thr Pro Gln Gln Lys Gly Trp Pro Met Tyr
    770                 775                 780
Ala Gln Leu Leu Ile Asp Leu Phe Lys Tyr Leu Ala Pro Phe Leu Arg
785                 790                 795                 800
Asn Val Glu Leu Thr Lys Pro Met Gln Ile Leu Tyr Lys Gly Thr Leu
                805                 810                 815
Arg Val Leu Leu Val Leu Leu His Asp Phe Pro Glu Phe Leu Cys Asp
            820                 825                 830
Tyr His Tyr Gly Phe Cys Asp Val Ile Pro Pro Asn Cys Ile Gln Leu
        835                 840                 845
Arg Asn Leu Ile Leu Ser Ala Phe Pro Arg Asn Met Arg Leu Pro Asp
    850                 855                 860
Pro Phe Thr Pro Asn Leu Lys Val Asp Met Leu Ser Glu Ile Asn Ile
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Ala Pro Arg Ile Leu Thr Asn Phe Thr Gly Val Met Pro Pro Gln Phe
                885                 890                 895
Lys Lys Asp Leu Asp Ser Tyr Leu Lys Thr Arg Ser Pro Val Thr Phe
            900                 905                 910
Leu Ser Asp Leu Arg Ser Asn Leu Gln Val Ser Asn Glu Pro Gly Asn
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Arg Tyr Asn Leu Gln Leu Ile Asn Ala Leu Val Leu Tyr Val Gly Thr
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Gln Ala Ile Ala His Ile His Asn Lys Gly Ser Thr Pro Ser Met Ser
945                 950                 955                 960
Thr Ile Thr His Ser Ala His Met Asp Ile Phe Gln Asn Leu Ala Val
                965                 970                 975
Asp Leu Asp Thr Glu Gly Arg Tyr Leu Phe Leu Asn Ala Ile Ala Asn
            980                 985                 990
Gln Leu Arg Tyr Pro Asn Ser His Thr His Tyr Phe Ser Cys Thr Met
        995                 1000                1005
Leu Tyr Leu Phe Ala Glu Ala Asn Thr Glu Ala Ile Gln Glu Gln Ile
    1010                1015                1020
Thr Arg Val Leu Leu Glu Arg Leu Ile Val Asn Arg Pro His Pro Trp
1025                1030                1035                1040
Gly Leu Leu Ile Thr Phe Ile Glu Leu Ile Lys Asn Pro Ala Phe Lys
                1045                1050                1055
Phe Trp Asn His Glu Phe Val His Cys Ala Pro Glu Ile Glu Lys Leu
            1060                1065                1070
Phe Gln Ser Val Ala Gln Cys Cys Met Gly Gln Lys Gln Ala Gln Gln
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<211> 320
<212> DNA
<213> Homo sapiens

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gtggggcagt ggtgggcatt gtggctctgt gatctgggcc aggctcccag ccaccctggg
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<210> 6036
<211> 102
<212> PRT
<213> Homo sapiens

<400> 6036
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20 25 30
Arg Gln Val Leu Gln Glu Pro Ser Arg Glu Pro Pro Gly Trp Leu Gly
35 40 45
Ala Trp Pro Arg Ser Gln Ser His Asn Ala His His Cys Pro Thr Met
50 55 60
Pro Phe Arg Met Glu Pro Leu Ile His Trp Ala His Ser His Gly Gln
65 70 75 80
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Gln Gln Gly Leu Cys Asp
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<210> 6037
<211> 3910
<212> DNA
<213> Homo sapiens

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<211> 214
<212> PRT
<213> Homo sapiens

<400> 6038
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His Gly Gly Thr Cys Ser Arg Gln Glu Leu Gly Val Ser Asp Val Leu
35 40 45
Gly Tyr Val His Pro Asp Leu Leu Lys Asp Phe Cys Met Asn Pro Gln
50 55 60
Thr Val Leu Leu Leu Arg Val Ile Ala Ala Phe Cys Phe Leu Gly Ile
65 70 75 80
Leu Cys Ser Leu Ser Ala Phe Leu Leu Asp Val Phe Gly Pro Lys His
85 90 95
Pro Ala Leu Lys Ile Thr Arg Arg Tyr Ala Phe Ala His Ile Leu Thr
100 105 110
Val Leu Gln Cys Ala Thr Val Ile Gly Phe Ser Tyr Trp Ala Ser Glu
115 120 125
Leu Ile Leu Ala Gln Gln Gln Gln His Lys Lys Tyr His Gly Ser Gln
130 135 140
Val Tyr Val Thr Phe Ala Val Ser Phe Tyr Leu Val Ala Gly Ala Gly
145 150 155 160
Gly Ala Ser Ile Leu Ala Thr Ala Ala Asn Leu Leu Arg His Tyr Pro
165 170 175
Thr Glu Glu Glu Glu Gln Ala Leu Glu Leu Leu Ser Glu Met Glu Glu
180 185 190
Asn Glu Pro Tyr Pro Ala Glu Tyr Glu Val Ile Asn Gln Phe Gln Pro
195 200 205
Pro Pro Ala Tyr Thr Pro
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<210> 6039
<211> 1130
<212> DNA
<213> Homo sapiens

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<210> 6040
<211> 312
<212> PRT
<213> Homo sapiens

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Gly Leu Leu Ala Val Leu Arg Ala Gly Pro Gly Pro Glu Ala Leu Leu

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Gln Val Trp Ala Ala Glu Ser Ala Leu Arg Gly Glu Pro Leu Trp Ala
        35                  40                  45
Gln Asn Val Val Pro Glu Ala Glu Gly Glu Asp Asp Pro Ala Gly Glu
    50                  55                  60
Ala Gln Ala Gly Arg Leu Pro Leu Leu Pro Cys Ala Arg Ala Tyr Val
65                  70                  75                  80
Ser Pro Arg Ala Pro Phe Tyr Arg Pro Leu Ala Pro Glu Leu Arg Ala
                85                  90                  95
Arg Gln Leu Glu Leu Gly Ala Glu His Ala Leu Leu Leu Asp Ala Ala
            100                 105                 110
Gly Gln Val Phe Ser Trp Gly Gly Gly Arg His Gly Gln Leu Gly His
        115                 120                 125
Gly Thr Leu Glu Ala Glu Leu Glu Pro Arg Leu Leu Glu Ala Leu Gln
    130                 135                 140
Gly Leu Val Met Ala Glu Val Ala Ala Gly Gly Trp His Ser Val Cys
145                 150                 155                 160
Val Ser Glu Thr Gly Asp Ile Tyr Ile Trp Gly Trp Asn Glu Ser Gly
                165                 170                 175
Gln Leu Ala Leu Pro Thr Arg Asn Leu Ala Glu Asp Gly Glu Thr Val
            180                 185                 190
Ala Arg Glu Ala Thr Glu Leu Asn Glu Asp Gly Ser Gln Val Lys Arg
        195                 200                 205
Thr Gly Gly Ala Glu Asp Gly Ala Pro Ala Pro Phe Ile Ala Val Gln
    210                 215                 220
Pro Phe Pro Ala Leu Leu Asp Leu Pro Met Gly Ser Asp Ala Val Lys
225                 230                 235                 240
Ala Ser Cys Gly Ser Arg His Thr Ala Val Val Thr Arg Thr Gly Glu
                245                 250                 255
Leu Tyr Thr Trp Gly Trp Gly Lys Tyr Gly Gln Leu Gly His Glu Asp
            260                 265                 270
Thr Thr Ser Leu Asp Arg Pro Arg Arg Val Glu Tyr Phe Val Asp Lys
        275                 280                 285
Gln Leu Gln Val Lys Ala Val Thr Cys Gly Pro Trp Asn Thr Tyr Val
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Tyr Ala Val Glu Lys Gly Lys Ser
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<210> 6041
<211> 291
<212> DNA
<213> Homo sapiens

<400> 6041

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180
ttccagcagt atgcagccca acagtatcca gggaactacg aacagcagca aattctcatc
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291
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<210> 6042
<211> 97
<212> PRT
<213> Homo sapiens

<400> 6042
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Arg Arg Ile Glu Glu Glu Arg Leu Arg Leu Glu Gln Gln Lys Gln Gln
35 40 45
Ile Met Ala Ala Leu Asn Ser Gln Thr Ala Val Gln Phe Gln Gln Tyr
50 55 60
Ala Ala Gln Gln Tyr Pro Gly Asn Tyr Glu Gln Gln Gln Ile Leu Ile
65 70 75 80
Arg Gln Leu Gln Glu Gln His Tyr Gln Gln Tyr Met Gln Gln Leu Tyr
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<210> 6043
<211> 558
<212> DNA
<213> Homo sapiens

<400> 6043
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<210> 6044
<211> 152
<212> PRT
<213> Homo sapiens

<400> 6044
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Cys Tyr Leu Ser Asn Val Asp Gly Gly Glu His Pro Cys Pro Arg Leu
20 25 30
Lys Ile Ala Pro Leu Glu Ser His His Arg Pro Lys Arg Pro Asp Asp
35 40 45
Pro Pro Gly Thr Leu Asn Pro Cys Pro Glu Arg Gly Gly Ala Gly Val
50 55 60
Trp Ile Pro Ala Gly Ser Phe Gly Thr Gly Lys Asn Arg Gly Cys Ser
65 70 75 80
Asp Arg Val Phe Thr Lys Thr Cys Ile Arg Gln Asp Pro Gly Arg Met
85 90 95
Trp Val Ala Pro Pro Leu Cys Trp Ala Arg Arg Met Cys Pro His Arg
100 105 110
Ser Gln Ile Leu Phe Pro Gln Trp Val Val Gln Asp Thr Leu Asn Phe
115 120 125
Cys Met Asn Trp Asp Ile Gln Asn Ser Leu Glu Gln Pro Pro Pro Ser
130 135 140
Thr Leu Cys Leu Asp Ile Ser Tyr
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<210> 6045
<211> 1916
<212> DNA
<213> Homo sapiens

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1800
gcatttttct taggttgtat gctcttctgt tttaaaggtt tgaatcacca gcatttttgt
1860
gatcaaaatc ctatttagaa aaaataaaac tactttctgt ttaaaaaaaa aacaaa
1916

<210> 6046
<211> 457
<212> PRT
<213> Homo sapiens

<400> 6046
Thr Arg Val Glu Thr His Phe Gln Pro Arg Gly Ala Gly Glu Gly Gly
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Pro Tyr Gly Cys Lys Asp Ala Leu Arg Gln Gln Leu Arg Ser Ala Arg
20 25 30
Glu Val Ile Ala Val Val Met Asp Val Phe Thr Asp Ile Asp Ile Phe
35 40 45
Arg Asp Leu Gln Glu Ile Cys Arg Lys Gln Gly Val Ala Val Tyr Ile
50 55 60
Leu Leu Asp Gln Ala Leu Leu Ser Gln Phe Leu Asp Met Cys Met Asp

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65                  70                  75                  80
Leu Lys Val His Pro Glu Gln Glu Lys Leu Met Thr Val Arg Thr Ile
                85                  90                  95
Thr Gly Asn Ile Tyr Tyr Ala Arg Ser Gly Thr Lys Ile Ile Gly Lys
            100                 105                 110
Val His Glu Lys Phe Thr Leu Ile Asp Gly Ile Arg Val Ala Thr Gly
        115                 120                 125
Ser Tyr Ser Phe Thr Trp Thr Asp Gly Lys Leu Asn Ser Ser Asn Leu
    130                 135                 140
Val Ile Leu Ser Gly Gln Val Val Glu His Phe Asp Leu Glu Phe Arg
145                 150                 155                 160
Ile Leu Tyr Ala Gln Ser Lys Pro Ile Ser Pro Lys Leu Leu Ser His
                165                 170                 175
Phe Gln Ser Ser Asn Lys Phe Asp His Leu Thr Asn Arg Lys Pro Gln
            180                 185                 190
Ser Lys Glu Leu Thr Leu Gly Asn Leu Leu Arg Met Arg Leu Ala Arg
        195                 200                 205
Leu Ser Ser Thr Pro Arg Lys Ala Asp Leu Asp Pro Glu Met Pro Ala
    210                 215                 220
Glu Gly Lys Ala Glu Arg Lys Pro His Asp Cys Glu Ser Ser Thr Val
225                 230                 235                 240
Ser Glu Glu Asp Tyr Phe Ser Ser His Arg Asp Glu Leu Gln Ser Arg
                245                 250                 255
Lys Ala Ile Asp Ala Ala Thr Gln Thr Glu Pro Gly Glu Glu Met Pro
            260                 265                 270
Gly Leu Ser Val Ser Glu Val Gly Thr Gln Thr Ser Ile Thr Thr Ala
        275                 280                 285
Cys Ala Gly Thr Gln Thr Ala Val Ile Thr Arg Ile Ala Ser Ser Gln
    290                 295                 300
Thr Thr Ile Trp Ser Arg Ser Thr Thr Thr Gln Thr Asp Met Asp Glu
305                 310                 315                 320
Asn Ile Leu Phe Pro Arg Gly Thr Gln Ser Thr Glu Gly Ser Pro Val
                325                 330                 335
Ser Lys Met Ser Val Ser Arg Ser Ser Ser Leu Lys Ser Ser Ser Ser
            340                 345                 350
Val Ser Ser Gln Gly Ser Val Ala Ser Ser Thr Gly Ser Pro Ala Ser
        355                 360                 365
Ile Arg Thr Thr Asp Phe His Asn Pro Gly Tyr Pro Lys Tyr Leu Gly
    370                 375                 380
Thr Pro His Leu Glu Leu Tyr Leu Ser Asp Ser Leu Arg Asn Leu Asn
385                 390                 395                 400
Lys Glu Arg Gln Phe His Phe Ala Gly Ile Arg Ser Arg Leu Asn His
                405                 410                 415
Met Leu Ala Met Leu Ser Arg Arg Thr Leu Phe Thr Glu Asn His Leu
            420                 425                 430
Gly Leu His Ser Gly Asn Phe Ser Arg Val Asn Leu Leu Ala Val Arg
        435                 440                 445
Asp Val Ala Leu Tyr Pro Ser Tyr Gln
    450                 455
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<210> 6047
<211> 773
<212> DNA
<213> Homo sapiens

<400> 6047
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120
gatgggaaat gggggatctc atcgcttgtg agtagaggag actttggggg gaaagtgatg
180
gaggatgggg caagggatcc ggtgtccaac tctgtgtgtc cctgcagctc ccgtagccca
240
gcagggaaga tgaccttctg gcccctaagc aggcggaagg caggtggccg ccgccggagc
300
aatggtgcaa acagctcttc tccagtgtgg tccccgtgct gctgggggac ccagaggagg
360
agccgggtgg gcggcagctc ctggacctca attgcttttt gtccgacatc tcggacactc
420
tcttcaccat gactcagtcc ggcccttcgc ccctgcagct gccgcctgag gatgcctacg
480
tcggcaatgc tgacatgatc cagccggacc tgacgccact gcagccaagc ctggatgact
540
tcatggacat ctcagatttc tttaccaact cccgcctccc acagccgccc atgccttcaa
600
acttcccaga gccccccaac ttcagccccg tggttgactc cctcttcagc agtgggaccc
660
tgggcccaga ggtgcccccg gcttcctcgg ccatgaccca cctctctgga cacagccgtc
720
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773

<210> 6048
<211> 129
<212> PRT
<213> Homo sapiens

<400> 6048
Met Val Lys Arg Val Ser Glu Met Ser Asp Lys Lys Gln Leu Arg Ser
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Arg Ser Cys Arg Pro Pro Gly Ser Ser Ser Gly Ser Pro Ser Ser Thr
20 25 30
Gly Thr Thr Leu Glu Lys Ser Cys Leu His His Cys Ser Gly Gly Gly
35 40 45
His Leu Pro Ser Ala Cys Leu Gly Ala Arg Arg Ser Ser Ser Leu Leu
50 55 60
Gly Tyr Gly Ser Cys Arg Asp Thr Gln Ser Trp Thr Pro Asp Pro Leu
65 70 75 80
Pro His Pro Pro Ser Leu Ser Pro Gln Ser Leu Leu Tyr Ser Gln Ala
85 90 95
Met Arg Ser Pro Ile Ser His Gln Glu Leu Thr Arg Pro Leu Gly Lys
100 105 110
Glu Ala Ala Arg Arg Arg Cys Gly His Thr Val Ala Leu Ser Ala Arg
115 120 125
Asp

<210> 6049
<211> 479
<212> DNA
<213> Homo sapiens

<400> 6049
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actgatggta ataccagcac cactccgccc acctctgcca agaagagaaa gttaaacagc
120
agcagcagta gcagcagtaa cagtagtaac gagagagaag actttgattc cacctcttcc
180
tcctcttcca ctcctccttt acaacccagg gattcggcat ccccttcaac ctcgtccttc
240
tgcctggggg tttcagtggc tgcttccagc cacgtaccga tacagaagaa gctgcgtttt
300
gaagacaccc tggagtttgt agggtttgat gcgaagatgg ctgaggaatc ctcctcctcc
360
tcctcctcat cttcaccaac tgctgcaaca tctcaggagc agcaacttaa aaataagagt
420
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479

<210> 6050
<211> 159
<212> PRT
<213> Homo sapiens

<400> 6050
Thr Gly Phe Ser Ser Pro Ser Pro Ser Ala Ala Ala Ala Ala Gln Glu
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Val Arg Ser Ala Thr Asp Gly Asn Thr Ser Thr Thr Pro Pro Thr Ser
            20   25   30
Ala Lys Lys Arg Lys Leu Asn Ser Ser Ser Ser Ser Ser Ser Ser Asn Ser
        35   40   45
Ser Asn Glu Arg Glu Asp Phe Asp Ser Thr Ser Ser Ser Ser Ser Thr
    50   55   60
Pro Pro Leu Gln Pro Arg Asp Ser Ala Ser Pro Ser Thr Ser Ser Phe
65   70   75   80
Cys Leu Gly Val Ser Val Ala Ala Ser Ser His Val Pro Ile Gln Lys
                85   90   95
Lys Leu Arg Phe Glu Asp Thr Leu Glu Phe Val Gly Phe Asp Ala Lys
            100   105   110
Met Ala Glu Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Pro Thr Ala
        115   120   125
Ala Thr Ser Gln Glu Gln Gln Leu Lys Asn Lys Ser Ile Leu Ile Ser
    130   135   140
Ser Val Gly Ser Val His His Ala Asp Gly Leu Ala Glu Ser Ser
145   150   155

<210> 6051
<211> 2404
<212> DNA
<213> Homo sapiens

<400> 6051
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120
ttacagcagc gtcgatttaa tggctcagac ggaggggttt catggtctcc tatggatgat
180
gaacttcttg cacagccaca ggttatgaaa ttattagatt cactccgaga gcaatatacc
240
cgctaccagg aagtttgtag gcaacgtagc aagcgcacac agttagaaga gattcaacag
300
aaggtaatgc aggtggtgaa ctggctagaa gggcctggat cagaacaact aagagcccag
360
tggggcattg gagactccat tagggcctcc caggccctac agcagaaaca cgaagagatt
420
gagagccagc acagtgaatg gtttgcagtg tatgtggaac ttaatcagca aattgcagca
480
ctcttgaatg ctggcgatga ggaagatctt gtggaactaa agtcactgca gcaacaactt
540
agtgatgttt gttatcgaca ggccagtcag ctggaattta ggcaaaatct cttacaagca
600
gctcttgaat ttcatggtgt tgcccaagat ttgtctcagc agttggatgg cttattaggg
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atgttgtgcg tagatgtagc accagctgat ggagcatcga ttcagcaaac tttaaaactg
720
cttgaagaga agctgaaaag tgttgatgtg ggattgcaag gtttgcgtga aaaaggtcaa
780
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840
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900
aaacaaagat gtgaagacat ggtagatgtg cgaaggttaa agatgcttca gatggtgcag
960
ttgtttaaat gtgaagaaga tgctgccaag gcagtagaat ggctaagtga acttctggat
1020
gctctgctta agactcacat cagattgggc gatgatgctc aagaaacgaa agttttgctg
1080
gaaaagcata gaaaatttgt tgatgttgca cagagcactt atgactatgg caggcagttg
1140
ctacaggcca cagttgtgtt atgccagtct ttgcgctgca cttctcggtc atctggggat
1200
acacttcctc gactgaacag agtatggaaa caatttacaa tagcatctga agagagagta
1260
catagattgg aaatggctat tgcatttcac tcaaatgctg aaaagatttt gcaggactgt
1320
ccagaagagc ctgaagctat taatgatgag gagcaatttg atgaaattga agcagttggg
1380
aaatcacttt tggatagatt aactgttcca gtagtttatc ctgatggaac cgaacaatat
1440
tttgggagtc caagtgacat ggcttctact gcagaaaaca tcagagacag gatgaaacta
1500
gttaatctca aaaggcagca gctgagacat cctgaaatgg tgaccacaga gagctaatag
1560

ctaccagcta cctacagatt tgcagttcat aatcccgcat gttgtcaaca tactacagca
1620
ttagccacca caccttaaga tgcatttcac agccaaaata agtctcattt cttttcatga
1680
cacatttctc tttacatgtt aacaccttgc tactaccaag gcataattac ttaacatgct
1740
tcgaggctgt agattccaag tatcttaaaa gaaggaacta taaacattgc actgaaaact
1800
tgctttaaag ctttacctga cctgtcagtt tgtagacaaa caactgataa taagctttga
1860
atggtgctaa taagagtagg aattctctct attaaaaaga aaaaaaaaag ttgcccttcc
1920
tccacaggtg atttagtaaa tttagacagt agttaaactc ttgttagtag acagtggtgt
1980
cctcaaaatt ttactttgta attcttcaga attgattatt tttattgtgt caatacagag
2040
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2100
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2160
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2280
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caac
2404

<210> 6052
<211> 518
<212> PRT
<213> Homo sapiens

<400> 6052
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Thr Gly His Glu Leu Leu Ser Glu Leu Gln Gln Arg Arg Phe Asn Gly
35 40 45
Ser Asp Gly Gly Val Ser Trp Ser Pro Met Asp Asp Glu Leu Leu Ala
50 55 60
Gln Pro Gln Val Met Lys Leu Leu Asp Ser Leu Arg Glu Gln Tyr Thr
65 70 75 80
Arg Tyr Gln Glu Val Cys Arg Gln Arg Ser Lys Arg Thr Gln Leu Glu
85 90 95
Glu Ile Gln Gln Lys Val Met Gln Val Val Asn Trp Leu Glu Gly Pro
100 105 110
Gly Ser Glu Gln Leu Arg Ala Gln Trp Gly Ile Gly Asp Ser Ile Arg
115 120 125
Ala Ser Gln Ala Leu Gln Gln Lys His Glu Glu Ile Glu Ser Gln His

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    130                 135                 140
Ser Glu Trp Phe Ala Val Tyr Val Glu Leu Asn Gln Gln Ile Ala Ala
145                 150                 155                 160
Leu Leu Asn Ala Gly Asp Glu Glu Asp Leu Val Glu Leu Lys Ser Leu
                165                 170                 175
Gln Gln Gln Leu Ser Asp Val Cys Tyr Arg Gln Ala Ser Gln Leu Glu
            180                 185                 190
Phe Arg Gln Asn Leu Leu Gln Ala Ala Leu Glu Phe His Gly Val Ala
        195                 200                 205
Gln Asp Leu Ser Gln Gln Leu Asp Gly Leu Leu Gly Met Leu Cys Val
    210                 215                 220
Asp Val Ala Pro Ala Asp Gly Ala Ser Ile Gln Gln Thr Leu Lys Leu
225                 230                 235                 240
Leu Glu Glu Lys Leu Lys Ser Val Asp Val Gly Leu Gln Gly Leu Arg
                245                 250                 255
Glu Lys Gly Gln Gly Leu Leu Asp Gln Ile Ser Asn Gln Ala Ser Xaa
            260                 265                 270
Gly Pro Met Glu Arg Met Xaa Thr Ile Glu Asn Lys Glu Asn Val Asp
        275                 280                 285
His Ile Gln Gly Val Met Glu Asp Met Gln Leu Arg Lys Gln Arg Cys
    290                 295                 300
Glu Asp Met Val Asp Val Arg Arg Leu Lys Met Leu Gln Met Val Gln
305                 310                 315                 320
Leu Phe Lys Cys Glu Glu Asp Ala Ala Lys Ala Val Glu Trp Leu Ser
                325                 330                 335
Glu Leu Leu Asp Ala Leu Leu Lys Thr His Ile Arg Leu Gly Asp Asp
            340                 345                 350
Ala Gln Glu Thr Lys Val Leu Leu Glu Lys His Arg Lys Phe Val Asp
        355                 360                 365
Val Ala Gln Ser Thr Tyr Asp Tyr Gly Arg Gln Leu Leu Gln Ala Thr
    370                 375                 380
Val Val Leu Cys Gln Ser Leu Arg Cys Thr Ser Arg Ser Ser Gly Asp
385                 390                 395                 400
Thr Leu Pro Arg Leu Asn Arg Val Trp Lys Gln Phe Thr Ile Ala Ser
                405                 410                 415
Glu Glu Arg Val His Arg Leu Glu Met Ala Ile Ala Phe His Ser Asn
            420                 425                 430
Ala Glu Lys Ile Leu Gln Asp Cys Pro Glu Glu Pro Glu Ala Ile Asn
        435                 440                 445
Asp Glu Glu Gln Phe Asp Glu Ile Glu Ala Val Gly Lys Ser Leu Leu
    450                 455                 460
Asp Arg Leu Thr Val Pro Val Val Tyr Pro Asp Gly Thr Glu Gln Tyr
465                 470                 475                 480
Phe Gly Ser Pro Ser Asp Met Ala Ser Thr Ala Glu Asn Ile Arg Asp
                485                 490                 495
Arg Met Lys Leu Val Asn Leu Lys Arg Gln Gln Leu Arg His Pro Glu
            500                 505                 510
Met Val Thr Thr Glu Ser
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<210> 6053
<211> 3257
<212> DNA
<213> Homo sapiens

<400> 6053
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120
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180
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240
cagcggcagg aatagcaggc aacgtgattt caaagctggg ctcagcctct gtttcttctc
300
tcgtgtaatc gcaaaaccca ttttggagca ggaattccaa tcatgtctgt gatggtggtg
360
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540
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600
agcttcagtg accctggagt gattcctcgg gcgctaccag atgaagcagc tttcatagaa
660
atggagatag aagctaccaa tggtgcggtg ccccagggcc agagaccacc gcctcgtatc
720
aagaatttcc agataaacaa ccagattgtg aaactgaaat actgttacac atgcaagatc
780
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1020
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1080
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1140
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1260
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1320
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1380
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1440
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1500
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1560

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1620
aggcagtggc agaagatgtc agtcacctct gataactgga aaaatgggtc tcttgggccc
1680
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1860
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2280
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2400
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2460
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2520
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3257

<210> 6054
<211> 382
<212> PRT
<213> Homo sapiens

<400> 6054
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20 25 30
Glu Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met
35 40 45
Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile Leu
50 55 60
Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu Ala Val
65 70 75 80
Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu Phe Leu Phe
85 90 95
Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp Pro Gly Val Ile
100 105 110
Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile Glu Met Glu Ile Glu
115 120 125
Ala Thr Asn Gly Ala Val Pro Gln Gly Gln Arg Pro Pro Pro Arg Ile
130 135 140
Lys Asn Phe Gln Ile Asn Asn Gln Ile Val Lys Leu Lys Tyr Cys Tyr
145 150 155 160
Thr Cys Lys Ile Phe Arg Pro Pro Arg Ala Ser His Cys Ser Ile Cys
165 170 175
Asp Asn Cys Val Glu Arg Phe Asp His His Cys Pro Trp Val Gly Asn
180 185 190
Cys Val Gly Lys Arg Asn Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser
195 200 205
Leu Ser Leu Leu Thr Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val
210 215 220
Ala Leu Lys Ser Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr
225 230 235 240
Pro Gly Thr Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser
245 250 255
Val Val Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln
260 265 270
Thr Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val
275 280 285
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu Val
290 295 300
Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly Ile Leu
305 310 315 320
Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln Glu Thr Ser
325 330 335
Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu His Leu Asn Ser

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            340                 345                 350
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        355                 360                 365
Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala Glu Ala Glu Lys
    370                 375                 380
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<210> 6055
<211> 2089
<212> DNA
<213> Homo sapiens

<400> 6055
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120
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180
tataacttgt cagcaaacta ctttcaggag aaatttttcc caggtcatga gtctcgggct
240
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300
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360
cctatttgga gcatggctgc cagccccagt ggctctcaac ttttggttgg ttgtgaagat
420
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<211> 285
<212> PRT
<213> Homo sapiens

<400> 6056
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50 55 60
Ala Asn Tyr Phe Gln Glu Lys Phe Phe Pro Gly His Glu Ser Arg Ala
65 70 75 80
Thr Glu Ala Leu Cys Trp Ala Glu Gly Gln Arg Leu Phe Ser Ala Gly
85 90 95
Leu Asn Gly Glu Ile Met Glu Tyr Asp Leu Gln Ala Leu Asn Ile Lys
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Tyr Ala Met Asp Ala Phe Gly Gly Pro Ile Trp Ser Met Ala Ala Ser
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225                 230                 235                 240
Ser Ala Thr Gly Thr Leu Val Lys Ser His Leu Ile Ala Asn Ala Asp
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<212> DNA
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<211> 500
<212> PRT
<213> Homo sapiens

<400> 6058
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35 40 45
Val Asn Arg Arg Arg His Asn Ser Ser Asp Gly Phe Asp Ser Ala Ile
50 55 60
Gly Arg Pro Asn Gly Gly Asn Phe Gly Arg Lys Glu Lys Asn Gly Trp
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Arg Thr His Gly Arg Asn Gly Thr Glu Asn Ile Asn His Arg Gly Gly
85 90 95
Tyr His Gly Gly Ser Ser Arg Ser Arg Ser Ser Ile Phe His Ala Gly
100 105 110
Lys Ser Gln Gly Leu His Glu Asn Asn Ile Pro Asp Asn Glu Thr Gly
115 120 125
Arg Lys Glu Asp Lys Arg Glu Arg Lys Gln Phe Glu Ala Glu Asp Phe
130 135 140
Pro Ser Leu Asn Pro Glu Tyr Glu Arg Glu Pro Asn His Asn Lys Ser
145 150 155 160
Leu Ala Ala Gly Val Trp Gly Leu His Ala Gln Thr His Thr Tyr Pro
165 170 175
Thr Lys Lys Ile Ser Gln Ala Pro Leu Leu Glu Tyr Pro Pro Asn Pro
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Lys Ser Arg Ala Pro Arg Met Leu Val Ile Lys Lys Gly Asn Thr Lys
195 200 205
Asp Leu Gln Leu Ser Gly Phe Pro Val Val Gly Asn Leu Pro Ser Gln
210 215 220
Pro Val Lys Asn Gly Thr Gly Pro Ser Val Tyr Lys Gly Leu Val Pro
225 230 235 240
Lys Pro Ala Ala Pro Pro Thr Lys Pro Thr Gln Trp Lys Ser Gln Thr
245 250 255
Lys Glu Asn Lys Val Gly Thr Ser Phe Pro His Glu Ser Thr Phe Gly
260 265 270
Val Gly Asn Phe Asn Ala Phe Lys Ser Thr Ala Lys Asn Phe Ser Pro
275 280 285
Ser Thr Asn Ser Val Lys Glu Cys Asn Arg Ser Asn Ser Ser Ser Pro
290 295 300
Val Asp Lys Leu Asn Gln Gln Pro Arg Leu Thr Lys Leu Thr Arg Met
305 310 315 320
Arg Thr Asp Lys Lys Ser Glu Phe Leu Lys Ala Leu Lys Arg Asp Arg
325 330 335
Val Glu Glu Glu His Glu Asp Glu Ser Arg Ala Gly Ser Glu Lys Asp
340 345 350
Asp Asp Ser Phe Asn Leu His Asn Ser Asn Ser Thr His Gln Glu Arg
355 360 365
Asp Ile Asn Arg Asn Phe Asp Glu Asn Glu Ile Pro Gln Glu Asn Gly
370 375 380
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385 390 395 400
Gln Thr Asp Val Leu Ser Ser Ser Leu Glu Ala Glu His Arg Leu Leu
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Lys Glu Met Gly Trp Gln Glu Asp Ser Glu Asn Asp Glu Thr Cys Ala

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Leu Gln Lys Asn Gly Leu Arg Lys Asn Gly Ile Leu Lys Asn Gly Leu
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Ile Cys Asp Phe Lys Phe Gly Pro Trp Lys Asn Ser Thr Phe Lys Pro
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<211> 1442
<212> DNA
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<210> 6060
<211> 313
<212> PRT
<213> Homo sapiens

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Ile Ser Tyr Thr Ile Thr Ile Phe Gly Asn Val Ser Ile Met Met Val
35 40 45
Cys Ile Leu Asp Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
50 55 60
Asn Leu Ser Ile Leu Asp Leu Cys Tyr Thr Thr Thr Thr Val Pro His
65 70 75 80
Met Leu Val Asn Ile Gly Cys Asn Lys Lys Thr Ile Ser Tyr Ala Gly
85 90 95
Cys Val Ala His Leu Ile Ile Phe Leu Ala Leu Gly Ala Thr Glu Cys
100 105 110
Leu Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Arg
115 120 125
Pro Leu His Tyr Val Val Ile Met Asn Tyr Trp Phe Cys Leu Arg Met
130 135 140
Ala Ala Phe Ser Trp Leu Ile Gly Phe Gly Asn Ser Val Leu Gln Ser
145 150 155 160
Ser Leu Thr Leu Asn Met Pro Arg Cys Gly His Gln Glu Val Asp His
165 170 175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
180 185 190
Lys Pro Ile Glu Ala Glu Leu Phe Phe Phe Ser Val Leu Ile Leu Leu
195 200 205
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Gly Phe Ile Ala Gln Ala
210 215 220
Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
225 230 235 240
Cys Gly Ser His Met Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
245 250 255
Tyr Met Tyr Leu Gln Pro Pro Ser Ser Thr Ser Lys Asp Trp Gly Lys

260 265 270
Met Val Ser Leu Phe Tyr Gly Ile Ile Thr Ser Met Leu Asn Ser Leu
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<210> 6061
<211> 1582
<212> DNA
<213> Homo sapiens

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<210> 6062
<211> 226
<212> PRT
<213> Homo sapiens

<400> 6062
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Asp Asp Val Val Ile Thr Asn Pro His Ile Glu Ala Ile Leu Glu Asn
65 70 75 80
Glu Asp Trp Ile Glu Asp Ala Ser Gly Leu Met Ser His Cys Ile Ala
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Ile Leu Lys Ile Cys His Thr Leu Thr Glu Lys Leu Val Ala Met Thr
100 105 110
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115 120 125
Ile Val Val Ala Lys Arg Ile Ser Pro Arg Val Asp Asp Val Val Lys
130 135 140
Ser Met Tyr Pro Pro Leu Asp Pro Lys Leu Leu Asp Ala Arg Thr Thr
145 150 155 160
Ala Leu Leu Leu Ser Val Ser His Leu Val Leu Val Thr Arg Asn Ala
165 170 175
Cys His Leu Thr Gly Gly Leu Asp Trp Ile Asp Gln Ser Leu Ser Ala
180 185 190
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<210> 6063
<211> 2286

<212> DNA
<213> Homo sapiens

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<210> 6064
<211> 233
<212> PRT
<213> Homo sapiens

<400> 6064
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Phe Leu His Pro Asp Leu Gly Val Gly Gly Ala Glu Arg Leu Val Leu
        35   40   45
Asp Ala Ala Leu Ala Leu Gln Ala Arg Gly Cys Ser Val Lys Ile Trp
    50   55   60
Thr Ala His Tyr Asp Pro Gly His Cys Phe Ala Glu Ser Arg Glu Leu
65   70   75   80
Pro Val Arg Cys Ala Gly Asp Trp Leu Pro Arg Gly Leu Gly Trp Gly
                85   90   95
Gly Arg Gly Ala Ala Val Cys Ala Tyr Val Arg Met Val Phe Leu Ala
            100   105   110
Leu Tyr Val Leu Phe Leu Ala Asp Glu Glu Phe Asp Val Val Val Cys
        115   120   125
Asp Gln Val Ser Ala Cys Ile Pro Val Phe Arg Leu Ala Arg Arg Arg
    130   135   140
Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp Leu Leu Leu Thr Lys

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Arg Asp Ser Phe Leu Lys Arg Leu Tyr Arg Ala Pro Ile Asp Trp Ile
                165                 170                 175
Glu Glu Tyr Thr Thr Gly Met Ala Asp Cys Ile Leu Val Asn Ser Gln
            180                 185                 190
Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile
        195                 200                 205
Asp Pro Asp Val Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser
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Val Val Pro Glu Xaa Ser Trp Met Thr
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<210> 6065
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<212> DNA
<213> Homo sapiens

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1980
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2084

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<211> 80
<212> PRT
<213> Homo sapiens

<400> 6066
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20 25 30
Ala Ile Asp Lys Pro Thr Tyr Ala Thr Lys Trp Pro Ile Arg His Gly
35 40 45
Ile Ile Glu Asp Trp Asp Leu Met Glu Arg Phe Met Glu Gln Val Val
50 55 60
Phe Lys Tyr Leu Arg Ala Glu Pro Glu Asp His Tyr Phe Leu Met Gly
65 70 75 80

<210> 6067
<211> 406

<212> DNA
<213> Homo sapiens

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406

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<212> PRT
<213> Homo sapiens

<400> 6068
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Ser Cys Cys Asp Tyr Tyr Ser Pro Phe Ser Thr Leu Ile Ile Pro Arg
            20   25   30
Ser Leu Phe Leu Ser Gly Asn Val Ser Ser Arg Arg Met Arg Thr Ala
        35   40   45
Ser Arg Ser Ser Glu Pro Pro Ala Cys Pro Arg His Trp Pro Cys Pro
    50   55   60
Pro Gly Leu Pro Phe Gly Gln Gly Ala Val Ala Arg Ala Ala Pro Cys
65   70   75   80
Pro Ala Tyr Ser His Ser Ala Val Gly Arg Pro Pro Leu Pro Arg Lys
                85   90   95
Arg Gly Ala Val Ser Ser Gly Arg Leu His Arg Arg Gly Thr Gly Ala
            100   105   110
Met Trp Trp Glu Gly
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<210> 6069
<211> 456
<212> DNA
<213> Homo sapiens

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180

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456

<210> 6070
<211> 148
<212> PRT
<213> Homo sapiens

<400> 6070
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Asn Val Lys Gln Ile Ile Pro Met Val Thr Glu Leu Ile Gly Arg Ser
20 25 30
His Arg Tyr His Arg Lys Glu Asn Leu Glu Tyr Cys Ile Met Val Ile
35 40 45
Gly Val Pro Asn Val Gly Lys Ser Ser Leu Ile Asn Ser Leu Arg Arg
50 55 60
Gln His Leu Arg Lys Gly Lys Ala Thr Arg Val Gly Gly Glu Pro Gly
65 70 75 80
Ile Thr Arg Ala Val Met Ser Lys Ile Gln Val Glu Ser Ser Gly Ala
85 90 95
Arg Pro Ser Thr Leu Ser Arg Ala Leu Gln Ala Ser Gly Thr Cys Arg
100 105 110
Pro Leu Cys Gly Phe Arg Leu Leu Thr Thr Leu Pro Ser Pro Pro Leu
115 120 125
Ser Val Pro Ala Glu His Pro Arg Gly Arg His Cys Pro Ala Leu Ile
130 135 140
Pro Gln Ser Ser
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<210> 6071
<211> 2633
<212> DNA
<213> Homo sapiens

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<211> 76
<212> PRT
<213> Homo sapiens

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            20   25   30
Pro Thr Trp Arg Asn Pro Ile Ser Thr Lys Asn Thr Lys Ile Asn Lys
        35   40   45
Ala Trp Trp Arg Val Pro Val Val Pro Ala Thr Arg Glu Ala Glu Ala
    50   55   60
Gly Glu Ser Leu Glu Pro Gly Arg Arg Arg Phe Gln
65   70   75

<210> 6073
<211> 387
<212> DNA
<213> Homo sapiens

<400> 6073
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<210> 6074
<211> 69
<212> PRT
<213> Homo sapiens

<400> 6074
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20 25 30
Ala Pro Thr Gly Pro Phe Ser Pro Arg Met Lys Pro Ala Gly Ser Val
35 40 45
Asn Asp Met Ala Leu Asp Ala Phe Asp Leu Asp Arg Met Lys Gln Glu
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Ile Leu Glu Glu Val
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<210> 6075
<211> 4668
<212> DNA
<213> Homo sapiens

<400> 6075
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3900

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4668

<210> 6076
<211> 601
<212> PRT
<213> Homo sapiens

<400> 6076
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Glu Val Gly Leu Ala Leu Lys Asp Leu Ala Lys Gln Tyr Ser Asp Arg
35 40 45
Leu Glu Cys Cys Glu Asn Glu Val Glu Lys Val Ile Glu Glu Ile Arg
50 55 60
Cys Lys Ala Ile Glu Arg Gly Thr Gly Asn Asp Asn Tyr Arg Thr Thr
65 70 75 80
Gly Ile Ala Thr Ile Glu Val Phe Leu Pro Pro Arg Leu Lys Lys Asp
85 90 95
Arg Lys Asn Leu Leu Glu Thr Arg Leu His Ile Thr Gly Arg Glu Leu
100 105 110
Arg Ser Lys Ile Ala Glu Thr Phe Gly Leu Gln Glu Asn Tyr Ile Lys
115 120 125
Ile Val Ile Asn Lys Lys Gln Leu Gln Leu Gly Lys Thr Leu Glu Glu
130 135 140
Gln Gly Val Ala His Asn Val Lys Ala Met Val Leu Glu Leu Lys Gln
145 150 155 160
Ser Glu Glu Asp Ala Arg Lys Asn Phe Gln Leu Glu Glu Glu Glu Gln

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                165                 170                 175
Asn Glu Ala Lys Leu Lys Glu Lys Gln Ile Gln Arg Thr Lys Arg Gly
            180                 185                 190
Leu Glu Ile Leu Ala Lys Arg Ala Ala Glu Thr Val Val Asp Pro Glu
        195                 200                 205
Met Thr Pro Tyr Leu Asp Ile Ala Asn Gln Thr Gly Arg Ser Ile Arg
    210                 215                 220
Ile Pro Pro Ser Glu Arg Lys Ala Leu Met Leu Ala Met Gly Tyr His
225                 230                 235                 240
Glu Lys Gly Arg Ala Phe Leu Lys Arg Lys Glu Tyr Gly Ile Ala Leu
                245                 250                 255
Pro Cys Leu Leu Asp Ala Asp Lys Tyr Phe Cys Glu Cys Cys Arg Glu
            260                 265                 270
Leu Leu Asp Thr Val Asp Asn Tyr Ala Val Leu Gln Leu Asp Ile Val
        275                 280                 285
Trp Cys Tyr Phe Arg Leu Glu Gln Leu Glu Cys Leu Asp Asp Ala Glu
    290                 295                 300
Lys Lys Leu Asn Leu Ala Gln Lys Cys Phe Lys Asn Cys Tyr Gly Glu
305                 310                 315                 320
Asn His Gln Arg Leu Val His Ile Lys Gly Asn Cys Gly Lys Glu Lys
                325                 330                 335
Val Leu Phe Leu Arg Leu Tyr Leu Leu Gln Gly Ile Arg Asn Tyr His
            340                 345                 350
Ser Gly Asn Asp Val Glu Ala Tyr Glu Tyr Leu Asn Arg His Val Ser
        355                 360                 365
Ser Leu Lys Ser Tyr Ile Leu Ile His Gln Lys Trp Thr Ile Cys Cys
    370                 375                 380
Ser Trp Gly Leu Leu Pro Arg Lys Xaa Arg Leu Gly Leu Arg Ala Cys
385                 390                 395                 400
Asp Gly Asn Val Asp His Ala Ala Thr His Ile Thr Asn Arg Arg Glu
                405                 410                 415
Glu Leu Ala Gln Ile Arg Lys Glu Glu Lys Glu Lys Lys Arg Arg Arg
            420                 425                 430
Leu Glu Asn Ile Arg Phe Leu Lys Gly Met Gly Tyr Ser Thr His Ala
        435                 440                 445
Ala Gln Gln Ile Leu Leu Ser Asn Pro Gln Met Trp Trp Leu Asn Asp
    450                 455                 460
Ser Asn Pro Glu Thr Asp Asn Arg Gln Glu Ser Pro Ser Gln Glu Asn
465                 470                 475                 480
Ile Asp Arg Leu Val Tyr Met Gly Phe Asp Ala Leu Val Ala Glu Ala
                485                 490                 495
Ala Leu Arg Val Phe Arg Gly Asn Val Gln Leu Ala Ala Gln Thr Leu
            500                 505                 510
Ala His Asn Gly Gly Ser Leu Pro Pro Glu Leu Pro Leu Ser Pro Glu
        515                 520                 525
Asp Ser Leu Ser Pro Pro Ala Thr Ser Pro Ser Asp Ser Ala Gly Thr
    530                 535                 540
Ser Ser Ala Ser Thr Asp Glu Asp Met Glu Thr Glu Ala Val Asn Glu
545                 550                 555                 560
Ile Leu Glu Asp Ile Pro Glu His Glu Glu Asp Tyr Leu Asp Ser Thr
                565                 570                 575
Leu Glu Asp Glu Glu Ile Ile Ile Ala Glu Tyr Leu Ser Tyr Val Glu
            580                 585                 590
Asn Arg Lys Ser Ala Thr Lys Lys Asn
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595 600

<210> 6077
<211> 2093
<212> DNA
<213> Homo sapiens

<400> 6077
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120
ccgggggttg ggccgcacat ttacgtgcgc gaagcggagg accgggagct ggtgacgatg
180
gcggggccgc agcccctggc gctgcaactg gaacagttgt tgaacccgcg accaagcgag
240
gcggaccctg aagcggaccc cgaggaagcc actgctgcca gggtgattga caggtttgat
300
gaaggggaag atggggaagg tgatttccta gtagtgggta gcattagaaa actggcatca
360
gcctccctct tggacacgga caaaaggtat tgcggcaaaa ccacctctag aaaagcatgg
420
aatgaagacc attgggagca gactctgcca ggatcgtctg atgaggaaat atctgatgag
480
gaagggtctg gagatgaaga ttcagaggga ctgggtctgg aggaatatga tgaggacgac
540
ctgggtgctg ctgaggaaca ggagtgtggt gatcagggag agcaagaaga cgagaagcca
600
ctctgcaaaa acaccgggct tcagtgtcca gagtatcagt gactttgaga aatttaccaa
660
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720
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780
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840
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1020
aaagcattgt tgaggtcatt ggtaggtctt caggaagagt tgcttttcca gtacccagac
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actagatatc tagtagatgg gacaaagccc aatgcgggaa gtgaggagat ttctagtgaa
1140
gatgatgagc tggtagaaga gaagaagcag caacgaagaa gggtccctgc aaagaggaag
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ctggagatgg aggactatcc cagcttcatg gcaaagcgct ttgccgactt tacagtctac
1260
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1320
aagggttttg gtgcctttga acgctcaatc ttgactcaga tcgaccatat tctgatggac
1380

aaagagagat tacttcgaag gacacagacc aagcgctctg tctatcgagt tcttggcaaa
1440
cctgagccag cagctcagcc tgtcccagag agtttgccag gggaaccgga gatccttcct
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caagcccctg ctaatgctca tctgaaggac ttggatgaag aaatctttga tgatgatgac
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ttttaccacc agctccttcg agaactcata gaacggaaga ccagctcctt ggatcccaac
1620
gatcaggtgg ccatgggaag gcagtggctt gcaatccaga agttacgaag caaaatccac
1680
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1920
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1980
gaacctgtgc ctaatacacg caagggcgct gtcccgccca accccgcctt taaacgccac
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2093

<210> 6078
<211> 213
<212> PRT
<213> Homo sapiens

<400> 6078
Arg Pro Gly Arg Ser Pro Gly Ser Gly Arg Ser Arg Ala Val Gly Cys
 1   5   10   15
Leu Arg Ala Val Ser Gly Gly Ser Gly Asn Arg Ile Lys Ala Arg Gly
            20   25   30
Ser Gly Arg Glu Gly Ala Ser Gly Pro Gly Val Gly Pro His Ile Tyr
        35   40   45
Val Arg Glu Ala Glu Asp Arg Glu Leu Val Thr Met Ala Gly Pro Gln
    50   55   60
Pro Leu Ala Leu Gln Leu Glu Gln Leu Leu Asn Pro Arg Pro Ser Glu
65   70   75   80
Ala Asp Pro Glu Ala Asp Pro Glu Glu Ala Thr Ala Ala Arg Val Ile
                85   90   95
Asp Arg Phe Asp Glu Gly Glu Asp Gly Glu Gly Asp Phe Leu Val Val
            100   105   110
Gly Ser Ile Arg Lys Leu Ala Ser Ala Ser Leu Leu Asp Thr Asp Lys
        115   120   125
Arg Tyr Cys Gly Lys Thr Thr Ser Arg Lys Ala Trp Asn Glu Asp His
    130   135   140
Trp Glu Gln Thr Leu Pro Gly Ser Ser Asp Glu Glu Ile Ser Asp Glu
145   150   155   160
Glu Gly Ser Gly Asp Glu Asp Ser Glu Gly Leu Gly Leu Glu Glu Tyr
                165   170   175
Asp Glu Asp Asp Leu Gly Ala Ala Glu Glu Gln Glu Cys Gly Asp Gln

```
            180                 185                 190
Gly Glu Gln Glu Asp Glu Lys Pro Leu Cys Lys Asn Thr Gly Leu Gln
        195                 200                 205
Cys Pro Glu Tyr Gln
    210
```

<210> 6079
<211> 651
<212> DNA
<213> Homo sapiens

<400> 6079
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120
catgcgcagc ggggccgtgg gtgtacgcgg cgcagcgcgg cagtcctgat ggcccggcat
180
gggttaccgc tgctgcccct gctgtcgctc ctggtcggcg cgtggctcaa gctaggaaat
240
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300
ccagacagca gagatggtga agggcctgtg cgggaggcga cagtgaaacc ctttgccatc
360
gacatatttc ctgtcaccaa caaagatttc agggattttg tcagggagaa aaagtatcgg
420
acagaagctg agatgtttgg atggagcttt gtctttgagg actttgtctc tgatgagctg
480
agaaacaaag ccacccagcc aatgaagtct gtactctggt ggcttccagt ggaaaaggca
540
ttttggaggc agcctgcagg tcctggctct ggcatccgag agagactgga gcacccagtg
600
ttacacgtga gctggaatga cgcccgtgcc tactgtgctt ggcggggaaa a
651

<210> 6080
<211> 162
<212> PRT
<213> Homo sapiens

<400> 6080
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Leu Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu
 1               5                  10                  15
Val Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val
            20                  25                  30
Gln Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser
        35                  40                  45
Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala
    50                  55                  60
Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg
65                  70                  75                  80
Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val
                85                  90                  95
Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro
```

```
            100                 105                 110
Met Lys Ser Val Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg
        115                 120                 125
Gln Pro Ala Gly Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro
    130                 135                 140
Val Leu His Val Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg
145                 150                 155                 160
Gly Lys
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<210> 6081
<211> 655
<212> DNA
<213> Homo sapiens

<400> 6081
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120
ggaccagctg ttataacatt gttactagat gaatgtccat tgcccactaa agatgcactc
180
cagaaattga ctgaaattct caatttaaat ggagaagtag cttgccagga ctcaagccat
240
cctgccaaac acaggaacac atctgcagtc ctaggctgct tggccgagaa actagcaggt
300
cctgcaagta taggtttact tagcccagga atactggaat acttgctaca gtgtctgaag
360
ttacagtccc accccacagt catgcttttt gcacttatcg cactggaaaa gtttgcacag
420
acaagtgaaa ataaattgac tatttctgaa tccagtatta gtgaccggct tgtcacattg
480
gagtcctggg ctaatgatcc tgattatctg aaacgtcaag ttggtttctg tgcccagtgg
540
agcttagaca atctcttttt aaaagaaggt agacagctga cctatgagaa agtgaacttg
600
agtagcatta gggccatgct gaatagcaat gatgtcagcg agtacctgaa gatct
655

<210> 6082
<211> 218
<212> PRT
<213> Homo sapiens

<400> 6082
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Asp Asn Asp Gln Glu Pro Pro Tyr Ser Met Ile Thr Leu His Glu Met
 1               5                  10                  15
Ala Glu Thr Asp Glu Gly Trp Leu Asp Val Val Gln Ser Leu Ile Arg
            20                  25                  30
Val Ile Pro Leu Glu Asp Pro Leu Gly Pro Ala Val Ile Thr Leu Leu
        35                  40                  45
Leu Asp Glu Cys Pro Leu Pro Thr Lys Asp Ala Leu Gln Lys Leu Thr
    50                  55                  60
Glu Ile Leu Asn Leu Asn Gly Glu Val Ala Cys Gln Asp Ser Ser His
```

```
65                  70                  75                  80
Pro Ala Lys His Arg Asn Thr Ser Ala Val Leu Gly Cys Leu Ala Glu
                85                  90                  95
Lys Leu Ala Gly Pro Ala Ser Ile Gly Leu Leu Ser Pro Gly Ile Leu
            100                 105                 110
Glu Tyr Leu Leu Gln Cys Leu Lys Leu Gln Ser His Pro Thr Val Met
        115                 120                 125
Leu Phe Ala Leu Ile Ala Leu Glu Lys Phe Ala Gln Thr Ser Glu Asn
    130                 135                 140
Lys Leu Thr Ile Ser Glu Ser Ser Ile Ser Asp Arg Leu Val Thr Leu
145                 150                 155                 160
Glu Ser Trp Ala Asn Asp Pro Asp Tyr Leu Lys Arg Gln Val Gly Phe
                165                 170                 175
Cys Ala Gln Trp Ser Leu Asp Asn Leu Phe Leu Lys Glu Gly Arg Gln
            180                 185                 190
Leu Thr Tyr Glu Lys Val Asn Leu Ser Ser Ile Arg Ala Met Leu Asn
        195                 200                 205
Ser Asn Asp Val Ser Glu Tyr Leu Lys Ile
    210                 215
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<210> 6083
<211> 358
<212> DNA
<213> Homo sapiens

<400> 6083
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gaaaaagaac aggagctcca ggcaaaaata gaagctttgc aagctgataa tgatttcacc
120
aatgaaaggc taacagcttt acaagagaag ctgatcgtcg aagggcatct aaccaaagcg
180
gtagaagaaa caaagctttc aaaagaaaat cagacaagag caaaagaatc tgatttttca
240
gatactctga gtccaagcaa ggaaaaaagc agtgacgaca ctacagacgc ccaaatggat
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gagcaagacc taaatgagcc tcttgccaaa gtgtcccttt taaaagatga cttgcagg
358

<210> 6084
<211> 101
<212> PRT
<213> Homo sapiens

<400> 6084
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 1               5                  10                  15
Ala Asp Asn Asp Phe Thr Asn Glu Arg Leu Thr Ala Leu Gln Glu Lys
            20                  25                  30
Leu Ile Val Glu Gly His Leu Thr Lys Ala Val Glu Glu Thr Lys Leu
        35                  40                  45
Ser Lys Glu Asn Gln Thr Arg Ala Lys Glu Ser Asp Phe Ser Asp Thr
    50                  55                  60
Leu Ser Pro Ser Lys Glu Lys Ser Ser Asp Asp Thr Thr Asp Ala Gln
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65 70 75 80
Met Asp Glu Gln Asp Leu Asn Glu Pro Leu Ala Lys Val Ser Leu Leu
85 90 95
Lys Asp Asp Leu Gln
100

<210> 6085
<211> 2307
<212> DNA
<213> Homo sapiens

<400> 6085
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agccaggtgg actttgacaa tcccgactac gagaggttcc ctaatttcca aaatgtggtt
120
ggttacgaaa cagtggttgg ccctggtgat gttctttaca tcccaatgta ctggtggcat
180
cacatagagt cattactaaa tgggggggatt accatcactg tgaacttctg gtataagggg
240
gctcccaccc ctaagagaat tgaatatcct ctcaaagctc atcagaaagt ggccataatg
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360
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420
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480
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660
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720
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840
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1020
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1080
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1140
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1200
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1260

ctgtgtgtgc gtatcacact aggggtgcaa gcctctgggt gtgtgtgtgt gtgtgcgtgc
1320
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1380
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1680
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1920
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1980
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2100
gatgcgtgtg gatgtgtgtg catgcctgag tgcgtttttt ggggaggggt gtttatttтt
2160
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2280
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2307

<210> 6086
<211> 84
<212> PRT
<213> Homo sapiens

<400> 6086
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Ile Thr Leu Gly Val Gln Ala Ser Gly Cys Val Cys Val Cys Ala Cys
        35   40   45
Val Cys Val Cys Val Ser Val Cys Val Cys Val Cys Val His Thr Gly
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Asp Ser Thr Val

<210> 6087
<211> 1506
<212> DNA
<213> Homo sapiens

<400> 6087
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<210> 6088
<211> 326
<212> PRT
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Ala Glu Thr His Phe Gly Phe Glu Thr Val Ser Glu Glu Glu Lys Gly
50 55 60
Gly Lys Val Tyr Gln Val Phe Glu Ser Val Ala Lys Lys Tyr Asp Val
65 70 75 80
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85 90 95
Leu Leu Trp Lys Met His Pro Leu Pro Gly Thr Gln Leu Leu Asp Met
100 105 110
Ala Gly Gly Thr Gly Asp Ile Ala Phe Arg Phe Leu Asn Tyr Val Gln
115 120 125
Ser Gln His Gln Arg Lys Gln Lys Arg Gln Leu Arg Ala Gln Gln Asn
130 135 140
Leu Ser Trp Glu Glu Ile Ala Lys Glu Tyr Gln Asn Glu Glu Asp Ser
145 150 155 160
Leu Gly Gly Ser Arg Val Val Val Cys Asp Ile Asn Lys Glu Met Leu
165 170 175
Lys Val Gly Lys Gln Lys Ala Leu Ala Gln Gly Tyr Arg Ala Gly Leu
180 185 190
Ala Trp Val Leu Gly Asp Ala Glu Glu Leu Pro Phe Asp Asp Asp Lys
195 200 205
Phe Asp Ile Tyr Thr Ile Ala Phe Gly Ile Arg Asn Val Thr His Ile
210 215 220
Asp Gln Ala Leu Gln Glu Ala His Arg Val Leu Lys Pro Gly Gly Arg
225 230 235 240
Phe Leu Cys Leu Glu Phe Ser Gln Val Asn Asn Pro Leu Ile Ser Arg
245 250 255
Leu Tyr Asp Leu Tyr Ser Phe Gln Val Ile Pro Val Leu Gly Glu Val
260 265 270
Ile Ala Gly Asp Trp Lys Ser Tyr Gln Tyr Leu Val Glu Ser Ile Arg
275 280 285
Arg Phe Pro Ser Gln Glu Glu Phe Lys Asp Met Ile Glu Asp Ala Gly
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325

<210> 6089
<211> 4211
<212> DNA
<213> Homo sapiens

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<210> 6090
<211> 839
<212> PRT
<213> Homo sapiens

<400> 6090
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Glu Asp Cys Thr Trp Met Gln Glu Tyr Asn Pro Pro Thr Phe Glu Thr

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Pro Glu Leu His Thr Lys Glu Gln Ile Leu Glu Leu Leu Val Leu Glu
                85                  90                  95
Gln Phe Leu Thr Ile Leu Pro Glu Glu Phe Gln Pro Trp Val Arg Glu
            100                 105                 110
His His Pro Glu Ser Gly Glu Glu Ala Val Ala Val Ile Glu Asn Ile
        115                 120                 125
Gln Arg Glu Leu Glu Glu Arg Arg Gln Gln Ile Val Ala Cys Pro Asp
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Val Leu Pro Arg Lys Met Ala Thr Pro Gly Ala Val Gln Glu Ser Cys
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Ser Pro His Pro Leu Thr Val Asp Thr Gln Pro Glu Gln Ala Pro Gln
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Lys Pro Arg Leu Leu Glu Glu Asn Ala Leu Pro Val Leu Gln Val Pro
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Ser Leu Pro Leu Lys Asp Ser Gln Glu Leu Thr Ala Ser Leu Leu Ser
        195                 200                 205
Thr Gly Ser Gln Lys Leu Val Lys Ile Glu Glu Val Ala Asp Val Ala
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Val Ser Phe Ile Leu Glu Glu Trp Gly His Leu Asp Gln Ser Gln Lys
225                 230                 235                 240
Ser Leu Tyr Arg Asp Asp Arg Lys Glu Asn Tyr Gly Ser Ile Thr Ser
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Met Gly Tyr Glu Ser Arg Asp Asn Met Glu Leu Ile Val Lys Gln Ile
            260                 265                 270
Ser Asp Asp Ser Glu Ser His Trp Val Ala Pro Glu His Thr Glu Arg
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Ser Val Pro Gln Asp Pro Asp Phe Ala Glu Val Ser Asp Leu Lys Gly
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Lys Gln Ser Thr His Gly Glu Arg Gly His Arg Cys Ser Asp Cys Gly
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Lys Phe Phe Leu Gln Ala Ser Asn Phe Ile Gln His Arg Arg Ile His
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Thr Gly Glu Lys Pro Phe Lys Cys Gly Glu Cys Gly Lys Ser Tyr Asn
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Gln Arg Val His Leu Thr Gln His Gln Arg Val His Thr Gly Glu Lys
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Pro Tyr Lys Cys Gln Val Cys Gly Lys Ala Phe Arg Val Ser Ser His
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Leu Val Gln His His Ser Val His Ser Gly Glu Arg Pro Tyr Gly Cys
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Asn Glu Cys Gly Lys Asn Phe Gly Arg His Ser His Leu Ile Glu His
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Ser Lys Asn Thr Lys Leu Ser Val Lys Lys Lys Ile Ser Glu Tyr Ser
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Lys Gln Gly Ile Pro Met Lys Glu Ile Leu Gly Gln Pro Ser Ser Lys
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Arg Met Asn Tyr Ser Glu Val Pro Tyr Val His Lys Lys Ser Ser Thr
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Gly Glu Arg Pro His Lys Cys Asn Glu Cys Gly Lys Ser Phe Ile Gln
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Ser Ala His Leu Ile Gln His Gln Arg Ile His Thr Gly Glu Lys Pro
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Phe Arg Cys Glu Glu Cys Gly Lys Ser Tyr Asn Gln Arg Val His Leu
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Thr Gln His Gln Arg Val His Thr Gly Glu Lys Pro Tyr Thr Cys Pro
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Leu Cys Gly Lys Ala Phe Arg Val Arg Ser His Leu Val Gln His Gln
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Ser Val His Ser Gly Glu Arg Pro Phe Lys Cys Asn Glu Cys Gly Lys
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Gly Phe Gly Arg Arg Ser His Leu Ala Gly His Leu Arg Leu His Ser
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Arg Glu Lys Ser His Gln Cys Arg Glu Cys Gly Glu Ile Phe Phe Gln
            660                 665                 670
Tyr Val Ser Leu Ile Glu His Gln Val Leu His Met Gly Gln Lys Asn
        675                 680                 685
Glu Lys Asn Gly Ile Cys Glu Glu Ala Tyr Ser Trp Asn Leu Thr Val
    690                 695                 700
Ile Glu Asp Lys Lys Ile Glu Leu Gln Glu Gln Pro Tyr Gln Cys Asp
705                 710                 715                 720
Ile Cys Gly Lys Ala Phe Gly Tyr Ser Ser Asp Leu Ile Gln His Tyr
                725                 730                 735
Arg Thr His Thr Ala Glu Lys Pro Tyr Gln Cys Asp Ile Cys Arg Glu
            740                 745                 750
Asn Val Gly Gln Cys Ser His Thr Lys Gln His Gln Lys Ile Tyr Ser
        755                 760                 765
Ser Thr Lys Ser His Gln Cys His Glu Cys Gly Arg Gly Phe Thr Leu
    770                 775                 780
Lys Ser His Leu Asn Gln His Gln Arg Ile His Thr Gly Glu Lys Pro
785                 790                 795                 800
Phe Gln Cys Lys Glu Cys Gly Met Asn Phe Ser Trp Ser Cys Ser Leu
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Phe Lys His Leu Arg Ser His Glu Arg Thr Asp Pro Ile Asn Thr Leu
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<212> DNA
<213> Homo sapiens

<400> 6091

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<210> 6092
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<400> 6092
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Val Thr Arg Gln Val Pro Ser Pro Pro Ser Gly Phe Arg Leu Pro Ser
    50                  55                  60
Ser Arg His Glu Gly Pro Ser Pro Pro Arg Asp Leu Gly Thr Ser Gly
65                  70                  75                  80
Pro Ser Arg Ala Ala Ser His Lys Pro Ser Asn Glu Gln Arg Asp Ala
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1740
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1860
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1920
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1980
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1998

<210> 6094
<211> 136
<212> PRT
<213> Homo sapiens

<400> 6094
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20 25 30
Thr Gly Pro Val Ser Gln Ser Phe Leu Gln Met Leu Ile Gly Val Cys
35 40 45
Trp Asn Pro Lys Pro Leu Pro Arg Leu Gln Ala Pro Asp Gly Leu Leu
50 55 60
Ser Cys Asn Phe Leu Gly Glu Glu Thr Phe Ser Ser Phe Pro Phe Leu
65 70 75 80
Val His Pro Cys Thr Leu Val Leu Ser Gln Pro Leu Pro His Ile Val

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                85                  90                  95
Pro Asp Ser Arg Gly Thr Ser Ser Leu His Arg Ala Ala Ala Ala Gly
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Leu Arg Ala Glu Pro Val Gly Ala Glu Ala Leu Ala Pro Glu Val Gln
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Pro Leu Ser Leu Gly Pro Leu Gly
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<210> 6095
<211> 441
<212> DNA
<213> Homo sapiens

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120
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180
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240
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300
tgggtggtcc aaagaatcgg caaatgagag tggttagaag gcttcttagc gcagttgttc
360
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420
aattcttcaa atagggaccg t
441

<210> 6096
<211> 97
<212> PRT
<213> Homo sapiens

<400> 6096

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Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
            20                  25                  30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys
    50                  55                  60
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
65                  70                  75                  80
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
                85                  90                  95
Lys
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<210> 6097
<211> 2404

<212> DNA
<213> Homo sapiens

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120
ctgctgaaga accagtggtt tgtccgctgc caggaaatgg gggcccgagc tgccaaggct
180
gtggagtcgg gggccctgga gctcagtccc tccttccacc agaagaactg gcaacactgg
240
ttttcccata ttggggactg gtgtgtctcc cggcagctgt ggtggggcca tcagattcca
300
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360
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420
gagccgaccc tggagaggga tcctgatgtc ctagacacat ggttttcttc tgccctgttc
480
ccctttctg ccctgggctg gccccaagag accccagacc ttgctcgttt ctacccccctg
540
tcacttttgg aaacgggcag cgaccttctg ctgttctggg tgggccgcat ggtcatgttg
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660
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720
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1500

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1980
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2100
aagtctggga atgaggagat tgagataaac ttttgaaatc ccaaacatgt ctgtttatgg
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2280
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<210> 6098
<211> 631
<212> PRT
<213> Homo sapiens

<400> 6098
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Arg Ser Gly Asp Val Ile Glu Tyr Leu Leu Lys Asn Gln Trp Phe Val
35 40 45
Arg Cys Gln Glu Met Gly Ala Arg Ala Ala Lys Ala Val Glu Ser Gly
50 55 60
Ala Leu Glu Leu Ser Pro Ser Phe His Gln Lys Asn Trp Gln His Trp
65 70 75 80
Phe Ser His Ile Gly Asp Trp Cys Val Ser Arg Gln Leu Trp Trp Gly
85 90 95
His Gln Ile Pro Ala Tyr Leu Val Xaa Xaa Gly Pro Cys Ala Xaa Gly
100 105 110
Glu Glu Xaa Thr Cys Trp Val Val Gly Arg Ser Gly Ala Glu Ala Arg

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        115                 120                 125
Glu Leu Ala Ala Glu Leu Thr Gly Arg Gln Gly Ala Glu Pro Thr Leu
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Glu Arg Asp Pro Asp Val Leu Asp Thr Trp Phe Ser Ser Ala Leu Phe
145                 150                 155                 160
Pro Phe Ser Ala Leu Gly Trp Pro Gln Glu Thr Pro Asp Leu Ala Arg
                165                 170                 175
Phe Tyr Pro Leu Ser Leu Leu Glu Thr Gly Ser Asp Leu Leu Leu Phe
            180                 185                 190
Trp Val Gly Arg Met Val Met Leu Gly Thr Gln Leu Thr Gly Gln Leu
        195                 200                 205
Pro Phe Ser Lys Val Leu Leu His Pro Met Val Arg Asp Arg Gln Gly
    210                 215                 220
Arg Lys Met Ser Lys Ser Leu Gly Asn Val Leu Asp Pro Arg Asp Ile
225                 230                 235                 240
Ile Ser Gly Val Glu Met Gln Leu Leu Gln Glu Lys Leu Arg Ser Gly
                245                 250                 255
Asn Leu Asp Pro Ala Glu Leu Ala Ile Val Ala Ala Ala Gln Lys Lys
            260                 265                 270
Asp Phe Pro His Gly Ile Pro Glu Cys Gly Thr Asp Ala Leu Arg Phe
        275                 280                 285
Thr Leu Cys Ser His Gly Val Gln Ala Gly Asp Leu His Leu Ser Val
    290                 295                 300
Ser Glu Val Gln Ser Cys Arg His Phe Cys Asn Lys Ile Trp Asn Ala
305                 310                 315                 320
Leu Arg Phe Ile Leu Asn Ala Leu Gly Glu Lys Phe Val Pro Gln Pro
                325                 330                 335
Ala Glu Glu Leu Ser Pro Ser Ser Pro Met Asp Ala Trp Ile Leu Ser
            340                 345                 350
Arg Leu Ala Leu Ala Ala Gln Glu Cys Glu Arg Gly Phe Leu Thr Arg
        355                 360                 365
Glu Leu Ser Leu Val Thr His Ala Leu His His Phe Trp Leu His Asn
    370                 375                 380
Leu Cys Asp Val Tyr Leu Glu Ala Val Lys Pro Val Leu Trp His Ser
385                 390                 395                 400
Pro Arg Pro Leu Gly Pro Pro Gln Val Leu Phe Ser Cys Ala Asp Leu
                405                 410                 415
Gly Leu Arg Leu Leu Ala Pro Leu Met Pro Phe Leu Ala Glu Glu Leu
            420                 425                 430
Trp Gln Arg Leu Pro Pro Arg Pro Gly Cys Pro Pro Ala Pro Ser Ile
        435                 440                 445
Ser Val Ala Pro Tyr Pro Ser Ala Cys Ser Leu Glu His Trp Arg Gln
    450                 455                 460
Pro Glu Leu Glu Arg Arg Phe Ser Arg Val Gln Glu Val Val Gln Val
465                 470                 475                 480
Leu Arg Ala Leu Arg Ala Thr Tyr Gln Leu Thr Lys Ala Arg Pro Arg
                485                 490                 495
Val Leu Leu Gln Ser Ser Glu Pro Gly Asp Gln Gly Leu Phe Glu Ala
            500                 505                 510
Phe Leu Glu Pro Leu Gly Thr Leu Gly Tyr Cys Gly Ala Val Gly Leu
        515                 520                 525
Leu Pro Pro Gly Thr Ala Ala Pro Ser Gly Trp Ala Gln Ala Pro Leu
    530                 535                 540
Ser Asp Thr Ala Gln Val Tyr Met Glu Leu Gln Gly Leu Val Asp Pro
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545 550 555 560
Gln Ile Gln Leu Pro Leu Leu Ala Ala Arg Arg Tyr Lys Leu Gln Lys
565 570 575
Gln Leu Asp Ser Leu Thr Ala Arg Thr Pro Ser Glu Gly Glu Ala Gly
580 585 590
Thr Gln Arg Gln Gln Lys Leu Ser Ser Leu Gln Leu Glu Leu Ser Lys
595 600 605
Leu Asp Lys Ala Ala Ser His Leu Arg Gln Leu Met Asp Glu Pro Pro
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Ala Pro Gly Ser Pro Glu Leu
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<210> 6099
<211> 3957
<212> DNA
<213> Homo sapiens

<400> 6099
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180
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240
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360
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3957

<210> 6100
<211> 1102
<212> PRT
<213> Homo sapiens

<400> 6100
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            20   25   30
Pro Ala Ala Gly Gln Pro Arg Pro Pro Ala Pro Ala Ser Arg Gly Pro

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        35                  40                  45
Met Pro Ala Arg Ile Gly Tyr Tyr Glu Ile Asp Arg Thr Ile Gly Lys
    50                  55                  60
Gly Asn Phe Ala Val Val Lys Arg Ala Thr His Leu Val Thr Lys Ala
65                  70                  75                  80
Lys Val Ala Ile Lys Ile Ile Asp Lys Thr Gln Leu Asp Glu Glu Asn
                85                  90                  95
Leu Lys Lys Ile Phe Arg Glu Val Gln Ile Met Lys Met Leu Cys His
            100                 105                 110
Pro His Ile Ile Arg Leu Tyr Gln Val Met Glu Thr Glu Arg Met Ile
        115                 120                 125
Tyr Leu Val Thr Glu Tyr Ala Ser Gly Gly Glu Ile Phe Asp His Leu
    130                 135                 140
Val Ala His Gly Arg Met Ala Glu Lys Glu Ala Arg Arg Lys Phe Lys
145                 150                 155                 160
Gln Ile Val Thr Ala Val Tyr Phe Cys His Cys Arg Asn Ile Val His
                165                 170                 175
Arg Asp Leu Lys Ala Glu Asn Leu Leu Leu Asp Ala Asn Leu Asn Ile
            180                 185                 190
Lys Ile Ala Asp Phe Gly Phe Ser Asn Leu Phe Thr Pro Gly Gln Leu
        195                 200                 205
Leu Lys Thr Trp Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe
    210                 215                 220
Glu Gly Lys Glu Tyr Asp Gly Pro Lys Val Asp Ile Trp Ser Leu Gly
225                 230                 235                 240
Val Val Leu Tyr Val Leu Val Cys Gly Ala Leu Pro Phe Asp Gly Ser
                245                 250                 255
Thr Leu Gln Asn Leu Arg Ala Arg Val Leu Ser Gly Lys Phe Arg Ile
            260                 265                 270
Pro Phe Phe Met Ser Thr Glu Cys Glu His Leu Ile Arg His Met Leu
        275                 280                 285
Val Leu Asp Pro Asn Lys Arg Leu Ser Met Glu Gln Ile Cys Lys His
    290                 295                 300
Lys Trp Met Lys Leu Gly Asp Ala Asp Pro Asn Phe Asp Arg Leu Ile
305                 310                 315                 320
Ala Glu Cys Gln Gln Leu Lys Glu Glu Arg Gln Val Asp Pro Leu Asn
                325                 330                 335
Glu Asp Val Leu Leu Ala Met Glu Asp Met Gly Leu Asp Lys Glu Gln
            340                 345                 350
Thr Leu Gln Ala Glu Gln Ala Gly Thr Ala Met Asn Ile Ser Val Pro
        355                 360                 365
Gln Val Gln Leu Ile Asn Pro Glu Asn Gln Ile Val Glu Pro Asp Gly
    370                 375                 380
Thr Leu Asn Leu Asp Ser Asp Glu Gly Glu Glu Pro Ser Pro Glu Ala
385                 390                 395                 400
Leu Val Arg Tyr Leu Ser Met Arg Arg His Thr Val Gly Val Ala Asp
                405                 410                 415
Pro Arg Thr Glu Val Met Glu Asp Leu Gln Lys Leu Leu Pro Gly Phe
            420                 425                 430
Pro Gly Val Asn Pro Gln Ala Pro Phe Leu Gln Val Ala Pro Asn Val
        435                 440                 445
Asn Phe Met His Asn Leu Leu Pro Met Gln Asn Leu Gln Pro Thr Gly
    450                 455                 460
Gln Leu Glu Tyr Lys Glu Gln Ser Leu Leu Gln Pro Pro Thr Leu Gln
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465                 470                 475                 480
Leu Leu Asn Gly Met Gly Pro Leu Gly Arg Arg Ala Ser Asp Gly Gly
                485                 490                 495
Ala Asn Ile Gln Leu His Ala Gln Gln Leu Leu Lys Arg Pro Arg Gly
            500                 505                 510
Pro Ser Pro Leu Val Thr Met Thr Pro Ala Val Pro Ala Val Thr Pro
        515                 520                 525
Val Asp Glu Glu Ser Ser Asp Gly Glu Pro Asp Gln Glu Ala Val Gln
    530                 535                 540
Ser Ser Thr Tyr Lys Asp Ser Asn Thr Leu His Leu Pro Thr Glu Arg
545                 550                 555                 560
Phe Ser Pro Val Arg Arg Phe Ser Asp Gly Ala Ala Ser Ile Gln Ala
                565                 570                 575
Phe Lys Ala His Leu Glu Lys Met Gly Asn Asn Ser Ser Ile Lys Gln
            580                 585                 590
Leu Gln Gln Glu Cys Glu Gln Leu Gln Lys Met Tyr Gly Gly Gln Ile
        595                 600                 605
Asp Glu Arg Thr Leu Glu Lys Thr Gln Gln Gln His Met Leu Tyr Gln
    610                 615                 620
Gln Glu Gln His His Gln Ile Leu Gln Gln Gln Ile Gln Asp Ser Ile
630                 635                 640
Cys Pro Pro Gln Pro Ser Pro Pro Leu Gln Ala Ala Cys Glu Asn Gln
                645                 650                 655
Pro Ala Leu Leu Thr His Gln Leu Gln Arg Leu Arg Ile Gln Pro Ser
            660                 665                 670
Ser Pro Pro Pro Asn His Pro Asn Asn His Leu Phe Arg Gln Pro Ser
        675                 680                 685
Asn Ser Pro Pro Pro Met Ser Ser Ala Met Ile Gln Pro His Gly Ala
    690                 695                 700
Ala Ser Ser Ser Gln Phe Gln Gly Leu Pro Ser Arg Ser Ala Ile Phe
705                 710                 715                 720
Gln Gln Gln Pro Glu Asn Cys Ser Ser Pro Pro Asn Val Ala Leu Thr
                725                 730                 735
Cys Leu Gly Met Gln Gln Pro Ala Gln Ser Gln Gln Val Thr Ile Gln
            740                 745                 750
Val Gln Glu Pro Val Asp Met Leu Ser Asn Met Pro Gly Thr Ala Ala
        755                 760                 765
Gly Ser Ser Gly Arg Gly Ile Ser Ile Ser Pro Ser Ala Gly Gln Met
    770                 775                 780
Gln Met Gln His Arg Thr Asn Leu Met Ala Thr Leu Ser Tyr Gly His
785                 790                 795                 800
Arg Pro Leu Ser Lys Gln Leu Ser Ala Asp Ser Ala Glu Ala His Ser
                805                 810                 815
Leu Asn Val Asn Arg Phe Ser Pro Ala Asn Tyr Asp Gln Ala His Leu
            820                 825                 830
His Pro His Leu Phe Ser Asp Gln Ser Arg Gly Ser Pro Ser Ser Tyr
        835                 840                 845
Ser Pro Ser Thr Gly Val Gly Phe Ser Pro Thr Gln Ala Leu Lys Val
    850                 855                 860
Pro Pro Leu Asp Gln Phe Pro Thr Phe Pro Pro Ser Ala His Gln Gln
865                 870                 875                 880
Pro Pro His Tyr Thr Thr Ser Ala Leu Gln Gln Ala Leu Leu Ser Pro
                885                 890                 895
Thr Pro Pro Asp Tyr Thr Arg His Gln Gln Val Pro His Ile Leu Gln
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            900                 905                 910
Gly Leu Leu Ser Pro Arg His Ser Leu Thr Gly Ser Asp Ile Arg
        915                 920                 925
Leu Pro Pro Thr Glu Phe Ala Gln Leu Ile Lys Arg Gln Gln Gln Gln
    930                 935                 940
Arg Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Tyr Gln Glu Leu
945                 950                 955                 960
Phe Arg His Met Asn Gln Gly Asp Ala Gly Ser Leu Ala Pro Ser Leu
                965                 970                 975
Gly Gly Gln Ser Met Thr Glu Arg Gln Ala Leu Ser Tyr Gln Asn Ala
            980                 985                 990
Asp Ser Tyr His His Thr Ile Gln Asn Ser Asp Asp Ala Tyr Val Gln
        995                 1000                1005
Leu Asp Asn Leu Pro Gly Met Ser Leu Val Ala Gly Lys Ala Leu Ser
    1010                1015                1020
Ser Ala Arg Met Ser Asp Ala Val Leu Ser Gln Ser Ser Leu Met Gly
1025                1030                1035                1040
Ser Gln Gln Phe Gln Asp Gly Glu Asn Glu Glu Cys Gly Ala Ser Leu
                1045                1050                1055
Gly Gly His Glu His Pro Asp Leu Ser Asp Gly Ser Gln His Leu Asn
            1060                1065                1070
Ser Ser Cys Tyr Pro Ser Thr Cys Ile Thr Asp Ile Leu Leu Ser Tyr
        1075                1080                1085
Lys His Pro Glu Val Ser Phe Ser Met Glu Gln Ala Gly Val
    1090                1095                1100
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<210> 6101
<211> 1447
<212> DNA
<213> Homo sapiens

<400> 6101

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180
gtttactaca gggatcccca aatattgtta gttgaatgaa caaacacaca tttcaaggag
240
ggcactacag tgagtagatg aacagttttc tgataggaga ttgtacaagt aatgttttca
300
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420
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480
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660
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840
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1200
ccaacgctga cgcccgcggt ctgaggtcgc catgggaaga gcggtaggcc accctgctcc
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1320
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1447

<210> 6102
<211> 123
<212> PRT
<213> Homo sapiens

<400> 6102
Met Ala Leu Asn Asn Val Ser Leu Ser Ser Gly Asp Gln Arg Ser Arg
 1   5   10   15
Val Ala Tyr Arg Ser Ser His Gly Asp Leu Arg Pro Arg Ala Ser Ala
            20   25   30
Leu Ala Met Val Ser Gly Asp Gly Phe Leu Val Ser Arg Pro Glu Ala
        35   40   45
Ile His Leu Gly Pro Arg Gln Ala Val Arg Pro Ser Val Arg Ala Glu
    50   55   60
Ser Arg Arg Val Asp Gly Gly Gly Arg Ser Pro Arg Glu Pro Asp Gly
65   70   75   80
Arg Gly Arg Ser Arg Gln Ala Arg Phe Ser Pro Tyr Pro Ile Pro Ala
                85   90   95
Val Glu Pro Asp Leu Leu Arg Ser Val Leu Gln Gln Arg Leu Ile Ala
            100   105   110
Leu Gly Gly Val Ile Ala Ala Arg Ile Ser Val
        115   120

<210> 6103
<211> 309

<212> DNA
<213> Homo sapiens

<400> 6103
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120
agaacctatg ccttgatgaa gaagattggg cagtccccag tgagagtcct gaaggagatt
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gacggcttcg tcctgaaccg cctgcagtac gccgtcatca gtgaggcctg gagactggtg
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gaggaagaaa tagtatctcc tagcgaccta gacctggtca tgtcagacgg gctgggcatg
300
cggtacgcg
309

<210> 6104
<211> 71
<212> PRT
<213> Homo sapiens

<400> 6104
Glu Thr Ala Pro Ala Thr Met Asp Arg Thr Tyr Ala Leu Met Lys Lys
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Ile Gly Gln Ser Pro Val Arg Val Leu Lys Glu Ile Asp Gly Phe Val
            20   25   30
Leu Asn Arg Leu Gln Tyr Ala Val Ile Ser Glu Ala Trp Arg Leu Val
        35   40   45
Glu Glu Glu Ile Val Ser Pro Ser Asp Leu Asp Leu Val Met Ser Asp
    50   55   60
Gly Leu Gly Met Arg Tyr Ala
65   70

<210> 6105
<211> 1846
<212> DNA
<213> Homo sapiens

<400> 6105
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caggggccag aaccggggat gccccccaac cctatgaact caacacagcc atcaactgca
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gggatgaagt ggtgtctccc cttccatctg ctctgcaggg gtccctcagg ctccctatca
180
gcccctccag ctgcctcagt tatctctgca cccccatctt cctcctcccg acatcgcaaa
240
cgtcgcagga cttccagcaa gtcggaggca ggggctaggg gtggaggcca gggttccaag
300
gaaaagggcc gagggagttg gggaggccgc caccaccacc accacccact gcctgcagca
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ggcttcaaaa agcaacagcg caagttccag tatgggaatt attgcaaata ctatgggtac
420

cgcaatcctt cctgtgagga tgggcgcctt cgggtgttga agcctgagtg gtttcggggc
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cgggacgtcc tagatctggg ctgcaatgtg ggccatctga ccctgagcat tgcctgcaag
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660
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720
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780
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1800
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1846

<210> 6106
<211> 405
<212> PRT
<213> Homo sapiens

<400> 6106
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20 25 30
Asn Ser Thr Gln Pro Ser Thr Ala Gly Met Lys Trp Cys Leu Pro Phe
35 40 45
His Leu Leu Cys Arg Gly Pro Ser Gly Ser Leu Ser Ala Pro Pro Ala
50 55 60
Ala Ser Val Ile Ser Ala Pro Pro Ser Ser Ser Ser Arg His Arg Lys
65 70 75 80
Arg Arg Arg Thr Ser Ser Lys Ser Glu Ala Gly Ala Arg Gly Gly Gly
85 90 95
Gln Gly Ser Lys Glu Lys Gly Arg Gly Ser Trp Gly Gly Arg His His
100 105 110
His His His Pro Leu Pro Ala Ala Gly Phe Lys Lys Gln Gln Arg Lys
115 120 125
Phe Gln Tyr Gly Asn Tyr Cys Lys Tyr Tyr Gly Tyr Arg Asn Pro Ser
130 135 140
Cys Glu Asp Gly Arg Leu Arg Val Leu Lys Pro Glu Trp Phe Arg Gly
145 150 155 160
Arg Asp Val Leu Asp Leu Gly Cys Asn Val Gly His Leu Thr Leu Ser
165 170 175
Ile Ala Cys Lys Trp Gly Pro Ser Arg Met Val Gly Leu Asp Ile Asp
180 185 190
Ser Arg Leu Ile His Ser Ala Arg Gln Asn Ile Arg His Tyr Leu Ser
195 200 205
Glu Glu Leu Arg Leu Pro Pro Gln Thr Leu Glu Gly Asp Pro Gly Ala
210 215 220
Glu Gly Glu Glu Gly Thr Thr Thr Val Arg Lys Arg Ser Cys Phe Pro
225 230 235 240
Ala Ser Leu Thr Ala Ser Arg Gly Pro Ile Ala Ala Pro Gln Val Pro
245 250 255
Leu Asp Gly Ala Asp Thr Ser Val Phe Pro Asn Asn Val Val Phe Val
260 265 270
Thr Gly Asn Tyr Val Leu Asp Arg Asp Asp Leu Val Glu Ala Gln Thr
275 280 285
Pro Glu Tyr Asp Val Val Leu Cys Leu Ser Leu Thr Lys Trp Val His
290 295 300
Leu Asn Trp Gly Asp Glu Gly Leu Lys Arg Met Phe Arg Arg Ile Tyr
305 310 315 320
Arg His Leu Arg Pro Gly Gly Ile Leu Val Leu Glu Pro Gln Pro Trp
325 330 335
Ser Ser Tyr Gly Lys Arg Lys Thr Leu Thr Glu Thr Ile Tyr Lys Asn
340 345 350
Tyr Tyr Arg Ile Gln Leu Lys Pro Glu Gln Phe Ser Ser Tyr Leu Thr
355 360 365
Ser Pro Asp Val Gly Phe Ser Ser Tyr Glu Leu Val Ala Thr Pro His
370 375 380
Asn Thr Ser Lys Gly Phe Gln Arg Pro Val Tyr Leu Phe His Lys Ala
385 390 395 400
Arg Ser Pro Ser His
405

<210> 6107
<211> 896
<212> DNA
<213> Homo sapiens

<400> 6107
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180
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240
tgggggagtt cagttggctc ggggttgcct tggcctgcca ccaggtggtc cacatgcccc
300
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420
cctgccacca ccatcacctc attacccaca ccctcaatga gggtgacatc agtgaccccc
480
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540
ggcagccctt cggttcgggt gggcccagac cccagtccaa cgccgaggga ataggaccat
600
ccaaaagcgg aaccttcgcc tcagaaaaag ggtgcgggac ccctcctcac cgtgcggtca
660
cggtacggac agggtagatc acaggctgag ggacagagca aagacccctg aggccggaca
720
cctggggtcc tgccgggccc ctccccacga gagttccctg tgtctgtgcc aatcgttttc
780
gtctttcttt gccgcagttt cttttcctgt aaatcatggt taatgacatt aaccttctta
840
ccatcagggg ttagttgtgg ttgtgataaa taattactac cgttattaag caattg
896

<210> 6108
<211> 124
<212> PRT
<213> Homo sapiens

<400> 6108
Xaa Asn Leu Thr Arg Thr Val Met Arg Pro Gly Leu Gly Gly Arg Gln
 1   5   10   15
Gly Leu Ser Ser Asp Leu Arg Gly Ala Ser Gly Leu Leu Leu Pro Ala
            20   25   30
Pro Ala Cys Leu Leu Gly Arg Pro Trp Met Ser Arg Arg Cys Ser Arg
        35   40   45
Leu Gly Ser Thr Pro Pro Pro Ala Pro Ala Ser Pro Val Glu Ser Pro
    50   55   60
Arg Pro Ser Pro Ala Ser Ser Ala Phe Ser Ser Leu Pro Ser Asp Gly
65   70   75   80
Trp Gly Ser Ser Val Gly Ser Gly Leu Pro Trp Pro Ala Thr Arg Trp

```
                85                  90                  95
Ser Thr Cys Pro Arg Trp Arg Thr Asp Val Ser Pro Ala Asp Thr Ile
            100                 105                 110
Ala Pro Arg Ser Trp Leu Leu Pro Leu Ser Ala Thr
        115                 120
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<210> 6109
<211> 2087
<212> DNA
<213> Homo sapiens

<400> 6109
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ggtagcttca gagcctccag tgcctgtggg gctggaggtg aagttggggg ccctggtgct
180
gctgctggtc tcaccctcct ctgcagcctg gtgcccatct gtgtgctgcg ccggccagga
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gctaaccatg aaggctcagc ttcccgccag aaagccctga gcctagtaag ctgtttcgcg
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480
tcagggccgt cacctctgga ggaaacaagg gctctgctgg gaacagtgaa tggtgggccg
540
cagcattggc atgatgggcc aggggtccca caggcgagtg gagccccagc aacccccctca
600
gccttgcgtg cctgtgtact ggtgttctcc ctggccctcc actccgtgtt cgaggggctg
660
gcggtagggc tgcagcgaga ccgggctcgg gccatggagc tgtgcctggc tttgctgctc
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780
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960
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1020
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1080
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atggtcaagt cgctagagac atatcagggg acattaggat tggggaagac acttgactgc
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2087

<210> 6110
<211> 323
<212> PRT
<213> Homo sapiens

<400> 6110
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Pro Gly Ala Ala Ala Gly Leu Thr Leu Leu Cys Ser Leu Val Pro Ile
35 40 45
Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser Arg
50 55 60
Gln Lys Ala Leu Ser Leu Val Ser Cys Phe Ala Gly Gly Val Phe Leu
65 70 75 80
Ala Thr Cys Leu Leu Asp Leu Leu Pro Asp Tyr Leu Ala Ala Ile Asp
85 90 95
Glu Ala Leu Ala Ala Leu His Val Thr Leu Gln Phe Pro Leu Gln Glu
100 105 110
Phe Ile Leu Ala Met Gly Phe Phe Leu Val Leu Val Met Glu Gln Ile
115 120 125
Thr Leu Ala Tyr Lys Glu Gln Ser Gly Pro Ser Pro Leu Glu Glu Thr
130 135 140
Arg Ala Leu Leu Gly Thr Val Asn Gly Gly Pro Gln His Trp His Asp

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145                 150                 155                 160
Gly Pro Gly Val Pro Gln Ala Ser Gly Ala Pro Ala Thr Pro Ser Ala
                165                 170                 175
Leu Arg Ala Cys Val Leu Val Phe Ser Leu Ala Leu His Ser Val Phe
            180                 185                 190
Glu Gly Leu Ala Val Gly Leu Gln Arg Asp Arg Ala Arg Ala Met Glu
        195                 200                 205
Leu Cys Leu Ala Leu Leu Leu His Lys Gly Ile Leu Ala Val Ser Leu
    210                 215                 220
Ser Leu Arg Leu Leu Gln Ser His Leu Arg Ala Gln Val Val Ala Gly
225                 230                 235                 240
Cys Gly Ile Leu Phe Ser Cys Met Thr Pro Leu Gly Ile Gly Leu Gly
                245                 250                 255
Ala Ala Leu Ala Glu Ser Ala Gly Pro Leu His Gln Leu Ala Gln Ser
            260                 265                 270
Val Leu Glu Gly Met Ala Ala Gly Thr Phe Leu Tyr Ile Thr Phe Leu
        275                 280                 285
Glu Ile Leu Pro Gln Glu Leu Ala Ser Ser Glu Gln Arg Ile Leu Lys
    290                 295                 300
Val Ile Leu Leu Leu Ala Gly Phe Ala Leu Leu Thr Gly Leu Leu Phe
305                 310                 315                 320
Ile Gln Ile
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<210> 6111
<211> 1706
<212> DNA
<213> Homo sapiens

<400> 6111

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180
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720
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1560
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1680
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1706

<210> 6112
<211> 110
<212> PRT
<213> Homo sapiens

<400> 6112
Met Ser Leu Phe Cys Phe Val Leu Phe Leu Arg Trp Ser Phe Pro Leu
 1   5   10   15
Val Ala Gln Ala Gly Val Xaa Trp His Ser Leu Gly Ser Leu Gln Pro
            20   25   30
Pro Leu Pro Gly Phe Lys Gln Phe Ser Cys Arg Ser Leu Pro Ser Ser
        35   40   45
Trp Asp Tyr Arg His Ala Pro Pro Arg Gln Ala Asn Phe Cys Ile Phe
    50   55   60
Ser Arg Asp Gly Val Ser Pro Cys Trp Pro Gly Trp Ser Gln Thr Pro
65   70   75   80
Asp Leu Arg Arg Ser Thr His Leu Ser Val Pro Lys Cys Trp Asp Tyr
                85   90   95
Arg Arg Glu Pro Pro His Leu Ala Tyr Glu Trp Ser Phe Asn

100 105 110

<210> 6113
<211> 1095
<212> DNA
<213> Homo sapiens

<400> 6113
nncggccgcc aagcgatccc tgctccgcgc gacactgcgt gcccgcgcac gcagagaggc
60
ggtgacgcac tttacggcgg cagcgtaagt gcgtgacgct cgtcagtggc ttcagttcac
120
acgtggcgcc agcggaggca ggttgatgtg tttgtgcttc cttctacagc caatatgaaa
180
aggcctagta agtggggtcg ggaggcgggc gtggagggac ccacgtctgg aagttgctgc
240
agccaccacg acgctcttct acggctacgg ctttgtctct gctggtatgg gggtgggagc
300
atacgcgtag gccttggccc tatttcctgg tagaaccgag agttggaagt ccctacggcg
360
atcatgttaa ccgcgcgggc tcattctgcg gaacgaagcc gggcagaggg tggggaagac
420
taggctagat tttcgtaagg aagcagcgtc tgagccaggt ttgaggccca atattttctt
480
tccgtggcca cgtgcagact ggcccaggtg agagctgaga atcgcctccc agactcagtg
540
ttcctctcct gccttatgat tcgtgctgtt tgacacgaag tggttgtcgt tttgtgtctc
600
atacgctgtt gtgtatgatc ccattctaat attgtgaggg taagtgcagg gaattttgac
660
tccattctgg atctactgaa tttaattctc tgggatttga aagtagcacg tatgtttgca
720
ttaggcattt cgcattagac ttaacgttag gtttggtagc caataacaca agaaaaggat
780
ataactccat agtgcgttaa cccagaacta atcatttggg ttaacagatt tgtgatgtgt
840
ttctttgtag agttaaagaa agcaagtaaa cgcatgacct gccataagcg gtataaaatc
900
caaaaaaagg ttcgagaaca tcatcgaaaa ttaagaaagg aggctaaaaa gcggggtcac
960
aagaagccta ggaaagaccc aggagttcca aacagtgctc cctttaagga ggctcttctt
1020
gaggaagctg agctaaggaa acagaggctt gaagaactaa aacagcagca gaaacttgac
1080
aggcagaagg aacta
1095

<210> 6114
<211> 87
<212> PRT
<213> Homo sapiens

<400> 6114
Met Cys Phe Phe Val Glu Leu Lys Lys Ala Ser Lys Arg Met Thr Cys

```
 1               5                  10                  15
His Lys Arg Tyr Lys Ile Gln Lys Lys Val Arg Glu His His Arg Lys
            20                  25                  30
Leu Arg Lys Glu Ala Lys Lys Arg Gly His Lys Lys Pro Arg Lys Asp
        35                  40                  45
Pro Gly Val Pro Asn Ser Ala Pro Phe Lys Glu Ala Leu Leu Glu Glu
    50                  55                  60
Ala Glu Leu Arg Lys Gln Arg Leu Glu Glu Leu Lys Gln Gln Gln Lys
65                  70                  75                  80
Leu Asp Arg Gln Lys Glu Leu
                85
```

<210> 6115
<211> 411
<212> DNA
<213> Homo sapiens

<400> 6115
gcgcgcctgg ccccgccagg gcctaagttc cctgcactcg cttccccgcc tgtcgccgcc
60
gccgccgccc gcagccctcc ttctcgtggg cgctggggaa gaaactcgtc ggcgggtcta
120
actgtggcgt cccagggcgg tggagggagc aacttcgggg gcacgtcctc gtaaatcccg
180
tggaggacac tgaccctgta ccccaccctc gaggccagaa gtcggttcct ttgggggaac
240
tgaggggcga gagcactcgc ccccctgact tgcaaagttg gcgtctttac ttggcctccg
300
ggattctgcg catggcgtgt ctccaggctg ctgatgggca agacagatgt gccaggtcca
360
gaatgaactt gagaagagtt tgtagccatt cctgaatcac cttatactag t
411

<210> 6116
<211> 129
<212> PRT
<213> Homo sapiens

<400> 6116
```
Met Ala Thr Asn Ser Ser Gln Val His Ser Gly Pro Gly Thr Ser Val
 1               5                  10                  15
Leu Pro Ile Ser Ser Leu Glu Thr Arg His Ala Gln Asn Pro Gly Gly
            20                  25                  30
Gln Val Lys Thr Pro Thr Leu Gln Val Arg Gly Ala Ser Ala Leu Ala
        35                  40                  45
Pro Gln Phe Pro Gln Arg Asn Arg Leu Leu Ala Ser Arg Val Gly Tyr
    50                  55                  60
Arg Val Ser Val Leu His Gly Ile Tyr Glu Asp Val Pro Pro Lys Leu
65                  70                  75                  80
Leu Pro Pro Pro Pro Trp Asp Ala Thr Val Arg Pro Ala Asp Glu Phe
                85                  90                  95
Leu Pro Gln Arg Pro Arg Glu Gly Gly Leu Arg Ala Ala Ala Ala Ala
            100                 105                 110
Thr Gly Gly Glu Ala Ser Ala Gly Asn Leu Gly Pro Gly Gly Ala Arg
```

115 120 125
Arg

<210> 6117
<211> 962
<212> DNA
<213> Homo sapiens

<400> 6117
cttccgcctt ccccaagcca acgtctccgc cgtcggctcc gcggcgccgc catggccgac
60
gtggaagacg gagaggaaac ctgcgccctg gcctctcact ccgggagctc aggctccaag
120
tcgggaggcg acaagatgtt ctccctcaag aagtggaacg cggtggccat gtggagctgg
180
gacgtggagt gcgatacgtg cgccatctgc agggtccagg tgatggatgc ctgtcttaga
240
tgtcaagctg aaaacaaaca agaggactgt gttgtggtct ggggagaatg taatcattcc
300
ttccacaact gctgcatgtc cctgtgggtg aaacagaaca atcgctgccc tctctgccag
360
caggactggg tggtccaaag aatcggcaaa tgagagtggt tagaaggctt cttagcgcag
420
ttgttcagag ccctggtgga tcttgtaatc cagtgcccta caaaggctag aacactacag
480
gggatgaatt cttcaaatag gagccgatgg atctgtggtc ctttgggact catcaaagcc
540
ttggtttagc attttgtcag ttttatcttc agaaattctc tgcgattaag aagataattt
600
attaaaggtg gtccttccta cctctgtggt gtgtgtcgcg cacacagctt agaagtgcta
660
taaaaaagga aagagctcca aattgaatca cctttataat ttacccattt ctatacaaca
720
ggcagtggaa gcagtttcag agaacttttt gcatgcttat ggttgatcag ttaaaaaaga
780
atgttacagt aacaaataaa gtgcagttta aaacccaact cttactctta atttgttcct
840
aatacgtatt tttggcaggg agagggaacg gtccatgaaa tctttatgtg atataaggat
900
tttaagtttg ggccagtgaa cagggtaaat aaaatttaac ttttgagcat aaaaaaaaaa
960
aa
962

<210> 6118
<211> 113
<212> PRT
<213> Homo sapiens

<400> 6118
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu

```
            20                  25                  30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
        35                  40                  45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
    50                  55                  60
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65                  70                  75                  80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
                85                  90                  95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
            100                 105                 110
Lys
```

<210> 6119
<211> 375
<212> DNA
<213> Homo sapiens

<400> 6119
accggttgac aacctcccta tggggaagct agatacagcc ccatggacat gccccactga
60
cccccacacc ccacacggac tgcacggaaa tatcacagta accatctctc agtcacagcg
120
tggccccaca gaactcatgc ctgcttgctt taaacccacc aatgaaaact ccccatggga
180
aacctgcttg gataatactt tggaccccaa taaatgcttt aatcccacaa gtcctctgtc
240
tctgcctctc tcttgccccc acccactggt tgagcatgtg tgtcccaaac ggccctgcaa
300
ggtgtgctgc cctgttcttt ctgggctctg tcaaggaatc aaactgcttc tgttatgtga
360
tgtgtcatgt tgtgc
375

<210> 6120
<211> 118
<212> PRT
<213> Homo sapiens

<400> 6120

```
Met Gly Lys Leu Asp Thr Ala Pro Trp Thr Cys Pro Thr Asp Pro His
 1               5                  10                  15
Thr Pro His Gly Leu His Gly Asn Ile Thr Val Thr Ile Ser Gln Ser
            20                  25                  30
Gln Arg Gly Pro Thr Glu Leu Met Pro Ala Cys Phe Lys Pro Thr Asn
        35                  40                  45
Glu Asn Ser Pro Trp Glu Thr Cys Leu Asp Asn Thr Leu Asp Pro Asn
    50                  55                  60
Lys Cys Phe Asn Pro Thr Ser Pro Leu Ser Leu Pro Leu Ser Cys Pro
65                  70                  75                  80
Tyr Pro Leu Val Glu His Val Cys Pro Lys Arg Pro Cys Lys Val Cys
                85                  90                  95
Cys Pro Val Leu Ser Gly Leu Cys Gln Gly Ile Lys Leu Leu Leu Leu
```

100 105 110
Cys Asp Val Ser Cys Cys
115

<210> 6121
<211> 1039
<212> DNA
<213> Homo sapiens

<400> 6121
gacggaacgg cggtggtggc ccgcggaccg gacggggcac tatgaacgaa gaggagcagt
60
ttgtaaacat tgatttgaat gatgacaaca tttgcagtgt ttgtaaactg ggaacagaca
120
aagaaacact ctccttctgc cacatttgtt ttgagctaaa tattgagggg gtaccaaagt
180
ctgatctctt gcacaccaaa tcattaaggg gccataaaga ctgctttgaa aaataccatt
240
taattgcaaa ccagggttgt cctcgatcta agctttcaaa aagtacttat gaagaagtta
300
aaaccatttt gagtaagaag ataaactgga ttgtgcagta tgcacaaaat aaggatctgg
360
attcagattc tgaatgttct aaaaagcccc agcatcatct gtttaatttc aggcataagc
420
cagaagaaaa attactccca cagtttgagt cccaagtacc aaaatattct gcaaaatgga
480
tagatggaag tgcaggtggc atctctaact gtacacaaag aattttggag cagagggaaa
540
atacagactt tggactttct atgttacaag attcaggtgc cactttatgt cgtaacagtg
600
tattgtggcc tcatagtcac aaccaggcac agaaaaaaga agagacaatc tctagtccag
660
aggctaatgt ccagacccag catccacatt acagcagaga ggaataagtt tttgaagagt
720
taactcacca agtgcaagaa aaagattctt tggcctcaca gctccatgtc cgccacgttg
780
ccatcgaaca gcttctgaag aactgttcta agttaccatg tctgcaagta gggcgaacag
840
gaatgaagtc gcacctaccc ataaacaact gacctaaaca gacttacttc gtatgccctg
900
ccctttattg gtctcccaga catgcaaact ttgaagaagt ttgaagaaag ttgtggtccg
960
ttttttttatg gtcattaaat ttgccaaaca taaggcagta tttaacatct ttgtcaaata
1020
aagcagatca ttatactct
1039

<210> 6122
<211> 221
<212> PRT
<213> Homo sapiens

<400> 6122
Met Asn Glu Glu Glu Gln Phe Val Asn Ile Asp Leu Asn Asp Asp Asn

```
 1               5                  10                  15
Ile Cys Ser Val Cys Lys Leu Gly Thr Asp Lys Glu Thr Leu Ser Phe
            20                  25                  30
Cys His Ile Cys Phe Glu Leu Asn Ile Glu Gly Val Pro Lys Ser Asp
        35                  40                  45
Leu Leu His Thr Lys Ser Leu Arg Gly His Lys Asp Cys Phe Glu Lys
    50                  55                  60
Tyr His Leu Ile Ala Asn Gln Gly Cys Pro Arg Ser Lys Leu Ser Lys
65                  70                  75                  80
Ser Thr Tyr Glu Glu Val Lys Thr Ile Leu Ser Lys Lys Ile Asn Trp
                85                  90                  95
Ile Val Gln Tyr Ala Gln Asn Lys Asp Leu Asp Ser Asp Ser Glu Cys
            100                 105                 110
Ser Lys Lys Pro Gln His His Leu Phe Asn Phe Arg His Lys Pro Glu
        115                 120                 125
Glu Lys Leu Leu Pro Gln Phe Glu Ser Gln Val Pro Lys Tyr Ser Ala
    130                 135                 140
Lys Trp Ile Asp Gly Ser Ala Gly Gly Ile Ser Asn Cys Thr Gln Arg
145                 150                 155                 160
Ile Leu Glu Gln Arg Glu Asn Thr Asp Phe Gly Leu Ser Met Leu Gln
                165                 170                 175
Asp Ser Gly Ala Thr Leu Cys Arg Asn Ser Val Leu Trp Pro His Ser
            180                 185                 190
His Asn Gln Ala Gln Lys Lys Glu Glu Thr Ile Ser Ser Pro Glu Ala
        195                 200                 205
Asn Val Gln Thr Gln His Pro His Tyr Ser Arg Glu Glu
    210                 215                 220
```

<210> 6123
<211> 900
<212> DNA
<213> Homo sapiens

<400> 6123

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ntgcatgcct gtataccaca gctactcggg aggctgaggc gggagaatcg cttgaaccca
60
ggaggcggag gttgcggtga gctgagatcg caccattgca ctccagcctg ggcaacaaga
120
gcgaaacaac aagagaaaaa aaaggaagct gccctctgcc caaaacccac gtcgaggtcc
180
ccaaacctgg gacccttagg tcttttctca cttagcgtgc ccaaccttct cctggcagga
240
aacaagcctc caggtctgct tccccgcaaa ggactataca tggcaaatga cttaaagctc
300
ctgagacacc atctccagat tcccatccac ttccccaagg atttcttgtc tgtgatgctt
360
gaaaaaggaa gtttgtctgc catgcgtttc ctcaccgccg tgaacttgga gcatccagag
420
atgctggaga aagcgtcccg ggagctgtgg atgcgcgtct ggtcaagggt gagtgtgggg
480
ctctgggaat cctctgggag gaccttggat gactttctga ccttccccag gcacgttttc
540
agggtcatga tcctgccccc gcccggggga tctactgtcc tcccagtcac acccctctcc
600
```

ccgcaccgcc ttcctgctgt cttctcttct tcccagaatg aagacatcac cgagccgcag
660
agcatcctgg cggctgcaga gaaggctggt atgtctgcag aacaagccca gggacttctg
720
gaaaagatcg caacgccaaa ggtgaagaac cagctcaagg agaccactga ggcagcctgc
780
agatacggag cctttgggct gcccatcacc gtggcccatg tggatggcca aacccacatg
840
ttatttggct ctgaccggat ggagctgctg gcgcacctgc tgggagagaa gtggatgggc
900

<210> 6124
<211> 300
<212> PRT
<213> Homo sapiens

<400> 6124
Xaa His Ala Cys Ile Pro Gln Leu Leu Gly Arg Leu Arg Arg Glu Asn
1 5 10 15
Arg Leu Asn Pro Gly Gly Gly Gly Cys Gly Glu Leu Arg Ser His His
20 25 30
Cys Thr Pro Ala Trp Ala Thr Arg Ala Lys Gln Gln Glu Lys Lys Lys
35 40 45
Glu Ala Ala Leu Cys Pro Lys Pro Thr Ser Arg Ser Pro Asn Leu Gly
50 55 60
Pro Leu Gly Leu Phe Ser Leu Ser Val Pro Asn Leu Leu Leu Ala Gly
65 70 75 80
Asn Lys Pro Pro Gly Leu Leu Pro Arg Lys Gly Leu Tyr Met Ala Asn
85 90 95
Asp Leu Lys Leu Leu Arg His His Leu Gln Ile Pro Ile His Phe Pro
100 105 110
Lys Asp Phe Leu Ser Val Met Leu Glu Lys Gly Ser Leu Ser Ala Met
115 120 125
Arg Phe Leu Thr Ala Val Asn Leu Glu His Pro Glu Met Leu Glu Lys
130 135 140
Ala Ser Arg Glu Leu Trp Met Arg Val Trp Ser Arg Val Ser Val Gly
145 150 155 160
Leu Trp Glu Ser Ser Gly Arg Thr Leu Asp Asp Phe Leu Thr Phe Pro
165 170 175
Arg His Val Phe Arg Val Met Ile Leu Pro Pro Pro Gly Gly Ser Thr
180 185 190
Val Leu Pro Val Thr Pro Leu Ser Pro His Arg Leu Pro Ala Val Phe
195 200 205
Ser Ser Ser Gln Asn Glu Asp Ile Thr Glu Pro Gln Ser Ile Leu Ala
210 215 220
Ala Ala Glu Lys Ala Gly Met Ser Ala Glu Gln Ala Gln Gly Leu Leu
225 230 235 240
Glu Lys Ile Ala Thr Pro Lys Val Lys Asn Gln Leu Lys Glu Thr Thr
245 250 255
Glu Ala Ala Cys Arg Tyr Gly Ala Phe Gly Leu Pro Ile Thr Val Ala
260 265 270
His Val Asp Gly Gln Thr His Met Leu Phe Gly Ser Asp Arg Met Glu
275 280 285
Leu Leu Ala His Leu Leu Gly Glu Lys Trp Met Gly

290 295 300

<210> 6125
<211> 468
<212> DNA
<213> Homo sapiens

<400> 6125
nctacagtca ctcaggagaa gtcccgcatg gaggcttctt acttggctga caagaaaaag
60
atgaaacagg acttagagga tgccagtaac aaggcggagg aggagagggc ccgcctggag
120
ggagaattga aggggctgca ggagcaaata gcagaaacca aagcccggct tatcacgcag
180
cagcatgatc gggcccaaga gcagagtgac catgccttga tgctgcgtga gctccagaag
240
ctgctgcagg aggagaggac ccagcgccag gacttggagc ttaggttaga agagacccga
300
gaagccttgg caggacgagc atatgcagct gaacagatgg aaggatttga actgcagacc
360
aagcagctga cccgtgaggt ggaggagctg aaaagtgaac tgcaggccat tcgagatgag
420
aagaatcagc cagacccccg gctgcaagaa cttcaggaag aggccgcc
468

<210> 6126
<211> 156
<212> PRT
<213> Homo sapiens

<400> 6126
Xaa Thr Val Thr Gln Glu Lys Ser Arg Met Glu Ala Ser Tyr Leu Ala
1 5 10 15
Asp Lys Lys Lys Met Lys Gln Asp Leu Glu Asp Ala Ser Asn Lys Ala
20 25 30
Glu Glu Glu Arg Ala Arg Leu Glu Gly Glu Leu Lys Gly Leu Gln Glu
35 40 45
Gln Ile Ala Glu Thr Lys Ala Arg Leu Ile Thr Gln Gln His Asp Arg
50 55 60
Ala Gln Glu Gln Ser Asp His Ala Leu Met Leu Arg Glu Leu Gln Lys
65 70 75 80
Leu Leu Gln Glu Glu Arg Thr Gln Arg Gln Asp Leu Glu Leu Arg Leu
85 90 95
Glu Glu Thr Arg Glu Ala Leu Ala Gly Arg Ala Tyr Ala Ala Glu Gln
100 105 110
Met Glu Gly Phe Glu Leu Gln Thr Lys Gln Leu Thr Arg Glu Val Glu
115 120 125
Glu Leu Lys Ser Glu Leu Gln Ala Ile Arg Asp Glu Lys Asn Gln Pro
130 135 140
Asp Pro Arg Leu Gln Glu Leu Gln Glu Glu Ala Ala
145 150 155

<210> 6127
<211> 1900

<212> DNA
<213> Homo sapiens

<400> 6127
gtttcctgga ttacaggcca ggcantggag ataggcagcn ncagcctgac tatcctggta
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gaatgctggg atgggcacct gacacccccc gaggttgcat ccctggctga cagggcatca
120
cgggcaagag actccaatat ggtgagggcg gcagcagagc tggccctgag ctgcctgcct
180
cacgcccatg cattgaaccc taatgagatc cagcgggccc tggtgcagtg caaggaacag
240
gacaacctga tgttggagaa ggcctgcatg gcagtggaag aggcagctaa gggtgggggc
300
gtgtaccctg aagtgttgtt tgaggttgct caccagtggt tctggctata tgagcaaact
360
gcaggtggct catccacagc ccgtgaaggg gctacaagct gtagtgccag tgggatcagg
420
gcaggtgggg aagctgggcg gggtatgcct gagggtagag ggggcccagg gactgagccg
480
gttacagtgg cagcggcagc agtgacagca gcagccacag tggtgcccgt catatcggtg
540
gggtctagtt tatacccggg tccaggactg gggcatggcc actcccctgg cctgcacccc
600
tacactgctc tacagcccca cctgccctgt agccctcagt atctcactca cccagctcac
660
cctgcccacc ccatgcctca catgccccgg cctgccgtct tccctgtgcc cagctctgca
720
tacccacagg gtgtgcatcc tgcattccta ggggctcagt acccttattc agtgactcct
780
ccctcacttg ctgccactgc tgtgtctttc cccgttcctt ccatggcacc catcacagta
840
catccctacc acacagagcc agggcttcca ctgcccacca gtgtggcctg tgagttgtgg
900
ggccagggaa cagtgagcag tgtccatcca gcatccacgt ttccagccat ccaaggtgcc
960
tcactgcctg ccctgaccac acagcccagc cctctggtga gcggaggttt tccaccgccc
1020
gaggaggaga cacacagtca gccagtcaat ccccacagcc tgcaccacct gcatgctgcc
1080
taccgtgtcg gaatgctggc actggagatg ctgggtcgcc gggcacacaa cgatcacccc
1140
aacaacttct cccgctcccc cccctacact gatgatgtca aatggttgct ggggctggca
1200
gcaaagctgg gagtgaacta cgtgcaccag ttctgtgtgg gggcagccaa gggggtgctg
1260
agcccgtttg tgctgcagga gatcgtcatg gagacgctgc agcggctgag tcccgctcat
1320
gcccacaacc acctgcgtgc cccggccttc caccaactgg tgcagcgctg ccagcaggca
1380
tacatgcagt acatccacca ccgcttgatt cacctgactc ctgcggacta cgacgacttt
1440
gtgaatgcga tccggagtgc ccgcagcgcc ttctgcctga cgcccatggg catgatgcag
1500

ttcaacgaca tcctacagaa cctcaagcgc agcaaacaga ccaaggagct gtggcagcgg
1560
gtctcactcg agatggccac cttctccccc tgagtctttc acccttaggg tcctatacag
1620
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1680
gatcatcctc actcagttcc ctggtagcac agactgacag ctgctcttgg gctatagctt
1740
ggggccaaga tgtctcacac cctagaagcc tagggctggg ggagacagcc ctgtctggga
1800
gggggcgttg ggtggcctct ggtatttatt tggcatttat aaatatataa actccttttt
1860
tactctagtc gacctgggcc tttcccttct ttccaaattt
1900

<210> 6128
<211> 530
<212> PRT
<213> Homo sapiens

<400> 6128
Val Ser Trp Ile Thr Gly Gln Ala Xaa Glu Ile Gly Ser Xaa Ser Leu
1 5 10 15
Thr Ile Leu Val Glu Cys Trp Asp Gly His Leu Thr Pro Pro Glu Val
20 25 30
Ala Ser Leu Ala Asp Arg Ala Ser Arg Ala Arg Asp Ser Asn Met Val
35 40 45
Arg Ala Ala Ala Glu Leu Ala Leu Ser Cys Leu Pro His Ala His Ala
50 55 60
Leu Asn Pro Asn Glu Ile Gln Arg Ala Leu Val Gln Cys Lys Glu Gln
65 70 75 80
Asp Asn Leu Met Leu Glu Lys Ala Cys Met Ala Val Glu Glu Ala Ala
85 90 95
Lys Gly Gly Gly Val Tyr Pro Glu Val Leu Phe Glu Val Ala His Gln
100 105 110
Trp Phe Trp Leu Tyr Glu Gln Thr Ala Gly Gly Ser Ser Thr Ala Arg
115 120 125
Glu Gly Ala Thr Ser Cys Ser Ala Ser Gly Ile Arg Ala Gly Gly Glu
130 135 140
Ala Gly Arg Gly Met Pro Glu Gly Arg Gly Gly Pro Gly Thr Glu Pro
145 150 155 160
Val Thr Val Ala Ala Ala Ala Val Thr Ala Ala Ala Thr Val Val Pro
165 170 175
Val Ile Ser Val Gly Ser Ser Leu Tyr Pro Gly Pro Gly Leu Gly His
180 185 190
Gly His Ser Pro Gly Leu His Pro Tyr Thr Ala Leu Gln Pro His Leu
195 200 205
Pro Cys Ser Pro Gln Tyr Leu Thr His Pro Ala His Pro Ala His Pro
210 215 220
Met Pro His Met Pro Arg Pro Ala Val Phe Pro Val Pro Ser Ser Ala
225 230 235 240
Tyr Pro Gln Gly Val His Pro Ala Phe Leu Gly Ala Gln Tyr Pro Tyr
245 250 255
Ser Val Thr Pro Pro Ser Leu Ala Ala Thr Ala Val Ser Phe Pro Val

```
            260                 265                 270
Pro Ser Met Ala Pro Ile Thr Val His Pro Tyr His Thr Glu Pro Gly
        275                 280                 285
Leu Pro Leu Pro Thr Ser Val Ala Cys Glu Leu Trp Gly Gln Gly Thr
    290                 295                 300
Val Ser Ser Val His Pro Ala Ser Thr Phe Pro Ala Ile Gln Gly Ala
305                 310                 315                 320
Ser Leu Pro Ala Leu Thr Thr Gln Pro Ser Pro Leu Val Ser Gly Gly
                325                 330                 335
Phe Pro Pro Pro Glu Glu Glu Thr His Ser Gln Pro Val Asn Pro His
            340                 345                 350
Ser Leu His His Leu His Ala Ala Tyr Arg Val Gly Met Leu Ala Leu
        355                 360                 365
Glu Met Leu Gly Arg Arg Ala His Asn Asp His Pro Asn Asn Phe Ser
    370                 375                 380
Arg Ser Pro Pro Tyr Thr Asp Asp Val Lys Trp Leu Leu Gly Leu Ala
385                 390                 395                 400
Ala Lys Leu Gly Val Asn Tyr Val His Gln Phe Cys Val Gly Ala Ala
                405                 410                 415
Lys Gly Val Leu Ser Pro Phe Val Leu Gln Glu Ile Val Met Glu Thr
            420                 425                 430
Leu Gln Arg Leu Ser Pro Ala His Ala His Asn His Leu Arg Ala Pro
        435                 440                 445
Ala Phe His Gln Leu Val Gln Arg Cys Gln Gln Ala Tyr Met Gln Tyr
    450                 455                 460
Ile His His Arg Leu Ile His Leu Thr Pro Ala Asp Tyr Asp Asp Phe
465                 470                 475                 480
Val Asn Ala Ile Arg Ser Ala Arg Ser Ala Phe Cys Leu Thr Pro Met
                485                 490                 495
Gly Met Met Gln Phe Asn Asp Ile Leu Gln Asn Leu Lys Arg Ser Lys
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<212> DNA
<213> Homo sapiens

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<212> PRT
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50 55 60
Thr Tyr Ile Phe Val Tyr Glu Asn Pro Ile Ser Leu Leu Cys Gly Ala
65 70 75 80
Ile Ile Ile Trp Arg Phe Ala Gly Asn Phe Glu Arg Thr Val Gly Thr
85 90 95
Val Arg His Cys Phe Phe Thr Val Ile Phe Ala Ile Phe Ser Ala Ile
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Ile Phe Leu Ser Phe Glu Ala Val Ser Ser Leu Ser Lys Leu Gly Glu
115 120 125
Val Glu Asp Ala Arg Gly Phe Thr Pro Val Ala Phe Ala Met Leu Gly
130 135 140
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Leu Ile Pro Gln Thr Ser Phe Leu Ser Asn Val Cys Gly Leu Ser Ile
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Gly Leu Ala Tyr Gly Leu Thr Tyr Cys Tyr Ser Ile Asp Leu Ser Glu
195 200 205
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Arg Ile Ser Val Phe Lys Tyr Val Ser Gly Ser Ser Ala Glu Arg Arg
225 230 235 240
Ala Ala Gln Ser Arg Lys Leu Asn Pro Val Pro Gly Ser Tyr Pro Thr
245 250 255
Gln Ser Cys His Pro His Leu Ser Pro Ser His Pro Val Ser Gln Thr
260 265 270
Gln His Ala Ser Gly Gln Lys Leu Ala Ser Trp Pro Ser Cys Thr Pro
275 280 285
Gly His Met Pro Thr Leu Pro Pro Tyr Gln Pro Ala Ser Gly Leu Cys
290 295 300
Tyr Val Gln Asn His Phe Gly Pro Asn Pro Thr Ser Ser Ser Val Tyr
305 310 315 320
Pro Ala Ser Ala Gly Thr Ser Leu Gly Ile Gln Pro Pro Thr Pro Val
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<212> DNA
<213> Homo sapiens

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<213> Homo sapiens

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35 40 45
Val Pro Ile Val Ile Gln Asp Asp Ser Leu Pro Ala Gly Pro Pro Pro
50 55 60
Gln Ile Arg Ile Leu Lys Arg Pro Thr Ser Asn Gly Val Val Ser Ser
65 70 75 80
Pro Asn Ser Thr Ser Arg Pro Thr Leu Pro Val Lys Ser Leu Ala Gln
85 90 95
Arg Glu Ala Glu Tyr Ala Glu Ala Arg Lys Arg Ile Leu Gly Ser Ala
100 105 110
Ser Pro Glu Glu Glu Gln Glu Lys Pro Ile Leu Asp Arg Ser Ser Ser
115 120 125
Asp Leu Leu Pro Phe Arg Pro Thr Arg Ile Ser Gln Pro Glu Asp Ser
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<210> 6133
<211> 4156
<212> DNA
<213> Homo sapiens

<400> 6133

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Arg Gly Leu Val Pro Thr Asp Tyr Val Glu Ile Leu Pro Ser Asp Gly
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Lys Asp Gln Phe Ser Cys Gly Asn Ser Val Ala Asp Gln Ala Phe Leu
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Asp Ser Leu Ser Ala Ser Thr Ala Gln Ala Ser Ser Ser Ala Ala Ser
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Asn Asn His Gln Val Gly Ser Gly Asn Asp Pro Trp Ser Ala Trp Ser
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Ala Ser Lys Ser Gly Asn Trp Glu Ser Ser Glu Gly Trp Gly Ala Gln

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Tyr Phe Lys Asp Ser Glu Ser Ala Asp Ala Gly Gly Ala Gln Arg Gly
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Pro Gly Phe Ala Lys Pro Gly Thr Glu Gln Tyr Leu Leu Ala Lys Gln
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Gln Leu Thr Pro Thr Asn Thr Asn Arg Ser Val Asn His Arg Tyr Lys
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Leu Thr Val Gly Gln Glu His Trp Lys Arg Cys Thr Gly Pro Leu Pro
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Lys Glu Tyr Gln Lys Ile Gly Lys Ala Leu Gln Ser Leu Ala Thr Val
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Phe Ser Ser Ser Gly Tyr Gln Gly Glu Thr Asp Leu Asn Asp Ala Ile
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Thr Glu Ala Gly Lys Thr Tyr Glu Glu Ile Ala Ser Leu Val Ala Glu
465                 470                 475                 480
Gln Pro Lys Lys Asp Leu His Phe Leu Met Glu Cys Asn His Glu Tyr
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Lys Gly Phe Leu Gly Cys Phe Pro Asp Ile Ile Gly Thr His Lys Gly
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Ala Ile Glu Lys Val Lys Glu Ser Asp Lys Leu Val Ala Thr Ser Lys
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Ile Thr Leu Gln Asp Lys Gln Asn Met Val Lys Arg Val Ser Ile Met
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Ser Tyr Ala Leu Gln Ala Glu Met Asn His Phe His Ser Asn Arg Ile
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Tyr Asp Tyr Asn Ser Val Ile Arg Leu Tyr Leu Glu Gln Gln Val Gln
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<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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Leu Leu Ser Leu Glu His Val Gly Ile Leu His Lys Asp Phe Glu Ser
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Ile Leu Pro Thr Arg Lys Asn His Asn Met Ala Ser Arg Pro Leu Thr
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Leu Val Lys Pro Ser Ala Ser Gln Tyr
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<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

<400> 6138

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Gly	Val	Pro	Asn	Ser	Ala	Pro	Phe	Lys	Glu	Ala	Leu	Leu	Arg	Glu	Ala
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Asp	Arg	Gln	Lys	Glu	Leu	Glu	Lys	Lys	Arg	Lys	Leu	Glu	Thr	Asn	Pro
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Asp	Ile	Lys	Xaa	Ile	Lys	Cys	Gly	Thr	Xaa	Met	Glu	Lys	Glu	Phe	Gly
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Asn Ser Leu Lys Gln Glu Gln Met Cys Asn Val Gly Val Ser Met Gly
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Leu Thr Arg Ser Met Gln Val Val Pro Leu Asp Lys Gln Ile Thr Ile
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Lys Tyr Thr Val Pro Gly Tyr Arg Asn Ser Leu Glu Phe Phe Thr Val
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Leu Ala Gln Arg Arg Gly Met His Gln Lys Gly Gly Ile Pro Asn Val
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Ala Tyr Tyr Cys His Pro Pro Thr Ser Trp Thr Pro Pro Pro Tyr Phe
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Asn Glu Ser Ile Val Val Asp Met Lys Ser Gly Phe Asn Leu Glu Glu
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Leu Glu Lys Asn Asn Ala Gln Ser Ile Arg Ala Ile Lys Gly Pro His
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Leu Ala Asn Ser Ile Leu Phe Gln Ser Ser Gly Leu Thr Asn Gly Ile
    450                 455                 460
Ile Glu Glu Lys Asp Ile His Glu Glu Leu Pro Lys Arg Lys Glu Arg
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Lys Gln Glu Glu Arg Glu Asp Asp Lys Asp Ser Asp Gln Glu Thr Val
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<212> PRT
<213> Homo sapiens

<400> 6140
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Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
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Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
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Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Xaa Phe Gly Pro Xaa
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Cys Lys Thr Arg Asp Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile
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Arg Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Tyr Lys Gly
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Thr Val Thr Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser Ser Ser
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Asp Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val Lys Val
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Asn Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser Gly Gly
            260                 265                 270
Tyr Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe Ser Met
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Leu Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile Phe Lys
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Gly Ser Cys Ala Gly Cys Asp Leu Leu Phe Ser Gln Glu Thr Val Met
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Lys Phe Val Pro Arg Tyr Ser Leu Val Leu Glu Leu Ser Asp Ser Gly
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Ala Phe Arg Arg Ser Leu His Asp Pro Asp Gly Leu Val Ala Thr Tyr
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<212> DNA
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3780
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3900
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5400
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5460
gcacacgtcg gagtgggccg tgcagtccac tttagccaca tagactttgg catcttccat
5520
gctgttgtat ttgtctccca ggtcattcca agtcggctgc agccgctggc agtgtccaca
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5640

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5651

<210> 6142
<211> 513
<212> PRT
<213> Homo sapiens

<400> 6142
Met Pro Gly Leu Gly Arg Arg Ala Gln Trp Leu Cys Trp Trp Trp Gly
1 5 10 15
Leu Leu Cys Ser Cys Cys Gly Pro Pro Pro Leu Arg Pro Pro Leu Pro
20 25 30
Ala Ala Ala Ala Ala Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly
35 40 45
Ser Pro Gly Arg Thr Glu Gln Pro Pro Pro Ser Pro Gln Ser Ser Ser
50 55 60
Gly Phe Leu Tyr Arg Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln
65 70 75 80
Lys Glu Ile Leu Ser Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu
85 90 95
His Gly Leu Gln Gln Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu
100 105 110
Gln Gln Gln Gln Gln Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg
115 120 125
Leu Lys Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser
130 135 140
Ala Asp Asn Asp Glu Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser
145 150 155 160
Trp Pro His Glu Ala Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro
165 170 175
Gly Ala Ala His Pro Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser
180 185 190
Gly Ser Gly Gly Ala Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe
195 200 205
Leu Asn Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu Tyr
210 215 220
Asp Lys Glu Phe Ser Pro Arg Gln Arg His His Lys Glu Phe Lys Phe
225 230 235 240
Asn Leu Ser Gln Ile Pro Glu Gly Gly Val Val Thr Ala Ala Glu Phe
245 250 255
Arg Ile Tyr Lys Asp Cys Val Met Gly Ser Phe Lys Asn Gln Thr Phe
260 265 270
Leu Ile Ser Ile Tyr Gln Val Leu Gln Glu His Gln His Arg Asp Ser
275 280 285
Asp Leu Phe Leu Leu Asp Thr Arg Val Val Trp Ala Ser Glu Glu Gly
290 295 300
Trp Leu Glu Phe Asp Ile Thr Ala Thr Ser Asn Leu Trp Val Val Thr
305 310 315 320
Pro Gln His Asn Met Gly Leu Gln Leu Ser Val Val Thr Arg Asp Gly
325 330 335
Val His Val His Pro Arg Ala Ala Gly Leu Val Gly Arg Asp Gly Pro
340 345 350
Tyr Asp Lys Gln Pro Phe Met Val Ala Phe Phe Lys Val Ser Glu Val

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        355                 360                 365
His Val Arg Thr Thr Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser
    370                 375                 380
Arg Asn Arg Ser Thr Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala
385                 390                 395                 400
Ser Asp Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu
                405                 410                 415
Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala
            420                 425                 430
Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro
        435                 440                 445
Leu Asn Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu
    450                 455                 460
Val His Leu Met Asn Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro
465                 470                 475                 480
Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asn Asp Asn Ser Lys
                485                 490                 495
Ile Thr Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Tyr
            500                 505                 510
Cys
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<210> 6143
<211> 1137
<212> DNA
<213> Homo sapiens

<400> 6143
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120
cacccacctg cccaacctag gacagctggg cctgagctgg gcgggcaggg gattccatct
180
cctgggtgcg cctgccagag gggagaggct ggaggcggcg ggaatgctgt tctcccccag
240
gagtcagtcc tcagggcttc tgccgtggga cgtggggccg agggacctgg ggcactgacc
300
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360
cggacagctt ctggtgctgg gcctagcgga gacagaggac cagaggtcca ggttcctggg
420
ggctgagctt ttctcagact tcggaggaaa aatgtcccag cccagcaggc agtgccgggg
480
cagggccagt gtgtcagagg cgtcaaagct ctttcgggtg gatgtggtac cggtgcgggg
540
gctccaggat cgacagcggg atgctcaccc tgcgcagggg ggctgacgtg cgctgctgcg
600
ccagggtccc agggccctgc tggtctcgcg atgtcctgca caggcggcag ggggtaccgg
660
gatccacagg caccgggaac aggcgccggt tgacacggta acagtacacg cattcatggt
720
cttcctccac gccgctgcca ctgctctcac gcaggcctgg caactggggt tcaggatggc
780

tgcagataca ctcctccttg ttggtttccc gaaactcctg cagcttggag aagaaggcct
840
caggctggct ggtgatggaa gagctggtgt ccagagaccc tgcaatccag tcatagccca
900
ggtatggcct gaggcgccag ctcctctcag gaactgcaga ctcctcagag aaggtcaccc
960
tgggcttgga cagcttgctc tgttgagcca ggatggacct cggggtctgt gcctcctggg
1020
gtcctggatc acccagcctc cctgagggct ctgggtccct caggcttgag gtgcccagcg
1080
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1137

<210> 6144
<211> 141
<212> PRT
<213> Homo sapiens

<400> 6144
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Ser Thr Glu Ser Leu Thr Leu His Pro Arg Val Leu Pro Leu Trp Asn
20 25 30
Ser Gly Ser Arg Gln Ala Trp Val His Pro Pro Ala Gln Pro Arg Thr
35 40 45
Ala Gly Pro Glu Leu Gly Gly Gln Gly Ile Pro Ser Pro Gly Cys Ala
50 55 60
Cys Gln Arg Gly Glu Ala Gly Gly Gly Gly Asn Ala Val Leu Pro Gln
65 70 75 80
Glu Ser Val Leu Arg Ala Ser Ala Val Gly Arg Gly Ala Glu Gly Pro
85 90 95
Gly Ala Leu Thr Arg Ser Gly Ser Gly Ala Ala Ser Ala Leu Val Arg
100 105 110
Pro Gly Glu Lys Gly Cys Trp Cys Arg Thr Ala Ser Gly Ala Gly Pro
115 120 125
Ser Gly Asp Arg Gly Pro Glu Val Gln Val Pro Gly Gly
130 135 140

<210> 6145
<211> 766
<212> DNA
<213> Homo sapiens

<400> 6145
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agagcaatgt cttcccagca gcagcagcgg caggcagcag tgcccacccc agaggcccag
120
cagcagcaag tgaagcagcc ttgtcagcca ccccctgtta aatgtcaaga gacatgtgca
180
cccaaaacca aggatccatg tgctccccag gtcaagaagc aatgcccacc gaaagacacc
240
atcattccag cccagcagaa gtgtccctca gcccagcaag cctccaagag caaacagaag
300

taaggatgga ctggatatta ccatcatcca ccatcctggc taccagatgg aaccttctct
360
tcttccttct cctcttccct ccagctcttg agcctaccct cctctcacat ctcctcctgc
420
ccaagatgta aggaagcatt gtaaggattt cttcccatcg taccttccc cacacatacc
480
accttggctt cttctatatc ccaccccgat gctctcccag gtgggtgtga gagagacctc
540
attctctgca ggctccagcg tggccacagc taaggcccat ccatttccca aagtgaggaa
600
agtgtctggg cttcttctgg ggttccaccc tgacaagtag ggtcacagag gctggtgcac
660
agtttctgcc tcattcctct ccatgatgcc ccctgctctg ggcttctctc ctgttttccc
720
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766

<210> 6146
<211> 100
<212> PRT
<213> Homo sapiens

<400> 6146
Xaa Lys Gly Ser Ala Ser Ser Pro Gly Val Gln Leu Val Ala Ser Gly
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Ser Pro Val Pro Arg Ala Met Ser Ser Gln Gln Gln Gln Arg Gln Ala
20 25 30
Ala Val Pro Thr Pro Glu Ala Gln Gln Gln Gln Val Lys Gln Pro Cys
35 40 45
Gln Pro Pro Pro Val Lys Cys Gln Glu Thr Cys Ala Pro Lys Thr Lys
50 55 60
Asp Pro Cys Ala Pro Gln Val Lys Lys Gln Cys Pro Pro Lys Asp Thr
65 70 75 80
Ile Ile Pro Ala Gln Gln Lys Cys Pro Ser Ala Gln Gln Ala Ser Lys
85 90 95
Ser Lys Gln Lys
100

<210> 6147
<211> 1852
<212> DNA
<213> Homo sapiens

<400> 6147
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120
acatagttct ctgtaaaact gacttacttt ccaaatatat tttgaaataa aacaatataa
180
aaatgttttc tgtttttagg aatggtggaa agcagcagac ataattggag tgggttggat
240
aagcaaagtg atattcaaaa tttaaatgaa gagagaatct tagctttaca gctttgtggg
300

tggataaaga aaggaacgga tgtagacgtg gggccatttt tgaactccct tgtacaagaa
360
ggggaatggg aaagagctgc tgctgtggca ttgttcaact tggatattcg ccgagcaatc
420
caaatcctga atgaaggggc atcttctgaa aaaggagatc tgaatctcaa tgtggtagca
480
atggctttat cgggttatac ggatgagaag aactcccttt ggagagaaat gtgtagcaca
540
ctgcgattac agctaaataa cccgtatttg tgtgtcatgt ttgcatttct gacaagtgaa
600
acaggatctt acgatggagt tttgtatgaa aacaaagttg cagtacgtga cagagtggca
660
tttgcttgta aattccttag tgatactcag ttaaatagat acatcgaaaa gttgaccaat
720
gaaatgaaag aggctggaaa tttggaagga attttgctta caggccttac taaagatgga
780
gtggacttaa tggagagtta tgttgataga actggagatg ttcaaacagc aagttactgt
840
atgttacagg gttcaccttt agatgttctt aaagatgaaa gggttcagta ctggattgag
900
aattatagaa atttattaga tgcctggagg ttttggcata aacgagctga atttgatatt
960
cacaggagta agttggatcc cagttccaag cctttagcac aagtttttgt gagttgcaat
1020
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1080
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1140
cgaaaaccac ttcctcgatg tgcgctttgt ctcattaata tgggaacacc agtttctagc
1200
tgtcctggag gaaccaaatc agatgaaaaa gtggacttga gcaaggacaa aaaattagcc
1260
caatttaaca actggtttac atggtgtcat aattgcaggc acggtggaca tgctggacat
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aaacatacct cagaacaagc cattcatgac ttacctgtaa tgggaaaata aatcattcta
1560
tcagatcagc agttttgatg tttgagtgat tttgatatgc ttcacagaga caaatgctgc
1620
caaaataaac atcgaagtat agacatgagt tctgttcagc aggttgaaaa gtctgattta
1680
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1740
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1800
atatgtgcac ttttaaaata aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa
1852

<210> 6148

<211> 410
<212> PRT
<213> Homo sapiens

<400> 6148
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Asp Ile Gln Asn Leu Asn Glu Glu Arg Ile Leu Ala Leu Gln Leu Cys
20 25 30
Gly Trp Ile Lys Lys Gly Thr Asp Val Asp Val Gly Pro Phe Leu Asn
35 40 45
Ser Leu Val Gln Glu Gly Glu Trp Glu Arg Ala Ala Ala Val Ala Leu
50 55 60
Phe Asn Leu Asp Ile Arg Arg Ala Ile Gln Ile Leu Asn Glu Gly Ala
65 70 75 80
Ser Ser Glu Lys Gly Asp Leu Asn Leu Asn Val Val Ala Met Ala Leu
85 90 95
Ser Gly Tyr Thr Asp Glu Lys Asn Ser Leu Trp Arg Glu Met Cys Ser
100 105 110
Thr Leu Arg Leu Gln Leu Asn Asn Pro Tyr Leu Cys Val Met Phe Ala
115 120 125
Phe Leu Thr Ser Glu Thr Gly Ser Tyr Asp Gly Val Leu Tyr Glu Asn
130 135 140
Lys Val Ala Val Arg Asp Arg Val Ala Phe Ala Cys Lys Phe Leu Ser
145 150 155 160
Asp Thr Gln Leu Asn Arg Tyr Ile Glu Lys Leu Thr Asn Glu Met Lys
165 170 175
Glu Ala Gly Asn Leu Glu Gly Ile Leu Leu Thr Gly Leu Thr Lys Asp
180 185 190
Gly Val Asp Leu Met Glu Ser Tyr Val Asp Arg Thr Gly Asp Val Gln
195 200 205
Thr Ala Ser Tyr Cys Met Leu Gln Gly Ser Pro Leu Asp Val Leu Lys
210 215 220
Asp Glu Arg Val Gln Tyr Trp Ile Glu Asn Tyr Arg Asn Leu Leu Asp
225 230 235 240
Ala Trp Arg Phe Trp His Lys Arg Ala Glu Phe Asp Ile His Arg Ser
245 250 255
Lys Leu Asp Pro Ser Ser Lys Pro Leu Ala Gln Val Phe Val Ser Cys
260 265 270
Asn Phe Cys Gly Lys Ser Ile Ser Tyr Ser Cys Ser Ala Val Pro His
275 280 285
Gln Gly Arg Gly Phe Ser Gln Tyr Gly Val Ser Gly Ser Pro Thr Lys
290 295 300
Ser Lys Val Thr Ser Cys Pro Gly Cys Arg Lys Pro Leu Pro Arg Cys
305 310 315 320
Ala Leu Cys Leu Ile Asn Met Gly Thr Pro Val Ser Ser Cys Pro Gly
325 330 335
Gly Thr Lys Ser Asp Glu Lys Val Asp Leu Ser Lys Asp Lys Lys Leu
340 345 350
Ala Gln Phe Asn Asn Trp Phe Thr Trp Cys His Asn Cys Arg His Gly
355 360 365
Gly His Ala Gly His Met Leu Ser Trp Phe Arg Asp His Ala Glu Cys
370 375 380
Pro Val Ser Ala Cys Thr Cys Lys Cys Met Gln Leu Asp Thr Thr Gly

385 390 395 400
Asn Leu Val Pro Ala Glu Thr Val Gln Pro
405 410

<210> 6149
<211> 1949
<212> DNA
<213> Homo sapiens

<400> 6149
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120
agacagtcct cgtcagcact gactttcagc tatggaatcg cagacggttg atgatgaagc
180
gccggccgtg taaatgaaga tcgggtgagg agcaggacga tgcccaaggg tgggtgccct
240
aaagcaccac agcaggaaga gcttcccctc agcagcgaca tggtggagaa gcagactggg
300
aaaaaggata aagataaagt ttctctaacc aagaccccaa aactggagcg tggcgatggc
360
gggaaggagg tgagggagcg agccagcaag cggaagctgc ccttcaccgc gggcgccaat
420
ggggagcaga aggactcgga cacagagaag cagggccctg agcggaagag gattaagaag
480
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540
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600
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660
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780
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960
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1020
gagacgccgc tgaaagtggc caactccccc acgatggtga acctcctgtt aggcaaaggc
1080
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1140
ttcgcacctt ccagttcagt cgacggcaac aacacggact ccgagttcga aaaaggcctc
1200
aagcacaagg ccaagaaccc agagccacag aaggccacgg cccccgtcaa ggacgagtat
1260
gagtttgatg aggacgacga gcaggacagg gttcctccgg tggacgacaa gcacctattg
1320

aaaaaggact acagaaaaga aacgaaatcc aatagtttta tctctatacc caaaatggag
1380
gttaaaagtt acactaaaaa taacacgatt gcaccaaaga aagcgtccca tcgtatcctg
1440
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1740
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1800
gctctgccgc ccagaagcag aaccccagcc acacagacca gcacaccaag cactggcgga
1860
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1920
ccacaaggac gagactgaca agcgagtct
1949

<210> 6150
<211> 508
<212> PRT
<213> Homo sapiens

<400> 6150
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Lys Val Ser Leu Thr Lys Thr Pro Lys Leu Glu Arg Gly Asp Gly Gly
35 40 45
Lys Glu Val Arg Glu Arg Ala Ser Lys Arg Lys Leu Pro Phe Thr Ala
50 55 60
Gly Ala Asn Gly Glu Gln Lys Asp Ser Asp Thr Glu Lys Gln Gly Pro
65 70 75 80
Glu Arg Lys Arg Ile Lys Lys Glu Pro Val Thr Arg Lys Ala Gly Leu
85 90 95
Leu Phe Gly Met Gly Leu Ser Gly Ile Arg Ala Gly Tyr Pro Leu Ser
100 105 110
Glu Arg Gln Gln Val Ala Leu Leu Met Gln Met Thr Ala Glu Glu Ser
115 120 125
Ala Asn Ser Pro Val Asp Thr Thr Pro Lys His Pro Ser Gln Ser Thr
130 135 140
Val Cys Gln Lys Gly Thr Pro Asn Ser Ala Ser Lys Thr Lys Asp Lys
145 150 155 160
Leu Asn Lys Arg Asn Glu Arg Gly Glu Thr Arg Leu His Arg Ala Ala
165 170 175
Ile Arg Gly Asp Ala Arg Arg Ile Lys Glu Leu Ile Ser Glu Gly Ala
180 185 190
Asp Val Asn Val Lys Asp Phe Ala Gly Trp Thr Ala Leu His Glu Ala

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        195                 200                 205
Cys Asn Arg Gly Tyr Tyr Asp Val Ala Lys Gln Leu Leu Ala Ala Gly
    210                 215                 220
Ala Glu Val Asn Thr Lys Gly Leu Asp Asp Asp Thr Pro Leu His Asp
225                 230                 235                 240
Ala Ala Asn Asn Gly His Tyr Lys Val Val Lys Leu Leu Leu Arg Tyr
                245                 250                 255
Gly Gly Asn Pro Gln Gln Ser Asn Arg Lys Gly Glu Thr Pro Leu Lys
            260                 265                 270
Val Ala Asn Ser Pro Thr Met Val Asn Leu Leu Leu Gly Lys Gly Thr
        275                 280                 285
Tyr Thr Ser Ser Glu Glu Ser Ser Thr Glu Ser Ser Glu Glu Glu Asp
    290                 295                 300
Ala Pro Ser Phe Ala Pro Ser Ser Ser Val Asp Gly Asn Asn Thr Asp
305                 310                 315                 320
Ser Glu Phe Glu Lys Gly Leu Lys His Lys Ala Lys Asn Pro Glu Pro
                325                 330                 335
Gln Lys Ala Thr Ala Pro Val Lys Asp Glu Tyr Glu Phe Asp Glu Asp
            340                 345                 350
Asp Glu Gln Asp Arg Val Pro Pro Val Asp Asp Lys His Leu Leu Lys
        355                 360                 365
Lys Asp Tyr Arg Lys Glu Thr Lys Ser Asn Ser Phe Ile Ser Ile Pro
    370                 375                 380
Lys Met Glu Val Lys Ser Tyr Thr Lys Asn Asn Thr Ile Ala Pro Lys
385                 390                 395                 400
Lys Ala Ser His Arg Ile Leu Ser Asp Thr Ser Asp Glu Glu Asp Ala
                405                 410                 415
Ser Val Thr Val Gly Thr Gly Glu Lys Leu Arg Leu Ser Ala His Thr
            420                 425                 430
Ile Leu Pro Gly Ser Lys Thr Arg Glu Pro Ser Asn Ala Lys Gln Gln
        435                 440                 445
Lys Glu Lys Asn Lys Val Lys Lys Lys Arg Lys Lys Glu Thr Lys Gly
    450                 455                 460
Arg Glu Val Arg Phe Gly Lys Arg Ser Xaa Ser Ser Ala Pro Arg Ser
465                 470                 475                 480
Arg Arg Ala Ser Pro Gln Arg Val Gly Arg Met Thr Gly Thr Leu Trp
                485                 490                 495
Gly Ala Leu Ala Ala Ser Arg Gly Pro Arg Trp Cys
            500                 505
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<210> 6151
<211> 648
<212> DNA
<213> Homo sapiens

<400> 6151
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120
gtggaggtca ccttctggta gacggagacc cgcttttcag actctgtggc gcagcaggcg
180
ggccaggaac atttgggcca ctattgctct tagccctgcc gcgcctgact ttctctcctc
240

tactttcctt ccgaccgtag ggacaagtgt ggggatccgc tttgggctcc aaggccctgc
300
ccgcactggc agcaccaagc gggtgtagaa tgactggaag gagcagggaa ggaagatggg
360
tgtcaactgt cccggccagt ggctgcgtgc atgtgtgtgt gaacagggaa aaggccaccc
420
tctcccatgt ttctcccgtc tcctcggttc tcctcggaga cccgcagggc tgcccgaggt
480
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648

<210> 6152
<211> 130
<212> PRT
<213> Homo sapiens

<400> 6152
Met Arg Thr Lys Pro Gln Arg Pro Arg Ala Thr Arg Ser Tyr Leu Gly
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Gln Pro Cys Gly Ser Pro Arg Arg Thr Glu Glu Thr Gly Glu Thr Trp
20 25 30
Glu Arg Val Ala Phe Ser Leu Phe Thr His Thr Cys Thr Gln Pro Leu
35 40 45
Ala Gly Thr Val Asp Thr His Leu Pro Ser Leu Leu Leu Pro Val Ile
50 55 60
Leu His Pro Leu Gly Ala Ala Ser Ala Gly Arg Ala Leu Glu Pro Lys
65 70 75 80
Ala Asp Pro His Thr Cys Pro Tyr Gly Arg Lys Glu Ser Arg Gly Glu
85 90 95
Lys Val Arg Arg Gly Arg Ala Lys Ser Asn Ser Gly Pro Asn Val Pro
100 105 110
Gly Pro Pro Ala Ala Pro Gln Ser Leu Lys Ser Gly Ser Pro Ser Thr
115 120 125
Arg Arg
130

<210> 6153
<211> 1810
<212> DNA
<213> Homo sapiens

<400> 6153
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gactcatgcc tcatggtctg gcacatgaag ctgcagtcac gcgcctaccg cttcactggc
120
cacaaggatg ccgtcacctg tgtgaacttc tctccttcgg gacacctgct tgcttccggc
180
tcccgagaca agactgtccg catctgggta cccaatgtca aaggtgagtc cactgtgttt
240

cgtgcacaca cagccacagt gaggagtgtc cacttctgca gtgatggcca gtccttcgtg
300
acagcctctg acgacaagac agtcaaagtg tgggcaactc atcgccagaa attcctgttc
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480
gtccactcgt attgtgagca tggcggcttt gtcacctatg tggacttcca ccccagtggg
540
acgtgcattg ccgctgccgg catggacaac acagtgaagg tgtgggacgt gcggactcac
600
cggctgctgc agcattatca gttgcacagt gcagcagtga acgggctctc tttccacccg
660
tcgggaaact acctgatcac agcctccagt gactcaaccc tgaagatcct ggacctgatg
720
gagggccggc tgctctacac actccacggg catcagggac cagccaccac tgttgccttt
780
tcaagaacgg gggagtattt tgcttctgga ggctctgatg aacaagtgat ggtttggaag
840
agtaactttg atattgttga tcatggagaa gtcacgaaag tgccgaggcc cccagccaca
900
ctggccagct ccatggggaa tctgccagaa gtggacttcc ctgtcccccc aggcagaggc
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1140
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1200
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1260
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1320
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1380
cacaaatgat gcttcagacc cgaatgagag gaccacattt tgcttaatgt aaaggagcca
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1500
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1620
gactaaaggc ccaaagtggg cccatctgag tcaggtttgt tgagaacaag ccctctcaag
1680
tgggtggtgg cttttcagtg gccctgattt ctgttccaca cgtgttcact ggagccaggt
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aaaaaaaaaa
1810

<210> 6154
<211> 388
<212> PRT
<213> Homo sapiens

<400> 6154
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Ser Gly Xaa Met Asp Ser Cys Leu Met Val Trp His Met Lys Leu Gln
20 25 30
Ser Arg Ala Tyr Arg Phe Thr Gly His Lys Asp Ala Val Thr Cys Val
35 40 45
Asn Phe Ser Pro Ser Gly His Leu Leu Ala Ser Gly Ser Arg Asp Lys
50 55 60
Thr Val Arg Ile Trp Val Pro Asn Val Lys Gly Glu Ser Thr Val Phe
65 70 75 80
Arg Ala His Thr Ala Thr Val Arg Ser Val His Phe Cys Ser Asp Gly
85 90 95
Gln Ser Phe Val Thr Ala Ser Asp Asp Lys Thr Val Lys Val Trp Ala
100 105 110
Thr His Arg Gln Lys Phe Leu Phe Ser Leu Ser Gln His Ile Asn Trp
115 120 125
Val Arg Cys Ala Lys Phe Ser Pro Asp Gly Arg Leu Ile Val Ser Ala
130 135 140
Ser Asp Asp Lys Thr Val Lys Leu Trp Asp Lys Ser Ser Arg Glu Cys
145 150 155 160
Val His Ser Tyr Cys Glu His Gly Gly Phe Val Thr Tyr Val Asp Phe
165 170 175
His Pro Ser Gly Thr Cys Ile Ala Ala Ala Gly Met Asp Asn Thr Val
180 185 190
Lys Val Trp Asp Val Arg Thr His Arg Leu Leu Gln His Tyr Gln Leu
195 200 205
His Ser Ala Ala Val Asn Gly Leu Ser Phe His Pro Ser Gly Asn Tyr
210 215 220
Leu Ile Thr Ala Ser Ser Asp Ser Thr Leu Lys Ile Leu Asp Leu Met
225 230 235 240
Glu Gly Arg Leu Leu Tyr Thr Leu His Gly His Gln Gly Pro Ala Thr
245 250 255
Thr Val Ala Phe Ser Arg Thr Gly Glu Tyr Phe Ala Ser Gly Gly Ser
260 265 270
Asp Glu Gln Val Met Val Trp Lys Ser Asn Phe Asp Ile Val Asp His
275 280 285
Gly Glu Val Thr Lys Val Pro Arg Pro Pro Ala Thr Leu Ala Ser Ser
290 295 300
Met Gly Asn Leu Pro Glu Val Asp Phe Pro Val Pro Pro Gly Arg Gly
305 310 315 320
Trp Ser Val Glu Ser Val Gln Ser Gln Pro Gln Glu Pro Val Ser Val
325 330 335
Pro Gln Thr Leu Thr Ser Thr Leu Glu His Ile Val Gly Gln Leu Asp
340 345 350
Val Leu Thr Gln Thr Val Ser Ile Leu Glu Gln Arg Leu Thr Leu Thr
355 360 365
Glu Asp Lys Leu Lys Gln Cys Leu Glu Asn Gln Gln Leu Ile Met Gln

370 375 380
Arg Ala Thr Pro
385

<210> 6155
<211> 995
<212> DNA
<213> Homo sapiens

<400> 6155
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120
aataacagcg atttattatt aaggaaatga tacgcttttg tcccattcaa ataatgtttt
180
tattcccctt ttctttattc ttgggaggtt cctattgttg tgccaggtcg ttttcactga
240
acgattttta aaggtattca ccagtcccac gtgtgaccgg ttgcattttt actgtgcagg
300
accatcgtga agcctgtggc caaagagttt gatccagaca tggtcttagt atctgctgga
360
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420
tttggtcatt tgacgaagca attgatgaca ttggctgatg gacgtgtggt gttggctcta
480
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540
ctaggaaatg agctggagcc acttgcagaa gatattctcc accaaagccc gaatatgaat
600
gctgttattt ctttacagaa gatcattgaa attcaaaaac tgctggtgag cctatggaag
660
aggagccagc cttgtgaagt gccaagtccc cctctgatat ttcctgtgtg tgacatcatt
720
gtgtatcccc ccaccccagt accctcagac atgtcttgtc tgctgcctgg gtggcacaga
780
ttcaatggaa cataaacact gggcacaaaa ttctgaacag cagcttcact tgttctttgg
840
atggacttga aagggcatta aagattcctt aaacgtaacc gctgtgattc tagagttaca
900
gtaaaccacg attggaagaa actgcttcca gcatgctttt aatatgctgg gtgacccact
960
cctagacacc aagtttgaac tagaaacatt cagta
995

<210> 6156
<211> 164
<212> PRT
<213> Homo sapiens

<400> 6156
Thr Ile Val Lys Pro Val Ala Lys Glu Phe Asp Pro Asp Met Val Leu
1 5 10 15
Val Ser Ala Gly Phe Asp Ala Leu Glu Gly His Thr Pro Pro Leu Gly

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            20                  25                  30
Gly Tyr Lys Val Thr Ala Lys Cys Phe Gly His Leu Thr Lys Gln Leu
        35                  40                  45
Met Thr Leu Ala Asp Gly Arg Val Val Leu Ala Leu Glu Gly Gly His
    50                  55                  60
Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Asn Ala Leu
65                  70                  75                  80
Leu Gly Asn Glu Leu Glu Pro Leu Ala Glu Asp Ile Leu His Gln Ser
                85                  90                  95
Pro Asn Met Asn Ala Val Ile Ser Leu Gln Lys Ile Ile Glu Ile Gln
            100                 105                 110
Lys Leu Leu Val Ser Leu Trp Lys Arg Ser Gln Pro Cys Glu Val Pro
        115                 120                 125
Ser Pro Pro Leu Ile Phe Pro Val Cys Asp Ile Ile Val Tyr Pro Pro
    130                 135                 140
Thr Pro Val Pro Ser Asp Met Ser Cys Leu Leu Pro Gly Trp His Arg
145                 150                 155                 160
Phe Asn Gly Thr
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<210> 6157
<211> 2135
<212> DNA
<213> Homo sapiens

<400> 6157
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120
ttgaacttca gtttgactaa ctatgaaact tttaactgct attctttctc aactttcctt
180
ttttctgcag gatctggcga catggccaga aaggctctca agcttgcttc gtggaccagc
240
atggctcttg ctgcctctgg catctacttc tacagtaaca agtacttgga ccctaatgac
300
tttggcgctg tcagggtggg cagagcagtt gctacgacgg ctgtcatcag ttacgactac
360
ctcacttccc tgaagagtgt cccttatggc tcagaggagt acttgcagct gagatctaag
420
atccatgatt tgttccagag cttcgatgac acccctctgg ggacggcctc cctggcccag
480
gtccacaagg cagtgctgca tgatgggcgg acggtggccg tgaaggtcca gcacccaaag
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gtgcgggctc agagctcgaa ggacattctc ctgatggagg tgctcgttct ggctgtgaag
600
cagctgttcc cagagtttga gtttatgtgg cttgtggatg aagccaagaa gaacctgcct
660
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720
cattttgact tcttgaaggt cccccgaatc cactgggacc tgtccacgga gcgggtcctc
780
ctgatggagt ttgtggatgg cgggcaggtc aatgacagag actacatgga gaggaacaag
840

atcgacgtca atgagatctc acgccacctg ggcaagatgt atagtgagat gatcttcgtc
900
aatggcttcg tgcactgcga tccccacccc ggcaacgtac tggtgcggaa gcaccccggc
960
acgggaaagg cggagattgt cctgttggac catgggcttt accagatgct cacggaagaa
1020
ttccgcctga attactgcca cctctggcag tctctgatct ggactgacat gaagagagtg
1080
aaggagtaca gccagcgact gggagccggg gatctctacc ccttgtttgc ctgcatgctg
1140
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1200
gaggacttag agattcgcaa caacgcggcc aactacctcc cccagatcag ccatctcctc
1260
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1320
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1380
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1440
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1500
gtgaaggggt tgaagctggc tgaccgggtc ttggccctaa tatgctggct gttccctgct
1560
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1620
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1680
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1740
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1800
gcagcctaca ttcccattcc tggtatgtgc cattgggttg gatgtcccca ctacttccgt
1860
taacccttcc cattgtcaag atgtgccacg ggtgccactg ggggcacact gaacttgtag
1920
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1980
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2040
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2100
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2135

<210> 6158
<211> 455
<212> PRT
<213> Homo sapiens

<400> 6158
Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu
1 5 10 15
Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu Asp Pro Asn

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Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val
        35                  40                  45
Ile Ser Tyr Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
    50                  55                  60
Glu Glu Tyr Leu Gln Leu Arg Ser Lys Ile His Asp Leu Phe Gln Ser
65                  70                  75                  80
Phe Asp Asp Thr Pro Leu Gly Thr Ala Ser Leu Ala Gln Val His Lys
                85                  90                  95
Ala Val Leu His Asp Gly Arg Thr Val Ala Val Lys Val Gln His Pro
            100                 105                 110
Lys Val Arg Ala Gln Ser Ser Lys Asp Ile Leu Leu Met Glu Val Leu
        115                 120                 125
Val Leu Ala Val Lys Gln Leu Phe Pro Glu Phe Glu Phe Met Trp Leu
    130                 135                 140
Val Asp Glu Ala Lys Lys Asn Leu Pro Leu Glu Leu Asp Phe Leu Asn
145                 150                 155                 160
Glu Gly Arg Asn Ala Glu Lys Val Ser Gln Met Leu Arg His Phe Asp
                165                 170                 175
Phe Leu Lys Val Pro Arg Ile His Trp Asp Leu Ser Thr Glu Arg Val
            180                 185                 190
Leu Leu Met Glu Phe Val Asp Gly Gly Gln Val Asn Asp Arg Asp Tyr
        195                 200                 205
Met Glu Arg Asn Lys Ile Asp Val Asn Glu Ile Ser Arg His Leu Gly
    210                 215                 220
Lys Met Tyr Ser Glu Met Ile Phe Val Asn Gly Phe Val His Cys Asp
225                 230                 235                 240
Pro His Pro Gly Asn Val Leu Val Arg Lys His Pro Gly Thr Gly Lys
                245                 250                 255
Ala Glu Ile Val Leu Leu Asp His Gly Leu Tyr Gln Met Leu Thr Glu
            260                 265                 270
Glu Phe Arg Leu Asn Tyr Cys His Leu Trp Gln Ser Leu Ile Trp Thr
        275                 280                 285
Asp Met Lys Arg Val Lys Glu Tyr Ser Gln Arg Leu Gly Ala Gly Asp
    290                 295                 300
Leu Tyr Pro Leu Phe Ala Cys Met Leu Thr Ala Arg Ser Trp Asp Ser
305                 310                 315                 320
Val Asn Arg Gly Ile Ser Gln Ala Pro Val Thr Ala Thr Glu Asp Leu
                325                 330                 335
Glu Ile Arg Asn Asn Ala Ala Asn Tyr Leu Pro Gln Ile Ser His Leu
            340                 345                 350
Leu Asn His Val Pro Arg Gln Met Leu Leu Ile Leu Lys Thr Asn Asp
        355                 360                 365
Leu Leu Arg Gly Ile Glu Ala Ala Leu Gly Thr Arg Ala Ser Ala Ser
    370                 375                 380
Ser Phe Leu Asn Met Ser Arg Cys Cys Ile Arg Ala Leu Ala Glu His
385                 390                 395                 400
Lys Lys Lys Asn Thr Cys Ser Phe Phe Arg Arg Thr Gln Ile Ser Phe
                405                 410                 415
Ser Glu Ala Phe Asn Leu Trp Gln Ile Asn Leu His Glu Leu Ile Leu
            420                 425                 430
Arg Val Lys Gly Leu Lys Leu Ala Asp Arg Val Leu Ala Leu Ile Cys
        435                 440                 445
Trp Leu Phe Pro Ala Pro Leu
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450 455

<210> 6159
<211> 4310
<212> DNA
<213> Homo sapiens

<400> 6159
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120
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240
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300
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660
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720
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780
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840
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900
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960
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1020
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1080
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1140
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1320
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1380

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1560
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2160
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2220
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2280
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2340
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2400
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2460
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2520
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2580
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2640
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2700
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2760
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2820
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3000

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3060
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3120
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3240
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3360
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3600
ggatggaggg gtccctcctc tgggccagca ccagcgtcag gttgccagtg acggccagga
3660
caaaggccaa cgtggcacag atccagaagg ggccatacag atccggccga ttccgcagat
3720
ggtgccgcac aaagttgtgg ccaggccggg gcagcagtga gcctttgatc cggtccagga
3780
cctgtgaggt gtccacgtca aagaagctct gatagtagct gaaggtccag aatcccggct
3840
gctgctgctg ctgctgctcc tgcaggagcg cggccttgtc actctcctcc tccacctcat
3900
cctcggctcc atagctgcca cctgagccca cggccacagc cacgtgccct tgtggggtca
3960
gctgatcgct tctgctggtg gtggctgcat ctggggtgtc agccagaaga ttagtggcct
4020
cctcgaattc atggaaggtc agctcgtcgg ccgatgccat ggtcgttcag gggcgtctcc
4080
gcatccctcg ctggcgacca actgcaccca cggaggcttg aactcgtcgt cccgtcccca
4140
caggtgcgct ccgccccccc tcacctgagg ccacctgggc cggcgtggct ggggctcatc
4200
cctgtgcctt ggctgcagtg gctctttggg gcgctggccc tgggcctgtc agccgccggg
4260
ctggtattca ccctctggcc cgtggtccgt gaggacacca ggctggtggc
4310

<210> 6160
<211> 551
<212> PRT
<213> Homo sapiens

<400> 6160
Leu Glu Val Arg Ala Gly Pro Asp Ser Ala Gly Ile Ala Leu Tyr Ser
1 5 10 15
His Glu Asp Val Cys Val Phe Lys Cys Ser Val Ser Arg Glu Thr Glu

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            20                  25                  30
Cys Ser Arg Val Gly Lys Gln Ser Phe Ile Ile Thr Leu Gly Cys Asn
        35                  40                  45
Ser Val Leu Ile Gln Phe Ala Thr Pro Asn Asp Phe Cys Ser Phe Tyr
    50                  55                  60
Asn Ile Leu Lys Thr Cys Arg Gly His Thr Leu Glu Arg Ser Val Phe
65                  70                  75                  80
Ser Glu Arg Thr Glu Glu Ser Ser Ala Val Gln Tyr Phe Gln Phe Tyr
                85                  90                  95
Gly Tyr Leu Ser Gln Gln Gln Asn Met Met Gln Asp Tyr Val Arg Thr
            100                 105                 110
Gly Thr Tyr Gln Arg Ala Ile Leu Gln Asn His Thr Asp Phe Lys Asp
        115                 120                 125
Lys Ile Val Leu Asp Val Gly Cys Gly Ser Gly Ile Leu Ser Phe Phe
    130                 135                 140
Ala Ala Gln Ala Gly Ala Arg Lys Ile Tyr Ala Val Glu Ala Ser Thr
145                 150                 155                 160
Met Ala Gln His Ala Glu Val Leu Val Lys Ser Asn Asn Leu Thr Asp
                165                 170                 175
Arg Ile Val Val Ile Pro Gly Lys Val Glu Glu Val Ser Leu Pro Glu
            180                 185                 190
Gln Val Asp Ile Ile Ile Ser Glu Pro Met Gly Tyr Met Leu Phe Asn
        195                 200                 205
Glu Arg Met Leu Glu Ser Tyr Leu His Ala Lys Lys Tyr Leu Lys Pro
    210                 215                 220
Ser Gly Asn Met Phe Pro Thr Ile Gly Asp Val His Leu Ala Pro Phe
225                 230                 235                 240
Thr Asp Glu Gln Leu Tyr Met Glu Gln Phe Thr Lys Ala Asn Phe Trp
                245                 250                 255
Tyr Gln Pro Ser Phe His Gly Val Asp Leu Ser Ala Leu Arg Gly Ala
            260                 265                 270
Ala Val Asp Glu Tyr Phe Arg Gln Pro Val Val Asp Thr Phe Asp Ile
        275                 280                 285
Arg Ile Leu Met Ala Lys Ser Val Lys Tyr Thr Val Asn Phe Leu Glu
    290                 295                 300
Ala Lys Glu Gly Asp Leu His Arg Ile Glu Ile Pro Phe Lys Phe His
305                 310                 315                 320
Met Leu His Ser Gly Leu Val His Gly Leu Ala Phe Trp Phe Asp Val
                325                 330                 335
Ala Phe Ile Gly Ser Ile Met Thr Val Trp Leu Ser Thr Ala Pro Thr
            340                 345                 350
Glu Pro Leu Thr His Trp Tyr Gln Val Arg Cys Leu Phe Gln Ser Pro
        355                 360                 365
Leu Phe Ala Lys Ala Gly Asp Thr Leu Ser Gly Thr Cys Leu Leu Ile
    370                 375                 380
Ala Asn Lys Arg Gln Ser Tyr Asp Ile Ser Ile Val Ala Gln Val Asp
385                 390                 395                 400
Gln Thr Gly Ser Lys Ser Ser Asn Leu Leu Asp Leu Lys Asn Pro Phe
                405                 410                 415
Phe Arg Tyr Thr Gly Thr Thr Pro Ser Pro Pro Pro Gly Ser His Tyr
            420                 425                 430
Thr Ser Pro Ser Glu Asn Met Trp Asn Thr Gly Ser Thr Tyr Asn Leu
        435                 440                 445
Ser Ser Gly Met Ala Val Ala Gly Met Pro Thr Ala Tyr Asp Leu Ser
```

```
    450                 455                 460
Ser Val Ile Ala Ser Gly Ser Ser Val Gly His Asn Asn Leu Ile Pro
465                 470                 475                 480
Leu Ala Asn Thr Gly Ile Val Asn His Thr His Ser Arg Met Gly Ser
                485                 490                 495
Ile Met Ser Thr Gly Ile Val Gln Gly Ser Ser Gly Ala Gln Gly Ser
            500                 505                 510
Gly Gly Gly Ser Thr Ser Ala His Tyr Ala Val Asn Ser Gln Phe Thr
        515                 520                 525
Met Gly Gly Pro Ala Ile Ser Met Ala Ser Pro Met Ser Ile Pro Thr
    530                 535                 540
Asn Thr Met His Tyr Gly Ser
545                 550
```

<210> 6161
<211> 1489
<212> DNA
<213> Homo sapiens

<400> 6161
ggctgcatga tcttcagcag attcagtaca gagggaagtg agctgtggga gaggaaggag
60
gatgggggaa atggcaagaa aaggagcacc ctgcttagaa agggaacgga gccgggtgtg
120
gtggctcacg cctgcaatcc anacaccttg ggaggccgaa gcaaggagat cacctgagcc
180
caagagtttg agaccaccca catagcaaga ccccatctct atttttgga aaaaaaaaaa
240
aaaagcagca accagcagga tgggtggaaa aaagttgctg aaggctcttc aagatcctct
300
ctgcctgctc cttctctcac agagggacag gggagggtga tgagtcagtg gactgaatgt
360
ccccatgggg atgaaggatg gttggggtca gggtcctaga gggagggctg gaaggaggga
420
aggagatggc cagagaagga tgtaggacac agaggtgccg ccgtggatca ccaagaggtt
480
caggactggc cagaggaagg agaggagatc aaggcaagca tgaggcactt gggagatgca
540
tctgtgcctg cacacagctg aaatccccag gaaataagac gggagcaggg tgggtttctg
600
cagccgaggt gagaccaaag tgccagctca ctgccaccct cagtaaagac taacttgccc
660
ttccccacaa ctccccctccc agaagtagct tgctctcctc tgcctgccac acatcggggg
720
gctcagggaa agctcccccc ccctggacag ctagtgttcc ctaggccaag gccagtccct
780
gcagagatga ggagctggga aatcccctcc tcccatcccg cacgtccacg cgtgccagat
840
cctgtgctgc gggcttttca cacacagcct cttagacgct tagcctgtga ggcgggtgct
900
gttgtccttc cttcccattt tgcaactgag caaacagcct gaaagagaca aaaaccaggt
960
agttagcatg accccaaagc cactccctgg tctacgctgt tctgcagcct gagcctgggg
1020

tggccaggtg gggttgtgca gtgaggggg gaaggagaat agcccccaaa aatgctgccg
1080
gaatggtaaa gggcctggac tgcaaagcta gtgacttgag ctttattttg tggcactgga
1140
ggttttccca gtcattgtaa tgatacaatc agatttgcgt tgtcttcaag ttaccatggt
1200
aaccgtactt ccacccacca agagtggatt ggagaaggca aaactagggc agagaagcca
1260
gggagtgttg agaaggtctg aacccagaca gtgggcagct gggccccaag acggatgggg
1320
gactccagaa gcgtggagct ggcagagaga aacctgcccg gggcatcaga gaaaagggcg
1380
actgtgcagg aacagagtag atgaggtggg gaacctttgg gtaagaagag ctgaatcagg
1440
agcattgagg cagcggtttt caaacctcag aagcaacagc agggccggc
1489

<210> 6162
<211> 58
<212> PRT
<213> Homo sapiens

<400> 6162
Gly Cys Met Ile Phe Ser Arg Phe Ser Thr Glu Gly Ser Glu Leu Trp
1 5 10 15
Glu Arg Lys Glu Asp Gly Gly Asn Gly Lys Lys Arg Ser Thr Leu Leu
20 25 30
Arg Lys Gly Thr Glu Pro Gly Val Val Ala His Ala Cys Asn Pro Xaa
35 40 45
Thr Leu Gly Gly Arg Ser Lys Glu Ile Thr
50 55

<210> 6163
<211> 713
<212> DNA
<213> Homo sapiens

<400> 6163
gtggaaatga gcctctcatt aaaacacgtg ctttctggga gccgtgatga acgtgagtgt
60
gagatgagtc cagctgcggt cagagccatg ggatgtgggt cactgtgacc cagtgggtca
120
caggtgctga gcaaggaagg gctgggaggc tcaagcaaaa tctacaagaa aaatctaaag
180
gggcccagcc tctgccagga aaagcaggcc tggctctgct gaaaccccaa tcacgctctg
240
atggataccg gtacctgggc aaggatacc tggatggact tgattcttct ctcctgaaat
300
gtacgagaag gtgcatgcgg ggatttcggc tgcctgaaaa gcaaccctct aaaacccgag
360
tgtcattttt agaatcaaaa aggaaggaag gcagtggctg gctgcactgg tcagtaacga
420
gatctggagc ttttcgcctt aaggtcactg tttaaaactc tgccctgggt cagttgtaac
480

agaaagtcac aactccctca caggcatcag ggtgcaactt tgaatgccaa gaggggctgt
540
gtctgttggt taccacgcgg cgagctcccg ggacacctcc tgacacctcc tgacagtgtc
600
tctttctcta ggagtctcct ctcttcccac ccaccatggc ggcctggcct ggaggggagg
660
cattggggac tgagtccttc cccgacaggg agtctctctc ccccctggcg cgc
713

<210> 6164
<211> 120
<212> PRT
<213> Homo sapiens

<400> 6164
Met Trp Val Thr Val Thr Gln Trp Val Thr Gly Ala Glu Gln Gly Arg
 1   5   10   15
Ala Gly Arg Leu Lys Gln Asn Leu Gln Glu Lys Ser Lys Gly Ala Gln
            20   25   30
Pro Leu Pro Gly Lys Ala Gly Leu Ala Leu Leu Lys Pro Gln Ser Arg
        35   40   45
Ser Asp Gly Tyr Arg Tyr Leu Gly Lys Asp Thr Val Asp Gly Leu Asp
    50   55   60
Ser Ser Leu Leu Lys Cys Thr Arg Arg Cys Met Arg Gly Phe Arg Leu
65   70   75   80
Pro Glu Lys Gln Pro Ser Lys Thr Arg Val Ser Phe Leu Glu Ser Lys
                85   90   95
Arg Lys Glu Gly Ser Gly Trp Leu His Trp Ser Val Thr Arg Ser Gly
            100   105   110
Ala Phe Arg Leu Lys Val Thr Val
        115   120

<210> 6165
<211> 1004
<212> DNA
<213> Homo sapiens

<400> 6165
cccagccgga tcgggcggcg aaggccggcg cggcgagcag caaccatgtc ggtgttcggg
60
aagctgttcg gggctggagg gggtaaggcc ggcaagggcg gcccgacccc ccaggaggcc
120
atccagcggc tgcgggacac ggaagagatg ttaagcaaga aacaggagtt cctggagaag
180
aaaatcgagc aggagctgac ggccgccaag aagcacggca ccaaaaacaa gcgcgcggcc
240
ctccaggcac tgaagcgtaa gaagaggtat gagaagcagc tggcgcagat cgacggcaca
300
ttatcaacca tcgagttcca gcgggaggcc ctggagaatg ccaacaccaa caccgaggtg
360
ctcaagaaca tgggctatgc cgccaaggcc atgaaggcgg cccatgacaa catggacatc
420
gataaagttg atgagttaat gcaggacatt gctgaccagc aagaacttgc agaggagatt
480

tcaacagcaa tttcgaaacc tgtagggttt ggagaagagt ttgacgagga tgagctcatg
540
gcggaattag aagaactaga acaggaggaa ctagacaaga atttgctgga aatcagtgga
600
cccgaaacag tccctctacc aaatgttccc tctatagccc taccatcaaa acccgccaag
660
aagaaagaag aggaggacga cgacatgaag gaattggaga actgggctgg atccatgtaa
720
tggggtccag cgctggctgg gcccagacag actgtggtgg cctgcgcagc gagcaggcgt
780
gtgcgtgtgt ggggcaggca ggatgtggtg caggcaggtt ccatcgcttt cgactctcac
840
tccaaagcag tagggccgcg ttgctgctca ctctctgcat agcatggtct gcacctggga
900
gttggccggg gggaggggggg cgagcgggct ggcacgtgcc tgctgtttat aatgttgaat
960
ttctgtaaaa taaactgtat ttgcaaatcc aaaaaaaaaa aaaa
1004

<210> 6166
<211> 239
<212> PRT
<213> Homo sapiens

<400> 6166
Pro Ser Arg Ile Gly Arg Arg Arg Pro Ala Arg Arg Ala Ala Thr Met
1 5 10 15
Ser Val Phe Gly Lys Leu Phe Gly Ala Gly Gly Gly Lys Ala Gly Lys
20 25 30
Gly Gly Pro Thr Pro Gln Glu Ala Ile Gln Arg Leu Arg Asp Thr Glu
35 40 45
Glu Met Leu Ser Lys Lys Gln Glu Phe Leu Glu Lys Lys Ile Glu Gln
50 55 60
Glu Leu Thr Ala Ala Lys Lys His Gly Thr Lys Asn Lys Arg Ala Ala
65 70 75 80
Leu Gln Ala Leu Lys Arg Lys Lys Arg Tyr Glu Lys Gln Leu Ala Gln
85 90 95
Ile Asp Gly Thr Leu Ser Thr Ile Glu Phe Gln Arg Glu Ala Leu Glu
100 105 110
Asn Ala Asn Thr Asn Thr Glu Val Leu Lys Asn Met Gly Tyr Ala Ala
115 120 125
Lys Ala Met Lys Ala Ala His Asp Asn Met Asp Ile Asp Lys Val Asp
130 135 140
Glu Leu Met Gln Asp Ile Ala Asp Gln Gln Glu Leu Ala Glu Glu Ile
145 150 155 160
Ser Thr Ala Ile Ser Lys Pro Val Gly Phe Gly Glu Glu Phe Asp Glu
165 170 175
Asp Glu Leu Met Ala Glu Leu Glu Glu Leu Glu Gln Glu Glu Leu Asp
180 185 190
Lys Asn Leu Leu Glu Ile Ser Gly Pro Glu Thr Val Pro Leu Pro Asn
195 200 205
Val Pro Ser Ile Ala Leu Pro Ser Lys Pro Ala Lys Lys Lys Glu Glu
210 215 220
Glu Asp Asp Asp Met Lys Glu Leu Glu Asn Trp Ala Gly Ser Met

225 230 235

<210> 6167
<211> 1220
<212> DNA
<213> Homo sapiens

<400> 6167
ngccatacag cattttagtt ttgttctttc cattaactga agtcacgagg tatgcctcct
60
tggaaactcc aacagttaag agattctcat gtattccatg aaataaaaag caaagaaaaa
120
tcaaacttgt cttaatgaga tggaagtgtt ggatcaaaca ctgattgagc tgttctatgt
180
cctccacttc cccagtgcct tctctcctcc cgggtctgcg cggacgcggc ctccttacct
240
catttgtcct cgcccctccc cgtccctcta cgcgttttgg tccctgtttg gtgctttctg
300
tttgcagcta cggcagtgag tatgtatgtg acggaccccg agtcacccgc ggcctgggac
360
ccctgcctac cctccgtctc gccagccgag ctgtggaact agcgcgtgcc ccctcgccga
420
cctcggcgtc tccggtccgc ccctcacttg tggtggggcg cagctcctgg tccctcagct
480
gcgcgccgcc ccacgcggcc gggctgcggg tctaggggggt ccgcatctcc ctggctttcc
540
aagggctaag gtcgtgattc tagggcggct gggcgtccag ggcctcggtg ggggtggcgt
600
gtctgccctt tttatctccc cgcaaggccc ccagtcttct agggaagcca gtcagtgaag
660
cgcggaggtc cgggcgcgcc gagagagagt ccagtctttg aggaccgagt agtcctgggc
720
cacctcccgc ctctgctgtc agaagcagca gctgccgccg tggaatccaa aatttcggga
780
gctgtgaccc tttcctcatg taaaacgagt agtcttggac gatctgggca taggaaccaa
840
tcagaaacaa tcgcttcagc aatcaagacc attgttcatc atggaggaac ccatggatac
900
ctctgagcct ctatctgcat taccattcac tgggcagcag tcttttgagc caagtggcaa
960
atttggacag tatccatcga tgcagatgaa ccacatccag gcactgggga agtggaggac
1020
atagaacagc tcaatcagtg tttgatccaa cacttccatc tcattaagac aagtttgatt
1080
tttctttgct ttttatttca tggaatacat gagaatctct taactgttgg agtttccaag
1140
gaggcatacc tcatgacttc agttaatgga aagaacaaaa ctaaaatgct gtatggccaa
1200
agccacaaag ggaaggatcc
1220

<210> 6168
<211> 90
<212> PRT

<213> Homo sapiens

<400> 6168
Ala Lys Trp Gln Ile Trp Thr Val Ser Ile Asp Ala Asp Glu Pro His
1 5 10 15
Pro Gly Thr Gly Glu Val Glu Asp Ile Glu Gln Leu Asn Gln Cys Leu
20 25 30
Ile Gln His Phe His Leu Ile Lys Thr Ser Leu Ile Phe Leu Cys Phe
35 40 45
Leu Phe His Gly Ile His Glu Asn Leu Leu Thr Val Gly Val Ser Lys
50 55 60
Glu Ala Tyr Leu Met Thr Ser Val Asn Gly Lys Asn Lys Thr Lys Met
65 70 75 80
Leu Tyr Gly Gln Ser His Lys Gly Lys Asp
85 90

<210> 6169
<211> 720
<212> DNA
<213> Homo sapiens

<400> 6169
tgagggcttc gatcccttct ctgatttgct gtcagccatg aacggatgga tgtgatgcct
60
gctagccaaa aggcttccct ctgtgtgttg cagtcctgtg gcattatgca tgccccctcc
120
cagtgacccc aggcttttta tggctgtgaa acacgttaaa atttcagggt aagacgtgac
180
cttttgaggt gactataact gaagattgct ttacagaagc ccaaaaaggt tttttgagtc
240
atgatgcaag aatctgggac tgagacaaaa agtaacggtt cagccatcca gaatgggtcg
300
ggcggcagca accacttact agagtgcggc ggtcttcggg aggggcggtc caacggagag
360
acgccggccg tggacatcgg ggcagctgac ctcgcccacg cccagcagca gcagcaacag
420
tggcatctca taaaccatca gccctctagg agtcccagca gttggcttaa gagactaatt
480
tcaagccctt gggagttgga agtcctgcag gtcccttgtg gggagcagtt gctgagacga
540
agatgagtgg acctgtgtgt cagcctaacc cttccccatt ttgaataaaa ttattctttg
600
gagaaatggt tcccactgct ttcatgcaaa aataaaaatt aaacgaaaaa cagcttaagc
660
ctgtgaagaa ggaaatactg agctagccag caaaagagag aaagaagagg aggggagagg
720

<210> 6170
<211> 101
<212> PRT
<213> Homo sapiens

<400> 6170
Met Met Gln Glu Ser Gly Thr Glu Thr Lys Ser Asn Gly Ser Ala Ile

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 1               5                  10                  15
Gln Asn Gly Ser Gly Gly Ser Asn His Leu Leu Glu Cys Gly Gly Leu
            20                  25                  30
Arg Glu Gly Arg Ser Asn Gly Glu Thr Pro Ala Val Asp Ile Gly Ala
        35                  40                  45
Ala Asp Leu Ala His Ala Gln Gln Gln Gln Gln Trp His Leu Ile
    50                  55                  60
Asn His Gln Pro Ser Arg Ser Pro Ser Ser Trp Leu Lys Arg Leu Ile
65                  70                  75                  80
Ser Ser Pro Trp Glu Leu Glu Val Leu Gln Val Pro Cys Gly Glu Gln
                85                  90                  95
Leu Leu Arg Arg Arg
            100
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<210> 6171
<211> 1130
<212> DNA
<213> Homo sapiens

<400> 6171
nncccgctag gagttcctag taaagtggcg ggagccgcag ctatggagcc gcaggaggag
60
agagaaacgc aggttgctgc gtggttaaaa aaaatatttg gagatcatcc tattccacag
120
tatgaggtga acccacggac cacagagatt ttacatcacc tttcagaacg caacagggtc
180
cgggacaggg atgtctacct ggtaatagag gacttgaagc agaaagcaag tgaatacgag
240
tcagaagcca agtatcttca agaccttctc atggagagtg tgaatttttc ccccgccaat
300
ctctctagca ctggttccag gtatctgaat gctttggttg acagtgcggt ggcccttgaa
360
acaaaggata cctcgctagc tagttttatc cctgcagtga atgatttgac ctctgatctc
420
tttcgtacca aatccaaaag tgaagaaatc aagattgaac tggaaaaact tgaaaaaaat
480
ttaactgcaa ctttagtatt agaaaaatgt ctacaagagg atgtcaagaa agcagagttg
540
catctgtcta cagaaagggc caaagttgat aatcgtcgtc agaacatgga ctttctaaaa
600
gcaaagtcag aggaattcag atttggaatc aaggctgcag aggagcaact ttcagccaga
660
ggcatggatg cttctctgtc tcatcagtcc ttagtagcac tatcagagaa actggcaaga
720
ttaaagcaac agactatacc tttgaagaaa aaattggagt cctatttaga cttaatgccg
780
aatccgtctc ttgctcaagt gaaaattgaa gaagcaaagc gagaactaga tagcattgaa
840
gctgaactta caagaagagt agacatgatg gaactgtgac aaaagccaaa taaacatcct
900
tttccctaac aaagtaaatt gaataggact ttacagagtt ctttttcctc ttggcatttc
960
ctaataacaa aactttctgt gttcttagat tacagaatat cataattgat agaatatggt
1020

ttcttactgt gtgttgcatt tttgtgccca aatacatagt tttcatatta aaaagccttt
1080
tctcttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
1130

<210> 6172
<211> 292
<212> PRT
<213> Homo sapiens

<400> 6172
Xaa Pro Leu Gly Val Pro Ser Lys Val Ala Gly Ala Ala Ala Met Glu
 1   5   10   15
Pro Gln Glu Glu Arg Glu Thr Gln Val Ala Ala Trp Leu Lys Lys Ile
            20   25   30
Phe Gly Asp His Pro Ile Pro Gln Tyr Glu Val Asn Pro Arg Thr Thr
        35   40   45
Glu Ile Leu His His Leu Ser Glu Arg Asn Arg Val Arg Asp Arg Asp
    50   55   60
Val Tyr Leu Val Ile Glu Asp Leu Lys Gln Lys Ala Ser Glu Tyr Glu
65   70   75   80
Ser Glu Ala Lys Tyr Leu Gln Asp Leu Leu Met Glu Ser Val Asn Phe
                85   90   95
Ser Pro Ala Asn Leu Ser Ser Thr Gly Ser Arg Tyr Leu Asn Ala Leu
            100   105   110
Val Asp Ser Ala Val Ala Leu Glu Thr Lys Asp Thr Ser Leu Ala Ser
        115   120   125
Phe Ile Pro Ala Val Asn Asp Leu Thr Ser Asp Leu Phe Arg Thr Lys
    130   135   140
Ser Lys Ser Glu Glu Ile Lys Ile Glu Leu Glu Lys Leu Glu Lys Asn
145   150   155   160
Leu Thr Ala Thr Leu Val Leu Glu Lys Cys Leu Gln Glu Asp Val Lys
                165   170   175
Lys Ala Glu Leu His Leu Ser Thr Glu Arg Ala Lys Val Asp Asn Arg
            180   185   190
Arg Gln Asn Met Asp Phe Leu Lys Ala Lys Ser Glu Glu Phe Arg Phe
        195   200   205
Gly Ile Lys Ala Ala Glu Glu Gln Leu Ser Ala Arg Gly Met Asp Ala
    210   215   220
Ser Leu Ser His Gln Ser Leu Val Ala Leu Ser Glu Lys Leu Ala Arg
225   230   235   240
Leu Lys Gln Gln Thr Ile Pro Leu Lys Lys Lys Leu Glu Ser Tyr Leu
                245   250   255
Asp Leu Met Pro Asn Pro Ser Leu Ala Gln Val Lys Ile Glu Glu Ala
            260   265   270
Lys Arg Glu Leu Asp Ser Ile Glu Ala Glu Leu Thr Arg Arg Val Asp
        275   280   285
Met Met Glu Leu
    290

<210> 6173
<211> 1483
<212> DNA
<213> Homo sapiens

<400> 6173
agagagagag actagttctc tcttactcta ggcctttcgg tttgcgcgac ggggcaggaa
60
agcgtgcgtg cggctaagag agtgggcgct ctcgcggcgc tgacgatgga agaactggag
120
caaggcctgt tgatgcagcc atgggcgtgg ctacagcttg cagagaactc cctcttggcc
180
aaggttttta tcaccaagca gggctatgcc ttgttggttt cagatcttca acaggtgtgg
240
catgaacagg tggacactag tgtggtcagc cagcgagcca aggagctgaa caagcggctc
300
actgctcctc ctgcagcttt cctctgtcat ttggataatc tccttcgccc attgttgaag
360
gacgctgctc accctagcga agctaccttc tcctgtgatt gtgtggcaga tgcactgatt
420
ctacgggtgc gaagtgagct ctctggcctc cccttctatt ggaatttcca ctgcatgcta
480
gctagtcctt ccctggtctc ccaacatttg attcgtcctc tgatgggcat gagtctggca
540
ttacagtgcc aagtgaggga gctagcaacg ttacttcata tgaaagacct agagatccaa
600
gactaccagg agagtggggc tacgctgatt cgagatcgat tgaagacaga accatttgaa
660
gaaaattcct tcttggaaca atttatgata gagaaactgc cagaggcatg cagcattggt
720
gatggaaagc cctttgtcat gaatctgcag gatctgtata tggcagtcac cacacaagag
780
gtccaagtgg gacagaagca tcaaggcgct ggagatcctc atacctcaaa cagtgcttcc
840
ctgcaaggaa tcgatagcca atgtgtaaac cagccagaac aactggtctc ctcagcccca
900
accctctcag cacctgagaa agagtccacg ggtacttcag gccctctgca gagacctcag
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<210> 6174

<211> 299
<212> PRT
<213> Homo sapiens

<400> 6174
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Gly Tyr Ala Leu Leu Val Ser Asp Leu Gln Gln Val Trp His Glu Gln
35 40 45
Val Asp Thr Ser Val Val Ser Gln Arg Ala Lys Glu Leu Asn Lys Arg
50 55 60
Leu Thr Ala Pro Pro Ala Ala Phe Leu Cys His Leu Asp Asn Leu Leu
65 70 75 80
Arg Pro Leu Leu Lys Asp Ala Ala His Pro Ser Glu Ala Thr Phe Ser
85 90 95
Cys Asp Cys Val Ala Asp Ala Leu Ile Leu Arg Val Arg Ser Glu Leu
100 105 110
Ser Gly Leu Pro Phe Tyr Trp Asn Phe His Cys Met Leu Ala Ser Pro
115 120 125
Ser Leu Val Ser Gln His Leu Ile Arg Pro Leu Met Gly Met Ser Leu
130 135 140
Ala Leu Gln Cys Gln Val Arg Glu Leu Ala Thr Leu Leu His Met Lys
145 150 155 160
Asp Leu Glu Ile Gln Asp Tyr Gln Glu Ser Gly Ala Thr Leu Ile Arg
165 170 175
Asp Arg Leu Lys Thr Glu Pro Phe Glu Glu Asn Ser Phe Leu Glu Gln
180 185 190
Phe Met Ile Glu Lys Leu Pro Glu Ala Cys Ser Ile Gly Asp Gly Lys
195 200 205
Pro Phe Val Met Asn Leu Gln Asp Leu Tyr Met Ala Val Thr Thr Gln
210 215 220
Glu Val Gln Val Gly Gln Lys His Gln Gly Ala Gly Asp Pro His Thr
225 230 235 240
Ser Asn Ser Ala Ser Leu Gln Gly Ile Asp Ser Gln Cys Val Asn Gln
245 250 255
Pro Glu Gln Leu Val Ser Ser Ala Pro Thr Leu Ser Ala Pro Glu Lys
260 265 270
Glu Ser Thr Gly Thr Ser Gly Pro Leu Gln Arg Pro Gln Leu Ser Lys
275 280 285
Val Lys Arg Lys Asn Pro Arg Gly Leu Phe Ser
290 295

<210> 6175
<211> 349
<212> DNA
<213> Homo sapiens

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120

aaaactgttc agtttggtgg aactgtgaca gaagtcttgc tgaagtacaa aaagggtgaa
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acaaatgact ttgagttgtt gaagaaccag ctgttagatc cagacataaa gagattgcct
240
tggttgaata gaagtcaaac agtagtggaa gagtatttgg cttttcttgg taatcttgta
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349

<210> 6176
<211> 90
<212> PRT
<213> Homo sapiens

<400> 6176
Met Arg Ala Leu Glu Asn Asp Phe Phe Asn Ser Pro Pro Arg Lys Thr
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Val Gln Phe Gly Gly Thr Val Thr Glu Val Leu Leu Lys Tyr Lys Lys
20 25 30
Gly Glu Thr Asn Asp Phe Glu Leu Leu Lys Asn Gln Leu Leu Asp Pro
35 40 45
Asp Ile Lys Arg Leu Pro Trp Leu Asn Arg Ser Gln Thr Val Val Glu
50 55 60
Glu Tyr Leu Ala Phe Leu Gly Asn Leu Val Ser Ala Gln Thr Val Phe
65 70 75 80
Leu Arg Pro Cys Leu Ser Met Ile Ala Ser
85 90

<210> 6177
<211> 1536
<212> DNA
<213> Homo sapiens

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360
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600

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720
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780
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1200
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1380
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1536

<210> 6178
<211> 310
<212> PRT
<213> Homo sapiens

<400> 6178
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Ser Gly Gly Phe Gln Val Lys Leu Tyr Asp Ile Glu Gln Gln Gln Ile
20 25 30
Arg Asn Ala Leu Glu Asn Ile Arg Lys Glu Met Lys Leu Leu Glu Gln
35 40 45
Ala Gly Ser Leu Lys Gly Ser Leu Ser Val Glu Glu Gln Leu Ser Leu
50 55 60
Ile Ser Gly Cys Pro Asn Ile Gln Glu Ala Val Glu Gly Ala Met His
65 70 75 80
Ile Gln Glu Cys Val Pro Glu Asp Leu Glu Leu Lys Lys Lys Ile Phe
85 90 95
Ala Gln Leu Asp Ser Ile Ile Asp Asp Arg Val Ile Leu Ser Ser Ser
100 105 110
Thr Ser Cys Leu Met Pro Ser Lys Leu Phe Ala Gly Leu Val His Val

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        115                 120                 125
Lys Gln Cys Ile Val Ala His Pro Val Asn Pro Pro Tyr Tyr Ile Pro
    130                 135                 140
Leu Val Glu Leu Val Pro His Pro Glu Thr Ala Pro Thr Thr Val Asp
145                 150                 155                 160
Arg Thr His Ala Leu Met Lys Lys Ile Gly Xaa Val Pro His Ala Ser
                165                 170                 175
Pro Glu Gly Gly Gly Arg Leu Arg Ser Glu Pro Pro Ala Ile Cys Asn
            180                 185                 190
His Gln Arg Gly Leu Ala Ala Ser Gly Gly Arg Asn Xaa Cys Leu Leu
        195                 200                 205
Val Thr Trp Xaa Leu Val Met Ser Glu Gly Leu Gly Met Arg Tyr Ala
    210                 215                 220
Phe Ile Gly Pro Leu Glu Thr Met His Leu Asn Ala Glu Gly Met Leu
225                 230                 235                 240
Ser Tyr Cys Asp Arg Tyr Ser Glu Gly Ile Lys His Val Leu Gln Thr
                245                 250                 255
Phe Gly Pro Ile Pro Glu Phe Ser Arg Ala Thr Ala Glu Lys Val Asn
            260                 265                 270
Gln Asp Met Cys Met Lys Val Pro Asp Asp Pro Glu His Leu Ala Ala
        275                 280                 285
Arg Arg Gln Trp Arg Asp Glu Cys Leu Met Arg Leu Ala Lys Leu Lys
    290                 295                 300
Ser Gln Val Gln Pro Gln
305                 310
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<210> 6179
<211> 2940
<212> DNA
<213> Homo sapiens

<400> 6179

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120
aagccataca ggctgtgaag gtccagtcat tccaaatgaa gagatgcctg gacaaaaaca
180
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360
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420
tatgtcaagt catttcctca gtccaggaag gatattttga aagatttggt agaaatgtgc
480
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660
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840
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2280

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2520
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<210> 6180
<211> 751
<212> PRT
<213> Homo sapiens

<400> 6180
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Trp Arg Xaa Tyr Leu Thr Asp Glu Phe Ala Lys Gly Arg Lys Val Ala
35 40 45
Asp Leu Tyr Glu Leu Val Gln Tyr Ala Gly Asn Ile Ile Pro Arg Leu
50 55 60
Tyr Leu Leu Ile Thr Val Gly Val Val Tyr Val Lys Ser Phe Pro Gln
65 70 75 80
Ser Arg Lys Asp Ile Leu Lys Asp Leu Val Glu Met Cys Arg Gly Val
85 90 95
Gln His Pro Leu Arg Gly Leu Phe Leu Arg Asn Tyr Leu Leu Gln Cys
100 105 110
Thr Arg Asn Ile Leu Pro Asp Glu Gly Glu Pro Thr Asp Glu Glu Thr
115 120 125
Thr Gly Asp Ile Ser Asp Ser Met Asp Phe Val Leu Leu Asn Phe Ala
130 135 140
Glu Met Asn Lys Leu Trp Val Arg Met Gln His Gln Gly His Ser Arg
145 150 155 160
Asp Arg Glu Lys Arg Glu Arg Glu Arg Gln Glu Leu Arg Ile Leu Val
165 170 175
Gly Thr Asn Leu Val Arg Leu Ser Xaa Ser Trp Arg Cys Lys Cys Gly
180 185 190
Thr Leu Gln Gln Ile Val Leu Thr Gly Ile Leu Glu Gln Val Val Asn

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        195                 200                 205
Cys Arg Asp Ala Leu Ala Gln Glu Tyr Leu Met Glu Cys Ile Ile Gln
    210                 215                 220
Val Phe Pro Asp Glu Phe His Leu Gln Thr Leu Asn Pro Phe Leu Arg
225                 230                 235                 240
Ala Cys Ala Glu Leu His Gln Asn Val Asn Val Lys Asn Ile Ile Ile
                245                 250                 255
Ala Leu Ile Asp Arg Leu Ala Leu Phe Ala His Arg Glu Asp Gly Pro
            260                 265                 270
Gly Ile Pro Ala Asp Ile Lys Leu Phe Asp Ile Phe Ser Gln Gln Val
        275                 280                 285
Ala Thr Val Ile Gln Ser Arg Gln Asp Met Pro Ser Glu Asp Val Val
    290                 295                 300
Ser Leu Gln Val Ser Leu Ile Asn Leu Ala Met Lys Cys Tyr Pro Asp
305                 310                 315                 320
Arg Val Asp Tyr Val Asp Lys Val Leu Glu Thr Thr Val Glu Ile Phe
                325                 330                 335
Asn Lys Leu Asn Leu Glu His Ile Ala Thr Ser Ser Ala Val Ser Lys
            340                 345                 350
Glu Leu Thr Arg Leu Leu Lys Ile Pro Val Asp Thr Tyr Asn Asn Ile
        355                 360                 365
Leu Thr Val Leu Lys Leu Lys His Phe His Pro Leu Phe Glu Tyr Phe
    370                 375                 380
Asp Tyr Glu Ser Arg Lys Ser Met Ser Cys Tyr Val Leu Ser Asn Val
385                 390                 395                 400
Leu Asp Tyr Asn Thr Glu Ile Val Ser Gln Asp Gln Val Asp Ser Ile
                405                 410                 415
Met Asn Leu Val Ser Thr Leu Ile Gln Asp Gln Pro Asp Gln Pro Val
            420                 425                 430
Glu Asp Pro Asp Pro Glu Asp Phe Ala Asp Glu Gln Ser Leu Val Gly
        435                 440                 445
Arg Phe Ile His Leu Leu Arg Ser Glu Asp Pro Asp Gln Gln Tyr Leu
    450                 455                 460
Ile Leu Asn Thr Ala Arg Lys His Phe Gly Ala Gly Gly Asn Gln Arg
465                 470                 475                 480
Ile Arg Phe Thr Leu Pro Pro Leu Val Phe Ala Ala Tyr Gln Leu Ala
                485                 490                 495
Phe Arg Tyr Lys Glu Asn Ser Lys Trp Met Thr Asn Gly Lys Arg Asn
            500                 505                 510
Ala Arg Arg Phe Phe His Leu Pro Xaa Gln Thr Ile Ser Ala Leu Ile
        515                 520                 525
Lys Ala Glu Leu Ala Glu Leu Pro Leu Arg Leu Phe Leu Gln Gly Ala
    530                 535                 540
Leu Ala Ala Gly Glu Ile Gly Phe Glu Asn His Glu Thr Val Ala Tyr
545                 550                 555                 560
Glu Phe Met Ser Gln Ala Phe Ser Leu Tyr Glu Asp Glu Ile Ser Asp
                565                 570                 575
Ser Lys Ala Gln Leu Ala Ala Ile Thr Leu Ile Ile Gly Thr Phe Glu
            580                 585                 590
Arg Met Lys Cys Phe Ser Glu Glu Asn His Glu Pro Leu Arg Thr Gln
        595                 600                 605
Cys Ala Leu Ala Ala Ser Lys Leu Leu Lys Lys Pro Asp Gln Gly Arg
    610                 615                 620
Ala Glu His Leu Cys Thr Ser Leu Trp Ser Gly Arg Asn Thr Asp Lys
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625 630 635 640
Asn Gly Glu Glu Leu His Gly Gly Lys Arg Val Met Glu Cys Leu Lys
645 650 655
Lys Ala Leu Lys Ile Ala Asn Gln Cys Met Asp Pro Ser Leu Gln Val
660 665 670
Gln Leu Phe Ile Glu Ile Leu Asn Arg Tyr Ile Tyr Phe Tyr Glu Lys
675 680 685
Glu Asn Asp Ala Val Thr Ile Gln Val Leu Asn Gln Leu Ile Gln Lys
690 695 700
Ile Arg Glu Asp Leu Pro Asn Leu Glu Ser Ser Glu Glu Thr Glu Gln
705 710 715 720
Ile Asn Lys His Phe His Asn Thr Leu Glu His Leu Arg Leu Arg Arg
725 730 735
Glu Ser Pro Glu Ser Glu Gly Pro Ile Tyr Glu Gly Leu Ile Leu
740 745 750

<210> 6181
<211> 1135
<212> DNA
<213> Homo sapiens

<400> 6181
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180
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240
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420
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480
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720
ccatgctgga gtcggcgaga agggccgagg cggggcctgg gcagactgtg gtccggtcca
780
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900
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960

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1020
agtctgtctt ctgttgctac ttgttttttt cagtgctctg aaatagagta actaaatggt
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1135

<210> 6182
<211> 236
<212> PRT
<213> Homo sapiens

<400> 6182
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Glu Val Phe Phe Leu Pro Asp Leu Pro Thr Thr Pro Tyr Phe Ser Arg
        35   40   45
Asp Ala Gln Lys His Asp Val Glu Val Leu Glu Arg Asn Phe Gln Thr
    50   55   60
Ile Leu Cys Glu Phe Glu Thr Leu Tyr Lys Ala Phe Ser Asn Cys Ser
65   70   75   80
Leu Pro Gln Gly Trp Lys Met Asn Ser Thr Pro Ser Gly Glu Trp Phe
                85   90   95
Thr Phe Tyr Leu Val Asn Gln Gly Val Cys Val Pro Arg Asn Cys Arg
            100   105   110
Lys Cys Pro Arg Thr Tyr Arg Leu Leu Gly Ser Leu Arg Thr Cys Ile
        115   120   125
Gly Asn Asn Val Phe Gly Asn Ala Cys Ile Ser Val Leu Ser Pro Gly
    130   135   140
Thr Val Ile Thr Glu His Tyr Gly Pro Thr Asn Ile Arg Ile Arg Cys
145   150   155   160
His Leu Gly Leu Lys Thr Pro Asn Gly Cys Glu Leu Val Val Gly Gly
                165   170   175
Glu Pro Gln Cys Trp Ala Glu Gly Arg Cys Leu Leu Phe Asp Asp Ser
            180   185   190
Phe Leu His Ala Ala Phe His Glu Gly Ser Ala Glu Asp Gly Pro Arg
        195   200   205
Val Val Phe Met Val Asp Leu Trp His Pro Asn Val Ala Ala Ala Glu
    210   215   220
Arg Gln Ala Leu Asp Phe Ile Phe Ala Pro Gly Arg
225   230   235

<210> 6183
<211> 2530
<212> DNA
<213> Homo sapiens

<400> 6183
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120

aggttgtgtt gcgggggtcg ggtagctgta ggtcttagaa atggcatcaa aggtggcctt
180
ggcgaagttg cccagggtgg cagtgcagcc ccgggctgag gtgtagcagt catcgatacc
240
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300
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420
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720
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<210> 6184
<211> 308
<212> PRT
<213> Homo sapiens

<400> 6184

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Leu	Gly	Pro	Gly	Pro	Val	His	Gly	Arg	Asp	Pro	Gly	Pro	Gly	Gly	Pro
			20					25					30		
Gly	Met	Gly	Asn	Arg	Gly	Gly	Phe	Arg	Gly	Gly	Phe	Gly	Ser	Gly	Ile
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Ala	Arg	Gly	Gly	Lys	Ala	Glu	Asp	Lys	Glu	Trp	Met	Pro	Val	Thr	Lys
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Leu	Gly	Arg	Leu	Val	Lys	Asp	Met	Lys	Ile	Lys	Ser	Leu	Glu	Glu	Ile
				85					90					95	
Tyr	Leu	Phe	Ser	Leu	Pro	Ile	Lys	Glu	Ser	Glu	Ile	Ile	Asp	Phe	Phe
			100					105					110		
Leu	Gly	Ala	Ser	Leu	Lys	Asp	Glu	Val	Leu	Lys	Ile	Met	Pro	Val	Gln
		115					120					125			
Lys	Gln	Thr	Arg	Ala	Gly	Gln	Arg	Thr	Arg	Phe	Lys	Ala	Phe	Val	Ala
	130					135					140				
Ile	Gly	Asp	Tyr	Asn	Gly	His	Val	Gly	Leu	Gly	Val	Lys	Cys	Ser	Lys

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Ile Val Pro Val Arg Arg Gly Tyr Trp Gly Asn Lys Ile Gly Lys Pro
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His Thr Val Pro Cys Lys Val Thr Gly Arg Cys Gly Ser Val Leu Val
        195                 200                 205
Arg Leu Ile Pro Ala Pro Arg Gly Thr Gly Ile Val Ser Ala Pro Val
    210                 215                 220
Pro Lys Lys Leu Leu Met Met Ala Gly Ile Asp Asp Cys Tyr Thr Ser
225                 230                 235                 240
Ala Arg Gly Cys Thr Ala Thr Leu Gly Asn Phe Ala Lys Ala Thr Phe
                245                 250                 255
Asp Ala Ile Ser Lys Thr Tyr Ser Tyr Leu Thr Pro Asp Leu Trp Lys
            260                 265                 270
Glu Thr Val Phe Thr Lys Ser Pro Tyr Gln Glu Phe Thr Asp His Leu
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Val Lys Thr His Thr Arg Val Ser Val Gln Arg Thr Gln Ala Pro Ala
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<212> DNA
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<211> 133
<212> PRT
<213> Homo sapiens

<400> 6186
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35 40 45
Ala Gln Leu Ser His Cys Lys Ser Leu Gly His Phe Glu Asn Leu Gln
50 55 60
Lys Tyr Lys Ala Ala Lys Asn Pro Ser Pro Thr Thr Arg Pro Val Ser
65 70 75 80
Arg Arg Cys Ala Ile Asn Ala Arg Asn Ala Leu Thr Ala Leu Phe Thr
85 90 95
Ser Ser Gly Arg Pro Pro Ser Gln Pro Asn Thr Gln Asp Lys Thr Pro
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Ser Lys Val Thr Ala Arg Pro Ser Gln Pro Pro Leu Pro Arg Arg Ser
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Thr Arg Leu Lys Thr
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<211> 909
<212> DNA
<213> Homo sapiens

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180

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300
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420
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<210> 6188
<211> 227
<212> PRT
<213> Homo sapiens

<400> 6188
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Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
        35   40   45
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
    50   55   60
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
65   70   75   80
Phe Pro Gly Ala Val Tyr Gly Ala Thr Tyr Ile Leu Val Met Val Asp
                85   90   95
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
            100   105   110
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
        115   120   125
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
    130   135   140
Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
145   150   155   160
Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys

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                165                 170                 175
Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
            180                 185                 190
Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
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Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
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<212> DNA
<213> Homo sapiens

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<210> 6190
<211> 576
<212> PRT
<213> Homo sapiens

<400> 6190
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35 40 45
Asn Asn Leu Asn Val Glu Glu Asn Ser Ser Gly Asp Gln Arg Arg Ala
50 55 60
Pro Leu Ala Ala Gly Thr Trp Arg Ser Ala Pro Val Pro Val Thr Thr
65 70 75 80
Gln Asn Pro Pro Gly Ala Pro Pro Asn Val Leu Trp Gln Thr Pro Leu
85 90 95
Ala Trp Gln Asn Pro Ser Gly Trp Gln Asn Gln Thr Ala Arg Gln Thr
100 105 110
Pro Pro Ala Arg Gln Ser Pro Pro Ala Arg Gln Thr Pro Pro Ala Trp
115 120 125
Gln Thr Gln Asn Pro Val Ala Trp Gln Asn Pro Val Ile Trp Pro Asn
130 135 140
Pro Val Ile Trp Gln Asn Pro Val Ile Trp Pro Asn Pro Ile Val Trp
145 150 155 160
Pro Gly Pro Val Val Trp Pro Asn Pro Leu Ala Trp Gln Asn Pro Pro
165 170 175
Gly Trp Gln Thr Pro Pro Gly Trp Gln Thr Pro Pro Gly Trp Gln Gly
180 185 190
Pro Pro Asp Trp Gln Gly Pro Pro Asp Trp Pro Leu Pro Pro Asp Trp
195 200 205
Pro Leu Pro Pro Asp Trp Pro Leu Pro Thr Asp Trp Pro Leu Pro Pro
210 215 220
Asp Trp Ile Pro Ala Asp Trp Pro Ile Pro Pro Asp Trp Gln Asn Leu
225 230 235 240
Arg Pro Ser Pro Asn Leu Arg Pro Ser Pro Asn Ser Arg Ala Ser Gln
245 250 255
Asn Pro Gly Ala Ala Gln Pro Arg Asp Val Ala Leu Leu Gln Glu Arg
260 265 270
Ala Asn Lys Leu Val Lys Tyr Leu Met Leu Lys Asp Tyr Thr Lys Val
275 280 285
Pro Ile Lys Arg Ser Glu Met Leu Arg Asp Ile Ile Arg Glu Tyr Thr
290 295 300
Asp Val Tyr Pro Glu Ile Ile Glu Arg Ala Cys Phe Val Leu Glu Lys
305 310 315 320
Lys Phe Gly Ile Gln Leu Lys Glu Ile Asp Lys Glu Glu His Leu Tyr
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340 345 350
Lys Asp Thr Pro Lys Leu Gly Leu Leu Leu Val Ile Leu Gly Val Ile

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Leu Arg Lys Leu Leu Thr Tyr Glu Phe Val Lys Gln Lys Tyr Leu Asp
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Tyr Arg Arg Val Pro Asn Ser Asn Pro Pro Glu Tyr Glu Phe Leu Trp
            420                 425                 430
Gly Leu Arg Ser Tyr His Glu Thr Ser Lys Met Lys Val Leu Arg Phe
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Ile Ala Glu Val Gln Lys Arg Asp Pro Arg Asp Trp Thr Ala Gln Phe
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Met Glu Ala Ala Asp Glu Ala Leu Asp Ala Leu Asp Ala Ala Ala Ala
465                 470                 475                 480
Glu Ala Glu Ala Arg Ala Glu Ala Arg Thr Arg Met Gly Ile Gly Asp
                485                 490                 495
Glu Ala Val Ser Gly Pro Trp Ser Trp Asp Asp Ile Glu Phe Glu Leu
            500                 505                 510
Leu Thr Trp Asp Glu Glu Gly Asp Phe Gly Asp Pro Trp Ser Arg Ile
        515                 520                 525
Pro Phe Thr Phe Trp Ala Arg Tyr His Gln Asn Ala Arg Ser Arg Phe
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Pro Gln Thr Phe Ala Gly Pro Ile Ile Gly Pro Gly Gly Thr Ala Ser
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<210> 6191
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<212> DNA
<213> Homo sapiens

<400> 6191

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<210> 6192
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<212> PRT
<213> Homo sapiens

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Arg Leu Gly Val Leu Arg Gln Asp Trp Pro Asp Thr Asn Arg Leu Leu
50 55 60
Gly Ser Ala Asn Val Val Thr Glu Ala Leu Gln Arg Phe Thr Arg Ala
65 70 75 80
Ala Ala Asp Phe Ala Thr His Gly Lys Leu Gly Lys Leu Glu Phe Ala
85 90 95
Gln Asp Ala His Gly Gln Pro Asp Val Ser Ala Phe Asp Phe Thr Ser
100 105 110
Met Met Arg Ala Glu Ser Ser Ala Arg Val Gln Glu Lys His Gly Ala
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Arg Leu Leu Leu Gly Leu Val Gly Asp Cys Leu Val Glu Pro Phe Trp
130 135 140
Pro Leu Gly Thr Gly Val Ala Arg Gly Phe Leu Ala Ala Phe Asp Ala

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Glu Asn Met His Arg Asn Val Ala Gln Tyr Gly Leu Asp Pro Ala Thr
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Arg Tyr Pro Asn Leu Asn Leu Arg Ala Val Thr Pro Asn Gln Val Arg
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Asp Leu Tyr Asp Val Leu Ala Lys Glu Pro Val Gln Arg Asn Asn Asp
225                 230                 235                 240
Lys Thr Asp Thr Gly Met Pro Ala Thr Gly Ser Ala Gly Thr Gln Glu
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Glu Leu Leu Arg Trp Cys Gln Glu Gln Thr Ala Gly Tyr Pro Gly Val
            260                 265                 270
His Val Ser Asp Leu Ser Ser Ser Trp Ala Asp Gly Leu Ala Leu Cys
        275                 280                 285
Ala Leu Val Tyr Arg Leu Gln Pro Gly Leu Leu Glu Pro Ser Glu Leu
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Gln Gly Leu Gly Ala Leu Glu Ala Thr Ala Trp Ala Leu Lys Val Ala
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Glu Asn Glu Leu Gly Ile Thr Pro Val Val Ser Ala Gln Ala Val Val
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Ala Gly Ser Asp Pro Leu Gly Leu Ile Ala Tyr Leu Ser His Phe His
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Ser Ala Phe Lys Ser Met Ala His Ser Pro Gly Pro Val Ser Gln Ala
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Ser Pro Gly Thr Ser Ser Ala Val Leu Phe Leu Ser Lys Leu Gln Arg
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Ser Thr Glu Val Pro Pro Asp Pro Glu Pro Gly Val Pro Leu Thr Pro
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Pro Ser Gln His Gln Glu Ala Gly Ala Gly Asp Leu Cys Ala Leu Cys
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Gly Glu His Leu Tyr Val Leu Glu Arg Leu Cys Val Asn Gly His Phe
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465                 470                 475                 480
Pro Gly Gly Tyr Glu Gln His Pro Gly Asp Gly His Phe Tyr Cys Leu
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Gln His Leu Pro Gln Thr Asp His Lys Ala Glu Gly Ser Asp Arg Gly
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Pro Pro Pro Lys Pro Pro Arg Ser Cys Ser Ala Leu Ala Arg His Ala
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Trp Arg Arg Thr Leu Leu Arg Arg Ala Lys Glu Glu Glu Met Lys Arg
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Phe Cys Lys Ala Gln Thr Ile Gln Arg Arg Leu Asn Glu Ile Glu Ala
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Ala Leu Arg Glu Leu Glu Ala Glu Gly Val Lys Leu Glu Leu Ala Leu
    690                 695                 700
Arg Arg Gln Ser Ser Ser Pro Glu Gln Gln Lys Lys Leu Trp Val Gly
705                 710                 715                 720
Gln Leu Leu Gln Leu Val Asp Lys Lys Asn Ser Leu Val Ala Glu Glu
                725                 730                 735
Ala Glu Leu Met Ile Thr Val Gln Glu Leu Asn Leu Glu Glu Lys Gln
            740                 745                 750
Trp Gln Leu Asp Gln Glu Leu Arg Gly Tyr Met Asn Arg Glu Glu Asn
        755                 760                 765
Leu Lys Thr Ala Ala Asp Arg Gln Ala Glu Asp Gln Val Leu Arg Lys
    770                 775                 780
Leu Val Asp Leu Val Asn Gln Arg Asp Ala Leu Ile Arg Phe Gln Glu
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<210> 6193
<211> 2893
<212> DNA
<213> Homo sapiens

<400> 6193

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<211> 621
<212> PRT
<213> Homo sapiens

<400> 6194
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35 40 45
Ala Glu Val Val Gln Tyr Ala Lys Glu Val Val Asp Phe Ser Ser His
50 55 60
Tyr Gly Ser Glu Asn Ser Met Ser Tyr Thr Met Trp Asn Leu Ala Gly
65 70 75 80
Val Pro Asn Val Phe Pro Ser Ser Gly Asp Phe Thr Gln Thr Ala Val
85 90 95
Phe Arg Thr Tyr Gly Thr Trp Trp Asp Gln Cys Pro Ser Ala Ser Leu
100 105 110
Pro Phe Lys Arg Thr Pro Pro Asn Phe Gln Ser Gln Asp Tyr Val Glu
115 120 125
Leu Thr Phe Glu Gln Gln Val Tyr Pro Thr Ala Val His Val Leu Glu
130 135 140
Thr Tyr His Pro Gly Ala Val Ile Arg Ile Leu Ala Cys Ser Ala Asn
145 150 155 160
Pro Tyr Ser Pro Asn Pro Pro Ala Glu Val Arg Trp Glu Ile Leu Trp

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                165                 170                 175
Ser Glu Arg Pro Thr Lys Val Asn Ala Ser Gln Ala Arg Gln Phe Lys
            180                 185                 190
Pro Cys Ile Lys Gln Ile Asn Phe Pro Thr Asn Leu Ile Arg Leu Glu
        195                 200                 205
Val Asn Ser Ser Leu Leu Glu Tyr Tyr Thr Glu Leu Asp Ala Val Val
    210                 215                 220
Leu His Gly Val Lys Asp Lys Pro Val Leu Ser Leu Lys Thr Ser Leu
225                 230                 235                 240
Ile Asp Met Asn Asp Ile Glu Asp Asp Ala Tyr Ala Glu Lys Asp Gly
                245                 250                 255
Cys Gly Met Asp Ser Leu Asn Lys Lys Phe Ser Ser Ala Val Leu Gly
            260                 265                 270
Glu Gly Pro Asn Asn Gly Tyr Phe Asp Lys Leu Pro Tyr Glu Leu Ile
        275                 280                 285
Gln Leu Ile Leu Asn His Leu Thr Leu Pro Asp Leu Cys Arg Leu Ala
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Gln Thr Cys Lys Leu Leu Ser Gln His Cys Cys Asp Pro Leu Gln Tyr
305                 310                 315                 320
Ile His Leu Asn Leu Gln Pro Tyr Trp Ala Lys Leu Asp Asp Thr Ser
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Leu Glu Phe Leu Gln Ser Arg Cys Thr Leu Val Gln Trp Leu Asn Leu
            340                 345                 350
Ser Trp Thr Gly Asn Arg Gly Phe Ile Ser Val Ala Gly Phe Ser Arg
        355                 360                 365
Phe Leu Lys Val Cys Gly Ser Glu Leu Val Arg Leu Glu Leu Ser Cys
    370                 375                 380
Ser His Phe Leu Asn Glu Thr Cys Leu Glu Val Ile Ser Glu Met Cys
385                 390                 395                 400
Pro Asn Leu Gln Ala Leu Asn Leu Ser Ser Cys Asp Lys Leu Pro Pro
                405                 410                 415
Gln Ala Phe Asn His Ile Ala Lys Leu Cys Ser Leu Lys Arg Leu Val
            420                 425                 430
Leu Tyr Arg Thr Lys Val Glu Gln Thr Ala Leu Leu Ser Ile Leu Asn
        435                 440                 445
Phe Cys Ser Glu Leu Gln His Leu Ser Leu Gly Ser Cys Val Met Ile
    450                 455                 460
Glu Asp Tyr Asp Val Ile Ala Ser Met Ile Gly Ala Lys Cys Lys Lys
465                 470                 475                 480
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                485                 490                 495
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            500                 505                 510
Gly Trp Cys Pro Thr Leu Gln Ser Ser Thr Gly Cys Phe Thr Arg Leu
        515                 520                 525
Ala His Gln Leu Pro Asn Leu Gln Lys Leu Phe Leu Thr Ala Asn Arg
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Ser Val Cys Asp Thr Asp Ile Asp Glu Leu Ala Cys Asn Cys Thr Arg
545                 550                 555                 560
Leu Gln Gln Leu Asp Ile Leu Gly Thr Arg Met Val Ser Pro Ala Ser
                565                 570                 575
Leu Arg Lys Leu Leu Glu Ser Cys Lys Asp Leu Ser Leu Leu Asp Val
            580                 585                 590
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<210> 6195
<211> 518
<212> DNA
<213> Homo sapiens

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<210> 6196
<211> 117
<212> PRT
<213> Homo sapiens

<400> 6196
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Leu Leu Leu Ser Arg Thr Thr Arg Val Lys Pro His Pro Tyr Lys Tyr
35 40 45
Gln Val His Pro Asn Ser Ser Leu Ala Gln Lys Trp Cys Tyr Ile His
50 55 60
Trp Glu Gln Thr Cys Ile Pro Thr Pro Arg His Val Thr Thr Gly Thr
65 70 75 80
Ala Asn Glu Leu Cys Pro Gly Asn Ser Phe Thr Pro Ser Ser Cys Ser
85 90 95
Phe His Ser His Leu Leu Ser Thr Asn Tyr Ala Lys Asn Tyr Val Gln
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His Arg Thr Gly Trp
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<210> 6197
<211> 2841

<212> DNA
<213> Homo sapiens

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<210> 6198
<211> 124
<212> PRT
<213> Homo sapiens

<400> 6198
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Pro Gly Trp Gly Met Trp Gly Gln Glu Ala Ala Gln Ser Gly Arg Gln
    50                  55                  60
Arg Glu Lys Cys Val Gln Arg Ala Pro Ile Ser Gly Cys Asn Val Val
65                  70                  75                  80
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<210> 6199
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<212> DNA
<213> Homo sapiens

<400> 6199

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960
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1777

<210> 6200
<211> 164
<212> PRT
<213> Homo sapiens

<400> 6200
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Phe Trp Glu Glu Gly Ser Ala Pro Arg Pro Gln Glu Ser Arg Gln Arg
20 25 30
Pro Pro Lys Pro Asp Cys Gln Gln Lys Pro Ser Pro Ser Glu Gly Gln
35 40 45
Val Gly Val Pro Xaa Arg Ser Pro His Pro Gln Gly Gly Phe Thr His
50 55 60
Cys Pro Val Pro Gly Met Pro Gly Gly Arg Pro Leu Cys Cys Cys His
65 70 75 80
Cys Cys Gln His Cys Pro Ala Cys Glu Ala Arg Arg Ser Pro Cys Pro
85 90 95
Thr Arg Cys Cys Cys Ser Ser Asp Pro Cys Cys Glu Glu Trp Asp Ser
100 105 110
Trp Ser Lys Lys Leu Val Phe Leu Phe Cys Ile Asn Glu Lys Asn Pro
115 120 125
Gly Glu Ala Ala Thr Leu Pro Ser Gln Arg Asp Ala Leu Pro Cys Phe
130 135 140
Gly Val Leu Ser Pro Phe Pro Pro Leu Val Gln Gly Gln Pro Ser Arg

145 150 155 160
Ser Ser Trp Phe

<210> 6201
<211> 604
<212> DNA
<213> Homo sapiens

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120
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240
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300
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360
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420
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480
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600
gccg
604

<210> 6202
<211> 124
<212> PRT
<213> Homo sapiens

<400> 6202
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Pro Ser Asp Arg Met Arg Asp Arg Asn Ala Gln Gln Arg Ala Ile Gln
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Gly Gln Trp Thr Leu Gly Arg Gly Ala Glu Trp Ala Ala Leu Arg Arg
35 40 45
Ala Gly Leu Arg Gly Cys Arg Glu Glu Phe Gly Gly Lys Gly Gln Pro
50 55 60
Gln Ser Leu Ser Cys Ala Ser Trp Glu Arg Gly Met Thr Gly Arg His
65 70 75 80
Thr Asn Val Ser Gln Gly Arg Trp Ala Trp Gly His Arg Ala Pro Arg
85 90 95
Gly Gly Ser Gly Glu Gly Glu Pro Ala Glu Glu Arg Pro Gly Arg Ala
100 105 110
Gly Asp His Ala Gly Ala Gln Gly Glu Arg Gln Asp

115 120

<210> 6203
<211> 3462
<212> DNA
<213> Homo sapiens

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120
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240
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300
atcgacgatg gccaccgcct gtgcagcgac ctcatgaact gcctgcatga gcgggcgcgc
360
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420
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480
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540
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600
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660
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720
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780
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1980
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2040
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2160
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2280
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2340
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2400
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2460
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2580
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2880
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2940
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3000

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3300
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3360
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3462

<210> 6204
<211> 486
<212> PRT
<213> Homo sapiens

<400> 6204
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            20                  25                  30
Asp Gly His Arg Leu Cys Ser Asp Leu Met Asn Cys Leu His Glu Arg
        35                  40                  45
Ala Arg Ile Glu Lys Ala Tyr Ala Gln Gln Leu Thr Glu Trp Ala Arg
    50                  55                  60
Arg Trp Arg Gln Leu Val Glu Lys Gly Pro Gln Tyr Gly Thr Val Glu
65                  70                  75                  80
Lys Ala Trp Met Ala Phe Met Ser Glu Ala Glu Arg Val Ser Glu Leu
                85                  90                  95
His Leu Glu Val Lys Ala Ser Leu Met Asn Asp Asp Phe Glu Lys Ile
            100                 105                 110
Lys Asn Trp Gln Lys Glu Ala Phe His Lys Gln Met Met Gly Gly Phe
        115                 120                 125
Lys Glu Thr Lys Glu Ala Glu Asp Gly Phe Arg Lys Ala Gln Lys Pro
    130                 135                 140
Trp Ala Lys Lys Leu Lys Glu Val Glu Ala Ala Lys Lys Ala His His
145                 150                 155                 160
Ala Ala Cys Lys Glu Glu Lys Leu Ala Ile Ser Arg Glu Ala Asn Ser
                165                 170                 175
Lys Ala Asp Pro Ser Leu Asn Pro Glu Gln Leu Lys Lys Leu Gln Asp
            180                 185                 190
Lys Ile Glu Lys Cys Lys Gln Asp Val Leu Lys Thr Lys Glu Lys Tyr
        195                 200                 205
Glu Lys Ser Leu Lys Glu Leu Asp Gln Gly Thr Pro Gln Tyr Met Glu
    210                 215                 220
Asn Met Glu Gln Val Phe Glu Gln Cys Gln Gln Phe Glu Glu Lys Arg
225                 230                 235                 240
Leu Arg Phe Phe Arg Glu Val Leu Leu Glu Val Gln Lys His Leu Asp
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                245                 250                 255
Leu Ser Asn Val Ala Gly Tyr Lys Ala Ile Tyr His Asp Leu Glu Gln
            260                 265                 270
Ser Ile Arg Ala Ala Asp Ala Val Glu Asp Leu Arg Trp Phe Arg Ala
        275                 280                 285
Asn His Gly Pro Gly Met Ala Met Asn Trp Pro Gln Phe Glu Glu Trp
    290                 295                 300
Ser Ala Asp Leu Asn Arg Thr Leu Ser Arg Arg Glu Lys Lys Lys Ala
305                 310                 315                 320
Thr Asp Gly Val Thr Leu Thr Gly Ile Asn Gln Thr Gly Asp Gln Ser
                325                 330                 335
Leu Pro Ser Lys Pro Ser Ser Thr Leu Asn Val Pro Ser Asn Pro Ala
            340                 345                 350
Gln Ser Ala Gln Ser Gln Ser Ser Tyr Asn Pro Phe Glu Asp Glu Asp
        355                 360                 365
Asp Thr Gly Ser Thr Val Ser Glu Lys Asp Asp Thr Lys Ala Lys Asn
    370                 375                 380
Val Ser Ser Tyr Glu Lys Thr Gln Ser Tyr Pro Thr Asp Trp Ser Asp
385                 390                 395                 400
Asp Glu Ser Asn Asn Pro Phe Ser Ser Thr Asp Ala Asn Gly Asp Ser
                405                 410                 415
Asn Pro Phe Asp Asp Asp Ala Thr Ser Gly Thr Glu Val Arg Val Arg
            420                 425                 430
Ala Leu Tyr Asp Tyr Glu Gly Gln Glu His Asp Glu Leu Ser Phe Lys
        435                 440                 445
Ala Gly Asp Glu Leu Thr Lys Met Glu Asp Glu Asp Glu Gln Gly Trp
    450                 455                 460
Cys Lys Gly Arg Leu Asp Asn Gly Gln Val Gly Leu Tyr Pro Ala Asn
465                 470                 475                 480
Tyr Val Glu Ala Ile Gln
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<210> 6205
<211> 926
<212> DNA
<213> Homo sapiens

<400> 6205
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120
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240
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420
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480

tggacggtgg ccccctcagc ctggcagcct ctggacagag aggaaggaag gattggaaaa
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600
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780
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926

<210> 6206
<211> 92
<212> PRT
<213> Homo sapiens

<400> 6206
Xaa Arg Leu Pro Xaa Arg Ile Gly Pro Ser Phe Asn Gly Gly Cys Gly
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Glu Met Glu Lys Trp Gly Glu Asp Phe Gly Glu Ser Arg Gly Arg Ala
            20   25   30
Arg Glu Gly Lys Glu Phe Ala Asp Ser Gln Lys Leu Leu Phe Met Glu
        35   40   45
Thr Ser Ala Lys Leu Asn His Gln Val Ser Glu Val Phe Asn Thr Val
    50   55   60
Ala Gln Glu Leu Leu Gln Arg Ser Asp Glu Glu Gly Gln Ala Leu Xaa
65   70   75   80
Gly Glu Asp Thr Pro Cys Leu Gly His Gly Gln Leu
                85   90

<210> 6207
<211> 1384
<212> DNA
<213> Homo sapiens

<400> 6207
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120
ggaaacaccg ggaatccctg cagctgagcc tgtctctcac gggaccggga agctggagag
180
agccccaacc ctgcccgctg gggccgagct ccctgctcct gcagcagtcc cgtgccccac
240
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300
acctacttcg gggcccactt tgctgtcatc cgccgagcgt ccctggagaa gaacccgtac
360

caggctgtgc accaatgggc cttctctgcg gggttgagcc tggtgggcct cctgactctg
420
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480
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1380
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<210> 6208
<211> 290
<212> PRT
<213> Homo sapiens

<400> 6208
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Ala Ser Leu Glu Lys Asn Pro Tyr Gln Ala Val His Gln Trp Ala Phe
20 25 30
Ser Ala Gly Leu Ser Leu Val Gly Leu Leu Thr Leu Gly Ala Val Leu
35 40 45
Ser Ala Ala Ala Thr Val Arg Glu Ala Gln Gly Leu Met Ala Gly Gly
50 55 60
Phe Leu Cys Phe Ser Leu Ala Phe Xaa Ala Gln Val Gln Val Val Phe
65 70 75 80
Trp Arg Leu His Ser Pro Thr Gln Val Glu Asp Ala Met Leu Asp Thr

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                85                  90                  95
Tyr Asp Leu Val Tyr Glu Gln Ala Met Lys Gly Thr Ser His Val Arg
            100                 105                 110
Arg Gln Glu Leu Ala Ala Ile Gln Asp Val Phe Leu Cys Cys Gly Lys
        115                 120                 125
Lys Ser Pro Phe Ser Arg Leu Gly Ser Thr Glu Ala Asp Leu Cys Gln
    130                 135                 140
Gly Glu Glu Ala Ala Arg Glu Asp Cys Leu Gln Gly Ile Arg Ser Phe
145                 150                 155                 160
Leu Arg Thr His Gln Gln Val Ala Ser Ser Leu Thr Ser Ile Gly Leu
                165                 170                 175
Ala Leu Thr Val Ser Ala Leu Leu Phe Ser Ser Phe Leu Trp Phe Ala
            180                 185                 190
Ile Arg Cys Gly Cys Ser Leu Asp Arg Lys Gly Lys Tyr Thr Leu Thr
        195                 200                 205
Pro Arg Ala Cys Gly Arg Gln Pro Gln Glu Pro Ser Leu Leu Arg Cys
    210                 215                 220
Ser Gln Gly Gly Pro Thr His Cys Leu His Ser Glu Ala Val Ala Ile
225                 230                 235                 240
Gly Pro Arg Gly Cys Ser Gly Ser Leu Arg Trp Leu Gln Glu Ser Asp
                245                 250                 255
Ala Ala Pro Leu Pro Leu Ser Cys His Leu Ala Ala His Arg Ala Leu
            260                 265                 270
Gln Gly Arg Ser Arg Gly Gly Leu Ser Gly Cys Pro Glu Arg Gly Leu
        275                 280                 285
Ser Asp
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<210> 6209
<211> 2269
<212> DNA
<213> Homo sapiens

<400> 6209
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120
gcggggaaac cctggatatt tcactctgaa gtggtttctt gaaagaaaac tcaactgact
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240
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300
gaccaagaaa tgggctgatc aagtccttgg ccactcactg ttaagagcca ggatttacag
360
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420
aaatttcaca gccagcagcg ctttcagtcc acaacagatt tctcagagga aacatggata
480
ttttgcgtag gcagaaacag tgaggagtac aaagcaaagc tataaatacc accaatggtt
540
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600

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720
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780
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900
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2269

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<211> 165
<212> PRT
<213> Homo sapiens

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Ser Pro Ser Leu Arg Gly Thr His Leu Leu Phe Leu Pro Gln Ala Asp
35 40 45
Val Val Asp Glu Ala Ile Asp Ser Leu Ala Arg Thr Lys Gly Val Met
50 55 60
Lys Pro Pro Cys Ser Glu Gly Ser Pro Trp Arg Cys Pro His Phe Thr
65 70 75 80
Cys Trp Val Leu Gln Ala Arg Lys Pro Gly Ser Gly Gly Thr Arg Glu
85 90 95
Arg Gln Ala Cys Val Trp Thr Ser Ala Gly Ala Ala Ala Leu Arg Leu
100 105 110
Ala Arg Glu Arg Gln Arg Trp Val Phe Arg Phe His Ala Tyr Val Trp
115 120 125
Ala His Ser Gln His Gly Arg Val Ser Ala Val Leu Val Leu Thr Leu
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Trp Pro Gln Pro Ser
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<210> 6211
<211> 2163
<212> DNA
<213> Homo sapiens

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2163

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<213> Homo sapiens

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35 40 45
Ala Phe Glu Gly Ser Tyr Leu Glu Asp Thr Gln Met Tyr Gly Asn Ile
50 55 60
Ile Arg Gly Trp Xaa Ser Val Ser Asp Gln Pro Xaa Lys Asn Ser Asn
65 70 75 80
Ser Lys Asn Asp Arg Arg Asn Arg Lys Phe Lys Glu Ala Glu Arg Leu
85 90 95
Phe Ser Lys Ser Ser Val Thr Ser Ala Ala Ala Val Ser Ala Leu Ala
100 105 110
Gly Val Gln Asp Gln Leu Ile Glu Lys Arg Glu Pro Gly Ser Gly Thr
115 120 125
Glu Ser Asp Thr Ser Pro Asp Phe His Asn Gln Glu Asn Glu Pro Ser
130 135 140
Gln Glu Asp Pro Glu Asp Leu Asp Gly Ser Val Gln Gly Val Lys Pro
145 150 155 160
Gln Lys Ala Ala Ser Ser Thr Ser Ser Gly Ser His His Ser Ser His
165 170 175
Lys Lys Arg Lys Asn Lys Asn Arg His Ser Pro Ser Gly Met Phe Asp
180 185 190
Tyr Asp Phe Glu Ile Asp Leu Lys Leu Asn Lys Lys Pro Arg Ala Asp
195 200 205
Tyr

<210> 6213
<211> 1160
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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Glu Pro Ala Xaa Cys Leu His Gln Thr Gly Pro His Leu Gly Pro Pro
35 40 45
Pro Pro Pro Pro Pro Thr Pro Pro Pro Thr Cys Ile Ala Gln Ile Gln
50 55 60
Val Met Met Glu Gln Ile Arg Pro Trp His Ser Arg Met Lys Arg Arg
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Lys Gly Val Met Glu Gly Gln Ser Leu Glu Pro Ala Ala Ser Ser Gly
85 90 95
Pro Leu Pro Thr Asp
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<210> 6215
<211> 651
<212> DNA
<213> Homo sapiens

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<210> 6216
<211> 87
<212> PRT
<213> Homo sapiens

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Glu Ala Val Ala Ile Gly Pro Arg Gly Cys Ser Gly Ser Leu Arg Trp
        35   40   45
Leu Gln Glu Ser Asp Ala Ala Pro Leu Pro Leu Ser Cys His Leu Ala
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Ala His Arg Ala Leu Gln Gly Arg Ser Arg Gly Gly Leu Ser Gly Cys
65   70   75   80
Pro Glu Arg Gly Leu Ser Asp
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<210> 6217
<211> 2955
<212> DNA
<213> Homo sapiens

<400> 6217

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<211> 133
<212> PRT
<213> Homo sapiens

<400> 6218
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Ala Gln Leu Ser His Cys Lys Ser Leu Gly His Phe Glu Asn Leu Gln
    50                  55                  60
Lys Tyr Lys Ala Ala Lys Asn Pro Ser Pro Thr Thr Arg Pro Val Ser
65                  70                  75                  80
Arg Arg Cys Ala Ile Asn Ala Arg Asn Ala Leu Thr Ala Leu Phe Thr
                85                  90                  95
Ser Ser Gly Arg Pro Pro Ser Gln Pro Asn Thr Gln Asp Lys Thr Pro
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<210> 6219
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<212> DNA
<213> Homo sapiens

<400> 6219

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2280
cggggcactc ccttggagcc cctggcgngc tgcccgccca gctttctggc agggcctgct
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2400
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2460
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2495

<210> 6220
<211> 179
<212> PRT
<213> Homo sapiens

<400> 6220
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20 25 30
Ser Ala Gly Asn Thr Ala Arg Cys Pro Gln Thr Pro Gly Ser Ala Gln
35 40 45
Gly Gly Pro Ala Pro Ser Pro Gln Xaa Tyr Ile His Asp Ser Pro Ser
50 55 60
Cys Trp Pro Trp Thr Lys Ala Gly Ser Ser Xaa Cys Pro Val Arg Ser
65 70 75 80
Pro Tyr Ser Pro Pro Ala Ala Arg Pro Gly Pro Gly Xaa Pro Leu Trp
85 90 95
Cys Gln Arg Val Ser Gln Asn Pro Gly Pro Ser Pro Ser Xaa Gly Pro
100 105 110
Leu Pro Ser Pro Arg Pro Val Cys Trp Asp Gly Ala Ser Thr Leu Arg
115 120 125
Leu Val Lys Ala Glu Leu Asn Ser Ser Asn Glu Ser Ala Gly Trp Ala
130 135 140
Trp Gly Asp Gly Glu Gln Ala Pro Pro Arg Ala Ser Ser Glu Gly Gly
145 150 155 160
Asp Ala Ala Pro Phe Leu Pro Ala Ala Gln Thr Ala Pro Thr Gly Ser
165 170 175
Gly Ala Gly

<210> 6221
<211> 1487
<212> DNA
<213> Homo sapiens

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180
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240
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300
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360
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420
tctgaagatt tagagtcata taagatatca gtggtaatgc aggaatcagc tgagaaactt
480

tcagaaaagt tacataagtg taaagaattt gtggacagtt gcaggcttac tttccctact
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600
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840
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960
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1020
atccatagtg gagaaaaacg ccataaatgc cttgagtgtg gaaaagcctt tggccggcat
1080
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1140
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1200
gaggaattct ttcaatgtgg agaatgtggg aaaacgttta gttttaagag gaatcttttt
1260
cgacatcagg tcattcacac tggaagccaa ctctaccaat gtgtcatatg tggaaaatct
1320
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1380
tgatgttaat tggaaagcag tcattggaga actagaactt ataaacctct acttcaagtg
1440
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1487

<210> 6222
<211> 330
<212> PRT
<213> Homo sapiens

<400> 6222
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Tyr Lys Ile Ser Val Val Met Gln Glu Ser Ala Glu Lys Leu Ser Glu
20 25 30
Lys Leu His Lys Cys Lys Glu Phe Val Asp Ser Cys Arg Leu Thr Phe
35 40 45
Pro Thr Ser Gly Asp Glu Tyr Ser Arg Gly Phe Leu Gln Asn Leu Asn
50 55 60
Leu Ile Gln Asp Gln Asn Ala Gln Thr Arg Trp Lys Gln Gly Arg Tyr
65 70 75 80
Asp Glu Asp Gly Lys Pro Phe Asn Gln Arg Ser Leu Leu Leu Gly His
85 90 95
Glu Arg Ile Leu Thr Arg Ala Lys Ser Tyr Glu Cys Ser Glu Cys Gly

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            100                 105                 110
Lys Val Ile Arg Arg Lys Ala Trp Phe Asp Gln His Gln Arg Ile His
        115                 120                 125
Phe Leu Glu Asn Pro Phe Glu Cys Lys Val Cys Gly Gln Ala Phe Arg
    130                 135                 140
Gln Arg Ser Ala Leu Thr Val His Lys Gln Cys His Leu Gln Asn Lys
145                 150                 155                 160
Pro Tyr Arg Cys His Asp Cys Gly Lys Cys Phe Arg Gln Leu Ala Tyr
                165                 170                 175
Leu Val Glu His Lys Arg Ile His Thr Lys Glu Lys Pro Tyr Lys Cys
            180                 185                 190
Ser Lys Cys Glu Lys Thr Phe Ser Gln Asn Ser Thr Leu Ile Arg His
        195                 200                 205
Gln Val Ile His Ser Gly Glu Lys Arg His Lys Cys Leu Glu Cys Gly
    210                 215                 220
Lys Ala Phe Gly Arg His Ser Thr Leu Leu Cys His Gln Gln Ile His
225                 230                 235                 240
Ser Lys Pro Asn Thr His Lys Cys Ser Glu Cys Gly Gln Ser Phe Gly
                245                 250                 255
Arg Asn Val Asp Leu Ile Gln His Gln Arg Ile His Thr Lys Glu Glu
            260                 265                 270
Phe Phe Gln Cys Gly Glu Cys Gly Lys Thr Phe Ser Phe Lys Arg Asn
        275                 280                 285
Leu Phe Arg His Gln Val Ile His Thr Gly Ser Gln Leu Tyr Gln Cys
    290                 295                 300
Val Ile Cys Gly Lys Ser Phe Lys Trp His Thr Ser Phe Ile Lys His
305                 310                 315                 320
Gln Gly Thr His Lys Gly Gln Ile Ser Thr
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<210> 6223
<211> 944
<212> DNA
<213> Homo sapiens

<400> 6223
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120
ccccaacttc ccatcccccc actcctctcc attccctctc ttgcttgtgc gcataagcaa
180
gtcccactca ttgcaactgt aaccaatacc aagcatgaga acaggaacta gctccaccct
240
ctaacccccа ctccagctgc agacgccacg gagtttgtgc aggggcgcag cgctccagcc
300
atggcgcgtt cgctcgtcca cgacaccgtg ttctactgcc tgagtgtata ccaggtaaaa
360
ataagcccca cacctcagct gggggcagca tcaagcgcag aaggccatgt tggccaagga
420
gctccaggcc tcatgggtaa tatgaaccct gagggcggtg tgaaccacga gaacggcatg
480
aaccgcgatg gcggcatgat ccccgagggc ggcggtggaa accaggagcc tcggcagcag
540

ccgcagcccc cgccggagga gccggcccag gcggccatgg agggtccgca gcccgagaac
600
atgcagccac gaactcggcg cacgaagttc acgctgttgc aggtggagga gctggaaagt
660
gttttccgac acactcaata ccctgatgtg cccacaagaa gggaacttgc cgaaaactta
720
ggtgtgactg aagacaaagt gcgggtcagt acacttgaaa aagcaatttg agaggacagc
780
cattctaaaa cctgcttcag ggcattgaag gctttgaagg ctttgtcctg aacgttctaa
840
agttgttgtt tttattattg tctttttttat gttgacaaat aagttttgaa gtttgggttc
900
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944

<210> 6224
<211> 156
<212> PRT
<213> Homo sapiens

<400> 6224
Met Ala Arg Ser Leu Val His Asp Thr Val Phe Tyr Cys Leu Ser Val
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Tyr Gln Val Lys Ile Ser Pro Thr Pro Gln Leu Gly Ala Ala Ser Ser
            20   25   30
Ala Glu Gly His Val Gly Gln Gly Ala Pro Gly Leu Met Gly Asn Met
        35   40   45
Asn Pro Glu Gly Gly Val Asn His Glu Asn Gly Met Asn Arg Asp Gly
    50   55   60
Gly Met Ile Pro Glu Gly Gly Gly Gly Asn Gln Glu Pro Arg Gln Gln
65   70   75   80
Pro Gln Pro Pro Pro Glu Glu Pro Ala Gln Ala Ala Met Glu Gly Pro
                85   90   95
Gln Pro Glu Asn Met Gln Pro Arg Thr Arg Arg Thr Lys Phe Thr Leu
            100   105   110
Leu Gln Val Glu Glu Leu Glu Ser Val Phe Arg His Thr Gln Tyr Pro
        115   120   125
Asp Val Pro Thr Arg Arg Glu Leu Ala Glu Asn Leu Gly Val Thr Glu
    130   135   140
Asp Lys Val Arg Val Ser Thr Leu Glu Lys Ala Ile
145   150   155

<210> 6225
<211> 3851
<212> DNA
<213> Homo sapiens

<400> 6225
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120
gaacagaaga cagatgcctt ggggaaacag tctgtgaaca gaggattcac taaggacaag
180

actctcagtt caatctttaa cattgagatg gtaaaagaaa aaactgcaga agaaataaaa
240
cagatttggc agcaatattt tgcagcaaaa gatacagtct acgcagttat tcctgcagaa
300
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420
gcacttataa atattcagac ccgaggggaa gctgcagcca gccagctgat tttatatcac
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720
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780
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1080
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1260
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1380
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1440
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1800

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aaaaaaaaaa a
3851

<210> 6226
<211> 246
<212> PRT
<213> Homo sapiens

<400> 6226
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            20   25   30
Gln Gly Asp Phe Ile Lys Cys Val Glu Gln Lys Thr Asp Ala Leu Gly
        35   40   45
Lys Gln Ser Val Asn Arg Gly Phe Thr Lys Asp Lys Thr Leu Ser Ser
    50   55   60
Ile Phe Asn Ile Glu Met Val Lys Glu Lys Thr Ala Glu Glu Ile Lys
65   70   75   80
Gln Ile Trp Gln Gln Tyr Phe Ala Ala Lys Asp Thr Val Tyr Ala Val
                85   90   95
Ile Pro Ala Glu Lys Phe Asp Leu Ile Trp Asn Arg Ala Gln Ser Cys
            100   105   110
Pro Thr Phe Leu Cys Ala Leu Pro Arg Arg Glu Gly Tyr Glu Phe Phe
        115   120   125
Val Gly Gln Trp Thr Gly Thr Glu Leu His Phe Thr Ala Leu Ile Asn
    130   135   140
Ile Gln Thr Arg Gly Glu Ala Ala Ala Ser Gln Leu Ile Leu Tyr His
145   150   155   160
Tyr Pro Glu Leu Lys Glu Glu Lys Gly Ile Val Leu Met Thr Ala Glu
                165   170   175
Met Asp Ser Thr Phe Leu Asn Val Ala Glu Ala Gln Cys Ile Ala Asn
            180   185   190
Gln Val Gln Leu Phe Tyr Ala Thr Asp Arg Lys Glu Thr Tyr Gly Leu
        195   200   205
Val Glu Thr Phe Asn Leu Arg Pro Asn Glu Phe Lys Tyr Met Ser Val
    210   215   220
Ile Ala Glu Leu Glu Gln Ser Gly Leu Gly Ala Glu Leu Lys Cys Ala
225   230   235   240
Gln Asn Gln Asn Lys Thr

245

<210> 6227
<211> 830
<212> DNA
<213> Homo sapiens

<400> 6227
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120
ccagggagag tcgctgcaga atgggaggta cagaatcgta tcccttctgg aactatatta
180
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240
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360
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420
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720
cggcctgtga aaaagacgat ggaaattccg aaagattcct tgcagaagta cctcaaagac
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<210> 6228
<211> 271
<212> PRT
<213> Homo sapiens

<400> 6228
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20 25 30
Ile Pro Ser Pro Gly Arg Val Ala Ala Glu Trp Glu Val Gln Asn Arg
35 40 45
Ile Pro Ser Gly Thr Ile Leu Lys Ala Leu Met Glu Gly Gly Glu Asn
50 55 60
Gly Pro Trp Met Arg Phe Met Arg Ala Glu Ile Thr Ala Glu Gly Phe
65 70 75 80
Leu Arg Glu Phe Gly Arg Leu Cys Ser Glu Met Leu Lys Thr Ser Val

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                85                  90                  95
Pro Val Asp Ser Phe Phe Ser Leu Leu Thr Ser Glu Arg Val Ala Lys
            100                 105                 110
Gln Phe Pro Val Met Thr Glu Ala Ile Thr Gln Ile Arg Ala Lys Gly
        115                 120                 125
Leu Gln Thr Ala Val Leu Ser Asn Asn Phe Tyr Leu Pro Asn Gln Lys
    130                 135                 140
Ser Phe Leu Pro Leu Asp Arg Lys Gln Phe Asp Val Ile Val Glu Ser
145                 150                 155                 160
Cys Met Glu Gly Ile Cys Lys Pro Asp Pro Arg Ile Tyr Lys Leu Cys
                165                 170                 175
Leu Glu Gln Leu Gly Leu Gln Pro Ser Glu Ser Ile Phe Leu Asp Asp
            180                 185                 190
Leu Gly Thr Asn Leu Lys Glu Ala Ala Arg Leu Gly Ile His Thr Ile
        195                 200                 205
Lys Val Asn Asp Pro Glu Thr Ala Val Lys Glu Leu Glu Ala Leu Leu
    210                 215                 220
Gly Phe Thr Leu Arg Val Gly Val Pro Asn Thr Arg Pro Val Lys Lys
225                 230                 235                 240
Thr Met Glu Ile Pro Lys Asp Ser Leu Gln Lys Tyr Leu Lys Asp Leu
                245                 250                 255
Leu Gly Ile Gln Thr Thr Gly Pro Leu Glu Leu Leu Gln Phe Asp
            260                 265                 270
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<210> 6229
<211> 3105
<212> DNA
<213> Homo sapiens

<400> 6229

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180
gacgagatca tcaccagcct cgtgtctgcc ttagactcca tgtgctcagc gctgtccaaa
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300
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360
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420
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480
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540
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720
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2100
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2280
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2340

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3105

<210> 6230
<211> 944
<212> PRT
<213> Homo sapiens

<400> 6230
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Ser Leu Val Ser Ala Leu Asp Ser Met Cys Ser Ala Leu Ser Lys Leu
35 40 45
Asn Ala Glu Val Ala Cys Val Ala Val His Asp Glu Ser Ala Phe Val
50 55 60
Val Gly Thr Glu Lys Gly Arg Met Phe Leu Asn Ala Arg Lys Glu Leu
65 70 75 80
Gln Ser Asp Phe Leu Arg Phe Cys Arg Gly Pro Pro Trp Lys Asp Pro
85 90 95
Glu Ala Glu His Pro Lys Lys Val Gln Arg Gly Glu Gly Gly Gly Arg
100 105 110
Ser Leu Pro Arg Ser Ser Leu Glu His Gly Ser Asp Val Tyr Leu Leu
115 120 125
Arg Lys Met Val Glu Glu Val Phe Asp Val Leu Tyr Ser Glu Ala Leu
130 135 140
Gly Arg Ala Ser Val Val Pro Leu Pro Tyr Glu Arg Leu Leu Arg Glu
145 150 155 160
Pro Gly Leu Leu Ala Val Gln Gly Leu Pro Glu Gly Leu Ala Phe Arg

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                165                 170                 175
Arg Pro Ala Glu Tyr Asp Pro Lys Ala Leu Met Ala Ile Leu Glu His
            180                 185                 190
Ser His Arg Ile Arg Phe Lys Leu Lys Arg Pro Leu Glu Asp Gly Gly
        195                 200                 205
Arg Asp Ser Lys Ala Leu Val Glu Leu Asn Gly Val Ser Leu Ile Pro
    210                 215                 220
Lys Gly Ser Arg Asp Cys Gly Leu His Gly Gln Ala Pro Lys Val Pro
225                 230                 235                 240
Pro Gln Asp Leu Pro Pro Thr Ala Thr Ser Ser Ser Met Ala Ser Phe
                245                 250                 255
Leu Tyr Ser Thr Ala Leu Pro Asn His Ala Ile Arg Glu Leu Lys Gln
            260                 265                 270
Glu Ala Pro Ser Cys Pro Leu Ala Pro Ser Asp Leu Gly Leu Ser Arg
        275                 280                 285
Pro Met Pro Glu Pro Lys Ala Thr Gly Ala Gln Asp Phe Ser Asp Cys
    290                 295                 300
Cys Gly Gln Lys Pro Thr Gly Pro Gly Gly Pro Leu Ile Gln Asn Val
305                 310                 315                 320
His Ala Ser Lys Arg Ile Leu Phe Ser Ile Val His Asp Lys Ser Glu
                325                 330                 335
Lys Trp Asp Ala Phe Ile Lys Glu Thr Glu Asp Ile Asn Thr Leu Arg
            340                 345                 350
Glu Cys Val Gln Ile Leu Phe Asn Ser Arg Tyr Ala Glu Ala Leu Gly
        355                 360                 365
Leu Gly Asn Met Val Pro Val Pro Tyr Arg Lys Ile Ala Cys Asp Pro
    370                 375                 380
Glu Ala Val Glu Ile Val Gly Ile Pro Asp Lys Ile Pro Phe Lys Arg
385                 390                 395                 400
Pro Cys Thr Tyr Gly Val Pro Lys Leu Lys Arg Ile Leu Glu Glu Arg
                405                 410                 415
His Ser Ile His Phe Ile Ile Lys Arg Met Phe Asp Glu Arg Ile Phe
            420                 425                 430
Thr Gly Asn Lys Phe Thr Lys Asp Thr Thr Lys Leu Glu Pro Ala Ser
        435                 440                 445
Pro Pro Glu Asp Thr Ser Ala Glu Val Ser Arg Ala Thr Val Leu Asp
    450                 455                 460
Leu Ala Gly Asn Ala Arg Ser Asp Lys Gly Ser Met Ser Glu Asp Cys
465                 470                 475                 480
Gly Pro Gly Thr Ser Gly Glu Leu Gly Gly Leu Arg Pro Ile Lys Ile
                485                 490                 495
Glu Pro Glu Asp Leu Asp Ile Ile Gln Val Thr Val Pro Asp Pro Ser
            500                 505                 510
Pro Thr Ser Glu Glu Met Thr Asp Ser Met Pro Gly His Leu Pro Ser
        515                 520                 525
Glu Asp Ser Gly Tyr Gly Met Glu Met Leu Thr Asp Lys Gly Leu Ser
    530                 535                 540
Glu Asp Ala Arg Pro Glu Glu Arg Pro Val Glu Asp Ser His Gly Asp
545                 550                 555                 560
Val Ile Arg Pro Leu Arg Lys Gln Val Glu Leu Leu Phe Asn Thr Arg
                565                 570                 575
Tyr Ala Lys Ala Ile Gly Ile Ser Glu Pro Val Lys Val Pro Tyr Ser
            580                 585                 590
Lys Phe Leu Met His Pro Glu Glu Leu Phe Val Val Gly Leu Pro Glu
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595 600 605
Gly Ile Ser Leu Arg Arg Pro Asn Cys Phe Gly Ile Ala Lys Leu Arg
610 615 620
Lys Ile Leu Glu Ala Ser Asn Ser Ile Gln Phe Val Ile Lys Arg Pro
625 630 635 640
Glu Leu Leu Thr Glu Gly Val Lys Glu Pro Ile Val Asp Ser Gln Glu
645 650 655
Arg Asp Ser Gly Asp Pro Leu Val Asp Glu Ser Leu Lys Arg Gln Gly
660 665 670
Phe Gln Glu Asn Tyr Asp Ala Arg Leu Ser Arg Ile Asp Ile Ala Asn
675 680 685
Thr Leu Arg Glu Gln Val Gln Asp Leu Phe Asn Lys Lys Tyr Gly Glu
690 695 700
Ala Leu Gly Ile Lys Tyr Pro Val Gln Val Pro Tyr Lys Arg Ile Lys
705 710 715 720
Ser Asn Pro Gly Ser Val Ile Ile Glu Gly Leu Pro Pro Gly Ile Pro
725 730 735
Phe Arg Lys Pro Cys Thr Phe Gly Ser Gln Asn Leu Glu Arg Ile Leu
740 745 750
Ala Val Ala Asp Lys Ile Lys Phe Thr Val Thr Arg Pro Phe Gln Gly
755 760 765
Leu Ile Pro Lys Pro Asp Glu Asp Asp Ala Asn Arg Leu Gly Glu Lys
770 775 780
Val Ile Leu Arg Glu Gln Val Lys Glu Leu Phe Asn Glu Lys Tyr Gly
785 790 795 800
Glu Ala Leu Gly Leu Asn Arg Pro Val Leu Val Pro Tyr Lys Leu Ile
805 810 815
Arg Asp Ser Pro Asp Ala Val Glu Val Thr Gly Leu Pro Asp Asp Ile
820 825 830
Pro Phe Arg Asn Pro Asn Thr Tyr Asp Ile His Arg Leu Glu Lys Ile
835 840 845
Leu Lys Ala Arg Glu His Val Arg Met Val Ile Ile Asn Gln Leu Gln
850 855 860
Pro Phe Ala Glu Ile Cys Asn Asp Ala Lys Val Pro Ala Lys Asp Ser
865 870 875 880
Ser Ile Pro Lys Arg Lys Arg Lys Arg Val Ser Glu Gly Asn Ser Val
885 890 895
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asn Pro Asp Ser
900 905 910
Val Ala Ser Ala Asn Gln Ile Ser Leu Val Gln Trp Pro Met Tyr Met
915 920 925
Val Asp Tyr Ala Gly Leu Asn Val Gln Leu Pro Gly Pro Leu Asn Tyr
930 935 940

<210> 6231
<211> 471
<212> DNA
<213> Homo sapiens

<400> 6231
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taccaatgac aggccctact cacagccact gcactccagc ttgggcgaca gaacgaggcc
120

ttgccttttt aaaaaaaaaa aaaaggctca aaaaaagagt atgctgggcc aaaaatctgg
180
cccctcaggc ctcctgacct ggaggagaaa aaggggcccg aagccccccg ttgcccccat
240
ctccatatgg aatggcacaa cccctcgagg ggaaccccccc cctaaccata gttctaaaaa
300
ggggacaaaa aaatgggcgc tggatttttc aacgccggaa acccaattcc cacccccctgg
360
ccggccgttc ttagggattc caacttggga cccaacctgg gcgtattctg ggccttactt
420
gtttcttgtg ggaattggta ttccgttccc atttcccccа ccttccaacc c
471

<210> 6232
<211> 138
<212> PRT
<213> Homo sapiens

<400> 6232
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Gly Asp Arg Thr Arg Pro Cys Leu Phe Lys Lys Lys Lys Lys Ala Gln
            20   25   30
Lys Lys Ser Met Leu Gly Gln Lys Ser Gly Pro Ser Gly Leu Leu Thr
        35   40   45
Trp Arg Arg Lys Arg Gly Pro Lys Pro Pro Val Ala Pro Ile Ser Ile
    50   55   60
Trp Asn Gly Thr Thr Pro Arg Gly Glu Pro Pro Pro Asn His Ser Ser
65   70   75   80
Lys Lys Gly Thr Lys Lys Trp Ala Leu Asp Phe Ser Thr Pro Glu Thr
                85   90   95
Gln Phe Pro Pro Pro Gly Arg Pro Phe Leu Gly Ile Pro Thr Trp Asp
            100   105   110
Pro Thr Trp Ala Tyr Ser Gly Pro Tyr Leu Phe Leu Val Gly Ile Gly
        115   120   125
Ile Pro Phe Pro Phe Pro Pro Pro Ser Asn
    130   135

<210> 6233
<211> 894
<212> DNA
<213> Homo sapiens

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120
agggaaggag acgattggag tcaactcaat gtgctcaaaa aaagaagagt cggggacctc
180
ctagccagtt acattccaga ggatgaggcg ctgatgcttc gggatggacg ctttgcttgt
240
gccatctgcc cccatcgacc ggtactggac accctggcca tgctgactgc ccaccgtgca
300

ggcaagaaac atctgtccag cttgcagctt ttctatggca agaagcagcc gggaaaggaa
360
agaaagcaga atccaaaaca tcagaatgaa ttgagaaggg aagaaaccaa agctgaggct
420
cctctgctaa ctcagacacg acttatcacc cagagtgctc tgcacagagc tccccactat
480
aacagttgct gccgccggaa gtacagacca gaagcccctg gtccctctgt ctccctttcc
540
cctatgccac cctcagaggt caaactccaa agtgggaaga tcagtaggga acctgaacct
600
gcggctggcc cacaggccga ggagtcagca actgtctcag cccctgcacc catgagcccc
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acaagaagac gagccctgga ccattatctc acccttcgaa gctctggatg gatcccagat
720
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780
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840
tgctgagaac ttaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa
894

<210> 6234
<211> 230
<212> PRT
<213> Homo sapiens

<400> 6234
Met Ser Phe Lys Arg Glu Gly Asp Asp Trp Ser Gln Leu Asn Val Leu
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Lys Lys Arg Arg Val Gly Asp Leu Leu Ala Ser Tyr Ile Pro Glu Asp
20 25 30
Glu Ala Leu Met Leu Arg Asp Gly Arg Phe Ala Cys Ala Ile Cys Pro
35 40 45
His Arg Pro Val Leu Asp Thr Leu Ala Met Leu Thr Ala His Arg Ala
50 55 60
Gly Lys Lys His Leu Ser Ser Leu Gln Leu Phe Tyr Gly Lys Lys Gln
65 70 75 80
Pro Gly Lys Glu Arg Lys Gln Asn Pro Lys His Gln Asn Glu Leu Arg
85 90 95
Arg Glu Glu Thr Lys Ala Glu Ala Pro Leu Leu Thr Gln Thr Arg Leu
100 105 110
Ile Thr Gln Ser Ala Leu His Arg Ala Pro His Tyr Asn Ser Cys Cys
115 120 125
Arg Arg Lys Tyr Arg Pro Glu Ala Pro Gly Pro Ser Val Ser Leu Ser
130 135 140
Pro Met Pro Pro Ser Glu Val Lys Leu Gln Ser Gly Lys Ile Ser Arg
145 150 155 160
Glu Pro Glu Pro Ala Ala Gly Pro Gln Ala Glu Glu Ser Ala Thr Val
165 170 175
Ser Ala Pro Ala Pro Met Ser Pro Thr Arg Arg Arg Ala Leu Asp His
180 185 190
Tyr Leu Thr Leu Arg Ser Ser Gly Trp Ile Pro Asp Gly Arg Gly Arg
195 200 205
Trp Val Lys Asp Glu Asn Val Glu Phe Asp Ser Asp Glu Glu Glu Pro

210 215 220
Pro Asp Leu Pro Leu Asp
225 230

<210> 6235
<211> 3427
<212> DNA
<213> Homo sapiens

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120
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180
gatgtgaagc ctggcgcgga agagcagacc caggtggcca aagctgcctt caagcgcttc
240
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300
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1020
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gccggcc
3427

<210> 6236
<211> 820
<212> PRT
<213> Homo sapiens

<400> 6236
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            20   25   30
Pro Glu Gly Gly Leu Pro Gly Pro Trp Ala Leu His Arg Gly Arg Lys
        35   40   45
Lys Ala Thr Gly Ser Pro Val Ser Ile Phe Val Tyr Asp Val Lys Pro
    50   55   60
Gly Ala Glu Glu Gln Thr Gln Val Ala Lys Ala Ala Phe Lys Arg Phe
65   70   75   80
Lys Thr Leu Arg His Pro Asn Ile Leu Ala Tyr Ile Asp Gly Leu Glu
                85   90   95
Thr Glu Lys Cys Leu His Val Val Thr Glu Ala Val Thr Pro Leu Gly
            100   105   110
Ile Tyr Leu Lys Ala Arg Val Glu Ala Gly Gly Leu Lys Glu Leu Glu
        115   120   125
Ile Ser Trp Gly Leu His Gln Ile Val Lys Ala Leu Ser Phe Leu Val
    130   135   140
Asn Asp Cys Ser Leu Ile His Asn Asn Val Cys Met Ala Ala Val Phe
145   150   155   160
Val Asp Arg Ala Gly Glu Trp Lys Leu Gly Gly Leu Asp Tyr Met Tyr
                165   170   175
Ser Ala Gln Gly Asn Gly Gly Gly Pro Pro Arg Lys Gly Ile Pro Glu
            180   185   190
Leu Glu Gln Tyr Asp Pro Pro Glu Leu Ala Asp Ser Ser Gly Arg Val
        195   200   205
Val Arg Glu Lys Trp Ser Ala Asp Met Trp Arg Leu Gly Cys Leu Ile
    210   215   220
Trp Glu Val Phe Asn Gly Pro Leu Pro Arg Ala Ala Ala Leu Arg Asn

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225                 230                 235                 240
Pro Gly Lys Ile Pro Lys Thr Leu Val Pro His Tyr Cys Glu Leu Val
                245                 250                 255
Gly Ala Asn Pro Lys Val Arg Pro Asn Pro Ala Arg Phe Leu Gln Asn
            260                 265                 270
Cys Arg Ala Pro Gly Gly Phe Met Ser Asn Arg Phe Val Glu Thr Asn
        275                 280                 285
Leu Phe Leu Glu Glu Ile Gln Ile Lys Glu Pro Ala Glu Lys Gln Lys
    290                 295                 300
Phe Phe Gln Glu Leu Ser Lys Ser Leu Asp Ala Phe Pro Glu Asp Phe
305                 310                 315                 320
Cys Arg His Lys Val Leu Pro Gln Leu Leu Thr Ala Phe Glu Phe Gly
                325                 330                 335
Asn Ala Gly Ala Val Val Leu Thr Pro Leu Phe Lys Val Gly Lys Phe
            340                 345                 350
Leu Ser Ala Glu Glu Tyr Gln Gln Lys Ile Ile Pro Val Val Val Lys
        355                 360                 365
Met Phe Ser Ser Thr Asp Arg Ala Met Arg Ile Arg Leu Leu Gln Gln
    370                 375                 380
Met Glu Gln Phe Ile Gln Tyr Leu Asp Glu Pro Thr Val Asn Thr Gln
385                 390                 395                 400
Ile Phe Pro His Val Val His Gly Phe Leu Asp Thr Asn Pro Ala Ile
                405                 410                 415
Arg Glu Gln Thr Val Lys Ser Met Leu Leu Leu Ala Pro Lys Leu Asn
            420                 425                 430
Glu Ala Asn Leu Asn Val Glu Leu Met Lys His Phe Ala Arg Leu Gln
        435                 440                 445
Ala Lys Asp Glu Gln Gly Pro Ile Arg Cys Asn Thr Thr Val Cys Leu
    450                 455                 460
Gly Lys Ile Gly Ser Tyr Leu Ser Ala Ser Thr Arg His Arg Val Leu
465                 470                 475                 480
Thr Ser Ala Phe Ser Arg Ala Thr Arg Asp Pro Phe Ala Pro Ser Arg
                485                 490                 495
Val Ala Gly Val Leu Gly Phe Ala Ala Thr His Asn Leu Tyr Ser Met
            500                 505                 510
Asn Asp Cys Ala Gln Lys Ile Leu Pro Val Leu Cys Gly Leu Thr Val
        515                 520                 525
Asp Pro Glu Lys Ser Val Arg Asp Gln Ala Phe Lys Ala Ile Arg Ser
    530                 535                 540
Phe Leu Ser Lys Leu Glu Ser Val Ser Glu Asp Pro Thr Gln Leu Glu
545                 550                 555                 560
Glu Val Glu Lys Asp Val His Ala Ala Ser Ser Pro Gly Met Gly Gly
                565                 570                 575
Ala Ala Ala Ser Trp Ala Gly Trp Ala Val Thr Gly Val Ser Ser Leu
            580                 585                 590
Thr Ser Lys Leu Ile Arg Ser His Pro Thr Thr Ala Pro Thr Glu Thr
        595                 600                 605
Asn Ile Pro Gln Arg Pro Thr Pro Glu Gly Val Pro Ala Pro Ala Pro
    610                 615                 620
Thr Pro Val Pro Ala Thr Pro Thr Thr Ser Gly His Trp Glu Thr Gln
625                 630                 635                 640
Glu Glu Asp Lys Asp Thr Ala Glu Asp Ser Ser Thr Ala Asp Arg Trp
                645                 650                 655
Asp Asp Glu Asp Trp Gly Ser Leu Glu Gln Glu Ala Glu Ser Val Leu
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660 665 670
Ala Gln Gln Asp Asp Trp Ser Thr Gly Gly Gln Val Ser Arg Ala Ser
675 680 685
Gln Val Ser Asn Ser Asp His Lys Ser Ser Lys Ser Pro Glu Ser Asp
690 695 700
Trp Ser Ser Trp Glu Ala Glu Gly Ser Trp Glu Gln Gly Trp Gln Glu
705 710 715 720
Pro Ser Ser Gln Glu Pro Pro Pro Asp Gly Thr Arg Leu Ala Ser Glu
725 730 735
Tyr Asn Trp Gly Gly Pro Glu Ser Ser Asp Lys Gly Asp Pro Phe Ala
740 745 750
Thr Leu Ser Ala Arg Pro Ser Thr Gln Pro Arg Pro Asp Ser Trp Gly
755 760 765
Glu Asp Asn Trp Glu Gly Leu Glu Thr Asp Ser Arg Gln Val Lys Ala
770 775 780
Glu Leu Ala Arg Lys Lys Arg Glu Glu Arg Arg Arg Glu Met Glu Ala
785 790 795 800
Lys Arg Ala Glu Arg Lys Val Ala Lys Gly Pro Met Lys Leu Gly Ala
805 810 815
Arg Lys Leu Asp
820

<210> 6237
<211> 494
<212> DNA
<213> Homo sapiens

<400> 6237
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tggcctttgt gagcctcagc ctgcagttct tccacctgat cccggtgtcg actcctaaga
180
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240
tgacagaccc cgtttatgaa gctcttttgt actgcaacat ccccagcgtg gccgagcgca
300
gcatggaagg tcatgccccg catcatttta agctggtctc agtgcatgtg ttcattcgcc
360
acggagacag gtacccactg tatgtcattc ccaaaacaaa gcgaccagaa attgactgca
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ctctggtggc taacaggaaa ccgtatcacc caaaactgga agctttcatt agtcacatgt
480
tgagaggatc cgga
494

<210> 6238
<211> 141
<212> PRT
<213> Homo sapiens

<400> 6238
Met Leu Phe Arg Asn Arg Phe Leu Leu Leu Leu Ala Leu Ala Ala Leu

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            20                  25                  30
Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys Arg Ile Met
        35                  40                  45
Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro Val Tyr Glu Ala
    50                  55                  60
Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu Arg Ser Met Glu Gly
65                  70                  75                  80
His Ala Pro His His Phe Lys Leu Val Ser Val His Val Phe Ile Arg
                85                  90                  95
His Gly Asp Arg Tyr Pro Leu Tyr Val Ile Pro Lys Thr Lys Arg Pro
            100                 105                 110
Glu Ile Asp Cys Thr Leu Val Ala Asn Arg Lys Pro Tyr His Pro Lys
        115                 120                 125
Leu Glu Ala Phe Ile Ser His Met Leu Arg Gly Ser Gly
    130                 135                 140
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<210> 6239
<211> 911
<212> DNA
<213> Homo sapiens

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gcctgtgtcc tcaccaccgc cgcggtgcag ctggagctcc tcagcccctt tcaactctac
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ttcaacccgc accttgtgtt ccggaagttc caggtctgga ggctcgtcac caacttcctc
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900

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911

<210> 6240
<211> 235
<212> PRT
<213> Homo sapiens

<400> 6240
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Leu Glu Leu Leu Ser Pro Phe Gln Leu Tyr Phe Asn Pro His Leu Val
35 40 45
Phe Arg Lys Phe Gln Val Trp Arg Leu Val Thr Asn Phe Leu Phe Phe
50 55 60
Gly Pro Leu Gly Phe Ser Phe Phe Phe Asn Met Leu Phe Val Phe Arg
65 70 75 80
Tyr Cys Arg Met Leu Glu Glu Gly Ser Phe Arg Gly Arg Thr Ala Asp
85 90 95
Phe Val Phe Met Phe Leu Phe Gly Gly Val Leu Met Thr Leu Leu Gly
100 105 110
Leu Leu Gly Ser Leu Phe Phe Leu Gly Gln Ala Leu Met Ala Met Leu
115 120 125
Val Tyr Val Trp Ser Arg Arg Ser Pro Arg Val Arg Val Asn Phe Phe
130 135 140
Gly Leu Leu Thr Phe Gln Ala Pro Phe Leu Pro Trp Ala Leu Met Gly
145 150 155 160
Phe Ser Leu Leu Leu Gly Asn Ser Ile Leu Val Asp Leu Leu Gly Ile
165 170 175
Ala Val Gly His Ile Tyr Tyr Phe Leu Glu Asp Val Phe Pro Asn Gln
180 185 190
Pro Gly Gly Lys Arg Leu Leu Gln Thr Pro Gly Phe Leu Lys Leu Leu
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Gln Pro Gly Pro His Leu Pro Pro Pro Gln Gln
225 230 235

<210> 6241
<211> 1515
<212> DNA
<213> Homo sapiens

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240

ctgggcgagc agcgggacgc ctgggagacg ttccagaagc ggcagaagct tacctccgag
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360
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420
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540
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600
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720
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<210> 6242
<211> 245
<212> PRT
<213> Homo sapiens

<400> 6242
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        35                  40                  45
Gly Glu Pro Pro Pro Pro Glu Leu Ala Leu Leu Pro Pro Pro Pro Pro
    50                  55                  60
Pro Pro Pro Thr Pro Ala Thr Pro Thr Ser Ser Ala Ser Asn Leu Asp
65                  70                  75                  80
Leu Gly Glu Gln Arg Asp Ala Trp Glu Thr Phe Gln Lys Arg Gln Lys
                85                  90                  95
Leu Thr Ser Glu Gly Ala Ala Lys Leu Leu Leu Asp Thr Phe Glu Tyr
            100                 105                 110
Gln Gly Leu Val Lys His Thr Gly Gly Cys His Cys Gly Ala Val Arg
        115                 120                 125
Phe Glu Val Trp Ala Ser Ala Asp Leu His Ile Phe Asp Cys Asn Cys
    130                 135                 140
Ser Ile Cys Lys Lys Lys Gln Asn Arg His Phe Ile Val Pro Ala Ser
145                 150                 155                 160
Arg Phe Lys Leu Leu Lys Gly Ala Glu His Ile Thr Thr Tyr Thr Phe
                165                 170                 175
Asn Thr His Lys Ala Gln His Thr Phe Cys Lys Arg Cys Gly Val Gln
            180                 185                 190
Ser Phe Tyr Thr Pro Arg Ser Asn Pro Gly Gly Phe Gly Ile Ala Pro
        195                 200                 205
His Cys Leu Asp Glu Gly Thr Val Arg Ser Met Val Thr Glu Glu Phe
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Asn Gly Ser Asp Trp Glu Lys Ala Met Lys Glu His Lys Thr Ile Lys
225                 230                 235                 240
Asn Met Ser Lys Glu
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<210> 6243
<211> 326
<212> DNA
<213> Homo sapiens

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326

<210> 6244
<211> 104
<212> PRT
<213> Homo sapiens

<400> 6244
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Gly Phe Leu Leu Trp Lys Ala Ile Pro Ser Phe Ala Ser Ser Thr Leu
35 40 45
Arg Met Ser Ser Ser Leu His Ser Leu Trp Phe Val Pro Leu Val Ser
50 55 60
Glu Glu Glu Val Leu Ile Ile Leu Ser Gly Ser Glu Cys Ser Thr Cys
65 70 75 80
Pro Tyr Val Leu Ser Tyr Pro Thr Ser Ser Leu Thr Leu Phe His Gln
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Phe Leu Ser Phe Ser Pro Trp Arg
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<210> 6245
<211> 6609
<212> DNA
<213> Homo sapiens

<400> 6245
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120
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6609

<210> 6246
<211> 1286
<212> PRT
<213> Homo sapiens

<400> 6246

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			20					25					30		
Ile	Leu	Ser	Glu	Gln	Lys	Ala	Met	Ile	Asn	Ala	Met	Asp	Ser	Lys	Ile
		35					40					45			
Arg	Ser	Leu	Glu	Gln	Arg	Ile	Val	Glu	Leu	Ser	Glu	Ala	Asn	Lys	Leu
	50					55					60				
Ala	Ala	Asn	Ser	Ser	Leu	Phe	Thr	Gln	Arg	Asn	Met	Lys	Ala	Gln	Glu
65					70					75					80
Glu	Met	Ile	Ser	Glu	Leu	Arg	Gln	Gln	Lys	Phe	Tyr	Leu	Glu	Thr	Gln
				85					90					95	
Ala	Gly	Lys	Leu	Glu	Ala	Gln	Asn	Arg	Lys	Leu	Glu	Glu	Gln	Leu	Glu
			100					105					110		
Lys	Ile	Ser	His	Gln	Asp	His	Ser	Asp	Lys	Asn	Arg	Leu	Leu	Glu	Leu
		115					120					125			
Glu	Thr	Arg	Leu	Arg	Glu	Val	Ser	Leu	Glu	His	Glu	Glu	Gln	Lys	Leu
	130					135					140				
Glu	Leu	Lys	Arg	Gln	Leu	Thr	Glu	Leu	Gln	Leu	Ser	Leu	Gln	Glu	Arg

```
145                 150                 155                 160
Glu Ser Gln Leu Thr Ala Leu Gln Ala Ala Arg Ala Ala Leu Glu Ser
                165                 170                 175
Gln Leu Arg Gln Ala Lys Thr Glu Leu Glu Glu Thr Thr Ala Glu Ala
            180                 185                 190
Glu Glu Glu Ile Gln Ala Leu Thr Ala His Arg Asp Glu Ile Gln Arg
        195                 200                 205
Lys Phe Asp Ala Leu Arg Asn Ser Cys Thr Val Ile Thr Asp Leu Glu
    210                 215                 220
Glu Gln Leu Asn Gln Leu Thr Glu Asp Asn Ala Glu Leu Asn Asn Gln
225                 230                 235                 240
Asn Phe Tyr Leu Ser Lys Gln Leu Asp Glu Ala Ser Gly Ala Asn Asp
                245                 250                 255
Glu Ile Val Gln Leu Arg Ser Glu Val Asp His Leu Arg Arg Glu Ile
            260                 265                 270
Thr Glu Arg Glu Met Gln Leu Thr Ser Gln Lys Gln Thr Met Glu Ala
        275                 280                 285
Leu Lys Thr Thr Cys Thr Met Leu Glu Glu Gln Val Met Asp Leu Glu
    290                 295                 300
Ala Leu Asn Asp Glu Leu Leu Glu Lys Glu Arg Gln Trp Glu Ala Trp
305                 310                 315                 320
Arg Ser Val Leu Gly Asp Glu Lys Ser Gln Phe Glu Cys Arg Val Arg
                325                 330                 335
Glu Leu Gln Arg Met Leu Asp Thr Glu Lys Gln Ser Arg Ala Arg Ala
            340                 345                 350
Asp Gln Arg Ile Thr Glu Ser Arg Gln Val Val Glu Leu Ala Val Lys
        355                 360                 365
Glu His Lys Ala Glu Ile Leu Ala Leu Gln Gln Ala Leu Lys Glu Gln
    370                 375                 380
Lys Leu Lys Ala Glu Ser Leu Ser Asp Lys Leu Asn Asp Leu Glu Lys
385                 390                 395                 400
Lys His Ala Met Leu Glu Met Asn Ala Arg Ser Leu Gln Gln Lys Leu
                405                 410                 415
Glu Thr Glu Arg Glu Leu Lys Gln Arg Leu Leu Glu Glu Gln Ala Lys
            420                 425                 430
Leu Gln Gln Gln Met Asp Leu Gln Lys Asn His Ile Phe Arg Leu Thr
        435                 440                 445
Gln Gly Leu Gln Glu Ala Leu Asp Arg Ala Asp Leu Leu Lys Thr Glu
    450                 455                 460
Arg Ser Asp Leu Glu Tyr Gln Leu Glu Asn Ile Gln Val Leu Tyr Ser
465                 470                 475                 480
His Glu Lys Val Lys Met Glu Gly Thr Ile Ser Gln Gln Thr Lys Leu
                485                 490                 495
Ile Asp Phe Leu Gln Ala Lys Met Asp Gln Pro Ala Lys Lys Lys Lys
            500                 505                 510
Val Pro Leu Gln Tyr Asn Glu Leu Lys Leu Ala Leu Glu Lys Glu Lys
        515                 520                 525
Ala Arg Cys Ala Glu Leu Glu Glu Ala Leu Gln Lys Thr Arg Ile Glu
    530                 535                 540
Leu Arg Ser Ala Arg Glu Glu Ala Ala His Arg Lys Ala Thr Asp His
545                 550                 555                 560
Pro His Pro Ser Thr Pro Ala Thr Ala Arg Gln Gln Ile Ala Met Ser
                565                 570                 575
Ala Ile Val Arg Ser Pro Glu His Gln Pro Ser Ala Met Ser Leu Leu
```

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            580                 585                 590
Ala Pro Pro Ser Ser Arg Arg Lys Glu Ser Ser Thr Pro Glu Glu Phe
        595                 600                 605
Ser Arg Arg Leu Lys Glu Arg Met His His Asn Ile Pro His Arg Phe
    610                 615                 620
Asn Val Gly Leu Asn Met Arg Ala Thr Lys Cys Ala Val Cys Leu Asp
625                 630                 635                 640
Thr Val His Phe Gly Arg Gln Ala Ser Lys Cys Leu Glu Cys Gln Val
                645                 650                 655
Met Cys His Pro Lys Cys Ser Thr Cys Leu Pro Ala Thr Cys Gly Leu
            660                 665                 670
Pro Ala Glu Tyr Ala Thr His Phe Thr Glu Ala Phe Cys Arg Asp Lys
        675                 680                 685
Met Asn Ser Pro Gly Leu Gln Thr Lys Glu Pro Ser Ser Ser Leu His
    690                 695                 700
Leu Glu Gly Trp Met Lys Val Pro Arg Asn Asn Lys Arg Gly Gln Gln
705                 710                 715                 720
Gly Trp Asp Arg Lys Tyr Ile Val Leu Glu Gly Ser Lys Val Leu Ile
                725                 730                 735
Tyr Asp Asn Glu Ala Arg Glu Ala Gly Gln Arg Pro Val Glu Glu Phe
            740                 745                 750
Glu Leu Cys Leu Pro Asp Gly Asp Val Ser Ile His Gly Ala Val Gly
        755                 760                 765
Ala Ser Glu Leu Ala Asn Thr Ala Lys Ala Asp Val Pro Tyr Ile Leu
    770                 775                 780
Lys Met Glu Ser His Pro His Thr Thr Cys Trp Pro Gly Arg Thr Leu
785                 790                 795                 800
Tyr Leu Leu Ala Pro Ser Phe Pro Asp Lys Gln Arg Trp Val Thr Ala
                805                 810                 815
Leu Glu Ser Val Val Ala Gly Gly Arg Val Ser Arg Glu Lys Ala Glu
            820                 825                 830
Ala Asp Ala Lys Leu Leu Gly Asn Ser Leu Leu Lys Leu Glu Gly Asp
        835                 840                 845
Asp Arg Leu Asp Met Asn Cys Thr Leu Pro Phe Ser Asp Gln Val Val
    850                 855                 860
Leu Val Gly Thr Glu Glu Gly Leu Tyr Ala Leu Asn Val Leu Lys Asn
865                 870                 875                 880
Ser Leu Thr His Val Pro Gly Ile Gly Ala Val Phe Gln Ile Tyr Ile
                885                 890                 895
Ile Lys Asp Leu Glu Lys Leu Leu Met Ile Ala Gly Glu Glu Arg Ala
            900                 905                 910
Leu Cys Leu Val Asp Val Lys Lys Val Lys Gln Ser Leu Ala Gln Ser
        915                 920                 925
His Leu Pro Ala Gln Pro Asp Ile Ser Pro Asn Ile Phe Glu Ala Val
    930                 935                 940
Lys Gly Cys His Leu Phe Gly Ala Gly Lys Ile Glu Asn Gly Leu Cys
945                 950                 955                 960
Ile Cys Ala Ala Met Pro Ser Lys Val Val Ile Leu Arg Tyr Asn Glu
                965                 970                 975
Asn Leu Ser Lys Tyr Cys Ile Arg Lys Glu Ile Glu Thr Ser Glu Pro
            980                 985                 990
Cys Ser Cys Ile His Phe Thr Asn Tyr Ser Ile Leu Ile Gly Thr Asn
        995                 1000                1005
Lys Phe Tyr Glu Ile Asp Met Lys Gln Tyr Thr Leu Glu Glu Phe Leu
```

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    1010                1015                1020
Asp Lys Asn Asp His Ser Leu Ala Pro Ala Val Phe Ala Ala Ser Ser
1025                1030                1035                1040
Asn Ser Phe Pro Val Ser Ile Val Gln Val Asn Ser Ala Gly Gln Arg
                1045                1050                1055
Glu Glu Tyr Leu Leu Cys Phe His Glu Phe Gly Val Phe Val Asp Ser
            1060                1065                1070
Tyr Gly Arg Arg Ser Arg Thr Asp Asp Leu Lys Trp Ser Arg Leu Pro
        1075                1080                1085
Leu Ala Phe Ala Tyr Arg Glu Pro Tyr Leu Phe Val Thr His Phe Asn
    1090                1095                1100
Ser Leu Glu Val Ile Glu Ile Gln Ala Arg Ser Ser Ala Gly Thr Pro
1105                1110                1115                1120
Ala Arg Ala Tyr Leu Asp Ile Pro Asn Pro Arg Tyr Leu Gly Pro Ala
                1125                1130                1135
Ile Ser Ser Gly Ala Ile Tyr Leu Ala Ser Ser Tyr Gln Asp Lys Leu
            1140                1145                1150
Arg Val Ile Cys Cys Lys Gly Asn Leu Val Lys Glu Ser Gly Thr Glu
        1155                1160                1165
His His Arg Gly Pro Ser Thr Ser Arg Ser Ser Pro Asn Lys Arg Gly
    1170                1175                1180
Pro Pro Thr Tyr Asn Glu His Ile Thr Lys Arg Val Ala Ser Ser Pro
1185                1190                1195                1200
Ala Pro Pro Glu Gly Pro Ser His Pro Arg Glu Pro Ser Thr Pro His
                1205                1210                1215
Arg Tyr Arg Glu Gly Arg Thr Glu Leu Arg Arg Asp Lys Ser Pro Gly
            1220                1225                1230
Arg Pro Leu Glu Arg Glu Lys Ser Pro Gly Arg Met Leu Ser Thr Arg
        1235                1240                1245
Arg Glu Arg Ser Pro Gly Arg Leu Phe Glu Asp Ser Ser Arg Gly Arg
    1250                1255                1260
Leu Pro Ala Gly Ala Val Arg Thr Pro Leu Ser Gln Val Asn Lys Val
1265                1270                1275                1280
Trp Asp Gln Ser Ser Val
                1285
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<210> 6247
<211> 497
<212> DNA
<213> Homo sapiens

<400> 6247

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gcggccgcag cgctgaatgg ggtggaccga cgttccctgc agcgttcaca aggctggctc
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tagaagtgct ggagagggcc aagaggaggg cggtggactg gcatgccctg gagcgtccca
120
aaggctgcat gggggtcctt gcccgggagg cgccccacct agagaaacag ccggcagccg
180
gcccgcagcg cgttctcccg ggagagaaat attattcatc tgtgccagag gaaggagggg
240
caacccatgt ctatcgttat cacagaggcg agtcgaagct gcacatgtgc ttggacatag
300
ggaatggtca gagaaaagac agaaaaaaga catcccttgg tcctggaggc agctatcaaa
360
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tatcagagca tgctccagag gcatcccagc ctgtgagtac ggaactgctt acgcactggg
420
tttcaccacc gttgcaactc catgaaccag ttgacatggt tcttagaggg ctatttgaat
480
tgagtctata gtatttt
497

<210> 6248
<211> 142
<212> PRT
<213> Homo sapiens

<400> 6248
Met Gly Trp Thr Asp Val Pro Cys Ser Val His Lys Ala Gly Ser Arg
1 5 10 15
Ser Ala Gly Glu Gly Gln Glu Glu Gly Gly Gly Leu Ala Cys Pro Gly
20 25 30
Ala Ser Gln Arg Leu His Gly Gly Pro Cys Pro Gly Gly Ala Pro Pro
35 40 45
Arg Glu Thr Ala Gly Ser Arg Pro Ala Ala Arg Ser Pro Gly Arg Glu
50 55 60
Ile Leu Phe Ile Cys Ala Arg Gly Arg Arg Gly Asn Pro Cys Leu Ser
65 70 75 80
Leu Ser Gln Arg Arg Val Glu Ala Ala His Val Leu Gly His Arg Glu
85 90 95
Trp Ser Glu Lys Arg Gln Lys Lys Asp Ile Pro Trp Ser Trp Arg Gln
100 105 110
Leu Ser Asn Ile Arg Ala Cys Ser Arg Gly Ile Pro Ala Cys Glu Tyr
115 120 125
Gly Thr Ala Tyr Ala Leu Gly Phe Thr Thr Val Ala Thr Pro
130 135 140

<210> 6249
<211> 1217
<212> DNA
<213> Homo sapiens

<400> 6249
nntgagcaac aaaccgagtt ctggagaacg ccatcagctc gctgcttaaa ctggaaacaa
60
aagtctcaac ttccaacctc tttgcagcta ggagtggcca agtagcatag atctggtgaa
120
tgaactgcag gtgggaattt ctgagaaggt ttccttctta aatagaaaga ttaaaccaca
180
ggttccatta tgggtcgact tgatgggaaa gtcatcatcc tgacggccgc tgctcagggg
240
attggccaag cagctgcctt agcttttgca agagaaggtg ccaaagtcat agccacagac
300
attaatgagt ccaaacttca ggaactggaa aagtacccgg gtattcaaac tcgtgtcctt
360
gatgtcacaa agaagaaaca aattgatcag tttgccaatg aagttgagag acttgatgtt
420
ctctttaatg ttgctggttt tgtccatcat ggaactgtcc tggattgtga ggagaaagac
480

tgggacttct cgatgaatct caatgtgcgc agcatgtacc tgatgatcaa ggcattcctt
540
cctaaaatgc ttgctcagaa atctggcaat attatcaaca tgtcttctgt ggcttccagc
600
gtcaaaggag ttgtgaacag atgtgtgtac agcacaacca aggcagccgt gattggcctc
660
acaaaatctg tggctgcaga tttcatccag cagggcatca ggtgcaactg tgtgtgccca
720
ggaacagttg atacgccatc tctacaagaa agaatacaag ccagaggaaa tcctgaagag
780
gcacggaatg atttcctgaa gagacaaaag acgggaagat tcgcaactgc agaagaaata
840
gccatgctct gcgtgtattt ggcttctgat gaatctgctt atgtaactgg taaccctgtc
900
atcattgatg gaggctggag cttgtgattt taggatctcc atggtgggaa ggaaggcagg
960
cccttcctat ccacagtgaa cctggttacg aagaaaactc accaatcatc tccttcctgt
1020
taatcacatg ttaatgaaaa taagctcttt ttaatgatgt cactgtttgc aagagtctga
1080
ttctttaagt atattaatct ctttgtaatc tcttctgaaa tcattgtaaa gaaataaaaa
1140
tattgaactc atagcaggag aatagttttt aaaataaatc tcgatttgtt agcaaaaaaa
1200
aaaaaaaaaa aaaaaaa
1217

<210> 6250
<211> 245
<212> PRT
<213> Homo sapiens

<400> 6250
Met Gly Arg Leu Asp Gly Lys Val Ile Ile Leu Thr Ala Ala Ala Gln
 1   5   10   15
Gly Ile Gly Gln Ala Ala Ala Leu Ala Phe Ala Arg Glu Gly Ala Lys
            20   25   30
Val Ile Ala Thr Asp Ile Asn Glu Ser Lys Leu Gln Glu Leu Glu Lys
        35   40   45
Tyr Pro Gly Ile Gln Thr Arg Val Leu Asp Val Thr Lys Lys Lys Gln
    50   55   60
Ile Asp Gln Phe Ala Asn Glu Val Glu Arg Leu Asp Val Leu Phe Asn
65   70   75   80
Val Ala Gly Phe Val His His Gly Thr Val Leu Asp Cys Glu Glu Lys
                85   90   95
Asp Trp Asp Phe Ser Met Asn Leu Asn Val Arg Ser Met Tyr Leu Met
            100   105   110
Ile Lys Ala Phe Leu Pro Lys Met Leu Ala Gln Lys Ser Gly Asn Ile
        115   120   125
Ile Asn Met Ser Ser Val Ala Ser Ser Val Lys Gly Val Val Asn Arg
    130   135   140
Cys Val Tyr Ser Thr Thr Lys Ala Ala Val Ile Gly Leu Thr Lys Ser
145   150   155   160
Val Ala Ala Asp Phe Ile Gln Gln Gly Ile Arg Cys Asn Cys Val Cys

```
                165                 170                 175
Pro Gly Thr Val Asp Thr Pro Ser Leu Gln Glu Arg Ile Gln Ala Arg
            180                 185                 190
Gly Asn Pro Glu Glu Ala Arg Asn Asp Phe Leu Lys Arg Gln Lys Thr
        195                 200                 205
Gly Arg Phe Ala Thr Ala Glu Glu Ile Ala Met Leu Cys Val Tyr Leu
    210                 215                 220
Ala Ser Asp Glu Ser Ala Tyr Val Thr Gly Asn Pro Val Ile Ile Asp
225                 230                 235                 240
Gly Gly Trp Ser Leu
                245
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<210> 6251
<211> 1611
<212> DNA
<213> Homo sapiens

<400> 6251
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tattgctgac atgcaggaag agtccccatg tagtacaaaa atatgtcttt atacaaactt
120
ttttgtgact ttttccgttt ctttacaata ggacttctct cagtgtgtga cacccagtga
180
gggctgaccc atcctcctct cctttgcttc accaggaatg tcatcagaca catggcttga
240
ccttggaagg gcccagtctg tctgacaggg ctttgcagac ccggcggcta ttgctttgaa
300
aaggaggaga aagaccacgc acgggcagca gcctggaggg acccggtggg ctgctgagag
360
ggggctccgc tgcgacgggc cctggcccag cttcaggccc tcacaggagg acagtcaagg
420
gctgggagcc ctaggccgga ctgcatttcc gctcccgcag gagactttct atgaaataaa
480
tatagaaaag agggcatccc ccagccccac agcacaagac cctggccctc agcgctggac
540
agctgagaca gacgcaggct cgctgctcag ggggagtaag tgctgggctc cagtaggctc
600
ccacaggccc actgaggcag aggcatgagt cgcccaagtg ctggatgggg catggggaga
660
aaggggcgtg ggcagccctg ctactgctgg caagaggtgg ccccattttt tccagatggg
720
gaaactgagg cacaaggagg tttgggaact tgcccaaggt cactcacagt gagtcagctt
780
tttaggggga ggagagcggc tcacactctg ggaaacacag tcacctcccc actggggagc
840
agggccaggc aggaggggcc tcagggccca tgactgcctg gaggggacac tcagcctctc
900
tgaggacata tgggggggtag gcctctgggg aagggtcttt gcttggcatc aggcagggcc
960
aagtccagta agggcaaggg gaggggggcat tctggtgaga acagcatttc tggcaagacg
1020
ggcatccact tcaaaatctc ggctcaaaag ggcagcaggg ctgttctcaa gccaggcagg
1080

cagggtcccc caatccctac aattctcctg agtccctcac caccatggag gacccttgct
1140
agggtctacc gggagagtca ccacatctat tatgaggcaa gggcactggg atatgttccc
1200
accatcccct aaacacaaga gtaggctagg ggagcgtgca ggcagccccc gctcacggcc
1260
aggcctgcag cccaacccat gggccccttc gcactgggag tccacgtgag ctcagtacca
1320
cggggaagga tagagaaggg aacaggttaa cgcgcgtgta cagcacctca gagaagccac
1380
tgagacggga gagaaagagc caggtctaga aaggcctccc atcaccggca gcagagaggg
1440
actggtgggc tgaaagggga cagggactgg caggaggggc ttccctgcct gggggtgagg
1500
agggagctca cgtgtgggct gtggattcct tgctgtccag ccaggctggg ggcagggagt
1560
ggccatggac tgagccacct agagatggga gagaagttgg tatgggtaan a
1611

<210> 6252
<211> 100
<212> PRT
<213> Homo sapiens

<400> 6252
Met Gly Gly Arg Pro Leu Gly Lys Gly Leu Cys Leu Ala Ser Gly Arg
 1   5   10   15
Ala Lys Ser Ser Lys Gly Lys Gly Arg Gly His Ser Gly Glu Asn Ser
            20   25   30
Ile Ser Gly Lys Thr Gly Ile His Phe Lys Ile Ser Ala Gln Lys Gly
        35   40   45
Ser Arg Ala Val Leu Lys Pro Gly Arg Gln Gly Pro Pro Ile Pro Thr
    50   55   60
Ile Leu Leu Ser Pro Ser Pro Pro Trp Arg Thr Leu Ala Arg Val Tyr
65   70   75   80
Arg Glu Ser His His Ile Tyr Tyr Glu Ala Arg Ala Leu Gly Tyr Val
                85   90   95
Pro Thr Ile Pro
            100

<210> 6253
<211> 1953
<212> DNA
<213> Homo sapiens

<400> 6253
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cggctccgag cggcggcggc ccggcttccg ctgcccgtga gctaaggacg gtccgctccc
120
tctagccagc tccgaatcct gatccaggcg ggggccaggg gcccctcgcc tcccctctga
180
ggaccgaaga tgagcttcct cttcagcagc cgctcttcta aaacattcaa accaaagaag
240

aatatccctg aaggatctca tcagtatgaa ctcttaaaac atgcagaagc aactctagga
300
agtgggaatc tgagacaagc tgttatgttg cctgagggag aggatctcaa tgaatggatt
360
gctgtgaaca ctgtggattt ctttaaccag atcaacatgt tatatggaac tattacagaa
420
ttctgcactg aagcaagctg tccagtcatg tctgcaggtc cgagatatga atatcactgg
480
gcagatggta ctaatattaa aaagccaatc aaatgttctg caccaaaata cattgactat
540
ttgatgactt gggttcaaga tcagcttgat gatgaaactc tttttccttc taagattggt
600
gtcccatttc ccaaaaactt tatgtctgtg gcaaagacta ttctaaagcg tctgttcagg
660
gtttatgccc atatttatca ccagcacttt gattctgtga tgcagctgca agaggaggcc
720
cacctcaaca cctcctttaa gcactttatt ttctttgttc aggagtttaa tctgattgat
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840
atgtttcttc tagaacacag ttacccccct gcttcatcta ttgctagaac tatctcattg
900
ctatctgtta tagactagtg atacaaactt taagaaaaca ggataaaaag atacccattg
960
cctgtgtcta ctgataaaat tatcccaaag gtaggttggt gtgatagttt ccgagtaaga
1020
ccttaaggac acagccaaat cttaagtact gtgtgaccac tcttgttgtt atcacatagt
1080
catacttggt tgtaatatgt gatggttaac ctgtagctta taaatttact tattattctt
1140
ttactcattt actcagtcat ttctttacaa gaaaatgatt gaatctgttt taggtgacag
1200
cacaatggac attaagaatt tccatcaata atttatgaat aagtttccag aacaaatttc
1260
ctaataacac aatcagattg gttttattct tttattttac gaataaaaaa tgtatttttc
1320
agtacccttg agatttagaa catctgtgtc acttcagata acattttagt ttcaagtttg
1380
tatggtagtg tttttataga taagatacgt ctatttttc aaaattcatg attgcagttt
1440
aaatcatcat atgacgtgtg ggtgggagca accaaagtta tttttacagg gactttattt
1500
tttgatcttt atttgagatt gttttcatat ctatctaaat tattaggagt gtgtgtatca
1560
gaagtaattt tttaatgtct tctaaggatg gtcttccagg cttttaaact gaaaagctta
1620
attcagatag tagcttttgg ctgagaaaag gaatccaaaa tattaataaa tttagatctc
1680
aaaaccacta tttttattat ttcattattt ttcagaggcc ttaaaattct gggtaagaga
1740
atggaggaaa atactcagag tacttgatta ttttatttcc ttttattaaa aaattacttc
1800
tatgttttta ttgtctcttg agccttagtt aagagtagtg tagaaatgca tgaacttcat
1860

cctaataagg ataaaactta aggaaaacca caataaacca tgaaggtgta cacatcttaa
1920
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa
1953

<210> 6254
<211> 216
<212> PRT
<213> Homo sapiens

<400> 6254
Met Ser Phe Leu Phe Ser Ser Arg Ser Ser Lys Thr Phe Lys Pro Lys
 1   5   10   15
Lys Asn Ile Pro Glu Gly Ser His Gln Tyr Glu Leu Leu Lys His Ala
            20   25   30
Glu Ala Thr Leu Gly Ser Gly Asn Leu Arg Gln Ala Val Met Leu Pro
        35   40   45
Glu Gly Glu Asp Leu Asn Glu Trp Ile Ala Val Asn Thr Val Asp Phe
    50   55   60
Phe Asn Gln Ile Asn Met Leu Tyr Gly Thr Ile Thr Glu Phe Cys Thr
65   70   75   80
Glu Ala Ser Cys Pro Val Met Ser Ala Gly Pro Arg Tyr Glu Tyr His
                85   90   95
Trp Ala Asp Gly Thr Asn Ile Lys Lys Pro Ile Lys Cys Ser Ala Pro
            100   105   110
Lys Tyr Ile Asp Tyr Leu Met Thr Trp Val Gln Asp Gln Leu Asp Asp
        115   120   125
Glu Thr Leu Phe Pro Ser Lys Ile Gly Val Pro Phe Pro Lys Asn Phe
    130   135   140
Met Ser Val Ala Lys Thr Ile Leu Lys Arg Leu Phe Arg Val Tyr Ala
145   150   155   160
His Ile Tyr His Gln His Phe Asp Ser Val Met Gln Leu Gln Glu Glu
                165   170   175
Ala His Leu Asn Thr Ser Phe Lys His Phe Ile Phe Phe Val Gln Glu
            180   185   190
Phe Asn Leu Ile Asp Arg Arg Glu Leu Ala Pro Leu Gln Glu Leu Ile
        195   200   205
Glu Lys Leu Gly Ser Lys Asp Arg
    210   215

<210> 6255
<211> 622
<212> DNA
<213> Homo sapiens

<400> 6255
nntccggagg ctgagacagg agaatcgctt gaacccagga ggccgaggtt gcagtgagcc
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gagatcatgc cattgcactc cagcctgggc aacagagtga gacttcatct caaaaaaaaa
120
aaagccacag tggctgcctt cacagccagc gagggccacg cacatcccag ggtagtggag
180
ctacccaaga cggatgaggg cctaggcttc aacatcatgg gtggcaaaga gcaaaactcg
240

cccatctaca tctcccgggt catcccaggg ggtgtggctg accgccatgg aggcctcaag
300
cgtggggatc aactgttgtc ggtgaacggt gtgagcgttg agggtgagca gcatgagaag
360
gcggtggagc tgctgaaggc ggcccagggc tcggtgaagc tggttgtccg ttacacaccg
420
cgagtgctgg aggagatgga ggcccggttc gagaagatgc gctctgcccg ccggcgccaa
480
cagcatcaga gctactcgtc cttggagtct cgaggttgaa accacagatc tggacgttca
540
cgtgcactct cttcctgtac agtatttatt gttcctggca ctttatttaa agatttttga
600
ccctcaaaaa aaaaaaaaaa aa
622

<210> 6256
<211> 150
<212> PRT
<213> Homo sapiens

<400> 6256
Met Pro Leu His Ser Ser Leu Gly Asn Arg Val Arg Leu His Leu Lys
 1   5   10   15
Lys Lys Lys Ala Thr Val Ala Ala Phe Thr Ala Ser Glu Gly His Ala
            20   25   30
His Pro Arg Val Val Glu Leu Pro Lys Thr Asp Glu Gly Leu Gly Phe
        35   40   45
Asn Ile Met Gly Gly Lys Glu Gln Asn Ser Pro Ile Tyr Ile Ser Arg
    50   55   60
Val Ile Pro Gly Gly Val Ala Asp Arg His Gly Gly Leu Lys Arg Gly
65   70   75   80
Asp Gln Leu Leu Ser Val Asn Gly Val Ser Val Glu Gly Glu Gln His
                85   90   95
Glu Lys Ala Val Glu Leu Leu Lys Ala Ala Gln Gly Ser Val Lys Leu
            100   105   110
Val Val Arg Tyr Thr Pro Arg Val Leu Glu Glu Met Glu Ala Arg Phe
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Glu Lys Met Arg Ser Ala Arg Arg Arg Gln Gln His Gln Ser Tyr Ser
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Ser Leu Glu Ser Arg Gly
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<210> 6257
<211> 2216
<212> DNA
<213> Homo sapiens

<400> 6257
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<210> 6258
<211> 340
<212> PRT
<213> Homo sapiens

<400> 6258
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35 40 45
Ala Ile Phe Ser Leu Ser Ser Ala Leu Ser Ser Glu Ala Lys Glu Glu
50 55 60
Ser Lys Lys Pro Val Val Thr Phe Gln Ala His Asp Gly Pro Val Tyr
65 70 75 80
Ser Met Val Ser Thr Asp Arg His Leu Leu Ser Ala Gly Asp Gly Glu
85 90 95
Val Lys Ala Trp Leu Trp Ala Glu Met Leu Lys Lys Gly Cys Lys Glu
100 105 110
Leu Trp Arg Arg Gln Pro Pro Tyr Arg Thr Ser Leu Glu Val Pro Glu
115 120 125
Ile Asn Ala Leu Leu Leu Val Pro Lys Glu Asn Ser Leu Ile Leu Ala
130 135 140
Gly Gly Asp Cys Gln Leu His Thr Met Asp Leu Glu Thr Gly Thr Phe
145 150 155 160
Thr Arg Val Leu Arg Gly His Thr Asp Tyr Ile His Cys Leu Ala Leu
165 170 175
Arg Glu Arg Ser Pro Glu Val Leu Ser Gly Gly Glu Asp Gly Ala Val
180 185 190
Arg Leu Trp Asp Leu Arg Thr Ala Lys Glu Val Gln Thr Ile Glu Ser
195 200 205
Ile Ser Thr Arg Ser Ala Arg Gly Pro Thr Met Gly Ala Gly Leu Asp
210 215 220
Val Trp Thr Asp Ser Asp Trp Met Val Cys Gly Gly Gly Pro Ala Leu
225 230 235 240
Thr Leu Trp His Leu Arg Ser Ser Thr Pro Thr Thr Ile Phe Pro Ile
245 250 255
Arg Ala Pro Gln Lys His Val Thr Phe Tyr Gln Asp Leu Ile Leu Ser

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            260                 265                 270
Ala Gly Gln Gly Arg Cys Val Asn Gln Trp Gln Leu Ser Gly Glu Leu
        275                 280                 285
Lys Ala Gln Val Pro Gly Ser Ser Pro Gly Leu Leu Ser Leu Ser Leu
    290                 295                 300
Asn Gln Gln Pro Ala Ala Pro Glu Cys Lys Val Leu Thr Ala Ala Gly
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Ser Leu Ser Phe
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<210> 6259
<211> 384
<212> DNA
<213> Homo sapiens

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240
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<210> 6260
<211> 128
<212> PRT
<213> Homo sapiens

<400> 6260

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            20                  25                  30
Gln Lys Asn Glu Lys Ile Lys Tyr Ser Arg Phe Ala Ala Thr Asn Thr
        35                  40                  45
Arg Val Lys Ala Lys Gln Lys Pro Leu Ile Ser Asn Ser His Thr Asp
    50                  55                  60
His Leu Met Gly Cys Thr Lys Ser Ala Glu Pro Gly Thr Glu Thr Ser
65                  70                  75                  80
Gln Val Asn Ser Phe Ser Asp Leu Lys Ala Ser Thr Leu Val His Lys
                85                  90                  95
Pro Gln Ser Asp Phe Thr Asn Asp Ala Leu Ser Pro Lys Phe Asn Leu
            100                 105                 110
Ser Ser Ser Ile Ser Ser Glu Asn Ser Leu Ile Lys Gly Gly Ala Ala
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<210> 6261
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<212> DNA
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<210> 6262
<211> 431
<212> PRT
<213> Homo sapiens

<400> 6262
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Val Arg Leu Gln Asn Glu Thr Ser Tyr Ser Arg Val Leu His Gly Tyr
        35   40   45
Ala Ala Gln Gln Leu Pro Ser Leu Leu Lys Glu Arg Glu Phe His Leu
    50   55   60
Gly Thr Leu Asn Lys Val Phe Ala Ser Gln Trp Leu Asn His Arg Gln
65   70   75   80
Val Val Cys Gly Thr Lys Cys Asn Thr Leu Phe Val Val Asp Val Gln
                85   90   95
Thr Ser Gln Ile Thr Lys Ile Pro Ile Leu Lys Asp Arg Glu Pro Gly
            100   105   110
Gly Val Thr Gln Gln Gly Cys Gly Ile His Ala Ile Glu Leu Asn Pro
        115   120   125
Ser Arg Thr Leu Leu Ala Thr Gly Gly Asp Asn Pro Asn Ser Leu Ala
    130   135   140
Ile Tyr Arg Leu Pro Thr Leu Asp Pro Val Cys Val Gly Asp Asp Gly
145   150   155   160
His Lys Asp Trp Ile Phe Ser Ile Ala Trp Ile Ser Asp Thr Met Ala
                165   170   175
Val Ser Gly Ser Arg Asp Gly Ser Met Gly Leu Trp Glu Val Thr Asp
            180   185   190
Asp Val Leu Thr Lys Ser Asp Ala Arg His Asn Val Ser Arg Val Pro

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        195                 200                 205
Val Tyr Ala His Ile Thr His Lys Ala Leu Lys Asp Ile Pro Lys Glu
    210                 215                 220
Asp Thr Asn Pro Asp Asn Cys Lys Val Arg Ala Leu Ala Phe Asn Asn
225                 230                 235                 240
Lys Asn Lys Glu Leu Gly Ala Val Ser Leu Asp Gly Tyr Phe His Leu
                245                 250                 255
Trp Lys Ala Glu Asn Thr Leu Ser Lys Leu Leu Ser Thr Lys Leu Pro
            260                 265                 270
Tyr Cys Arg Glu Asn Val Cys Leu Ala Tyr Gly Ser Glu Trp Ser Val
        275                 280                 285
Tyr Ala Val Gly Ser Gln Ala His Val Ser Phe Leu Asp Pro Arg Gln
    290                 295                 300
Pro Ser Tyr Asn Val Lys Ser Val Cys Ser Arg Glu Arg Gly Ser Gly
305                 310                 315                 320
Ile Arg Ser Val Ser Phe Tyr Glu His Ile Ile Thr Val Gly Thr Gly
                325                 330                 335
Gln Gly Ser Leu Leu Phe Tyr Asp Ile Arg Ala Gln Arg Phe Leu Glu
            340                 345                 350
Glu Arg Leu Ser Ala Cys Tyr Gly Ser Lys Pro Arg Leu Ala Gly Glu
        355                 360                 365
Asn Leu Lys Leu Thr Thr Gly Lys Gly Trp Leu Asn His Asp Glu Thr
    370                 375                 380
Trp Arg Asn Tyr Phe Ser Asp Ile Asp Phe Phe Pro Asn Ala Val Tyr
385                 390                 395                 400
Thr His Cys Tyr Asp Ser Ser Gly Thr Lys Leu Phe Val Ala Gly Gly
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<212> DNA
<213> Homo sapiens

<400> 6263
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<210> 6264
<211> 654
<212> PRT
<213> Homo sapiens

<400> 6264
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Asn Asn Trp Asp Leu Val Ala Ala Ile Asn Gly Val Ile Pro Gln Glu
35 40 45
Asn Gly Ile Leu Gln Ser Glu Tyr Gly Gly Glu Thr Ile Pro Gly Pro
50 55 60
Ala Phe Asn Pro Ala Ser His Pro Ala Ser Ala Pro Thr Ser Ser Ser
65 70 75 80
Ser Ser Ala Phe Arg Pro Val Met Pro Ser Arg Gln Ile Val Glu Arg
85 90 95
Gln Pro Arg Met Leu Asp Phe Arg Val Glu Tyr Arg Asp Arg Asn Val
100 105 110
Asp Val Val Leu Glu Asp Thr Cys Thr Val Gly Glu Ile Lys Gln Ile
115 120 125
Leu Glu Asn Glu Leu Gln Ile Pro Val Ser Lys Met Leu Leu Lys Gly
130 135 140
Trp Lys Thr Gly Asp Val Glu Asp Ser Thr Val Leu Lys Ser Leu His
145 150 155 160
Leu Pro Lys Asn Asn Ser Leu Tyr Val Leu Thr Pro Asp Leu Pro Pro
165 170 175
Pro Ser Ser Ser Ser His Ala Gly Ala Leu Gln Glu Ser Leu Asn Gln
180 185 190
Asn Phe Met Leu Ile Ile Thr His Arg Glu Val Gln Arg Glu Tyr Asn
195 200 205
Leu Asn Phe Ser Gly Ser Ser Thr Ile Gln Glu Val Lys Arg Asn Val
210 215 220
Tyr Asp Leu Thr Ser Ile Pro Val Arg His Gln Leu Trp Glu Gly Trp
225 230 235 240
Pro Thr Ser Ala Thr Asp Asp Ser Met Cys Leu Ala Glu Ser Gly Leu
245 250 255
Ser Tyr Pro Cys His Arg Leu Thr Val Gly Arg Arg Ser Ser Pro Ala
260 265 270
Gln Thr Arg Glu Gln Ser Glu Glu Gln Ile Thr Asp Val His Met Val

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        275                 280                 285
Ser Asp Ser Asp Gly Asp Asp Phe Glu Asp Ala Thr Glu Phe Gly Val
    290                 295                 300
Asp Asp Gly Glu Val Phe Gly Met Ala Ser Ser Ala Leu Arg Lys Ser
305                 310                 315                 320
Pro Met Ile Cys Phe Leu Val Pro Glu Asn Ala Glu Asn Glu Gly Asp
                325                 330                 335
Ala Leu Leu Gln Phe Thr Ala Glu Phe Ser Ser Arg Tyr Gly Asp Cys
            340                 345                 350
His Pro Val Phe Phe Ile Gly Ser Leu Glu Ala Ala Phe Gln Glu Ala
        355                 360                 365
Phe Tyr Val Lys Ala Arg Asp Arg Lys Leu Leu Ala Ile Tyr Leu His
    370                 375                 380
His Asp Glu Ser Val Leu Thr Asn Val Phe Cys Ser Gln Met Leu Cys
385                 390                 395                 400
Ala Glu Ser Ile Val Ser Tyr Leu Ser Gln Asn Phe Ile Thr Trp Ala
                405                 410                 415
Trp Asp Leu Thr Lys Asp Ser Asn Arg Ala Arg Phe Leu Thr Met Cys
            420                 425                 430
Asn Arg His Phe Gly Ser Val Val Ala Gln Thr Ile Arg Thr Gln Lys
        435                 440                 445
Thr Asp Gln Phe Pro Leu Phe Leu Ile Ile Met Gly Lys Arg Ser Ser
    450                 455                 460
Asn Glu Val Leu Asn Val Ile Gln Gly Asn Thr Thr Val Asp Glu Leu
465                 470                 475                 480
Met Met Arg Leu Met Ala Ala Met Glu Ile Phe Thr Ala Gln Gln Gln
                485                 490                 495
Glu Asp Ile Lys Asp Glu Asp Glu Arg Glu Ala Arg Glu Asn Val Lys
            500                 505                 510
Arg Glu Gln Asp Glu Ala Tyr Arg Leu Ser Leu Glu Ala Asp Arg Ala
        515                 520                 525
Lys Arg Glu Ala His Glu Arg Glu Met Ala Glu Gln Phe Arg Leu Glu
    530                 535                 540
Gln Ile Arg Lys Glu Gln Glu Glu Glu Arg Glu Ala Ile Arg Leu Ser
545                 550                 555                 560
Leu Glu Gln Ala Leu Pro Pro Glu Pro Lys Glu Glu Asn Ala Glu Pro
                565                 570                 575
Val Ser Lys Leu Arg Ile Arg Thr Pro Ser Gly Glu Phe Leu Glu Arg
            580                 585                 590
Arg Phe Leu Ala Ser Asn Lys Leu Gln Ile Val Phe Asp Phe Val Ala
        595                 600                 605
Ser Lys Gly Phe Pro Trp Asp Glu Tyr Lys Leu Leu Ser Thr Phe Pro
    610                 615                 620
Arg Arg Asp Val Thr Gln Leu Asp Pro Asn Lys Ser Leu Leu Glu Val
625                 630                 635                 640
Lys Leu Phe Pro Gln Glu Thr Leu Phe Leu Glu Ala Lys Glu
                645                 650
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<210> 6265
<211> 1344
<212> DNA
<213> Homo sapiens

<400> 6265

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120
tctgtggagg aagagatgca aagtacagtt cgagagcaca gagatggagg tcatgcaggt
180
ggaatcttca acagatacaa tattctcaag attcagaagg tttgtaacaa gaaactatgg
240
gaaagataca ctcaccggag aaaagaagtt tctgaagaaa accacaacca tgccaatgaa
300
cgaatgctat ttcatgggtc tccttttgtg aatgcaatta tccacaaagg ctttgatgaa
360
aggcatgcgt acataggtgg tatgtttgga gctggcattt attttgctga aaactcttcc
420
aaaagcaatc aatatgtata tggaattgga ggaggtactg ggtgtccagt tcacaaagac
480
agatcttgtt acatttgcca caggcagctg ctcttttgcc gggtaacctt gggaaagtct
540
ttcctgcagt tcagtgcaat gaaaatggca cattctcctc caggtcatca ctcagtcact
600
ggtaggccca gtgtaaatgg cctagcatta gctgaatatg ttatttacag aggagaacag
660
gcttatcctg agtatttaat tacttaccag attatgaggc ctgaaggtat ggtcgatgga
720
taaatagtta ttttaagaaa ctaattccac tgaacctaaa atcatcaaag cagcagtggc
780
ctctacgttt tactcctttg ctgaaaaaaa atcatcttgc ccacaggcct gtggcaaaag
840
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1020
tctaacaaac tgtaatgccc tcaacagaac taattttact aatacaatac tgtgttcttt
1080
aaaacacagc atttacactg aatacaattt catttgtaaa actgtaaata agagcttttg
1140
tactagccca gtatttattt acattgcttt gtaatataaa tctgttttag aactgcagcg
1200
gtttacaaaa ttttttcata tgtattgttc atctatactt catcttacat cgtcatgatt
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gagtgatctt tacatttgat tccagaggct atgttcagtt gttagttggg aaagattgag
1320
ttatcagatt taatttgccg atgg
1344

<210> 6266
<211> 240
<212> PRT
<213> Homo sapiens

<400> 6266
Xaa Ala Leu Pro Ala Ser His Arg Pro Gly Gln Gln Gly Leu Asn Pro

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 1               5                  10                  15
Tyr Leu Thr Leu Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile Asp Leu
            20                  25                  30
Ser Pro Asp Asp Lys Glu Phe Gln Ser Val Glu Glu Glu Met Gln Ser
        35                  40                  45
Thr Val Arg Glu His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn
    50                  55                  60
Arg Tyr Asn Ile Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp
65                  70                  75                  80
Glu Arg Tyr Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn
                85                  90                  95
His Ala Asn Glu Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala
            100                 105                 110
Ile Ile His Lys Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly Met
        115                 120                 125
Phe Gly Ala Gly Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser Asn Gln
    130                 135                 140
Tyr Val Tyr Gly Ile Gly Gly Gly Thr Gly Cys Pro Val His Lys Asp
145                 150                 155                 160
Arg Ser Cys Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg Val Thr
                165                 170                 175
Leu Gly Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala His Ser
            180                 185                 190
Pro Pro Gly His His Ser Val Thr Gly Arg Pro Ser Val Asn Gly Leu
        195                 200                 205
Ala Leu Ala Glu Tyr Val Ile Tyr Arg Gly Glu Gln Ala Tyr Pro Glu
    210                 215                 220
Tyr Leu Ile Thr Tyr Gln Ile Met Arg Pro Glu Gly Met Val Asp Gly
225                 230                 235                 240
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<210> 6267
<211> 328
<212> DNA
<213> Homo sapiens

<400> 6267
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gggagagggg agggctaagc agagtgggga tgcccggcag tgacccagcc tctctcccca
120
gatgagcctt tcctgcagtt ccgaaggaac gtgttcttcc caaagcggcg ggagctccag
180
atccatgacg aggaggtcct gcggctgctc tatgaggagg ccaagggcaa cgtgctggct
240
gcacggtacc cgtgcgacgt ggaggactgc gaggctctgg gcgccctggt gtgccgcgtg
300
cagcttgggc cctaccagcc cggccggc
328

<210> 6268
<211> 83
<212> PRT
<213> Homo sapiens

<400> 6268
Ala Glu Trp Gly Cys Pro Ala Val Thr Gln Pro Leu Ser Pro Asp Glu
1 5 10 15
Pro Phe Leu Gln Phe Arg Arg Asn Val Phe Phe Pro Lys Arg Arg Glu
20 25 30
Leu Gln Ile His Asp Glu Glu Val Leu Arg Leu Leu Tyr Glu Glu Ala
35 40 45
Lys Gly Asn Val Leu Ala Ala Arg Tyr Pro Cys Asp Val Glu Asp Cys
50 55 60
Glu Ala Leu Gly Ala Leu Val Cys Arg Val Gln Leu Gly Pro Tyr Gln
65 70 75 80
Pro Gly Arg

<210> 6269
<211> 923
<212> DNA
<213> Homo sapiens

<400> 6269
nggcggaaga tggcgacgcc cctcgggtgg tcgaaggcgg ggtcaggatc tgtgtgtctc
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gctttagatc aactgcggga cgtgattgag tctcaggagg aactaatcca ccagctgagg
120
aacgtgatgg ttctccagga cgaaaatttt gtcagtaaag aagagttcca ggcagtggag
180
aagaagctgg tggaagagaa agctgcccat gccaaaacca aggtcctcct ggccaaggaa
240
gaggagaagt tacagtttgc cctcggagag gtagaggtgc tatccaagca gctggagaaa
300
gagaagctgg cctttgaaaa agcgctctcc agtgtcaaga gcaaagtcct tcaggagtcc
360
agcaagaagg accagctcat caccaagtgc aatgagattg agtctcacat tataaagcaa
420
gaagatatac ttaatggcaa agagaatgag attaaagagt tgcagcaagt tatcagccag
480
cagaaacaga tcttcagccc accaccagcc ggctccgttg caggaatcac atgtctgact
540
tccggatcca gaagcagcag gaaagctaca tggcccaggt gctggaccag aagcataaga
600
aagcctcagg gacacgtcag gcccgcagcc accagcatcc cagggaaaaa taaaatggcc
660
gccgctttcc tgttctctgg ctgtaatccc cagcctctgc cttctctgct ctgggagtcc
720
ccagcctcta gcccctgcta cttccctccc tcttggatag tggtaggggt ccacaaggtg
780
ggggcttgta gcctagggga ggagctgggt ctttgttgtc tggtaggcac caccgcttcc
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900
actcccagtg tcctggtaaa ttt
923

<210> 6270

<211> 307
<212> PRT
<213> Homo sapiens

<400> 6270
Xaa Arg Lys Met Ala Thr Pro Leu Gly Trp Ser Lys Ala Gly Ser Gly
1 5 10 15
Ser Val Cys Leu Ala Leu Asp Gln Leu Arg Asp Val Ile Glu Ser Gln
20 25 30
Glu Glu Leu Ile His Gln Leu Arg Asn Val Met Val Leu Gln Asp Glu
35 40 45
Asn Phe Val Ser Lys Glu Glu Phe Gln Ala Val Glu Lys Lys Leu Val
50 55 60
Glu Glu Lys Ala Ala His Ala Lys Thr Lys Val Leu Leu Ala Lys Glu
65 70 75 80
Glu Glu Lys Leu Gln Phe Ala Leu Gly Glu Val Glu Val Leu Ser Lys
85 90 95
Gln Leu Glu Lys Glu Lys Leu Ala Phe Glu Lys Ala Leu Ser Ser Val
100 105 110
Lys Ser Lys Val Leu Gln Glu Ser Ser Lys Lys Asp Gln Leu Ile Thr
115 120 125
Lys Cys Asn Glu Ile Glu Ser His Ile Ile Lys Gln Glu Asp Ile Leu
130 135 140
Asn Gly Lys Glu Asn Glu Ile Lys Glu Leu Gln Gln Val Ile Ser Gln
145 150 155 160
Gln Lys Gln Ile Phe Ser Pro Pro Pro Ala Gly Ser Val Ala Gly Ile
165 170 175
Thr Cys Leu Thr Ser Gly Ser Arg Ser Ser Arg Lys Ala Thr Trp Pro
180 185 190
Arg Cys Trp Thr Arg Ser Ile Arg Lys Pro Gln Gly His Val Arg Pro
195 200 205
Ala Ala Thr Ser Ile Pro Gly Lys Asn Lys Met Ala Ala Ala Phe Leu
210 215 220
Phe Ser Gly Cys Asn Pro Gln Pro Leu Pro Ser Leu Leu Trp Glu Ser
225 230 235 240
Pro Ala Ser Ser Pro Cys Tyr Phe Pro Pro Ser Trp Ile Val Val Gly
245 250 255
Val His Lys Val Gly Ala Cys Ser Leu Gly Glu Glu Leu Gly Leu Cys
260 265 270
Cys Leu Val Gly Thr Thr Ala Ser Phe Gly Tyr Leu Ile Pro Ser Tyr
275 280 285
Ile Asn Ser Pro Gly Tyr Pro Val Ile Phe His Pro Thr Pro Ser Val
290 295 300
Leu Val Asn
305

<210> 6271
<211> 1437
<212> DNA
<213> Homo sapiens

<400> 6271
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tgtggaggca cagttggtgc tattttcact tgtccactag aagtcattaa gacacggttg
120
cagtcttcaa gattagctct ccggacagtc tactatcctc aggttcatct ggggaccatt
180
agtggagctg gaatggtgag accaacatcc gtgacacctg gactctttca ggttctgaag
240
gctgtatact ttgcatgtta ctccaaagcc aaagagcaat ttaatggcat tttcgtgcct
300
aacagcaata ttgtgcatct tttctcagct ggctctgcag cttttatcac aaattcctta
360
atgaatccta tatggatggt taaaacccga atgcagctag aacagaaagt gaggggctct
420
aagcagatga atacactcca gtgtgctcgt tacgtttacc agaccgaagg cattcgtggc
480
ttctatagag gattaactgc ctcgtatgct ggaatttccg aaactataat ctgctttgct
540
atttatgaaa gtttaaagaa gtatctgaaa gaagctccat tagcctcttc tgcaaatggg
600
actgagaaaa attccacaag ttttttgga cttatggcag ctgctgctct ttctaagggc
660
tgtgcctcct gcattgctta tccacacgaa gtcataagga cgaggctccg ggaagagggc
720
accaagtaca agtcttttgt ccagacggcg cgcctggtgt tccgggaaga aggctacctt
780
gccttttata gaggactgtt tgcccagctt atccggcaga tcccaaatac tgccattgtg
840
ttgtctactt atgagttaat tgtgtacctg ttagaagacc gtactcagta acaggccgga
900
aaattgtgct ctagaagaat aaaactgaaa aactctagag aatttttttt ccccattgat
960
gtttagaaag tttgagactg aaacaggaaa ggccataaaa tatctggttc atatcacctg
1020
ttggacattt ccttttggat tcatgctttc tggaaggttt aaattcatta acgttaatag
1080
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1140
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1260
gagaatacaa cttgttttat aatctgactt taagatcttg cactgctaga cagggaagaa
1320
gtgtcgcatt ttggctgggc actgtggctc acgcctgtaa tcccagcact ttgggaggcc
1380
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1437

<210> 6272
<211> 296
<212> PRT
<213> Homo sapiens

<400> 6272
Xaa Met Ala Thr Gly Gly Gln Gln Lys Glu Asn Thr Leu Leu His Leu

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Phe Ala Gly Gly Cys Gly Gly Thr Val Gly Ala Ile Phe Thr Cys Pro
            20                  25                  30
Leu Glu Val Ile Lys Thr Arg Leu Gln Ser Ser Arg Leu Ala Leu Arg
        35                  40                  45
Thr Val Tyr Tyr Pro Gln Val His Leu Gly Thr Ile Ser Gly Ala Gly
    50                  55                  60
Met Val Arg Pro Thr Ser Val Thr Pro Gly Leu Phe Gln Val Leu Lys
65                  70                  75                  80
Ala Val Tyr Phe Ala Cys Tyr Ser Lys Ala Lys Glu Gln Phe Asn Gly
                85                  90                  95
Ile Phe Val Pro Asn Ser Asn Ile Val His Leu Phe Ser Ala Gly Ser
            100                 105                 110
Ala Ala Phe Ile Thr Asn Ser Leu Met Asn Pro Ile Trp Met Val Lys
        115                 120                 125
Thr Arg Met Gln Leu Glu Gln Lys Val Arg Gly Ser Lys Gln Met Asn
    130                 135                 140
Thr Leu Gln Cys Ala Arg Tyr Val Tyr Gln Thr Glu Gly Ile Arg Gly
145                 150                 155                 160
Phe Tyr Arg Gly Leu Thr Ala Ser Tyr Ala Gly Ile Ser Glu Thr Ile
                165                 170                 175
Ile Cys Phe Ala Ile Tyr Glu Ser Leu Lys Lys Tyr Leu Lys Glu Ala
            180                 185                 190
Pro Leu Ala Ser Ser Ala Asn Gly Thr Glu Lys Asn Ser Thr Ser Phe
        195                 200                 205
Phe Gly Leu Met Ala Ala Ala Ala Leu Ser Lys Gly Cys Ala Ser Cys
    210                 215                 220
Ile Ala Tyr Pro His Glu Val Ile Arg Thr Arg Leu Arg Glu Glu Gly
225                 230                 235                 240
Thr Lys Tyr Lys Ser Phe Val Gln Thr Ala Arg Leu Val Phe Arg Glu
                245                 250                 255
Glu Gly Tyr Leu Ala Phe Tyr Arg Gly Leu Phe Ala Gln Leu Ile Arg
            260                 265                 270
Gln Ile Pro Asn Thr Ala Ile Val Leu Ser Thr Tyr Glu Leu Ile Val
        275                 280                 285
Tyr Leu Leu Glu Asp Arg Thr Gln
    290                 295
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<210> 6273
<211> 2355
<212> DNA
<213> Homo sapiens

<400> 6273
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ccccagacat gccggtgttc acagagcaga tgatccagca ggagcagctg gactcggtga
120
tggactggct caccaaccag ccgcggccgg cagctggtgg acaaggacag caccttcctc
180
agcacgctgg agcaccacct gagccgctac ctgaaggacg tgaagcagca ccacgtcaag
240
gctgacaagc gggacccaga gtttgtcttc tacgaccagc tgaagcaagt gatgaatgcg
300

tacagagtca agccggccgt ctttgacctg ctcctggctg ttggcattgc tgcctacctc
360
ggcatggcct acgtggctgt ccaggtgagc agtgcccagg ctcagcactt cagcctcctc
420
tacaagaccg tccagaggct gctcgtgaag gccaagacac agtgacacag ccacccccac
480
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ccgccgcggg cggccctgca gggacagggg ccctctccct ccccggcggt ggttggaaca
600
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660
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720
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780
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1620
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1740
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1920

tggccaccag ttcttcggcc agcacctctg ccctccagaa cctgcagcct ggaggggtga
1980
ggggacaacc acccctcttt cctccaggtt ggcaggggac cctcttctcc cgtctgccct
2040
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2340
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2355

<210> 6274
<211> 70
<212> PRT
<213> Homo sapiens

<400> 6274
Asp Pro Glu Phe Val Phe Tyr Asp Gln Leu Lys Gln Val Met Asn Ala
1 5 10 15
Tyr Arg Val Lys Pro Ala Val Phe Asp Leu Leu Leu Ala Val Gly Ile
20 25 30
Ala Ala Tyr Leu Gly Met Ala Tyr Val Ala Val Gln Val Ser Ser Ala
35 40 45
Gln Ala Gln His Phe Ser Leu Leu Tyr Lys Thr Val Gln Arg Leu Leu
50 55 60
Val Lys Ala Lys Thr Gln
65 70

<210> 6275
<211> 1534
<212> DNA
<213> Homo sapiens

<400> 6275
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120
gcctcctgcc ccgcgcgatg agacttcccc ggcggacgct gtgtgccctg gccttggacg
180
tgacctctgt gggtcctccc gttgctgcct gcggccgccg agccaacctg attggaagga
240
gccgagcggc gcagctttgc gggcccgacc ggctccgcgt ggcaggtgaa gtgcaccggt
300
ttagaacctc tgacgtctct caagccactt tagccagtgt agccccagta tttactgtga
360
caaaatttga caaacaggga aacgttactt cttttgaaag gaagaaaact gaattatacc
420

aagagttagg tcttcaagcc agagatttga gatttcagca tgtaatgagt atcacagtca
480
gaaacaatag gattatcatg agaatggagt atttgaaagc tgtgataact ccagagtgtc
540
ttctgatatt agattatcgt aatttaaact tagagcaatg gctgttccgg gaactcccct
600
cacagttgtc tggagagggt caactcgtta catacccttt acctttgag tttagagcta
660
tagaagcact cctgcaatat tggatcatgt tgttatctag atcaacaccc ttcaggggaa
720
acttagcatt ttgcagccac tgatccttga gaccttggat gctttggtgg accccaaaca
780
ttcttctgta gacagaagca aactgcacat tttactacag aatggcaaaa gtctatcaga
840
gttagaaaca gatattaaaa ttttcaaaga gtcaattttg gagatcttgg atgaggaaga
900
gttgctagaa gagctctgtg tatcaaaatg ggagtgaccc acaagtcttt gnaaaagagc
960
agtgctggga ttgaccatgc agaagaaatg gagttgctgt tggaaaacta ctaccgattg
1020
gctgacgatc tctccaatgc agctcgtgag cttagggtgc tgattgatga ttcacaaagt
1080
attattttca ttaatctgga cagccaccga aacgtgatga ttaggttgaa tctacagctg
1140
accatgggaa ccttctctct ttcgctcttt ggactaatgg gagttgcttt tggaatgaat
1200
ttggaatctt cccttgaaga ggaccataga atttttggc tgattacagg aattatgttc
1260
atgggaagtg gcctcatctg gaggcgcctg ctttcattcc ttggacgaca gctagaagct
1320
ccattgcctc ctatgatggc ttctttacct aaaaagactc ttctggcaga tagaagcatg
1380
gaattgaaaa atagcctcag actggatgga cttggatcag gaaggagcat cctaacaaac
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cgttaggaac agccccgtgg atactgaagt ttttttatg gtagttacag gaaacttctg
1500
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1534

<210> 6276
<211> 172
<212> PRT
<213> Homo sapiens

<400> 6276
Met Gly Val Thr His Lys Ser Leu Xaa Lys Ser Ser Ala Gly Ile Asp
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His Ala Glu Glu Met Glu Leu Leu Leu Glu Asn Tyr Tyr Arg Leu Ala
            20   25   30
Asp Asp Leu Ser Asn Ala Ala Arg Glu Leu Arg Val Leu Ile Asp Asp
        35   40   45
Ser Gln Ser Ile Ile Phe Ile Asn Leu Asp Ser His Arg Asn Val Met
    50   55   60
Ile Arg Leu Asn Leu Gln Leu Thr Met Gly Thr Phe Ser Leu Ser Leu

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65                  70                  75                  80
Phe Gly Leu Met Gly Val Ala Phe Gly Met Asn Leu Glu Ser Ser Leu
                85                  90                  95
Glu Glu Asp His Arg Ile Phe Trp Leu Ile Thr Gly Ile Met Phe Met
            100                 105                 110
Gly Ser Gly Leu Ile Trp Arg Arg Leu Leu Ser Phe Leu Gly Arg Gln
        115                 120                 125
Leu Glu Ala Pro Leu Pro Pro Met Met Ala Ser Leu Pro Lys Lys Thr
    130                 135                 140
Leu Leu Ala Asp Arg Ser Met Glu Leu Lys Asn Ser Leu Arg Leu Asp
145                 150                 155                 160
Gly Leu Gly Ser Gly Arg Ser Ile Leu Thr Asn Arg
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<210> 6277
<211> 1206
<212> DNA
<213> Homo sapiens

<400> 6277
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<210> 6278
<211> 399
<212> PRT
<213> Homo sapiens

<400> 6278
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35 40 45
Asp Gly Ser Thr Val Val Pro Ala Gly Pro Glu Pro Pro Pro Gln Ser
50 55 60
Ser Arg Ala Glu Ser Ser Ser Gly Gly Gly Thr Val Pro Ser Ser Ala
65 70 75 80
Gly Ile Leu Glu Gln Gly Pro Ser Pro Gly Asp Gly Ser Pro Pro Lys
85 90 95
Pro Lys Asp Pro Val Ser Ala Ala Val Pro Ala Pro Xaa Glu Lys Gln
100 105 110
Gln Ser Asp Ser Ile Trp Pro Lys Ser Ala Pro Gly Ser Cys Trp Leu
115 120 125
Pro Pro Ala Leu His Gly Pro Pro His Asn Ala Ala Gly Pro Ser Pro
130 135 140
His Thr Leu Arg Arg Ala Val Lys Lys Pro Ala Pro Ala Pro Pro Lys
145 150 155 160
Pro Gly Asn Pro Pro Pro Gly His Pro Gly Gly Gln Ser Ser Ser Gly
165 170 175
Thr Ser Gln His Pro Pro Ser Leu Ser Pro Lys Pro Pro Thr Arg Ser
180 185 190
Pro Ser Pro Pro Pro Ser Thr Arg Ala Ser Leu Gln Ala Ser Pro Pro
195 200 205
Pro Pro Pro Ser Ser Gln His Pro Gly Gly Thr Pro Xaa Ser Leu Ser
210 215 220
Pro Ile Gln Ala Pro Asn His Pro Pro Pro Gln Pro Pro Thr Gln Ala
225 230 235 240
Thr Pro Leu Met His Thr Lys Pro Asn Ser Gln Gly Pro Pro Asn Pro
245 250 255
Met Ala Leu Pro Ser Glu His Gly Leu Glu Gln Pro Ser His Thr Pro
260 265 270
Pro Gln Thr Pro Thr Pro Pro Ser Thr Pro Pro Leu Gly Lys Gln Asn
275 280 285
Pro Ser Leu Pro Ala Pro Gln Thr Leu Ala Gly Gly Asn Pro Glu Thr
290 295 300
Ala Gln Pro His Ala Gly Thr Leu Pro Arg Pro Arg Pro Val Pro Lys

305 310 315 320
Pro Arg Asn Arg Pro Ser Val Pro Pro Pro Pro Gln Pro Pro Gly Val
325 330 335
His Ser Ala Gly Asp Ser Ser Leu Thr Asn Thr Ala Pro Thr Ala Ser
340 345 350
Lys Ile Val Thr Asp Ser Asn Ser Arg Val Ser Glu Pro His Arg Ser
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Ile Phe Pro Glu Met His Ser Asp Ser Ala Ser Lys Asp Val Pro Gly
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Arg Ile Leu Leu Asp Ile Asp Asn Asp Thr Glu Ser Thr Ala Leu
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<210> 6279
<211> 2795
<212> DNA
<213> Homo sapiens

<400> 6279
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<210> 6280
<211> 619
<212> PRT
<213> Homo sapiens

<400> 6280
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        35   40   45
Ser Leu Ser Leu Glu Ile Leu Gln Ile Ile Lys Glu Ser Gln Gln Gln
    50   55   60
His Gly Leu Arg His Gly Asp Phe Gln Arg Tyr Arg Gly Tyr Cys Ser
65   70   75   80
Arg Arg Gln Arg Arg Leu Arg Lys Thr Leu Asn Phe Lys Met Gly Asn
                85   90   95
Arg His Lys Phe Thr Gly Lys Lys Val Thr Glu Glu Leu Leu Thr Asp
            100   105   110
Asn Arg Tyr Leu Leu Leu Val Leu Met Asp Ala Glu Arg Ala Trp Ser
115   120   125
Tyr Ala Met Gln Leu Lys Gln Glu Ala Asn Thr Glu Pro Arg Lys Arg
    130   135   140
Phe His Leu Leu Ser Arg Leu Arg Lys Ala Val Lys His Ala Glu Glu
145   150   155   160
Leu Glu Arg Leu Cys Lys Ser Asn Arg Val Asp Ala Lys Thr Lys Leu
                165   170   175
Glu Ala Gln Ala Tyr Thr Ala Tyr Leu Ser Gly Met Leu Arg Phe Glu
            180   185   190
His Gln Glu Trp Lys Ala Ala Ile Glu Ala Phe Asn Lys Cys Lys Thr
        195   200   205
Ile Tyr Glu Lys Leu Ala Ser Ala Phe Thr Glu Glu Gln Ala Val Leu
    210   215   220
Tyr Asn Gln Arg Val Glu Glu Ile Ser Pro Asn Ile Arg Tyr Cys Ala
225   230   235   240
Tyr Asn Ile Gly Asp Gln Ser Ala Ile Asn Glu Leu Met Gln Met Arg
                245   250   255
Leu Arg Ser Gly Gly Thr Glu Gly Leu Leu Ala Glu Lys Leu Glu Ala
            260   265   270
Leu Ile Thr Gln Thr Arg Ala Lys Gln Ala Ala Thr Met Ser Glu Val
        275   280   285
Glu Trp Arg Gly Arg Thr Val Pro Val Lys Ile Asp Lys Val Arg Ile
    290   295   300
Phe Leu Leu Gly Leu Ala Asp Asn Glu Ala Ala Ile Val Gln Ala Glu
305   310   315   320
Ser Glu Glu Thr Lys Glu Arg Leu Phe Glu Ser Met Leu Ser Glu Cys
                325   330   335
Arg Asp Ala Ile Gln Val Val Arg Glu Glu Leu Lys Pro Asp Gln Lys

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Gln Arg Asp Tyr Ile Leu Glu Gly Glu Pro Gly Lys Val Ser Asn Leu
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Gln Tyr Leu His Ser Tyr Leu Thr Tyr Ile Lys Leu Ser Thr Ala Ile
    370                 375                 380
Lys Arg Asn Glu Asn Met Ala Lys Gly Leu His Arg Ala Leu Leu Gln
385                 390                 395                 400
Gln Gln Pro Glu Asp Asp Ser Lys Arg Ser Pro Arg Pro Gln Asp Leu
                405                 410                 415
Ile Arg Leu Tyr Asp Ile Ile Leu Gln Asn Leu Val Glu Leu Leu Gln
            420                 425                 430
Leu Pro Gly Leu Glu Glu Asp Lys Ala Phe Gln Lys Glu Ile Gly Leu
        435                 440                 445
Lys Thr Leu Val Phe Lys Ala Tyr Arg Cys Phe Phe Ile Ala Gln Ser
    450                 455                 460
Tyr Val Leu Val Lys Lys Trp Ser Glu Ala Leu Val Leu Tyr Asp Arg
465                 470                 475                 480
Val Leu Lys Tyr Ala Asn Glu Val Asn Ser Asp Ala Gly Ala Phe Lys
                485                 490                 495
Asn Ser Leu Lys Asp Leu Pro Asp Val Gln Glu Leu Ile Thr Gln Val
            500                 505                 510
Arg Ser Glu Lys Cys Ser Leu Gln Ala Ala Ala Ile Leu Asp Ala Asn
        515                 520                 525
Asp Ala His Gln Thr Glu Thr Ser Ser Ser Gln Val Lys Asp Asn Lys
    530                 535                 540
Pro Leu Val Glu Arg Phe Glu Thr Phe Cys Leu Asp Pro Ser Leu Val
545                 550                 555                 560
Thr Lys Gln Ala Asn Leu Val His Phe Pro Pro Gly Phe Gln Pro Ile
                565                 570                 575
Pro Cys Lys Pro Leu Phe Phe Asp Leu Ala Leu Asn His Val Ala Phe
            580                 585                 590
Pro Pro Leu Glu Asp Lys Leu Glu Gln Lys Thr Lys Ser Gly Leu Thr
        595                 600                 605
Gly Tyr Ile Lys Gly Ile Phe Gly Phe Arg Ser
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<210> 6281
<211> 741
<212> DNA
<213> Homo sapiens

<400> 6281

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240
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360
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<210> 6282
<211> 162
<212> PRT
<213> Homo sapiens

<400> 6282
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35 40 45
Lys Glu Leu Leu Glu Gln Met Asp Leu Glu Val Arg Glu Ile Pro Pro
50 55 60
Gln Ser Arg Gly Met Tyr Ser Asn Arg Met Arg Ser Tyr Lys Gln Glu
65 70 75 80
Met Gly Lys Leu Glu Thr Asp Phe Lys Arg Ser Arg Ile Ala Tyr Ser
85 90 95
Asp Glu Val Arg Asn Glu Leu Leu Gly Asp Asp Gly Asn Ser Ser Glu
100 105 110
Asn Gln Arg Ala His Leu Leu Asp Asn Thr Glu Arg Leu Glu Arg Ser
115 120 125
Ser Arg Arg Leu Glu Ala Gly Tyr Gln Ile Ala Val Glu Thr Gly Glu
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<210> 6283
<211> 2312
<212> DNA
<213> Homo sapiens

<400> 6283
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<210> 6284
<211> 122
<212> PRT
<213> Homo sapiens

<400> 6284
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Lys Pro Ile His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile
35 40 45
Ala Ser Val Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe Ser Leu Lys
50 55 60
Asn Thr Thr Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala
65 70 75 80
Asn Ser Thr Gly Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr
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Ile Leu Leu Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr
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Asp Arg Gln Pro Leu Leu His Asp Gly Glu
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<210> 6285
<211> 2542
<212> DNA
<213> Homo sapiens

<400> 6285
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2340
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<210> 6286
<211> 57
<212> PRT
<213> Homo sapiens

<400> 6286
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Ser Cys Gly Gln His Glu Gln Gln Ile Pro Pro Asp His His Lys Asp
            20   25   30
Ala Gly Asn Ile Tyr Leu Gly Thr Ser Pro Pro Ser Gln Glu Pro Ser
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Ser Pro Trp Ala Ser Trp His Arg Ser
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<210> 6287
<211> 1674
<212> DNA
<213> Homo sapiens

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240
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300
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420
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480
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<210> 6288

<211> 269
<212> PRT
<213> Homo sapiens

<400> 6288
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35 40 45
Ser Val Lys Leu Asp Glu His Ile Ile Pro Leu Gly Ser Met Ala Ile
50 55 60
Asn Ser Ile Ser Lys Leu Thr Gln Leu Thr Gln Ser Ser Met Tyr Ser
65 70 75 80
Leu Pro Asn Ala Pro Thr Leu Ala Asp Leu Glu Asp Asp Thr His Glu
85 90 95
Ala Ser Asp Asp Gln Pro Glu Lys Pro His Phe Asp Ser Arg Ser Val
100 105 110
Ile Phe Glu Leu Asp Ser Cys Asn Gly Ser Gly Lys Val Cys Leu Val
115 120 125
Tyr Lys Ser Gly Lys Pro Ala Leu Ala Glu Asp Thr Glu Ile Trp Phe
130 135 140
Leu Asp Arg Ala Leu Tyr Trp His Phe Leu Thr Asp Thr Phe Thr Ala
145 150 155 160
Tyr Tyr Arg Leu Leu Ile Thr His Leu Gly Leu Pro Gln Trp Gln Tyr
165 170 175
Ala Phe Thr Ser Tyr Gly Ile Ser Pro Gln Ala Lys Gln Trp Phe Ser
180 185 190
Met Tyr Lys Pro Ile Thr Tyr Asn Thr Asn Leu Leu Thr Glu Glu Thr
195 200 205
Asp Ser Phe Val Asn Lys Leu Asp Pro Ser Lys Val Phe Lys Ser Lys
210 215 220
Asn Lys Ile Val Ile Pro Lys Lys Lys Gly Pro Val Gln Pro Ala Gly
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Gly Gln Lys Gly Pro Ser Gly Pro Ser Gly Pro Ser Thr Ser Ser Thr
245 250 255
Ser Lys Ser Ser Ser Gly Ser Gly Asn Pro Thr Arg Lys
260 265

<210> 6289
<211> 1321
<212> DNA
<213> Homo sapiens

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240

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420
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540
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600
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660
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720
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1321

<210> 6290
<211> 172
<212> PRT
<213> Homo sapiens

<400> 6290
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Pro Tyr Cys Leu Glu Ala Gly Glu Pro Thr Pro Gly Leu Ser Asp Thr
20 25 30
Ser Pro Asp Glu Gly Leu Ile Glu Asp Leu Thr Ile Glu Asp Lys Ala
35 40 45
Val Glu Gln Leu Ala Glu Gly Leu Leu Ser His Tyr Leu Pro Asp Leu
50 55 60
Gln Arg Ser Lys Gln Ala Leu Gln Glu Leu Thr Gln Asn Gln Val Val

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65                  70                  75                  80
Leu Leu Asp Thr Leu Glu Gln Glu Ile Ser Lys Phe Lys Glu Cys His
                85                  90                  95
Ser Met Leu Asp Ile Asn Ala Leu Phe Ala Glu Ala Lys His Tyr His
            100                 105                 110
Ala Lys Leu Val Asn Ile Arg Lys Glu Met Leu Met Leu His Glu Lys
        115                 120                 125
Thr Ser Lys Leu Lys Lys Arg Ala Leu Lys Leu Gln Gln Lys Arg Gln
    130                 135                 140
Lys Glu Glu Leu Glu Arg Glu Gln Gln Arg Glu Lys Gly Phe Glu Arg
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Glu Lys Gln Leu Thr Ala Arg Pro Ala Lys Arg Met
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<210> 6291
<211> 2718
<212> DNA
<213> Homo sapiens

<400> 6291

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<210> 6292
<211> 497
<212> PRT
<213> Homo sapiens

<400> 6292
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Leu Ser Arg Pro Gln Pro Pro Pro Asp Pro Leu Leu Leu Gln Arg Leu
        35   40   45
Pro Arg Pro Ser Ser Leu Ser Asp Lys Thr Gln Leu His Ser Arg Trp
    50   55   60
Leu Asp Ser Ser Arg Cys Leu Met Gln Gln Gly Ile Lys Ala Gly Asp
65   70   75   80
Ala Leu Trp Leu Arg Phe Lys Tyr Tyr Ser Phe Phe Asp Leu Asp Pro
                85   90   95
Lys Thr Asp Pro Val Arg Leu Thr Gln Leu Tyr Glu Gln Ala Arg Trp
            100   105   110
Asp Leu Leu Leu Glu Glu Ile Asp Cys Thr Glu Glu Glu Met Met Val
        115   120   125
Phe Ala Ala Leu Gln Tyr His Ile Asn Lys Leu Ser Gln Ser Gly Glu
    130   135   140
Val Gly Glu Pro Ala Gly Thr Asp Pro Gly Leu Asp Asp Leu Asp Val
145   150   155   160
Ala Leu Ser Asn Leu Glu Val Lys Leu Glu Gly Ser Ala Pro Thr Asp
                165   170   175
Val Leu Asp Ser Leu Thr Thr Ile Pro Glu Leu Lys Asp Tyr Leu Arg
            180   185   190
Ile Phe Arg Pro Arg Lys Leu Thr Leu Lys Gly Tyr Arg Gln His Trp
        195   200   205
Val Val Phe Lys Glu Thr Thr Leu Ser Tyr Tyr Lys Ser Gln Asp Glu
    210   215   220
Ala Pro Gly Asp Pro Ile Gln Gln Leu Asn Leu Lys Gly Cys Glu Val
225   230   235   240
Val Pro Asp Val Asn Val Ser Gly Gln Lys Phe Cys Ile Lys Leu Leu
                245   250   255
Val Pro Ser Pro Glu Gly Met Ser Glu Ile Tyr Leu Arg Cys Gln Asp
            260   265   270
Glu Gln Gln Tyr Ala Arg Trp Met Ala Gly Cys Arg Leu Ala Ser Lys
        275   280   285
Gly Arg Thr Met Ala Asp Ser Ser Tyr Thr Ser Glu Val Gln Ala Ile
    290   295   300
Leu Ala Phe Leu Ser Leu Gln His Gly Gln Trp Gly Pro Arg Gln Pro
305   310   315   320
Pro Pro Arg Pro Asp Ala Ser Ala Glu Gly Leu Asn Pro Tyr Gly Leu
                325   330   335
Val Ala Pro Arg Phe Gln Arg Lys Phe Lys Ala Lys Gln Leu Thr Pro

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            340                 345                 350
Arg Ile Leu Glu Ala His Gln Asn Val Ala Gln Leu Ser Leu Ala Glu
        355                 360                 365
Ala Gln Leu Arg Phe Ile Gln Ala Trp Gln Ser Leu Pro Asp Phe Gly
    370                 375                 380
Ile Ser Tyr Val Met Val Arg Phe Lys Gly Ser Arg Lys Asp Glu Ile
385                 390                 395                 400
Leu Gly Ile Ala Asn Asn Arg Leu Ile Arg Ile Asp Leu Ala Val Gly
                405                 410                 415
Asp Val Val Lys Thr Trp Arg Phe Ser Asn Met Arg Gln Trp Asn Val
            420                 425                 430
Asn Trp Asp Ile Arg Gln Val Ala Ile Glu Phe Asp Glu His Ile Asn
        435                 440                 445
Val Ala Phe Ser Cys Val Ser Ala Ser Cys Arg Ile Val His Glu Tyr
    450                 455                 460
Ile Gly Gly Tyr Ile Phe Leu Ser Thr Arg Glu Arg Ala Arg Gly Glu
465                 470                 475                 480
Glu Leu Asp Glu Asp Leu Phe Leu Gln Leu Thr Gly Gly His Glu Ala
                485                 490                 495
Phe
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<210> 6293
<211> 750
<212> DNA
<213> Homo sapiens

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<210> 6294
<211> 250
<212> PRT
<213> Homo sapiens

<400> 6294
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20 25 30
Gly Gly Thr Ala Ile Ala Gly Ser Val Glu Ala Val Ala Arg Leu Lys
35 40 45
Arg Ser Arg Leu Lys Val Arg Phe Cys Thr Asn Glu Ser Gln Lys Ser
50 55 60
Arg Ala Glu Leu Val Gly Gln Leu Gln Arg Leu Gly Phe Asp Ile Ser
65 70 75 80
Glu Gln Glu Val Thr Ala Pro Ala Pro Ala Ala Cys Gln Ile Leu Lys
85 90 95
Glu Arg Gly Leu Arg Pro Tyr Leu Leu Ile His Asp Gly Val Arg Ser
100 105 110
Glu Phe Asp Gln Ile Asp Thr Ser Asn Pro Asn Cys Val Val Ile Ala
115 120 125
Asp Ala Gly Glu Ser Phe Ser Tyr Gln Asn Met Asn Asn Ala Phe Gln
130 135 140
Val Leu Met Glu Leu Glu Lys Pro Val Leu Ile Ser Leu Gly Lys Gly
145 150 155 160
Arg Tyr Tyr Lys Glu Thr Ser Gly Leu Met Leu Asp Val Gly Pro Tyr
165 170 175
Met Lys Ala Leu Glu Tyr Ala Cys Gly Ile Lys Ala Glu Val Val Gly
180 185 190
Lys Pro Ser Pro Glu Phe Phe Lys Ser Ala Leu Gln Ala Ile Gly Val
195 200 205
Glu Ala His Gln Ala Val Met Ile Gly Asp Asp Ile Val Gly Asp Val
210 215 220
Gly Gly Ala Gln Arg Cys Gly Met Arg Ala Leu Gln Val Arg Thr Gly
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Lys Phe Arg Pro Ser Asp Glu His His Pro
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<210> 6295
<211> 2091
<212> DNA
<213> Homo sapiens

<400> 6295
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1260
gtgcagcggg aaactgggaa gcttgatgga ccagacaaat aggatgatgg cttgaccgag
1320
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1440
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1680
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1800
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1860

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1980
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2091

<210> 6296
<211> 399
<212> PRT
<213> Homo sapiens

<400> 6296
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Ala Cys Gly Cys Arg Leu Val Leu Gly Gly Arg Asp Asp Val Ser Ala
35 40 45
Gly Leu Arg Gly Ser His Gly Ala Arg Gly Glu Pro Leu Asp Pro Ala
50 55 60
Arg Pro Leu Gln Arg Pro Pro Arg Pro Glu Val Pro Arg Ala Phe Arg
65 70 75 80
Arg Gln Pro Arg Ala Ala Ala Pro Ser Phe Phe Phe Ser Ser Ile Lys
85 90 95
Gly Gly Arg Arg Ser Ile Ser Phe Ser Val Gly Ala Ser Ser Val Val
100 105 110
Gly Ser Gly Gly Ser Ser Asp Lys Gly Lys Leu Ser Leu Gln Asp Val
115 120 125
Ala Glu Leu Ile Arg Ala Arg Ala Cys Gln Arg Val Val Val Met Val
130 135 140
Gly Ala Gly Ile Ser Thr Pro Ser Gly Ile Pro Asp Phe Arg Ser Pro
145 150 155 160
Gly Ser Gly Leu Tyr Ser Asn Leu Gln Gln Tyr Asp Leu Pro Tyr Pro
165 170 175
Glu Ala Ile Phe Glu Leu Pro Phe Phe Phe His Asn Pro Lys Pro Phe
180 185 190
Phe Thr Leu Ala Lys Glu Leu Tyr Pro Gly Asn Tyr Lys Pro Asn Val
195 200 205
Thr His Tyr Phe Leu Arg Leu Leu His Asp Lys Gly Leu Leu Leu Arg
210 215 220
Leu Tyr Thr Gln Asn Ile Asp Gly Leu Glu Arg Val Ser Gly Ile Pro
225 230 235 240
Ala Ser Lys Leu Val Glu Ala His Gly Thr Phe Ala Ser Ala Thr Cys
245 250 255
Thr Val Cys Gln Arg Pro Phe Pro Gly Glu Asp Ile Arg Ala Asp Val
260 265 270
Met Ala Asp Arg Val Pro Arg Cys Pro Val Cys Thr Gly Val Val Lys
275 280 285
Pro Asp Ile Val Phe Phe Gly Glu Pro Leu Pro Gln Arg Phe Leu Leu
290 295 300
His Val Val Asp Phe Pro Met Ala Asp Leu Leu Leu Ile Leu Gly Thr

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305                 310                 315                 320
Ser Leu Glu Val Glu Pro Phe Ala Ser Leu Thr Glu Ala Val Arg Ser
                325                 330                 335
Ser Val Pro Arg Leu Leu Ile Asn Arg Asp Leu Val Gly Pro Leu Ala
            340                 345                 350
Trp His Pro Arg Ser Arg Asp Val Ala Gln Leu Gly Asp Val Val His
        355                 360                 365
Gly Val Glu Ser Leu Val Glu Leu Leu Gly Trp Thr Glu Glu Met Arg
    370                 375                 380
Asp Leu Val Gln Arg Glu Thr Gly Lys Leu Asp Gly Pro Asp Lys
385                 390                 395
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<210> 6297
<211> 472
<212> DNA
<213> Homo sapiens

<400> 6297
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120
ttcggaagcc cgttcggcct ggaggagccg cagtgggtcc cggacaagga gtgtcggaga
180
tgtatgcagt gtgacgccaa gtttgacttt ctcaccagaa agcaccactg tcgccgctgc
240
gggaagtgct tctgcgacag gtgctgcagc cagaaggtgc cgctgcggcg catgtgcttt
300
gtggaccccg tgcggcagtg cgcggagtgc gccctggtgt ccctcaagga ggcggagttc
360
tacgacaagc agctcaaagt gctcctgagc ggtaaggacg ggtgtcctgc acagtcctgc
420
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472

<210> 6298
<211> 146
<212> PRT
<213> Homo sapiens

<400> 6298
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Ser Pro Ser Gly Leu Arg Met Val Pro Glu His Arg Ala Phe Gly Ser
            20                  25                  30
Pro Phe Gly Leu Glu Glu Pro Gln Trp Val Pro Asp Lys Glu Cys Arg
        35                  40                  45
Arg Cys Met Gln Cys Asp Ala Lys Phe Asp Phe Leu Thr Arg Lys His
    50                  55                  60
His Cys Arg Arg Cys Gly Lys Cys Phe Cys Asp Arg Cys Cys Ser Gln
65                  70                  75                  80
Lys Val Pro Leu Arg Arg Met Cys Phe Val Asp Pro Val Arg Gln Cys
                85                  90                  95
Ala Glu Cys Ala Leu Val Ser Leu Lys Glu Ala Glu Phe Tyr Asp Lys
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            100                 105                 110
Gln Leu Lys Val Leu Leu Ser Gly Lys Asp Gly Cys Pro Ala Gln Ser
        115                 120                 125
Cys Ala Leu Arg Gln Pro Ala Pro Arg Val Cys Gly Asp Ala Val Gly
    130                 135                 140
Cys Ala
145
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<210> 6299
<211> 1466
<212> DNA
<213> Homo sapiens

<400> 6299
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gcccatctcc gcgctggaga gcgatgcggc caagccagcg gaggcccccg acgctcccga
120
ggcggccagc ccgcccattg gcccagggag agcctggttc tgtaccactg gacccagtcc
180
ttcagctcgc agaaggtgcg gctggtgatc gccgagaagg gcctggtgtg cgaggagcgg
240
gacgtgagcc tgccacagag cgagcacaag gagccctggt tcatgcggct caacctgggc
300
gaggaggtgc ccgtcatcat ccaccgcgac aacatcatca gtgactatga ccagatcatt
360
gactatgtgg agcgcacctt cacaggagag cacgtggtgg ccctgatgcc cgaggtgggc
420
agcctgcagc acgcacgggt gctgcagtac cgggagctgc tggacgcact gcccatggat
480
gcctacacgc atggctgcat cctgcatccc gagctcacca ccgactccat gatccccaag
540
tacgccacgg ccgagatccg cagacattta gccaatgcca ccacggacct catgaaactg
600
gaccatgaag aggagcccca gctctccgag ccctaccttt ctaaacaaaa gaagctcatg
660
gccaagatct tggagcatga tgatgtgagc tacctgaaga agatcctcgg ggaactggcc
720
atggtgctgg accagattga ggcggagctg gagaagagga agctggagaa cgaggggcag
780
aaatgcgagc tgtggctctg tggctgtgcc ttcaccctcg ctgatgtcct cctgggagcc
840
accctgcacc gcctcaagtt cctgggactg tccaagaaat actgggaaga tggcagccgg
900
cccaacctgc agtccttctt tgagagggtc cagagacgct ttgccttccg gaaagtcctg
960
ggtgacatcc acaccaccct gctgtcggcc gtcatcccca atgctttccg gctggtcaag
1020
aggaaacccc catccttctt cggggcgtcc ttcctcatgg gctccctggg tgggatgggc
1080
tactttgcct actggtacct caagaaaaaa tacatctagg gccaggcctg gggcttggtg
1140
tctgactgtc ggtgtctctg tgctgtgtga ttccccgtga gctctcagta actcactgtc
1200

tcatgaacac ttggacagcc ctccccgccc ttcgttctga gtaataatac cgtcagtgtg
1260
aaaacattcc gtagtttaga agtagacgtt gcaaatgctg tgactcaagg ccacggctct
1320
gctaaaagag agagaaggaa cgagagagag agagaaaaaa caaaaaacca gaaaaccacg
1380
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1440
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1466

<210> 6300
<211> 372
<212> PRT
<213> Homo sapiens

<400> 6300
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Leu Gln Leu Val Ala His Leu Arg Ala Gly Glu Arg Cys Gly Gln Ala
            20   25   30
Ser Gly Gly Pro Arg Arg Ser Arg Gly Gly Gln Pro Ala His Trp Pro
        35   40   45
Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln
    50   55   60
Lys Val Arg Leu Val Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg
65   70   75   80
Asp Val Ser Leu Pro Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg
                85   90   95
Leu Asn Leu Gly Glu Glu Val Pro Val Ile Ile His Arg Asp Asn Ile
            100   105   110
Ile Ser Asp Tyr Asp Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr
        115   120   125
Gly Glu His Val Val Ala Leu Met Pro Glu Val Gly Ser Leu Gln His
    130   135   140
Ala Arg Val Leu Gln Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp
145   150   155   160
Ala Tyr Thr His Gly Cys Ile Leu His Pro Glu Leu Thr Thr Asp Ser
                165   170   175
Met Ile Pro Lys Tyr Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn
            180   185   190
Ala Thr Thr Asp Leu Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu
        195   200   205
Ser Glu Pro Tyr Leu Ser Lys Gln Lys Lys Leu Met Ala Lys Ile Leu
    210   215   220
Glu His Asp Asp Val Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala
225   230   235   240
Met Val Leu Asp Gln Ile Glu Ala Glu Leu Glu Lys Arg Lys Leu Glu
                245   250   255
Asn Glu Gly Gln Lys Cys Glu Leu Trp Leu Cys Gly Cys Ala Phe Thr
            260   265   270
Leu Ala Asp Val Leu Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu
        275   280   285
Gly Leu Ser Lys Lys Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln

290 295 300
Ser Phe Phe Glu Arg Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu
305 310 315 320
Gly Asp Ile His Thr Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe
325 330 335
Arg Leu Val Lys Arg Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu
340 345 350
Met Gly Ser Leu Gly Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys
355 360 365
Lys Lys Tyr Ile
370

<210> 6301
<211> 911
<212> DNA
<213> Homo sapiens

<400> 6301
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120
ccgaagctct cgctgactct gtccagctca gtgtctcgag ggaatgtgtc cactccccca
180
cgccacagca gtggaagcct tactcccccc gtgaccccac ccatcacccc ctcctcttca
240
ttccgcagca gcactccgac aggcagcgag tatgacgagg aggaggtgga ctatgaggag
300
tcggacagcg atgagtcctg gaccacagag agtgccatca gctccgaagc catcctcagc
360
tccatgtgca tgaatggagg ggaagagaag ccttttgcct gcccagttcc tggatgtaaa
420
aagagataca agaatgtgaa tggcataaag tatcacgcta agaatggtca cagaacacag
480
attcgtgtcc gcaaaccatt caagtgtcgc tgtgggaaga gttacaagac agctcagggc
540
ctgcggcacc acacaatcaa tttccatccc ccggtgtcgg ctgagattat caggaagatg
600
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660
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720
atgcatgctt taaatttttt ctgtaatttt ggaatgatgt atctttgtag agttaatgat
780
tttgtacatt tgcacatgta atcatcatac ccattttcat tactttgata taaggtgcta
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911

<210> 6302
<211> 202
<212> PRT

<213> Homo sapiens

<400> 6302
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Leu Ser Tyr Ile Asn Arg Phe Met Thr Asp Ala Ala Arg Arg Glu Gln
20 25 30
Glu Ser Leu Lys Lys Lys Ile Gln Pro Lys Leu Ser Leu Thr Leu Ser
35 40 45
Ser Ser Val Ser Arg Gly Asn Val Ser Thr Pro Pro Arg His Ser Ser
50 55 60
Gly Ser Leu Thr Pro Pro Val Thr Pro Pro Ile Thr Pro Ser Ser Ser
65 70 75 80
Phe Arg Ser Ser Thr Pro Thr Gly Ser Glu Tyr Asp Glu Glu Glu Val
85 90 95
Asp Tyr Glu Glu Ser Asp Ser Asp Glu Ser Trp Thr Thr Glu Ser Ala
100 105 110
Ile Ser Ser Glu Ala Ile Leu Ser Ser Met Cys Met Asn Gly Gly Glu
115 120 125
Glu Lys Pro Phe Ala Cys Pro Val Pro Gly Cys Lys Lys Arg Tyr Lys
130 135 140
Asn Val Asn Gly Ile Lys Tyr His Ala Lys Asn Gly His Arg Thr Gln
145 150 155 160
Ile Arg Val Arg Lys Pro Phe Lys Cys Arg Cys Gly Lys Ser Tyr Lys
165 170 175
Thr Ala Gln Gly Leu Arg His His Thr Ile Asn Phe His Pro Pro Val
180 185 190
Ser Ala Glu Ile Ile Arg Lys Met Gln Gln
195 200

<210> 6303
<211> 676
<212> DNA
<213> Homo sapiens

<400> 6303
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120
gctgaaacaa tgagaatagt gctggaacgc tgctacaatg atttgcgtct tctcagtgtc
180
tccagtaaaa ccctgaaagc tgaaggattt tttagaagta acaaggtgtt tgttgaaagc
240
tccgagactt tggattacca gatggccttt gcagactctc atttatggaa actcctggat
300
cggcatgcaa atacaatcag attatttgtt ttgctacctg aacaatcccc agtatcttat
360
tccaaaagga cagcatacca gaaagctgga ggcgattctg gtaatgtgga tgatgactgt
420
gaaagagtca aaggacctgt aggaagccta aagtctgtgg aagctattct agaagaaagc
480
actgaaaaac tcaaaagctt gtcactgcag caacagcagg atggagataa tggggacagc
540

agcaaaagta ctgagacaag tgactttgaa aacatcgaat cacctctcaa tgagagggac
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660
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676

<210> 6304
<211> 181
<212> PRT
<213> Homo sapiens

<400> 6304
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Val Ser Ser Lys Thr Leu Lys Ala Glu Gly Phe Phe Arg Ser Asn Lys
20 25 30
Val Phe Val Glu Ser Ser Glu Thr Leu Asp Tyr Gln Met Ala Phe Ala
35 40 45
Asp Ser His Leu Trp Lys Leu Leu Asp Arg His Ala Asn Thr Ile Arg
50 55 60
Leu Phe Val Leu Leu Pro Glu Gln Ser Pro Val Ser Tyr Ser Lys Arg
65 70 75 80
Thr Ala Tyr Gln Lys Ala Gly Gly Asp Ser Gly Asn Val Asp Asp Asp
85 90 95
Cys Glu Arg Val Lys Gly Pro Val Gly Ser Leu Lys Ser Val Glu Ala
100 105 110
Ile Leu Glu Glu Ser Thr Glu Lys Leu Lys Ser Leu Ser Leu Gln Gln
115 120 125
Gln Gln Asp Gly Asp Asn Gly Asp Ser Ser Lys Ser Thr Glu Thr Ser
130 135 140
Asp Phe Glu Asn Ile Glu Ser Pro Leu Asn Glu Arg Asp Ser Ser Ala
145 150 155 160
Ser Val Asp Asn Arg Glu Leu Glu Gln His Ile Gln Thr Ser Asp Pro
165 170 175
Glu Lys Phe Ser Val
180

<210> 6305
<211> 3853
<212> DNA
<213> Homo sapiens

<400> 6305
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240
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360
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420
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480
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1680
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1920

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1980
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2220
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2880
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3060
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3480
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3540

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3720
gaattactcc taggtcggct cttatagagt ggccatagtg ttctgtcaaa acacttgctt
3780
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3840
aaaaaaaaaa aaa
3853

<210> 6306
<211> 474
<212> PRT
<213> Homo sapiens

<400> 6306
Met Arg Arg Val Val Arg Gln Ser Lys Phe Arg His Val Phe Gly Gln
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Pro Val Lys Asn Asp Gln Cys Tyr Glu Asp Ile Arg Val Ser Arg Val
20 25 30
Thr Trp Asp Ser Thr Phe Cys Ala Val Asn Pro Lys Phe Leu Ala Val
35 40 45
Ile Val Glu Ala Ser Gly Gly Gly Ala Phe Leu Val Leu Pro Leu Ser
50 55 60
Lys Thr Gly Arg Ile Asp Lys Ala Tyr Pro Thr Val Cys Gly His Thr
65 70 75 80
Gly Pro Val Leu Asp Ile Asp Trp Cys Pro His Asn Asp Gln Val Ile
85 90 95
Ala Ser Gly Ser Glu Asp Cys Thr Val Met Val Trp Gln Ile Pro Glu
100 105 110
Asn Gly Leu Thr Ser Pro Leu Thr Glu Pro Val Val Val Leu Glu Gly
115 120 125
His Thr Lys Arg Val Gly Ile Ile Ala Trp His Pro Thr Ala Arg Asn
130 135 140
Val Leu Leu Ser Ala Gly Cys Asp Asn Val Val Leu Ile Trp Asn Val
145 150 155 160
Gly Thr Ala Glu Glu Leu Tyr Arg Leu Asp Ser Leu His Pro Asp Leu
165 170 175
Ile Tyr Asn Val Ser Trp Asn His Asn Gly Ser Leu Phe Cys Ser Ala
180 185 190
Cys Lys Asp Lys Ser Val Arg Ile Ile Asp Pro Arg Arg Gly Thr Leu
195 200 205
Val Ala Glu Arg Glu Lys Ala His Glu Gly Ala Arg Pro Met Arg Ala
210 215 220
Ile Phe Leu Ala Asp Gly Lys Val Phe Thr Thr Gly Phe Ser Arg Met
225 230 235 240
Ser Glu Arg Gln Leu Ala Leu Trp Asn Pro Lys Asn Met Gln Glu Pro
245 250 255
Ile Ala Leu His Glu Met Asp Thr Ser Asn Gly Val Leu Leu Pro Phe
260 265 270
Tyr Asp Pro Asp Thr Ser Ile Ile Tyr Leu Cys Gly Lys Gly Asp Ser

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        275                 280                 285
Ser Ile Arg Tyr Phe Glu Ile Thr Asp Glu Ser Pro Tyr Val His Tyr
    290                 295                 300
Leu Asn Thr Phe Ser Ser Lys Glu Pro Gln Arg Gly Met Gly Tyr Met
305                 310                 315                 320
Pro Lys Arg Gly Leu Asp Val Asn Lys Cys Glu Ile Ala Arg Phe Phe
                325                 330                 335
Lys Leu His Glu Arg Lys Cys Glu Pro Ile Ile Met Thr Val Pro Arg
            340                 345                 350
Lys Ser Asp Leu Phe Gln Asp Asp Leu Tyr Pro Asp Thr Ala Gly Pro
        355                 360                 365
Glu Ala Ala Leu Glu Ala Glu Glu Trp Phe Glu Gly Lys Asn Ala Asp
    370                 375                 380
Pro Ile Leu Ile Ser Leu Lys His Gly Tyr Ile Pro Gly Lys Asn Arg
385                 390                 395                 400
Asp Leu Lys Val Val Lys Lys Asn Ile Leu Asp Ser Lys Pro Thr Ala
                405                 410                 415
Asn Lys Lys Cys Asp Leu Ile Ser Ile Pro Lys Lys Thr Thr Asp Thr
            420                 425                 430
Ala Ser Val Gln Asn Glu Ala Lys Leu Asp Glu Ile Leu Lys Glu Ile
        435                 440                 445
Lys Ser Ile Lys Asp Thr Ile Cys Asn Gln Asp Glu Arg Ile Ser Lys
    450                 455                 460
Leu Glu Gln Gln Met Ala Lys Ile Ala Ala
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<210> 6307
<211> 2119
<212> DNA
<213> Homo sapiens

<400> 6307

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180
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240
caagattacg aagtttagat gaccaaaatg gatatccgag gtgctgtgga tgctgctgtc
300
cccaccaata ttattgctgc caaggctgca gaagttcgtg caaacaaagt caactggcaa
360
tcctatcttc agggacagat gatttctgct gaagattgtg agtttattca gaggtttgaa
420
atgaaacgaa gccctgaaga gaagcaagag atgcttcaaa ctgaaggcag ccagtgtgct
480
aaaacattta taaatctgat gactcatatc tgcaaagaac agaccgttca gtatatacta
540
actatggtgg atgatatgct gcaggaaaat catcagcgtg ttagcatttt ctttgactat
600
gcaagatgta gcaagaacac tgcgtggccc tactttctgc caatgttgaa tcgccaggat
660
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ccccttcactg ttcatatggc agcaagaatt attgccaagt tagcagcttg gggaaaagaa
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780
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1140
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1260
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1440
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2119

<210> 6308
<211> 483
<212> PRT

<213> Homo sapiens

<400> 6308

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Asn Ile Ile Ala Ala Lys Ala Ala Glu Val Arg Ala Asn Lys Val Asn
            20                  25                  30
Trp Gln Ser Tyr Leu Gln Gly Gln Met Ile Ser Ala Glu Asp Cys Glu
        35                  40                  45
Phe Ile Gln Arg Phe Glu Met Lys Arg Ser Pro Glu Glu Lys Gln Glu
    50                  55                  60
Met Leu Gln Thr Glu Gly Ser Gln Cys Ala Lys Thr Phe Ile Asn Leu
65                  70                  75                  80
Met Thr His Ile Cys Lys Glu Gln Thr Val Gln Tyr Ile Leu Thr Met
                85                  90                  95
Val Asp Asp Met Leu Gln Glu Asn His Gln Arg Val Ser Ile Phe Phe
            100                 105                 110
Asp Tyr Ala Arg Cys Ser Lys Asn Thr Ala Trp Pro Tyr Phe Leu Pro
        115                 120                 125
Met Leu Asn Arg Gln Asp Pro Phe Thr Val His Met Ala Ala Arg Ile
    130                 135                 140
Ile Ala Lys Leu Ala Ala Trp Gly Lys Glu Leu Met Glu Gly Ser Asp
145                 150                 155                 160
Leu Asn Tyr Tyr Phe Asn Trp Ile Lys Thr Gln Leu Ser Ser Gln Lys
                165                 170                 175
Leu Arg Gly Ser Gly Val Ala Val Glu Thr Gly Thr Val Ser Ser Ser
            180                 185                 190
Asp Ser Ser Gln Tyr Val Gln Cys Val Ala Gly Cys Leu Gln Leu Met
        195                 200                 205
Leu Arg Val Asn Glu Tyr Arg Phe Ala Trp Val Glu Ala Asp Gly Val
    210                 215                 220
Asn Cys Ile Met Gly Val Leu Ser Asn Lys Cys Gly Phe Gln Leu Gln
225                 230                 235                 240
Tyr Gln Met Ile Phe Ser Ile Trp Leu Leu Ala Phe Ser Pro Gln Met
                245                 250                 255
Cys Glu His Leu Arg Arg Tyr Asn Ile Ile Pro Val Leu Ser Asp Ile
            260                 265                 270
Leu Gln Glu Ser Val Lys Glu Lys Val Thr Arg Ile Ile Leu Ala Ala
        275                 280                 285
Phe Arg Asn Phe Leu Glu Lys Ser Thr Glu Arg Glu Thr Arg Gln Glu
    290                 295                 300
Tyr Ala Leu Ala Met Ile Gln Cys Lys Val Leu Lys Gln Leu Glu Asn
305                 310                 315                 320
Leu Glu Gln Gln Lys Tyr Asp Asp Glu Asp Ile Ser Glu Asp Ile Lys
                325                 330                 335
Phe Leu Leu Glu Lys Leu Gly Glu Ser Val Gln Asp Leu Ser Ser Phe
            340                 345                 350
Asp Glu Tyr Ser Ser Glu Leu Lys Ser Gly Arg Leu Glu Trp Ser Pro
        355                 360                 365
Val His Lys Ser Glu Lys Phe Trp Arg Glu Asn Ala Val Arg Leu Asn
    370                 375                 380
Glu Lys Asn Tyr Glu Leu Leu Lys Ile Leu Thr Lys Leu Leu Glu Val
385                 390                 395                 400
Ser Asp Asp Pro Gln Val Leu Ala Val Ala Ala His Asp Val Gly Glu
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                405                 410                 415
Tyr Val Arg His Tyr Pro Arg Gly Lys Arg Val Ile Glu Gln Leu Gly
            420                 425                 430
Gly Lys Gln Leu Val Met Asn His Met His His Glu Asp Gln Gln Val
        435                 440                 445
Arg Tyr Asn Ala Leu Leu Ala Val Gln Lys Leu Met Val His Asn Trp
    450                 455                 460
Glu Tyr Leu Gly Lys Gln Leu Gln Ser Glu Gln Pro Gln Thr Ala Ala
465                 470                 475                 480
Ala Arg Ser
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<210> 6309
<211> 564
<212> DNA
<213> Homo sapiens

<400> 6309
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120
ccaggcgcct cccacggggt tcccccgcag ccgcgacacc accaacagtc gccgcaaccg
180
ccgcgtggaa cagacgaccc gggtctcaaa gaggcggcgc gggcgggacg cagcccctgg
240
tccatctcgg gcgccgcctg atgcactcct actgcgcccg ggtcctcccg gcctgtctca
300
ctttgggggg ctcagggtcc tcacgggggа cgcctgcacg taagccagga cggcgttctg
360
caggaagctc gccctctggg cctcctcgtc ccggatgcgg gcgatctccg cctcccggag
420
ccgcagcttc tcccggagag acgcgttctc gctctccctg tccagcagcg cgatctgagc
480
tcactggaac ctccacctcc caggttcgag tgattctcct gcctcagcct cctgagtagc
540
tggtattaca gggtgccacc acta
564

<210> 6310
<211> 83
<212> PRT
<213> Homo sapiens

<400> 6310
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Cys Thr Pro Thr Ala Pro Gly Ser Ser Arg Pro Val Ser Leu Trp Gly
 1               5                  10                  15
Ala Gln Gly Pro His Gly Gly Arg Leu His Val Ser Gln Asp Gly Val
            20                  25                  30
Leu Gln Glu Ala Arg Pro Leu Gly Leu Leu Val Pro Asp Ala Gly Asp
        35                  40                  45
Leu Arg Leu Pro Glu Pro Gln Leu Leu Pro Glu Arg Arg Val Leu Ala
    50                  55                  60
Leu Pro Val Gln Gln Arg Asp Leu Ser Ser Leu Glu Pro Pro Pro Pro
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65 70 75 80
Arg Phe Glu

<210> 6311
<211> 1548
<212> DNA
<213> Homo sapiens

<400> 6311
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120
tttaaagatc ttatggggct caaatactaa cttcataaat ggccttttga ataacagcag
180
caaataatct ctcagctgat atttcaattt actaaggaag cacaaattaa aacattcctg
240
ctacacagtc atgggctggc acatgtctgg ttggatgaat acaaggagca gtatttttcc
300
ttaagacctg acctgaagac gaaaagctat ggcaatatca gtgagcgtgt ggaactgaga
360
aagaagttgg gctgtaaatc atttaaatgg tatttggata atgtataccc agagatgcag
420
atatctgggt cccacgccaa accccaacaa cccatttttg tcaatagagg gccaaaacga
480
cccaaagtcc ttcaacgtgg aaggctctat cacctccaga ccaacaaatg cctggtggcc
540
cagggccgcc caagtcagaa gggaggtctc gtggtgctta aggcctgtga ctacagtgac
600
ccaaatcaga tctggatcta taatgaagag catgaattgg ttttaaatag tctcctttgt
660
ctagatatgt cagagactcg ctcatcagac ccgccacggc tcatgaaatg ccacgggtca
720
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780
cagtgcctga gagcagtgga tcccctgggt cagaagggct ctgtcgccat ggcgatctgc
840
gatggctcct cttcacagca gtggcatttg gaaggttaag gtggatgctg tggcgggaac
900
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960
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1020
tgtgttagca gaggtgacac gtgtctgaca gagacgggag ctctgagtgt ccacgggtga
1080
agaagtgagt gtccacgggt gaagaagtga gtatgtttca cctggacatt aaggtgatgt
1140
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1200
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1260
atttatgcct ctttttaatc ccctttaatg atgcagtggt ttttatctga tcaggaactt
1320

gtcatgattt cctttcttag acttcatagg agatagtgct ttaaaaaaaa aaaaacttct
1380
attatttgtt tagtatgttg taagtagatc attttaaaaa actgaatcta tattatgttt
1440
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1548

<210> 6312
<211> 234
<212> PRT
<213> Homo sapiens

<400> 6312
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Gln Ile Lys Thr Phe Leu Leu His Ser His Gly Leu Ala His Val Trp
20 25 30
Leu Asp Glu Tyr Lys Glu Gln Tyr Phe Ser Leu Arg Pro Asp Leu Lys
35 40 45
Thr Lys Ser Tyr Gly Asn Ile Ser Glu Arg Val Glu Leu Arg Lys Lys
50 55 60
Leu Gly Cys Lys Ser Phe Lys Trp Tyr Leu Asp Asn Val Tyr Pro Glu
65 70 75 80
Met Gln Ile Ser Gly Ser His Ala Lys Pro Gln Gln Pro Ile Phe Val
85 90 95
Asn Arg Gly Pro Lys Arg Pro Lys Val Leu Gln Arg Gly Arg Leu Tyr
100 105 110
His Leu Gln Thr Asn Lys Cys Leu Val Ala Gln Gly Arg Pro Ser Gln
115 120 125
Lys Gly Gly Leu Val Val Leu Lys Ala Cys Asp Tyr Ser Asp Pro Asn
130 135 140
Gln Ile Trp Ile Tyr Asn Glu Glu His Glu Leu Val Leu Asn Ser Leu
145 150 155 160
Leu Cys Leu Asp Met Ser Glu Thr Arg Ser Ser Asp Pro Pro Arg Leu
165 170 175
Met Lys Cys His Gly Ser Gly Gly Ser Gln Gln Trp Thr Phe Gly Lys
180 185 190
Asn Asn Arg Leu Tyr Gln Val Ser Val Gly Gln Cys Leu Arg Ala Val
195 200 205
Asp Pro Leu Gly Gln Lys Gly Ser Val Ala Met Ala Ile Cys Asp Gly
210 215 220
Ser Ser Ser Gln Gln Trp His Leu Glu Gly
225 230

<210> 6313
<211> 725
<212> DNA
<213> Homo sapiens

<400> 6313
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gagaaaatat acagcaggag ggatgaggag tacacatagg aaatttctgt gattttcttc
120
attttgatcg tattgctttc ttgtcttcag gagggaagat ttcgacttca aaagtaacaa
180
aatatttaag aagagaattc acatctttct gttctagctg gtattcttgc attattttct
240
cagcagtcca ggtttctggg aaaagcttat gattattgag aagtgtcaat gcttctacaa
300
tggaaatttt gcctttggga atgctcttaa tatttatcat atcaaaatga tggtctttcg
360
gcaatctgaa ttccttcggc tcttgacatg tttcagcagc ttttacctgc aaggaagaca
420
caggatcttt ggaatcaaca tacacatctt ttagaaacga cagcagcttt tcatctttac
480
gagcaatctc tcctttaact tctggataga gactaatctg ctctcgcagg aggctgttgg
540
tagaggggtg tctgggagcg acagagggct tcatcttgct gatttcccgt tccgctcggt
600
tctctaggtt gaaattcctg ataccgcgaa tcactagtgc tcccatctcc tcataacatt
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720
ggagc
725

<210> 6314
<211> 175
<212> PRT
<213> Homo sapiens

<400> 6314

Met	Gly	Ala	Leu	Val	Ile	Arg	Gly	Ile	Arg	Asn	Phe	Asn	Leu	Glu	Asn
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Arg	Ala	Glu	Arg	Glu	Ile	Ser	Lys	Met	Lys	Pro	Ser	Val	Ala	Pro	Arg
			20					25					30		
His	Pro	Ser	Thr	Asn	Ser	Leu	Leu	Arg	Glu	Gln	Ile	Ser	Leu	Tyr	Pro
		35					40					45			
Glu	Val	Lys	Gly	Glu	Ile	Ala	Arg	Lys	Asp	Glu	Lys	Leu	Leu	Ser	Phe
	50					55					60				
Leu	Lys	Asp	Val	Tyr	Val	Asp	Ser	Lys	Asp	Pro	Val	Ser	Ser	Leu	Gln
65					70					75					80
Val	Lys	Ala	Ala	Glu	Thr	Cys	Gln	Glu	Pro	Lys	Glu	Phe	Arg	Leu	Pro
				85					90					95	
Lys	Asp	His	His	Phe	Asp	Met	Ile	Asn	Ile	Lys	Ser	Ile	Pro	Lys	Gly
			100					105					110		
Lys	Ile	Ser	Ile	Val	Glu	Ala	Leu	Thr	Leu	Leu	Asn	Asn	His	Lys	Leu
		115					120					125			
Phe	Pro	Glu	Thr	Trp	Thr	Ala	Glu	Lys	Ile	Met	Gln	Glu	Tyr	Gln	Leu
	130					135					140				
Glu	Gln	Lys	Asp	Val	Asn	Ser	Leu	Leu	Lys	Tyr	Phe	Val	Thr	Phe	Glu
145					150					155					160
Val	Glu	Ile	Phe	Pro	Pro	Glu	Asp	Lys	Lys	Ala	Ile	Arg	Ser	Lys	
				165					170					175	

<210> 6315
<211> 378
<212> DNA
<213> Homo sapiens

<400> 6315
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gctcaaaaca gaaaacttgt ggaggccata aaacaaggtc acattcctga gctccaggag
120
tatgtaaaat ataaatatgc aatggatgaa gctgatgaaa aaggatggtt tccattgcat
180
gaagctgttg ttcaacccat tcaacaaata cttgagattg ttctggatgc atcctataag
240
acactctggg aattcaagac ctgtgatgga gaaacaccct tgactttggc agtcaaagct
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ggtctggtgg aaaatgtaag aactttatta gaaaagggag tgtggcccaa cacaaaaaat
360
gataaaggag agaccccc
378

<210> 6316
<211> 126
<212> PRT
<213> Homo sapiens

<400> 6316
Gln Glu Ser Ile Glu Ala Ser Lys Thr Ala Leu Cys Pro Glu Arg Phe
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Val Pro Leu Ser Ala Gln Asn Arg Lys Leu Val Glu Ala Ile Lys Gln
            20   25   30
Gly His Ile Pro Glu Leu Gln Glu Tyr Val Lys Tyr Lys Tyr Ala Met
        35   40   45
Asp Glu Ala Asp Glu Lys Gly Trp Phe Pro Leu His Glu Ala Val Val
    50   55   60
Gln Pro Ile Gln Gln Ile Leu Glu Ile Val Leu Asp Ala Ser Tyr Lys
65   70   75   80
Thr Leu Trp Glu Phe Lys Thr Cys Asp Gly Glu Thr Pro Leu Thr Leu
                85   90   95
Ala Val Lys Ala Gly Leu Val Glu Asn Val Arg Thr Leu Leu Glu Lys
            100   105   110
Gly Val Trp Pro Asn Thr Lys Asn Asp Lys Gly Glu Thr Pro
        115   120   125

<210> 6317
<211> 1201
<212> DNA
<213> Homo sapiens

<400> 6317
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ttcttaagat gtcttgccga agtagcaaga gcggagggtg actgtgtgag caggagcgag
120

agggcgccag ctcctgcggg ggaggttcct actgcgcgcc ccaccctgtg caagaatgtc
180
aggctttagg gcagctgcca taggccccag gggcatcagg actctgcctc tgaaccagag
240
ctgctttccc gactaacttc aatctggaga gatggtaagt tatctaaccg gctcttcttt
300
tggcgagact gctctttctc cttaatcaga gccccccatg ccctttgcag ctcagagtcg
360
tcttcctcag cgccaggcac cctgtgatcc actttcttcg tattcttttc tttggtcttg
420
ggtgcagttc ctaggcgagt ccataaatta cctgatttct tctcccgagt atcggcgtag
480
aggcctttac tatcctgcct gggaacacct agcctactat gcacatcaga agagggctct
540
ctccgaacga cggggttact actaaaagcc ttttccggag aatgtggtct ttttcctaac
600
cgctggcgta tatctgattt agtactgctg actggtggcc gtggacggga gtgctgacgt
660
ttctcatcta atagatgtcg gacatctgca aatttctcag gtggtaattt gttaccaatt
720
cggtttttga tattgcttga agatacacta tctgccctca tggagttcct aatatttttc
780
aactgagatt ccacttcgtc agcatacata gtcattttca tgcttttctt tggtgaaggc
840
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1080
gaatgtcgat gtttatacga cgtcaagcca acgtcatccc caatcagggc tctcttcttg
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1200
c
1201

<210> 6318
<211> 94
<212> PRT
<213> Homo sapiens

<400> 6318
Ser Ile Ser Ser Glu Ser Glu Leu Leu Ala Leu Asp Arg Leu Asp Ala
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Leu Arg Ser Arg Gly Cys Leu Arg Ala Gly Ser Ser Ser Trp Tyr Ser
20 25 30
Thr Thr Thr Leu Ser Ser Ala Ser Met Ser Trp Ser Ser Ser Ser Ser
35 40 45
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Met Gly Ser Ser
50 55 60
Gly Thr Phe Thr Ser Pro Glu Cys Arg Cys Leu Tyr Asp Val Lys Pro

65 70 75 80
Thr Ser Ser Pro Ile Arg Ala Leu Phe Leu Ile Thr Ser Arg
85 90

<210> 6319
<211> 345
<212> DNA
<213> Homo sapiens

<400> 6319
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120
tgcttcgacg gccacctgga ggtggtgcgc tacctggtcg gcgagcacca ggccgacctg
180
gaggtggcca accggcacgg ccacacgtgc ctcatgatct cgtgctacaa gggccaccgt
240
gagatcgccc gctacctgct ggagcagggc gcccaggtga accggcgcag cgccaagggc
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aacacggccc tgcatgactg cgccgagtcc ggcagcctgg agatc
345

<210> 6320
<211> 115
<212> PRT
<213> Homo sapiens

<400> 6320
Ala Pro Pro Leu Trp Ala Ala Ser Ala Ala Gly His Leu Asp Val Val
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Arg Ser Leu Leu Arg Arg Gly Ala Ser Val Asn Arg Thr Thr Arg Thr
20 25 30
Asn Ser Thr Pro Leu Arg Ala Ala Cys Phe Asp Gly His Leu Glu Val
35 40 45
Val Arg Tyr Leu Val Gly Glu His Gln Ala Asp Leu Glu Val Ala Asn
50 55 60
Arg His Gly His Thr Cys Leu Met Ile Ser Cys Tyr Lys Gly His Arg
65 70 75 80
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What is claimed is:

1. An isolated nucleic acid molecule encoding a polypeptide comprising an amin acid sequence that is at least 85% identical to a polypeptide including an amino acid sequence selected from the group consisting of SEQ ID NO:2*n*, wherein *n* is any integer 1-3161, or the complement thereof.

2. The isolated nucleic acid molecule of claim 1, said molecule hybridizing under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule comprising the sequence of nucleotides selected from the group consisting of SEQ ID NO:2*n*- wherein *n* is any integer 1-3161, or the complement thereof.

3. The isolated nucleic acid molecule of claim 1, said molecule encoding a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ I NO: 2*n*, wherein n is any integer 1-3161, or an amino acid sequence comprising one or more conservative substitutions in the amino acid sequence selected from the group consisting of S ID NO: 2*n*.

4. The isolated nucleic acid molecule of claim 1, wherein said molecule encodes polypeptide comprising the amino acid sequence selected from the group consisting of SEQ I NO: 2*n*, wherein *n* is any integer 1-3161.

5. The isolated nucleic acid molecule of claim 1, wherein said molecule comprise the sequence of nucleotides selected from the group consisting of SEQ ID NO:2*n*-1, wherein any integer 1-3161, or the complement thereof.

6. An oligonucleotide less than 100 nucleotides in length and comprising at least contiguous nucleotides selected from the group consisting of SEQ ID NO:2*n*-1, wherein *n* is a integer 1-3161, or the complement thereof.

7. A vector comprising the nucleic acid molecule of claim 1.

8. The vector of claim 7, wherein said vector is an expression vector.

9 A host cell comprising the isolated nucleic acid molecule of claim 1.

10. A substantially purified polypeptide comprising an amino acid sequence at least 80% identical to a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 2*n*, wherein *n* is any integer 1-3161.

11. The polypeptide of claim 10, wherein said polypeptide comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 2*n*, wherein *n* is any integer 1-3161.

12. An antibody that selectively binds to the polypeptide of claim 10.

13. A pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a therapeutic selected from the group consisting of:

a) the nucleic acid of claim 1;

b) the polypeptide of claim 10; and

c) the antibody of claim 12;

and a pharmaceutically acceptable carrier.

14. A kit comprising in one or more containers, a therapeutically or prophylactically effective amount of the pharmaceutical composition of claim 13.

15. A method of producing the polypeptide of claim 10, said method comprising culturing the host cell of claim 9 under conditions in which the nucleic acid molecule is expressed.

16. A method of detecting the presence of the polypeptide of claim 10 in a sample, comprising contacting the sample with a compound that selectively binds to said polypeptide under conditions allowing the formation of a complex between said polypeptide and said

compound, and detecting said complex, if present, thereby identifying said polypeptide in said sample.

17. A method of detecting the presence of a nucleic acid molecule of claim 1 in a sample, the method comprising contacting the sample with a nucleic acid probe or primer that selectively binds to the nucleic acid molecule and determining whether the nucleic acid probe c primer bound to the nucleic acid molecule of claim 1 is present in the sample.

18. A method for modulating the activity of the polypeptide of claim 10, the methoc comprising contacting a cell sample comprising the polypeptide of claim 10 with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptid

19. The use of a therapeutic in the manufacture of a medicament for treating a syndrome associated with a ORFX-associated disorder, wherein said therapeutic is selected fro the group consisting of:

a) the nucleic acid of claim 1;

b) the polypeptide of claim 10; and

c) the antibody of claim 12.

20. A method for screening for a modulator of activity or of latency or predispositio to an ORFX-associated disorder, said method comprising:

a) contacting a test compound with the polypeptide of claim 10; and

b) determining if said test compound binds to said polypeptide,

wherein binding of said test compound to said polypeptide indicates the test compound is a modulator of activity or of latency or predisposition to an ORFX-associated disorder.

21. A method for screening for a modulator of activity or of latency or predispositio to an ORFX-associated disorder, said method comprising:

a) administering a test compound to a test subject at an increased risk ORFX-associated disorder, wherein said test subject recombinantly expresses a polypeptide encoded by the nucleotide of claim 1;

b) measuring expression the activity of said protein in said test subject;

c) measuring the activity of said protein in a control subject that recombinantly expresses said protein and is not at increased risk for an ORFX-associated disorder; and

d) comparing expression of said protein in said test subject and said control subject, wherein a change in the activity of said protein in said test subject relative to said control subject indicates the test compound is a modulator or of latency of predispostition to an ORFX-associated disorder.

22. The method of claim 20, wherein said test animal is a recombinant test animal that expresses a test protein transgene or expresses said transgene under the control of a promoter at an increased level relative to a wild-type test animal, and wherein said promoter is not the native gene promoter of said transgene.

23. A method for determining the presence of or predisposition to a disease associated with altered levels of a polypeptide of claim 11 in a subject, the method comprising:

a) measuring the amount of the polypeptide in a sample from said subject; and

b) comparing the amount of said polypeptide in step (a) to the amount of the polypeptide present in a control sample,

wherein an alteration in the level of the polypeptide in step (a) as compared to the control sample indicates the presence of or predisposition to a disease in said subject.

24. The method of claim 23, wherein said subject is a human.

25. A method for determining the presence of or predisposition to a disease associated with altered levels the nucleic acid molecule of claim 1 in a subject, the method comprising:

a) measuring the amount of the nucleic acid in a sample from the mammalian subject; and

b) comparing the amount of said nucleic acid in step (a) to the amount of the nucleic acid present in a control sample,

wherein an alteration in the level of the nucleic acid in step (a) as compared to the co sample indicates the presence of or predisposition to said disease in said subject.

26. The method of claim 25, wherein said subject is a human.

27. A method of treating or preventing a pathological condition associated with a ORFX-associated disorder in a subject, the method comprising administering to said subject polypeptide of claim 10 in an amount sufficient to alleviate or prevent said pathological condition.

28. The method of claim 27, wherein said subject is a human.

29. A method of treating or preventing a pathological condition associated with a ORFX-associated disorder in a subject, the method comprising administering to said subject nucleic acid molecule of claim 1 in an amount sufficient to alleviate or prevent said patholog condition.

30. The method of claim 29, wherein said subject is a human.

31. A method of treating or preventing a pathological condition associated with a ORFX-associated disorder in a subject, the method comprising administering to said subject antibody of claim 12 in an amount sufficient to alleviate or prevent said pathological conditio

32. The method of claim 31, wherein said subject is a human.

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